



# Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 08:55 am BST

PDB ID : 4QOQ  
Title : Structure of Bacillus pumilus catalase with guaiacol bound  
Authors : Loewen, P.C.  
Deposited on : 2014-06-20  
Resolution : 1.70 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

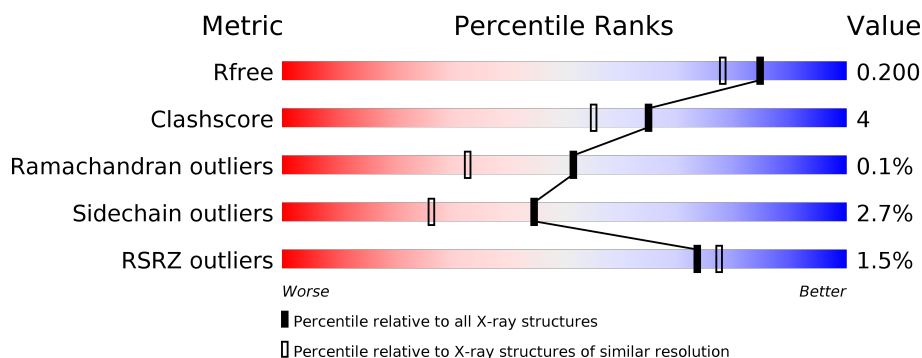
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	491	<div> <div>2%</div> <div> <div></div> <div>88%</div> <div>9%</div> <div>..</div> </div> </div>
1	B	491	<div> <div>%</div> <div> <div></div> <div>89%</div> <div>8%</div> <div>..</div> </div> </div>
1	C	491	<div> <div>%</div> <div> <div></div> <div>89%</div> <div>8%</div> <div>..</div> </div> </div>
1	D	491	<div> <div>2%</div> <div> <div></div> <div>89%</div> <div>8%</div> <div>.</div> </div> </div>

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 crite-

ria:

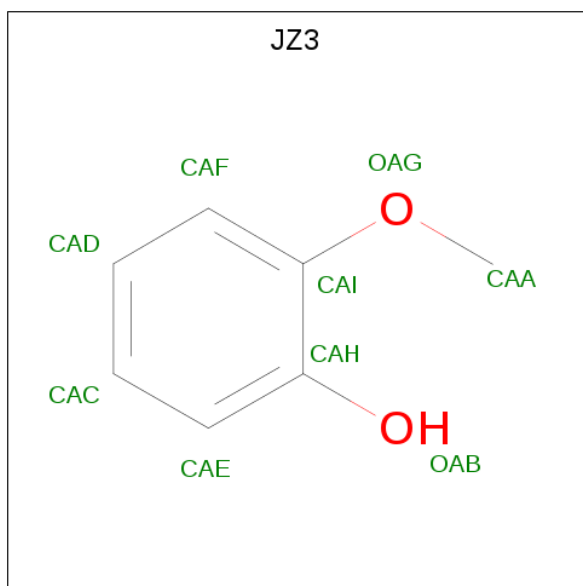
Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	JZ3	A	503	-	-	X	-
3	JZ3	B	503	-	-	X	-
3	JZ3	D	503	-	-	X	-



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

- Molecule 3 is Guaiacol (three-letter code: JZ3) (formula: C<sub>7</sub>H<sub>8</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O		
			9	7	2		
3	B	1	Total	C	O		
			9	7	2		
3	B	1	Total	C	O		
			9	7	2		
3	C	1	Total	C	O		
			9	7	2		
3	D	1	Total	C	O		
			9	7	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	1	Total	C	O	0	0
			9	7	2		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Na	0	0
			1	1		
5	A	1	Total	Na	0	0
			1	1		

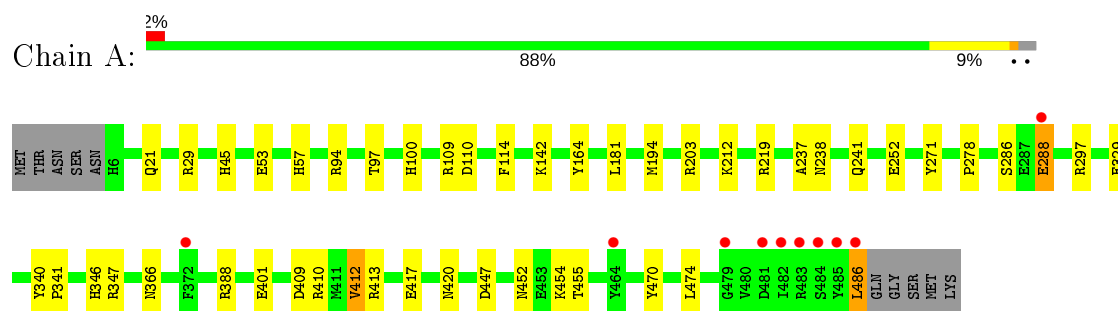
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	434	Total	O	0	0
			434	434		
6	B	429	Total	O	0	0
			429	429		
6	C	435	Total	O	0	0
			435	435		
6	D	408	Total	O	0	0
			408	408		

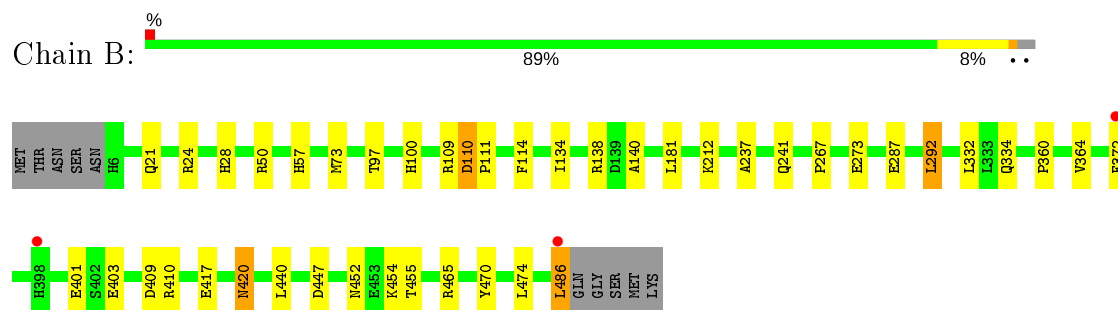
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: Catalase



#### • Molecule 1: Catalase







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	91.79Å 108.11Å 103.41Å 90.00° 91.98° 90.00°	Depositor
Resolution (Å)	103.35 – 1.70 46.62 – 1.70	Depositor EDS
% Data completeness (in resolution range)	95.0 (103.35-1.70) 95.0 (46.62-1.70)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.13 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0069	Depositor
R, $R_{free}$	0.162 , 0.190 0.172 , 0.200	Depositor DCC
$R_{free}$ test set	10488 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	17.6	Xtriage
Anisotropy	0.741	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 45.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.045 for -h,-l,-k 0.038 for -h,l,k 0.095 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	17970	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.68% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: HEM, CL, JZ3, NA

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	0.93	2/4082 (0.0%)	0.94	14/5535 (0.3%)
1	B	0.95	0/4077	0.94	6/5527 (0.1%)
1	C	1.01	3/4094 (0.1%)	0.96	13/5550 (0.2%)
1	D	0.95	1/4084 (0.0%)	0.91	7/5537 (0.1%)
All	All	0.96	6/16337 (0.0%)	0.94	40/22149 (0.2%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	85	GLU	CD-OE1	6.74	1.33	1.25
1	A	329	GLU	CG-CD	6.57	1.61	1.51
1	C	85	GLU	CD-OE2	5.91	1.32	1.25
1	A	53	GLU	CD-OE2	5.62	1.31	1.25
1	C	262	TYR	CG-CD1	5.36	1.46	1.39
1	D	234	GLU	CD-OE1	5.23	1.31	1.25

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	50	ARG	NE-CZ-NH1	7.04	123.82	120.30
1	A	203	ARG	NE-CZ-NH2	-6.97	116.82	120.30
1	A	413	ARG	NE-CZ-NH1	-6.77	116.92	120.30
1	C	413	ARG	NE-CZ-NH1	-6.60	117.00	120.30
1	A	329	GLU	OE1-CD-OE2	-6.58	115.40	123.30
1	A	410	ARG	NE-CZ-NH2	6.38	123.49	120.30
1	A	470	TYR	CB-CG-CD2	-6.20	117.28	121.00
1	C	410	ARG	NE-CZ-NH2	6.12	123.36	120.30
1	B	109	ARG	NE-CZ-NH1	6.07	123.33	120.30
1	D	50	ARG	NE-CZ-NH1	6.06	123.33	120.30
1	D	413	ARG	NE-CZ-NH1	-6.06	117.27	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	50	ARG	NE-CZ-NH2	-6.04	117.28	120.30
1	A	203	ARG	NE-CZ-NH1	5.89	123.24	120.30
1	A	388	ARG	NE-CZ-NH2	-5.85	117.38	120.30
1	C	194	MET	CG-SD-CE	5.75	109.40	100.20
1	C	138	ARG	NE-CZ-NH1	5.74	123.17	120.30
1	D	194	MET	CG-SD-CE	5.71	109.33	100.20
1	B	138	ARG	NE-CZ-NH2	-5.69	117.45	120.30
1	B	486	LEU	CA-CB-CG	5.68	128.36	115.30
1	C	138	ARG	NE-CZ-NH2	-5.65	117.48	120.30
1	C	430	ARG	NE-CZ-NH1	5.64	123.12	120.30
1	D	486	LEU	CA-CB-CG	5.55	128.07	115.30
1	B	73	MET	CG-SD-CE	-5.54	91.33	100.20
1	D	48	ARG	NE-CZ-NH2	-5.52	117.54	120.30
1	A	252	GLU	CG-CD-OE2	5.48	129.27	118.30
1	C	465	ARG	NE-CZ-NH1	5.44	123.02	120.30
1	C	470	TYR	CB-CG-CD2	-5.42	117.75	121.00
1	A	194	MET	CG-SD-CE	5.39	108.82	100.20
1	A	347	ARG	NE-CZ-NH2	-5.39	117.61	120.30
1	A	470	TYR	CB-CG-CD1	5.37	124.22	121.00
1	A	29	ARG	NE-CZ-NH1	5.36	122.98	120.30
1	C	388	ARG	NE-CZ-NH2	-5.34	117.63	120.30
1	C	473	ARG	NE-CZ-NH2	-5.33	117.63	120.30
1	D	388	ARG	NE-CZ-NH2	-5.30	117.65	120.30
1	A	297	ARG	NE-CZ-NH1	5.28	122.94	120.30
1	A	109	ARG	NE-CZ-NH1	5.15	122.88	120.30
1	C	430	ARG	NE-CZ-NH2	-5.12	117.74	120.30
1	B	24	ARG	NE-CZ-NH2	-5.12	117.74	120.30
1	B	50	ARG	NE-CZ-NH2	-5.05	117.78	120.30
1	D	297	ARG	NE-CZ-NH1	5.02	122.81	120.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3960	0	3764	30	0
1	B	3959	0	3767	34	0
1	C	3973	0	3787	28	0
1	D	3966	0	3769	25	0
2	A	86	0	60	9	0
2	B	86	0	60	9	0
2	C	86	0	60	12	0
2	D	86	0	60	2	0
3	A	9	0	8	4	0
3	B	18	0	16	5	0
3	C	9	0	8	3	0
3	D	18	0	15	4	0
4	A	2	0	0	0	0
4	B	1	0	0	0	0
4	C	2	0	0	0	0
4	D	1	0	0	0	0
5	A	1	0	0	1	0
5	B	1	0	0	0	0
6	A	434	0	0	10	0
6	B	429	0	0	5	0
6	C	435	0	0	11	0
6	D	408	0	0	9	0
All	All	17970	0	15374	130	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 (130) 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:C:212:LYS:HE2	6:C:905:HOH:O	1.24	1.31
1:D:72[B]:SER:OG	1:D:74:GLU:OE1	1.60	1.17
1:B:372[A]:PHE:CE2	6:D:904:HOH:O	2.06	1.05
1:D:212:LYS:HE2	6:D:714:HOH:O	1.63	0.96
1:A:212:LYS:HE2	6:A:699:HOH:O	1.67	0.95
1:D:181:LEU:HD21	3:D:503:JZ3:HAF	1.48	0.94
2:B:501[A]:HEM:CMC	2:B:501[A]:HEM:HBC2	2.00	0.89
2:C:501[A]:HEM:HMB2	2:C:501[A]:HEM:HBB2	1.57	0.87
1:A:181:LEU:HD21	3:A:503:JZ3:HAF	1.58	0.86
2:C:501[A]:HEM:CMB	2:C:501[A]:HEM:HBB2	2.08	0.83
2:B:501[A]:HEM:HBC2	2:B:501[A]:HEM:HMC2	1.58	0.83
1:C:181:LEU:HD21	3:C:503:JZ3:HAF	1.60	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:287:GLU:HG2	1:B:292:LEU:HD21	1.61	0.80
5:A:506:NA:NA	6:A:843:HOH:O	1.56	0.78
2:C:502[B]:HEM:HBC2	2:C:502[B]:HEM:HMC2	1.67	0.75
2:A:501[A]:HEM:HBC2	2:A:501[A]:HEM:CMC	2.15	0.74
1:B:287:GLU:CG	1:B:292:LEU:HD21	2.17	0.73
1:A:452:ASN:HD22	1:A:455:THR:H	1.38	0.70
1:B:452:ASN:HD22	1:B:455:THR:H	1.39	0.70
1:C:212:LYS:NZ	6:C:906:HOH:O	2.26	0.68
2:C:501[A]:HEM:HMB2	2:C:501[A]:HEM:CBB	2.24	0.68
1:A:45:HIS:HE1	1:C:351:ASN:OD1	1.76	0.68
1:B:292:LEU:HD23	6:B:999:HOH:O	1.94	0.67
2:B:501[A]:HEM:CBC	2:B:501[A]:HEM:HMC2	2.27	0.65
2:B:501[A]:HEM:CMB	2:B:501[A]:HEM:HBB2	2.26	0.64
1:C:219:ARG:HD2	6:C:1001:HOH:O	1.97	0.64
1:B:110:ASP:OD1	3:B:503:JZ3:OAG	2.16	0.64
1:A:412[A]:VAL:HG13	1:B:403:GLU:OE2	1.98	0.63
1:B:465:ARG:CZ	6:B:926:HOH:O	2.45	0.63
2:C:502[B]:HEM:CMB	2:C:502[B]:HEM:HBB2	2.29	0.62
1:B:292:LEU:CD2	1:B:292:LEU:N	2.63	0.61
1:C:465:ARG:NE	6:C:1032:HOH:O	2.33	0.61
1:D:483:ARG:O	1:D:484:SER:CB	2.47	0.61
1:D:181:LEU:CD2	3:D:503:JZ3:HAF	2.29	0.61
2:A:501[A]:HEM:HBC2	2:A:501[A]:HEM:HMC2	1.84	0.60
6:A:803:HOH:O	1:D:100:HIS:HE1	1.85	0.60
1:B:372[A]:PHE:CD2	6:D:904:HOH:O	2.39	0.59
1:B:212:LYS:NZ	6:B:898:HOH:O	2.35	0.59
1:D:332:LEU:HD12	2:D:501[A]:HEM:HBB1	1.85	0.59
1:A:100:HIS:HE1	6:A:673:HOH:O	1.85	0.59
2:C:501[A]:HEM:HBC2	2:C:501[A]:HEM:CMC	2.32	0.58
1:A:346:HIS:HE1	6:D:904:HOH:O	1.87	0.58
1:B:181:LEU:HD21	3:B:503:JZ3:CAF	2.33	0.57
1:A:417:GLU:HG2	1:D:28:HIS:CD2	2.39	0.57
1:B:452:ASN:HD21	1:B:454:LYS:HB3	1.68	0.57
1:B:465:ARG:NH2	6:B:926:HOH:O	2.37	0.57
1:D:181:LEU:HD21	3:D:503:JZ3:CAF	2.28	0.56
1:A:238:ASN:HB2	6:A:781:HOH:O	2.06	0.54
1:A:452:ASN:HD21	1:A:454:LYS:HB3	1.71	0.54
2:B:501[A]:HEM:HMB2	2:B:501[A]:HEM:HBB2	1.87	0.54
1:C:219:ARG:HD2	6:C:727:HOH:O	2.07	0.54
1:D:219:ARG:HD3	6:D:855:HOH:O	2.07	0.53
1:B:292:LEU:HD22	1:B:292:LEU:N	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:240:PHE:C	1:C:241:GLN:HG3	2.28	0.53
2:A:501[A]:HEM:CMB	2:A:501[A]:HEM:HBB2	2.38	0.52
1:D:219:ARG:CG	6:D:855:HOH:O	2.58	0.52
3:C:503:JZ3:HAC	6:C:940:HOH:O	2.09	0.51
2:C:501[A]:HEM:HBC2	2:C:501[A]:HEM:HMC2	1.91	0.51
2:C:502[B]:HEM:HMB1	2:C:502[B]:HEM:HBB2	1.92	0.51
1:A:181:LEU:CD2	3:A:503:JZ3:HAF	2.36	0.51
1:C:465:ARG:CD	6:C:1032:HOH:O	2.58	0.51
1:A:271:TYR:CD1	1:A:278:PRO:HD2	2.45	0.51
1:B:237:ALA:HB2	1:C:237:ALA:HB2	1.93	0.51
1:C:461[B]:CYS:SG	1:C:465:ARG:CZ	3.00	0.50
1:A:271:TYR:HD1	1:A:278:PRO:HD2	1.75	0.50
1:B:292:LEU:CD2	1:B:292:LEU:H	2.24	0.50
1:D:435:GLU:HG3	6:D:897:HOH:O	2.12	0.50
1:B:181:LEU:HD21	3:B:503:JZ3:HAF	1.93	0.50
2:A:501[A]:HEM:CBC	2:A:501[A]:HEM:HMC2	2.41	0.49
1:A:219:ARG:HD2	6:A:836:HOH:O	2.13	0.49
2:B:501[A]:HEM:HMB2	2:B:501[A]:HEM:CBB	2.43	0.49
1:A:45:HIS:HD2	6:A:688:HOH:O	1.96	0.48
1:A:181:LEU:HD21	3:A:503:JZ3:CAF	2.38	0.48
1:B:134[B]:ILE:HD13	1:B:134[B]:ILE:H	1.78	0.47
1:C:134[B]:ILE:HD11	1:C:180:TRP:CD1	2.48	0.47
1:B:332:LEU:HD12	2:B:501[A]:HEM:HBB1	1.96	0.47
1:C:140:ALA:HA	2:C:501[A]:HEM:HBB1	1.95	0.47
1:C:271:TYR:HD1	1:C:278:PRO:HD2	1.79	0.47
1:A:164:TYR:OH	3:A:503:JZ3:HAC	2.15	0.46
1:C:336:ARG:HG2	2:C:502[B]:HEM:C2C	2.50	0.46
1:B:181:LEU:HD21	3:B:503:JZ3:CAD	2.45	0.46
1:B:420:ASN:ND2	6:B:729:HOH:O	2.43	0.46
1:B:334:GLN:HG3	6:C:704:HOH:O	2.16	0.45
1:B:100:HIS:HE1	6:C:703:HOH:O	1.99	0.45
1:D:57:HIS:HA	1:D:97:THR:O	2.17	0.45
1:A:417:GLU:H	1:D:28:HIS:CD2	2.35	0.45
1:C:219:ARG:CD	6:C:727:HOH:O	2.65	0.45
2:A:502[B]:HEM:HBC2	2:A:502[B]:HEM:CMC	2.47	0.44
1:A:21:GLN:HA	1:D:142:LYS:HD3	1.99	0.44
1:B:28:HIS:CE1	1:C:417:GLU:CG	3.01	0.44
1:C:461[B]:CYS:SG	1:C:465:ARG:NH2	2.91	0.44
6:A:984:HOH:O	1:D:334:GLN:HG3	2.16	0.44
1:A:286:SER:OG	1:A:288:GLU:HG2	2.17	0.44
2:A:502[B]:HEM:HBB2	2:A:502[B]:HEM:CMB	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:452:ASN:ND2	1:A:455:THR:H	2.11	0.43
6:A:667:HOH:O	1:B:410:ARG:HD2	2.17	0.43
1:C:110:ASP:OD1	3:C:503:JZ3:OAG	2.36	0.43
1:A:366:ASN:HA	1:C:9[B]:LEU:CD2	2.48	0.43
1:D:302:ARG:HD2	6:D:823:HOH:O	2.18	0.43
1:D:332:LEU:CD1	2:D:501[A]:HEM:HBB1	2.48	0.43
2:C:502[B]:HEM:HMB1	2:C:502[B]:HEM:CBB	2.48	0.43
1:D:483:ARG:O	1:D:484:SER:HB3	2.18	0.43
2:B:502[B]:HEM:CMC	2:B:502[B]:HEM:HBC2	2.48	0.43
1:B:287:GLU:HG2	1:B:292:LEU:CD2	2.40	0.43
1:D:392:GLN:NE2	6:D:892:HOH:O	2.44	0.43
1:C:199:VAL:HG11	2:C:502[B]:HEM:HBB1	2.01	0.43
1:D:134[B]:ILE:H	1:D:134[B]:ILE:HD13	1.83	0.43
1:A:57:HIS:HA	1:A:97:THR:O	2.19	0.42
1:A:486:LEU:HA	1:A:486:LEU:HD12	1.84	0.42
1:C:340:TYR:HB2	1:C:341:PRO:HD3	2.01	0.42
1:B:57:HIS:HA	1:B:97:THR:O	2.19	0.42
1:A:57:HIS:CD2	2:A:501[A]:HEM:C4D	3.08	0.42
1:B:140:ALA:HA	2:B:501[A]:HEM:HBB1	2.02	0.42
1:B:111:PRO:HD3	3:B:503:JZ3:HAAB	2.02	0.41
2:A:501[A]:HEM:CMB	2:A:501[A]:HEM:CBB	2.98	0.41
1:B:292:LEU:H	1:B:292:LEU:HD23	1.84	0.41
1:C:271:TYR:CD1	1:C:278:PRO:HD2	2.54	0.41
1:A:142:LYS:HD3	1:D:21:GLN:HA	2.02	0.41
1:A:237:ALA:HB2	1:D:237:ALA:HB2	2.03	0.41
1:A:340:TYR:HB2	1:A:341:PRO:HD3	2.02	0.41
1:C:57:HIS:CE1	1:C:98:VAL:HG22	2.55	0.41
1:B:360:PRO:HG2	1:B:364:VAL:CG2	2.51	0.41
1:A:219:ARG:HG2	6:A:1015:HOH:O	2.21	0.41
1:D:340:TYR:HB2	1:D:341:PRO:HD3	2.03	0.40
1:B:417:GLU:HG3	1:C:28:HIS:CE1	2.56	0.40
1:C:465:ARG:CZ	6:C:1032:HOH:O	2.69	0.40
1:A:94:ARG:HD3	2:A:501[A]:HEM:O1D	2.21	0.40
1:B:21:GLN:HA	1:C:142:LYS:HD3	2.03	0.40
1:C:462:ASN:OD1	1:C:465:ARG:NH1	2.54	0.40
1:D:150:LEU:HD13	3:D:503:JZ3:HAAA	2.02	0.40

There are no symmetry-related clashes.

## 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	485/491 (99%)	475 (98%)	10 (2%)	0	100	100
1	B	484/491 (99%)	472 (98%)	12 (2%)	0	100	100
1	C	486/491 (99%)	474 (98%)	12 (2%)	0	100	100
1	D	485/491 (99%)	469 (97%)	15 (3%)	1 (0%)	47	30
All	All	1940/1964 (99%)	1890 (97%)	49 (2%)	1 (0%)	51	33

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	484	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	428/432 (99%)	416 (97%)	12 (3%)	43	25
1	B	427/432 (99%)	413 (97%)	14 (3%)	38	19
1	C	429/432 (99%)	421 (98%)	8 (2%)	57	41
1	D	428/432 (99%)	416 (97%)	12 (3%)	43	25
All	All	1712/1728 (99%)	1666 (97%)	46 (3%)	44	26

All (46) residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	A	110	ASP
1	A	114	PHE
1	A	241	GLN
1	A	288	GLU
1	A	401	GLU
1	A	409	ASP
1	A	412[A]	VAL
1	A	412[B]	VAL
1	A	420	ASN
1	A	447	ASP
1	A	474	LEU
1	A	486	LEU
1	B	110	ASP
1	B	114	PHE
1	B	241	GLN
1	B	267	PRO
1	B	273	GLU
1	B	292	LEU
1	B	401	GLU
1	B	409	ASP
1	B	420	ASN
1	B	440	LEU
1	B	447	ASP
1	B	470	TYR
1	B	474	LEU
1	B	486	LEU
1	C	110	ASP
1	C	114	PHE
1	C	120	THR
1	C	241	GLN
1	C	401	GLU
1	C	409	ASP
1	C	420	ASN
1	C	447	ASP
1	D	75	LYS
1	D	110	ASP
1	D	114	PHE
1	D	241	GLN
1	D	267	PRO
1	D	273	GLU
1	D	401	GLU
1	D	409	ASP
1	D	447	ASP

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Mol	Chain	Res	Type
1	D	470	TYR
1	D	474	LEU
1	D	486	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	45	HIS
1	A	100	HIS
1	A	157	ASN
1	A	226	ASN
1	A	346	HIS
1	A	420	ASN
1	A	452	ASN
1	B	100	HIS
1	B	157	ASN
1	B	226	ASN
1	B	420	ASN
1	B	452	ASN
1	C	100	HIS
1	C	226	ASN
1	C	420	ASN
1	D	28	HIS
1	D	100	HIS
1	D	157	ASN
1	D	226	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 carbohydrates in this entry.

## 5.6 Ligand geometry

Of 22 ligands modelled in this entry, 8 are monoatomic - leaving 14 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	JZ3	A	503	-	9,9,9	1.85	1 (11%)	11,11,11	3.24	4 (36%)
2	HEM	D	501[A]	1	27,50,50	1.04	2 (7%)	17,82,82	1.68	5 (29%)
3	JZ3	D	504	-	9,9,9	1.64	1 (11%)	11,11,11	2.09	3 (27%)
3	JZ3	D	503	-	9,9,9	2.08	2 (22%)	11,11,11	3.67	5 (45%)
2	HEM	D	502[B]	1	27,50,50	1.21	2 (7%)	17,82,82	1.77	6 (35%)
3	JZ3	B	503	-	9,9,9	2.29	1 (11%)	11,11,11	3.57	5 (45%)
2	HEM	C	502[B]	1	27,50,50	1.43	3 (11%)	17,82,82	2.43	5 (29%)
3	JZ3	B	504	-	9,9,9	1.45	1 (11%)	11,11,11	0.90	0
2	HEM	C	501[A]	1	27,50,50	1.52	3 (11%)	17,82,82	1.77	3 (17%)
2	HEM	A	501[A]	1	27,50,50	1.19	2 (7%)	17,82,82	2.01	6 (35%)
2	HEM	B	502[B]	1,6	27,50,50	1.04	1 (3%)	17,82,82	1.90	7 (41%)
3	JZ3	C	503	-	9,9,9	1.71	1 (11%)	11,11,11	3.16	5 (45%)
2	HEM	A	502[B]	1	27,50,50	1.27	4 (14%)	17,82,82	2.21	7 (41%)
2	HEM	B	501[A]	1,6	27,50,50	1.25	3 (11%)	17,82,82	1.18	2 (11%)

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	JZ3	A	503	-	-	2/2/2/2	0/1/1/1
2	HEM	D	501[A]	1	-	0/6/54/54	-
3	JZ3	D	504	-	-	0/2/2/2	0/1/1/1
3	JZ3	D	503	-	-	2/2/2/2	0/1/1/1
2	HEM	D	502[B]	1	-	0/6/54/54	-
3	JZ3	B	503	-	-	0/2/2/2	0/1/1/1
2	HEM	C	502[B]	1	-	0/6/54/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	JZ3	B	504	-	-	0/2/2/2	0/1/1/1
2	HEM	C	501[A]	1	-	0/6/54/54	-
2	HEM	A	501[A]	1	-	0/6/54/54	-
2	HEM	B	502[B]	1,6	-	0/6/54/54	-
3	JZ3	C	503	-	-	2/2/2/2	0/1/1/1
2	HEM	A	502[B]	1	-	0/6/54/54	-
2	HEM	B	501[A]	1,6	-	0/6/54/54	-

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	503	JZ3	CAH-CAI	6.19	1.51	1.40
3	D	503	JZ3	CAH-CAI	5.58	1.50	1.40
3	A	503	JZ3	CAH-CAI	5.14	1.49	1.40
3	C	503	JZ3	CAH-CAI	4.81	1.49	1.40
3	D	504	JZ3	CAH-CAI	4.71	1.48	1.40
2	C	501[A]	HEM	C3B-C2B	-4.66	1.33	1.40
2	C	501[A]	HEM	C4D-C3D	4.08	1.51	1.42
2	C	502[B]	HEM	C3C-C2C	-3.92	1.34	1.40
2	D	502[B]	HEM	C4D-C3D	3.83	1.51	1.42
3	B	504	JZ3	CAH-CAI	3.67	1.46	1.40
2	C	502[B]	HEM	C4D-C3D	3.59	1.50	1.42
2	C	501[A]	HEM	C4A-NA	3.43	1.43	1.36
2	A	501[A]	HEM	C3B-C2B	-3.41	1.35	1.40
2	B	501[A]	HEM	C4D-C3D	3.30	1.50	1.42
2	D	501[A]	HEM	C3B-C2B	-3.26	1.35	1.40
2	C	502[B]	HEM	C1A-NA	3.21	1.42	1.36
2	B	501[A]	HEM	C3B-C2B	-3.20	1.35	1.40
2	A	502[B]	HEM	C4D-C3D	3.13	1.49	1.42
2	B	502[B]	HEM	C4D-C3D	2.93	1.49	1.42
2	A	501[A]	HEM	C4D-C3D	2.75	1.48	1.42
2	D	501[A]	HEM	C4D-C3D	2.73	1.48	1.42
3	D	503	JZ3	OAG-CAI	2.41	1.41	1.37
2	A	502[B]	HEM	C3B-C2B	-2.34	1.37	1.40
2	A	502[B]	HEM	C4B-NB	-2.33	1.31	1.36
2	B	501[A]	HEM	C4A-NA	2.28	1.40	1.36
2	D	502[B]	HEM	C3C-CAC	-2.27	1.43	1.47
2	A	502[B]	HEM	C4A-NA	2.14	1.40	1.36

All (63) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	503	JZ3	CAA-OAG-CAI	9.32	131.60	117.53
3	B	503	JZ3	CAA-OAG-CAI	8.48	130.32	117.53
3	A	503	JZ3	CAA-OAG-CAI	8.25	129.99	117.53
3	C	503	JZ3	CAA-OAG-CAI	7.65	129.08	117.53
3	B	503	JZ3	OAG-CAI-CAH	6.30	123.70	114.57
2	C	502[B]	HEM	CMD-C2D-C1D	-6.09	119.10	128.46
3	D	503	JZ3	OAG-CAI-CAH	5.63	122.73	114.57
3	C	503	JZ3	OAG-CAI-CAH	5.24	122.16	114.57
3	A	503	JZ3	OAG-CAI-CAH	5.20	122.10	114.57
2	C	502[B]	HEM	CMD-C2D-C3D	4.56	133.55	124.94
2	C	501[A]	HEM	C4C-C3C-C2C	4.49	110.03	106.90
2	A	501[A]	HEM	CMA-C3A-C4A	-4.49	121.57	128.46
3	D	504	JZ3	OAG-CAI-CAH	4.44	121.00	114.57
3	D	504	JZ3	CAA-OAG-CAI	4.32	124.05	117.53
2	A	502[B]	HEM	CAA-CBA-CGA	-4.23	105.57	112.67
2	C	502[B]	HEM	CAD-CBD-CGD	3.32	118.24	112.67
2	A	502[B]	HEM	C3C-C4C-NC	-3.29	104.73	110.94
2	C	502[B]	HEM	CBD-CAD-C3D	-3.29	106.42	112.48
2	C	501[A]	HEM	C3B-C4B-NB	-3.25	105.01	109.21
2	A	502[B]	HEM	C3B-C4B-NB	-3.21	105.06	109.21
2	A	501[A]	HEM	CMA-C3A-C2A	3.19	130.96	124.94
2	B	502[B]	HEM	C4A-C3A-C2A	3.19	109.22	107.00
2	D	502[B]	HEM	CAA-CBA-CGA	-3.14	107.41	112.67
3	D	503	JZ3	CAF-CAI-CAH	-3.12	115.97	119.86
2	A	502[B]	HEM	C1D-C2D-C3D	-3.02	104.90	107.00
2	D	501[A]	HEM	CMA-C3A-C4A	-2.88	124.04	128.46
2	A	501[A]	HEM	C3C-C4C-NC	-2.77	105.71	110.94
2	B	502[B]	HEM	CMD-C2D-C1D	-2.76	124.22	128.46
3	B	503	JZ3	CAF-CAI-CAH	-2.71	116.47	119.86
2	D	502[B]	HEM	C4A-C3A-C2A	2.67	108.85	107.00
2	D	502[B]	HEM	CBD-CAD-C3D	-2.66	107.58	112.48
3	B	503	JZ3	OAG-CAI-CAF	-2.66	119.81	124.37
2	D	501[A]	HEM	CMD-C2D-C1D	-2.65	124.39	128.46
2	C	501[A]	HEM	CBA-CAA-C2A	-2.58	107.73	112.49
2	A	502[B]	HEM	CBA-CAA-C2A	2.55	117.18	112.49
3	B	503	JZ3	OAB-CAH-CAI	2.54	126.02	120.09
2	A	501[A]	HEM	CAA-CBA-CGA	2.49	116.86	112.67
3	D	503	JZ3	CAD-CAF-CAI	2.49	124.29	119.71
3	A	503	JZ3	OAG-CAI-CAF	-2.45	120.17	124.37
3	C	503	JZ3	CAE-CAH-CAI	-2.44	116.69	119.53
2	B	502[B]	HEM	CAD-CBD-CGD	2.43	116.75	112.67
2	B	502[B]	HEM	CMD-C2D-C3D	2.41	129.48	124.94
2	D	502[B]	HEM	CMB-C2B-C3B	2.41	129.18	124.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501[A]	HEM	C3B-C4B-NB	-2.40	106.11	109.21
2	D	502[B]	HEM	CMD-C2D-C1D	-2.36	124.83	128.46
3	C	503	JZ3	OAG-CAI-CAF	-2.34	120.35	124.37
2	C	502[B]	HEM	CAA-CBA-CGA	-2.34	108.74	112.67
2	A	502[B]	HEM	CBD-CAD-C3D	-2.34	108.17	112.48
2	D	501[A]	HEM	CAD-CBD-CGD	-2.29	108.83	112.67
2	B	502[B]	HEM	CAA-CBA-CGA	-2.28	108.84	112.67
2	A	502[B]	HEM	CMD-C2D-C3D	2.25	129.19	124.94
2	B	502[B]	HEM	CMC-C2C-C3C	2.24	128.87	124.68
2	A	501[A]	HEM	C1D-C2D-C3D	-2.24	105.44	107.00
3	D	503	JZ3	CAC-CAE-CAH	2.23	122.87	120.05
2	B	501[A]	HEM	C3C-C4C-NC	-2.21	106.77	110.94
2	D	501[A]	HEM	CAA-CBA-CGA	2.10	116.20	112.67
3	A	503	JZ3	CAE-CAH-CAI	-2.08	117.11	119.53
2	D	502[B]	HEM	CMC-C2C-C3C	2.07	128.56	124.68
2	A	501[A]	HEM	CMD-C2D-C3D	2.07	128.85	124.94
3	D	504	JZ3	OAG-CAI-CAF	-2.04	120.87	124.37
2	D	501[A]	HEM	C3B-C4B-NB	-2.04	106.58	109.21
2	B	502[B]	HEM	CBA-CAA-C2A	-2.03	108.73	112.49
3	C	503	JZ3	CAD-CAF-CAI	2.03	123.44	119.71

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	503	JZ3	CAH-CAI-OAG-CAA
3	C	503	JZ3	CAF-CAI-OAG-CAA
3	A	503	JZ3	CAF-CAI-OAG-CAA
3	D	503	JZ3	CAF-CAI-OAG-CAA
3	C	503	JZ3	CAH-CAI-OAG-CAA
3	A	503	JZ3	CAH-CAI-OAG-CAA

There are no ring outliers.

11 monomers are involved in 48 short contacts:

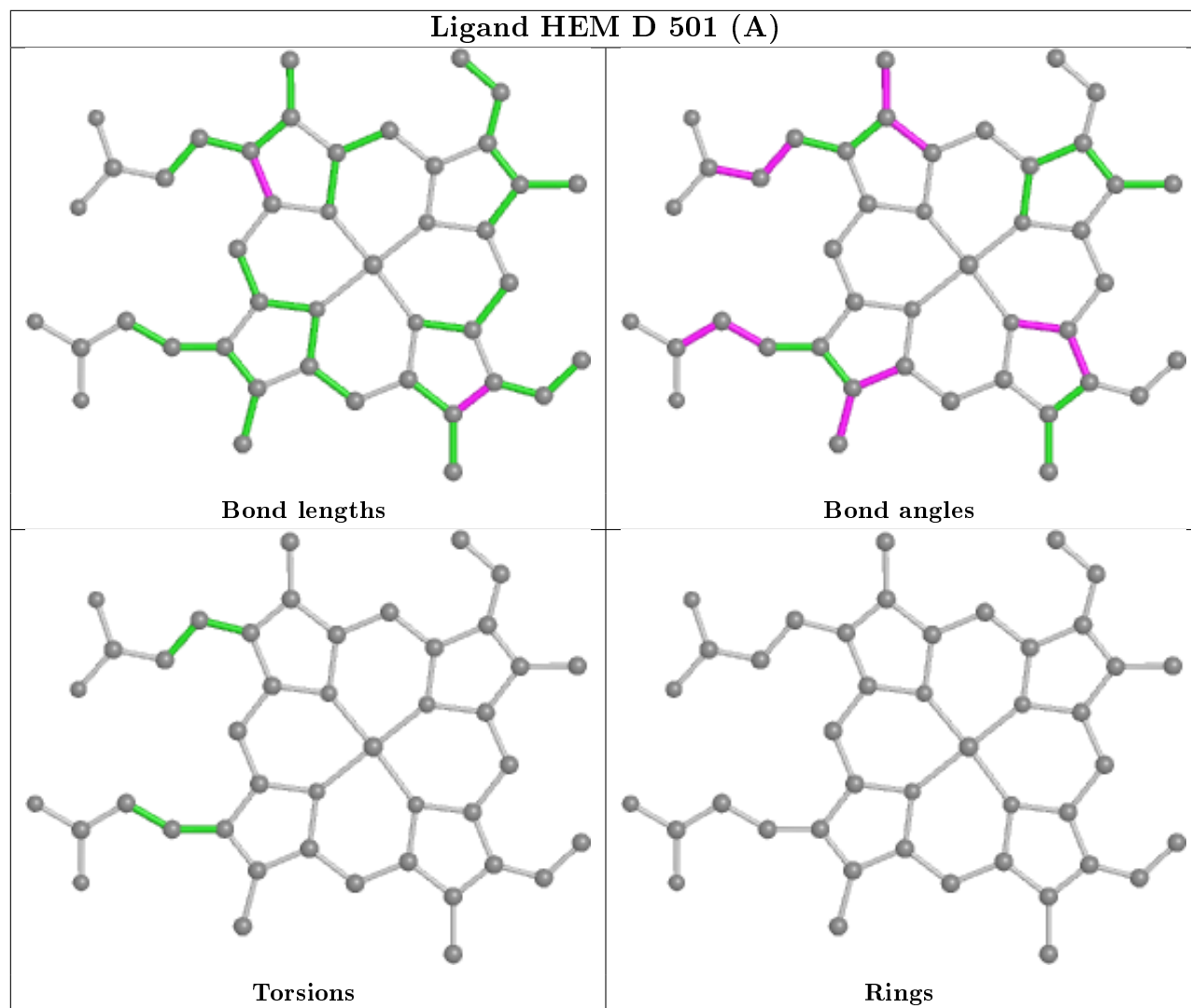
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	503	JZ3	4	0
2	D	501[A]	HEM	2	0
3	D	503	JZ3	4	0
3	B	503	JZ3	5	0
2	C	502[B]	HEM	6	0

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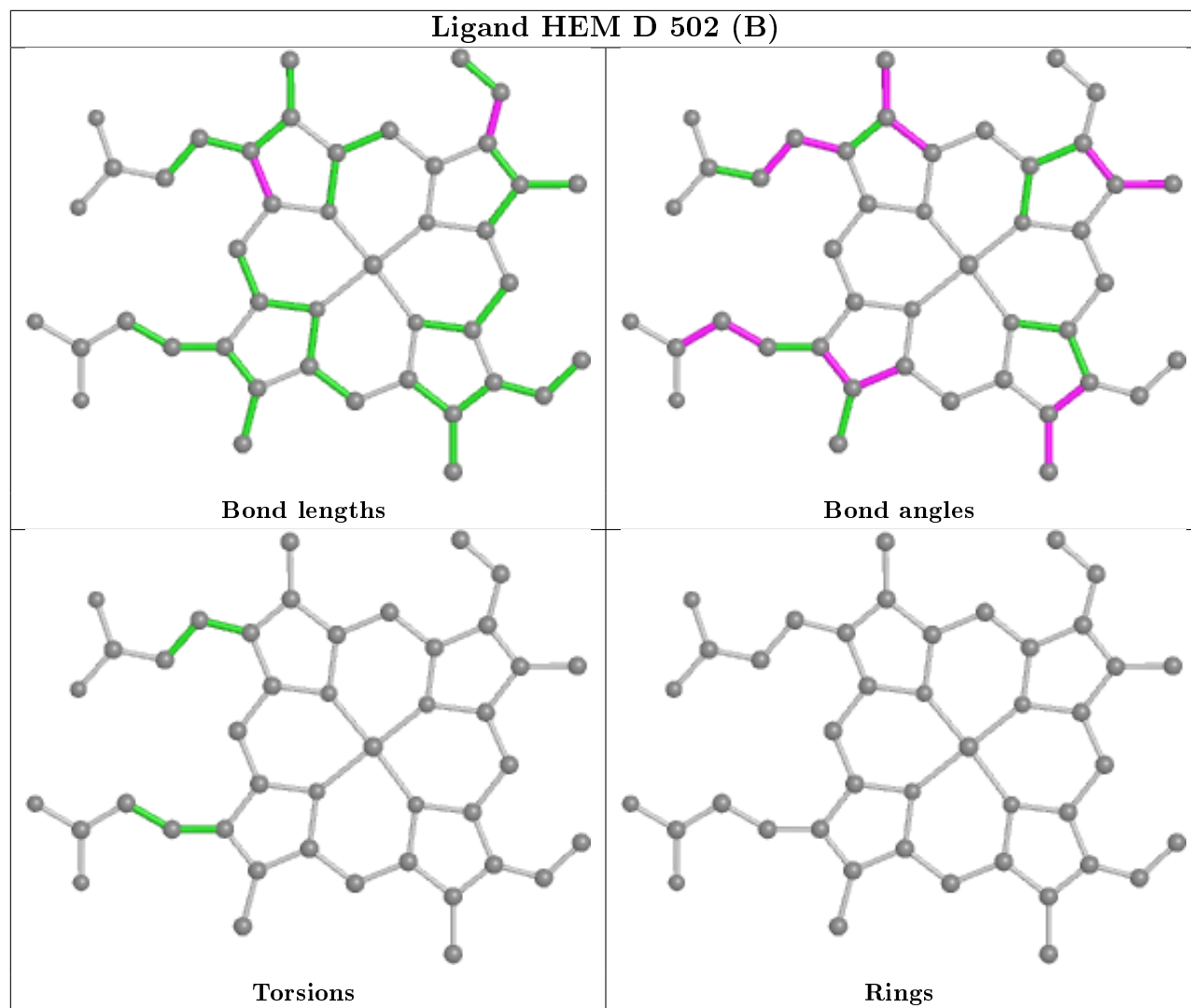
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	501[A]	HEM	6	0
2	A	501[A]	HEM	7	0
2	B	502[B]	HEM	1	0
3	C	503	JZ3	3	0
2	A	502[B]	HEM	2	0
2	B	501[A]	HEM	8	0

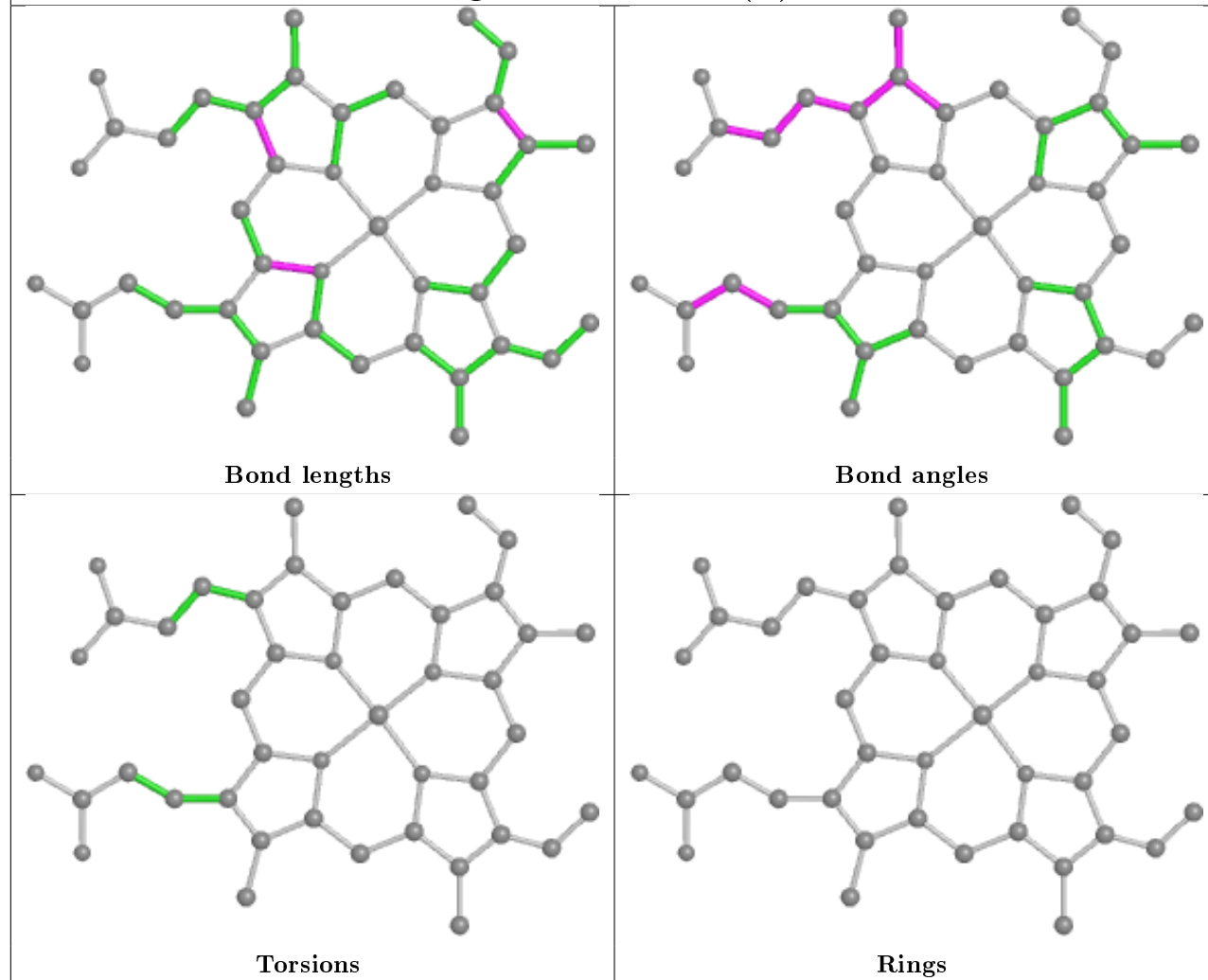
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



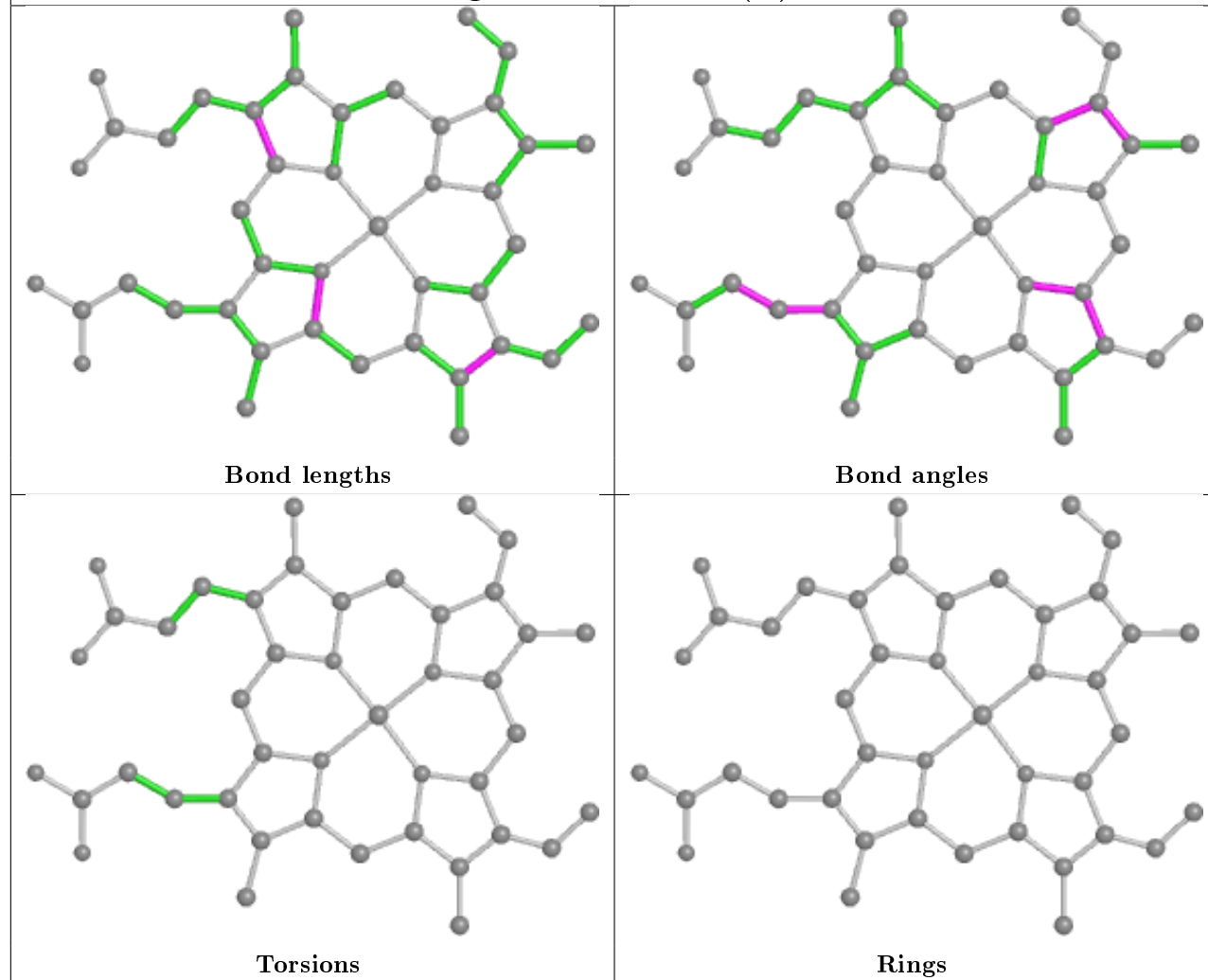




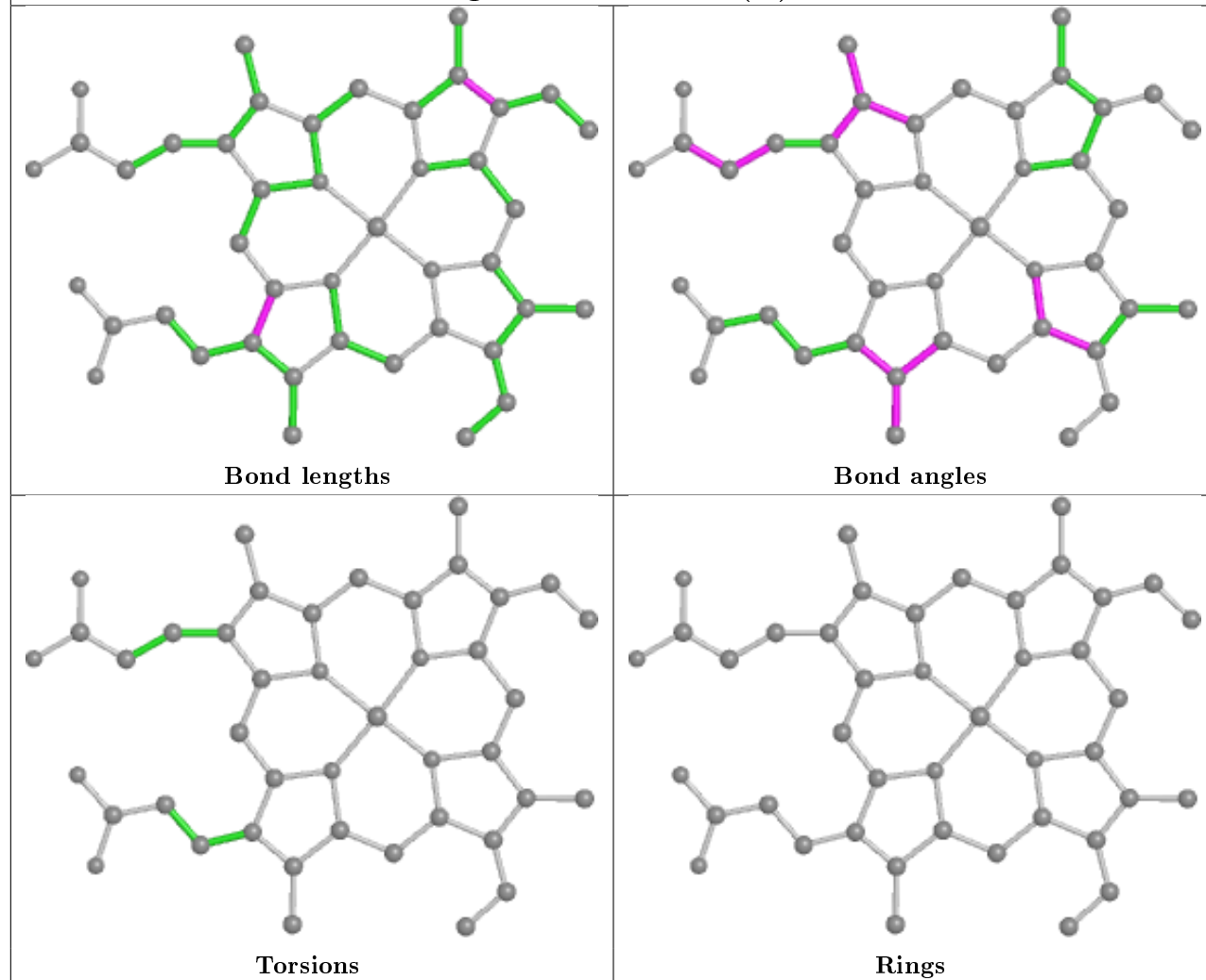
## Ligand HEM C 502 (B)



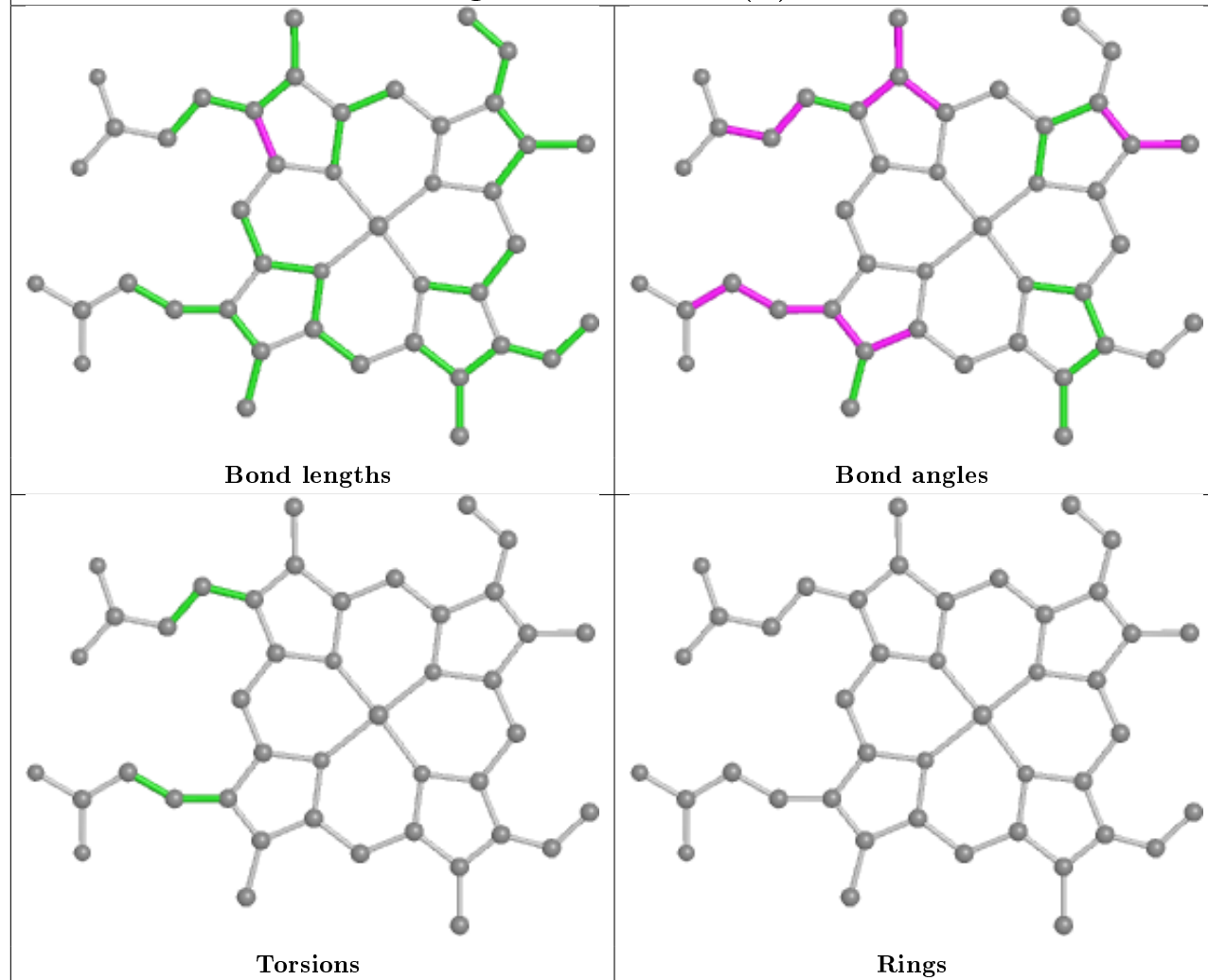
## Ligand HEM C 501 (A)



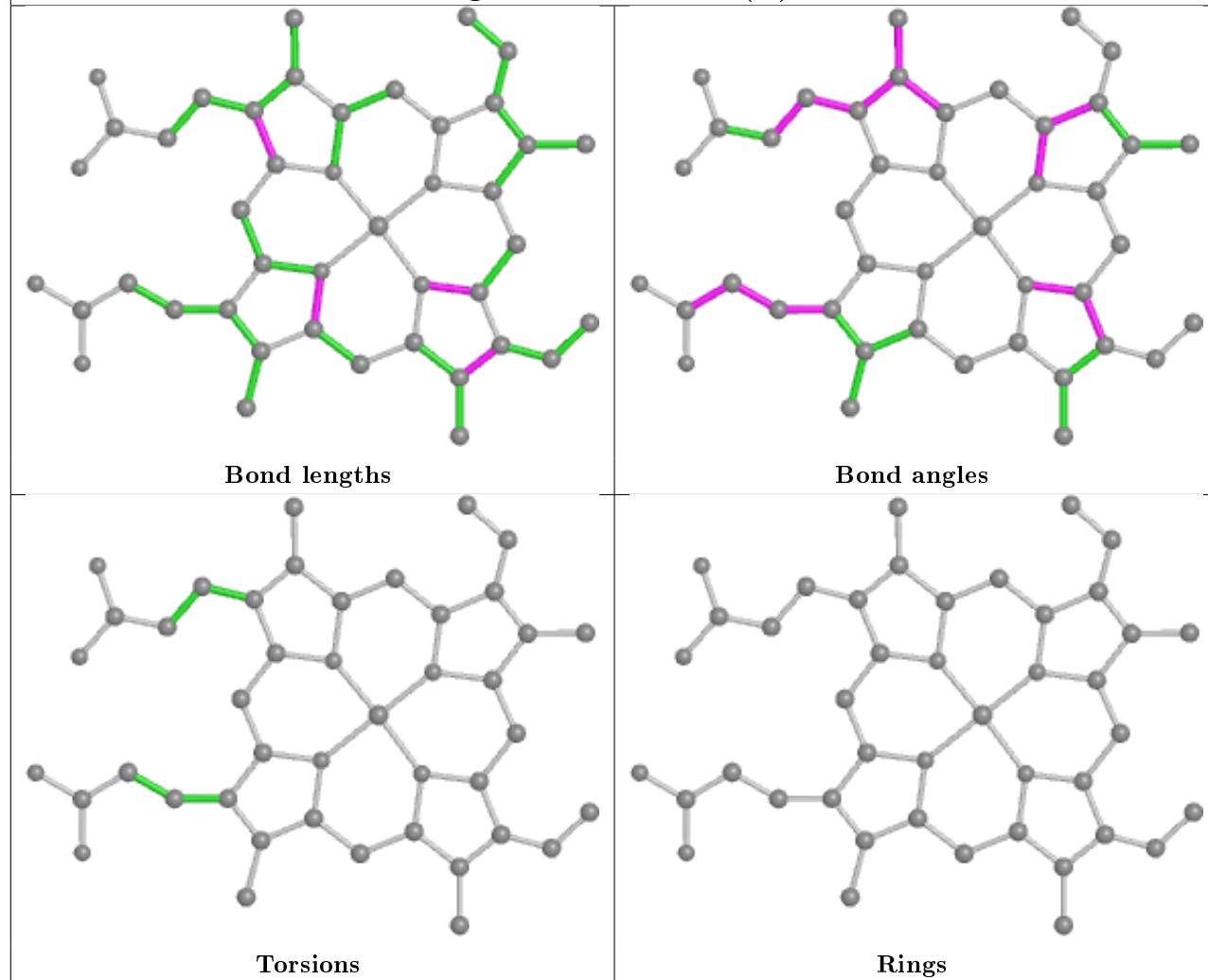
## Ligand HEM A 501 (A)

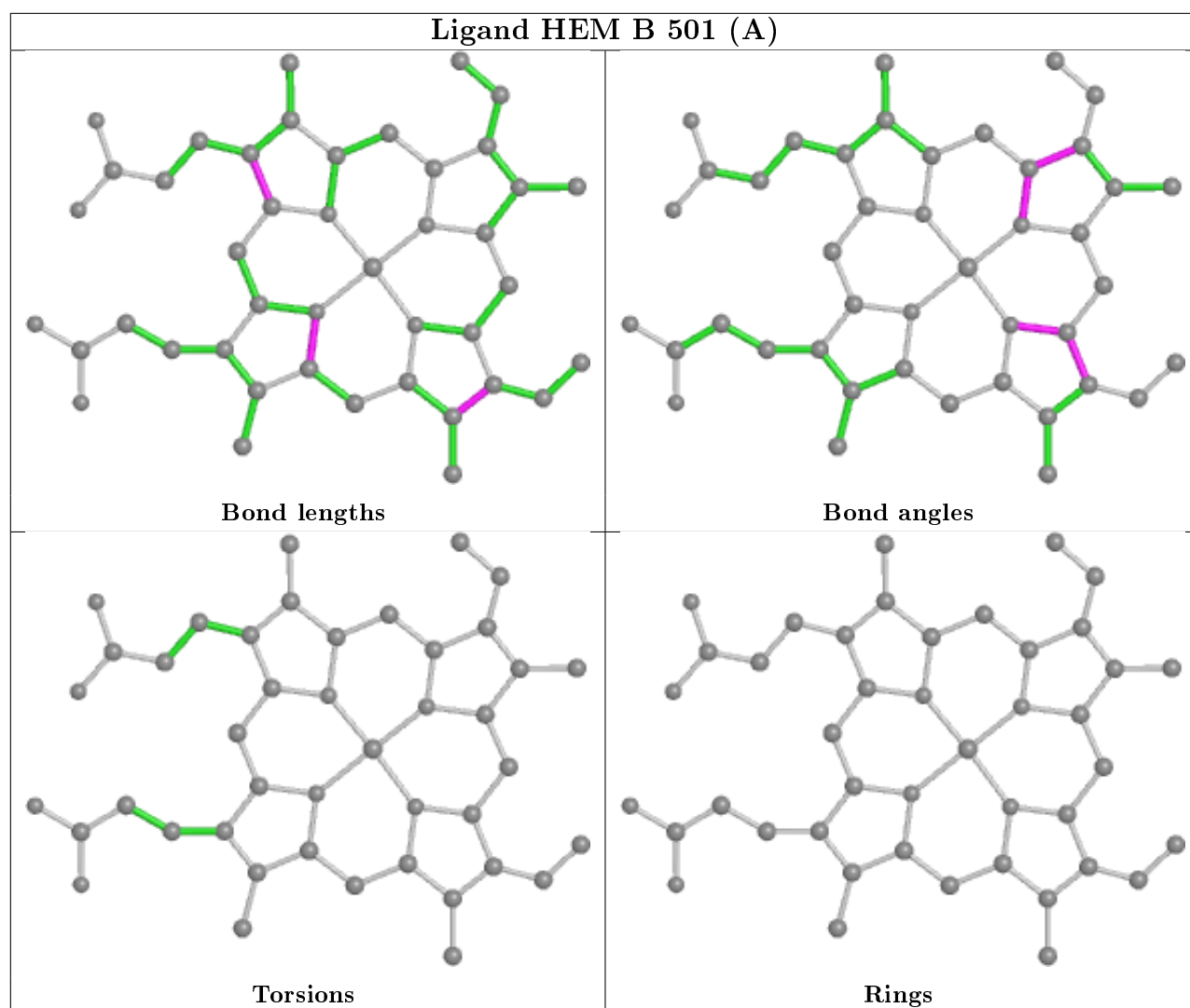


## Ligand HEM B 502 (B)



## Ligand HEM A 502 (B)





## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	481/491 (97%)	-0.10	10 (2%) 63 67	13, 21, 36, 63	0
1	B	481/491 (97%)	-0.20	3 (0%) 89 91	12, 19, 33, 55	0
1	C	481/491 (97%)	-0.07	7 (1%) 73 77	12, 18, 32, 71	0
1	D	481/491 (97%)	-0.04	9 (1%) 66 70	13, 21, 36, 60	0
All	All	1924/1964 (97%)	-0.10	29 (1%) 73 77	12, 19, 35, 71	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	486	LEU	7.5
1	A	485	TYR	5.9
1	C	485	TYR	5.8
1	A	486	LEU	5.5
1	A	484	SER	4.0
1	D	484	SER	3.9
1	C	484	SER	3.8
1	D	485	TYR	3.6
1	D	483	ARG	3.6
1	D	486	LEU	3.6
1	C	482	ILE	3.1
1	D	479	GLY	3.0
1	C	372[A]	PHE	3.0
1	D	481	ASP	2.9
1	B	486	LEU	2.8
1	C	483	ARG	2.8
1	A	372[A]	PHE	2.8
1	A	479	GLY	2.6
1	A	288	GLU	2.6
1	D	480	VAL	2.6
1	D	372[A]	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	398	HIS	2.4
1	A	464	TYR	2.4
1	B	372[A]	PHE	2.3
1	A	481	ASP	2.3
1	C	6	HIS	2.2
1	A	482	ILE	2.1
1	A	483	ARG	2.0
1	D	475	ALA	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 carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	JZ3	D	503	9/9	0.61	0.34	49,56,62,64	0
3	JZ3	C	503	9/9	0.64	0.25	42,45,52,52	0
3	JZ3	B	503	9/9	0.66	0.31	45,53,59,60	0
3	JZ3	A	503	9/9	0.67	0.28	54,57,64,66	0
3	JZ3	D	504	9/9	0.87	0.25	40,43,50,51	0
3	JZ3	B	504	9/9	0.91	0.14	34,38,40,45	0
2	HEM	D	502[B]	43/43	0.97	0.11	10,12,13,14	43
2	HEM	C	501[A]	43/43	0.97	0.10	10,13,15,19	43
2	HEM	C	502[B]	43/43	0.97	0.10	10,11,13,13	43
2	HEM	D	501[A]	43/43	0.97	0.11	14,16,17,24	43
2	HEM	A	502[B]	43/43	0.97	0.09	11,13,14,15	43
4	CL	B	505	1/1	0.98	0.08	18,18,18,18	0
5	NA	B	506	1/1	0.98	0.05	19,19,19,19	0
2	HEM	B	502[B]	43/43	0.98	0.09	8,10,11,11	43
2	HEM	B	501[A]	43/43	0.98	0.09	11,15,16,23	43

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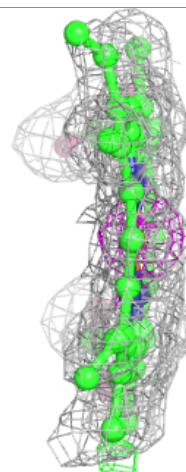
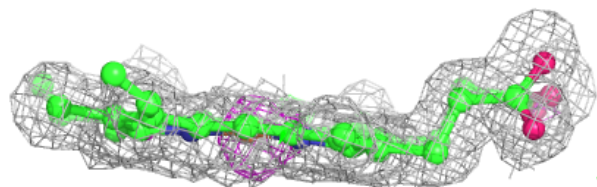
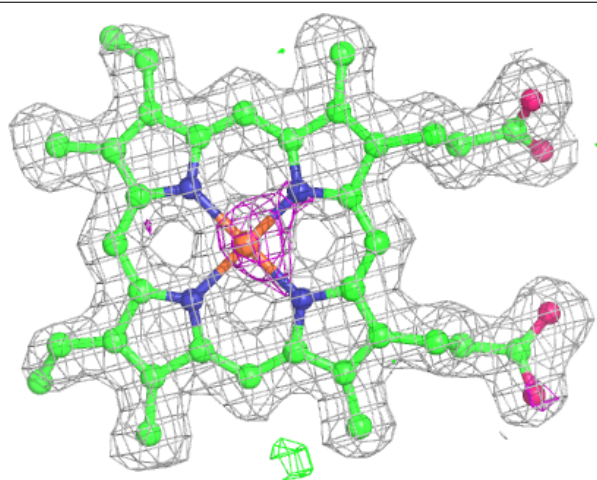
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	HEM	A	501[A]	43/43	0.98	0.09	12,15,16,20	43
5	NA	A	506	1/1	0.99	0.08	6,6,6,6	0
4	CL	C	504	1/1	0.99	0.12	23,23,23,23	0
4	CL	D	505	1/1	0.99	0.05	18,18,18,18	0
4	CL	A	504	1/1	0.99	0.17	25,25,25,25	0
4	CL	A	505	1/1	1.00	0.06	18,18,18,18	0
4	CL	C	505	1/1	1.00	0.05	20,20,20,20	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.

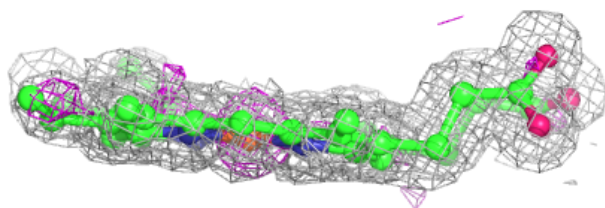
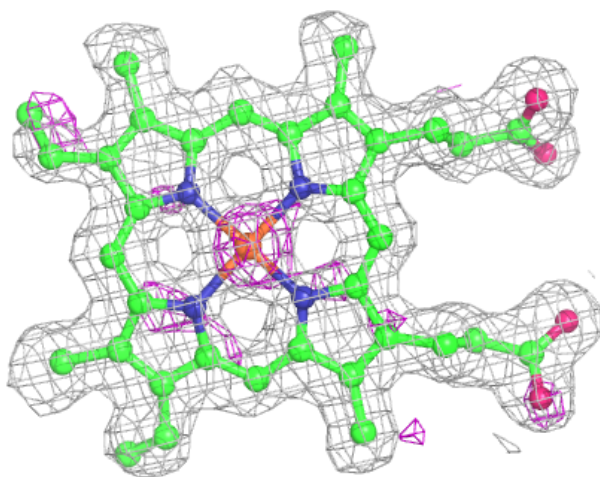
**Electron density around HEM D 502 (B):**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)



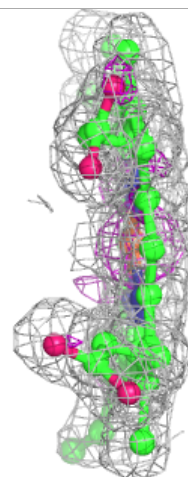
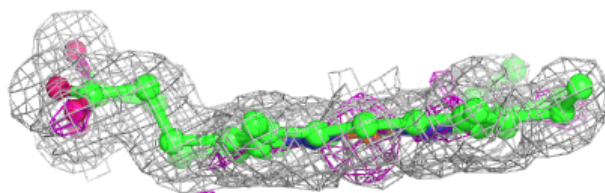
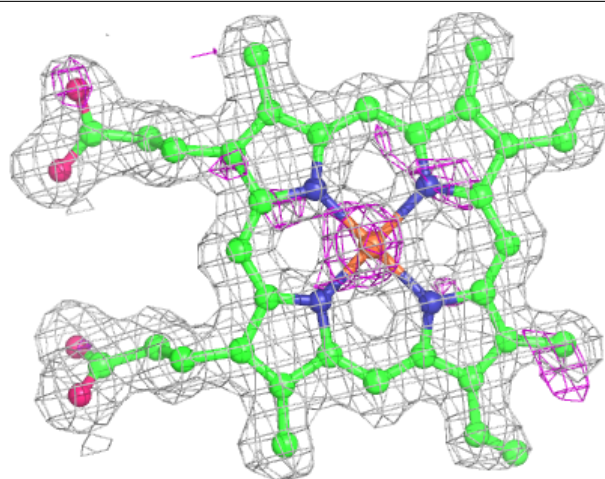
**Electron density around HEM C 501 (A):**

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



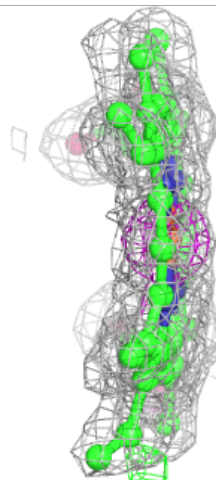
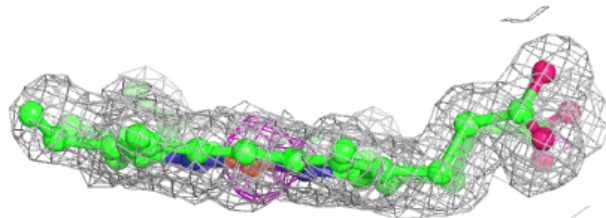
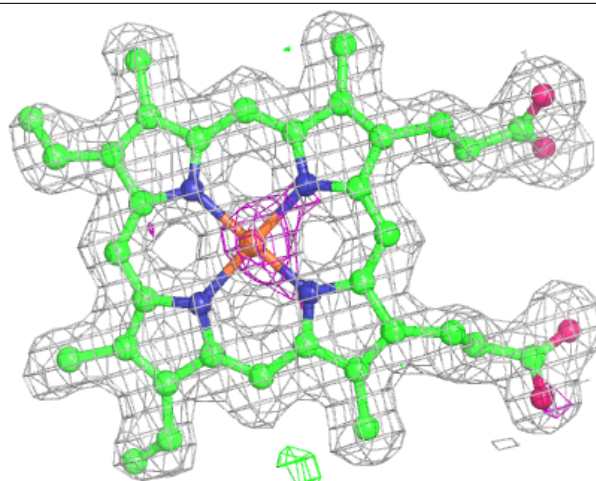
**Electron density around HEM C 502 (B):**

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



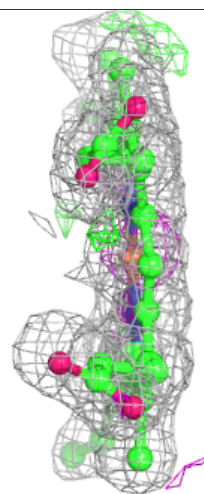
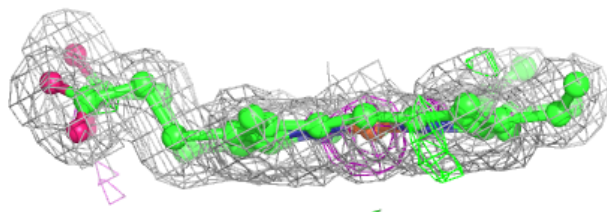
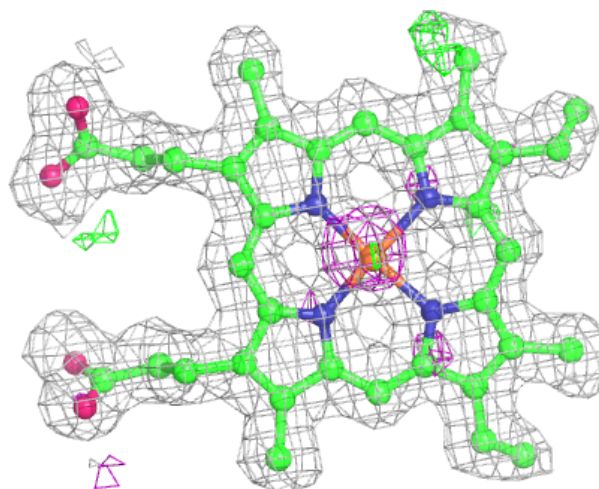
**Electron density around HEM D 501 (A):**

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



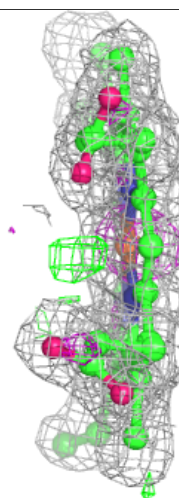
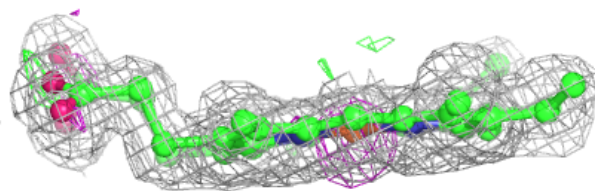
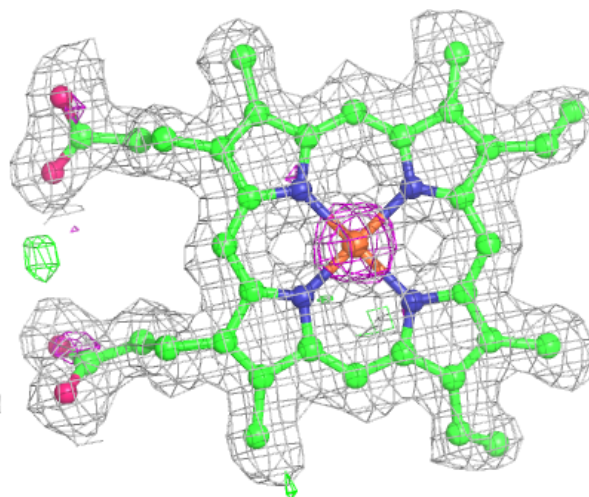
**Electron density around HEM A 502 (B):**

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



**Electron density around HEM B 502 (B):**

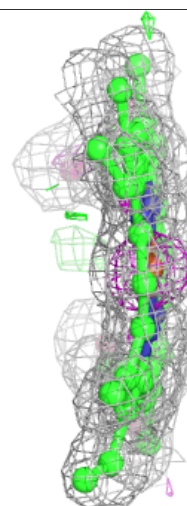
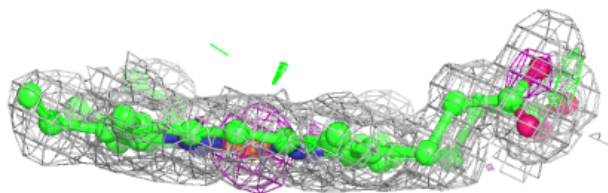
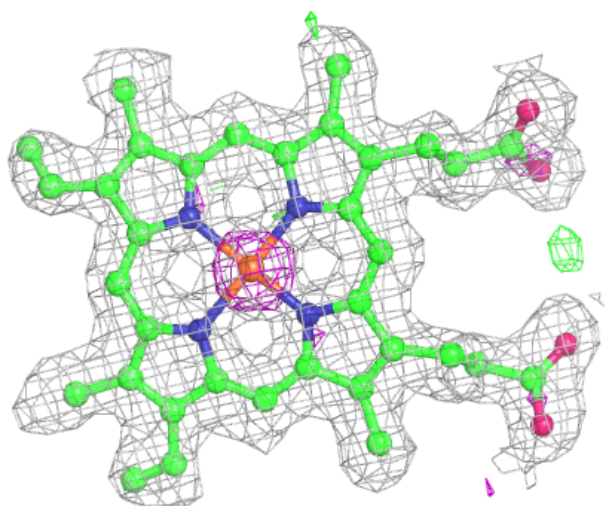
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around HEM B 501 (A):**

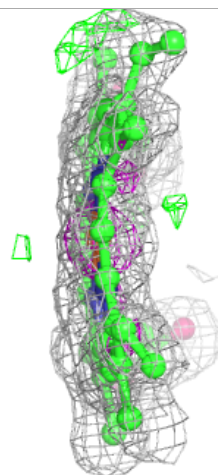
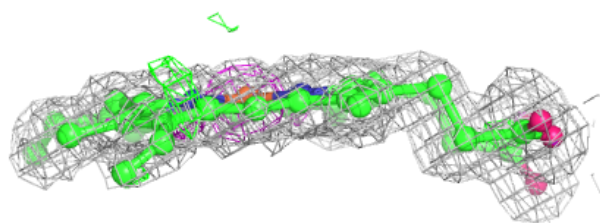
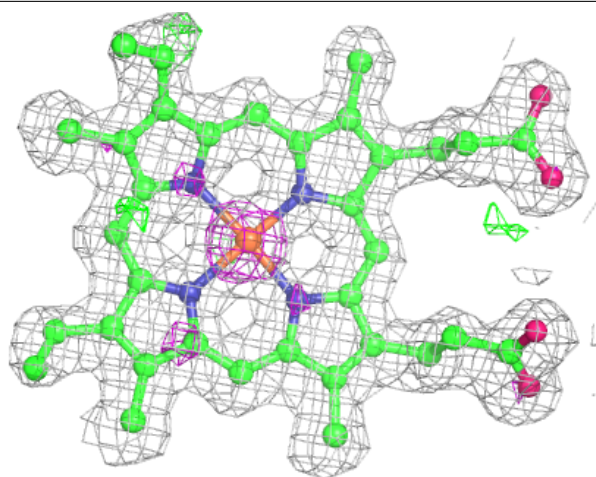
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





**Electron density around HEM A 501 (A):**

$2mF_o-DF_c$  (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.