



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:17 AM UTC

PDB ID : 6NH8 / pdb_00006nh8
Title : Structure of human endothelial nitric oxide synthase heme domain in complex with 6-(5-(3-(dimethylamino)propyl)-2,3,4-trifluorophenethyl)-4-methylpyridine-2-amine
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Deposited on : 2018-12-21
Resolution : 1.80 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

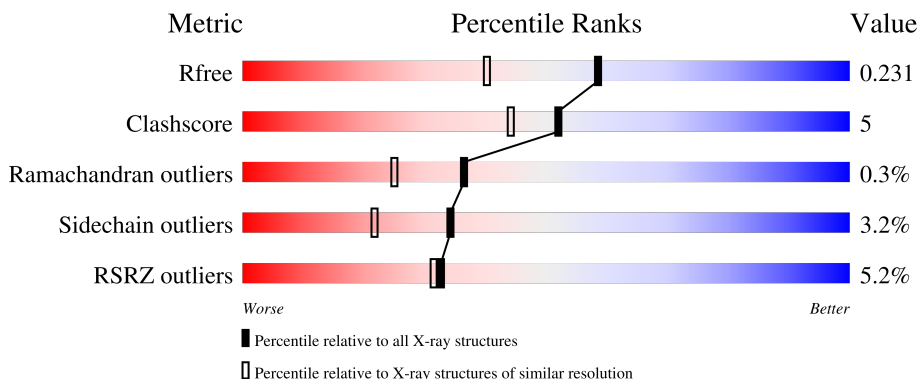
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	9% 77% 13% • 9%
1	B	440	0% 83% 7% • 9%
1	C	440	7% 79% 11% • 9%
1	D	440	2% 83% 8% 9%

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 14166 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 Endothelial nitric oxide synthase splice variant eNOS13A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	401	Total	C	N	O	S	0	2	0
			3215	2047	566	586	16			
1	B	402	Total	C	N	O	S	0	3	0
			3220	2051	566	587	16			
1	C	401	Total	C	N	O	S	0	2	0
			3209	2044	563	586	16			
1	D	402	Total	C	N	O	S	0	3	0
			3218	2050	565	587	16			

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



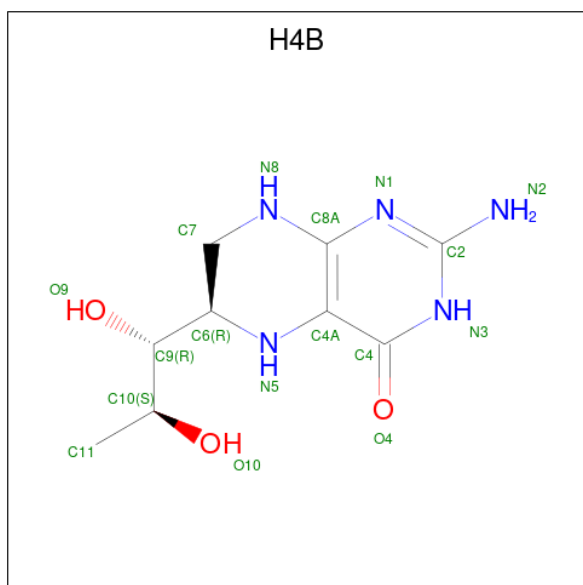
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	Fe	N O	0	0
			43	34	1	4 4		
2	B	1	Total	C	Fe	N O	0	0
			43	34	1	4 4		

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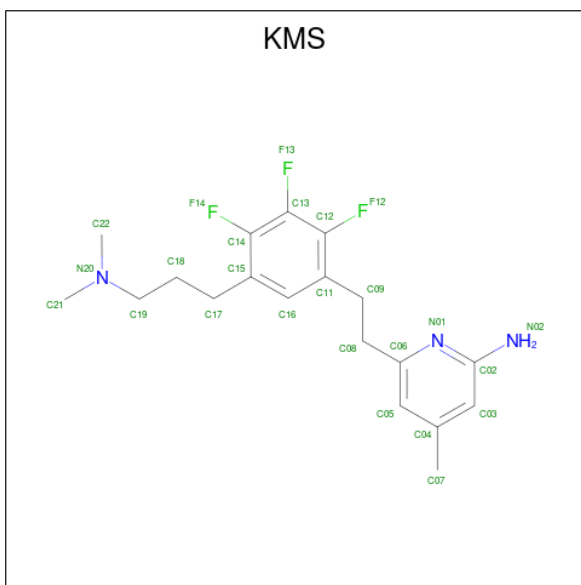
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	D	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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



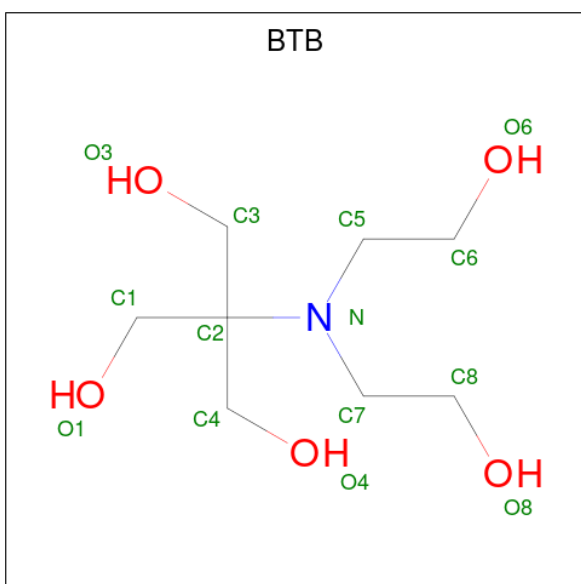
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			17	9	5	3		
3	B	1	Total	C	N	O	0	0
			17	9	5	3		
3	C	1	Total	C	N	O	0	0
			17	9	5	3		
3	D	1	Total	C	N	O	0	0
			17	9	5	3		

- Molecule 4 is 6-(2-{5-[3-(dimethylamino)propyl]-2,3,4-trifluorophenyl}ethyl)-4-methylpyridine-2-amine (CCD ID: KMS) (formula: $C_{19}H_{24}F_3N_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total 25	C 19	F 3	N 3	0	0
4	B	1	Total 25	C 19	F 3	N 3	0	0
4	C	1	Total 25	C 19	F 3	N 3	0	0
4	D	1	Total 25	C 19	F 3	N 3	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 14 8 1 5	0	0
5	A	1	Total C N O 14 8 1 5	0	0
5	A	1	Total C N O 14 8 1 5	0	0
5	B	1	Total C N O 14 8 1 5	0	0
5	B	1	Total C N O 14 8 1 5	0	0
5	B	1	Total C N O 14 8 1 5	0	0
5	C	1	Total C N O 14 8 1 5	0	0
5	C	1	Total C N O 14 8 1 5	0	0
5	C	1	Total C N O 14 8 1 5	0	0
5	D	1	Total C N O 14 8 1 5	0	0
5	D	1	Total C N O 14 8 1 5	0	0

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

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

- Molecule 7 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

- Molecule 8 is CHLORIDE ION (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		
8	D	1	Total	Cl	0	0
			1	1		

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

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

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

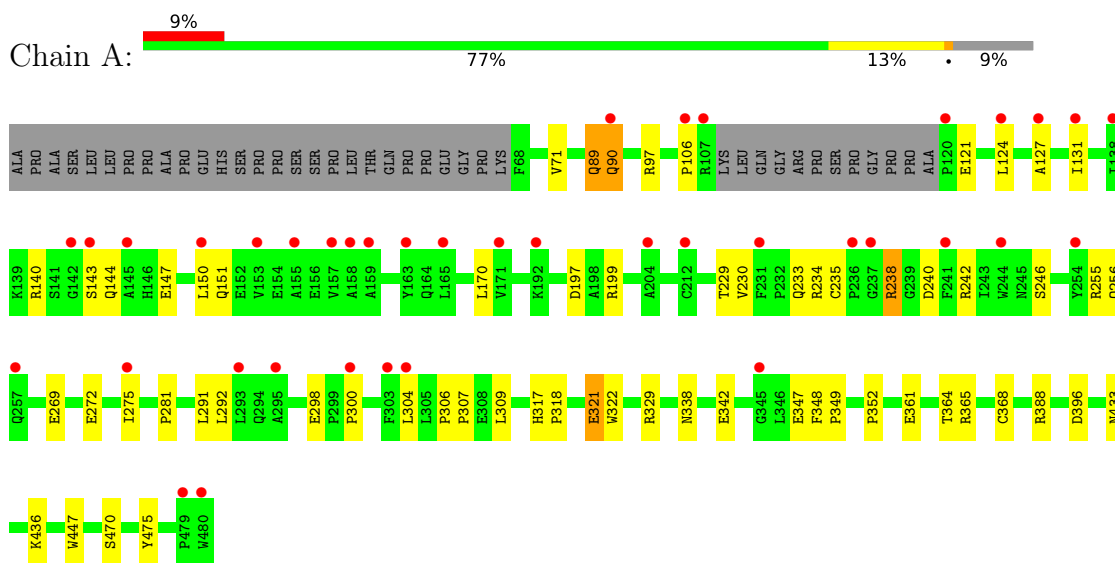
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	143	Total 143	O 143	0	0
10	B	216	Total 216	O 216	0	0
10	C	171	Total 171	O 171	0	0
10	D	258	Total 258	O 258	0	0

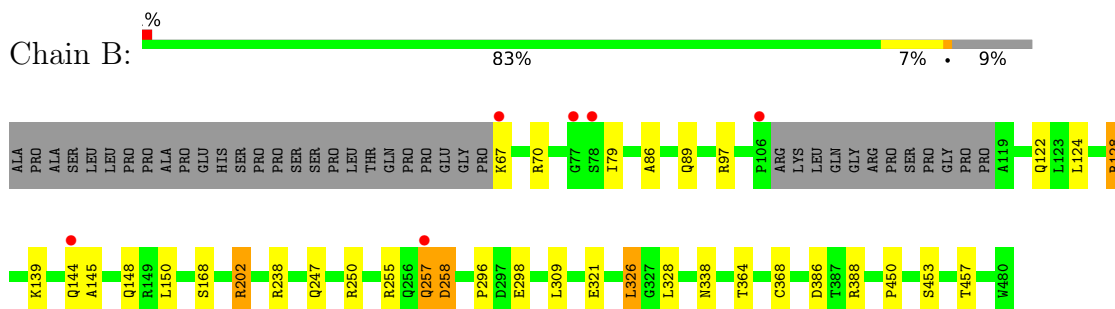
3 Residue-property plots [i](#)

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.

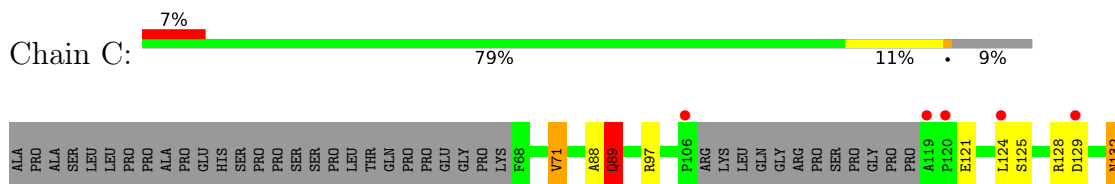
- Molecule 1: Endothelial nitric oxide synthase splice variant eNOS13A

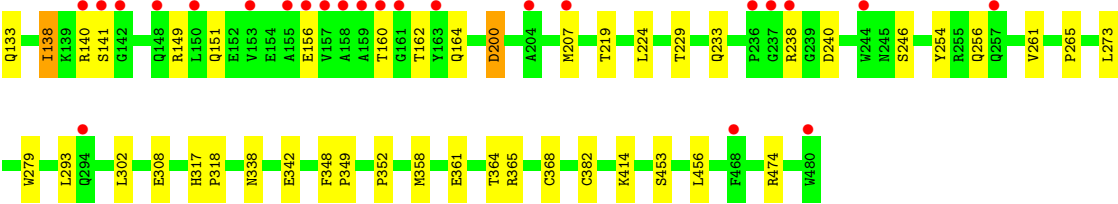


- Molecule 1: Endothelial nitric oxide synthase splice variant eNOS13A

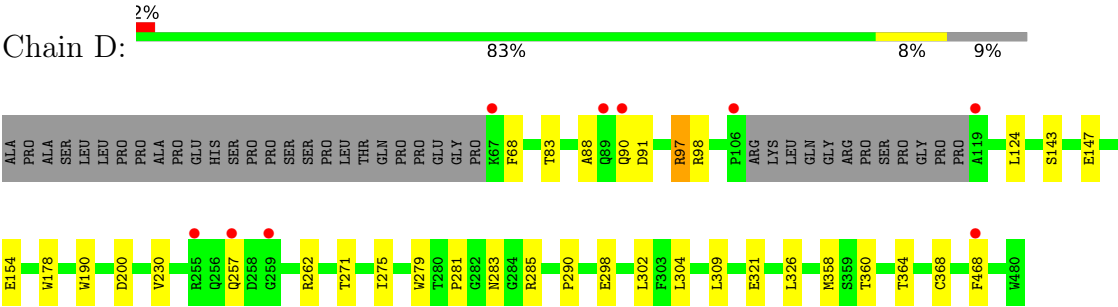


- Molecule 1: Endothelial nitric oxide synthase splice variant eNOS13A





● Molecule 1: Endothelial nitric oxide synthase splice variant eNOS13A



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	59.72Å 152.51Å 108.53Å 90.00° 90.70° 90.00°	Depositor
Resolution (Å)	55.60 – 1.80 55.60 – 1.80	Depositor EDS
% Data completeness (in resolution range)	94.2 (55.60-1.80) 98.8 (55.60-1.80)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.34 (at 1.80Å)	Xtriage
Refinement program	PHENIX 1.11.1-2575_1496	Depositor
R, R_{free}	0.200 , 0.234 0.196 , 0.231	Depositor DCC
R_{free} test set	8869 reflections (4.19%)	wwPDB-VP
Wilson B-factor (Å ²)	25.4	Xtriage
Anisotropy	0.712	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 51.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.126 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	14166	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.28% 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, BTB, H4B, HEM, KMS, GD, GOL, ZN

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	0/3313	0.46	0/4513
1	B	0.34	0/3321	0.52	0/4525
1	C	0.26	0/3307	0.45	0/4507
1	D	0.35	0/3319	0.54	0/4522
All	All	0.30	0/13260	0.49	0/18067

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	B	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	B	257	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	3215	0	3118	34	0
1	B	3220	0	3127	22	0
1	C	3209	0	3109	34	0
1	D	3218	0	3126	19	0
2	A	43	0	30	5	0
2	B	43	0	30	2	0
2	C	43	0	30	3	0
2	D	43	0	30	3	0
3	A	17	0	15	1	0
3	B	17	0	15	0	0
3	C	17	0	15	1	0
3	D	17	0	15	0	0
4	A	25	0	0	2	0
4	B	25	0	0	1	0
4	C	25	0	0	1	0
4	D	25	0	0	1	0
5	A	42	0	56	10	0
5	B	42	0	55	8	0
5	C	42	0	55	6	0
5	D	28	0	36	6	0
6	A	1	0	0	0	0
6	C	1	0	0	0	0
7	A	6	0	8	0	0
7	C	6	0	8	0	0
8	A	1	0	0	0	0
8	B	1	0	0	0	0
8	C	1	0	0	0	0
8	D	1	0	0	0	0
9	A	1	0	0	0	0
9	B	1	0	0	0	0
9	C	1	0	0	0	0
9	D	1	0	0	0	0
10	A	143	0	0	3	0
10	B	216	0	0	1	1
10	C	171	0	0	5	0
10	D	258	0	0	3	1
All	All	14166	0	12878	135	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 5.

All (135) 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:C:504:BTB:O3	10:C:601:HOH:O	1.82	0.95
1:C:128:ARG:O	1:C:132:ASN:ND2	2.19	0.76
2:A:501:HEM:HBB2	2:A:501:HEM:HHC	1.73	0.71
1:A:240:ASP:OD1	10:A:601:HOH:O	2.08	0.70
1:D:321:GLU:OE2	5:D:504:BTB:O4	2.08	0.70
5:A:505:BTB:O3	5:A:505:BTB:O1	2.08	0.69
1:B:258:ASP:OD2	1:B:258:ASP:N	2.26	0.69
2:D:501:HEM:HMC2	2:D:501:HEM:HBC2	1.74	0.68
1:D:275:ILE:HD12	1:D:281:PRO:HG3	1.74	0.68
2:B:501:HEM:HBC2	2:B:501:HEM:HMC2	1.75	0.67
1:A:433:ASN:HA	1:A:436:LYS:HE3	1.76	0.66
1:C:88:ALA:HB3	1:D:97:ARG:HD2	1.78	0.66
1:A:321:GLU:H	1:A:321:GLU:CD	2.02	0.65
1:C:160:THR:HG23	1:C:162:THR:H	1.60	0.65
2:A:501:HEM:HMC2	2:A:501:HEM:HBC2	1.80	0.64
2:C:501:HEM:HBB2	2:C:501:HEM:HHC	1.81	0.63
1:B:238:ARG:HG2	1:B:296:PRO:HB3	1.80	0.63
1:C:200:ASP:OD1	1:C:200:ASP:N	2.25	0.63
1:B:70:ARG:HD2	1:B:79:ILE:HD13	1.80	0.63
1:B:247:GLN:HB2	1:B:250:ARG:HD3	1.82	0.62
1:C:238:ARG:NH1	10:C:603:HOH:O	2.32	0.62
1:D:271:THR:O	1:D:275:ILE:HG12	2.00	0.61
1:C:97:ARG:HG3	1:D:88:ALA:HB3	1.82	0.61
2:C:501:HEM:HBC2	2:C:501:HEM:HMC2	1.84	0.58
1:B:128:ARG:HG3	1:B:150:LEU:HD22	1.85	0.58
1:D:279:TRP:HB2	1:D:302:LEU:HD21	1.86	0.58
1:C:207:MET:HE3	1:C:293:LEU:HB3	1.87	0.56
2:B:501:HEM:HHC	2:B:501:HEM:HBB2	1.87	0.55
1:C:138:ILE:HD12	1:C:140:ARG:HB2	1.87	0.55
2:D:501:HEM:HBB2	2:D:501:HEM:HHC	1.87	0.55
1:B:202:ARG:HH11	1:B:202:ARG:HB2	1.72	0.55
1:D:290:PRO:HB3	1:D:304:LEU:HD23	1.90	0.54
1:C:133:GLN:NE2	10:C:606:HOH:O	2.43	0.52
1:C:125:SER:O	1:C:128:ARG:NH1	2.43	0.51
5:D:504:BTB:O4	5:D:504:BTB:H82	2.10	0.51
1:A:238:ARG:NH2	10:A:609:HOH:O	2.41	0.51
1:A:322:TRP:CD1	5:A:504:BTB:H62	2.46	0.51
1:C:342:GLU:HG3	1:C:474:ARG:NH2	2.26	0.51
1:A:97:ARG:NH2	1:B:86:ALA:O	2.43	0.51
1:B:321:GLU:OE1	5:B:504:BTB:H82	2.10	0.50
1:B:326:LEU:HB3	1:B:328:LEU:HG	1.93	0.50
1:A:147:GLU:HA	1:A:150:LEU:HD12	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:106:PRO:O	10:A:602:HOH:O	2.20	0.49
1:B:386:ASP:OD1	1:B:388:ARG:HG2	2.13	0.49
1:D:298:GLU:CD	5:D:505:BTB:H41	2.38	0.48
1:C:364:THR:O	1:C:368:CYS:HB2	2.13	0.48
5:A:506:BTB:H42	5:A:506:BTB:H72	1.67	0.48
1:C:125:SER:O	1:C:128:ARG:HG3	2.14	0.48
5:C:506:BTB:H82	5:C:506:BTB:O6	2.15	0.47
1:A:388:ARG:HA	5:A:505:BTB:H81	1.96	0.47
1:C:279:TRP:HB2	1:C:302:LEU:HD11	1.95	0.47
1:D:143:SER:O	1:D:147:GLU:HG2	2.14	0.47
1:D:358:MET:HE3	1:D:360:THR:OG1	2.15	0.47
1:A:269:GLU:O	1:A:272:GLU:HG2	2.15	0.47
1:B:364:THR:O	1:B:368:CYS:HB2	2.15	0.47
1:A:89:GLN:HB3	1:A:90:GLN:H	1.55	0.46
1:A:475:TYR:OH	2:A:501:HEM:O1D	2.25	0.46
1:A:342:GLU:OE1	1:A:470:SER:OG	2.31	0.46
1:D:178:TRP:CE3	1:D:190:TRP:HA	2.50	0.46
5:C:505:BTB:H72	5:C:505:BTB:H42	1.52	0.46
5:B:505:BTB:H72	5:B:505:BTB:H11	1.46	0.46
5:A:504:BTB:H11	5:A:504:BTB:H51	1.84	0.46
1:D:91:ASP:OD1	10:D:601:HOH:O	2.21	0.46
1:A:242:ARG:HD2	1:A:349:PRO:HB2	1.98	0.46
1:D:364:THR:O	1:D:368:CYS:HB2	2.16	0.45
1:C:233:GLN:HB3	1:C:348:PHE:CE2	2.51	0.45
1:C:240:ASP:OD1	1:C:349:PRO:HG2	2.15	0.45
5:C:506:BTB:H72	5:C:506:BTB:H11	1.66	0.45
1:C:149:ARG:NH2	1:C:164:GLN:O	2.43	0.45
2:A:501:HEM:HBA1	4:A:503:KMS:C08	2.47	0.45
5:A:505:BTB:H11	5:A:505:BTB:H51	1.46	0.45
5:D:504:BTB:O4	5:D:504:BTB:C8	2.65	0.45
1:A:298:GLU:OE2	5:A:506:BTB:H41	2.17	0.45
1:A:396:ASP:OD2	1:B:453:SER:OG	2.33	0.44
1:A:233:GLN:HB3	1:A:348:PHE:CE2	2.53	0.44
1:A:197:ASP:OD2	1:A:199:ARG:NH2	2.42	0.44
1:A:234:ARG:NH1	1:A:347:GLU:OE1	2.50	0.44
1:A:292:LEU:HD22	1:A:300:PRO:HB2	1.99	0.44
1:A:317:HIS:CG	1:A:318:PRO:HD2	2.52	0.44
1:A:365:ARG:HH12	3:A:502:H4B:C4	2.30	0.44
1:B:250:ARG:HA	1:B:250:ARG:HD2	1.81	0.44
1:A:147:GLU:O	1:A:151:GLN:NE2	2.44	0.44
1:C:361:GLU:OE2	4:C:503:KMS:N02	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:275:ILE:HD11	1:A:281:PRO:HB3	2.00	0.43
1:A:246:SER:HA	1:A:338:ASN:HB3	2.01	0.43
1:B:238:ARG:NH2	10:B:606:HOH:O	2.46	0.43
5:B:505:BTB:O3	5:B:505:BTB:O1	2.32	0.43
1:C:382:CYS:HA	5:C:504:BTB:H12	2.00	0.43
1:C:156:GLU:O	1:C:160:THR:HG22	2.19	0.43
1:D:285:ARG:NH2	10:D:616:HOH:O	2.51	0.43
5:D:505:BTB:H51	5:D:505:BTB:H32	1.63	0.43
1:D:257:GLN:NE2	10:D:614:HOH:O	2.51	0.43
1:A:447:TRP:HZ3	2:A:501:HEM:HBA2	1.84	0.43
1:C:71:VAL:HG12	10:C:673:HOH:O	2.18	0.43
1:D:262:ARG:HD3	1:D:283:ASN:O	2.19	0.43
1:B:450:PRO:HG3	1:B:457:THR:HG21	2.00	0.42
1:C:414:LYS:HA	1:C:414:LYS:HD3	1.73	0.42
5:A:505:BTB:H41	5:A:505:BTB:H72	1.43	0.42
1:B:202:ARG:HB2	1:B:202:ARG:NH1	2.33	0.42
5:B:506:BTB:H31	5:B:506:BTB:H51	1.82	0.42
1:C:365:ARG:HH12	3:C:502:H4B:C4	2.33	0.42
5:C:504:BTB:H12	5:C:504:BTB:H51	1.83	0.42
1:B:298:GLU:OE2	5:B:505:BTB:H31	2.20	0.42
1:C:358:MET:HE1	10:C:680:HOH:O	2.19	0.42
1:D:68:PHE:CD2	1:D:83:THR:HA	2.55	0.42
1:C:229:THR:O	1:C:352:PRO:HD2	2.20	0.42
1:C:317:HIS:CG	1:C:318:PRO:HD2	2.54	0.42
1:B:124:LEU:O	1:B:128:ARG:HD3	2.19	0.42
1:A:127:ALA:O	1:A:131:ILE:HG12	2.20	0.42
1:A:364:THR:O	1:A:368:CYS:HB2	2.20	0.41
1:C:89:GLN:H	1:C:89:GLN:HG2	1.58	0.41
1:A:298:GLU:OE1	5:A:506:BTB:H32	2.20	0.41
1:A:306:PRO:HA	1:A:307:PRO:HD3	1.97	0.41
1:A:388:ARG:HG2	5:A:505:BTB:H82	2.01	0.41
1:B:321:GLU:OE2	5:B:504:BTB:O4	2.39	0.41
5:D:505:BTB:H52	5:D:505:BTB:H81	1.50	0.41
1:B:338:ASN:HD21	4:B:503:KMS:C22	2.32	0.41
1:C:219:THR:HA	1:C:224:LEU:HD22	2.03	0.41
2:C:501:HEM:HBB2	2:C:501:HEM:CHC	2.48	0.41
5:B:505:BTB:H71	5:B:505:BTB:H62	1.81	0.41
2:D:501:HEM:O2A	4:D:503:KMS:C12	2.69	0.41
1:A:361:GLU:OE2	4:A:503:KMS:N02	2.53	0.41
1:A:229:THR:O	1:A:352:PRO:HD2	2.21	0.41
5:B:506:BTB:H11	5:B:506:BTB:H72	1.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:124:LEU:HD21	1:D:154:GLU:HA	2.03	0.41
1:B:144:GLN:NE2	1:B:145:ALA:H	2.19	0.40
1:C:453:SER:HB3	1:C:456:LEU:HD12	2.03	0.40
1:D:90:GLN:HB3	1:D:468:PHE:CD2	2.57	0.40
1:A:170:LEU:HD11	1:A:230:VAL:HG11	2.03	0.40
1:C:261:VAL:HG11	1:C:265:PRO:HA	2.03	0.40
1:B:97:ARG:CZ	1:B:97:ARG:HB3	2.51	0.40
1:C:273:LEU:HD23	1:C:273:LEU:HA	1.94	0.40
1:C:129:ASP:HA	1:C:132:ASN:ND2	2.37	0.40
1:C:246:SER:HA	1:C:338:ASN:HB3	2.04	0.40
1:C:254:TYR:O	1:C:261:VAL:HA	2.21	0.40

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)
10:B:647:HOH:O	10:D:628:HOH:O[1_556]	2.19	0.01

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	399/440 (91%)	386 (97%)	10 (2%)	3 (1%)	16	6
1	B	401/440 (91%)	392 (98%)	9 (2%)	0	100	100
1	C	399/440 (91%)	383 (96%)	15 (4%)	1 (0%)	36	25
1	D	401/440 (91%)	393 (98%)	8 (2%)	0	100	100
All	All	1600/1760 (91%)	1554 (97%)	42 (3%)	4 (0%)	36	25

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	89	GLN
1	A	89	GLN
1	A	144	GLN
1	A	255	ARG

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%)	329 (96%)	14 (4%)	27	15
1	B	344/373 (92%)	330 (96%)	14 (4%)	27	15
1	C	342/373 (92%)	331 (97%)	11 (3%)	34	22
1	D	344/373 (92%)	338 (98%)	6 (2%)	53	45
All	All	1373/1492 (92%)	1328 (97%)	45 (3%)	34	21

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	71	VAL
1	A	90	GLN
1	A	121	GLU
1	A	124	LEU
1	A	140	ARG
1	A	143	SER
1	A	235	CYS
1	A	238	ARG
1	A	256	GLN
1	A	291	LEU
1	A	304	LEU
1	A	309	LEU
1	A	321	GLU
1	A	329	ARG
1	B	67	LYS
1	B	89	GLN
1	B	122	GLN
1	B	128	ARG

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Mol	Chain	Res	Type
1	B	139	LYS
1	B	148	GLN
1	B	168[A]	SER
1	B	168[B]	SER
1	B	202	ARG
1	B	255	ARG
1	B	257	GLN
1	B	258	ASP
1	B	309	LEU
1	B	326	LEU
1	C	71	VAL
1	C	89	GLN
1	C	121	GLU
1	C	124	LEU
1	C	132	ASN
1	C	138	ILE
1	C	141	SER
1	C	151	GLN
1	C	200	ASP
1	C	256	GLN
1	C	308	GLU
1	D	97	ARG
1	D	98	ARG
1	D	200	ASP
1	D	230	VAL
1	D	309	LEU
1	D	326	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	133	GLN
1	A	148	GLN
1	C	133	GLN
1	C	256	GLN
1	C	403	ASN
1	D	126	GLN
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 ⓘ

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 35 ligands modelled in this entry, 10 are monoatomic - leaving 25 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	BTB	C	504	9	13,13,13	0.38	0	7,16,16	0.65	0
5	BTB	C	505	-	13,13,13	0.69	0	7,16,16	1.02	1 (14%)
5	BTB	B	506	-	13,13,13	0.34	0	7,16,16	0.50	0
5	BTB	A	504	9	13,13,13	0.37	0	7,16,16	0.73	0
4	KMS	B	503	-	26,26,26	0.57	0	33,36,36	1.84	7 (21%)
3	H4B	C	502	-	17,18,18	0.93	0	14,26,26	1.89	5 (35%)
2	HEM	B	501	1	50,50,50	1.62	9 (18%)	67,82,82	1.32	6 (8%)
2	HEM	C	501	1	50,50,50	1.64	7 (14%)	67,82,82	1.49	9 (13%)
5	BTB	D	505	-	13,13,13	0.41	0	7,16,16	0.84	0
5	BTB	C	506	-	13,13,13	0.36	0	7,16,16	0.31	0
2	HEM	A	501	1	50,50,50	1.62	8 (16%)	67,82,82	1.39	8 (11%)
5	BTB	B	504	9	13,13,13	0.44	0	7,16,16	0.85	0
5	BTB	A	505	-	13,13,13	0.40	0	7,16,16	0.46	0
4	KMS	C	503	-	26,26,26	0.57	0	33,36,36	2.22	8 (24%)
5	BTB	A	506	-	13,13,13	0.34	0	7,16,16	0.43	0
5	BTB	B	505	-	13,13,13	0.50	0	7,16,16	0.93	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	H4B	D	502	-	17,18,18	0.95	1 (5%)	14,26,26	1.82	4 (28%)
7	GOL	C	508	-	5,5,5	0.34	0	5,5,5	0.37	0
4	KMS	A	503	-	26,26,26	0.52	0	33,36,36	1.83	6 (18%)
5	BTB	D	504	9	13,13,13	0.39	0	7,16,16	0.95	0
2	HEM	D	501	1	50,50,50	1.76	10 (20%)	67,82,82	1.36	11 (16%)
7	GOL	A	508	-	5,5,5	0.33	0	5,5,5	0.40	0
3	H4B	B	502	-	17,18,18	0.92	0	14,26,26	1.81	4 (28%)
4	KMS	D	503	-	26,26,26	0.42	0	33,36,36	2.21	8 (24%)
3	H4B	A	502	-	17,18,18	0.92	0	14,26,26	1.82	4 (28%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	BTB	C	504	9	-	2/21/21/21	-
5	BTB	C	505	-	-	9/21/21/21	-
5	BTB	B	506	-	-	0/21/21/21	-
5	BTB	A	504	9	-	3/21/21/21	-
4	KMS	B	503	-	-	5/11/11/11	0/2/2/2
3	H4B	C	502	-	-	0/8/17/17	0/2/2/2
2	HEM	B	501	1	-	3/14/54/54	-
2	HEM	C	501	1	-	3/14/54/54	-
5	BTB	D	505	-	-	2/21/21/21	-
5	BTB	C	506	-	-	9/21/21/21	-
2	HEM	A	501	1	-	3/14/54/54	-
5	BTB	B	504	9	-	0/21/21/21	-
5	BTB	A	505	-	-	14/21/21/21	-
4	KMS	C	503	-	-	9/11/11/11	0/2/2/2
5	BTB	A	506	-	-	4/21/21/21	-
5	BTB	B	505	-	-	5/21/21/21	-
3	H4B	D	502	-	-	0/8/17/17	0/2/2/2
7	GOL	C	508	-	-	2/4/4/4	-
4	KMS	A	503	-	-	5/11/11/11	0/2/2/2
5	BTB	D	504	9	-	5/21/21/21	-
2	HEM	D	501	1	-	1/14/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	GOL	A	508	-	-	2/4/4/4	-
3	H4B	B	502	-	-	0/8/17/17	0/2/2/2
4	KMS	D	503	-	-	7/11/11/11	0/2/2/2
3	H4B	A	502	-	-	0/8/17/17	0/2/2/2

All (35) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	501	HEM	FE-NB	5.87	2.13	1.94
2	B	501	HEM	FE-NB	5.28	2.11	1.94
2	C	501	HEM	FE-NA	4.93	2.11	1.95
2	D	501	HEM	FE-NC	4.82	2.11	1.95
2	C	501	HEM	FE-NC	4.55	2.10	1.95
2	A	501	HEM	FE-NB	4.53	2.08	1.94
2	A	501	HEM	FE-NA	4.39	2.09	1.95
2	A	501	HEM	FE-NC	3.94	2.08	1.95
2	C	501	HEM	FE-ND	3.78	2.06	1.94
2	A	501	HEM	FE-ND	3.77	2.06	1.94
2	C	501	HEM	FE-NB	3.74	2.06	1.94
2	B	501	HEM	FE-NC	3.74	2.07	1.95
2	D	501	HEM	FE-NA	3.43	2.06	1.95
2	B	501	HEM	FE-NA	3.22	2.05	1.95
2	D	501	HEM	CAC-C3C	3.05	1.55	1.47
2	C	501	HEM	CAC-C3C	3.04	1.55	1.47
2	B	501	HEM	CAC-C3C	3.01	1.55	1.47
2	A	501	HEM	CAB-C3B	2.99	1.55	1.47
2	D	501	HEM	CAB-C3B	2.99	1.55	1.47
2	B	501	HEM	CAB-C3B	2.97	1.55	1.47
2	A	501	HEM	CAC-C3C	2.91	1.55	1.47
2	C	501	HEM	CAB-C3B	2.85	1.55	1.47
2	B	501	HEM	CMA-C3A	2.79	1.56	1.50
2	D	501	HEM	CMA-C3A	2.65	1.56	1.50
2	B	501	HEM	FE-ND	2.60	2.02	1.94
2	D	501	HEM	CMD-C2D	2.51	1.55	1.50
2	B	501	HEM	CMD-C2D	2.51	1.55	1.50
2	D	501	HEM	CMB-C2B	2.50	1.55	1.50
2	D	501	HEM	FE-ND	2.35	2.02	1.94
2	C	501	HEM	CMC-C2C	2.22	1.55	1.50
2	B	501	HEM	C2A-C3A	-2.17	1.33	1.38
2	A	501	HEM	CMC-C2C	2.13	1.55	1.50
2	D	501	HEM	O2D-CGD	-2.09	1.23	1.30
2	A	501	HEM	CMB-C2B	2.05	1.55	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	502	H4B	C4-N3	-2.02	1.35	1.38

All (81) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	503	KMS	C02-N01-C06	8.14	124.16	118.07
4	A	503	KMS	C02-N01-C06	6.89	123.22	118.07
4	B	503	KMS	C02-N01-C06	6.55	122.97	118.07
4	D	503	KMS	C02-N01-C06	5.36	122.08	118.07
4	D	503	KMS	C09-C11-C12	4.94	124.70	120.73
4	C	503	KMS	F12-C12-C11	4.58	124.20	118.00
4	D	503	KMS	F12-C12-C11	4.58	124.19	118.00
4	D	503	KMS	C17-C15-C14	4.47	124.32	120.73
3	B	502	H4B	C2-N1-C8A	4.19	120.75	113.36
3	A	502	H4B	C2-N1-C8A	4.05	120.51	113.36
3	D	502	H4B	C2-N1-C8A	3.92	120.28	113.36
3	C	502	H4B	C2-N1-C8A	3.89	120.22	113.36
4	C	503	KMS	C09-C11-C12	3.82	123.80	120.73
2	C	501	HEM	C3B-C4B-NB	-3.80	106.74	109.47
4	D	503	KMS	C18-C19-N20	-3.78	103.93	113.71
4	B	503	KMS	C05-C06-N01	-3.78	118.43	122.73
4	D	503	KMS	F14-C14-C15	3.70	123.00	118.00
2	D	501	HEM	CBD-CAD-C3D	-3.57	102.67	112.53
2	B	501	HEM	C2A-C1A-NA	-3.52	106.25	110.15
2	D	501	HEM	C2A-C1A-NA	-3.51	106.25	110.15
4	C	503	KMS	C05-C06-N01	-3.50	118.75	122.73
2	A	501	HEM	C3B-C4B-NB	-3.39	107.03	109.47
4	B	503	KMS	F14-C14-C15	3.37	122.56	118.00
2	C	501	HEM	C3D-C4D-ND	-3.33	106.52	110.17
4	A	503	KMS	C05-C06-N01	-3.29	118.98	122.73
3	D	502	H4B	O4-C4-C4A	-3.17	119.61	127.26
4	D	503	KMS	C05-C06-N01	-3.15	119.14	122.73
3	C	502	H4B	O4-C4-C4A	-3.10	119.79	127.26
4	B	503	KMS	F12-C12-C11	3.09	122.18	118.00
2	A	501	HEM	C1B-NB-C4B	2.98	108.74	105.21
4	C	503	KMS	F14-C14-C15	2.95	121.99	118.00
3	A	502	H4B	O4-C4-C4A	-2.92	120.22	127.26
4	A	503	KMS	C09-C08-C06	2.90	119.47	113.01
2	C	501	HEM	C4D-ND-C1D	2.83	108.56	105.21
2	C	501	HEM	C2A-C1A-NA	-2.81	107.03	110.15
3	B	502	H4B	O4-C4-C4A	-2.79	120.52	127.26
2	A	501	HEM	C4D-ND-C1D	2.77	108.48	105.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	501	HEM	C1B-NB-C4B	2.75	108.46	105.21
4	A	503	KMS	C17-C15-C14	-2.73	118.54	120.73
2	A	501	HEM	C3D-C4D-ND	-2.72	107.19	110.17
2	D	501	HEM	C4A-NA-C1A	2.71	110.23	105.82
2	D	501	HEM	C4C-NC-C1C	2.67	110.18	105.82
2	B	501	HEM	CBD-CAD-C3D	-2.65	105.22	112.53
2	A	501	HEM	C3B-C2B-C1B	2.61	108.37	106.41
2	C	501	HEM	CBD-CAD-C3D	-2.61	105.33	112.53
2	B	501	HEM	CHC-C1C-NC	2.59	127.28	124.45
3	B	502	H4B	C4A-C4-N3	2.58	119.22	112.13
3	D	502	H4B	C2-N3-C4	-2.56	120.47	125.11
3	D	502	H4B	C4A-C4-N3	2.54	119.12	112.13
3	A	502	H4B	C4A-C4-N3	2.51	119.03	112.13
4	A	503	KMS	F12-C12-C11	2.51	121.39	118.00
2	C	501	HEM	CHA-C4D-ND	2.49	127.45	124.37
2	C	501	HEM	CAD-CBD-CGD	-2.49	107.07	113.67
4	C	503	KMS	C09-C08-C06	2.48	118.54	113.01
3	A	502	H4B	C2-N3-C4	-2.48	120.62	125.11
4	B	503	KMS	C08-C06-C05	2.45	125.21	121.65
2	D	501	HEM	C3D-C4D-ND	-2.45	107.48	110.17
4	B	503	KMS	C09-C08-C06	2.41	118.37	113.01
2	C	501	HEM	C3B-C2B-C1B	2.38	108.20	106.41
2	B	501	HEM	CHA-C1A-NA	2.37	128.16	123.86
2	B	501	HEM	C3B-C2B-C1B	2.37	108.19	106.41
2	B	501	HEM	C4A-NA-C1A	2.37	109.68	105.82
3	C	502	H4B	C4A-C4-N3	2.36	118.62	112.13
4	D	503	KMS	C18-C17-C15	2.36	121.35	114.13
3	C	502	H4B	C11-C10-C9	-2.31	109.28	112.11
2	A	501	HEM	CBD-CAD-C3D	-2.30	106.19	112.53
2	D	501	HEM	CBA-CAA-C2A	-2.30	106.19	112.53
2	D	501	HEM	CHD-C4C-NC	2.28	126.94	124.45
2	D	501	HEM	CMB-C2B-C1B	2.25	128.56	125.03
5	C	505	BTB	O3-C3-C2	-2.25	106.10	111.40
4	A	503	KMS	N02-C02-N01	2.24	120.19	116.59
4	C	503	KMS	C03-C04-C05	2.21	120.57	118.11
4	C	503	KMS	C14-C13-C12	2.21	121.77	119.53
2	A	501	HEM	CAD-CBD-CGD	-2.20	107.83	113.67
2	D	501	HEM	CHC-C1C-NC	2.17	126.81	124.45
2	D	501	HEM	C3A-C4A-NA	-2.16	106.68	110.14
3	B	502	H4B	C2-N3-C4	-2.15	121.21	125.11
3	C	502	H4B	C2-N3-C4	-2.14	121.22	125.11
2	A	501	HEM	C2A-C1A-NA	-2.11	107.81	110.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	503	KMS	C07-C04-C03	-2.11	118.06	120.92
2	D	501	HEM	C4D-ND-C1D	2.03	107.61	105.21

There are no chirality outliers.

All (93) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	503	KMS	C15-C17-C18-C19
4	B	503	KMS	C14-C15-C17-C18
4	C	503	KMS	C08-C09-C11-C12
4	C	503	KMS	C08-C09-C11-C16
4	C	503	KMS	C15-C17-C18-C19
4	D	503	KMS	C08-C09-C11-C12
4	D	503	KMS	C08-C09-C11-C16
4	D	503	KMS	C14-C15-C17-C18
4	D	503	KMS	C16-C15-C17-C18
5	A	504	BTB	O1-C1-C2-C3
5	A	504	BTB	O1-C1-C2-N
5	A	504	BTB	C3-C2-C4-O4
5	A	505	BTB	C1-C2-C3-O3
5	A	505	BTB	C4-C2-C3-O3
5	A	505	BTB	N-C2-C3-O3
5	A	505	BTB	C1-C2-C4-O4
5	A	505	BTB	C3-C2-C4-O4
5	A	505	BTB	C1-C2-N-C5
5	A	505	BTB	C1-C2-N-C7
5	A	505	BTB	C3-C2-N-C5
5	A	505	BTB	C3-C2-N-C7
5	A	505	BTB	C4-C2-N-C5
5	A	505	BTB	C4-C2-N-C7
5	A	506	BTB	O1-C1-C2-C3
5	A	506	BTB	O1-C1-C2-C4
5	A	506	BTB	O1-C1-C2-N
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	C	505	BTB	O1-C1-C2-C3
5	C	505	BTB	O1-C1-C2-C4
5	C	505	BTB	O1-C1-C2-N
5	C	505	BTB	C1-C2-C3-O3
5	C	505	BTB	C4-C2-C3-O3
5	C	505	BTB	N-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
5	C	505	BTB	C3-C2-C4-O4
5	C	505	BTB	N-C2-C4-O4
5	C	506	BTB	O1-C1-C2-C4
5	C	506	BTB	O1-C1-C2-N
5	C	506	BTB	C1-C2-C3-O3
5	C	506	BTB	C4-C2-C3-O3
5	C	506	BTB	N-C2-C3-O3
5	C	506	BTB	C3-C2-C4-O4
5	C	506	BTB	N-C2-C4-O4
5	D	504	BTB	O1-C1-C2-C4
5	D	504	BTB	O1-C1-C2-N
5	D	504	BTB	C1-C2-C4-O4
5	D	504	BTB	C3-C2-C4-O4
5	D	504	BTB	N-C2-C4-O4
5	D	505	BTB	C8-C7-N-C5
7	C	508	GOL	C1-C2-C3-O3
4	B	503	KMS	C16-C15-C17-C18
2	A	501	HEM	C2A-CAA-CBA-CGA
2	B	501	HEM	C2A-CAA-CBA-CGA
2	C	501	HEM	C2A-CAA-CBA-CGA
4	D	503	KMS	C18-C19-N20-C21
4	B	503	KMS	C17-C18-C19-N20
4	B	503	KMS	C08-C09-C11-C16
4	C	503	KMS	C16-C15-C17-C18
4	D	503	KMS	C17-C18-C19-N20
4	C	503	KMS	C18-C19-N20-C21
4	C	503	KMS	C18-C19-N20-C22
4	D	503	KMS	C18-C19-N20-C22
4	A	503	KMS	C18-C19-N20-C22
7	A	508	GOL	C1-C2-C3-O3
4	A	503	KMS	C18-C19-N20-C21
5	A	505	BTB	O1-C1-C2-C4
7	C	508	GOL	O2-C2-C3-O3
2	C	501	HEM	C1A-C2A-CAA-CBA
4	A	503	KMS	C17-C18-C19-N20
4	A	503	KMS	C08-C09-C11-C16
5	B	505	BTB	C3-C2-C4-O4
5	A	505	BTB	N-C7-C8-O8
7	A	508	GOL	O2-C2-C3-O3
2	A	501	HEM	C4B-C3B-CAB-CBB
2	B	501	HEM	C4B-C3B-CAB-CBB
5	A	506	BTB	N-C7-C8-O8

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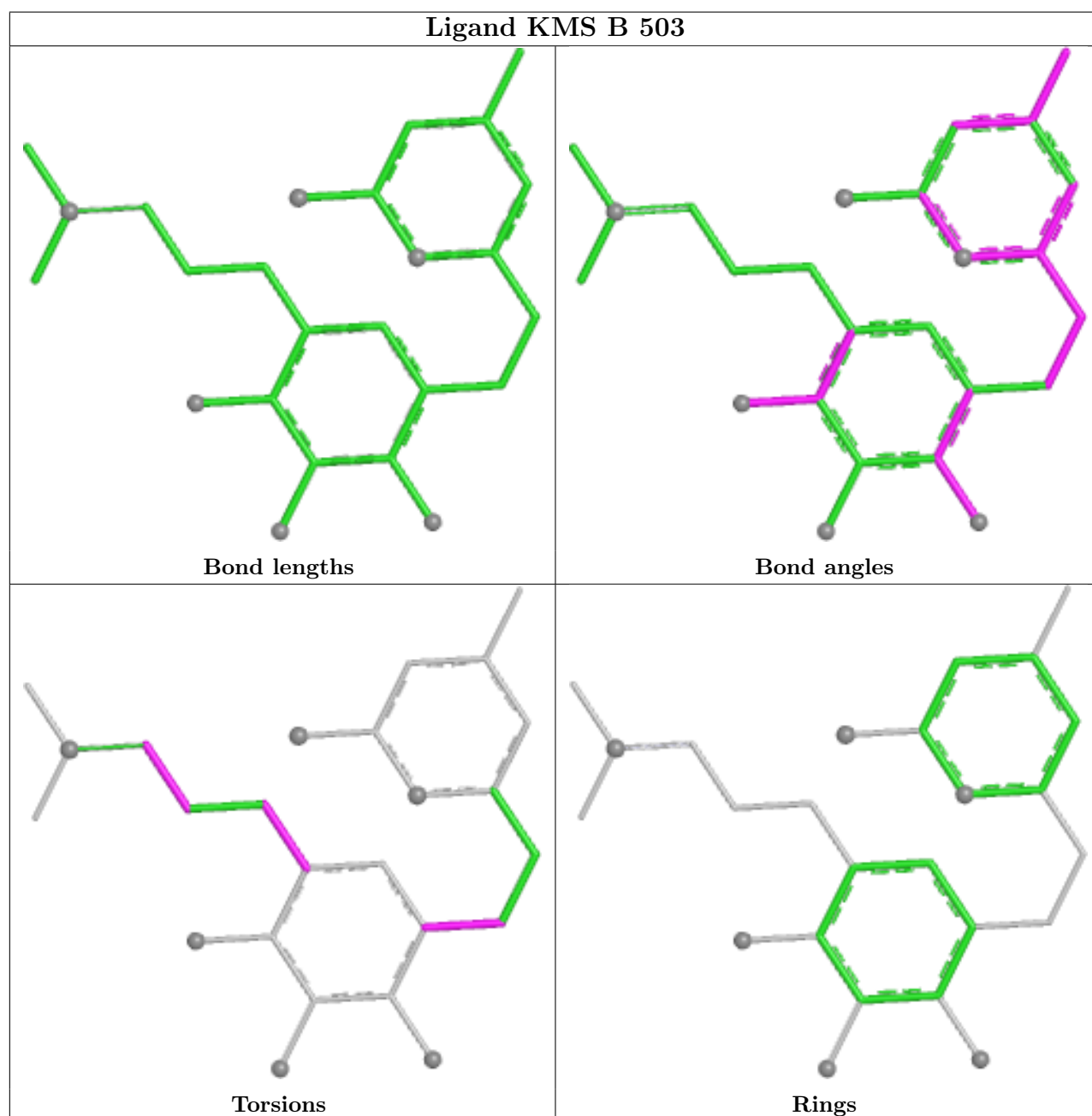
Mol	Chain	Res	Type	Atoms
5	A	505	BTB	N-C2-C4-O4
4	B	503	KMS	C08-C09-C11-C12
4	C	503	KMS	C14-C15-C17-C18
2	A	501	HEM	C1A-C2A-CAA-CBA
2	D	501	HEM	C2A-CAA-CBA-CGA
5	C	506	BTB	O1-C1-C2-C3
2	C	501	HEM	C3A-C2A-CAA-CBA
5	C	505	BTB	N-C5-C6-O6
2	B	501	HEM	C1A-C2A-CAA-CBA
5	B	505	BTB	N-C7-C8-O8
4	C	503	KMS	N01-C06-C08-C09
5	C	504	BTB	C4-C2-C3-O3
5	C	506	BTB	C1-C2-C4-O4
4	C	503	KMS	C05-C06-C08-C09
5	C	504	BTB	O1-C1-C2-N
5	D	505	BTB	C1-C2-N-C7

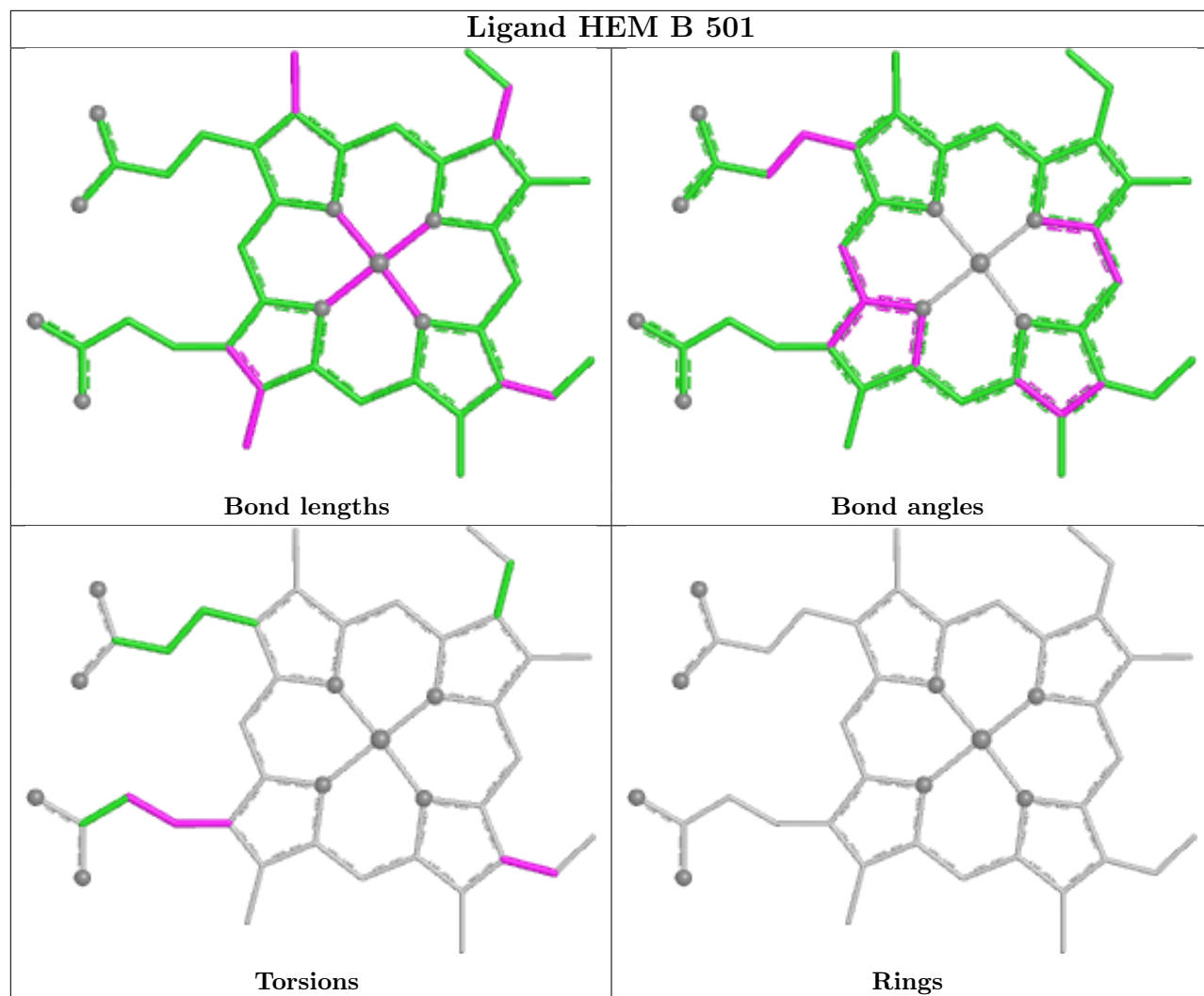
There are no ring outliers.

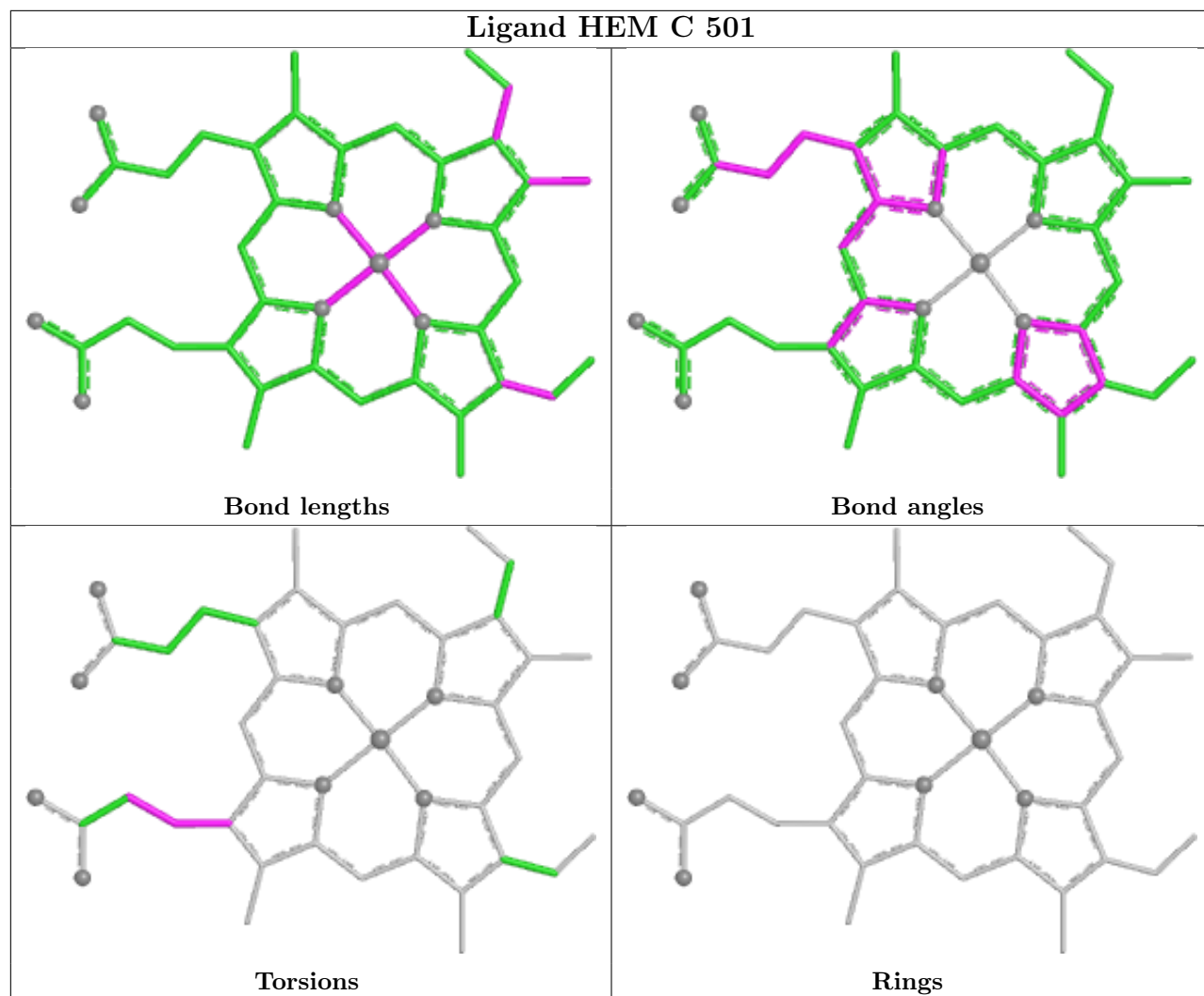
21 monomers are involved in 48 short contacts:

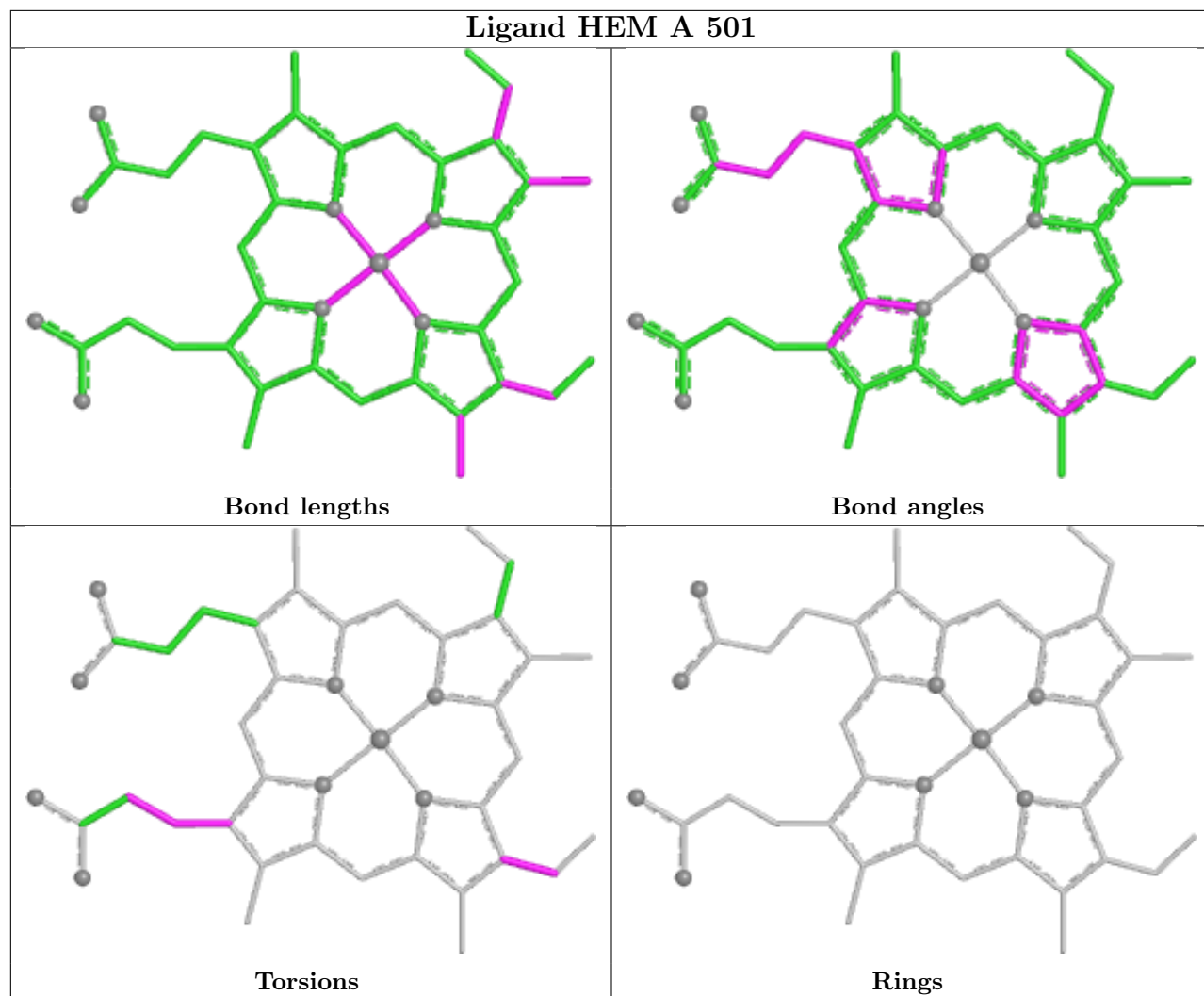
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	504	BTB	3	0
5	C	505	BTB	1	0
5	B	506	BTB	2	0
5	A	504	BTB	2	0
4	B	503	KMS	1	0
3	C	502	H4B	1	0
2	B	501	HEM	2	0
2	C	501	HEM	3	0
5	D	505	BTB	3	0
5	C	506	BTB	2	0
2	A	501	HEM	5	0
5	B	504	BTB	2	0
5	A	505	BTB	5	0
4	C	503	KMS	1	0
5	A	506	BTB	3	0
5	B	505	BTB	4	0
4	A	503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

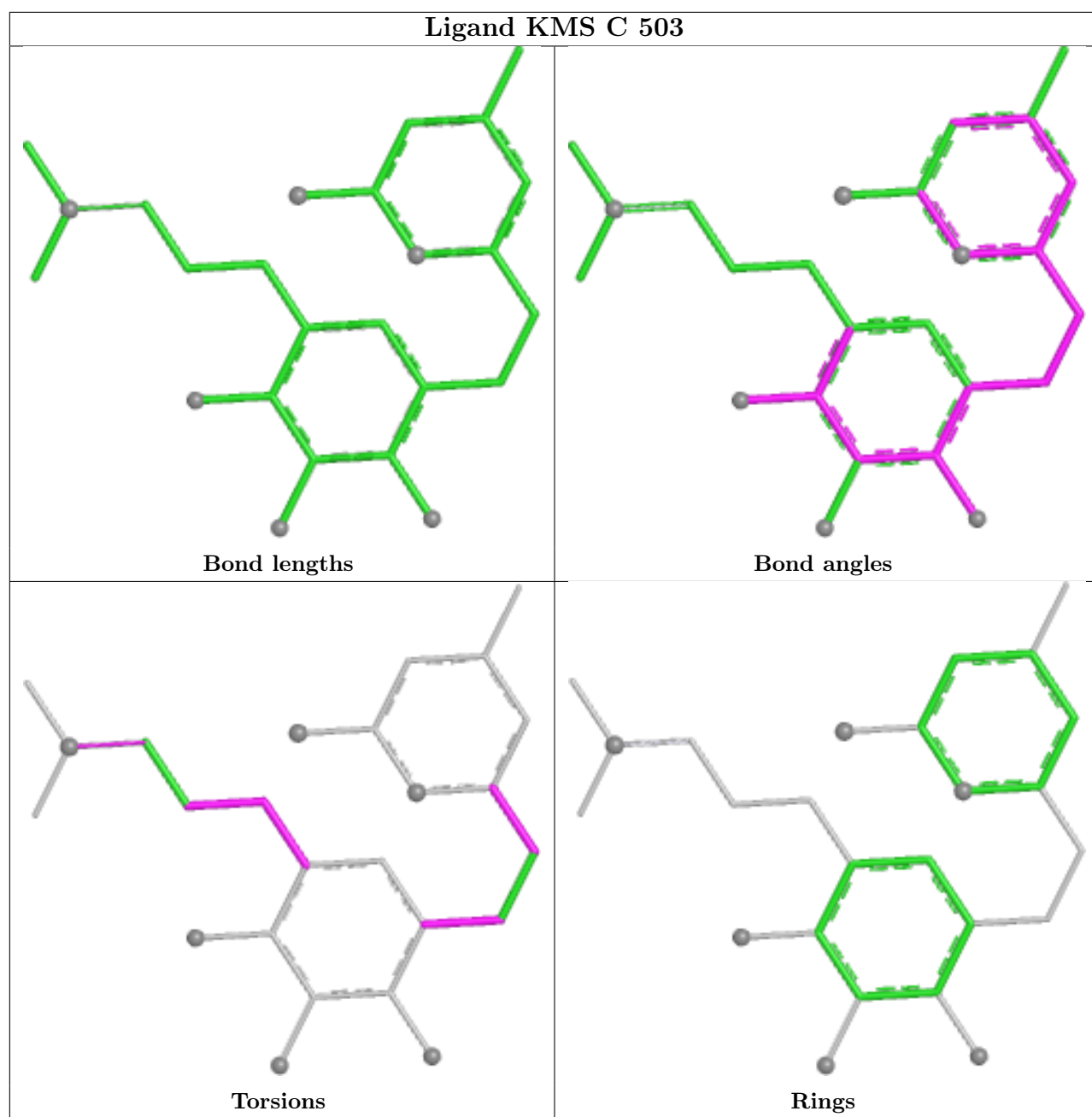
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

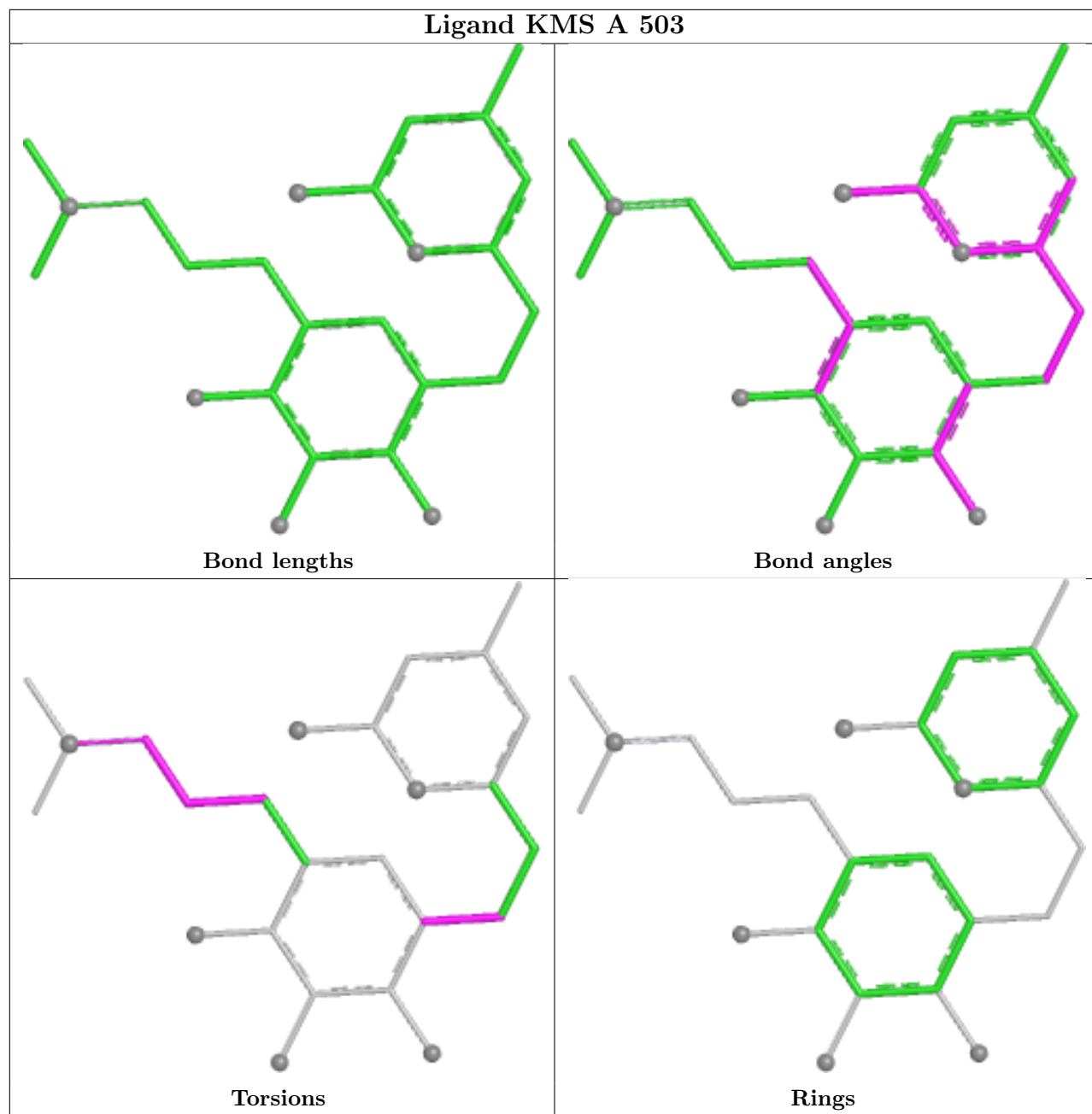


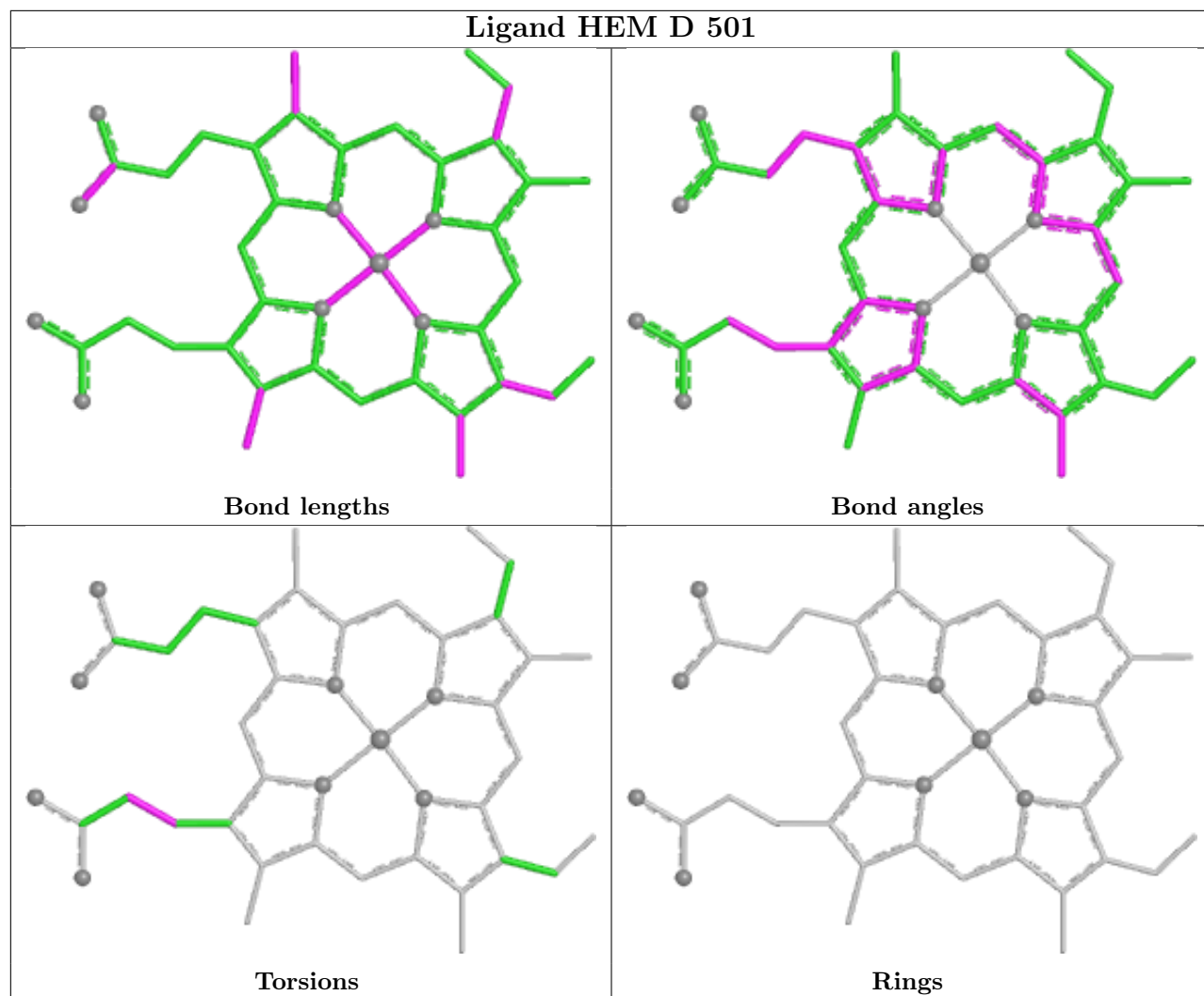


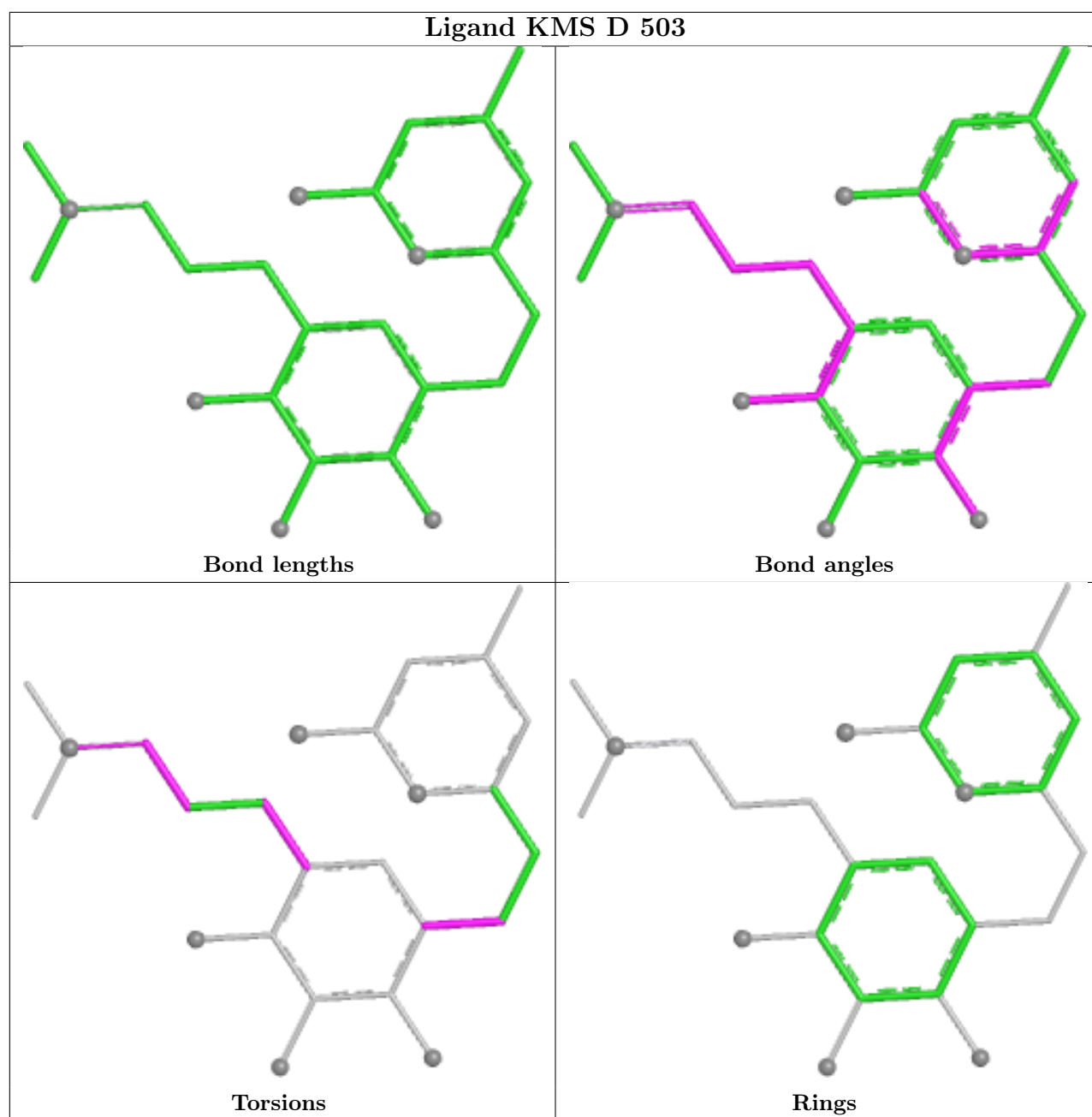












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	401/440 (91%)	0.80	39 (9%) 13 11	22, 50, 95, 118	2 (0%)
1	B	402/440 (91%)	0.13	6 (1%) 72 72	18, 33, 64, 96	3 (0%)
1	C	401/440 (91%)	0.58	29 (7%) 21 20	20, 46, 90, 119	2 (0%)
1	D	402/440 (91%)	0.07	9 (2%) 62 62	18, 31, 57, 108	3 (0%)
All	All	1606/1760 (91%)	0.40	83 (5%) 33 31	18, 39, 85, 119	10 (0%)

All (83) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	120	PRO	5.2
1	D	119	ALA	4.8
1	C	155	ALA	4.4
1	C	106	PRO	4.2
1	A	204	ALA	4.1
1	B	106	PRO	3.7
1	D	106	PRO	3.6
1	C	124	LEU	3.4
1	A	106	PRO	3.4
1	C	142	GLY	3.4
1	C	150	LEU	3.4
1	C	159	ALA	3.2
1	C	157	VAL	3.2
1	A	295	ALA	3.1
1	C	158	ALA	3.1
1	C	237	GLY	3.1
1	A	153	VAL	3.0
1	A	237	GLY	3.0
1	C	257	GLN	3.0
1	C	148	GLN	2.9
1	A	158	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	145	ALA	2.8
1	C	119	ALA	2.8
1	A	107	ARG	2.8
1	B	144	GLN	2.8
1	A	165	LEU	2.8
1	B	257	GLN	2.7
1	A	143	SER	2.7
1	A	155	ALA	2.7
1	A	131	ILE	2.7
1	A	345	GLY	2.7
1	C	238	ARG	2.7
1	C	120	PRO	2.6
1	C	163	TYR	2.6
1	A	163	TYR	2.5
1	A	304	LEU	2.5
1	C	160	THR	2.5
1	A	157	VAL	2.5
1	D	259	GLY	2.4
1	A	254	TYR	2.4
1	B	77	GLY	2.4
1	C	161	GLY	2.4
1	A	480	TRP	2.4
1	A	303	PHE	2.3
1	A	142	GLY	2.3
1	D	67	LYS	2.3
1	C	140	ARG	2.3
1	A	171	VAL	2.3
1	D	89	GLN	2.3
1	A	138	ILE	2.3
1	A	127	ALA	2.2
1	A	236	PRO	2.2
1	A	275	ILE	2.2
1	A	257	GLN	2.2
1	C	141	SER	2.2
1	A	159	ALA	2.2
1	C	204	ALA	2.2
1	A	241	PHE	2.2
1	C	468	PHE	2.2
1	D	468	PHE	2.2
1	A	244	TRP	2.2
1	A	124	LEU	2.2
1	A	293	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	479	PRO	2.2
1	A	192	LYS	2.2
1	D	90	GLN	2.1
1	C	129	ASP	2.1
1	C	153	VAL	2.1
1	B	78	SER	2.1
1	A	150	LEU	2.1
1	A	300	PRO	2.1
1	B	67	LYS	2.1
1	C	244	TRP	2.1
1	D	257	GLN	2.1
1	C	156	GLU	2.1
1	C	207	MET	2.1
1	A	90	GLN	2.1
1	D	255	ARG	2.1
1	A	231	PHE	2.0
1	A	212	CYS	2.0
1	C	480	TRP	2.0
1	C	294	GLN	2.0
1	C	236	PRO	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($\text{\AA}^2$)	Q<0.9
5	BTB	C	506	14/14	0.61	0.16	76,83,85,86	0
5	BTB	B	506	14/14	0.63	0.15	86,89,100,101	0
5	BTB	A	506	14/14	0.65	0.17	84,102,113,114	0

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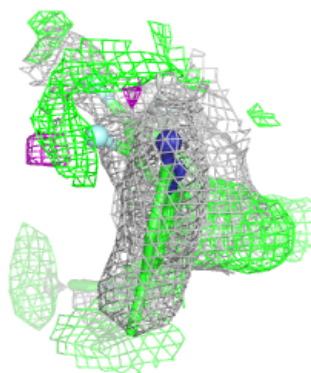
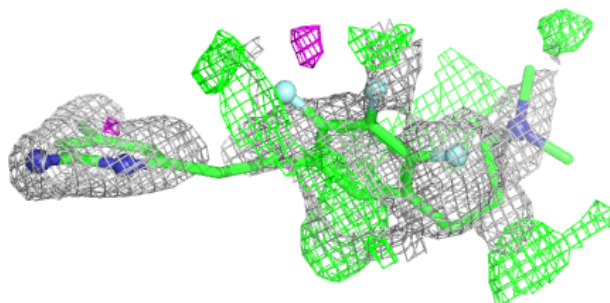
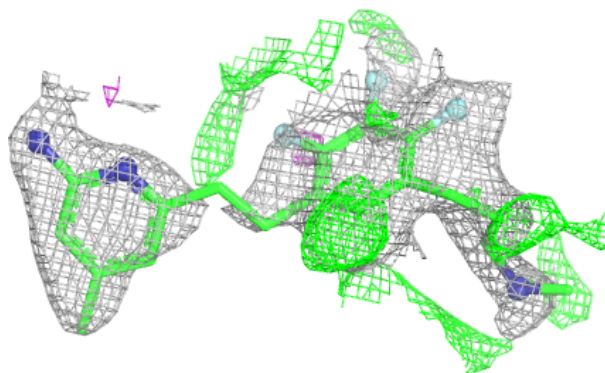
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	KMS	A	503	25/25	0.67	0.26	48,96,105,108	0
4	KMS	C	503	25/25	0.71	0.25	35,80,116,125	0
5	BTB	C	505	14/14	0.72	0.20	46,64,71,73	0
5	BTB	A	505	14/14	0.75	0.17	65,81,87,89	0
5	BTB	D	505	14/14	0.76	0.16	59,63,75,75	0
7	GOL	A	508	6/6	0.78	0.16	53,67,78,81	0
5	BTB	D	504	14/14	0.79	0.18	37,59,78,84	0
5	BTB	B	505	14/14	0.80	0.15	31,54,62,71	0
7	GOL	C	508	6/6	0.80	0.14	57,65,75,75	0
4	KMS	B	503	25/25	0.81	0.21	28,83,118,121	0
4	KMS	D	503	25/25	0.85	0.20	27,86,107,114	0
5	BTB	A	504	14/14	0.88	0.13	47,73,78,79	0
5	BTB	B	504	14/14	0.88	0.14	30,47,66,68	0
3	H4B	C	502	17/17	0.90	0.11	34,48,53,54	0
3	H4B	A	502	17/17	0.92	0.09	37,48,56,57	0
3	H4B	D	502	17/17	0.92	0.09	29,38,46,47	0
3	H4B	B	502	17/17	0.93	0.09	25,38,45,50	0
2	HEM	A	501	43/43	0.95	0.12	33,46,61,63	0
5	BTB	C	504	14/14	0.95	0.11	12,56,64,68	0
8	CL	A	509	1/1	0.95	0.09	59,59,59,59	0
9	GD	A	510	1/1	0.95	0.09	90,90,90,90	0
8	CL	B	507	1/1	0.96	0.14	41,41,41,41	0
2	HEM	C	501	43/43	0.96	0.09	24,35,61,67	0
9	GD	C	510	1/1	0.96	0.11	80,80,80,80	0
9	GD	D	507	1/1	0.96	0.06	36,36,36,36	0
8	CL	D	506	1/1	0.97	0.09	38,38,38,38	0
8	CL	C	509	1/1	0.97	0.07	46,46,46,46	0
2	HEM	D	501	43/43	0.98	0.07	14,22,43,56	0
9	GD	B	508	1/1	0.98	0.04	34,34,34,34	0
2	HEM	B	501	43/43	0.98	0.07	14,22,52,65	0
6	ZN	A	507	1/1	0.98	0.05	32,32,32,32	0
6	ZN	C	507	1/1	1.00	0.01	28,28,28,28	0

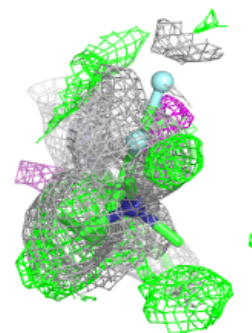
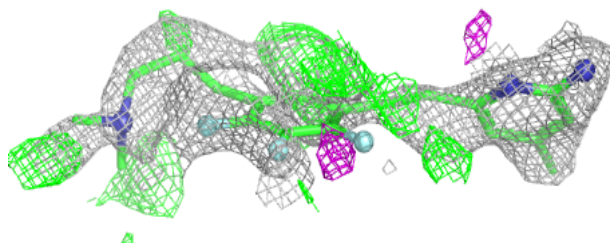
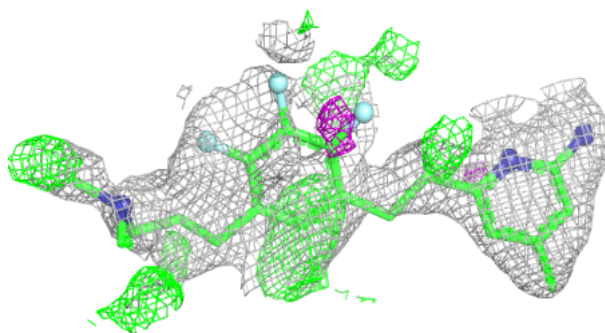
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around KMS 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)

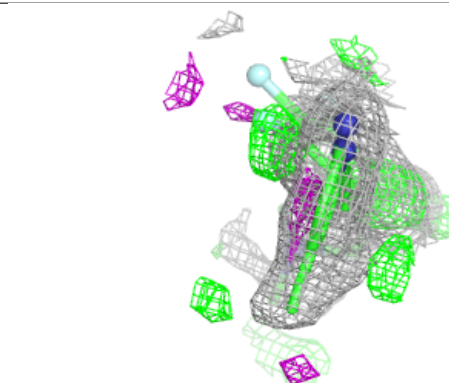
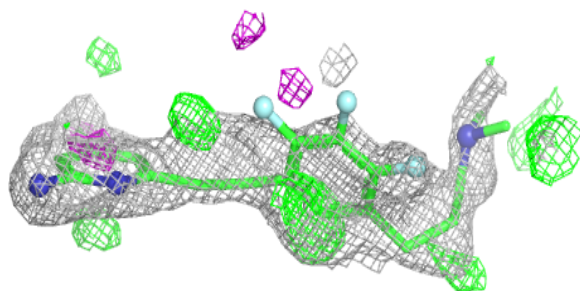
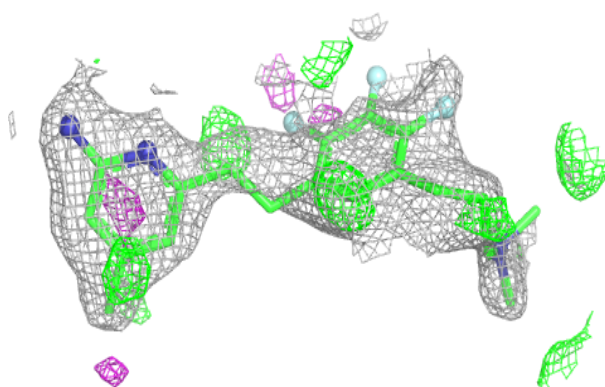
**Electron density around KMS C 503:**

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

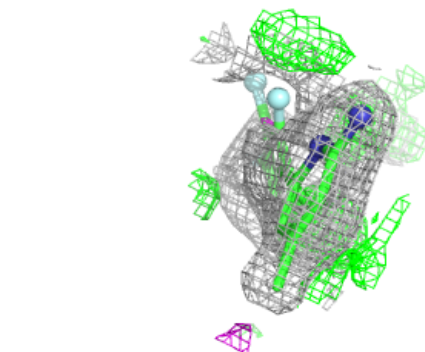
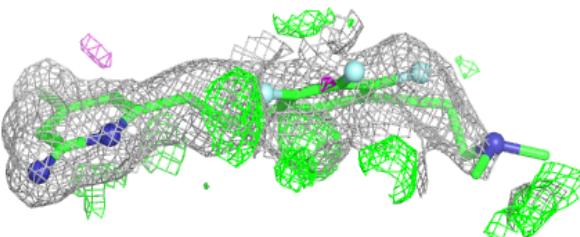
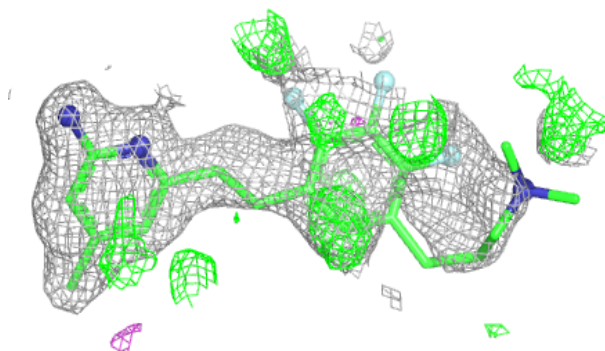


Electron density around KMS B 503:

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

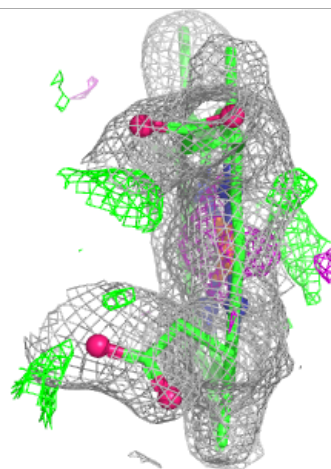
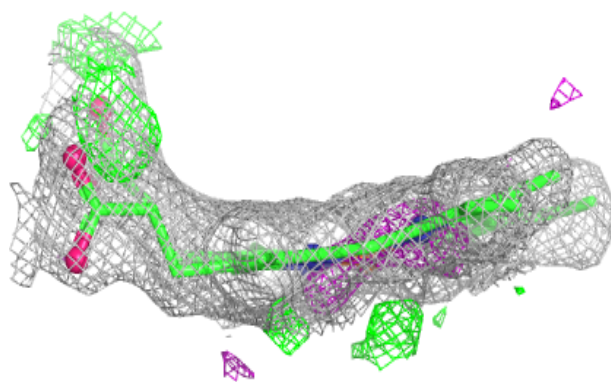
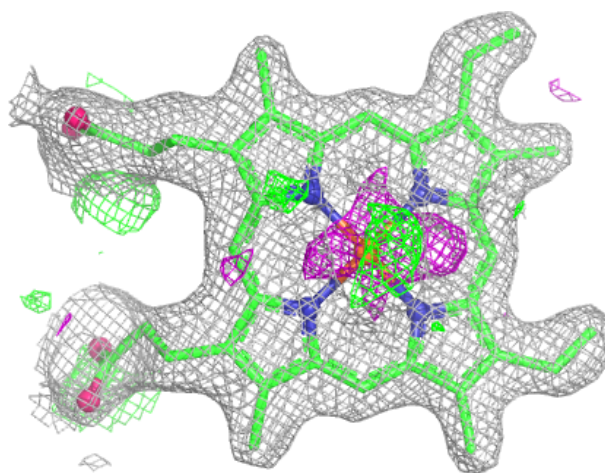
**Electron density around KMS D 503:**

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



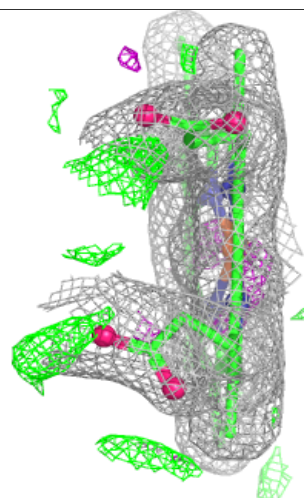
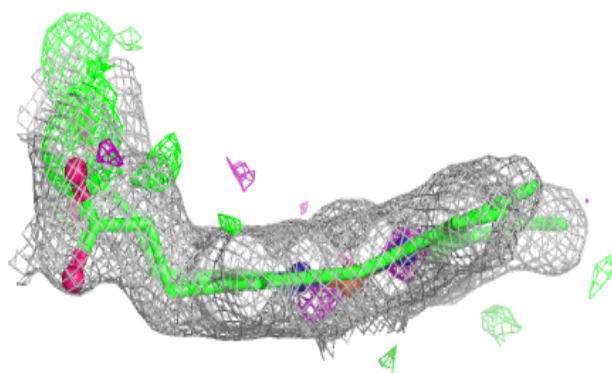
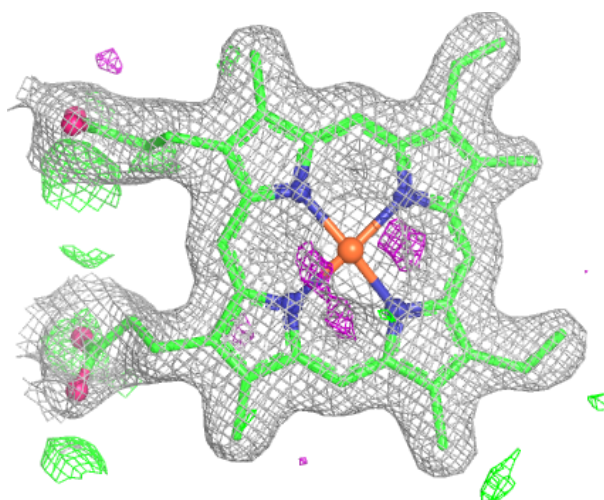
Electron density around HEM A 501:

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



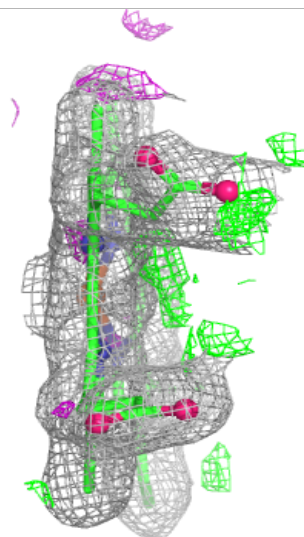
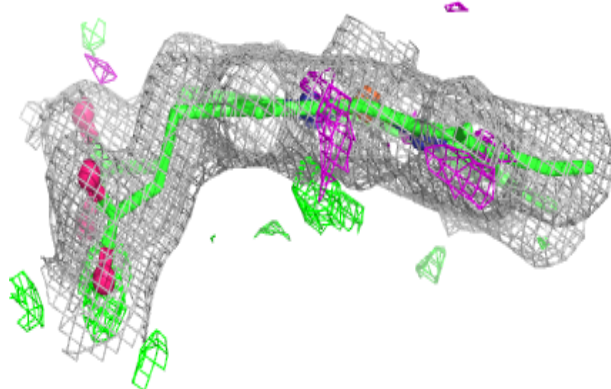
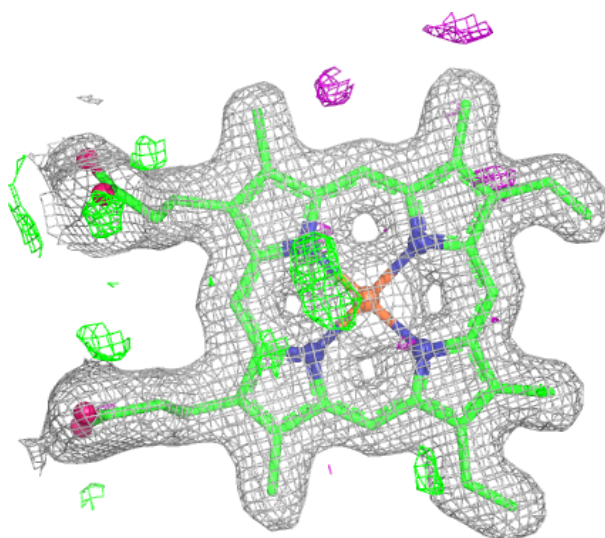
Electron density around HEM C 501:

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



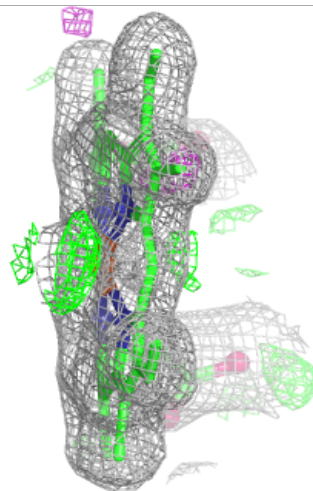
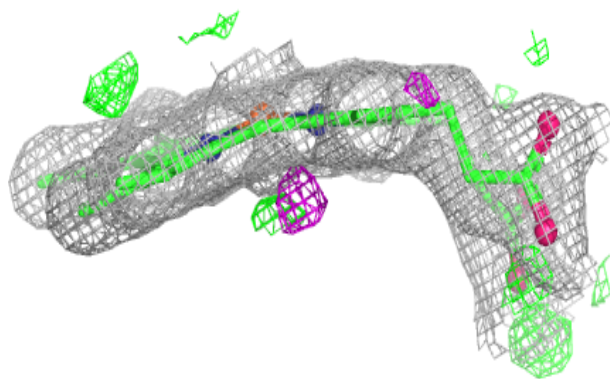
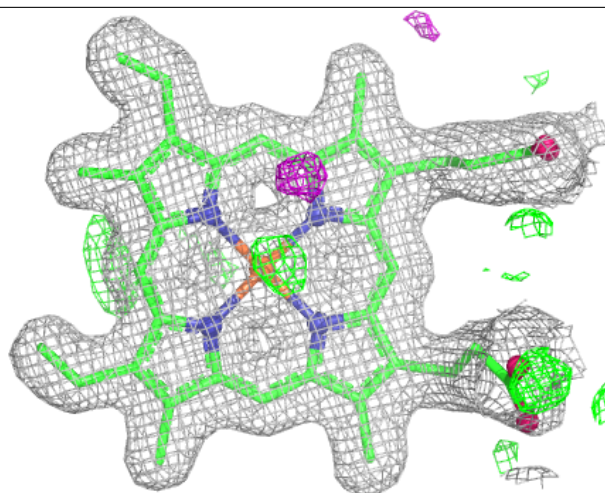
Electron density around HEM D 501:

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



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 ⓘ

There are no such residues in this entry.