



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 18, 2026 – 08:35 PM UTC

PDB ID : 9CW7 / pdb_00009cw7
Title : Structure of human endothelial nitric oxide synthase heme domain bound with 4-methyl-5'-((methylamino)methyl)-[2,3'-bipyridin]-6-amine dihydrochloride
Authors : Li, H.; Poulos, T.L.
Deposited on : 2024-07-29
Resolution : 1.83 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

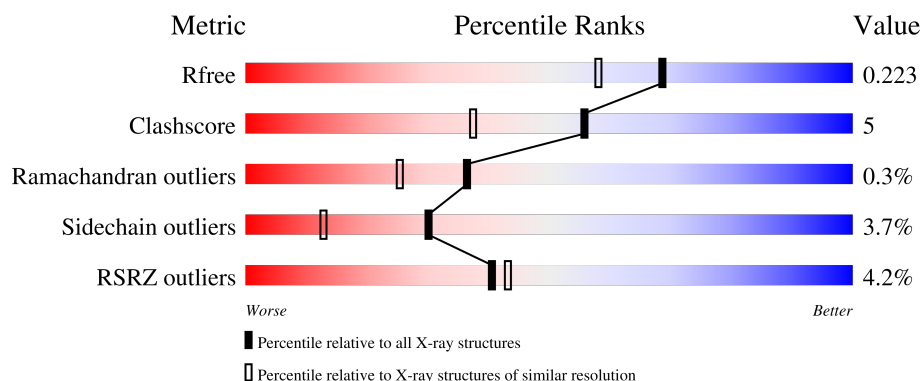
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.83 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1296 (1.84-1.84)
Clashscore	190562	1329 (1.84-1.84)
Ramachandran outliers	187476	1318 (1.84-1.84)
Sidechain outliers	187428	1318 (1.84-1.84)
RSRZ outliers	180081	1296 (1.84-1.84)

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	440	11% 75% 13% • 9%
1	B	440	% 85% 5% • 9%
1	C	440	2% 80% 11% • 9%
1	D	440	% 84% 8% 9%

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	GOL	A	512	-	X	-	-

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 14314 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.

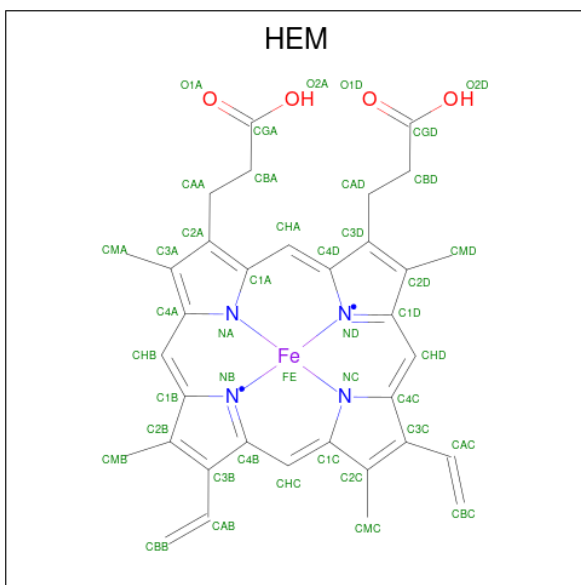
- Molecule 1 is a protein called Nitric oxide synthase, endothelial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	400	Total	C	N	O	S	0	1	0
			3200	2038	563	583	16			
1	B	401	Total	C	N	O	S	0	2	0
			3206	2042	563	585	16			
1	C	402	Total	C	N	O	S	0	1	0
			3212	2046	565	585	16			
1	D	402	Total	C	N	O	S	0	0	0
			3211	2044	567	584	16			

There are 4 discrepancies between the modelled and reference sequences:

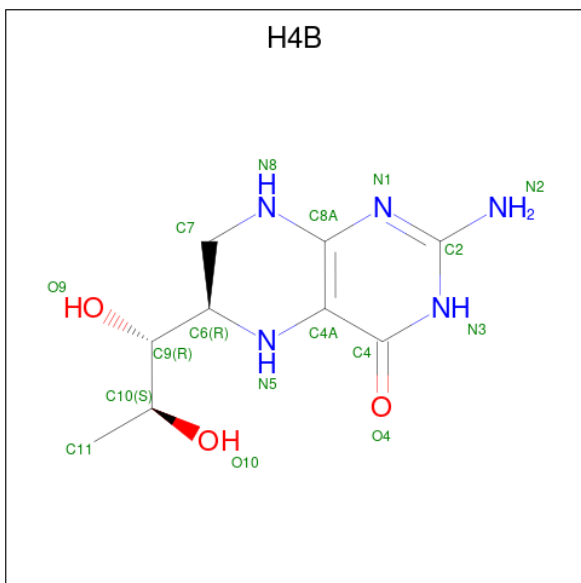
Chain	Residue	Modelled	Actual	Comment	Reference
A	298	GLU	ASP	variant	UNP P29474
B	298	GLU	ASP	variant	UNP P29474
C	298	GLU	ASP	variant	UNP P29474
D	298	GLU	ASP	variant	UNP P29474

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



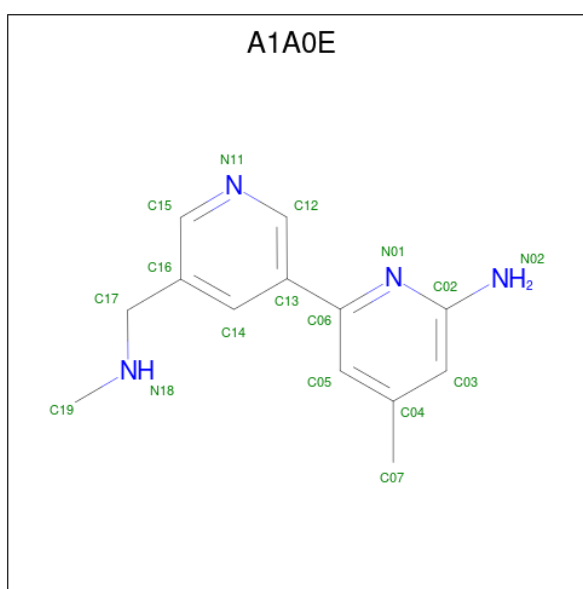
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

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



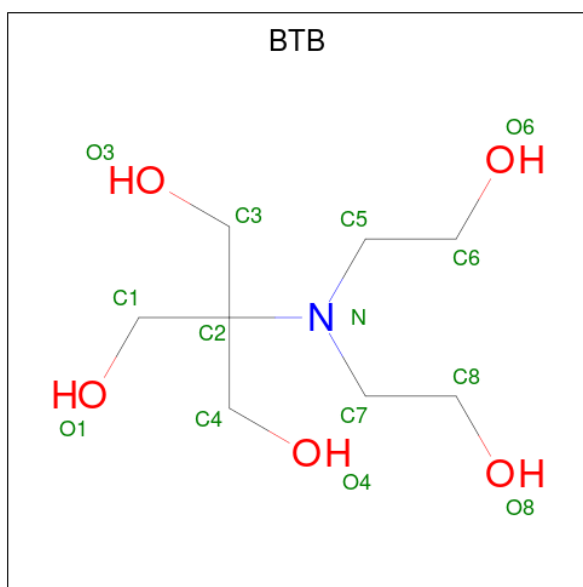
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 17 9 5 3	0	0
3	B	1	Total C N O 17 9 5 3	0	0
3	C	1	Total C N O 17 9 5 3	0	0
3	D	1	Total C N O 17 9 5 3	0	0

- Molecule 4 is (2M)-4-methyl-5'-[(methylamino)methyl][2,3'-bipyridin]-6-amine (CCD ID: A1A0E) (formula: C₁₃H₁₆N₄) (labeled as "Ligand of Interest" by depositor).



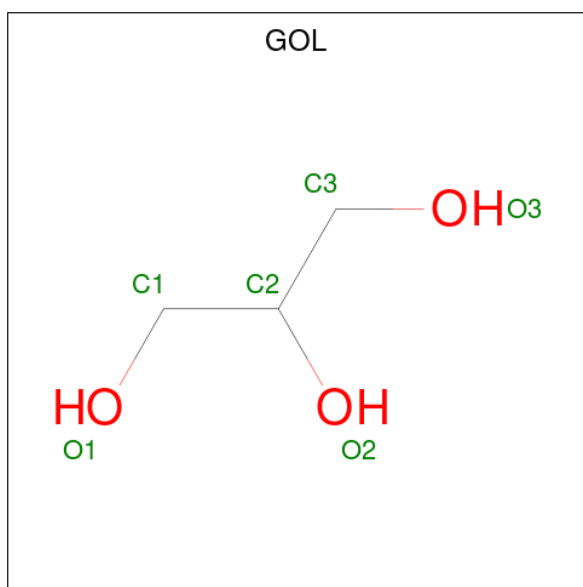
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N 17 13 4	0	0
4	B	1	Total C N 17 13 4	0	0
4	C	1	Total C N 17 13 4	0	0
4	D	1	Total C N 17 13 4	0	0

- Molecule 5 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPAN E-1,3-DIOL (CCD ID: BTB) (formula: C₈H₁₉NO₅).



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	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 GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

- Molecule 7 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

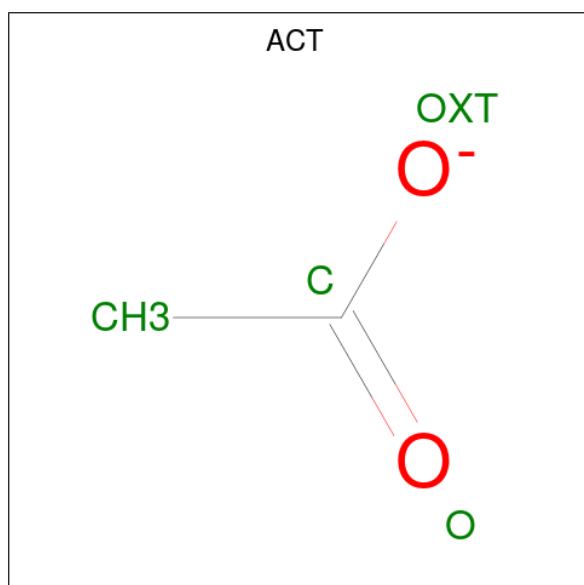
- Molecule 8 is GADOLINIUM ION (CCD ID: GD3) (formula: Gd).

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

- Molecule 9 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	1	Total	Zn	0	0
			1	1		
9	C	1	Total	Zn	0	0
			1	1		

- Molecule 10 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	B	1	Total	C	O	0	0
			4	2	2		
10	C	1	Total	C	O	0	0
			4	2	2		
10	D	1	Total	C	O	0	0
			4	2	2		

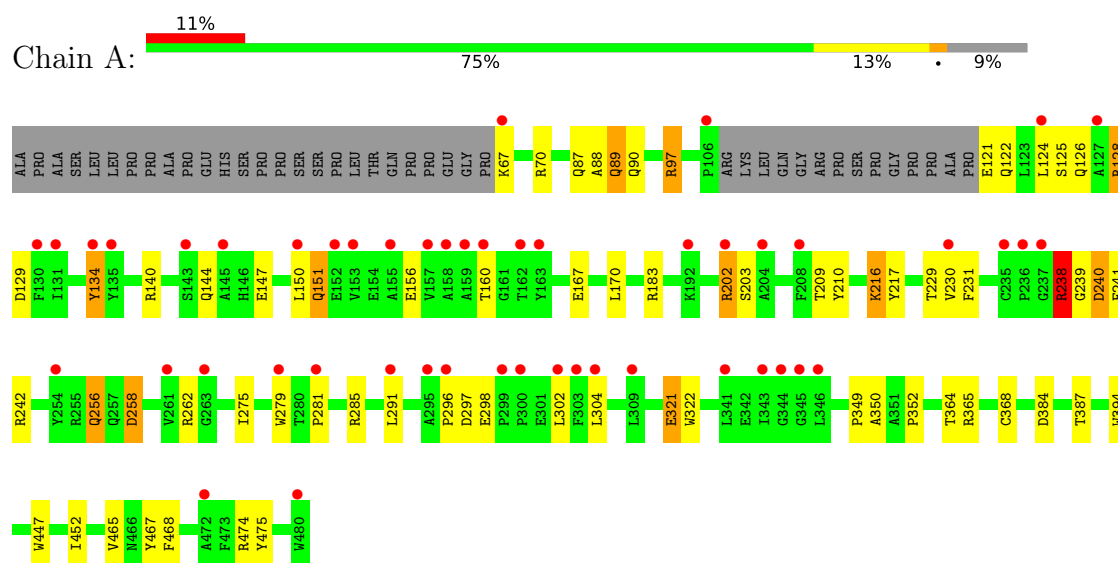
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	148	Total 148	O 148	0	0
11	B	293	Total 293	O 293	0	0
11	C	223	Total 223	O 223	0	0
11	D	317	Total 317	O 317	0	0

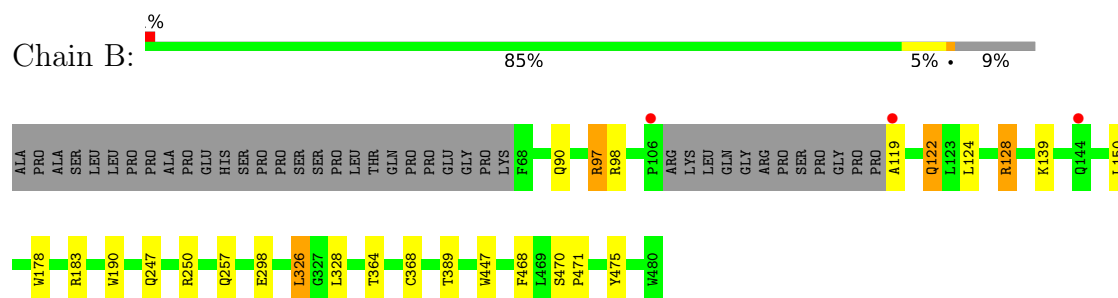
3 Residue-property plots [i](#)

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.

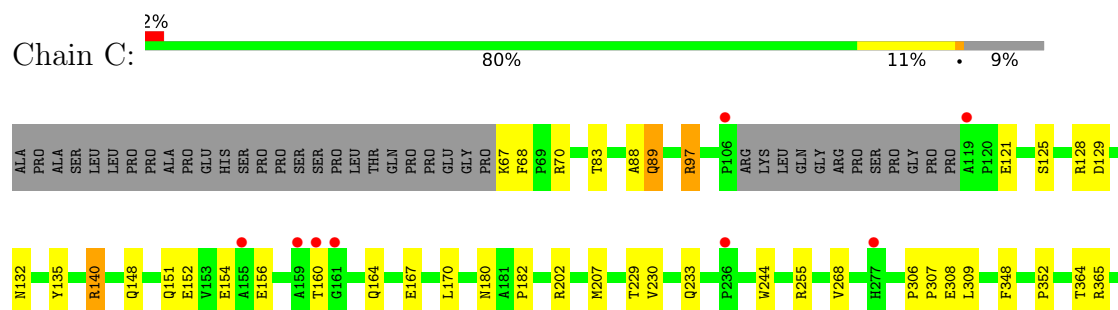
• Molecule 1: Nitric oxide synthase, endothelial



• Molecule 1: Nitric oxide synthase, endothelial

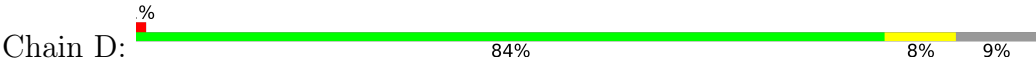


• Molecule 1: Nitric oxide synthase, endothelial





● Molecule 1: Nitric oxide synthase, endothelial



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	59.95Å 152.42Å 108.69Å 90.00° 90.80° 90.00°	Depositor
Resolution (Å)	49.37 – 1.83 49.37 – 1.83	Depositor EDS
% Data completeness (in resolution range)	98.6 (49.37-1.83) 98.5 (49.37-1.83)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.26 (at 1.83Å)	Xtriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, R_{free}	0.189 , 0.228 0.183 , 0.223	Depositor DCC
R_{free} test set	8502 reflections (1.51%)	wwPDB-VP
Wilson B-factor (Å ²)	31.9	Xtriage
Anisotropy	0.510	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 51.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.067 for h,-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	14314	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.96% 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: GD3, HEM, CL, ZN, H4B, ACT, A1A0E, GOL, BTB

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	0.25	0/3294	0.49	0/4487
1	B	0.32	0/3304	0.49	0/4503
1	C	0.27	0/3307	0.47	0/4506
1	D	0.35	0/3303	0.50	0/4501
All	All	0.30	0/13208	0.49	0/17997

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	238	ARG	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	3200	0	3104	44	0
1	B	3206	0	3108	17	0
1	C	3212	0	3116	26	0
1	D	3211	0	3111	19	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	1	0
3	B	17	0	15	1	0
3	C	17	0	15	1	0
3	D	17	0	15	0	0
4	A	17	0	0	0	0
4	B	17	0	0	0	0
4	C	17	0	0	0	0
4	D	17	0	0	0	0
5	A	42	0	56	10	0
5	B	42	0	55	3	0
5	C	14	0	18	3	0
5	D	28	0	36	4	0
6	A	18	0	24	1	0
6	B	6	0	8	0	0
6	C	18	0	24	1	0
6	D	6	0	8	0	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
8	A	1	0	0	0	0
8	B	2	0	0	0	0
8	D	1	0	0	0	0
9	A	1	0	0	0	0
9	C	1	0	0	0	0
10	B	4	0	3	1	0
10	C	4	0	3	0	0
10	D	4	0	3	0	0
11	A	148	0	0	5	0
11	B	293	0	0	0	0
11	C	223	0	0	3	0
11	D	317	0	0	0	0
All	All	14314	0	12857	123	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.

All (123) 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:D:475:TYR:OH	2:D:501:HEM:O1D	2.08	0.72
1:D:386:ASP:OD1	1:D:388:ARG:NH1	2.24	0.70
1:B:247:GLN:HB2	1:B:250:ARG:HD3	1.72	0.70
1:A:242:ARG:HD2	1:A:349:PRO:HB2	1.76	0.68
1:A:275:ILE:HD11	1:A:281:PRO:HB3	1.76	0.68
2:D:501:HEM:HMC2	2:D:501:HEM:HBC2	1.75	0.67
1:C:382:CYS:HA	5:C:505:BTB:H12	1.77	0.67
1:A:128:ARG:HH11	1:A:128:ARG:HB2	1.61	0.65
1:B:475:TYR:OH	2:B:501:HEM:O1D	2.16	0.63
1:A:90:GLN:HB3	1:A:468:PHE:CD2	2.34	0.63
2:D:501:HEM:HBB2	2:D:501:HEM:HHC	1.81	0.62
1:A:70:ARG:NH2	11:A:604:HOH:O	2.32	0.61
5:A:504:BTB:O3	5:A:504:BTB:O4	2.16	0.61
2:C:501:HEM:HBB2	2:C:501:HEM:HHC	1.82	0.60
1:B:124:LEU:HB3	1:B:128:ARG:HH12	1.65	0.60
1:A:125:SER:HA	1:A:128:ARG:NH1	2.16	0.60
1:D:321:GLU:OE2	5:D:505:BTB:O4	2.19	0.60
1:A:475:TYR:OH	2:A:501:HEM:O1D	2.18	0.59
1:A:321:GLU:H	1:A:321:GLU:CD	2.09	0.59
1:A:170:LEU:HD11	1:A:230:VAL:HG21	1.83	0.59
1:A:239:GLY:HA3	1:A:296:PRO:HB3	1.84	0.59
1:C:129:ASP:HA	1:C:132:ASN:HD22	1.68	0.58
1:A:124:LEU:O	1:A:128:ARG:HD3	2.03	0.58
5:A:504:BTB:O3	11:A:601:HOH:O	2.17	0.58
2:C:501:HEM:HBC2	2:C:501:HEM:HMC2	1.86	0.57
1:D:124:LEU:HD11	1:D:154:GLU:HG3	1.87	0.57
1:B:90:GLN:HB3	1:B:468:PHE:CD2	2.39	0.57
1:A:156:GLU:O	1:A:160:THR:OG1	2.15	0.57
1:A:147:GLU:O	1:A:151:GLN:NE2	2.38	0.56
1:D:298:GLU:OE1	5:D:506:BTB:H42	2.05	0.56
1:C:128:ARG:HH21	1:C:154:GLU:CD	2.13	0.56
2:A:501:HEM:HMC2	2:A:501:HEM:HBC2	1.87	0.56
1:D:290:PRO:HB3	1:D:304:LEU:HD23	1.88	0.56
1:C:156:GLU:O	1:C:160:THR:HG22	2.07	0.55
1:A:97:ARG:HH11	1:A:97:ARG:HB2	1.72	0.55
1:C:128:ARG:O	1:C:132:ASN:ND2	2.40	0.54
1:A:364:THR:O	1:A:368:CYS:HB2	2.08	0.54
2:A:501:HEM:HBB2	2:A:501:HEM:HHC	1.88	0.54
1:A:238:ARG:HG2	1:A:297:ASP:OD2	2.08	0.54
1:A:240:ASP:N	11:A:602:HOH:O	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:ARG:HD3	1:A:447:TRP:CD2	2.46	0.51
1:C:156:GLU:OE2	1:C:164:GLN:HG2	2.11	0.51
1:B:298:GLU:OE2	5:B:506:BTB:N	2.44	0.50
1:A:134:TYR:C	1:A:134:TYR:CD2	2.90	0.50
1:A:238:ARG:O	11:A:602:HOH:O	2.20	0.50
1:A:89:GLN:HG3	1:A:90:GLN:H	1.77	0.50
1:C:233:GLN:HB3	1:C:348:PHE:CE2	2.45	0.50
1:A:258:ASP:N	1:A:258:ASP:OD1	2.45	0.49
2:B:501:HEM:HHC	2:B:501:HEM:HBB2	1.94	0.49
1:C:68:PHE:CD1	1:C:83:THR:HG22	2.47	0.49
1:A:147:GLU:HA	1:A:150:LEU:HD12	1.94	0.48
1:A:150:LEU:HB2	1:A:151:GLN:HE21	1.78	0.48
1:C:244:TRP:CD1	1:C:479:PRO:HG2	2.48	0.48
5:B:505:BTB:H12	11:C:626:HOH:O	2.14	0.47
1:A:134:TYR:C	1:A:134:TYR:HD2	2.22	0.47
1:C:255:ARG:HH12	1:C:268:VAL:HG11	1.80	0.47
1:A:256:GLN:C	1:A:258:ASP:H	2.23	0.47
1:B:447:TRP:HA	3:B:502:H4B:N1	2.29	0.47
1:D:271:THR:O	1:D:275:ILE:HG12	2.15	0.47
1:A:298:GLU:OE2	5:A:506:BTB:H32	2.15	0.47
1:B:250:ARG:NH2	10:B:504:ACT:OXT	2.47	0.47
1:A:279:TRP:HB2	1:A:302:LEU:HD13	1.96	0.47
1:C:97:ARG:HD2	1:D:88:ALA:HB3	1.97	0.47
1:D:298:GLU:OE1	5:D:506:BTB:H52	2.15	0.46
1:C:364:THR:O	1:C:368:CYS:HB2	2.15	0.46
1:A:238:ARG:HE	1:A:239:GLY:HA3	1.80	0.46
1:A:322:TRP:CD1	5:A:504:BTB:H61	2.51	0.46
5:B:510:BTB:H42	5:B:510:BTB:H51	1.38	0.46
1:C:128:ARG:NH2	1:C:154:GLU:OE1	2.48	0.46
1:A:167:GLU:OE1	6:A:507:GOL:H2	2.16	0.46
1:B:183:ARG:HD3	1:B:447:TRP:CD2	2.50	0.45
1:A:262:ARG:HG3	1:A:285:ARG:HG3	1.97	0.45
1:A:387:THR:HA	1:A:394:TRP:CD1	2.51	0.45
1:A:202:ARG:HB2	1:A:202:ARG:NH1	2.31	0.45
5:A:506:BTB:H41	5:A:506:BTB:H72	1.46	0.45
1:B:326:LEU:HB3	1:B:328:LEU:HG	1.97	0.45
1:D:298:GLU:CD	5:D:506:BTB:H42	2.42	0.45
5:C:505:BTB:O3	5:C:505:BTB:O6	2.32	0.45
1:A:216:LYS:HG3	1:A:217:TYR:N	2.32	0.45
5:A:504:BTB:H32	5:A:504:BTB:H51	1.70	0.45
1:B:139:LYS:N	1:B:139:LYS:HD2	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:ARG:HH21	1:A:240:ASP:H	1.65	0.44
1:B:250:ARG:HA	1:B:250:ARG:HD2	1.71	0.44
1:C:479:PRO:HD2	1:C:480:TRP:CZ3	2.52	0.44
1:C:160:THR:HG21	11:C:683:HOH:O	2.16	0.44
1:D:178:TRP:CE3	1:D:190:TRP:HA	2.52	0.44
1:D:387:THR:HG22	1:D:394:TRP:CD2	2.53	0.44
1:A:365:ARG:HH12	3:A:502:H4B:C4	2.30	0.43
1:B:364:THR:O	1:B:368:CYS:HB2	2.18	0.43
1:C:135:TYR:HD1	1:C:140:ARG:HB2	1.84	0.43
1:C:450:PRO:HG2	1:C:457:THR:HG21	2.00	0.43
1:D:93:PRO:HB3	1:D:106:PRO:HB2	2.00	0.43
1:A:229:THR:O	1:A:352:PRO:HD2	2.19	0.43
2:B:501:HEM:HBC2	2:B:501:HEM:HMC2	2.00	0.43
1:C:365:ARG:HH12	3:C:502:H4B:C4	2.30	0.43
5:A:506:BTB:H11	5:A:506:BTB:H51	1.52	0.43
1:D:233:GLN:HB3	1:D:348:PHE:CE2	2.54	0.43
1:C:453:SER:HB3	1:C:456:LEU:HD12	2.01	0.42
1:A:140:ARG:HD3	1:A:140:ARG:HA	1.88	0.42
1:A:465:VAL:HG12	1:A:467:TYR:HD1	1.85	0.42
1:A:364:THR:HG21	1:A:452:ILE:HG23	2.02	0.42
1:A:384:ASP:OD1	5:A:504:BTB:O3	2.38	0.42
5:A:504:BTB:H41	5:A:504:BTB:H72	1.68	0.42
1:B:119:ALA:HB1	1:B:122:GLN:HG2	2.01	0.42
1:C:167:GLU:OE1	6:C:506:GOL:H31	2.20	0.42
5:C:505:BTB:H41	5:C:505:BTB:H72	1.59	0.42
1:D:306:PRO:HA	1:D:307:PRO:HD2	1.94	0.42
1:A:241:PHE:HD1	11:A:611:HOH:O	2.03	0.41
1:D:124:LEU:HD13	1:D:128:ARG:NH2	2.35	0.41
1:C:170:LEU:HD11	1:C:230:VAL:HG11	2.02	0.41
1:C:88:ALA:HB3	1:D:97:ARG:HD2	2.02	0.41
1:B:178:TRP:CE3	1:B:190:TRP:HA	2.56	0.41
1:B:470:SER:HA	1:B:471:PRO:C	2.46	0.40
1:C:229:THR:O	1:C:352:PRO:HD2	2.22	0.40
1:D:238:ARG:HG2	1:D:296:PRO:HB3	2.02	0.40
1:B:128:ARG:HG3	1:B:150:LEU:HD22	2.02	0.40
1:B:97:ARG:CZ	1:B:97:ARG:HB3	2.51	0.40
1:C:70:ARG:NH2	11:C:607:HOH:O	2.44	0.40
1:C:180:ASN:O	1:C:182:PRO:HD3	2.21	0.40
1:C:306:PRO:HA	1:C:307:PRO:HD2	1.95	0.40
1:D:455:SER:HA	1:D:460:PHE:CG	2.56	0.40
1:A:231:PHE:HB2	1:A:350:ALA:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:505:BTB:H11	5:A:505:BTB:H51	1.60	0.40

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	397/440 (90%)	374 (94%)	19 (5%)	4 (1%)	12	4
1	B	399/440 (91%)	389 (98%)	10 (2%)	0	100	100
1	C	399/440 (91%)	391 (98%)	7 (2%)	1 (0%)	36	25
1	D	398/440 (90%)	392 (98%)	6 (2%)	0	100	100
All	All	1593/1760 (90%)	1546 (97%)	42 (3%)	5 (0%)	36	25

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	144	GLN
1	A	240	ASP
1	A	88	ALA
1	A	203	SER
1	C	89	GLN

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	341/373 (91%)	319 (94%)	22 (6%)	15	3
1	B	342/373 (92%)	335 (98%)	7 (2%)	48	32
1	C	342/373 (92%)	328 (96%)	14 (4%)	27	10
1	D	341/373 (91%)	334 (98%)	7 (2%)	47	30
All	All	1366/1492 (92%)	1316 (96%)	50 (4%)	30	13

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	67	LYS
1	A	87	GLN
1	A	89	GLN
1	A	97	ARG
1	A	121	GLU
1	A	122	GLN
1	A	126	GLN
1	A	128	ARG
1	A	129	ASP
1	A	134	TYR
1	A	151	GLN
1	A	202	ARG
1	A	209	THR
1	A	210	TYR
1	A	216	LYS
1	A	238	ARG
1	A	256	GLN
1	A	258	ASP
1	A	291	LEU
1	A	304	LEU
1	A	321	GLU
1	A	474	ARG
1	B	97	ARG
1	B	98	ARG
1	B	122	GLN
1	B	128	ARG
1	B	257	GLN
1	B	326	LEU
1	B	389	THR
1	C	67	LYS
1	C	89	GLN
1	C	97	ARG
1	C	121	GLU

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Mol	Chain	Res	Type
1	C	125	SER
1	C	140	ARG
1	C	148	GLN
1	C	151	GLN
1	C	152	GLU
1	C	202	ARG
1	C	207	MET
1	C	308	GLU
1	C	309	LEU
1	C	397	LYS
1	D	124	LEU
1	D	192	LYS
1	D	200	ASP
1	D	255	ARG
1	D	257	GLN
1	D	258	ASP
1	D	262	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	151	GLN
1	A	256	GLN
1	B	122	GLN
1	B	213	ASN
1	B	276	GLN
1	C	87	GLN
1	C	132	ASN
1	C	133	GLN
1	C	148	GLN
1	C	256	GLN
1	C	283	ASN
1	D	256	GLN

5.3.3 RNA ⓘ

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 42 ligands modelled in this entry, 10 are monoatomic - leaving 32 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	B	506	-	13,13,13	0.61	0	7,16,16	1.17	0
5	BTB	A	505	-	13,13,13	0.46	0	7,16,16	0.94	0
5	BTB	B	510	-	13,13,13	0.48	0	7,16,16	0.68	0
3	H4B	C	502	-	17,18,18	0.95	0	14,26,26	2.11	5 (35%)
5	BTB	D	506	-	13,13,13	0.63	0	7,16,16	1.13	1 (14%)
5	BTB	B	505	8	13,13,13	0.43	0	7,16,16	0.38	0
5	BTB	D	505	8	13,13,13	0.35	0	7,16,16	0.70	0
10	ACT	C	504	-	3,3,3	1.01	0	3,3,3	0.91	0
6	GOL	A	512	-	5,5,5	0.69	0	5,5,5	2.44	2 (40%)
6	GOL	C	507	-	5,5,5	0.38	0	5,5,5	0.27	0
2	HEM	C	501	1	50,50,50	1.70	7 (14%)	67,82,82	1.45	10 (14%)
3	H4B	A	502	-	17,18,18	0.82	0	14,26,26	1.88	4 (28%)
6	GOL	C	508	-	5,5,5	0.37	0	5,5,5	0.20	0
6	GOL	D	507	-	5,5,5	0.34	0	5,5,5	0.34	0
4	A1A0E	A	503	-	18,18,18	0.33	0	23,24,24	1.86	7 (30%)
4	A1A0E	B	503	-	18,18,18	0.40	0	23,24,24	1.89	8 (34%)
6	GOL	A	507	-	5,5,5	0.37	0	5,5,5	0.30	0
2	HEM	D	501	1	50,50,50	1.62	10 (20%)	67,82,82	1.14	4 (5%)
3	H4B	D	502	-	17,18,18	0.88	0	14,26,26	1.75	3 (21%)
3	H4B	B	502	-	17,18,18	0.92	1 (5%)	14,26,26	1.99	4 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HEM	A	501	1	50,50,50	1.69	8 (16%)	67,82,82	1.30	8 (11%)
2	HEM	B	501	1	50,50,50	1.59	9 (18%)	67,82,82	1.30	6 (8%)
10	ACT	B	504	-	3,3,3	0.94	0	3,3,3	0.75	0
10	ACT	D	504	-	3,3,3	1.03	0	3,3,3	0.79	0
5	BTB	A	506	-	13,13,13	0.32	0	7,16,16	0.74	0
6	GOL	C	506	-	5,5,5	0.32	0	5,5,5	0.29	0
4	A1A0E	C	503	-	18,18,18	0.32	0	23,24,24	2.31	8 (34%)
5	BTB	C	505	8	13,13,13	0.37	0	7,16,16	1.07	1 (14%)
6	GOL	B	507	-	5,5,5	0.31	0	5,5,5	0.44	0
6	GOL	A	508	-	5,5,5	0.56	0	5,5,5	0.44	0
4	A1A0E	D	503	-	18,18,18	0.53	0	23,24,24	2.31	7 (30%)
5	BTB	A	504	8	13,13,13	0.39	0	7,16,16	0.62	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
5	BTB	B	506	-	-	9/21/21/21	-
5	BTB	A	505	-	-	5/21/21/21	-
5	BTB	B	510	-	-	15/21/21/21	-
3	H4B	C	502	-	-	0/8/17/17	0/2/2/2
5	BTB	D	506	-	-	9/21/21/21	-
5	BTB	B	505	8	-	3/21/21/21	-
5	BTB	D	505	8	-	6/21/21/21	-
6	GOL	A	512	-	-	4/4/4/4	-
6	GOL	C	507	-	-	4/4/4/4	-
2	HEM	C	501	1	-	2/14/54/54	-
3	H4B	A	502	-	-	0/8/17/17	0/2/2/2
6	GOL	C	508	-	-	2/4/4/4	-
6	GOL	D	507	-	-	2/4/4/4	-
4	A1A0E	A	503	-	-	5/7/7/7	0/2/2/2
4	A1A0E	B	503	-	-	5/7/7/7	0/2/2/2
6	GOL	A	507	-	-	0/4/4/4	-
2	HEM	D	501	1	-	0/14/54/54	-
3	H4B	D	502	-	-	0/8/17/17	0/2/2/2
3	H4B	B	502	-	-	0/8/17/17	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEM	A	501	1	-	0/14/54/54	-
2	HEM	B	501	1	-	1/14/54/54	-
5	BTB	A	506	-	-	10/21/21/21	-
6	GOL	C	506	-	-	2/4/4/4	-
4	A1A0E	C	503	-	-	4/7/7/7	0/2/2/2
5	BTB	C	505	8	-	4/21/21/21	-
6	GOL	B	507	-	-	2/4/4/4	-
6	GOL	A	508	-	-	2/4/4/4	-
4	A1A0E	D	503	-	-	5/7/7/7	0/2/2/2
5	BTB	A	504	8	-	4/21/21/21	-

All (35) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	501	HEM	FE-NB	5.47	2.11	1.94
2	A	501	HEM	FE-NB	5.47	2.11	1.94
2	C	501	HEM	FE-NB	5.23	2.11	1.94
2	C	501	HEM	FE-NA	5.07	2.11	1.95
2	A	501	HEM	FE-NC	4.83	2.11	1.95
2	B	501	HEM	FE-NA	4.47	2.09	1.95
2	A	501	HEM	FE-ND	4.33	2.08	1.94
2	D	501	HEM	FE-NC	4.14	2.08	1.95
2	C	501	HEM	FE-ND	4.10	2.07	1.94
2	B	501	HEM	FE-NB	4.02	2.07	1.94
2	C	501	HEM	FE-NC	3.94	2.08	1.95
2	B	501	HEM	FE-NC	3.73	2.07	1.95
2	B	501	HEM	FE-ND	3.62	2.06	1.94
2	D	501	HEM	FE-NA	3.24	2.05	1.95
2	A	501	HEM	FE-NA	3.23	2.05	1.95
2	B	501	HEM	CAC-C3C	3.14	1.55	1.47
2	A	501	HEM	CAB-C3B	3.13	1.55	1.47
2	C	501	HEM	CAB-C3B	3.13	1.55	1.47
2	D	501	HEM	CAB-C3B	3.09	1.55	1.47
2	B	501	HEM	CAB-C3B	3.03	1.55	1.47
2	A	501	HEM	CAC-C3C	2.99	1.55	1.47
2	D	501	HEM	FE-ND	2.90	2.03	1.94
2	C	501	HEM	CAC-C3C	2.89	1.55	1.47
2	D	501	HEM	CAC-C3C	2.68	1.54	1.47
2	C	501	HEM	CMC-C2C	2.52	1.55	1.50
2	D	501	HEM	CMC-C2C	2.42	1.55	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	501	HEM	CMD-C2D	2.39	1.55	1.50
2	A	501	HEM	CMC-C2C	2.35	1.55	1.50
2	B	501	HEM	CMB-C2B	2.16	1.55	1.50
2	D	501	HEM	CMB-C2B	2.15	1.55	1.50
2	B	501	HEM	CMA-C3A	2.10	1.55	1.50
2	B	501	HEM	CMC-C2C	2.06	1.55	1.50
2	D	501	HEM	CMA-C3A	2.05	1.55	1.50
3	B	502	H4B	C4-N3	-2.03	1.35	1.38
2	A	501	HEM	CMD-C2D	2.01	1.54	1.50

All (78) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	503	A1A0E	C06-N01-C02	5.51	121.94	118.52
4	C	503	A1A0E	C06-N01-C02	4.99	121.62	118.52
6	A	512	GOL	O1-C1-C2	-4.66	89.39	110.38
4	C	503	A1A0E	C14-C16-C15	4.61	121.17	116.90
4	A	503	A1A0E	C06-N01-C02	4.56	121.35	118.52
4	D	503	A1A0E	C12-C13-C06	-4.34	114.87	121.29
3	B	502	H4B	C2-N1-C8A	4.25	120.87	113.36
4	D	503	A1A0E	C14-C13-C06	4.21	126.48	120.59
3	D	502	H4B	C2-N1-C8A	4.07	120.55	113.36
3	C	502	H4B	C2-N1-C8A	4.06	120.52	113.36
3	A	502	H4B	C2-N1-C8A	4.03	120.47	113.36
4	B	503	A1A0E	C14-C16-C15	3.99	120.60	116.90
4	C	503	A1A0E	C12-C13-C06	-3.84	115.61	121.29
4	D	503	A1A0E	C14-C16-C15	3.82	120.44	116.90
2	C	501	HEM	C3B-C4B-NB	-3.42	107.01	109.47
4	C	503	A1A0E	C13-C14-C16	-3.40	116.67	121.20
4	B	503	A1A0E	C06-N01-C02	3.40	120.63	118.52
2	D	501	HEM	CBD-CAD-C3D	-3.32	103.36	112.53
3	C	502	H4B	O4-C4-C4A	-3.28	119.35	127.26
2	C	501	HEM	C2A-C1A-NA	-3.19	106.62	110.15
4	A	503	A1A0E	C14-C16-C15	3.14	119.81	116.90
4	D	503	A1A0E	C13-C06-N01	3.14	120.57	116.04
3	B	502	H4B	O4-C4-C4A	-3.10	119.79	127.26
4	B	503	A1A0E	C13-C06-N01	3.07	120.48	116.04
2	C	501	HEM	C1B-NB-C4B	3.05	108.82	105.21
4	B	503	A1A0E	C12-C13-C06	-3.05	116.78	121.29
2	A	501	HEM	C3B-C2B-C1B	2.99	108.65	106.41
4	C	503	A1A0E	C14-C13-C06	2.96	124.73	120.59
3	A	502	H4B	O4-C4-C4A	-2.96	120.12	127.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	HEM	CBA-CAA-C2A	-2.95	104.37	112.53
2	C	501	HEM	C3B-C2B-C1B	2.94	108.62	106.41
4	C	503	A1A0E	C16-C17-N18	-2.93	105.63	112.67
2	B	501	HEM	C3B-C2B-C1B	2.91	108.59	106.41
4	B	503	A1A0E	C13-C14-C16	-2.91	117.33	121.20
4	A	503	A1A0E	C13-C06-N01	2.86	120.17	116.04
2	C	501	HEM	CBD-CAD-C3D	-2.86	104.63	112.53
4	D	503	A1A0E	C13-C14-C16	-2.79	117.47	121.20
2	A	501	HEM	C3B-C4B-NB	-2.75	107.49	109.47
2	A	501	HEM	C1B-NB-C4B	2.74	108.45	105.21
3	B	502	H4B	C4A-C4-N3	2.72	119.61	112.13
3	C	502	H4B	O10-C10-C9	-2.72	105.27	109.77
2	A	501	HEM	C4D-ND-C1D	2.67	108.37	105.21
3	A	502	H4B	C2-N3-C4	-2.65	120.31	125.11
6	A	512	GOL	O2-C2-C1	-2.64	98.25	109.18
3	A	502	H4B	C4A-C4-N3	2.58	119.21	112.13
4	D	503	A1A0E	C05-C06-N01	-2.58	119.35	122.34
2	C	501	HEM	C3D-C4D-ND	-2.56	107.36	110.17
2	C	501	HEM	CBA-CAA-C2A	-2.54	105.51	112.53
3	D	502	H4B	C4A-C4-N3	2.53	119.08	112.13
4	A	503	A1A0E	C15-N11-C12	2.53	120.94	117.51
2	A	501	HEM	C2A-C1A-NA	-2.53	107.35	110.15
3	C	502	H4B	C4A-C4-N3	2.52	119.05	112.13
4	A	503	A1A0E	C12-C13-C06	-2.50	117.59	121.29
3	B	502	H4B	C2-N3-C4	-2.48	120.61	125.11
2	A	501	HEM	C3D-C4D-ND	-2.47	107.46	110.17
4	C	503	A1A0E	C13-C06-N01	2.45	119.58	116.04
2	B	501	HEM	C3B-C4B-NB	-2.44	107.72	109.47
3	C	502	H4B	C2-N3-C4	-2.43	120.70	125.11
2	A	501	HEM	CAD-CBD-CGD	-2.37	107.38	113.67
3	D	502	H4B	O4-C4-C4A	-2.36	121.57	127.26
4	C	503	A1A0E	C14-C13-C12	2.33	119.59	117.10
2	C	501	HEM	C4D-ND-C1D	2.30	107.93	105.21
4	B	503	A1A0E	C14-C13-C12	2.26	119.53	117.10
2	D	501	HEM	C2A-C1A-NA	-2.24	107.66	110.15
2	B	501	HEM	C3D-C4D-ND	-2.24	107.72	110.17
4	A	503	A1A0E	C13-C14-C16	-2.23	118.23	121.20
2	B	501	HEM	C1B-NB-C4B	2.22	107.84	105.21
5	D	506	BTB	C6-C5-N	2.21	120.20	111.59
4	B	503	A1A0E	C14-C13-C06	2.18	123.64	120.59
2	D	501	HEM	C4D-ND-C1D	2.17	107.78	105.21
4	A	503	A1A0E	C05-C06-N01	-2.16	119.83	122.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	HEM	C4D-ND-C1D	2.16	107.76	105.21
2	C	501	HEM	C2B-C1B-NB	-2.15	107.37	109.84
4	B	503	A1A0E	C05-C06-C13	-2.11	118.95	121.82
2	D	501	HEM	CBA-CAA-C2A	-2.10	106.74	112.53
2	A	501	HEM	CBD-CAD-C3D	-2.09	106.76	112.53
5	C	505	BTB	O3-C3-C2	2.07	116.26	111.40
2	C	501	HEM	CHA-C4D-ND	2.04	126.89	124.37

There are no chirality outliers.

All (105) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	503	A1A0E	C16-C17-N18-C19
4	B	503	A1A0E	C16-C17-N18-C19
4	D	503	A1A0E	C16-C17-N18-C19
5	A	504	BTB	C1-C2-C4-O4
5	A	504	BTB	C3-C2-C4-O4
5	A	504	BTB	N-C2-C4-O4
5	A	505	BTB	C1-C2-C4-O4
5	A	505	BTB	C3-C2-C4-O4
5	A	505	BTB	N-C2-C4-O4
5	A	506	BTB	O1-C1-C2-N
5	A	506	BTB	C1-C2-N-C5
5	A	506	BTB	C1-C2-N-C7
5	A	506	BTB	C3-C2-N-C5
5	A	506	BTB	C3-C2-N-C7
5	A	506	BTB	C4-C2-N-C5
5	A	506	BTB	C4-C2-N-C7
5	B	505	BTB	O1-C1-C2-C3
5	B	505	BTB	O1-C1-C2-C4
5	B	505	BTB	O1-C1-C2-N
5	B	506	BTB	O1-C1-C2-C3
5	B	506	BTB	O1-C1-C2-C4
5	B	506	BTB	O1-C1-C2-N
5	B	506	BTB	C1-C2-C3-O3
5	B	506	BTB	C4-C2-C3-O3
5	B	506	BTB	N-C2-C3-O3
5	B	506	BTB	C1-C2-C4-O4
5	B	506	BTB	C3-C2-C4-O4
5	B	506	BTB	N-C2-C4-O4
5	B	510	BTB	O1-C1-C2-C3
5	B	510	BTB	O1-C1-C2-C4

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Mol	Chain	Res	Type	Atoms
5	B	510	BTB	O1-C1-C2-N
5	B	510	BTB	C1-C2-C3-O3
5	B	510	BTB	C4-C2-C3-O3
5	B	510	BTB	N-C2-C3-O3
5	B	510	BTB	N-C2-C4-O4
5	B	510	BTB	C1-C2-N-C5
5	B	510	BTB	C1-C2-N-C7
5	B	510	BTB	C3-C2-N-C5
5	B	510	BTB	C3-C2-N-C7
5	B	510	BTB	C4-C2-N-C5
5	B	510	BTB	C4-C2-N-C7
5	C	505	BTB	C1-C2-C4-O4
5	C	505	BTB	C3-C2-C4-O4
5	C	505	BTB	N-C2-C4-O4
5	D	505	BTB	O1-C1-C2-C3
5	D	505	BTB	O1-C1-C2-C4
5	D	505	BTB	O1-C1-C2-N
5	D	505	BTB	C3-C2-C4-O4
5	D	506	BTB	C1-C2-C3-O3
5	D	506	BTB	C4-C2-C3-O3
5	D	506	BTB	N-C2-C3-O3
5	D	506	BTB	C1-C2-C4-O4
5	D	506	BTB	C3-C2-C4-O4
5	D	506	BTB	N-C2-C4-O4
5	D	506	BTB	C6-C5-N-C2
5	D	506	BTB	C8-C7-N-C5
6	A	512	GOL	O1-C1-C2-C3
6	A	512	GOL	C1-C2-C3-O3
6	A	512	GOL	O2-C2-C3-O3
6	B	507	GOL	O1-C1-C2-O2
6	B	507	GOL	O1-C1-C2-C3
6	C	506	GOL	O1-C1-C2-C3
6	C	507	GOL	O2-C2-C3-O3
6	D	507	GOL	C1-C2-C3-O3
4	B	503	A1A0E	N01-C06-C13-C12
4	C	503	A1A0E	N01-C06-C13-C12
4	B	503	A1A0E	C05-C06-C13-C12
4	C	503	A1A0E	C05-C06-C13-C12
6	C	507	GOL	O1-C1-C2-O2
4	D	503	A1A0E	C05-C06-C13-C12
4	C	503	A1A0E	C05-C06-C13-C14
6	A	508	GOL	C1-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
6	C	507	GOL	O1-C1-C2-C3
6	C	507	GOL	C1-C2-C3-O3
5	B	510	BTB	N-C7-C8-O8
4	D	503	A1A0E	N01-C06-C13-C12
4	B	503	A1A0E	C05-C06-C13-C14
5	B	510	BTB	C3-C2-C4-O4
6	C	506	GOL	O1-C1-C2-O2
4	A	503	A1A0E	C05-C06-C13-C12
4	C	503	A1A0E	N01-C06-C13-C14
5	C	505	BTB	N-C7-C8-O8
4	B	503	A1A0E	N01-C06-C13-C14
6	A	512	GOL	O1-C1-C2-O2
4	A	503	A1A0E	N01-C06-C13-C12
4	D	503	A1A0E	C05-C06-C13-C14
6	A	508	GOL	O2-C2-C3-O3
6	D	507	GOL	O2-C2-C3-O3
5	A	506	BTB	N-C7-C8-O8
6	C	508	GOL	O1-C1-C2-C3
2	C	501	HEM	C4B-C3B-CAB-CBB
5	A	506	BTB	O1-C1-C2-C4
6	C	508	GOL	O1-C1-C2-O2
4	A	503	A1A0E	C05-C06-C13-C14
4	D	503	A1A0E	N01-C06-C13-C14
5	D	506	BTB	N-C5-C6-O6
5	A	504	BTB	N-C7-C8-O8
2	C	501	HEM	C3D-CAD-CBD-CGD
4	A	503	A1A0E	N01-C06-C13-C14
5	A	505	BTB	N-C7-C8-O8
2	B	501	HEM	C4B-C3B-CAB-CBB
5	A	505	BTB	N-C5-C6-O6
5	D	505	BTB	C1-C2-C4-O4
5	A	506	BTB	N-C5-C6-O6
5	D	505	BTB	N-C2-C4-O4

There are no ring outliers.

19 monomers are involved in 37 short contacts:

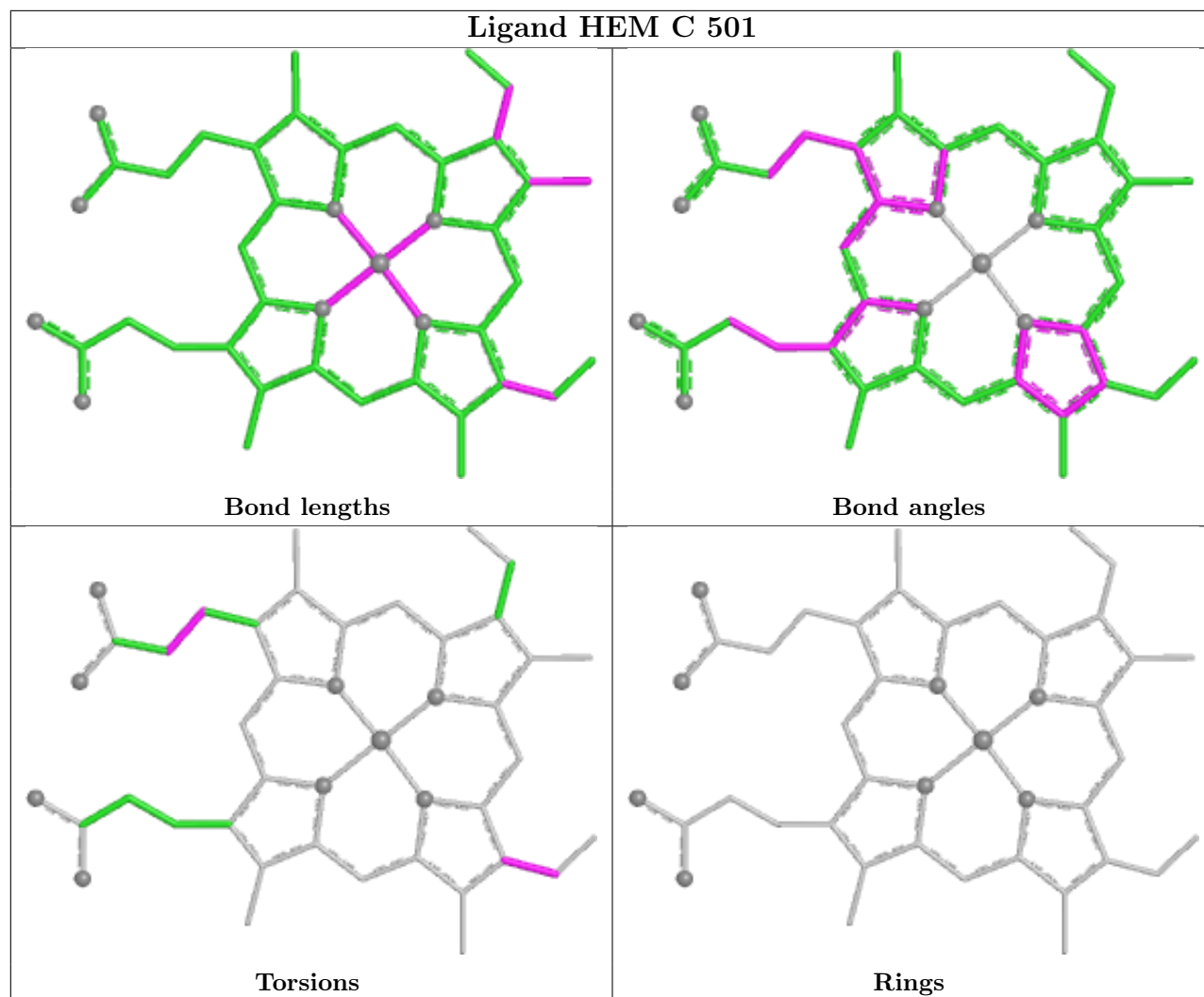
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	506	BTB	1	0
5	A	505	BTB	1	0
5	B	510	BTB	1	0
3	C	502	H4B	1	0

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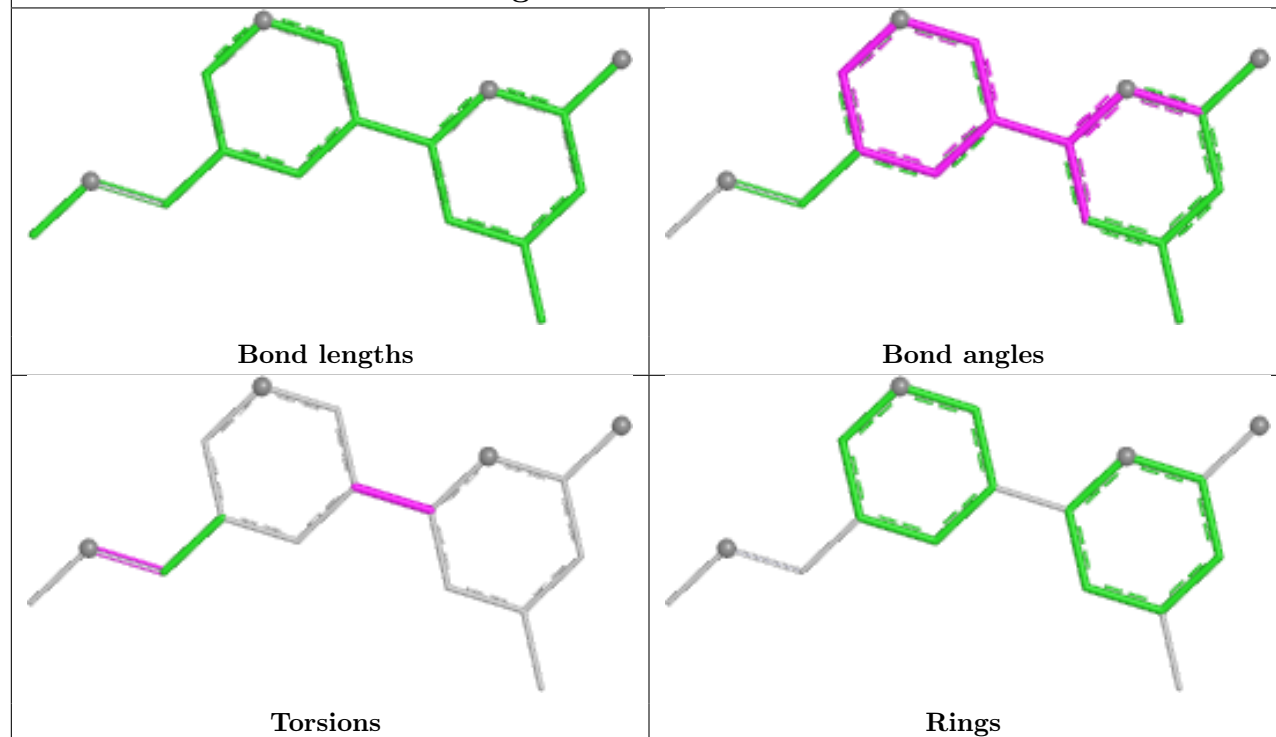
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	506	BTB	3	0
5	B	505	BTB	1	0
5	D	505	BTB	1	0
2	C	501	HEM	2	0
3	A	502	H4B	1	0
6	A	507	GOL	1	0
2	D	501	HEM	3	0
3	B	502	H4B	1	0
2	A	501	HEM	3	0
2	B	501	HEM	3	0
10	B	504	ACT	1	0
5	A	506	BTB	3	0
6	C	506	GOL	1	0
5	C	505	BTB	3	0
5	A	504	BTB	6	0

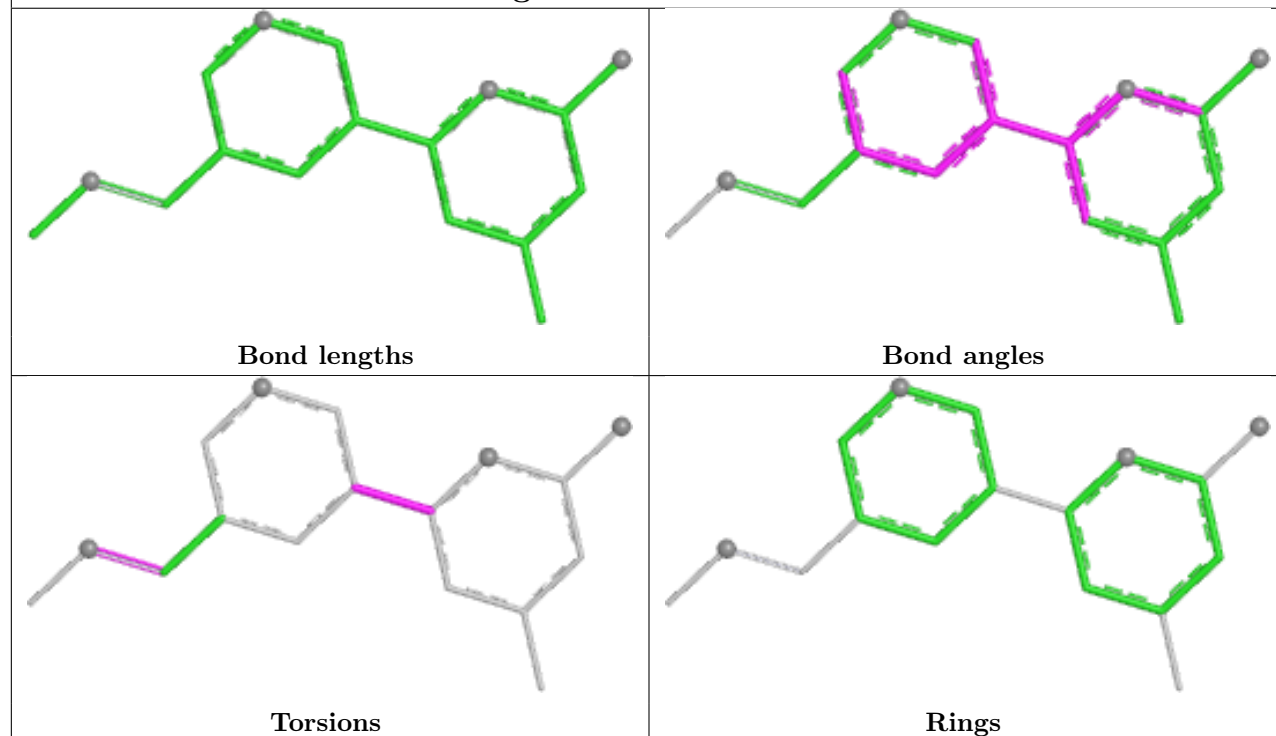
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

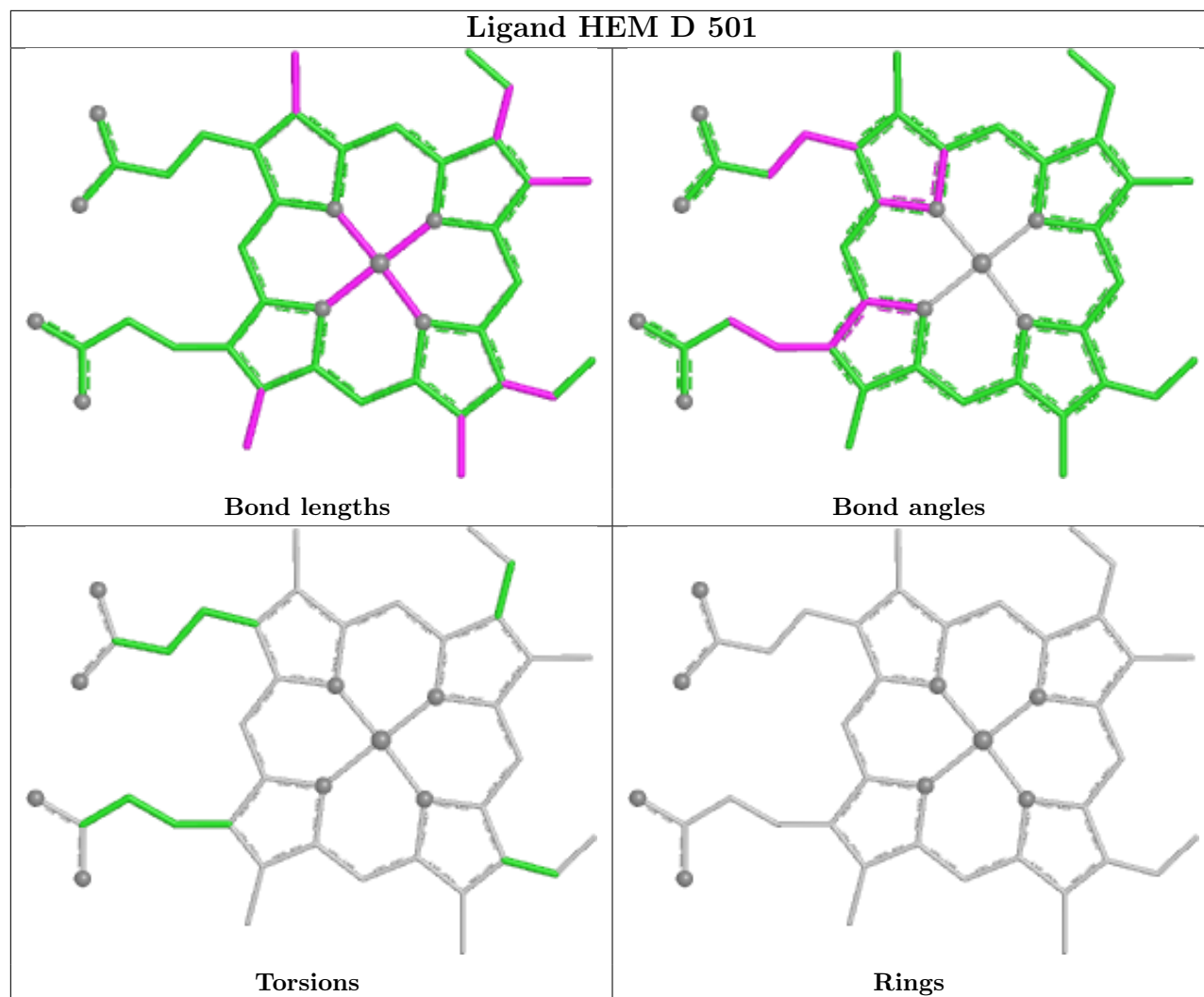


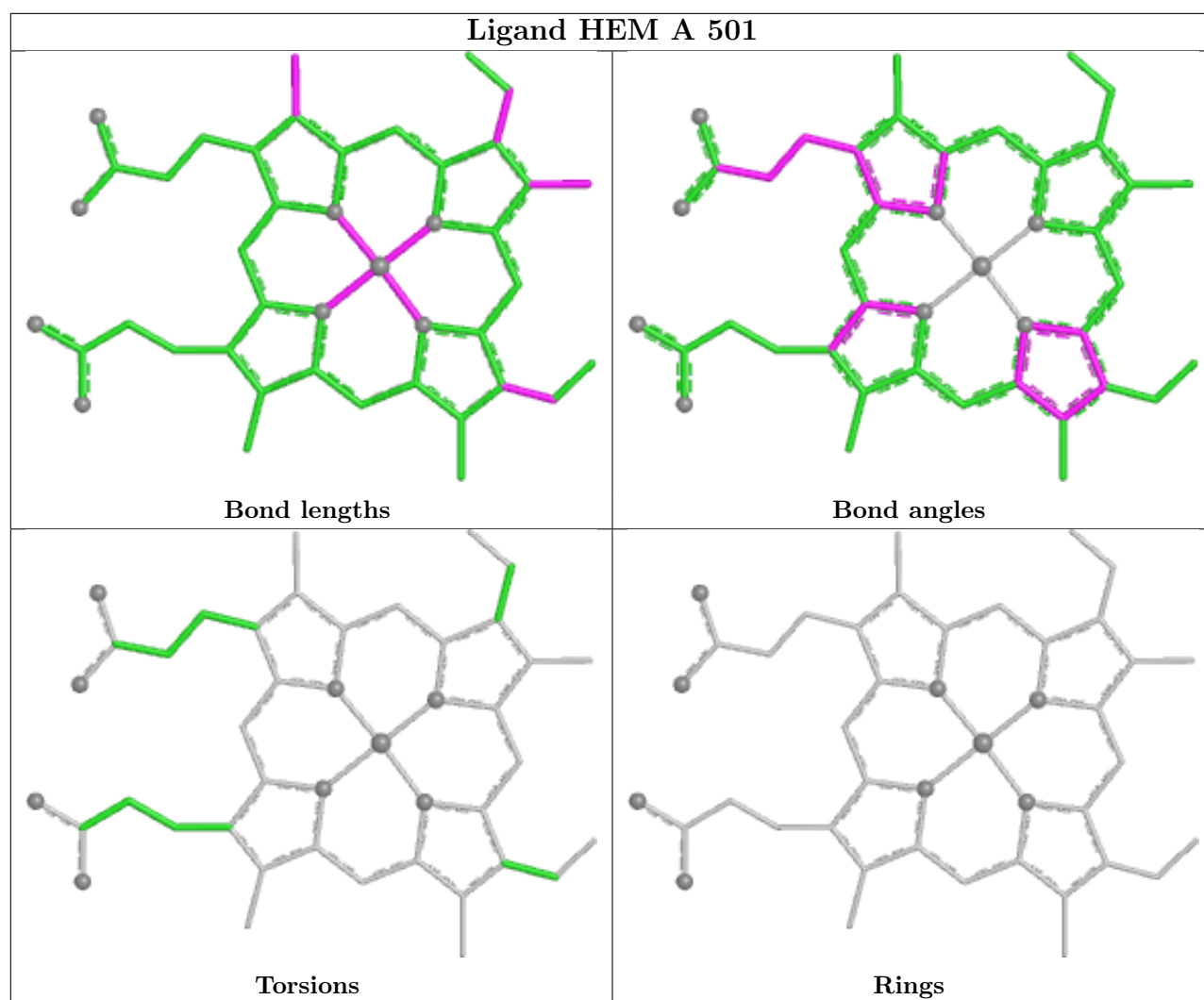
Ligand A1A0E A 503

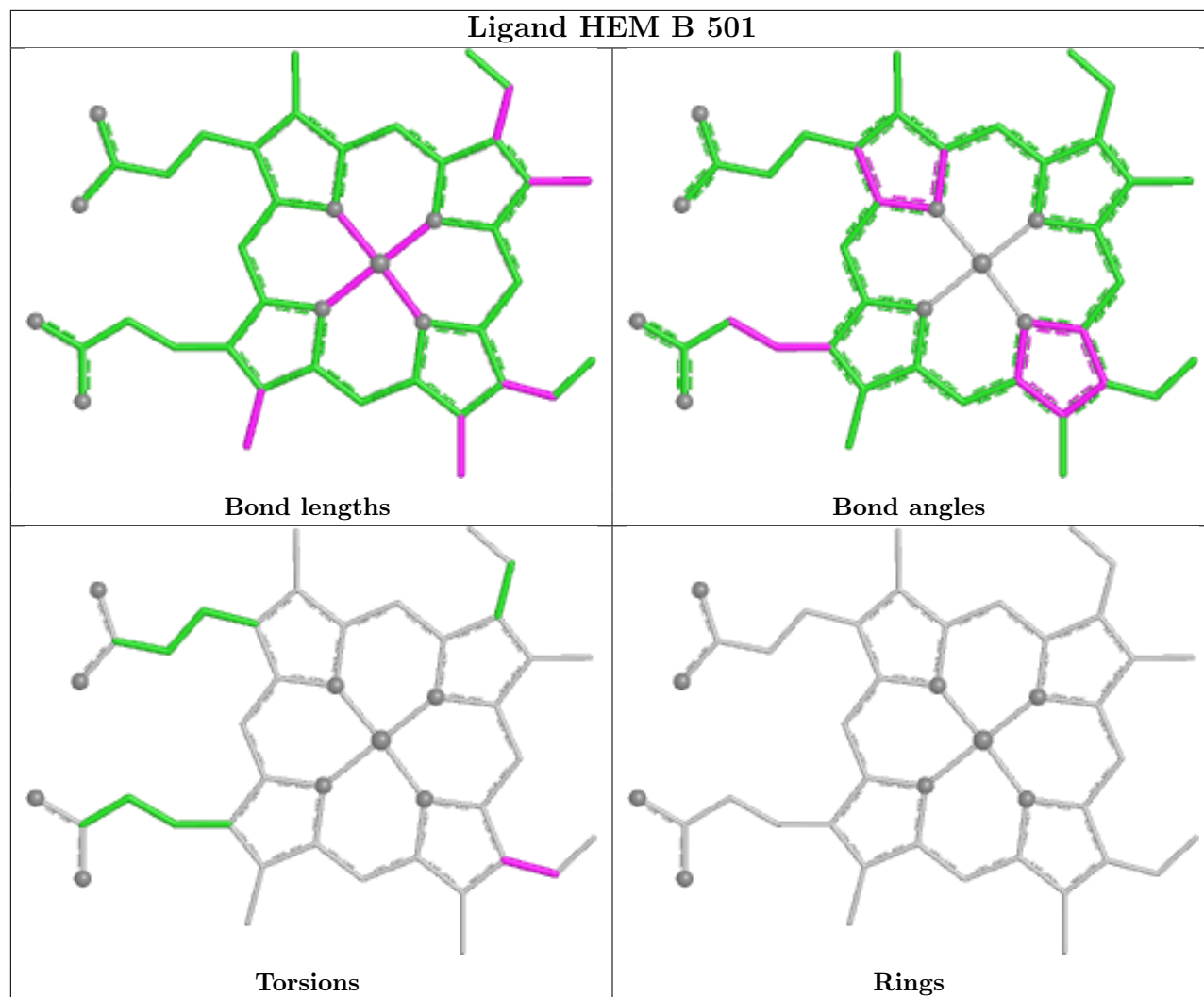


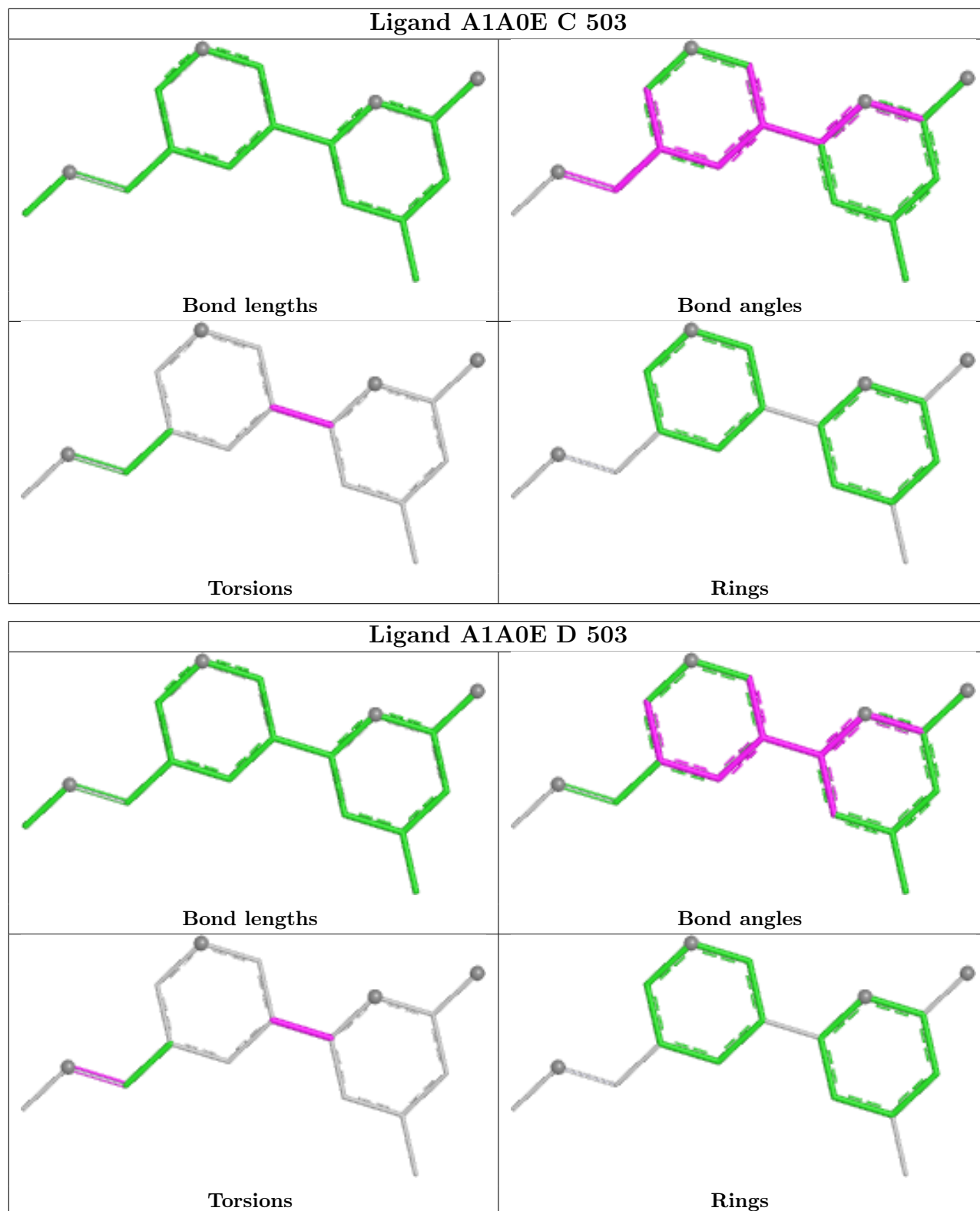
Ligand A1A0E B 503











5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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	400/440 (90%)	0.74	49 (12%) 8 8	23, 59, 116, 147	1 (0%)
1	B	401/440 (91%)	-0.13	3 (0%) 84 90	23, 37, 71, 109	2 (0%)
1	C	402/440 (91%)	0.20	10 (2%) 58 64	23, 48, 86, 107	1 (0%)
1	D	402/440 (91%)	-0.21	5 (1%) 76 82	21, 35, 61, 126	0
All	All	1605/1760 (91%)	0.15	67 (4%) 40 43	21, 43, 94, 147	4 (0%)

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	106	PRO	5.8
1	A	106	PRO	5.0
1	A	153	VAL	4.6
1	A	204	ALA	4.4
1	A	163	TYR	3.9
1	A	159	ALA	3.9
1	A	145	ALA	3.7
1	A	134	TYR	3.4
1	A	155	ALA	3.1
1	C	155	ALA	3.1
1	A	131	ILE	3.0
1	A	235	CYS	3.0
1	A	295	ALA	3.0
1	A	158	ALA	2.9
1	A	472	ALA	2.9
1	A	150	LEU	2.9
1	A	300	PRO	2.8
1	A	345	GLY	2.7
1	A	341	LEU	2.7
1	B	106	PRO	2.7
1	D	89	GLN	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	119	ALA	2.7
1	D	257	GLN	2.7
1	A	143	SER	2.7
1	C	159	ALA	2.6
1	A	124	LEU	2.6
1	C	161	GLY	2.6
1	A	254	TYR	2.5
1	A	291	LEU	2.5
1	C	480	TRP	2.5
1	A	157	VAL	2.5
1	A	281	PRO	2.5
1	A	299	PRO	2.5
1	A	346	LEU	2.5
1	B	144	GLN	2.5
1	A	127	ALA	2.5
1	D	106	PRO	2.5
1	A	237	GLY	2.4
1	D	258	ASP	2.4
1	A	344	GLY	2.4
1	A	303	PHE	2.4
1	A	279	TRP	2.4
1	A	304	LEU	2.3
1	A	230	VAL	2.3
1	A	208	PHE	2.3
1	A	135	TYR	2.2
1	A	263	GLY	2.2
1	C	468	PHE	2.2
1	A	236	PRO	2.2
1	A	309	LEU	2.2
1	C	119	ALA	2.2
1	A	480	TRP	2.2
1	A	192	LYS	2.2
1	A	202	ARG	2.2
1	A	130	PHE	2.1
1	A	152	GLU	2.1
1	A	296	PRO	2.1
1	B	119	ALA	2.1
1	A	343	ILE	2.1
1	A	67	LYS	2.0
1	A	160	THR	2.0
1	A	302	LEU	2.0
1	C	277	HIS	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	162	THR	2.0
1	C	160	THR	2.0
1	C	236	PRO	2.0
1	A	261	VAL	2.0

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 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	BTB	D	506	14/14	0.69	0.19	51,69,75,77	0
6	GOL	C	508	6/6	0.71	0.11	73,78,84,89	0
5	BTB	A	506	14/14	0.72	0.15	89,96,100,102	0
5	BTB	B	506	14/14	0.73	0.18	48,71,80,80	0
6	GOL	C	507	6/6	0.74	0.14	75,76,79,81	0
6	GOL	A	507	6/6	0.75	0.13	63,73,78,82	0
10	ACT	C	504	4/4	0.80	0.21	61,74,77,82	0
5	BTB	A	505	14/14	0.84	0.14	60,71,82,83	0
5	BTB	B	510	14/14	0.85	0.16	22,62,72,73	0
6	GOL	D	507	6/6	0.86	0.17	54,63,64,66	0
5	BTB	D	505	14/14	0.87	0.15	41,66,82,87	0
6	GOL	A	508	6/6	0.88	0.18	26,56,66,70	0
10	ACT	D	504	4/4	0.88	0.20	55,65,68,79	0
4	A1A0E	A	503	17/17	0.89	0.13	33,54,76,78	0
5	BTB	B	505	14/14	0.90	0.14	39,52,72,76	0
5	BTB	A	504	14/14	0.90	0.15	45,83,95,101	0
6	GOL	C	506	6/6	0.91	0.09	48,61,64,67	0
10	ACT	B	504	4/4	0.91	0.13	31,48,51,59	0
4	A1A0E	C	503	17/17	0.92	0.12	33,46,80,81	0

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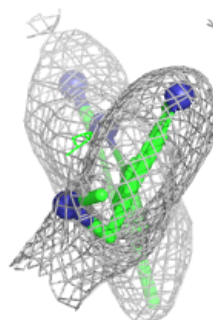
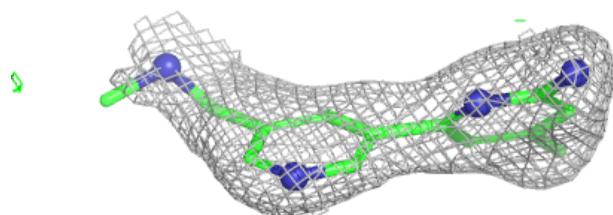
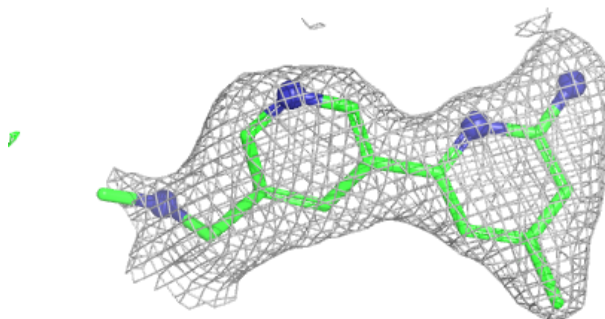
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	H4B	C	502	17/17	0.93	0.08	33,41,47,51	0
3	H4B	A	502	17/17	0.93	0.09	42,48,58,60	0
5	BTB	C	505	14/14	0.94	0.12	20,67,75,78	0
3	H4B	B	502	17/17	0.94	0.08	27,35,41,42	0
4	A1A0E	D	503	17/17	0.94	0.10	20,30,68,68	0
6	GOL	B	507	6/6	0.95	0.14	53,56,62,63	0
7	CL	A	509	1/1	0.95	0.11	51,51,51,51	0
4	A1A0E	B	503	17/17	0.95	0.09	22,30,65,72	0
3	H4B	D	502	17/17	0.95	0.07	26,35,41,42	0
6	GOL	A	512	6/6	0.95	0.12	14,37,55,56	0
2	HEM	A	501	43/43	0.96	0.10	35,52,67,74	0
8	GD3	A	510	1/1	0.96	0.06	91,91,91,91	1
8	GD3	D	509	1/1	0.96	0.05	43,43,43,43	0
8	GD3	B	511	1/1	0.97	0.05	63,63,63,63	1
2	HEM	C	501	43/43	0.97	0.07	28,37,63,88	0
9	ZN	A	511	1/1	0.97	0.05	40,40,40,40	0
2	HEM	D	501	43/43	0.98	0.06	19,23,43,64	0
7	CL	C	509	1/1	0.99	0.09	44,44,44,44	0
7	CL	D	508	1/1	0.99	0.11	40,40,40,40	0
2	HEM	B	501	43/43	0.99	0.06	18,27,49,70	0
8	GD3	B	509	1/1	0.99	0.03	38,38,38,38	0
7	CL	B	508	1/1	0.99	0.11	37,37,37,37	0
9	ZN	C	510	1/1	1.00	0.03	29,29,29,29	0

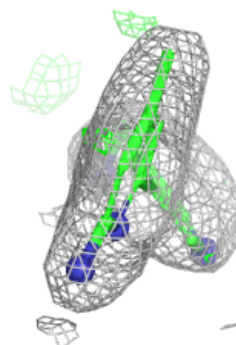
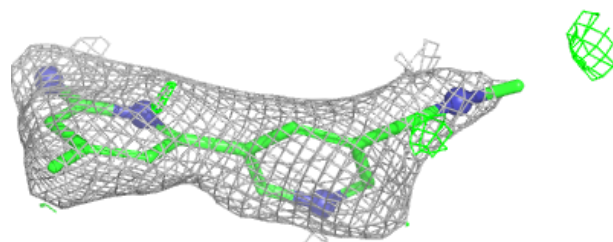
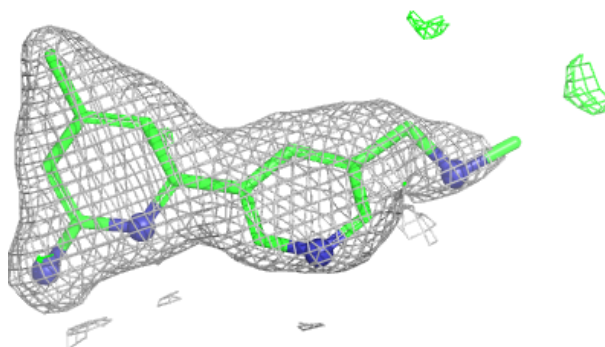
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around A1A0E 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)

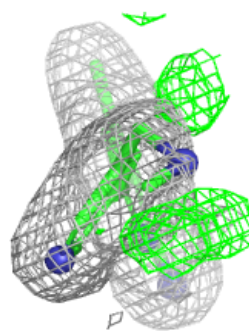
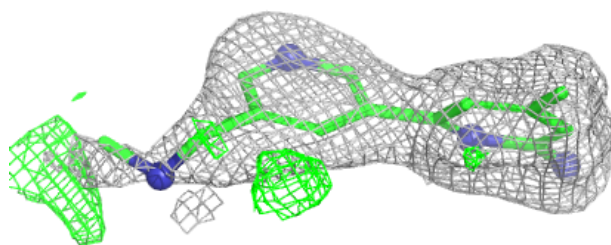
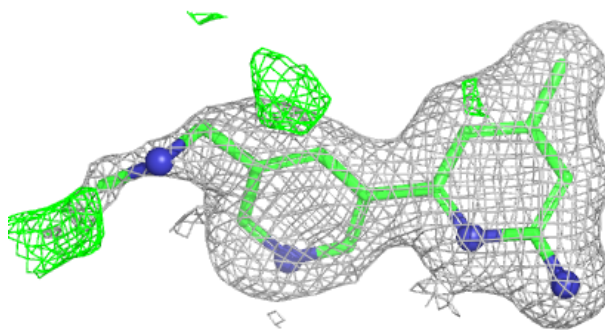
**Electron density around A1A0E C 503:**

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

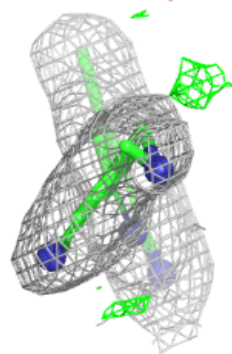
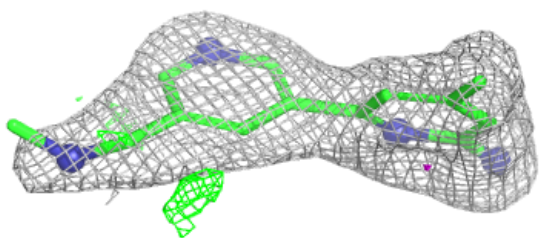
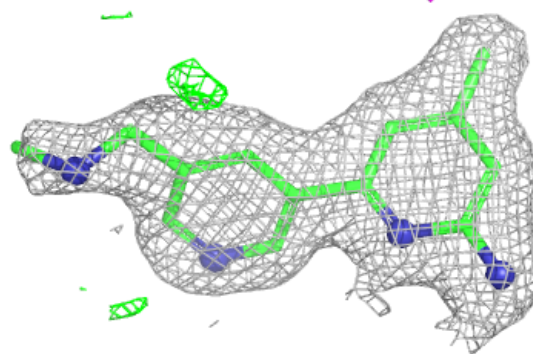


Electron density around A1A0E D 503:

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

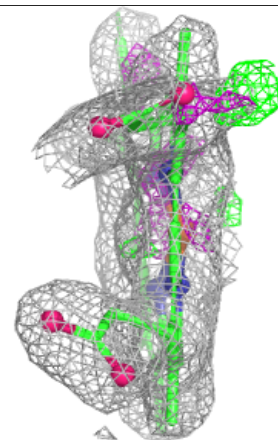
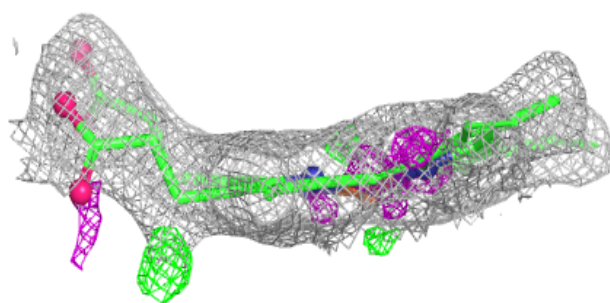
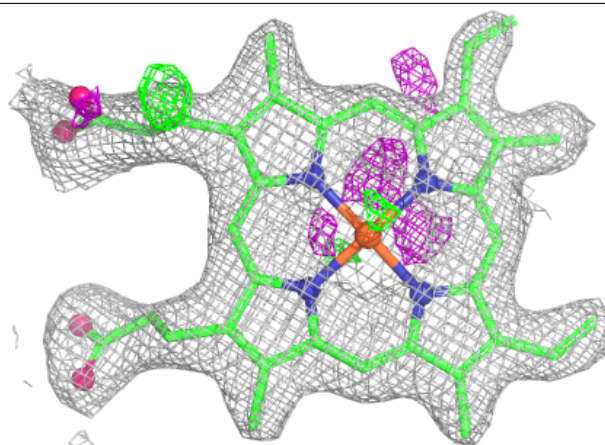
**Electron density around A1A0E B 503:**

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



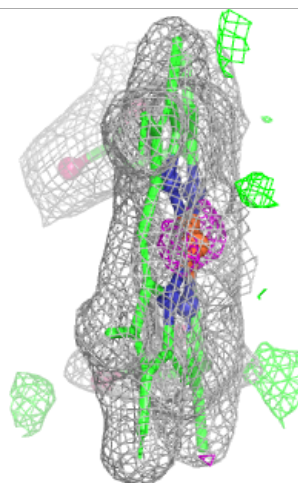
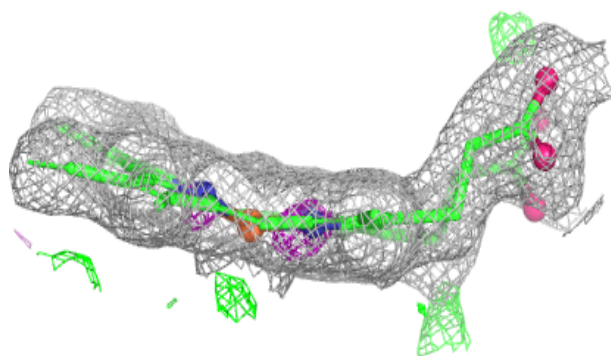
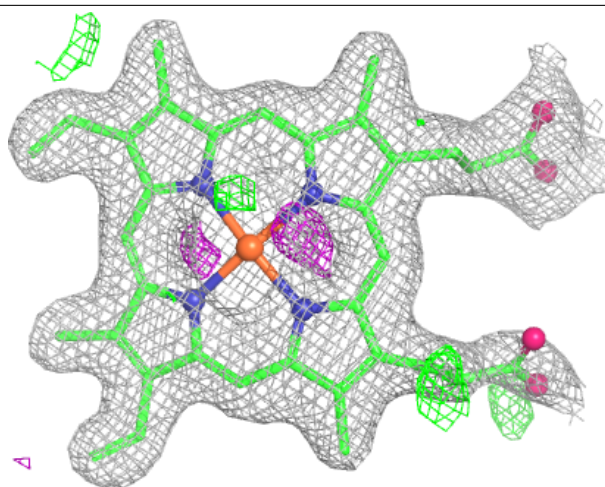
Electron density around HEM A 501:

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



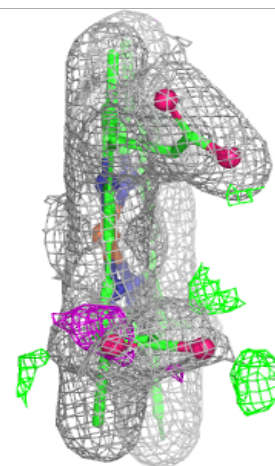
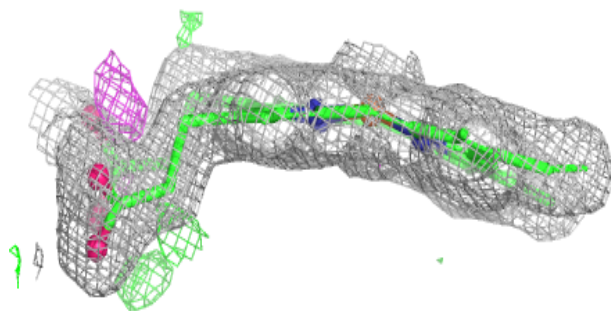
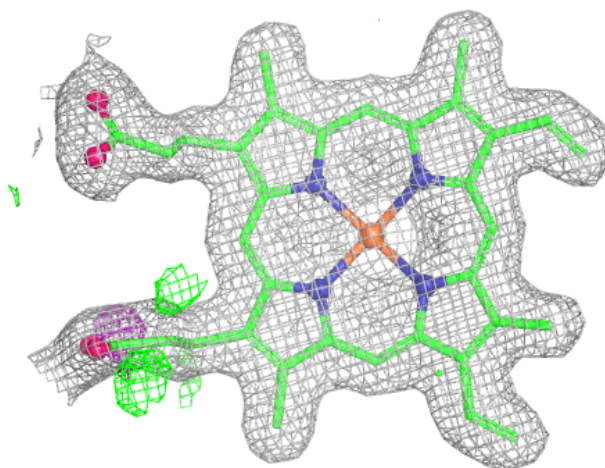
Electron density around HEM C 501:

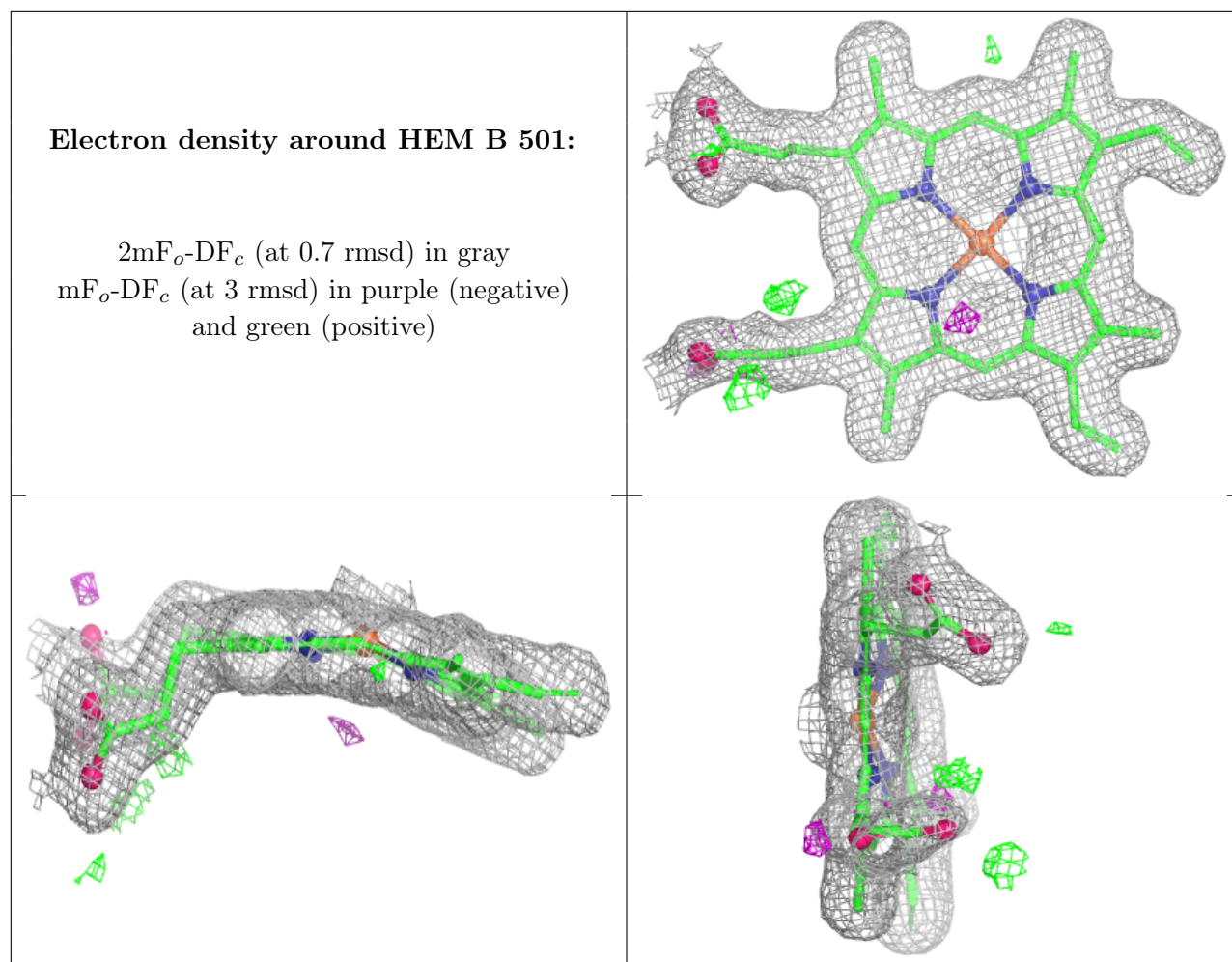
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM 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)





6.5 Other polymers ⓘ

There are no such residues in this entry.