



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 07:45 AM UTC

PDB ID : 9MWV / pdb_00009mwv
Title : Structure of human endothelial nitric oxide synthase heme domain bound with N-(3-(((2-(3-(aminomethyl)-[1,1'-biphenyl]-4-yl)ethyl)amino)methyl)phenyl)thiophene-2-carboximidamide
Authors : Li, H.; Poulos, T.L.
Deposited on : 2025-01-17
Resolution : 1.90 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	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

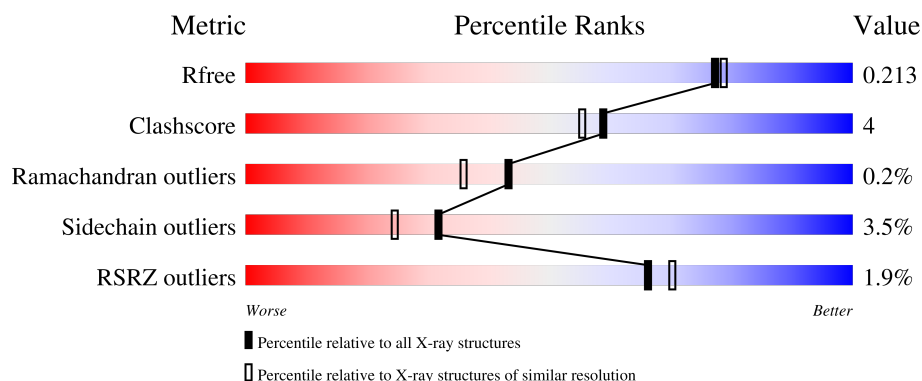
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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}	180053	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (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	2% 81% 9% • 9%
1	B	440	0% 85% 6% 8%
1	C	440	3% 79% 11% • 9%
1	D	440	0% 85% 5% • 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
5	ACT	B	501	-	-	X	-
5	ACT	C	504	-	-	X	-

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 14179 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.

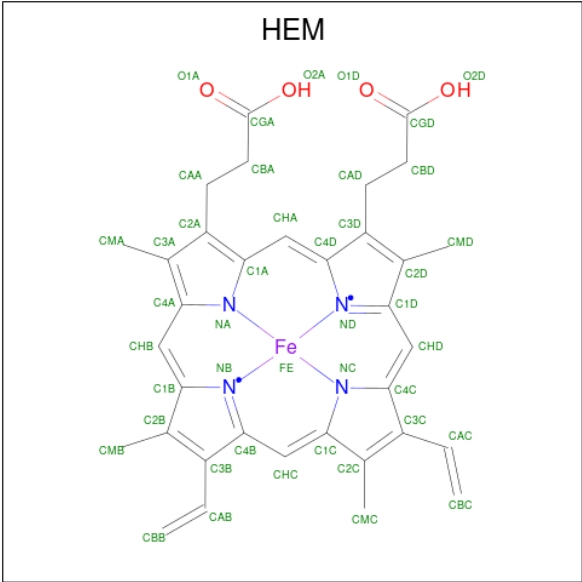
- Molecule 1 is a protein called Nitric oxide synthase, endothelial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	400	Total	C	N	O	S	0	1	0
			3198	2037	562	583	16			
1	B	403	Total	C	N	O	S	0	2	0
			3226	2054	569	587	16			
1	C	401	Total	C	N	O	S	0	1	0
			3207	2043	564	584	16			
1	D	401	Total	C	N	O	S	0	3	0
			3211	2045	564	586	16			

There are 4 discrepancies between the modelled and reference sequences:

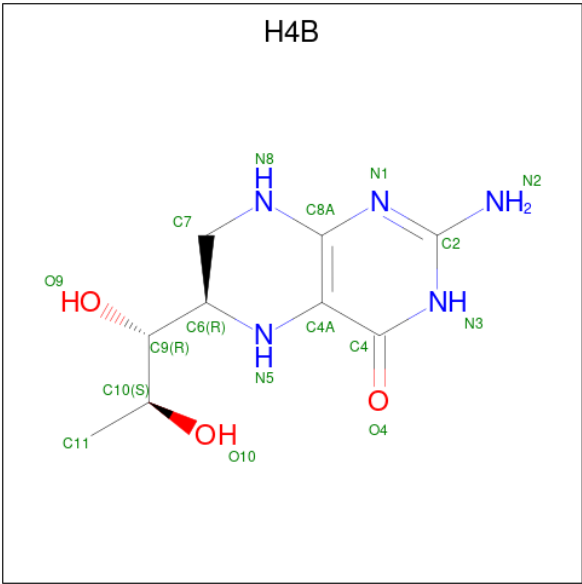
Chain	Residue	Modelled	Actual	Comment	Reference
A	298	GLU	ASP	variant	UNP P29474
B	298	GLU	ASP	variant	UNP P29474
C	298	GLU	ASP	variant	UNP P29474
D	298	GLU	ASP	variant	UNP P29474

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



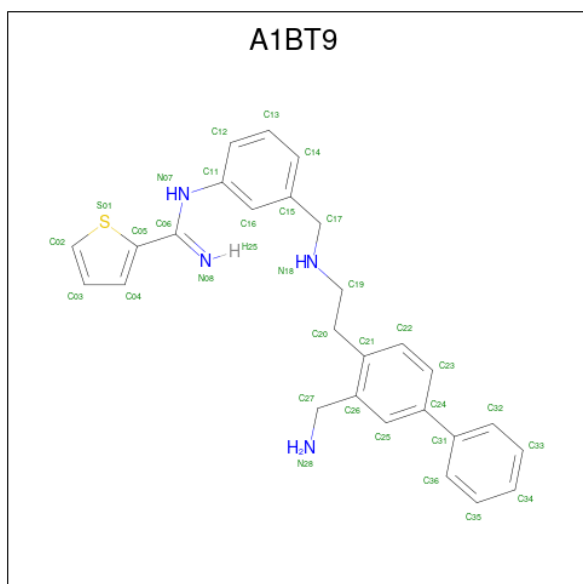
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	D	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 3 is 5,6,7,8-TETRAHYDROBIOPTERIN (CCD ID: H4B) (formula: C₉H₁₅N₅O₃).



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 N-{3-[(2-[3-(aminomethyl)[1,1'-biphenyl]-4-yl]ethyl)amino)methyl]phenyl}thiophene-2-carboximidamide (CCD ID: A1BT9) (formula: C₂₇H₂₈N₄S) (labeled as "Ligand of Interest" by depositor).



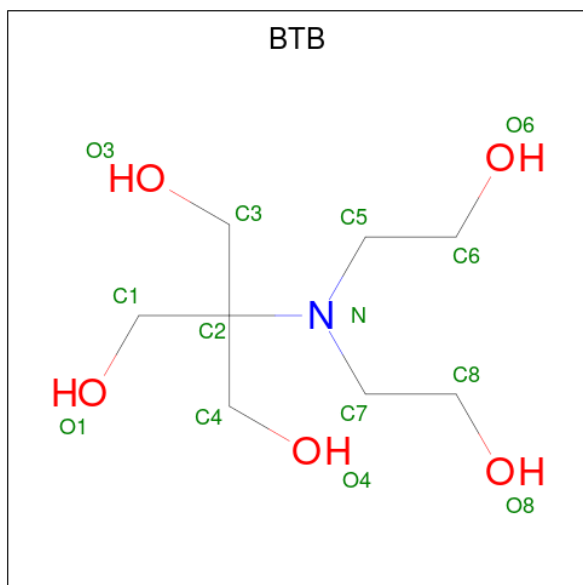
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	S	0	0
			32	27	4	1		
4	B	1	Total	C	N	S	0	0
			32	27	4	1		
4	C	1	Total	C	N	S	0	0
			32	27	4	1		
4	D	1	Total	C	N	S	0	0
			32	27	4	1		

- Molecule 5 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



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

- Molecule 6 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
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		
6	C	1	Total	C	N	O	0	0
			14	8	1	5		
6	D	1	Total	C	N	O	0	0
			14	8	1	5		
6	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 7 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 8 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

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

- Molecule 9 is GADOLINIUM ATOM (CCD ID: GD) (formula: Gd).

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

- Molecule 10 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 11 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

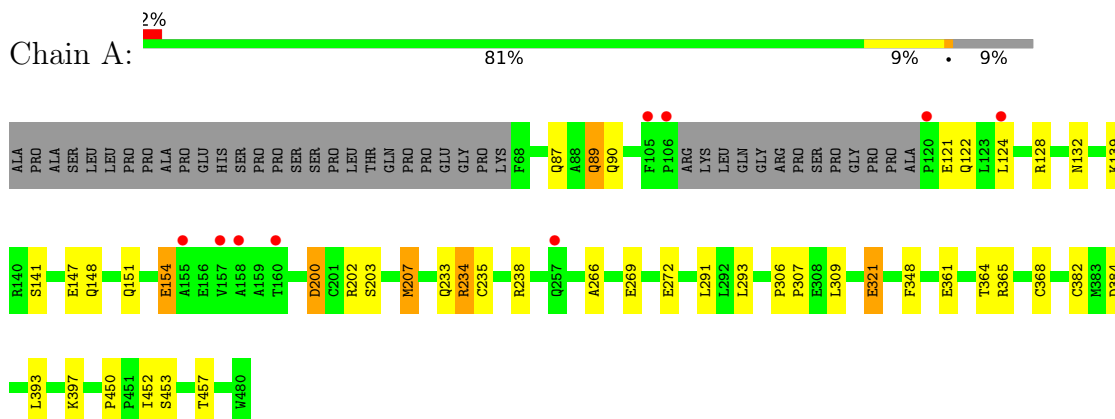
- Molecule 12 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
12	A	167	Total O 167 167	0	0
12	B	243	Total O 243 243	0	0
12	C	143	Total O 143 143	0	0
12	D	232	Total O 232 232	0	0

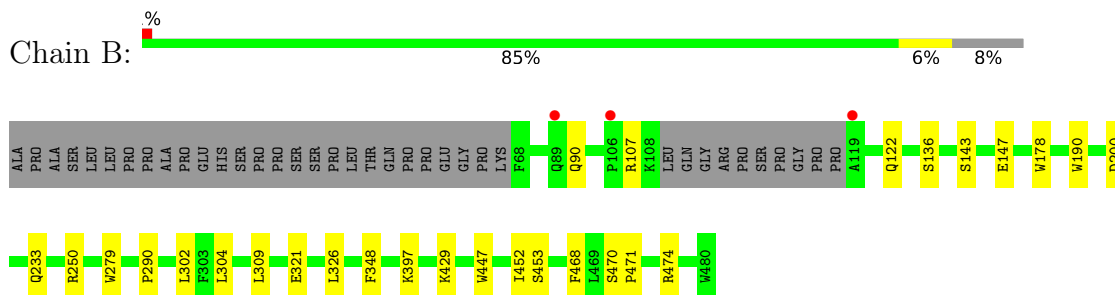
3 Residue-property plots [i](#)

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.

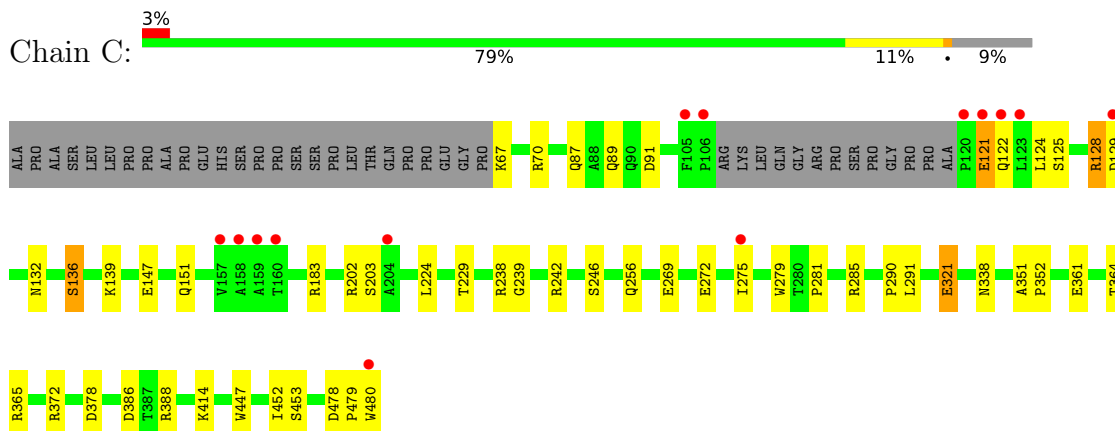
- Molecule 1: Nitric oxide synthase, endothelial



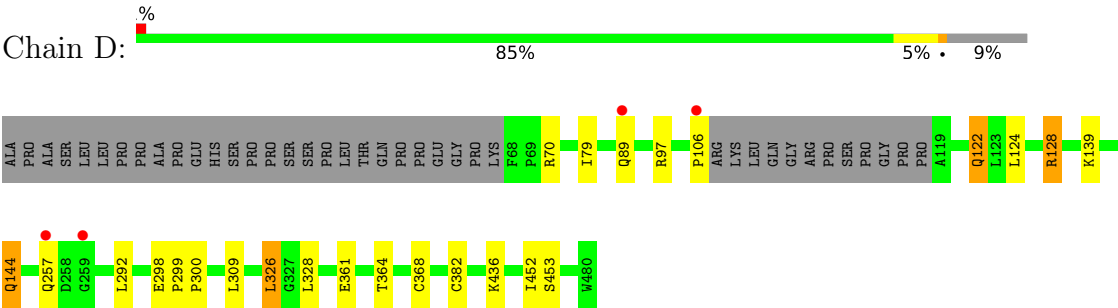
- Molecule 1: Nitric oxide synthase, endothelial



- 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	59.76Å 152.65Å 108.81Å 90.00° 90.86° 90.00°	Depositor
Resolution (Å)	39.17 – 1.90 39.17 – 1.90	Depositor EDS
% Data completeness (in resolution range)	92.5 (39.17-1.90) 95.4 (39.17-1.90)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.17 (at 1.89Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
R, R_{free}	0.181 , 0.218 0.178 , 0.213	Depositor DCC
R_{free} test set	7380 reflections (3.80%)	wwPDB-VP
Wilson B-factor (Å ²)	32.5	Xtriage
Anisotropy	0.364	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 56.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.063 for h,-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	14179	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 3.85% 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: H4B, GD, BTB, HEM, ACT, A1BT9, ZN, CA, GOL, CL

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	0.27	0/3293	0.46	0/4487
1	B	0.34	0/3324	0.51	0/4528
1	C	0.26	0/3302	0.46	0/4498
1	D	0.33	0/3312	0.50	0/4514
All	All	0.30	0/13231	0.48	0/18027

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	C	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	C	122	GLN	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	3198	0	3099	25	0
1	B	3226	0	3134	18	0
1	C	3207	0	3112	29	0
1	D	3211	0	3114	20	0
2	A	43	0	30	2	0
2	B	43	0	30	2	0
2	C	43	0	30	2	0
2	D	43	0	30	2	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	32	0	0	2	0
4	B	32	0	0	1	0
4	C	32	0	0	1	0
4	D	32	0	0	1	0
5	A	4	0	3	0	0
5	B	8	0	6	7	0
5	C	4	0	3	7	0
5	D	4	0	3	0	0
6	A	28	0	36	6	0
6	B	28	0	36	5	0
6	C	14	0	19	2	0
6	D	28	0	36	7	0
7	A	18	0	24	1	0
7	B	12	0	16	1	0
7	C	12	0	16	0	0
7	D	12	0	16	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	1	0	0	0	0
9	D	1	0	0	0	0
10	A	1	0	0	0	0
10	C	1	0	0	0	0
11	A	1	0	0	0	0
11	B	1	0	0	0	0
11	C	1	0	0	0	0
12	A	167	0	0	4	0
12	B	243	0	0	4	1
12	C	143	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	D	232	0	0	4	1
All	All	14179	0	12853	115	1

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.

The worst 5 of 115 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:B:290:PRO:HB3	1:B:304:LEU:HD23	1.64	0.79
1:C:238:ARG:NH1	1:C:239:GLY:O	2.20	0.73
7:A:509:GOL:O2	12:A:601:HOH:O	2.07	0.73
1:B:453:SER:H	5:B:501:ACT:H2	1.55	0.71
1:C:91:ASP:OD1	12:C:601:HOH:O	2.09	0.70

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:B:753:HOH:O	12:D:737:HOH:O[1_456]	2.14	0.06

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%)	387 (98%)	10 (2%)	0	100	100
1	B	401/440 (91%)	390 (97%)	11 (3%)	0	100	100
1	C	398/440 (90%)	384 (96%)	12 (3%)	2 (0%)	24	16
1	D	400/440 (91%)	392 (98%)	7 (2%)	1 (0%)	36	29
All	All	1596/1760 (91%)	1553 (97%)	40 (2%)	3 (0%)	43	36

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	121	GLU
1	D	89	GLN
1	C	203	SER

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	341/373 (91%)	322 (94%)	19 (6%)	19	11
1	B	344/373 (92%)	338 (98%)	6 (2%)	53	52
1	C	342/373 (92%)	327 (96%)	15 (4%)	25	17
1	D	343/373 (92%)	335 (98%)	8 (2%)	44	40
All	All	1370/1492 (92%)	1322 (96%)	48 (4%)	32	24

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	121	GLU
1	C	256	GLN
1	C	124	LEU
1	C	139	LYS
1	C	291	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	408	HIS
1	C	133	GLN
1	D	403	ASN
1	C	256	GLN
1	A	403	ASN

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 45 ligands modelled in this entry, 12 are monoatomic - leaving 33 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	$\# Z > 2$
6	BTB	B	507	-	13,13,13	0.47	0	7,16,16	1.10	1 (14%)
5	ACT	A	504	-	3,3,3	0.78	0	3,3,3	0.85	0
6	BTB	C	505	-	13,13,13	0.47	0	7,16,16	0.62	0
3	H4B	D	502	-	17,18,18	0.95	1 (5%)	14,26,26	1.89	5 (35%)
7	GOL	A	509	-	5,5,5	0.54	0	5,5,5	0.45	0
3	H4B	B	503	-	17,18,18	1.01	2 (11%)	14,26,26	1.72	3 (21%)
6	BTB	A	506	-	13,13,13	0.48	0	7,16,16	0.73	0
4	A1BT9	A	503	-	35,35,35	0.91	3 (8%)	43,46,46	1.49	9 (20%)
4	A1BT9	C	503	-	35,35,35	0.84	2 (5%)	43,46,46	1.18	4 (9%)
6	BTB	D	505	9	13,13,13	0.40	0	7,16,16	0.58	0
7	GOL	C	507	-	5,5,5	0.36	0	5,5,5	0.29	0
2	HEM	A	501	1	50,50,50	1.62	10 (20%)	67,82,82	1.33	8 (11%)
5	ACT	B	501	-	3,3,3	1.06	0	3,3,3	1.05	0
5	ACT	C	504	-	3,3,3	0.86	0	3,3,3	0.94	0
3	H4B	A	502	-	17,18,18	0.94	0	14,26,26	1.84	4 (28%)
7	GOL	A	508	-	5,5,5	0.37	0	5,5,5	0.30	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	GOL	B	509	-	5,5,5	0.35	0	5,5,5	0.56	0
6	BTB	D	506	-	13,13,13	0.35	0	7,16,16	0.57	0
4	A1BT9	D	503	-	35,35,35	0.78	3 (8%)	43,46,46	1.22	5 (11%)
4	A1BT9	B	504	-	35,35,35	0.85	2 (5%)	43,46,46	1.14	4 (9%)
2	HEM	B	502	1	50,50,50	1.73	8 (16%)	67,82,82	1.33	7 (10%)
2	HEM	C	501	1	50,50,50	1.58	8 (16%)	67,82,82	1.33	9 (13%)
6	BTB	B	506	9	13,13,13	0.70	0	7,16,16	1.26	2 (28%)
5	ACT	B	505	-	3,3,3	0.78	0	3,3,3	0.80	0
7	GOL	A	507	-	5,5,5	0.38	0	5,5,5	0.28	0
5	ACT	D	504	-	3,3,3	0.78	0	3,3,3	0.81	0
2	HEM	D	501	1	50,50,50	1.69	10 (20%)	67,82,82	1.35	10 (14%)
7	GOL	C	506	-	5,5,5	0.38	0	5,5,5	0.58	0
7	GOL	D	508	-	5,5,5	0.37	0	5,5,5	0.33	0
7	GOL	B	508	-	5,5,5	0.34	0	5,5,5	0.32	0
3	H4B	C	502	-	17,18,18	0.75	0	14,26,26	1.91	6 (42%)
7	GOL	D	507	-	5,5,5	0.36	0	5,5,5	0.34	0
6	BTB	A	505	9	13,13,13	0.40	0	7,16,16	0.65	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
6	BTB	B	507	-	-	4/21/21/21	-
6	BTB	C	505	-	-	4/21/21/21	-
3	H4B	D	502	-	-	0/8/17/17	0/2/2/2
7	GOL	A	509	-	-	2/4/4/4	-
3	H4B	B	503	-	-	0/8/17/17	0/2/2/2
6	BTB	A	506	-	-	10/21/21/21	-
4	A1BT9	A	503	-	-	4/17/21/21	0/4/4/4
4	A1BT9	C	503	-	-	0/17/21/21	0/4/4/4
6	BTB	D	505	9	-	3/21/21/21	-
7	GOL	C	507	-	-	4/4/4/4	-
2	HEM	A	501	1	-	2/14/54/54	-
3	H4B	A	502	-	-	0/8/17/17	0/2/2/2
7	GOL	A	508	-	-	4/4/4/4	-
7	GOL	B	509	-	-	2/4/4/4	-
6	BTB	D	506	-	-	7/21/21/21	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	A1BT9	D	503	-	-	0/17/21/21	0/4/4/4
4	A1BT9	B	504	-	-	1/17/21/21	0/4/4/4
2	HEM	B	502	1	-	1/14/54/54	-
2	HEM	C	501	1	-	1/14/54/54	-
6	BTB	B	506	9	-	6/21/21/21	-
7	GOL	A	507	-	-	4/4/4/4	-
2	HEM	D	501	1	-	1/14/54/54	-
7	GOL	C	506	-	-	2/4/4/4	-
7	GOL	D	508	-	-	2/4/4/4	-
7	GOL	B	508	-	-	3/4/4/4	-
3	H4B	C	502	-	-	0/8/17/17	0/2/2/2
7	GOL	D	507	-	-	2/4/4/4	-
6	BTB	A	505	9	-	4/21/21/21	-

The worst 5 of 49 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	502	HEM	FE-NB	5.34	2.11	1.94
2	D	501	HEM	FE-NC	5.00	2.11	1.95
2	C	501	HEM	FE-NB	4.69	2.09	1.94
2	D	501	HEM	FE-NA	4.60	2.10	1.95
2	A	501	HEM	FE-NA	4.58	2.10	1.95

The worst 5 of 77 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	502	H4B	C2-N1-C8A	4.25	120.85	113.36
3	A	502	H4B	C2-N1-C8A	4.22	120.81	113.36
3	D	502	H4B	C2-N1-C8A	4.09	120.57	113.36
3	B	503	H4B	C2-N1-C8A	4.05	120.51	113.36
2	B	502	HEM	C4D-ND-C1D	3.55	109.41	105.21

There are no chirality outliers.

5 of 73 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	503	A1BT9	C19-C20-C21-C22
4	A	503	A1BT9	C19-C20-C21-C26
4	B	504	A1BT9	C21-C26-C27-N28
6	A	505	BTB	O1-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
6	A	505	BTB	O1-C1-C2-C4

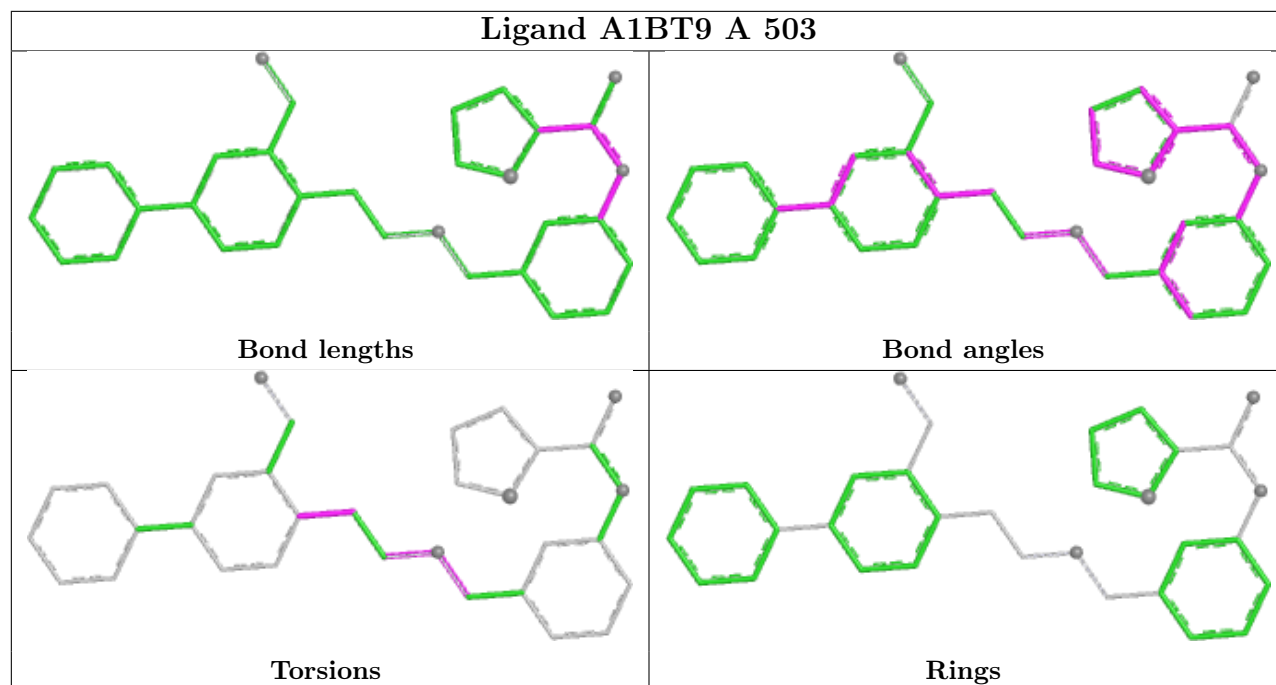
There are no ring outliers.

22 monomers are involved in 51 short contacts:

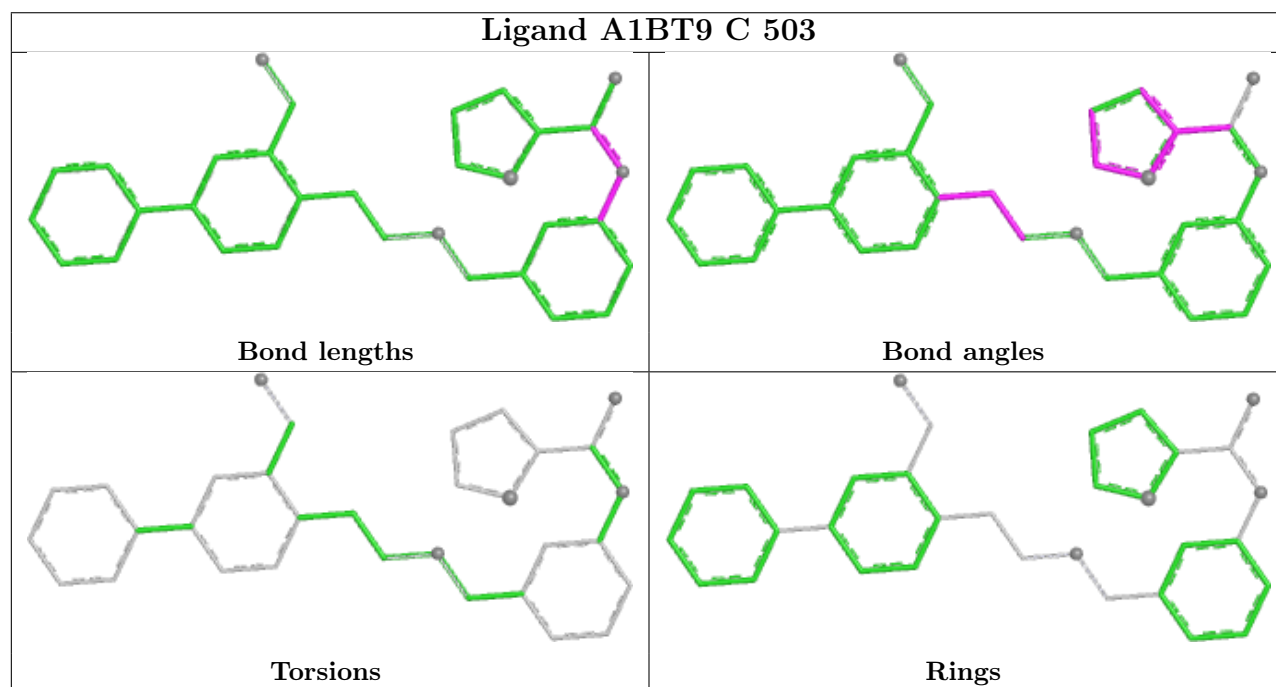
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	507	BTB	1	0
6	C	505	BTB	2	0
7	A	509	GOL	1	0
3	B	503	H4B	1	0
6	A	506	BTB	1	0
4	A	503	A1BT9	2	0
4	C	503	A1BT9	1	0
6	D	505	BTB	2	0
2	A	501	HEM	2	0
5	B	501	ACT	7	0
5	C	504	ACT	7	0
3	A	502	H4B	1	0
7	B	509	GOL	1	0
6	D	506	BTB	5	0
4	D	503	A1BT9	1	0
4	B	504	A1BT9	1	0
2	B	502	HEM	2	0
2	C	501	HEM	2	0
6	B	506	BTB	4	0
2	D	501	HEM	2	0
3	C	502	H4B	1	0
6	A	505	BTB	5	0

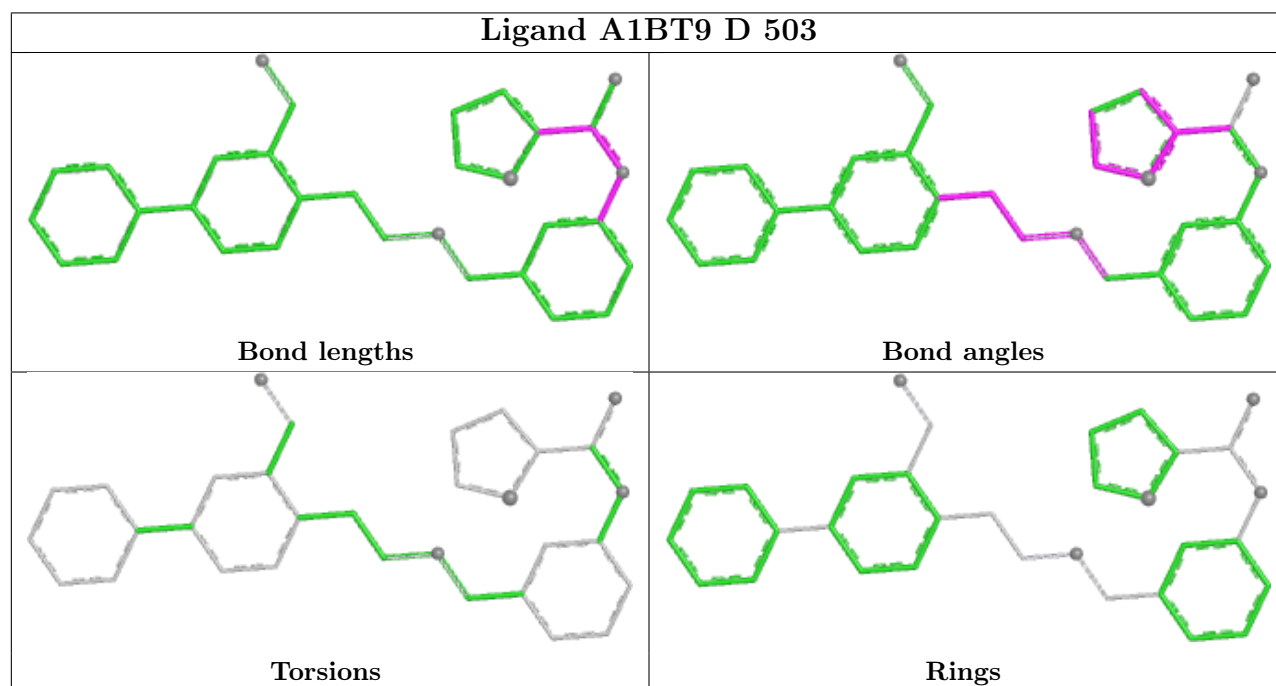
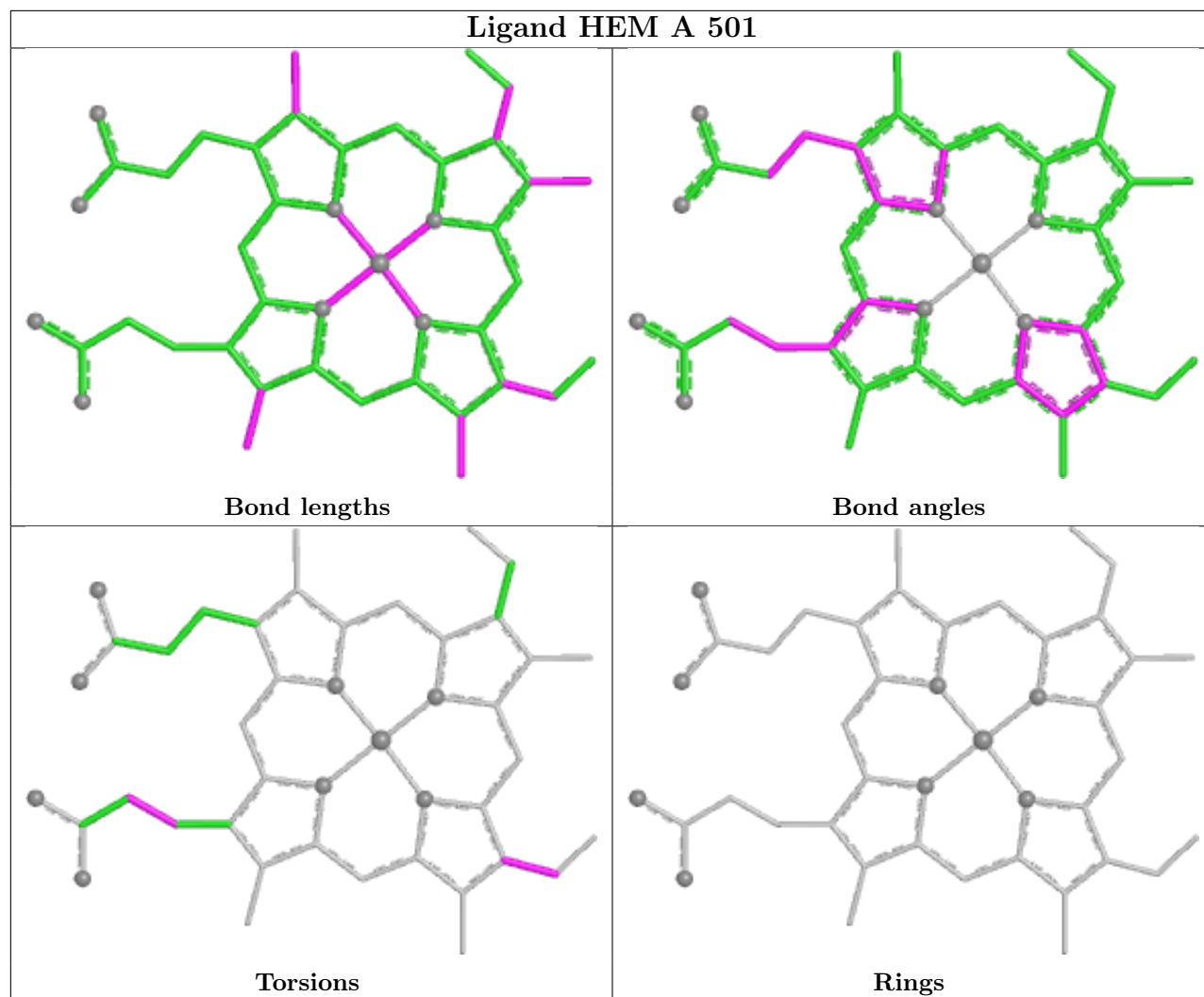
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 A1BT9 A 503

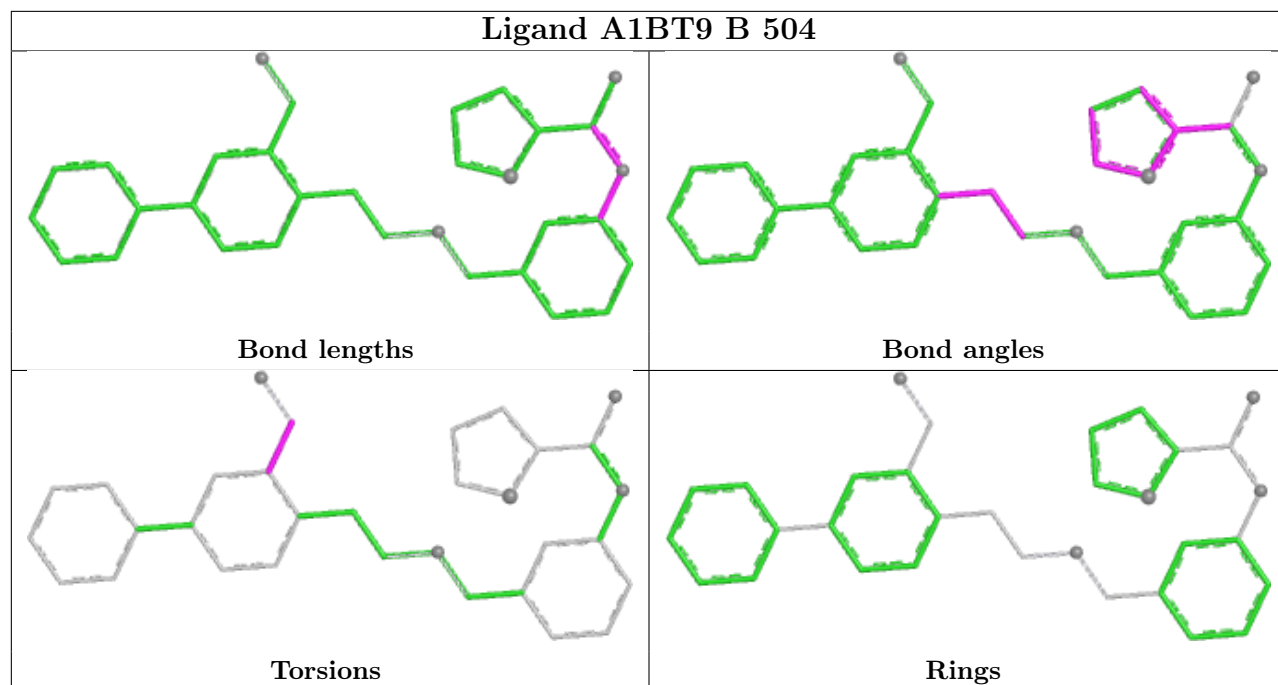


Ligand A1BT9 C 503

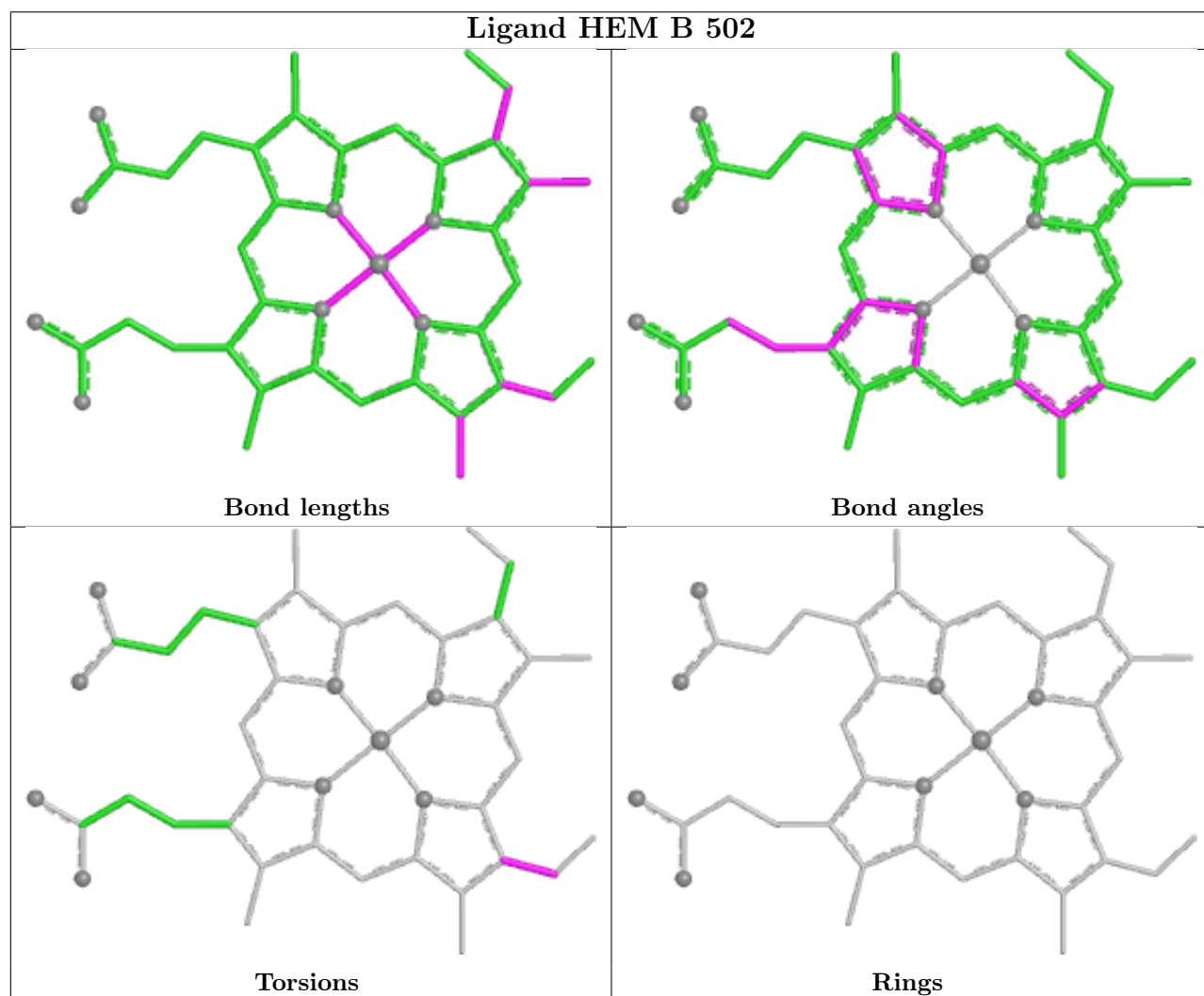


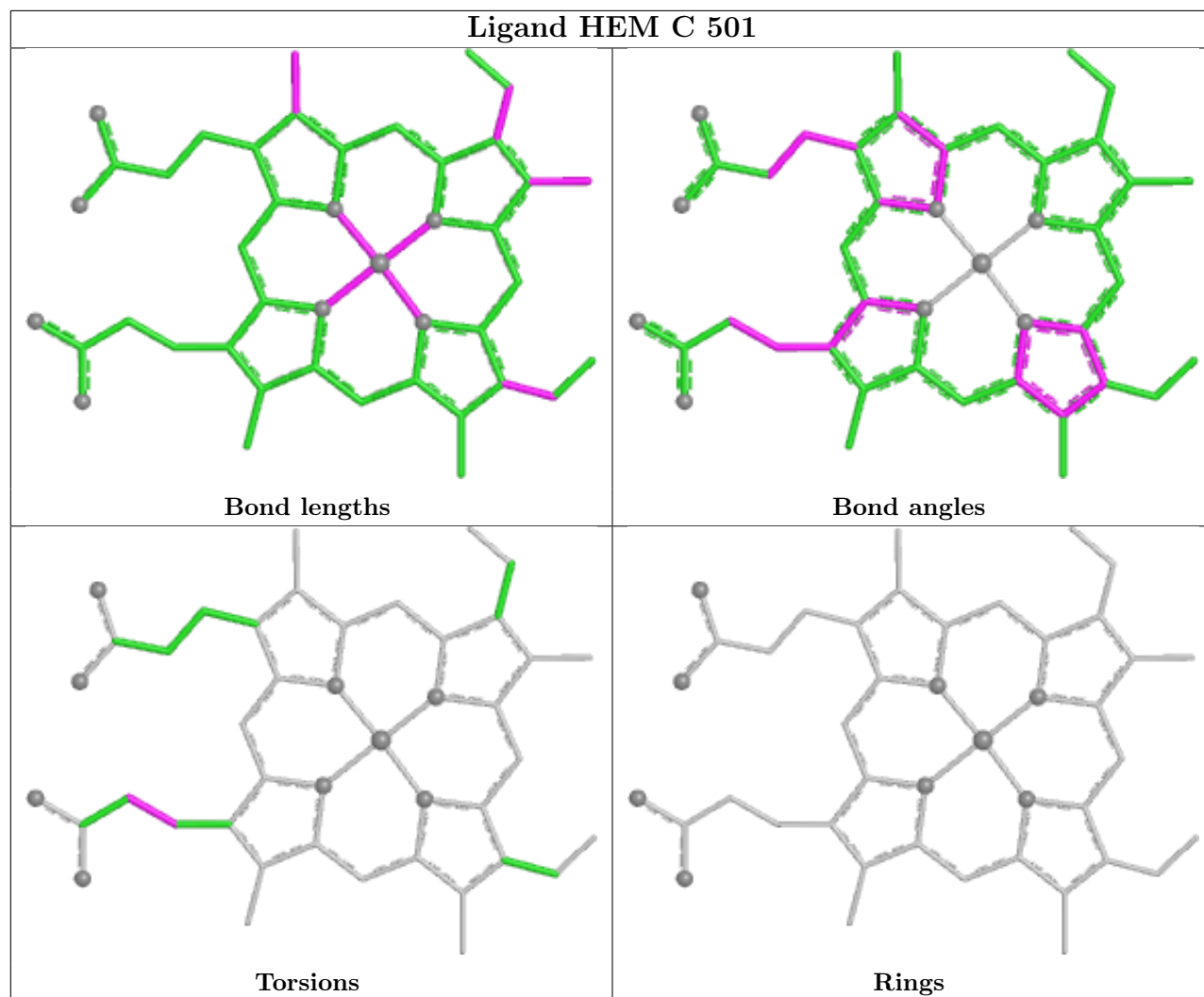


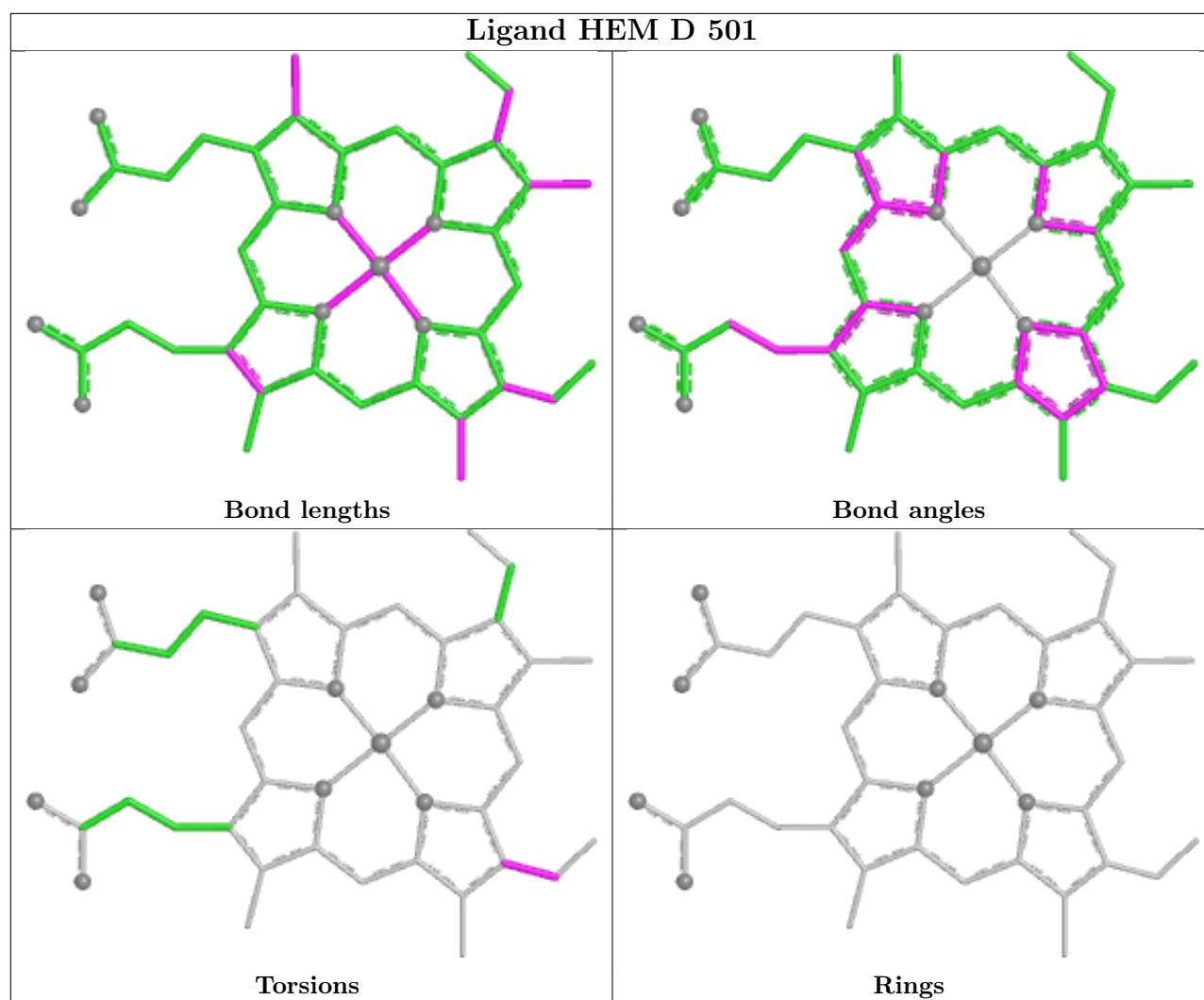
Ligand A1BT9 B 504



Ligand HEM B 502







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	400/440 (90%)	0.14	9 (2%) 61 65	24, 48, 91, 131	1 (0%)
1	B	403/440 (91%)	-0.27	3 (0%) 84 86	20, 35, 66, 126	2 (0%)
1	C	401/440 (91%)	0.45	14 (3%) 47 50	22, 55, 103, 153	1 (0%)
1	D	401/440 (91%)	-0.21	4 (0%) 79 82	20, 36, 70, 130	3 (0%)
All	All	1605/1760 (91%)	0.03	30 (1%) 66 70	20, 43, 90, 153	7 (0%)

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	204	ALA	5.8
1	A	106	PRO	4.4
1	C	106	PRO	4.3
1	A	120	PRO	4.3
1	C	121	GLU	3.6

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($\text{\AA}^2$)	Q<0.9
6	BTB	C	505	14/14	0.59	0.17	87,91,98,101	0
7	GOL	A	508	6/6	0.67	0.13	81,89,92,93	0
6	BTB	B	507	14/14	0.73	0.16	74,86,93,95	0
7	GOL	C	506	6/6	0.73	0.15	68,75,95,101	0
7	GOL	D	507	6/6	0.76	0.12	62,70,73,77	0
7	GOL	C	507	6/6	0.78	0.10	80,83,85,86	0
7	GOL	B	508	6/6	0.78	0.12	69,72,75,75	0
6	BTB	D	506	14/14	0.79	0.13	47,67,75,75	0
4	A1BT9	A	503	32/32	0.80	0.21	53,71,109,113	0
4	A1BT9	C	503	32/32	0.82	0.20	52,68,114,115	0
6	BTB	A	506	14/14	0.84	0.14	47,70,76,82	0
7	GOL	A	509	6/6	0.85	0.22	73,88,88,94	0
7	GOL	A	507	6/6	0.86	0.09	58,72,78,78	0
6	BTB	B	506	14/14	0.87	0.14	45,61,82,83	0
6	BTB	D	505	14/14	0.87	0.14	38,56,80,83	0
4	A1BT9	B	504	32/32	0.91	0.15	27,47,99,102	0
4	A1BT9	D	503	32/32	0.91	0.15	30,55,97,100	0
7	GOL	B	509	6/6	0.91	0.12	52,57,59,62	0
5	ACT	B	505	4/4	0.92	0.11	43,45,48,57	0
5	ACT	C	504	4/4	0.92	0.13	40,43,56,56	0
3	H4B	A	502	17/17	0.92	0.09	41,52,64,67	0
3	H4B	C	502	17/17	0.92	0.09	48,57,70,70	0
8	CL	C	508	1/1	0.92	0.12	66,66,66,66	0
6	BTB	A	505	14/14	0.93	0.11	28,74,90,95	0
5	ACT	A	504	4/4	0.93	0.12	52,54,57,62	0
3	H4B	D	502	17/17	0.94	0.09	28,43,51,51	0
9	GD	A	511	1/1	0.94	0.10	108,108,108,108	0
7	GOL	D	508	6/6	0.95	0.09	49,52,54,62	0
5	ACT	D	504	4/4	0.95	0.09	53,55,56,60	0
5	ACT	B	501	4/4	0.95	0.11	23,29,53,54	0
2	HEM	C	501	43/43	0.96	0.09	34,49,60,67	0
8	CL	A	510	1/1	0.96	0.07	55,55,55,55	0
3	H4B	B	503	17/17	0.97	0.05	29,35,39,41	0
8	CL	B	510	1/1	0.97	0.07	49,49,49,49	0
9	GD	B	511	1/1	0.97	0.05	45,45,45,45	0
2	HEM	A	501	43/43	0.98	0.07	28,34,54,70	0
11	CA	C	510	1/1	0.98	0.06	45,45,45,45	0
2	HEM	B	502	43/43	0.99	0.05	17,21,37,51	0
2	HEM	D	501	43/43	0.99	0.05	18,26,44,51	0
9	GD	D	510	1/1	0.99	0.04	43,43,43,43	0
10	ZN	C	509	1/1	0.99	0.05	38,38,38,38	0
11	CA	A	513	1/1	0.99	0.07	39,39,39,39	0
11	CA	B	512	1/1	0.99	0.09	41,41,41,41	0

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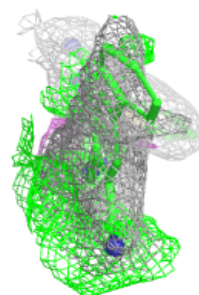
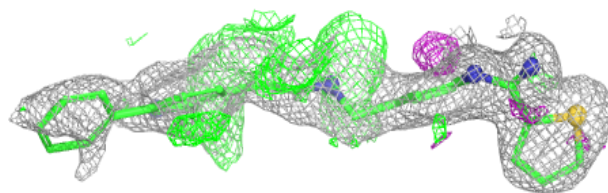
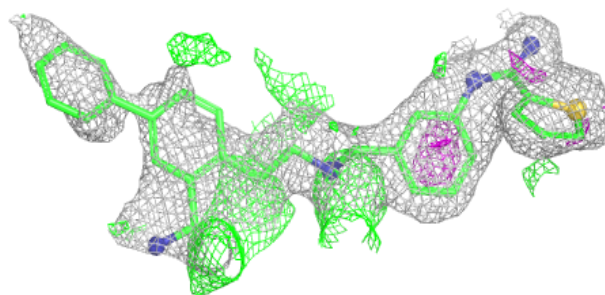
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
8	CL	D	509	1/1	0.99	0.05	42,42,42,42	0
10	ZN	A	512	1/1	1.00	0.02	32,32,32,32	0

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.

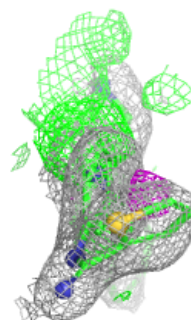
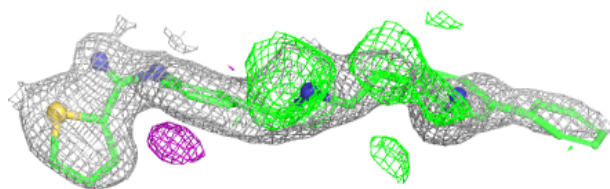
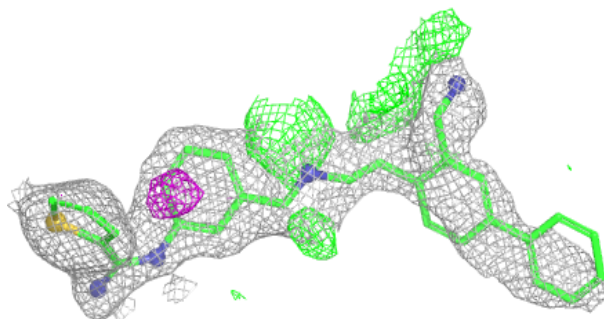
Electron density around A1BT9 A 503:

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

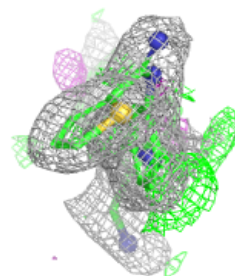
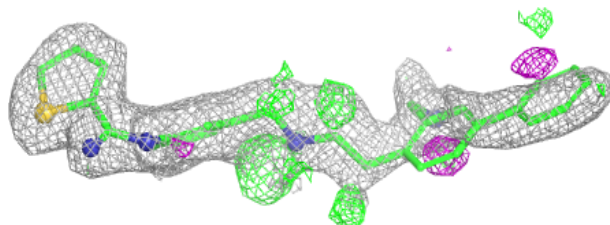
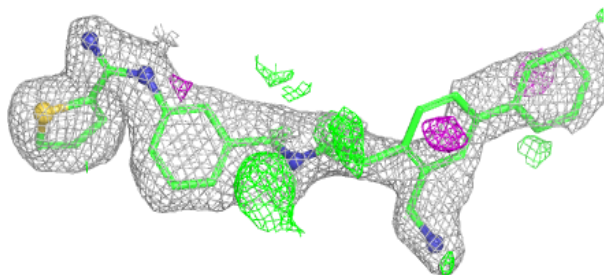


Electron density around A1BT9 C 503:

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

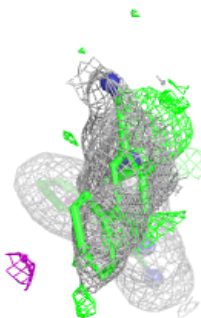
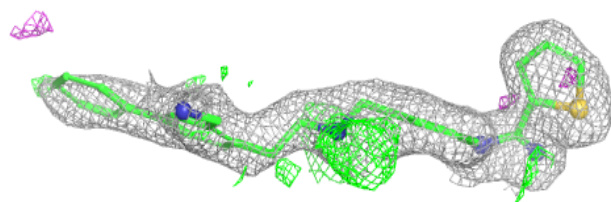
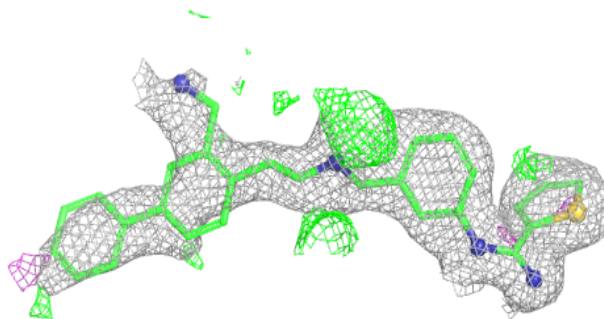
**Electron density around A1BT9 B 504:**

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and green (positive)

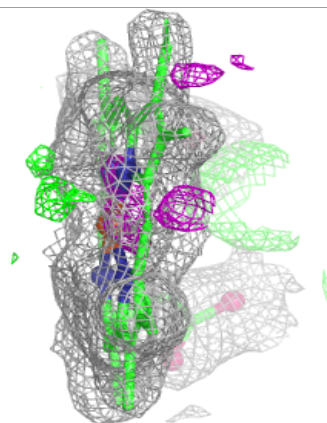
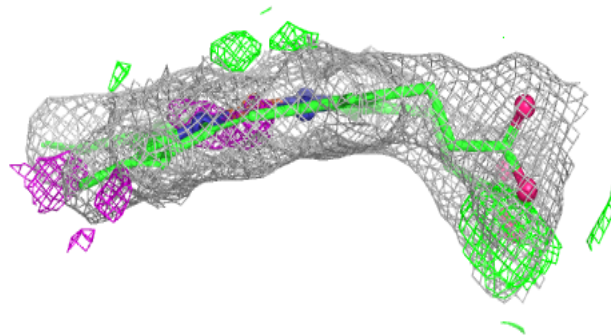
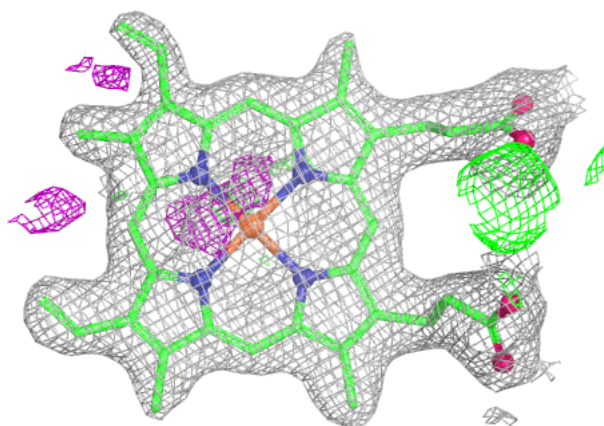


Electron density around A1BT9 D 503:

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

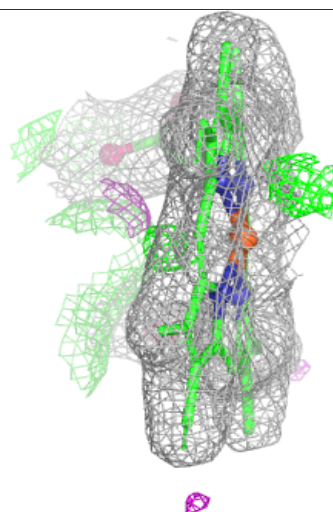
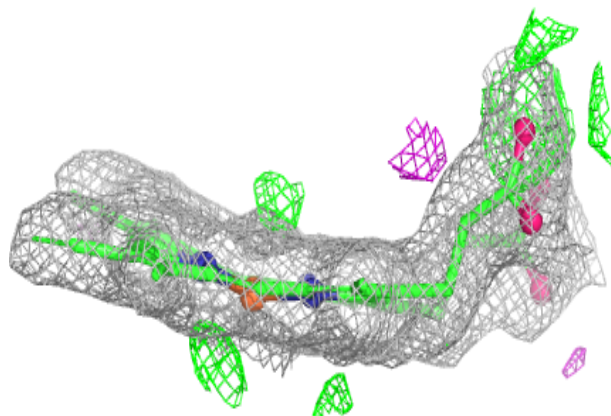
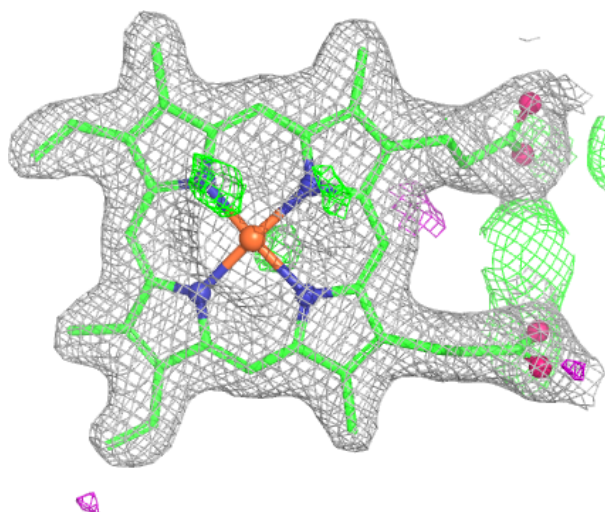
**Electron density around HEM C 501:**

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and green (positive)



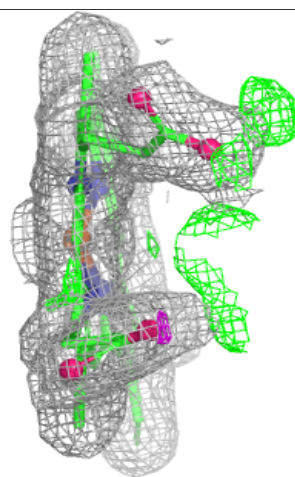
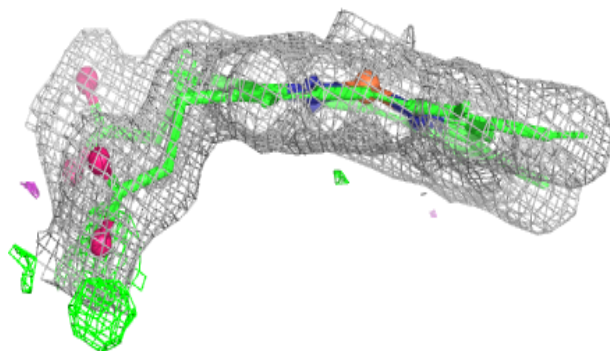
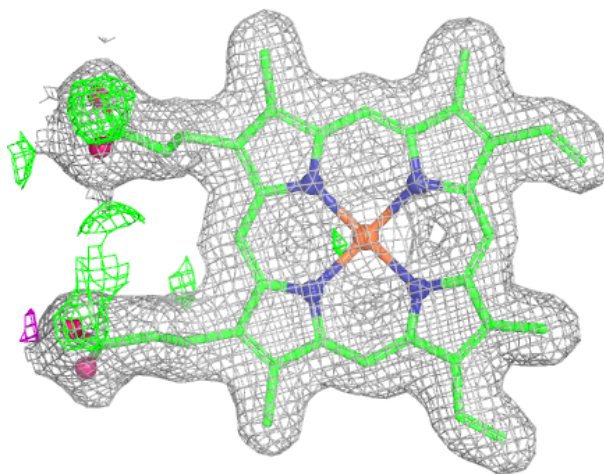
Electron density around HEM A 501:

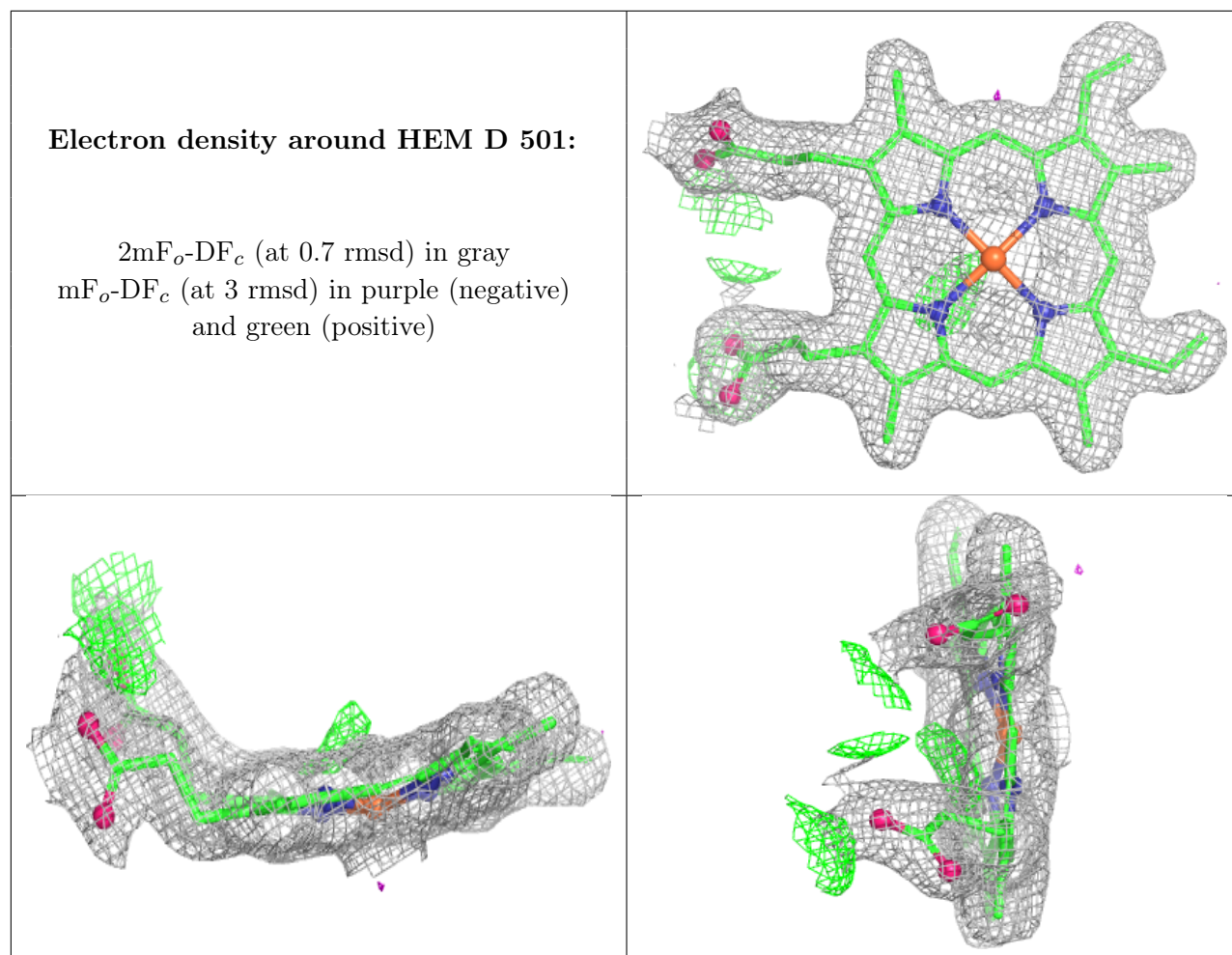
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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM B 502:

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





6.5 Other polymers [i](#)

There are no such residues in this entry.