



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 18, 2025 – 10:21 AM EST

PDB ID : 9MWS / pdb_00009mws
Title : Structure of human endothelial nitric oxide synthase heme domain bound with N-(3-(2-((3-(thiazole-5-carboximidamido)benzyl)amino)ethyl)phenyl)thiazole-5-carboximidamide
Authors : Li, H.; Poulos, T.L.
Deposited on : 2025-01-17
Resolution : 1.90 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	:	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

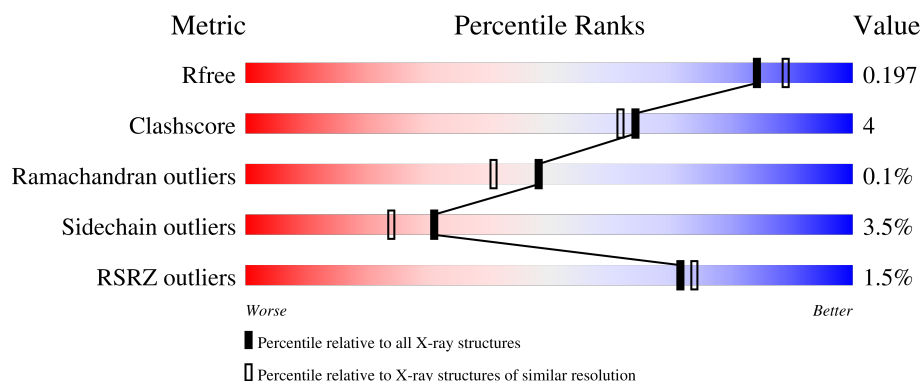
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7293 (1.90-1.90)
Clashscore	180529	8090 (1.90-1.90)
Ramachandran outliers	177936	8022 (1.90-1.90)
Sidechain outliers	177891	8022 (1.90-1.90)
RSRZ outliers	164620	7292 (1.90-1.90)

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	<div> <div>2%</div> <div> <div></div> <div>83%</div> <div>7%</div> <div>8%</div> </div> </div>
1	B	440	<div> <div>%</div> <div> <div></div> <div>85%</div> <div>6%</div> <div>8%</div> </div> </div>
1	C	440	<div> <div>%</div> <div> <div></div> <div>83%</div> <div>8%</div> <div>8%</div> </div> </div>
1	D	440	<div> <div>%</div> <div> <div></div> <div>85%</div> <div>6%</div> <div>8%</div> </div> </div>

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 14548 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.

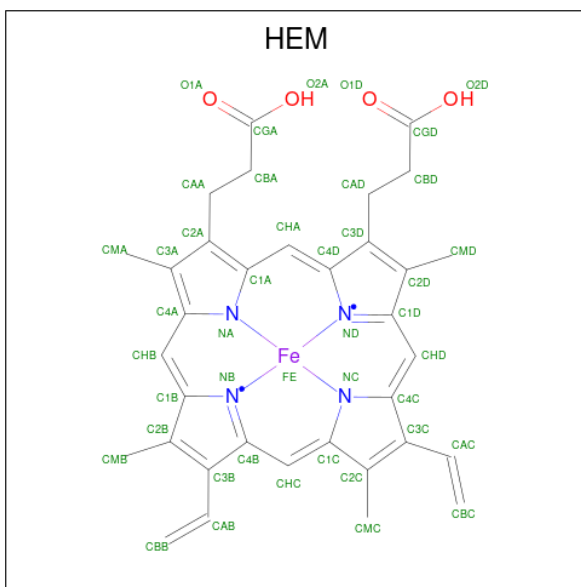
- Molecule 1 is a protein called Nitric oxide synthase, endothelial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	403	Total	C	N	O	S	0	1	0
			3223	2052	569	586	16			
1	B	403	Total	C	N	O	S	0	2	0
			3226	2054	569	587	16			
1	C	403	Total	C	N	O	S	0	1	0
			3227	2055	570	586	16			
1	D	405	Total	C	N	O	S	0	3	0
			3246	2068	572	590	16			

There are 4 discrepancies between the modelled and reference sequences:

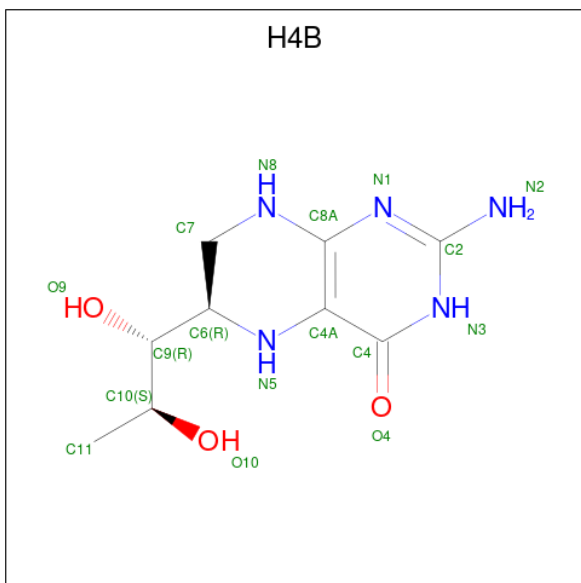
Chain	Residue	Modelled	Actual	Comment	Reference
A	298	GLU	ASP	variant	UNP P29474
B	298	GLU	ASP	variant	UNP P29474
C	298	GLU	ASP	variant	UNP P29474
D	298	GLU	ASP	variant	UNP P29474

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



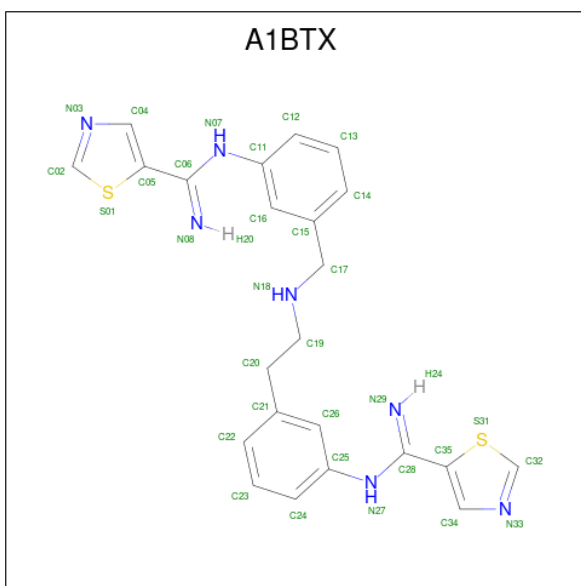
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

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



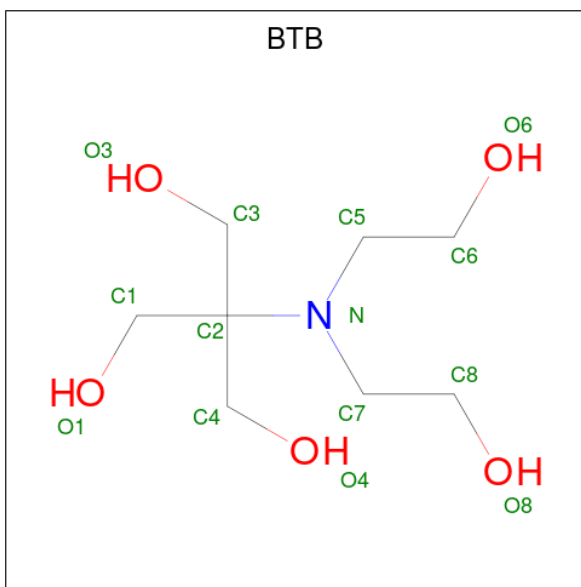
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 17	C 9	N 5	O 3	0	0
3	B	1	Total 17	C 9	N 5	O 3	0	0
3	C	1	Total 17	C 9	N 5	O 3	0	0
3	D	1	Total 17	C 9	N 5	O 3	0	0

- Molecule 4 is N-[3-(2-(3-((Z)-imino(1,3-thiazol-5-yl)methyl)amino)phenyl)ethyl]amino-3-methylphenyl-1,3-thiazole-5-carboximidamide (CCD ID: A1BTX) (formula: C₂₃H₂₃N₇S₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total 32	C 23	N 7	S 2	0	0
4	B	1	Total 32	C 23	N 7	S 2	0	0
4	C	1	Total 32	C 23	N 7	S 2	0	0
4	D	1	Total 32	C 23	N 7	S 2	0	0

- Molecule 5 is 2-[BIS-(2-HYDROXY-ETHYL)-AMINO]-2-HYDROXYMETHYL-PROPAN E-1,3-DIOL (CCD ID: BTB) (formula: $C_8H_{19}NO_5$).



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

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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 ATOM (CCD ID: GD) (formula: Gd).

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

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

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

- Molecule 10 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	B	1	Total 1	Ca 1	0	0
10	C	1	Total 1	Ca 1	0	0

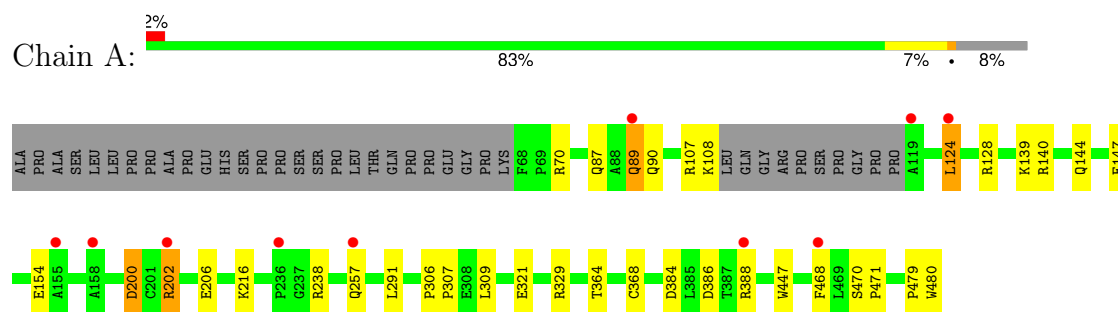
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	246	Total 246	O 246	0	0
11	B	307	Total 307	O 307	0	0
11	C	235	Total 235	O 235	0	0
11	D	312	Total 312	O 312	0	0

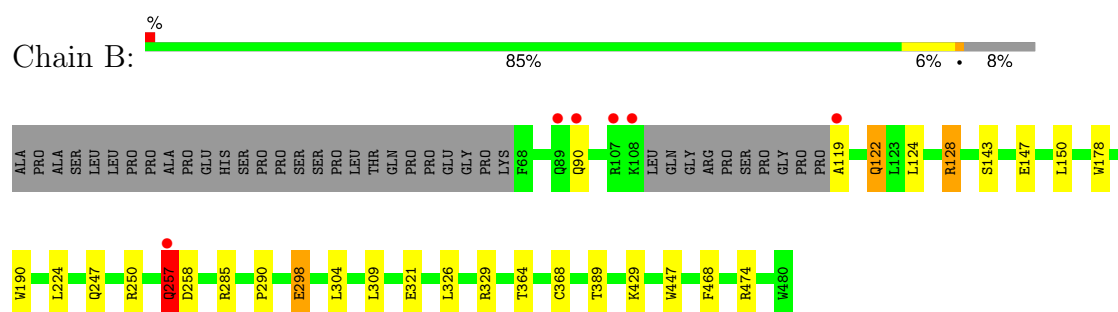
3 Residue-property plots [i](#)

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.

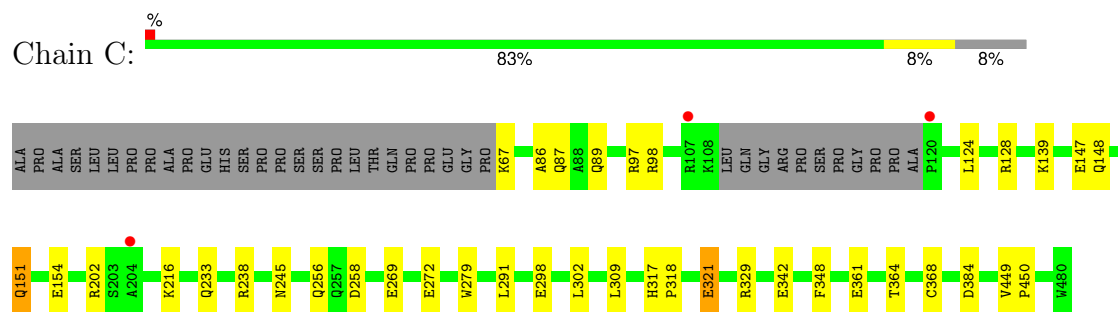
- Molecule 1: Nitric oxide synthase, endothelial



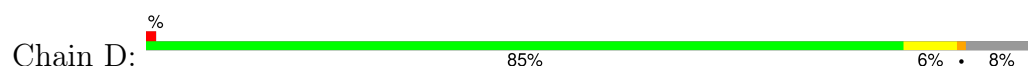
- Molecule 1: Nitric oxide synthase, endothelial

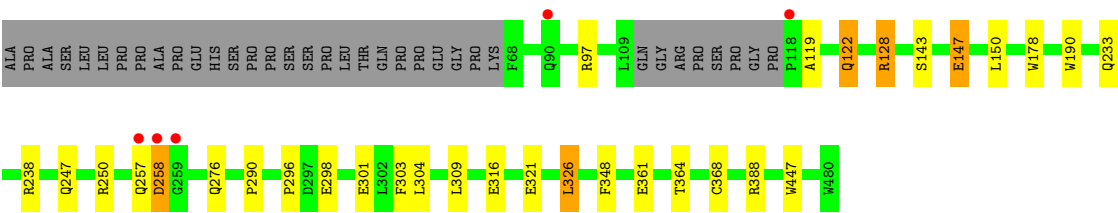


- Molecule 1: Nitric oxide synthase, endothelial



- 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	59.52Å 153.27Å 108.65Å 90.00° 90.72° 90.00°	Depositor
Resolution (Å)	39.04 – 1.90 39.04 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.8 (39.04-1.90) 98.9 (39.04-1.90)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.60 (at 1.89Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
R, R_{free}	0.170 , 0.203 0.164 , 0.197	Depositor DCC
R_{free} test set	7654 reflections (3.96%)	wwPDB-VP
Wilson B-factor (Å ²)	25.6	Xtriage
Anisotropy	0.492	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 58.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.037 for h,-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	14548	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.35% 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: CL, GD, GOL, HEM, ZN, H4B, CA, BTB, A1BTX

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	0.26	0/3318	0.46	0/4520
1	B	0.32	0/3324	0.50	0/4528
1	C	0.27	0/3322	0.46	0/4523
1	D	0.31	0/3348	0.50	0/4561
All	All	0.29	0/13312	0.48	0/18132

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3223	0	3129	16	0
1	B	3226	0	3134	22	0
1	C	3227	0	3138	20	0
1	D	3246	0	3159	25	0
2	A	43	0	30	2	0
2	B	43	0	30	2	0
2	C	43	0	30	1	0
2	D	43	0	30	2	0
3	A	17	0	15	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	17	0	15	1	0
3	C	17	0	15	0	0
3	D	17	0	15	1	0
4	A	32	0	0	0	0
4	B	32	0	0	0	0
4	C	32	0	0	1	0
4	D	32	0	0	1	0
5	A	14	0	19	2	0
5	B	28	0	36	6	0
5	C	14	0	19	2	0
5	D	42	0	55	13	0
6	A	18	0	24	0	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	2	0	0	0	0
8	B	1	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	1	0	0	0	0
10	C	1	0	0	0	0
11	A	246	0	0	2	0
11	B	307	0	0	3	0
11	C	235	0	0	3	0
11	D	312	0	0	3	0
All	All	14548	0	12933	101	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 4.

All (101) 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)
5:D:501:BTB:O3	11:D:601:HOH:O	2.05	0.74
1:D:119:ALA:HB1	1:D:122:GLN:HG2	1.69	0.73
1:B:321:GLU:OE2	5:B:504:BTB:O4	2.10	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:148:GLN:NE2	11:C:602:HOH:O	2.24	0.68
1:D:258:ASP:OD1	1:D:258:ASP:N	2.21	0.68
1:B:128:ARG:HG3	1:B:150:LEU:HD22	1.78	0.65
1:D:316:GLU:OE2	11:D:602:HOH:O	2.13	0.65
2:B:501:HEM:HBC2	2:B:501:HEM:HMC2	1.79	0.65
1:C:321:GLU:H	1:C:321:GLU:CD	2.04	0.65
1:B:285:ARG:NH1	11:B:601:HOH:O	2.25	0.62
1:A:128:ARG:NH2	11:A:603:HOH:O	2.31	0.61
1:D:321:GLU:OE2	5:D:505:BTB:O4	2.19	0.60
2:C:501:HEM:HBB2	2:C:501:HEM:HHC	1.82	0.60
1:B:290:PRO:HB3	1:B:304:LEU:HD23	1.83	0.59
5:D:505:BTB:O4	5:D:505:BTB:H82	2.03	0.59
1:D:143:SER:O	1:D:147:GLU:HG2	2.03	0.58
1:C:147:GLU:O	1:C:151:GLN:HG2	2.03	0.58
2:A:501:HEM:HBB2	2:A:501:HEM:HHC	1.86	0.58
1:A:200:ASP:OD1	1:A:200:ASP:N	2.32	0.57
1:C:89:GLN:NE2	11:C:605:HOH:O	2.35	0.57
1:A:89:GLN:HG3	1:A:90:GLN:H	1.69	0.57
1:B:474:ARG:NH2	11:B:604:HOH:O	2.37	0.56
2:A:501:HEM:HMC2	2:A:501:HEM:HBC2	1.88	0.55
2:D:502:HEM:HBB2	2:D:502:HEM:HHC	1.88	0.55
1:C:86:ALA:HA	1:D:97:ARG:HH22	1.72	0.54
1:A:124:LEU:HD21	1:A:154:GLU:HG2	1.91	0.53
1:D:247:GLN:HB2	1:D:250:ARG:HD3	1.91	0.53
1:B:258:ASP:OD1	1:B:258:ASP:N	2.36	0.52
1:B:298:GLU:CD	5:B:505:BTB:HO4	2.17	0.51
2:B:501:HEM:HHC	2:B:501:HEM:HBB2	1.92	0.51
1:B:247:GLN:HB2	1:B:250:ARG:HD3	1.94	0.50
5:B:504:BTB:O4	5:B:504:BTB:H82	2.12	0.49
1:B:298:GLU:OE1	5:B:505:BTB:O4	2.29	0.49
2:D:502:HEM:HMC2	2:D:502:HEM:HBC2	1.93	0.49
1:A:364:THR:O	1:A:368:CYS:HB2	2.12	0.49
1:B:90:GLN:HB2	1:B:468:PHE:CD2	2.48	0.49
1:C:279:TRP:HB2	1:C:302:LEU:HD11	1.94	0.49
1:C:86:ALA:O	1:D:97:ARG:NH2	2.46	0.48
5:C:504:BTB:H32	5:C:504:BTB:H51	1.65	0.48
1:A:479:PRO:HD2	1:A:480:TRP:CZ3	2.49	0.48
1:C:384:ASP:HB3	11:C:743:HOH:O	2.13	0.47
1:D:298:GLU:CD	5:D:506:BTB:H31	2.38	0.47
1:A:386:ASP:OD2	1:A:388:ARG:HG2	2.14	0.47
1:C:317:HIS:CG	1:C:318:PRO:HD2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:447:TRP:HA	3:D:503:H4B:N1	2.29	0.47
1:C:361:GLU:OE1	4:C:503:A1BTX:N07	2.48	0.47
1:D:128:ARG:HG3	1:D:150:LEU:HD22	1.96	0.47
1:D:388:ARG:HE	1:D:388:ARG:HB2	1.61	0.46
5:A:504:BTB:H11	5:A:504:BTB:H51	1.50	0.46
1:A:89:GLN:HG3	1:A:90:GLN:N	2.30	0.46
1:C:364:THR:O	1:C:368:CYS:HB2	2.15	0.46
5:D:501:BTB:H32	5:D:501:BTB:H51	1.81	0.46
1:D:290:PRO:HB3	1:D:304:LEU:HD23	1.98	0.46
1:A:124:LEU:O	1:A:128:ARG:HG3	2.16	0.45
1:A:202:ARG:HD2	1:A:206:GLU:OE2	2.16	0.45
5:B:505:BTB:H11	5:B:505:BTB:H51	1.67	0.45
1:D:321:GLU:CD	5:D:505:BTB:O4	2.59	0.45
1:B:143:SER:O	1:B:147:GLU:HG2	2.16	0.45
1:B:257:GLN:H	1:B:257:GLN:CD	2.23	0.45
1:B:447:TRP:HA	3:B:502:H4B:N1	2.32	0.45
1:D:364:THR:O	1:D:368:CYS:HB2	2.16	0.45
1:D:147:GLU:HG2	1:D:147:GLU:H	1.58	0.45
1:D:233:GLN:HB3	1:D:348:PHE:CE2	2.52	0.45
1:C:233:GLN:HB3	1:C:348:PHE:CE2	2.52	0.44
1:D:238:ARG:HG2	1:D:296:PRO:HB3	1.98	0.44
1:C:269:GLU:O	1:C:272:GLU:HG2	2.18	0.44
1:D:298:GLU:OE1	5:D:506:BTB:H42	2.17	0.44
1:B:122:GLN:H	1:B:122:GLN:HG2	1.59	0.44
1:B:298:GLU:OE2	1:B:298:GLU:HA	2.18	0.44
1:D:250:ARG:HD2	1:D:250:ARG:HA	1.78	0.44
1:B:90:GLN:NE2	11:B:618:HOH:O	2.51	0.43
1:B:119:ALA:HB1	1:B:122:GLN:HG3	2.00	0.43
1:B:250:ARG:HA	1:B:250:ARG:HD2	1.78	0.43
5:A:504:BTB:H72	5:A:504:BTB:H41	1.44	0.43
5:C:504:BTB:H41	5:C:504:BTB:H72	1.84	0.43
1:B:364:THR:O	1:B:368:CYS:HB2	2.18	0.43
1:C:124:LEU:HD11	1:C:154:GLU:HG2	2.00	0.42
1:C:97:ARG:CG	1:C:98:ARG:HG2	2.50	0.42
1:C:256:GLN:C	1:C:258:ASP:H	2.28	0.42
1:C:298:GLU:OE2	6:C:506:GOL:O3	2.38	0.42
1:A:447:TRP:HA	3:A:502:H4B:N1	2.35	0.42
1:B:178:TRP:CE3	1:B:190:TRP:HA	2.55	0.41
1:D:361:GLU:OE1	4:D:504:A1BTX:N07	2.53	0.41
5:D:501:BTB:H12	5:D:501:BTB:H72	1.59	0.41
1:D:326:LEU:HD12	5:D:501:BTB:H42	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:506:BTB:H11	5:D:506:BTB:H51	1.53	0.41
1:B:298:GLU:OE2	5:B:505:BTB:H81	2.20	0.41
1:D:238:ARG:NE	11:D:615:HOH:O	2.50	0.41
5:D:506:BTB:H42	5:D:506:BTB:H72	1.44	0.41
1:A:384:ASP:OD1	5:D:501:BTB:O3	2.39	0.41
1:C:67:LYS:HE2	1:C:67:LYS:HB3	1.81	0.41
1:C:245:ASN:OD1	1:C:245:ASN:N	2.53	0.41
1:D:178:TRP:CE3	1:D:190:TRP:HA	2.56	0.41
1:D:301:GLU:HB3	1:D:303:PHE:CE1	2.56	0.41
1:A:70:ARG:NE	11:A:613:HOH:O	2.53	0.41
5:D:505:BTB:H72	5:D:505:BTB:H11	1.75	0.41
1:B:124:LEU:HD23	1:B:124:LEU:HA	1.95	0.40
1:C:449:VAL:HA	1:C:450:PRO:HD3	1.95	0.40
1:A:470:SER:HA	1:A:471:PRO:C	2.45	0.40
1:A:89:GLN:OE1	1:A:468:PHE:HE2	2.05	0.40
1:A:306:PRO:HA	1:A:307:PRO:HD3	1.97	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	400/440 (91%)	391 (98%)	9 (2%)	0	100	100
1	B	401/440 (91%)	395 (98%)	5 (1%)	1 (0%)	44	36
1	C	400/440 (91%)	389 (97%)	11 (3%)	0	100	100
1	D	404/440 (92%)	395 (98%)	9 (2%)	0	100	100
All	All	1605/1760 (91%)	1570 (98%)	34 (2%)	1 (0%)	48	41

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	257	GLN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	343/373 (92%)	325 (95%)	18 (5%)	19	12
1	B	344/373 (92%)	334 (97%)	10 (3%)	37	31
1	C	344/373 (92%)	332 (96%)	12 (4%)	31	24
1	D	347/373 (93%)	339 (98%)	8 (2%)	45	41
All	All	1378/1492 (92%)	1330 (96%)	48 (4%)	31	24

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	87	GLN
1	A	89	GLN
1	A	107	ARG
1	A	108	LYS
1	A	124	LEU
1	A	139	LYS
1	A	140	ARG
1	A	144	GLN
1	A	147	GLU
1	A	200	ASP
1	A	202	ARG
1	A	216	LYS
1	A	238	ARG
1	A	257	GLN
1	A	291	LEU
1	A	309	LEU
1	A	321	GLU
1	A	329	ARG
1	B	122	GLN
1	B	128	ARG
1	B	224	LEU

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Mol	Chain	Res	Type
1	B	257	GLN
1	B	298	GLU
1	B	309	LEU
1	B	326	LEU
1	B	329	ARG
1	B	389	THR
1	B	429	LYS
1	C	87	GLN
1	C	128	ARG
1	C	139	LYS
1	C	151	GLN
1	C	202	ARG
1	C	216	LYS
1	C	238	ARG
1	C	291	LEU
1	C	309	LEU
1	C	321	GLU
1	C	329	ARG
1	C	342	GLU
1	D	122	GLN
1	D	128	ARG
1	D	147	GLU
1	D	257	GLN
1	D	258	ASP
1	D	276	GLN
1	D	309	LEU
1	D	326	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	144	GLN
1	A	213	ASN
1	C	87	GLN
1	C	89	GLN
1	C	256	GLN
1	C	435	GLN
1	D	122	GLN
1	D	408	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 39 ligands modelled in this entry, 12 are monoatomic - leaving 27 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	$\# Z > 2$
3	H4B	B	502	-	16,18,18	0.91	0	14,26,26	2.49	5 (35%)
6	GOL	D	507	-	5,5,5	0.35	0	5,5,5	0.40	0
2	HEM	A	501	1	42,50,50	1.58	6 (14%)	46,82,82	1.80	11 (23%)
4	A1BTX	D	504	-	31,35,35	1.22	3 (9%)	29,46,46	2.21	3 (10%)
2	HEM	C	501	1	42,50,50	1.53	4 (9%)	46,82,82	1.63	10 (21%)
5	BTB	C	504	8	13,13,13	0.46	0	7,16,16	0.82	0
6	GOL	A	505	-	5,5,5	0.35	0	5,5,5	0.55	0
6	GOL	C	506	-	5,5,5	0.39	0	5,5,5	0.28	0
6	GOL	A	507	-	5,5,5	0.35	0	5,5,5	0.56	0
2	HEM	B	501	1	42,50,50	1.57	6 (14%)	46,82,82	1.63	8 (17%)
5	BTB	B	504	8	13,13,13	0.49	0	7,16,16	0.88	1 (14%)
2	HEM	D	502	1	42,50,50	1.49	8 (19%)	46,82,82	1.64	6 (13%)
5	BTB	D	505	8	13,13,13	0.45	0	7,16,16	1.00	1 (14%)
6	GOL	B	506	-	5,5,5	0.40	0	5,5,5	0.36	0
3	H4B	A	502	-	16,18,18	0.94	0	14,26,26	2.59	6 (42%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	H4B	C	502	-	16,18,18	0.82	0	14,26,26	2.41	6 (42%)
5	BTB	A	504	-	13,13,13	0.62	0	7,16,16	1.26	0
6	GOL	C	505	-	5,5,5	0.35	0	5,5,5	0.43	0
4	A1BTX	B	503	-	31,35,35	1.30	6 (19%)	29,46,46	2.26	5 (17%)
3	H4B	D	503	-	16,18,18	0.97	0	14,26,26	2.62	5 (35%)
4	A1BTX	A	503	-	31,35,35	1.29	6 (19%)	29,46,46	2.17	5 (17%)
4	A1BTX	C	503	-	31,35,35	1.27	6 (19%)	29,46,46	2.20	5 (17%)
5	BTB	B	505	-	13,13,13	0.65	0	7,16,16	1.48	3 (42%)
5	BTB	D	506	-	13,13,13	0.76	1 (7%)	7,16,16	1.25	0
6	GOL	A	506	-	5,5,5	0.37	0	5,5,5	0.48	0
5	BTB	D	501	8	13,13,13	0.48	0	7,16,16	1.01	1 (14%)
6	GOL	C	507	-	5,5,5	0.35	0	5,5,5	0.40	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
3	H4B	B	502	-	-	0/8/17/17	0/2/2/2
6	GOL	D	507	-	-	2/4/4/4	-
2	HEM	A	501	1	-	0/12/54/54	-
4	A1BTX	D	504	-	-	2/15/23/23	0/4/4/4
2	HEM	C	501	1	-	1/12/54/54	-
5	BTB	C	504	8	-	0/21/21/21	-
6	GOL	A	505	-	-	3/4/4/4	-
6	GOL	C	506	-	-	2/4/4/4	-
6	GOL	A	507	-	-	2/4/4/4	-
2	HEM	B	501	1	-	0/12/54/54	-
5	BTB	B	504	8	-	3/21/21/21	-
2	HEM	D	502	1	-	0/12/54/54	-
5	BTB	D	505	8	-	8/21/21/21	-
6	GOL	B	506	-	-	0/4/4/4	-
3	H4B	A	502	-	-	0/8/17/17	0/2/2/2
3	H4B	C	502	-	-	0/8/17/17	0/2/2/2
5	BTB	A	504	-	-	8/21/21/21	-
6	GOL	C	505	-	-	2/4/4/4	-
4	A1BTX	B	503	-	-	1/15/23/23	0/4/4/4
3	H4B	D	503	-	-	0/8/17/17	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	A1BTX	A	503	-	-	5/15/23/23	0/4/4/4
4	A1BTX	C	503	-	-	5/15/23/23	0/4/4/4
5	BTB	B	505	-	-	10/21/21/21	-
5	BTB	D	506	-	-	15/21/21/21	-
6	GOL	A	506	-	-	2/4/4/4	-
5	BTB	D	501	8	-	6/21/21/21	-
6	GOL	C	507	-	-	3/4/4/4	-

All (46) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	HEM	C3C-C2C	-4.01	1.34	1.40
2	B	501	HEM	C3C-C2C	-3.89	1.35	1.40
2	C	501	HEM	C3C-C2C	-3.77	1.35	1.40
2	A	501	HEM	C3C-C4C	3.67	1.46	1.41
2	C	501	HEM	C3C-CAC	3.58	1.55	1.47
2	B	501	HEM	C3C-C4C	3.45	1.46	1.41
4	D	504	A1BTX	C35-C28	3.44	1.50	1.46
4	B	503	A1BTX	C35-C28	3.39	1.50	1.46
2	D	502	HEM	C3C-C2C	-3.30	1.35	1.40
2	A	501	HEM	C3C-CAC	3.28	1.55	1.47
2	B	501	HEM	C3C-CAC	3.28	1.55	1.47
2	D	502	HEM	CAB-C3B	3.28	1.56	1.47
2	A	501	HEM	CAB-C3B	3.08	1.55	1.47
2	C	501	HEM	CAB-C3B	3.05	1.55	1.47
4	A	503	A1BTX	C35-C28	3.02	1.50	1.46
4	A	503	A1BTX	C05-C06	3.01	1.50	1.46
2	D	502	HEM	C3C-C4C	3.00	1.45	1.41
4	B	503	A1BTX	C06-N07	-2.98	1.33	1.38
2	C	501	HEM	C3C-C4C	2.96	1.45	1.41
4	D	504	A1BTX	C06-N07	-2.91	1.33	1.38
2	B	501	HEM	CAB-C3B	2.89	1.55	1.47
2	D	502	HEM	C3C-CAC	2.83	1.54	1.47
4	C	503	A1BTX	C25-N27	-2.82	1.36	1.41
4	C	503	A1BTX	C06-N07	-2.79	1.33	1.38
4	C	503	A1BTX	C28-N27	-2.76	1.33	1.38
4	B	503	A1BTX	C05-C06	2.74	1.49	1.46
4	A	503	A1BTX	C11-N07	-2.74	1.36	1.41
4	C	503	A1BTX	C35-C28	2.66	1.49	1.46
4	C	503	A1BTX	C05-C06	2.59	1.49	1.46
4	A	503	A1BTX	C06-N07	-2.59	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	503	A1BTX	C04-C05	2.58	1.42	1.37
2	A	501	HEM	FE-ND	2.55	2.12	1.98
2	D	502	HEM	CMD-C2D	2.53	1.56	1.50
4	A	503	A1BTX	C25-N27	-2.52	1.36	1.41
4	A	503	A1BTX	C28-N27	-2.50	1.34	1.38
2	B	501	HEM	CMD-C2D	2.48	1.55	1.50
4	C	503	A1BTX	C11-N07	-2.44	1.36	1.41
2	A	501	HEM	CMB-C2B	2.33	1.55	1.50
4	D	504	A1BTX	C25-N27	-2.28	1.37	1.41
4	B	503	A1BTX	C11-N07	-2.26	1.37	1.41
2	B	501	HEM	FE-NB	2.19	2.10	1.98
2	D	502	HEM	CMA-C3A	2.15	1.55	1.51
2	D	502	HEM	CMB-C2B	2.14	1.55	1.50
5	D	506	BTB	C3-C2	-2.14	1.50	1.53
4	B	503	A1BTX	C25-N27	-2.13	1.37	1.41
2	D	502	HEM	C3D-C2D	-2.06	1.32	1.36

All (81) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	504	A1BTX	C04-N03-C02	8.42	119.04	105.72
4	B	503	A1BTX	C04-N03-C02	7.91	118.24	105.72
4	A	503	A1BTX	C04-N03-C02	7.67	117.86	105.72
4	C	503	A1BTX	C04-N03-C02	7.48	117.55	105.72
4	A	503	A1BTX	C34-N33-C32	7.04	116.85	105.72
4	C	503	A1BTX	C34-N33-C32	6.98	116.76	105.72
4	D	504	A1BTX	C34-N33-C32	6.94	116.70	105.72
4	B	503	A1BTX	C34-N33-C32	6.70	116.32	105.72
2	A	501	HEM	CBA-CAA-C2A	-5.77	102.84	112.54
2	B	501	HEM	CBA-CAA-C2A	-5.70	102.96	112.54
3	D	503	H4B	C8A-C4A-C4	5.60	119.60	114.50
3	B	502	H4B	C8A-C4A-C4	5.57	119.57	114.50
3	A	502	H4B	C8A-C4A-C4	5.48	119.48	114.50
3	C	502	H4B	C8A-C4A-C4	5.30	119.32	114.50
2	D	502	HEM	CBA-CAA-C2A	-4.98	104.17	112.54
3	A	502	H4B	C2-N3-C4	4.42	122.11	115.96
2	D	502	HEM	C4B-CHC-C1C	4.42	128.38	122.56
3	D	503	H4B	C2-N3-C4	4.15	121.73	115.96
3	A	502	H4B	N1-C2-N3	-4.13	119.14	125.48
3	C	502	H4B	C2-N3-C4	4.10	121.67	115.96
2	A	501	HEM	C4B-CHC-C1C	4.05	127.91	122.56
2	C	501	HEM	C4B-CHC-C1C	4.05	127.90	122.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	503	H4B	N1-C2-N3	-4.01	119.34	125.48
2	C	501	HEM	CBA-CAA-C2A	-3.90	105.98	112.54
3	B	502	H4B	C2-N3-C4	3.58	120.94	115.96
3	C	502	H4B	N1-C2-N3	-3.54	120.06	125.48
2	A	501	HEM	CMA-C3A-C4A	-3.54	123.28	128.46
2	C	501	HEM	C3B-C2B-C1B	3.35	108.93	106.41
2	B	501	HEM	C4B-CHC-C1C	3.34	126.97	122.56
3	B	502	H4B	N1-C2-N3	-3.26	120.49	125.48
4	B	503	A1BTX	C35-C34-N33	3.12	115.07	108.95
4	B	503	A1BTX	C25-N27-C28	3.02	135.37	128.41
3	B	502	H4B	O10-C10-C9	-3.01	104.78	109.77
4	C	503	A1BTX	C25-N27-C28	-2.95	121.62	128.41
2	B	501	HEM	C3B-C2B-C1B	2.84	108.55	106.41
2	A	501	HEM	CBD-CAD-C3D	-2.80	104.80	112.53
4	C	503	A1BTX	C15-C17-N18	-2.70	104.29	112.79
3	A	502	H4B	N2-C2-N1	2.66	121.21	117.22
3	D	503	H4B	C2-N1-C8A	2.66	120.92	114.59
3	A	502	H4B	C2-N1-C8A	2.62	120.81	114.59
2	A	501	HEM	C4D-ND-C1D	2.59	108.27	105.21
2	A	501	HEM	C3D-C4D-ND	-2.57	107.36	110.17
4	D	504	A1BTX	C35-C34-N33	2.55	113.96	108.95
3	D	503	H4B	N2-C2-N1	2.55	121.04	117.22
2	C	501	HEM	C4D-ND-C1D	2.53	108.20	105.21
2	C	501	HEM	C1B-NB-C4B	2.52	108.19	105.21
2	B	501	HEM	C4C-CHD-C1D	2.52	125.88	122.56
2	D	502	HEM	CMA-C3A-C4A	-2.50	124.79	128.46
5	D	505	BTB	O3-C3-C2	-2.49	105.54	111.40
2	C	501	HEM	CBD-CAD-C3D	-2.49	105.66	112.53
2	C	501	HEM	C3B-C4B-NB	-2.48	107.69	109.47
2	B	501	HEM	C4D-ND-C1D	2.47	108.13	105.21
2	B	501	HEM	CMA-C3A-C4A	-2.43	124.90	128.46
2	A	501	HEM	C3B-C2B-C1B	2.42	108.23	106.41
4	A	503	A1BTX	C35-C34-N33	2.41	113.67	108.95
3	B	502	H4B	C2-N1-C8A	2.37	120.22	114.59
2	A	501	HEM	CMC-C2C-C3C	2.36	129.39	124.68
2	D	502	HEM	C3B-C2B-C1B	2.34	108.17	106.41
2	D	502	HEM	CHD-C1D-ND	2.32	126.93	124.44
3	C	502	H4B	C2-N1-C8A	2.30	120.06	114.59
5	B	505	BTB	O3-C3-C2	-2.26	106.10	111.40
5	B	505	BTB	O4-C4-C2	2.22	116.63	111.40
2	A	501	HEM	C3B-C4B-NB	-2.21	107.88	109.47
5	B	504	BTB	O1-C1-C2	-2.20	106.22	111.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	501	HEM	CMA-C3A-C4A	-2.20	125.24	128.46
4	A	503	A1BTX	C15-C17-N18	-2.17	105.95	112.79
4	C	503	A1BTX	C35-C34-N33	2.17	113.20	108.95
4	B	503	A1BTX	C15-C17-N18	-2.16	105.99	112.79
4	A	503	A1BTX	C11-N07-C06	-2.14	123.50	128.41
3	C	502	H4B	N2-C2-N1	2.13	120.42	117.22
2	D	502	HEM	CMC-C2C-C3C	2.11	128.90	124.68
2	A	501	HEM	C4C-CHD-C1D	2.11	125.34	122.56
2	C	501	HEM	C3D-C4D-ND	-2.08	107.89	110.17
5	B	505	BTB	O1-C1-C2	-2.08	106.52	111.40
2	B	501	HEM	CMC-C2C-C3C	2.06	128.79	124.68
2	B	501	HEM	C3D-C4D-ND	-2.04	107.94	110.17
3	C	502	H4B	C4A-C4-N3	-2.02	118.80	123.91
2	C	501	HEM	C2B-C1B-NB	-2.02	107.52	109.84
5	D	501	BTB	O3-C3-C2	2.01	116.13	111.40
3	A	502	H4B	C4A-C4-N3	-2.01	118.84	123.91
2	A	501	HEM	CMA-C3A-C2A	2.01	128.73	124.94

There are no chirality outliers.

All (80) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	503	A1BTX	N18-C19-C20-C21
4	A	503	A1BTX	C35-C28-N27-C25
4	A	503	A1BTX	N29-C28-N27-C25
4	C	503	A1BTX	C35-C28-N27-C25
4	C	503	A1BTX	N29-C28-N27-C25
4	D	504	A1BTX	N29-C28-N27-C25
5	A	504	BTB	C1-C2-N-C5
5	A	504	BTB	C4-C2-N-C5
5	A	504	BTB	C4-C2-N-C7
5	B	504	BTB	C1-C2-C4-O4
5	B	504	BTB	C3-C2-C4-O4
5	B	504	BTB	N-C2-C4-O4
5	B	505	BTB	C1-C2-C3-O3
5	B	505	BTB	C4-C2-C3-O3
5	B	505	BTB	N-C2-C3-O3
5	B	505	BTB	C1-C2-N-C5
5	B	505	BTB	C1-C2-N-C7
5	B	505	BTB	C3-C2-N-C5
5	B	505	BTB	C3-C2-N-C7
5	B	505	BTB	C4-C2-N-C5

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Mol	Chain	Res	Type	Atoms
5	B	505	BTB	C4-C2-N-C7
5	D	501	BTB	C1-C2-C4-O4
5	D	501	BTB	C3-C2-C4-O4
5	D	501	BTB	N-C2-C4-O4
5	D	505	BTB	C1-C2-C4-O4
5	D	505	BTB	C3-C2-C4-O4
5	D	505	BTB	N-C2-C4-O4
5	D	505	BTB	C1-C2-N-C5
5	D	505	BTB	C3-C2-N-C5
5	D	505	BTB	C4-C2-N-C5
5	D	506	BTB	C1-C2-C3-O3
5	D	506	BTB	N-C2-C3-O3
5	D	506	BTB	C3-C2-C4-O4
5	D	506	BTB	N-C2-C4-O4
5	D	506	BTB	C1-C2-N-C5
5	D	506	BTB	C1-C2-N-C7
5	D	506	BTB	C3-C2-N-C5
5	D	506	BTB	C3-C2-N-C7
5	D	506	BTB	C4-C2-N-C5
5	D	506	BTB	C4-C2-N-C7
6	A	505	GOL	O1-C1-C2-C3
6	A	506	GOL	O1-C1-C2-O2
6	A	506	GOL	O1-C1-C2-C3
6	A	507	GOL	O1-C1-C2-C3
6	C	505	GOL	O1-C1-C2-C3
6	C	507	GOL	O1-C1-C2-O2
6	C	507	GOL	O1-C1-C2-C3
6	D	507	GOL	O1-C1-C2-C3
5	D	506	BTB	N-C5-C6-O6
5	A	504	BTB	N-C7-C8-O8
4	D	504	A1BTX	C15-C17-N18-C19
6	C	506	GOL	C1-C2-C3-O3
5	B	505	BTB	N-C5-C6-O6
5	D	506	BTB	N-C7-C8-O8
6	A	507	GOL	O1-C1-C2-O2
6	C	505	GOL	O1-C1-C2-O2
6	D	507	GOL	O1-C1-C2-O2
6	A	505	GOL	O1-C1-C2-O2
5	A	504	BTB	N-C5-C6-O6
5	D	501	BTB	N-C5-C6-O6
5	D	506	BTB	C4-C2-C3-O3
6	A	505	GOL	O2-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
6	C	506	GOL	O2-C2-C3-O3
2	C	501	HEM	C2A-CAA-CBA-CGA
5	D	501	BTB	N-C7-C8-O8
4	C	503	A1BTX	N18-C19-C20-C21
5	A	504	BTB	C3-C2-N-C5
5	A	504	BTB	C3-C2-N-C7
5	D	505	BTB	C1-C2-N-C7
5	D	505	BTB	C4-C2-N-C7
5	D	506	BTB	O1-C1-C2-N
4	A	503	A1BTX	C26-C25-N27-C28
5	D	506	BTB	C1-C2-C4-O4
4	C	503	A1BTX	C26-C25-N27-C28
4	A	503	A1BTX	C24-C25-N27-C28
4	C	503	A1BTX	C24-C25-N27-C28
6	C	507	GOL	O2-C2-C3-O3
4	B	503	A1BTX	N18-C19-C20-C21
5	A	504	BTB	C1-C2-N-C7
5	D	501	BTB	O1-C1-C2-N

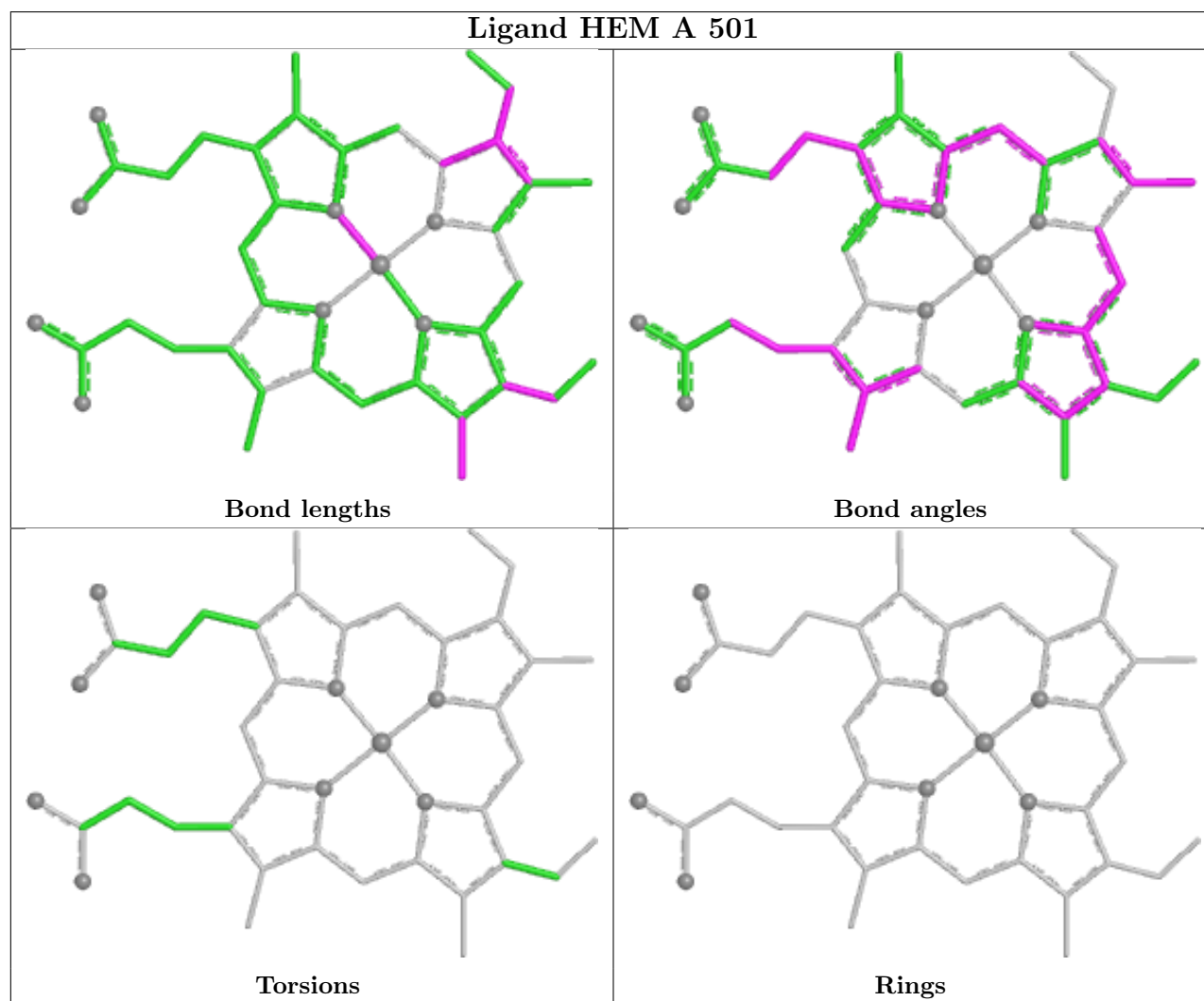
There are no ring outliers.

17 monomers are involved in 36 short contacts:

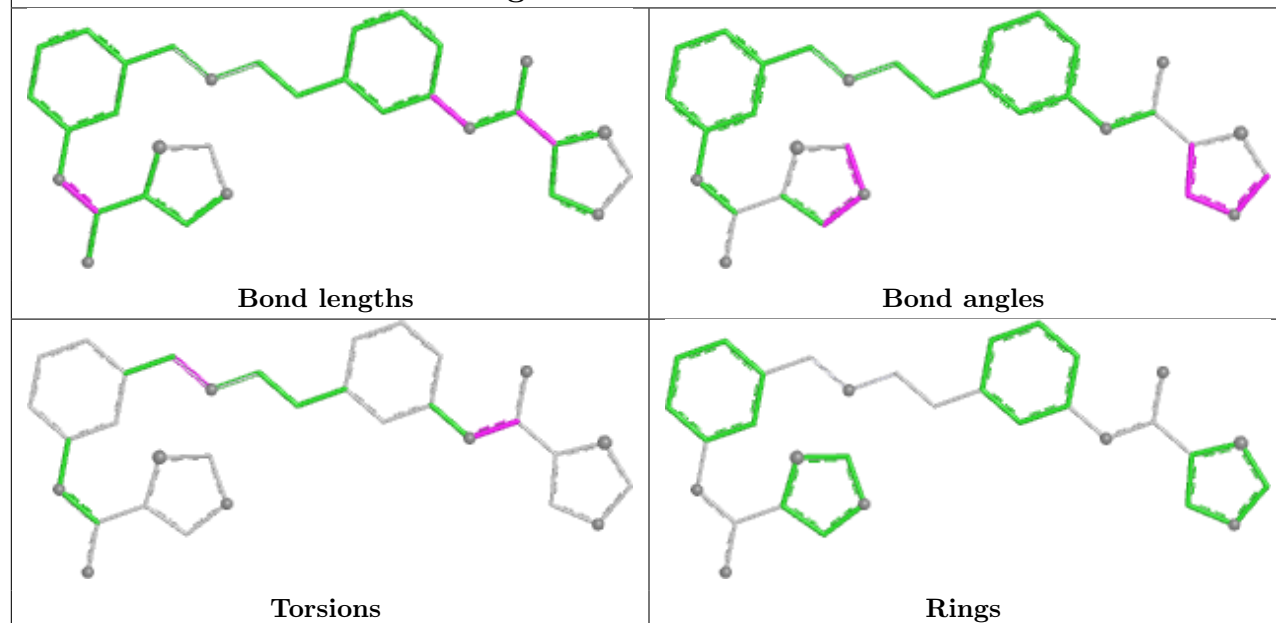
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	502	H4B	1	0
2	A	501	HEM	2	0
4	D	504	A1BTX	1	0
2	C	501	HEM	1	0
5	C	504	BTB	2	0
6	C	506	GOL	1	0
2	B	501	HEM	2	0
5	B	504	BTB	2	0
2	D	502	HEM	2	0
5	D	505	BTB	4	0
3	A	502	H4B	1	0
5	A	504	BTB	2	0
3	D	503	H4B	1	0
4	C	503	A1BTX	1	0
5	B	505	BTB	4	0
5	D	506	BTB	4	0
5	D	501	BTB	5	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

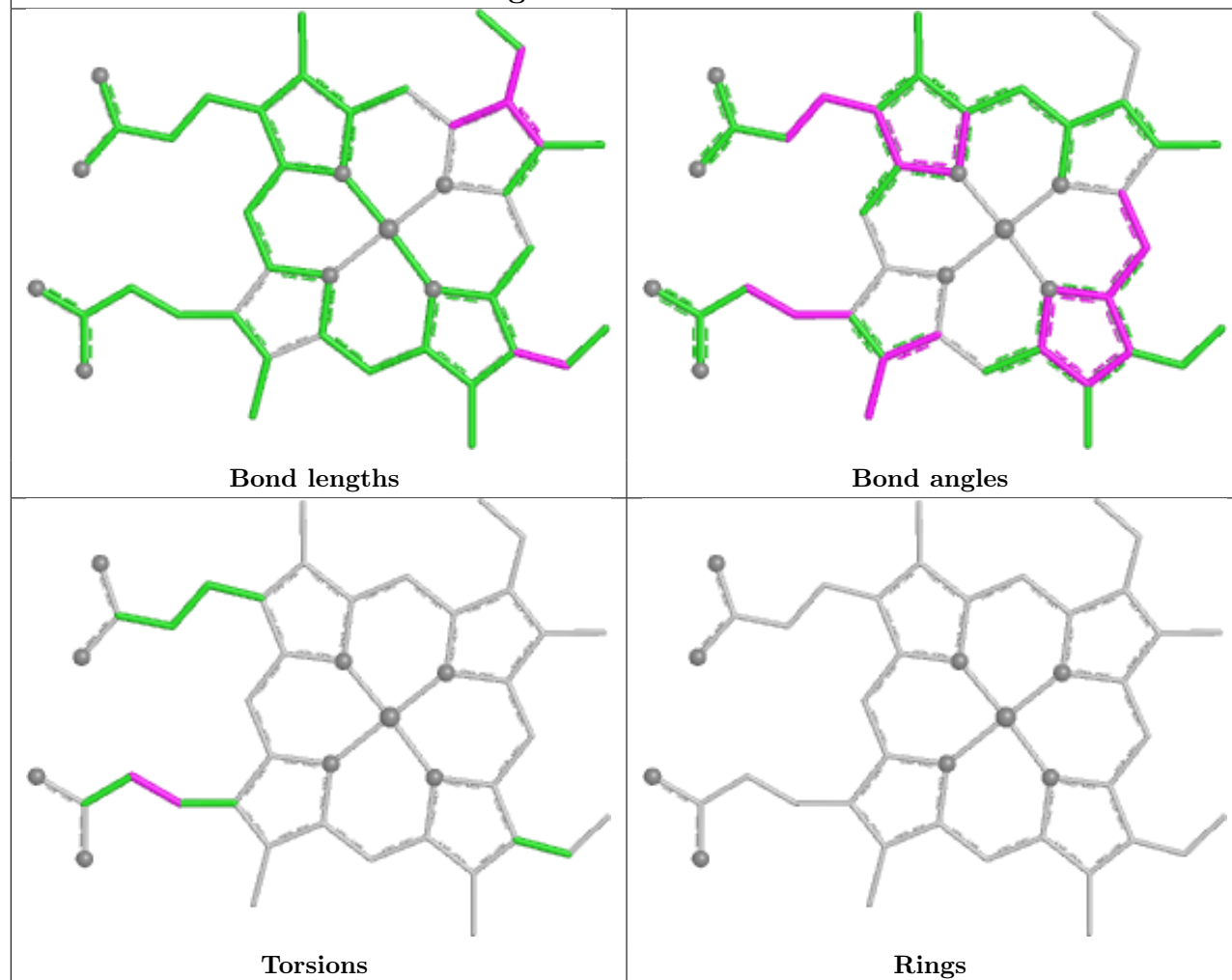
bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 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.

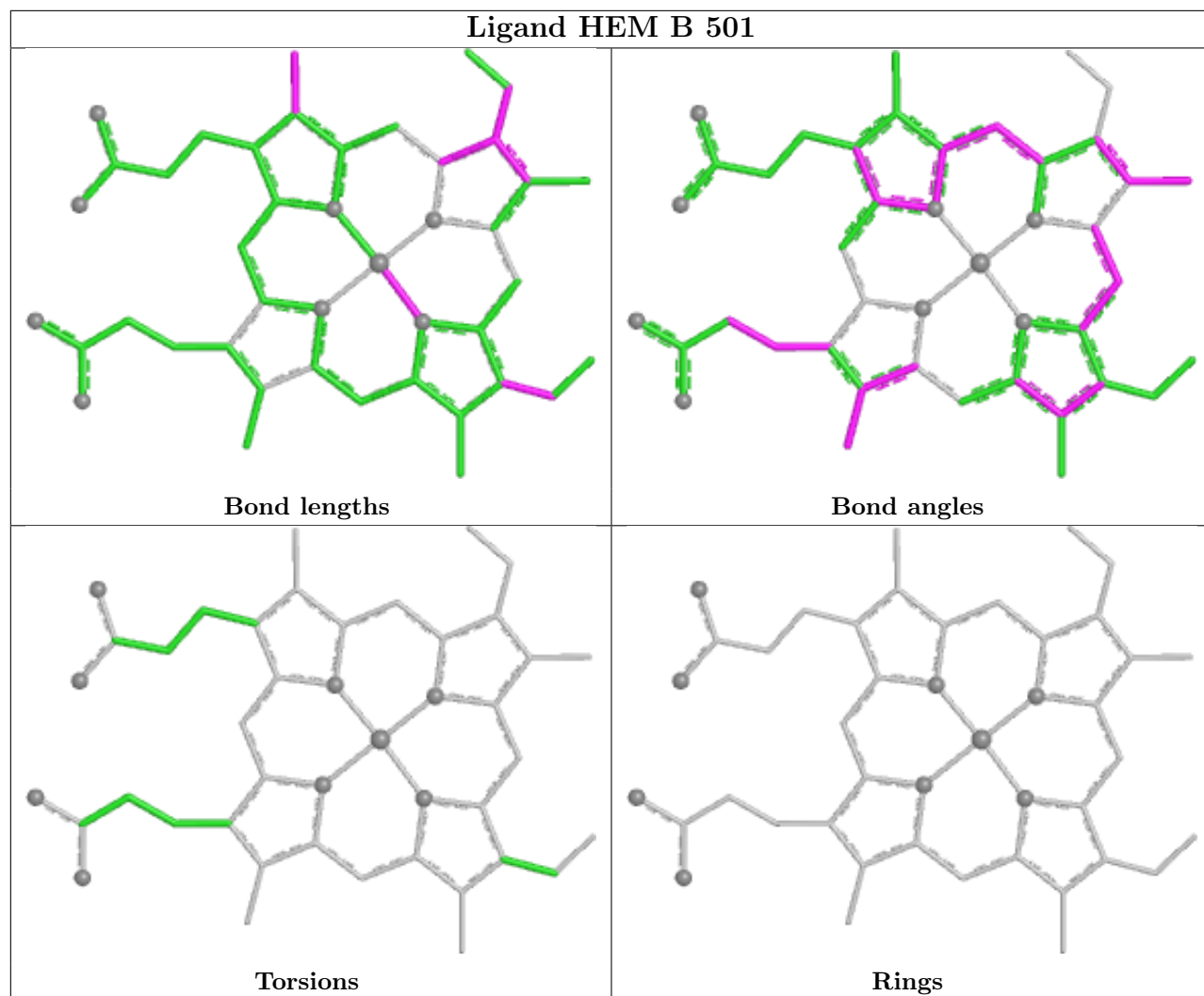


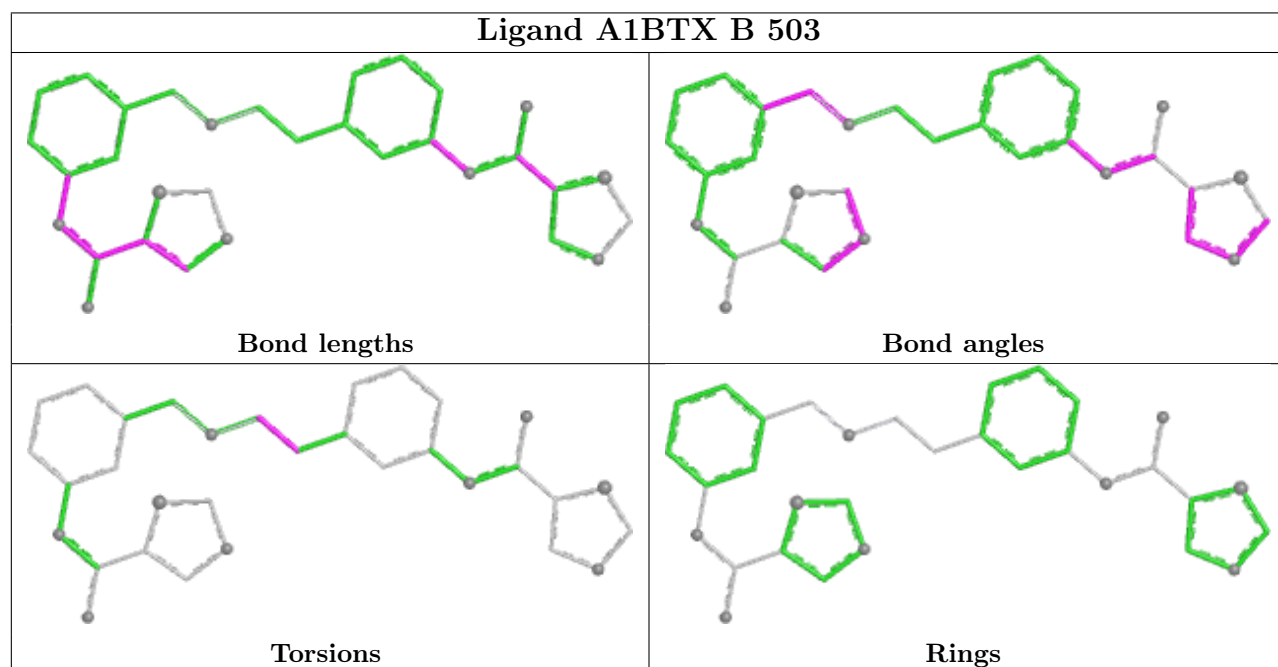
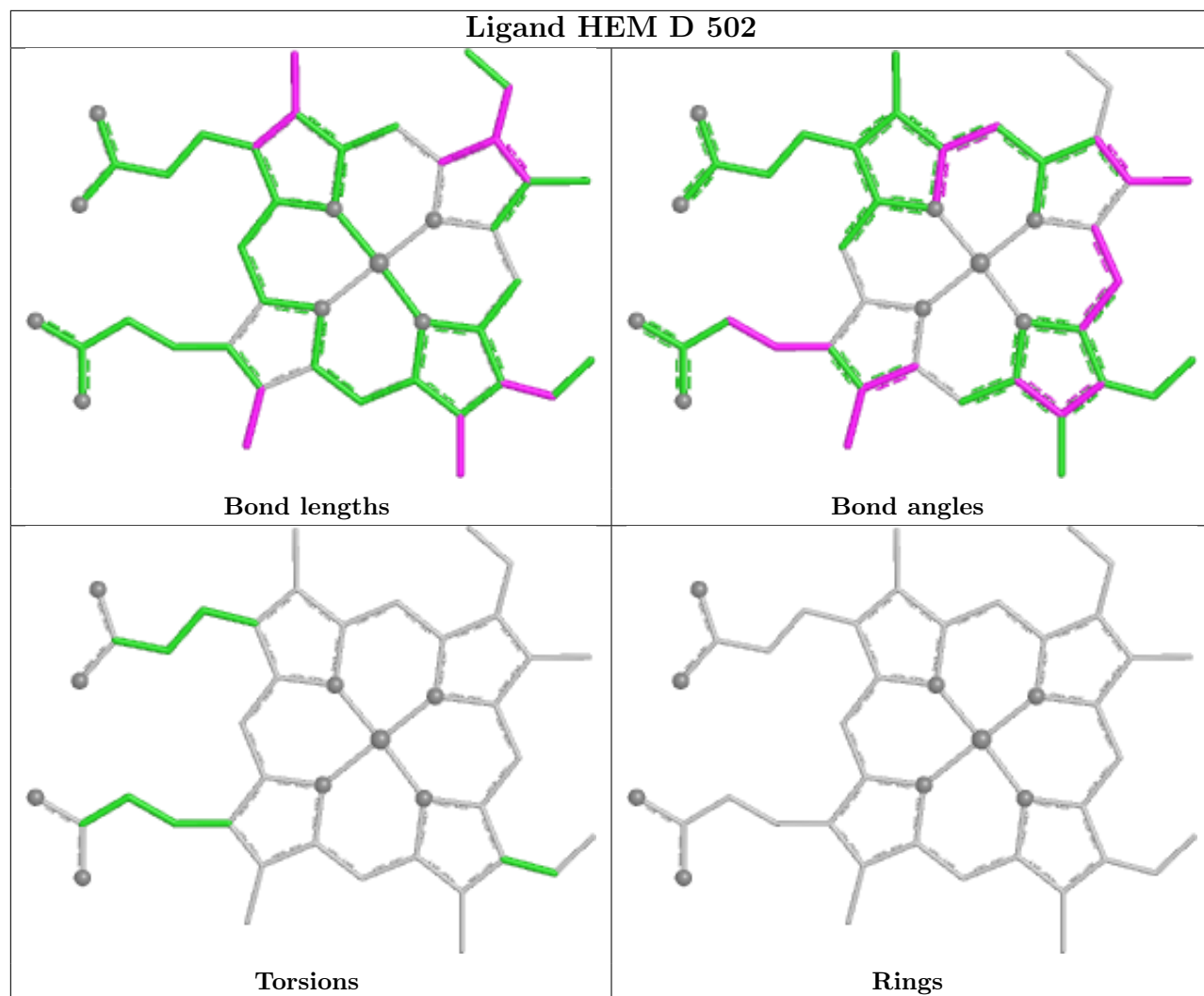
Ligand A1BTX D 504

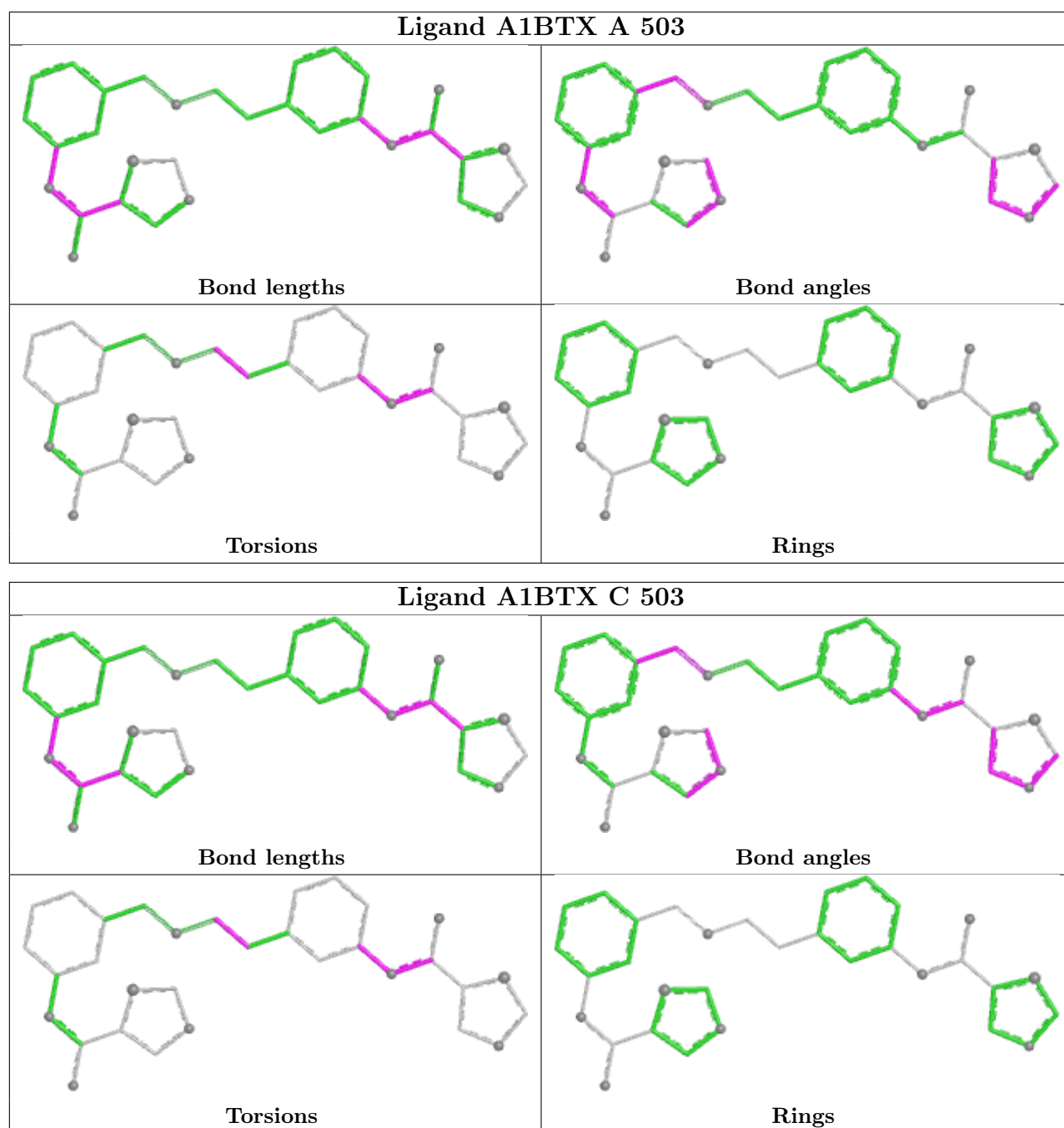


Ligand HEM C 501









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

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	403/440 (91%)	0.01	10 (2%) 58 60	16, 36, 76, 118	1 (0%)
1	B	403/440 (91%)	-0.42	6 (1%) 71 74	14, 26, 53, 108	2 (0%)
1	C	403/440 (91%)	-0.08	3 (0%) 84 86	16, 35, 70, 109	1 (0%)
1	D	405/440 (92%)	-0.36	5 (1%) 76 78	15, 27, 57, 120	3 (0%)
All	All	1614/1760 (91%)	-0.21	24 (1%) 71 74	14, 31, 69, 120	7 (0%)

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	120	PRO	5.4
1	D	257	GLN	4.6
1	B	108	LYS	3.9
1	D	118	PRO	3.5
1	B	119	ALA	3.3
1	A	155	ALA	3.3
1	A	119	ALA	3.1
1	A	257	GLN	2.6
1	A	236	PRO	2.6
1	A	158	ALA	2.6
1	B	257	GLN	2.5
1	D	259	GLY	2.4
1	D	258	ASP	2.4
1	A	89	GLN	2.4
1	A	124	LEU	2.4
1	B	90	GLN	2.3
1	A	468	PHE	2.2
1	A	202	ARG	2.2
1	C	204	ALA	2.2
1	B	107	ARG	2.2
1	C	107	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	90	GLN	2.1
1	B	89	GLN	2.0
1	A	388	ARG	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
6	GOL	A	506	6/6	0.61	0.17	74,77,81,82	0
6	GOL	A	505	6/6	0.66	0.17	65,73,75,84	0
5	BTB	B	505	14/14	0.70	0.20	62,76,80,82	0
6	GOL	C	506	6/6	0.71	0.14	68,73,77,79	0
6	GOL	C	507	6/6	0.71	0.17	64,68,73,74	0
5	BTB	C	504	14/14	0.75	0.18	63,72,78,78	0
5	BTB	D	506	14/14	0.75	0.17	37,62,73,79	0
5	BTB	A	504	14/14	0.77	0.18	44,66,75,78	0
6	GOL	B	506	6/6	0.77	0.21	53,61,64,64	0
6	GOL	C	505	6/6	0.79	0.15	47,56,77,85	0
5	BTB	B	504	14/14	0.82	0.19	43,58,84,92	0
5	BTB	D	505	14/14	0.85	0.15	39,45,58,64	0
6	GOL	A	507	6/6	0.85	0.20	65,68,72,72	0
6	GOL	D	507	6/6	0.86	0.20	59,63,66,69	0
4	A1BTX	A	503	32/32	0.90	0.14	15,49,109,119	0
3	H4B	A	502	17/17	0.92	0.09	26,43,48,49	0
4	A1BTX	C	503	32/32	0.92	0.14	11,49,112,119	0
3	H4B	C	502	17/17	0.92	0.09	41,46,51,54	0
3	H4B	D	503	17/17	0.92	0.08	19,33,39,42	0
3	H4B	B	502	17/17	0.93	0.07	24,31,36,37	0

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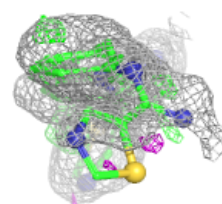
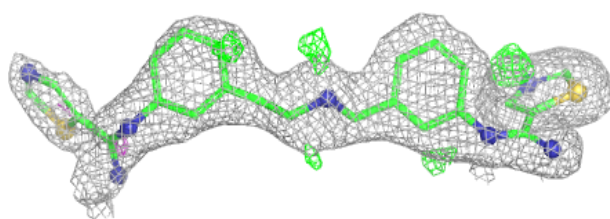
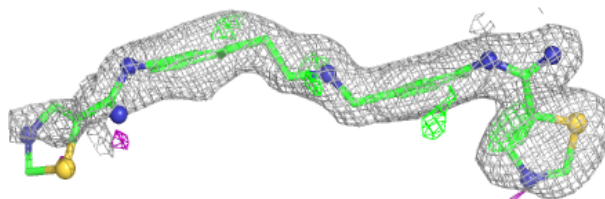
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	BTB	D	501	14/14	0.93	0.13	16,70,81,83	0
8	GD	A	509	1/1	0.93	0.17	96,96,96,96	0
4	A1BTX	D	504	32/32	0.94	0.12	5,40,106,111	0
4	A1BTX	B	503	32/32	0.95	0.10	3,39,109,111	0
10	CA	C	510	1/1	0.96	0.05	32,32,32,32	0
10	CA	B	509	1/1	0.97	0.05	30,30,30,30	0
8	GD	A	511	1/1	0.97	0.18	84,84,84,84	0
2	HEM	C	501	43/43	0.98	0.06	16,26,45,47	0
2	HEM	A	501	43/43	0.98	0.06	19,24,45,48	0
8	GD	B	508	1/1	0.98	0.04	33,33,33,33	0
8	GD	D	509	1/1	0.98	0.04	33,33,33,33	0
7	CL	B	507	1/1	0.98	0.08	35,35,35,35	0
7	CL	C	508	1/1	0.98	0.06	40,40,40,40	0
2	HEM	B	501	43/43	0.99	0.05	13,17,34,38	0
7	CL	D	508	1/1	0.99	0.07	33,33,33,33	0
7	CL	A	508	1/1	0.99	0.05	42,42,42,42	0
2	HEM	D	502	43/43	0.99	0.05	13,18,36,39	0
9	ZN	A	510	1/1	1.00	0.01	23,23,23,23	0
9	ZN	C	509	1/1	1.00	0.02	26,26,26,26	0

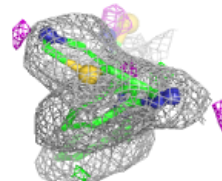
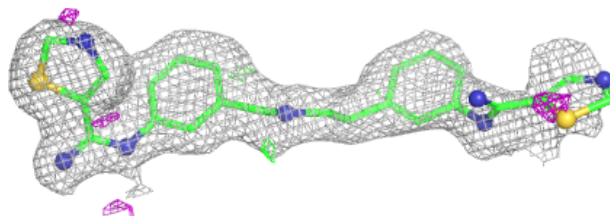
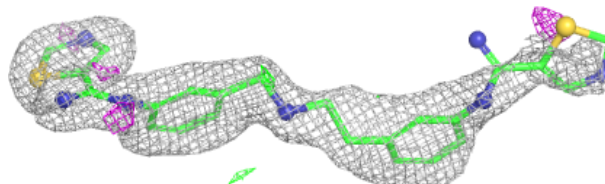
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around A1BTX 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)

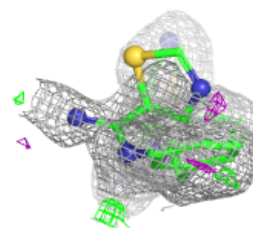
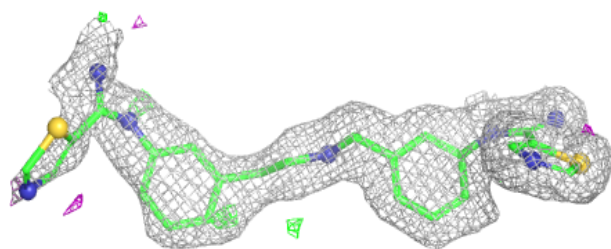
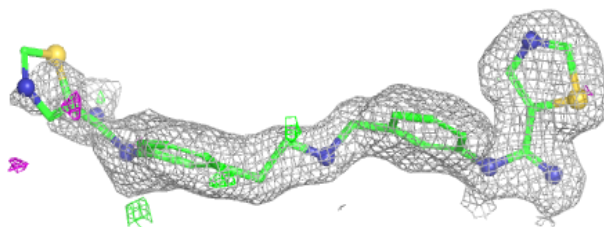
**Electron density around A1BTX C 503:**

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

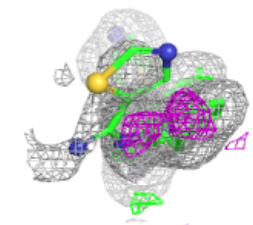
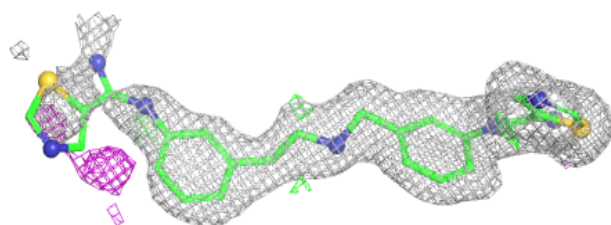
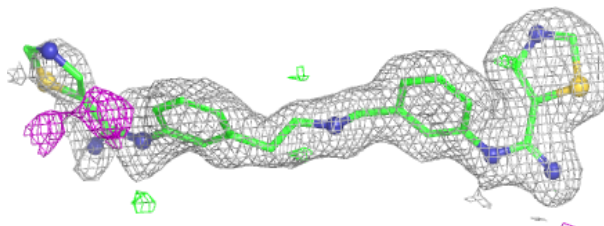


Electron density around A1BTX D 504:

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

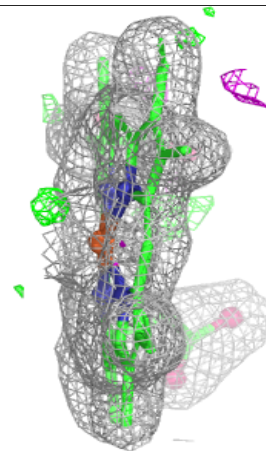
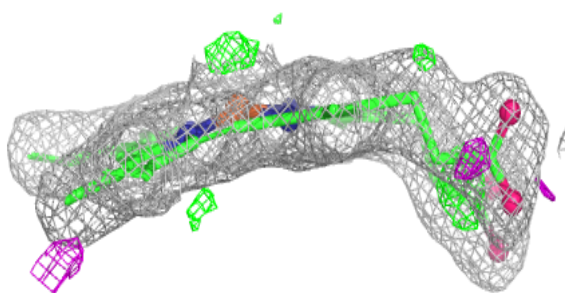
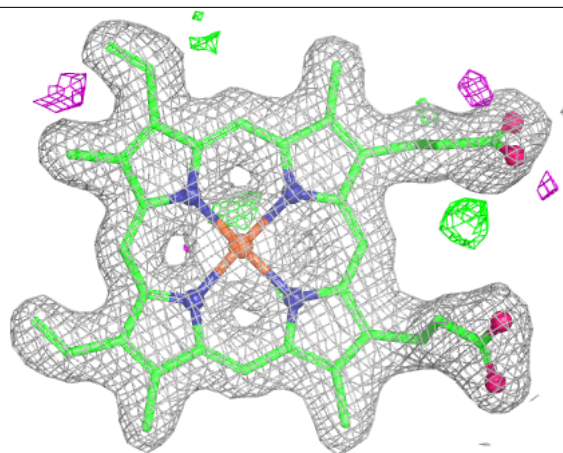
**Electron density around A1BTX B 503:**

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



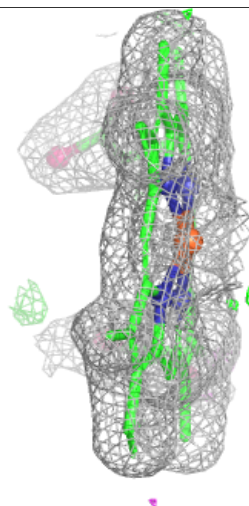
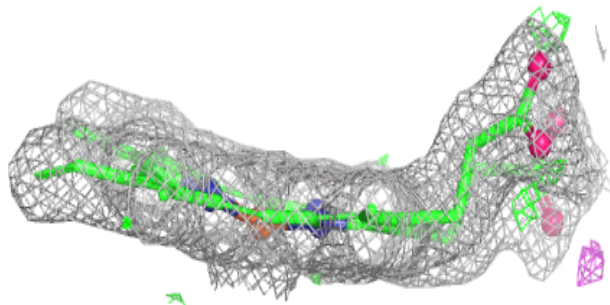
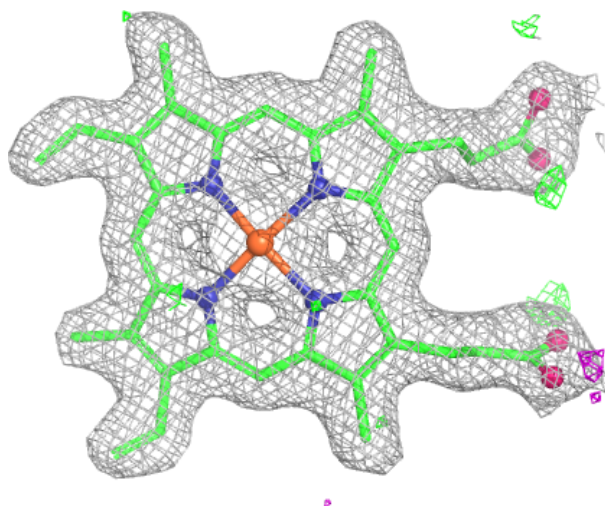
Electron density around HEM C 501:

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



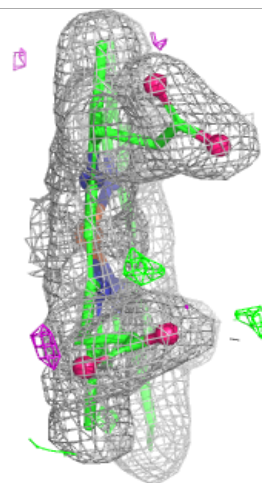
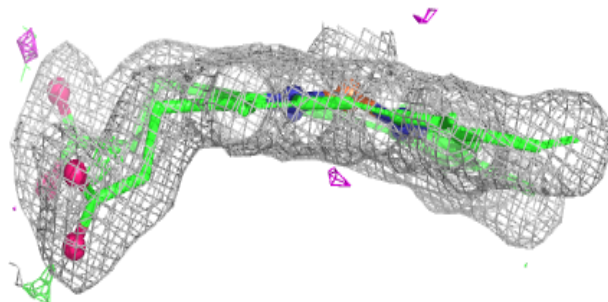
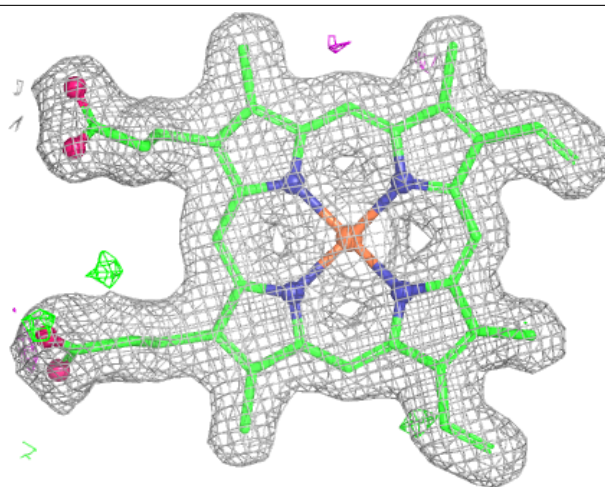
Electron density around HEM A 501:

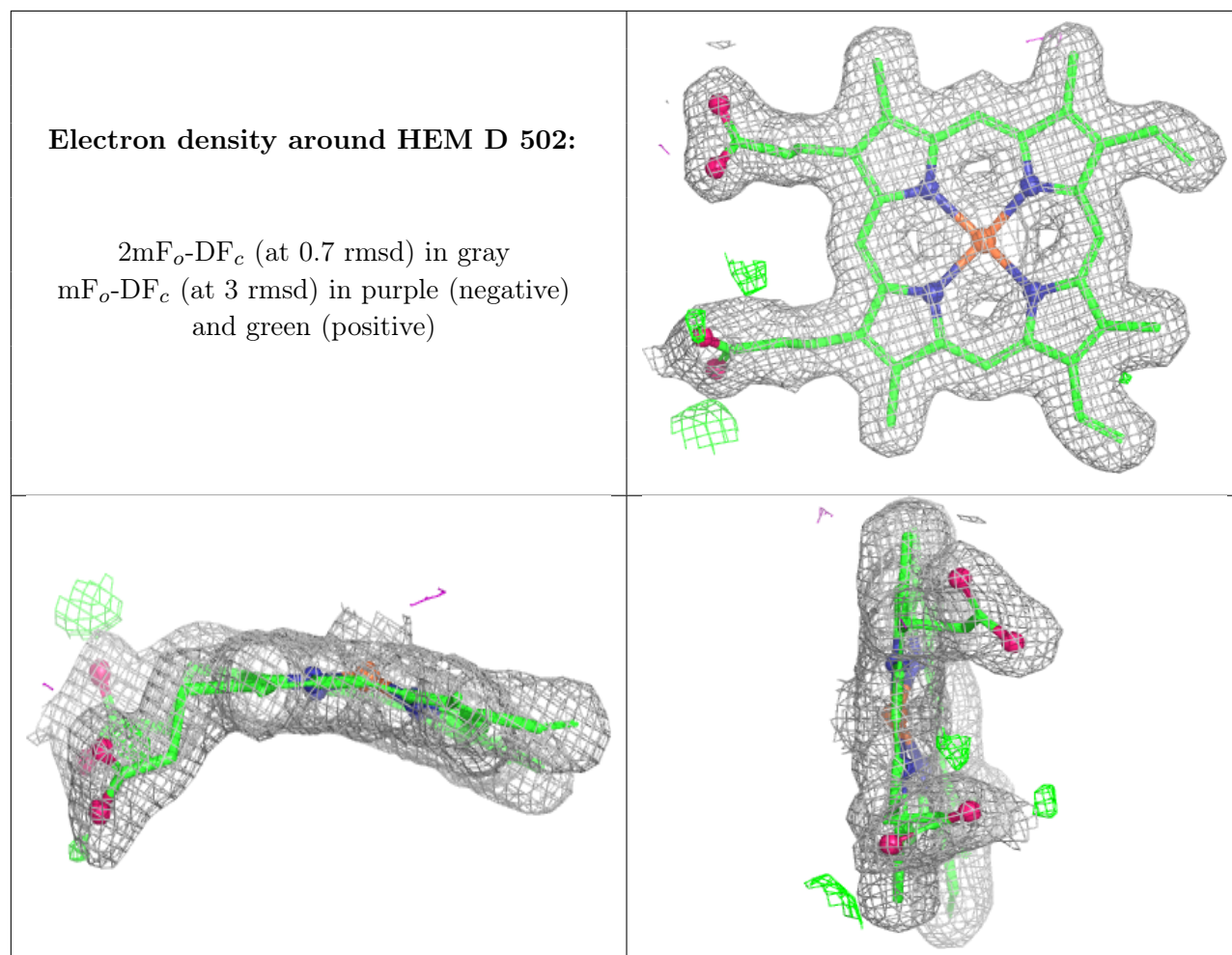
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM B 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 [i](#)

There are no such residues in this entry.