



# Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 12:37 pm BST

PDB ID : 5YQH  
Title : The crystal structure of CYP19A4 binding with 4-n-Propyl benzoic acid  
Authors : Zhou, W.; Zhang, T.; Qiao, R.; Bell, S.; Coleman, T.  
Deposited on : 2017-11-06  
Resolution : 2.30 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

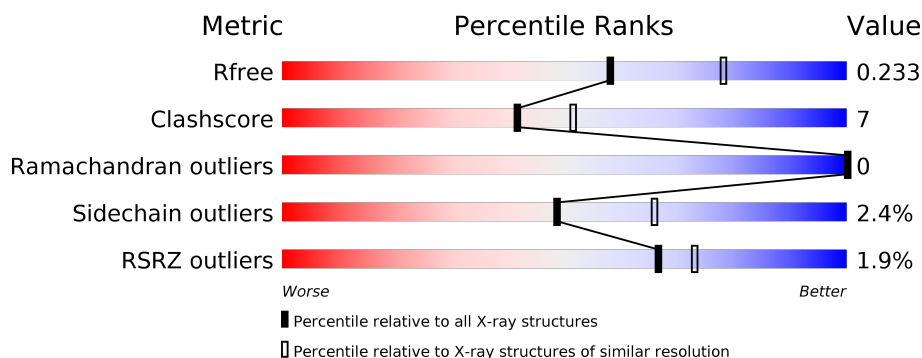
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	410	<div> <div>85%</div> <div>10%</div> <div>• •</div> </div>
1	B	410	<div> <div>84%</div> <div>11%</div> <div>• •</div> </div>
1	C	410	<div> <div>3%</div> <div>78%</div> <div>17%</div> <div>• •</div> </div>
1	D	410	<div> <div>4%</div> <div>84%</div> <div>12%</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:

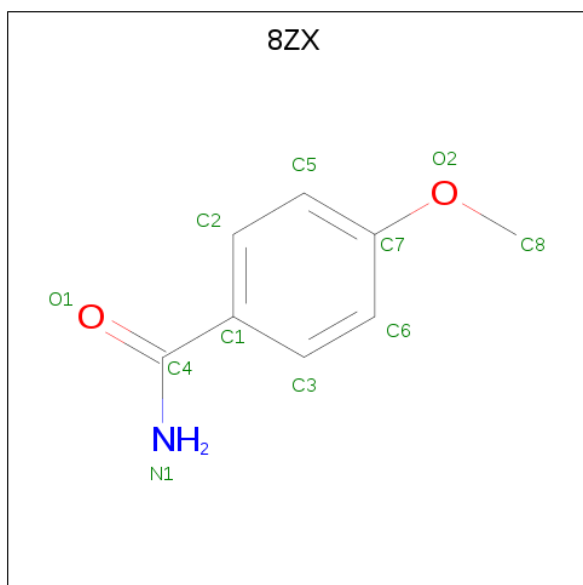
Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	8ZX	A	502	-	-	X	-
4	CL	C	503	-	-	X	-
5	GOL	B	507	-	-	X	-



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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 4-methoxybenzamide (three-letter code: 8ZX) (formula: C<sub>8</sub>H<sub>9</sub>NO<sub>2</sub>).

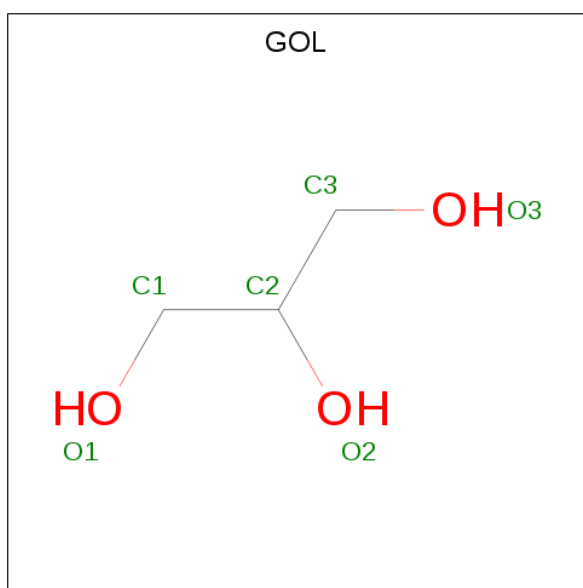


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			11	8	1	2		
3	A	1	Total	C	N	O	0	0
			11	8	1	2		
3	A	1	Total	C	N	O	0	0
			11	8	1	2		
3	B	1	Total	C	N	O	0	0
			11	8	1	2		
3	B	1	Total	C	N	O	0	0
			11	8	1	2		
3	B	1	Total	C	N	O	0	0
			11	8	1	2		
3	C	1	Total	C	N	O	0	0
			11	8	1	2		
3	D	1	Total	C	N	O	0	0
			11	8	1	2		

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

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

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



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

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).



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

- Molecule 7 is water.

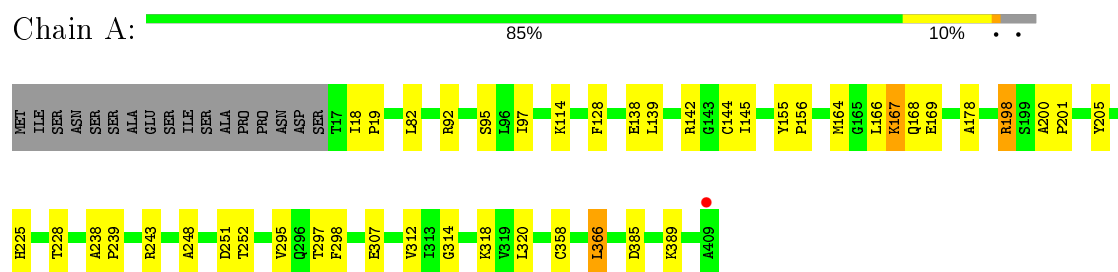
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	197	Total 197	O 197	0	0
7	B	172	Total 172	O 172	0	0
7	C	95	Total 95	O 95	0	0
7	D	79	Total 79	O 79	0	0



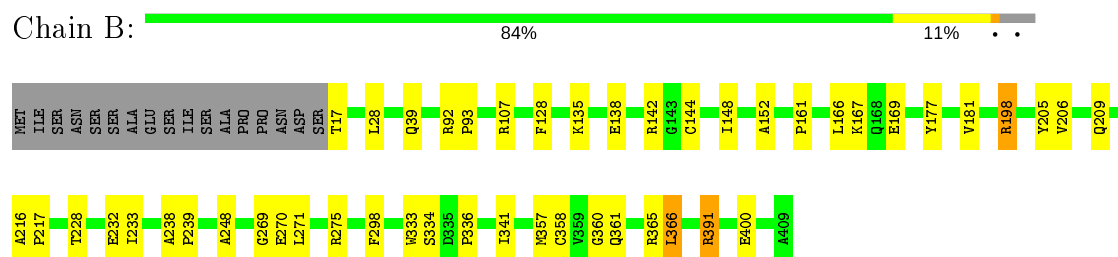
### 3 Residue-property plots [i](#)

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.

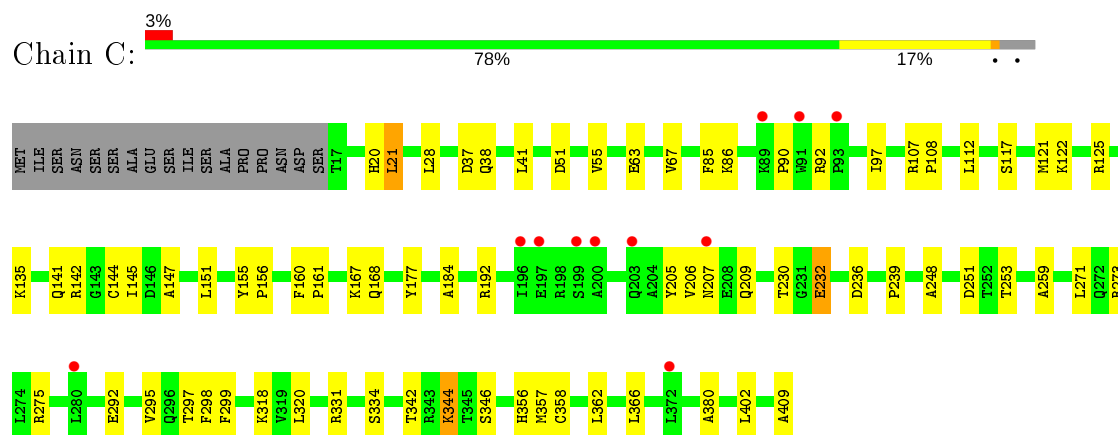
#### • Molecule 1: Cytochrome P450



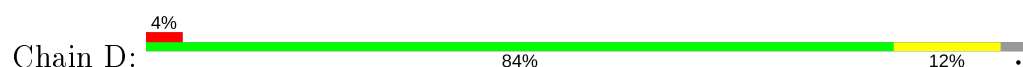
#### • Molecule 1: Cytochrome P450

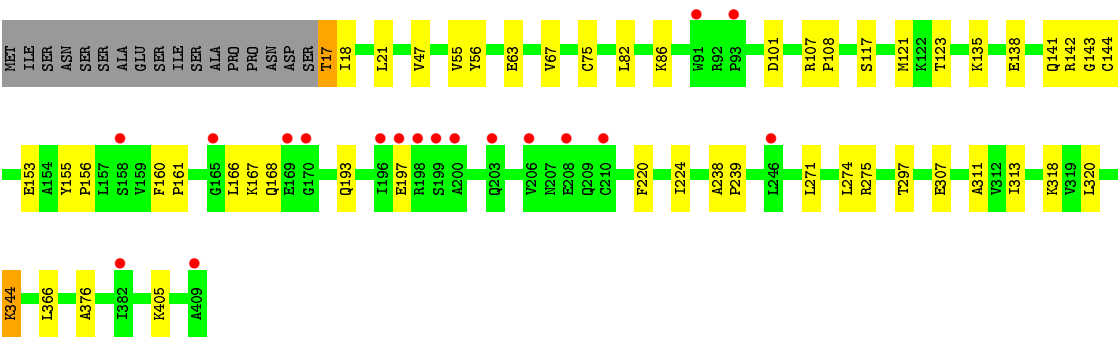


#### • Molecule 1: Cytochrome P450



#### • Molecule 1: Cytochrome P450





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	105.93Å 143.24Å 171.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.53 – 2.30 49.68 – 2.30	Depositor EDS
% Data completeness (in resolution range)	92.9 (43.53-2.30) 99.5 (49.68-2.30)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.58 (at 2.29Å)	Xtrriage
Refinement program	PHENIX 1.6.2_432	Depositor
R, $R_{free}$	0.196 , 0.237 0.199 , 0.233	Depositor DCC
$R_{free}$ test set	5827 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	36.9	Xtrriage
Anisotropy	0.832	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 38.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	13011	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 44.69 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.4708e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: GOL, SO4, 8ZX, HEM, 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	0.40	0/3093	0.55	0/4209
1	B	0.42	0/3104	0.55	0/4223
1	C	0.39	0/3093	0.52	0/4209
1	D	0.37	0/3093	0.50	0/4209
All	All	0.39	0/12383	0.53	0/16850

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3021	0	2993	38	0
1	B	3029	0	3006	43	0
1	C	3021	0	2993	49	0
1	D	3021	0	2993	34	0
2	A	43	0	30	7	0
2	B	43	0	30	6	0
2	C	43	0	30	7	0
2	D	43	0	30	2	0
3	A	33	0	0	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	33	0	0	5	0
3	C	11	0	0	2	0
3	D	11	0	0	1	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	2	0
4	D	1	0	0	0	0
5	A	6	0	8	0	0
5	B	12	0	16	5	0
5	C	12	0	16	3	0
5	D	12	0	16	0	0
6	A	30	0	0	0	0
6	B	20	0	0	0	0
6	C	15	0	0	1	0
6	D	5	0	0	0	0
7	A	197	0	0	2	0
7	B	172	0	0	6	0
7	C	95	0	0	0	0
7	D	79	0	0	3	0
All	All	13011	0	12161	172	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 7.

All (172) 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:391:ARG:HH11	1:B:391:ARG:HG3	1.33	0.92
2:B:501:HEM:HBC2	2:B:501:HEM:HMC1	1.55	0.88
2:C:501:HEM:HMB2	2:C:501:HEM:HBB2	1.68	0.76
1:B:269:GLY:HA3	5:B:507:GOL:H11	1.69	0.75
3:B:504:8ZX:N1	7:B:601:HOH:O	2.22	0.72
1:D:138:GLU:HB3	1:D:142:ARG:NH2	2.04	0.72
1:A:243:ARG:HE	3:A:502:8ZX:C8	2.03	0.71
1:C:92:ARG:NH2	4:C:503:CL:CL	2.60	0.71
1:A:238:ALA:HB3	1:A:239:PRO:HD3	1.72	0.70
1:B:144:CYS:SG	7:B:765:HOH:O	2.49	0.70
1:A:142:ARG:NH2	1:B:169:GLU:OE1	2.24	0.70
1:C:55:VAL:HG23	1:C:318:LYS:HB2	1.74	0.69
1:D:47:VAL:HG11	1:D:313:ILE:HD11	1.73	0.68
1:C:122:LYS:HD3	1:C:125:ARG:HH22	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:VAL:HG21	1:D:17:THR:HG22	1.75	0.68
1:C:167:LYS:HG3	1:C:168:GLN:N	2.10	0.67
1:B:391:ARG:HG3	1:B:391:ARG:NH1	2.07	0.67
2:B:501:HEM:HBC2	2:B:501:HEM:CMC	2.25	0.66
1:A:167:LYS:HG3	1:A:169:GLU:H	1.61	0.66
1:D:144:CYS:SG	7:D:676:HOH:O	2.54	0.64
1:D:55:VAL:HG23	1:D:318:LYS:HB2	1.80	0.64
1:A:169:GLU:OE1	1:B:142:ARG:NH2	2.30	0.64
1:A:167:LYS:HG3	1:A:168:GLN:N	2.13	0.63
1:C:55:VAL:HG23	1:C:318:LYS:CB	2.27	0.63
1:B:92:ARG:HH22	3:B:502:8ZX:C6	2.10	0.63
2:C:501:HEM:HBC2	2:C:501:HEM:HMC2	1.81	0.62
1:B:269:GLY:CA	5:B:507:GOL:H11	2.30	0.62
2:A:501:HEM:HBC2	2:A:501:HEM:HMC2	1.81	0.61
1:A:205:TYR:HA	1:B:142:ARG:HD3	1.82	0.61
1:C:21:LEU:HD23	1:C:41:LEU:HD23	1.83	0.61
1:D:297:THR:HB	1:D:320:LEU:HD11	1.84	0.60
1:C:167:LYS:HG3	1:C:168:GLN:H	1.67	0.60
2:D:501:HEM:HBC2	2:D:501:HEM:HMC2	1.83	0.60
5:C:505:GOL:H31	6:C:508:SO4:O4	2.02	0.60
1:D:138:GLU:HB3	1:D:142:ARG:HH21	1.65	0.59
1:D:274:LEU:HG	1:D:376:ALA:HB2	1.84	0.59
2:C:501:HEM:CMB	2:C:501:HEM:HBB2	2.31	0.58
1:A:92:ARG:NH2	3:A:502:8ZX:C5	2.66	0.58
1:C:155:TYR:HB3	1:C:156:PRO:HD3	1.84	0.58
1:D:160:PHE:HB3	1:D:161:PRO:HD3	1.87	0.57
2:D:501:HEM:HBC2	2:D:501:HEM:CMC	2.35	0.57
1:B:177:TYR:O	1:B:181:VAL:HG23	2.05	0.56
1:B:269:GLY:H	5:B:507:GOL:C1	2.19	0.56
1:B:361:GLN:O	1:B:365:ARG:HG3	2.06	0.56
1:C:177:TYR:CD2	1:C:206:VAL:HG21	2.41	0.55
2:A:501:HEM:HMB2	2:A:501:HEM:HBB2	1.87	0.55
1:B:17:THR:O	1:B:17:THR:HG22	2.06	0.55
1:C:236:ASP:O	1:C:239:PRO:HD2	2.06	0.54
1:D:55:VAL:HG23	1:D:318:LYS:CB	2.36	0.54
7:A:784:HOH:O	1:C:144:CYS:SG	2.59	0.54
1:C:85:PHE:CD2	1:C:90:PRO:HG3	2.42	0.54
1:A:92:ARG:HH22	3:A:502:8ZX:C5	2.21	0.54
1:B:391:ARG:CG	1:B:391:ARG:NH1	2.64	0.53
1:B:92:ARG:NH2	3:B:502:8ZX:C6	2.70	0.53
1:C:184:ALA:HA	1:C:192:ARG:HG3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:502:8ZX:C8	7:D:606:HOH:O	2.56	0.53
1:B:161:PRO:HD2	7:B:660:HOH:O	2.09	0.53
1:C:122:LYS:HD3	1:C:125:ARG:NH2	2.23	0.53
3:C:502:8ZX:N1	4:C:503:CL:CL	2.77	0.53
1:D:17:THR:HG23	1:D:18:ILE:N	2.23	0.53
1:C:259:ALA:HB1	1:C:292:GLU:HG3	1.91	0.53
1:C:253:THR:HG22	2:C:501:HEM:HAB	1.90	0.53
1:C:230:THR:OG1	1:C:232:GLU:OE1	2.23	0.52
1:C:92:ARG:NH1	1:C:177:TYR:OH	2.41	0.52
1:B:177:TYR:CD2	1:B:206:VAL:HG21	2.44	0.52
1:B:205:TYR:O	1:B:209:GLN:HG2	2.10	0.52
1:C:331:ARG:HE	5:C:505:GOL:H12	1.75	0.52
1:C:151:LEU:C	1:C:151:LEU:HD23	2.29	0.52
1:D:155:TYR:HB3	1:D:156:PRO:HD3	1.91	0.52
2:A:501:HEM:HBC2	2:A:501:HEM:CMC	2.40	0.52
1:C:358:CYS:HA	2:C:501:HEM:CHA	2.41	0.51
1:A:312:VAL:CG2	1:D:17:THR:HG22	2.41	0.51
2:C:501:HEM:HBC2	2:C:501:HEM:CMC	2.40	0.51
1:B:298:PHE:CE1	2:B:501:HEM:HBA2	2.46	0.51
1:A:142:ARG:HH22	1:B:169:GLU:CD	2.14	0.50
1:B:357:MET:O	1:B:358:CYS:C	2.49	0.50
1:C:402:LEU:O	1:C:402:LEU:HG	2.10	0.50
1:D:82:LEU:O	1:D:318:LYS:HE3	2.12	0.50
1:A:314:GLY:HA3	1:D:21:LEU:HD21	1.94	0.50
1:D:107:ARG:HB3	1:D:108:PRO:CD	2.41	0.50
1:B:228:THR:HG22	1:B:233:ILE:HG13	1.94	0.49
1:C:344:LYS:HE2	1:C:346:SER:H	1.78	0.49
1:C:177:TYR:CG	1:C:206:VAL:HG21	2.48	0.48
1:C:380:ALA:HB2	1:C:409:ALA:HA	1.95	0.48
1:D:274:LEU:HG	1:D:376:ALA:CB	2.44	0.48
1:A:169:GLU:HG3	1:B:138:GLU:OE1	2.14	0.47
1:A:243:ARG:HH11	3:A:502:8ZX:C8	2.27	0.47
1:C:37:ASP:O	1:C:41:LEU:HG	2.14	0.47
1:A:178:ALA:HB3	1:A:251:ASP:CG	2.35	0.47
2:A:501:HEM:HBB2	2:A:501:HEM:CMB	2.44	0.47
1:A:297:THR:HB	1:A:320:LEU:HD11	1.96	0.47
1:B:333:TRP:O	1:B:336:PRO:HD3	2.15	0.47
1:C:273:ARG:NH2	1:C:342:THR:CG2	2.78	0.47
1:A:389:LYS:HD2	1:B:198:ARG:NE	2.30	0.47
3:B:503:8ZX:C3	7:B:618:HOH:O	2.63	0.47
1:C:55:VAL:HG21	1:C:299:PHE:HE2	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:18:ILE:HD11	1:D:311:ALA:HB1	1.97	0.47
1:C:38:GLN:HA	1:C:41:LEU:HD12	1.97	0.46
1:D:143:GLY:O	1:D:405:LYS:HD2	2.15	0.46
1:B:248:ALA:HB2	3:B:502:8ZX:C4	2.44	0.46
1:D:56:TYR:CD1	1:D:313:ILE:HD12	2.50	0.46
1:A:248:ALA:HB2	3:A:502:8ZX:C4	2.46	0.46
1:A:138:GLU:OE1	1:B:169:GLU:HG3	2.15	0.46
1:C:86:LYS:HG2	1:C:86:LYS:O	2.14	0.46
1:D:344:LYS:HE2	1:D:344:LYS:HA	1.97	0.46
1:A:97:ILE:HG12	2:A:501:HEM:CGD	2.45	0.46
1:C:160:PHE:HB3	1:C:161:PRO:HD3	1.98	0.46
1:A:295:VAL:HG11	1:A:298:PHE:CE1	2.49	0.46
1:B:238:ALA:HB3	1:B:239:PRO:HD3	1.98	0.46
1:C:147:ALA:HB3	1:C:402:LEU:HD23	1.98	0.46
1:C:20:HIS:HD2	1:C:51:ASP:OD1	1.97	0.46
1:B:269:GLY:H	5:B:507:GOL:H11	1.81	0.46
1:A:155:TYR:HB3	1:A:156:PRO:HD3	1.98	0.46
3:A:503:8ZX:C8	1:C:141:GLN:HB2	2.45	0.46
1:B:269:GLY:N	5:B:507:GOL:H11	2.30	0.46
1:D:193:GLN:O	1:D:197:GLU:HB2	2.16	0.45
1:D:117:SER:O	1:D:121:MET:HG2	2.16	0.45
1:C:97:ILE:HD13	1:C:112:LEU:HD12	1.99	0.45
1:D:220:PHE:O	1:D:224:ILE:HG13	2.15	0.45
1:A:198:ARG:HD2	7:B:648:HOH:O	2.16	0.45
1:A:164:MET:HB3	1:A:166:LEU:HD13	1.99	0.45
1:A:389:LYS:HE3	1:B:198:ARG:HD3	2.00	0.44
1:D:271:LEU:O	1:D:275:ARG:HG3	2.17	0.44
1:C:295:VAL:HG11	1:C:298:PHE:CE1	2.52	0.44
1:C:107:ARG:HB3	1:C:108:PRO:CD	2.48	0.44
1:A:200:ALA:HB3	1:A:201:PRO:HD3	2.00	0.44
1:D:271:LEU:O	1:D:271:LEU:HD12	2.17	0.44
1:B:128:PHE:CD2	1:B:366:LEU:HD13	2.53	0.44
1:A:167:LYS:HG3	1:A:169:GLU:N	2.30	0.44
1:A:82:LEU:O	1:A:318:LYS:HE3	2.17	0.44
1:B:248:ALA:HB1	7:B:684:HOH:O	2.17	0.44
1:C:121:MET:HG3	1:C:362:LEU:HB3	2.00	0.43
1:B:107:ARG:HD2	1:B:232:GLU:O	2.18	0.43
1:D:193:GLN:HG2	7:D:610:HOH:O	2.18	0.43
1:D:86:LYS:O	1:D:86:LYS:HG2	2.18	0.43
1:B:270:GLU:OE2	1:B:341:ILE:HG12	2.19	0.43
1:B:177:TYR:CE2	1:B:206:VAL:HG21	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:271:LEU:O	1:B:275:ARG:HG3	2.19	0.43
1:B:358:CYS:HA	2:B:501:HEM:CHA	2.49	0.43
1:D:75:CYS:HB2	1:D:101:ASP:OD2	2.19	0.43
1:D:238:ALA:HB3	1:D:239:PRO:HD3	2.00	0.43
1:C:205:TYR:O	1:C:209:GLN:HG2	2.19	0.42
1:C:331:ARG:HH21	5:C:505:GOL:H32	1.84	0.42
1:C:63:GLU:O	1:C:67:VAL:HG23	2.19	0.42
1:A:95:SER:HB2	3:A:502:8ZX:C7	2.49	0.42
1:A:225:HIS:O	1:A:228:THR:HG23	2.20	0.42
1:B:92:ARG:HB2	1:B:93:PRO:HD2	2.01	0.42
1:B:391:ARG:HG2	1:B:400:GLU:HB2	2.00	0.42
2:B:501:HEM:HBB2	2:B:501:HEM:CMB	2.49	0.42
1:A:114:LYS:HB2	1:A:114:LYS:HE3	1.56	0.41
1:D:153:GLU:O	1:D:156:PRO:HD2	2.20	0.41
1:D:63:GLU:O	1:D:67:VAL:HG23	2.19	0.41
1:C:142:ARG:HD2	1:C:145:ILE:HG22	2.02	0.41
1:C:271:LEU:O	1:C:275:ARG:HG3	2.19	0.41
1:D:167:LYS:HG3	1:D:168:GLN:N	2.36	0.41
1:A:139:LEU:HD13	1:A:145:ILE:HD13	2.03	0.41
1:B:360:GLY:HA3	2:B:501:HEM:C3C	2.56	0.41
1:A:252:THR:HB	2:A:501:HEM:C3B	2.56	0.41
1:C:20:HIS:CD2	1:C:51:ASP:OD1	2.74	0.41
1:D:193:GLN:HA	1:D:193:GLN:NE2	2.36	0.41
1:B:148:ILE:HA	1:B:152:ALA:HB3	2.03	0.41
1:C:248:ALA:HB2	3:C:502:8ZX:C5	2.51	0.41
1:B:216:ALA:HA	1:B:217:PRO:HD3	1.98	0.40
1:C:117:SER:O	1:C:121:MET:HG2	2.21	0.40
1:A:144:CYS:SG	7:A:646:HOH:O	2.63	0.40
2:C:501:HEM:HMB2	2:C:501:HEM:CBB	2.44	0.40
1:A:358:CYS:HA	2:A:501:HEM:CHA	2.51	0.40
1:A:18:ILE:HA	1:A:19:PRO:HD2	1.98	0.40
1:A:128:PHE:CD2	1:A:366:LEU:HD13	2.57	0.40
1:C:299:PHE:CZ	1:C:320:LEU:HD13	2.57	0.40
1:C:297:THR:HB	1:C:320:LEU:HD11	2.02	0.40
1:C:356:HIS:O	1:C:357:MET:C	2.60	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	391/410 (95%)	383 (98%)	8 (2%)	0	100	100
1	B	392/410 (96%)	382 (97%)	10 (3%)	0	100	100
1	C	391/410 (95%)	380 (97%)	11 (3%)	0	100	100
1	D	391/410 (95%)	375 (96%)	16 (4%)	0	100	100
All	All	1565/1640 (95%)	1520 (97%)	45 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	319/334 (96%)	314 (98%)	5 (2%)	62	78
1	B	320/334 (96%)	311 (97%)	9 (3%)	43	60
1	C	319/334 (96%)	310 (97%)	9 (3%)	43	60
1	D	319/334 (96%)	311 (98%)	8 (2%)	47	65
All	All	1277/1336 (96%)	1246 (98%)	31 (2%)	49	66

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	167	LYS
1	A	198	ARG

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Mol	Chain	Res	Type
1	A	307	GLU
1	A	366	LEU
1	A	385	ASP
1	B	28	LEU
1	B	39	GLN
1	B	135	LYS
1	B	166	LEU
1	B	167	LYS
1	B	198	ARG
1	B	334	SER
1	B	366	LEU
1	B	391	ARG
1	C	21	LEU
1	C	28	LEU
1	C	135	LYS
1	C	207	ASN
1	C	232	GLU
1	C	251	ASP
1	C	334	SER
1	C	344	LYS
1	C	366	LEU
1	D	17	THR
1	D	123	THR
1	D	135	LYS
1	D	141	GLN
1	D	166	LEU
1	D	307	GLU
1	D	344	LYS
1	D	366	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	39	GLN
1	C	20	HIS
1	D	38	GLN
1	D	69	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 37 ligands modelled in this entry, 4 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	SO4	A	511	-	4,4,4	0.11	0	6,6,6	0.10	0
5	GOL	B	506	-	5,5,5	0.27	0	5,5,5	0.91	0
2	HEM	A	501	1	27,50,50	2.15	6 (22%)	17,82,82	1.57	3 (17%)
6	SO4	B	510	-	4,4,4	0.14	0	6,6,6	0.14	0
6	SO4	A	510	-	4,4,4	0.19	0	6,6,6	0.24	0
2	HEM	D	501	1,7	27,50,50	2.10	6 (22%)	17,82,82	1.58	4 (23%)
3	8ZX	A	502	-	11,11,11	0.75	0	14,14,14	1.44	3 (21%)
5	GOL	D	504	-	5,5,5	0.37	0	5,5,5	0.26	0
6	SO4	C	506	-	4,4,4	0.17	0	6,6,6	0.09	0
5	GOL	C	505	-	5,5,5	0.38	0	5,5,5	0.27	0
3	8ZX	A	504	-	11,11,11	0.71	0	14,14,14	0.80	1 (7%)
3	8ZX	B	504	-	11,11,11	0.55	0	14,14,14	0.65	0
6	SO4	B	511	-	4,4,4	0.24	0	6,6,6	0.16	0
6	SO4	C	508	-	4,4,4	0.15	0	6,6,6	0.17	0
5	GOL	B	507	-	5,5,5	0.33	0	5,5,5	0.38	0
6	SO4	A	509	-	4,4,4	0.17	0	6,6,6	0.32	0
2	HEM	C	501	1	27,50,50	2.18	6 (22%)	17,82,82	1.52	4 (23%)
6	SO4	C	507	-	4,4,4	0.19	0	6,6,6	0.19	0
5	GOL	D	505	-	5,5,5	0.28	0	5,5,5	0.50	0
6	SO4	B	509	-	4,4,4	0.18	0	6,6,6	0.18	0
3	8ZX	B	503	-	11,11,11	0.77	0	14,14,14	1.29	1 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	SO4	D	506	-	4,4,4	0.18	0	6,6,6	0.08	0
6	SO4	A	512	-	4,4,4	0.18	0	6,6,6	0.13	0
6	SO4	A	508	-	4,4,4	0.17	0	6,6,6	0.31	0
6	SO4	B	508	-	4,4,4	0.16	0	6,6,6	0.23	0
3	8ZX	A	503	-	11,11,11	0.50	0	14,14,14	0.72	0
6	SO4	A	507	-	4,4,4	0.22	0	6,6,6	0.28	0
5	GOL	A	506	-	5,5,5	0.17	0	5,5,5	1.19	1 (20%)
2	HEM	B	501	1,7	27,50,50	2.05	6 (22%)	17,82,82	1.77	3 (17%)
3	8ZX	B	502	-	11,11,11	0.84	0	14,14,14	1.78	2 (14%)
3	8ZX	C	502	-	11,11,11	0.54	0	14,14,14	1.02	0
3	8ZX	D	502	-	11,11,11	0.55	0	14,14,14	1.20	1 (7%)
5	GOL	C	504	-	5,5,5	0.41	0	5,5,5	0.22	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	8ZX	A	503	-	-	0/6/6/6	0/1/1/1
5	GOL	B	506	-	-	0/4/4/4	-
2	HEM	C	501	1	-	0/6/54/54	-
2	HEM	D	501	1,7	-	0/6/54/54	-
5	GOL	C	505	-	-	0/4/4/4	-
5	GOL	D	504	-	-	0/4/4/4	-
3	8ZX	A	504	-	-	0/6/6/6	0/1/1/1
3	8ZX	B	504	-	-	0/6/6/6	0/1/1/1
5	GOL	A	506	-	-	0/4/4/4	-
3	8ZX	B	503	-	-	2/6/6/6	0/1/1/1
5	GOL	B	507	-	-	2/4/4/4	-
2	HEM	B	501	1,7	-	0/6/54/54	-
3	8ZX	B	502	-	-	2/6/6/6	0/1/1/1
5	GOL	D	505	-	-	2/4/4/4	-
3	8ZX	A	502	-	-	2/6/6/6	0/1/1/1
2	HEM	A	501	1	-	0/6/54/54	-
3	8ZX	C	502	-	-	2/6/6/6	0/1/1/1
3	8ZX	D	502	-	-	2/6/6/6	0/1/1/1
5	GOL	C	504	-	-	2/4/4/4	-

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	HEM	C3D-C2D	5.27	1.53	1.37
2	D	501	HEM	C3D-C2D	5.27	1.53	1.37
2	C	501	HEM	C3D-C2D	5.09	1.52	1.37
2	B	501	HEM	C3D-C2D	5.01	1.52	1.37
2	A	501	HEM	C3B-C2B	-4.67	1.33	1.40
2	C	501	HEM	C3B-C2B	-4.57	1.34	1.40
2	C	501	HEM	C3C-C2C	-4.57	1.34	1.40
2	D	501	HEM	C3B-C2B	-4.07	1.34	1.40
2	B	501	HEM	C3C-C2C	-3.92	1.34	1.40
2	D	501	HEM	C3C-C2C	-3.91	1.34	1.40
2	B	501	HEM	C3B-C2B	-3.70	1.35	1.40
2	A	501	HEM	C3C-CAC	3.69	1.55	1.47
2	A	501	HEM	C3C-C2C	-3.69	1.35	1.40
2	A	501	HEM	C3B-CAB	3.68	1.55	1.47
2	B	501	HEM	C3B-CAB	3.61	1.55	1.47
2	C	501	HEM	C3B-CAB	3.60	1.55	1.47
2	C	501	HEM	C3C-CAC	3.57	1.55	1.47
2	D	501	HEM	C3B-CAB	3.44	1.54	1.47
2	D	501	HEM	C3C-CAC	3.26	1.54	1.47
2	B	501	HEM	C3C-CAC	3.18	1.54	1.47
2	D	501	HEM	CAA-C2A	2.61	1.55	1.52
2	A	501	HEM	CAA-C2A	2.36	1.55	1.52
2	C	501	HEM	CAA-C2A	2.23	1.55	1.52
2	B	501	HEM	CAA-C2A	2.20	1.55	1.52

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	502	8ZX	C8-O2-C7	4.38	127.00	117.51
2	B	501	HEM	CBD-CAD-C3D	-4.17	104.80	112.48
2	D	501	HEM	CBD-CAD-C3D	-3.61	105.83	112.48
2	B	501	HEM	C1D-C2D-C3D	-3.57	104.51	107.00
3	A	502	8ZX	C8-O2-C7	3.51	125.12	117.51
3	D	502	8ZX	C8-O2-C7	3.43	124.94	117.51
2	C	501	HEM	CBD-CAD-C3D	-3.22	106.55	112.48
2	A	501	HEM	CBD-CAD-C3D	-3.17	106.64	112.48
3	B	503	8ZX	O1-C4-C1	-3.09	115.93	119.63
2	A	501	HEM	C4A-C3A-C2A	2.79	108.93	107.00
3	B	502	8ZX	C3-C6-C7	2.71	123.05	119.73
2	C	501	HEM	C1D-C2D-C3D	-2.57	105.21	107.00
2	C	501	HEM	CMA-C3A-C4A	-2.45	124.69	128.46
3	A	502	8ZX	O1-C4-C1	-2.44	116.71	119.63
2	D	501	HEM	C1D-C2D-C3D	-2.41	105.32	107.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	HEM	CMA-C3A-C4A	-2.36	124.84	128.46
2	D	501	HEM	C4A-C3A-C2A	2.35	108.63	107.00
5	A	506	GOL	C3-C2-C1	-2.29	102.82	111.70
2	D	501	HEM	C4C-C3C-C2C	2.26	108.48	106.90
3	A	504	8ZX	C8-O2-C7	2.21	122.31	117.51
3	A	502	8ZX	C1-C4-N1	2.17	120.36	117.75
2	A	501	HEM	CMA-C3A-C4A	-2.17	125.13	128.46
2	C	501	HEM	C4A-C3A-C2A	2.10	108.46	107.00

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	507	GOL	O1-C1-C2-C3
5	C	504	GOL	O1-C1-C2-C3
3	D	502	8ZX	C6-C7-O2-C8
3	D	502	8ZX	C5-C7-O2-C8
5	C	504	GOL	O1-C1-C2-O2
3	B	502	8ZX	C5-C7-O2-C8
3	C	502	8ZX	C6-C7-O2-C8
3	C	502	8ZX	C5-C7-O2-C8
3	B	502	8ZX	C6-C7-O2-C8
5	D	505	GOL	O1-C1-C2-C3
5	B	507	GOL	O1-C1-C2-O2
3	B	503	8ZX	C6-C7-O2-C8
3	B	503	8ZX	C5-C7-O2-C8
5	D	505	GOL	O1-C1-C2-O2
3	A	502	8ZX	C6-C7-O2-C8
3	A	502	8ZX	C5-C7-O2-C8

There are no ring outliers.

14 monomers are involved in 45 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	HEM	7	0
2	D	501	HEM	2	0
3	A	502	8ZX	6	0
5	C	505	GOL	3	0
3	B	504	8ZX	1	0
6	C	508	SO4	1	0
5	B	507	GOL	5	0

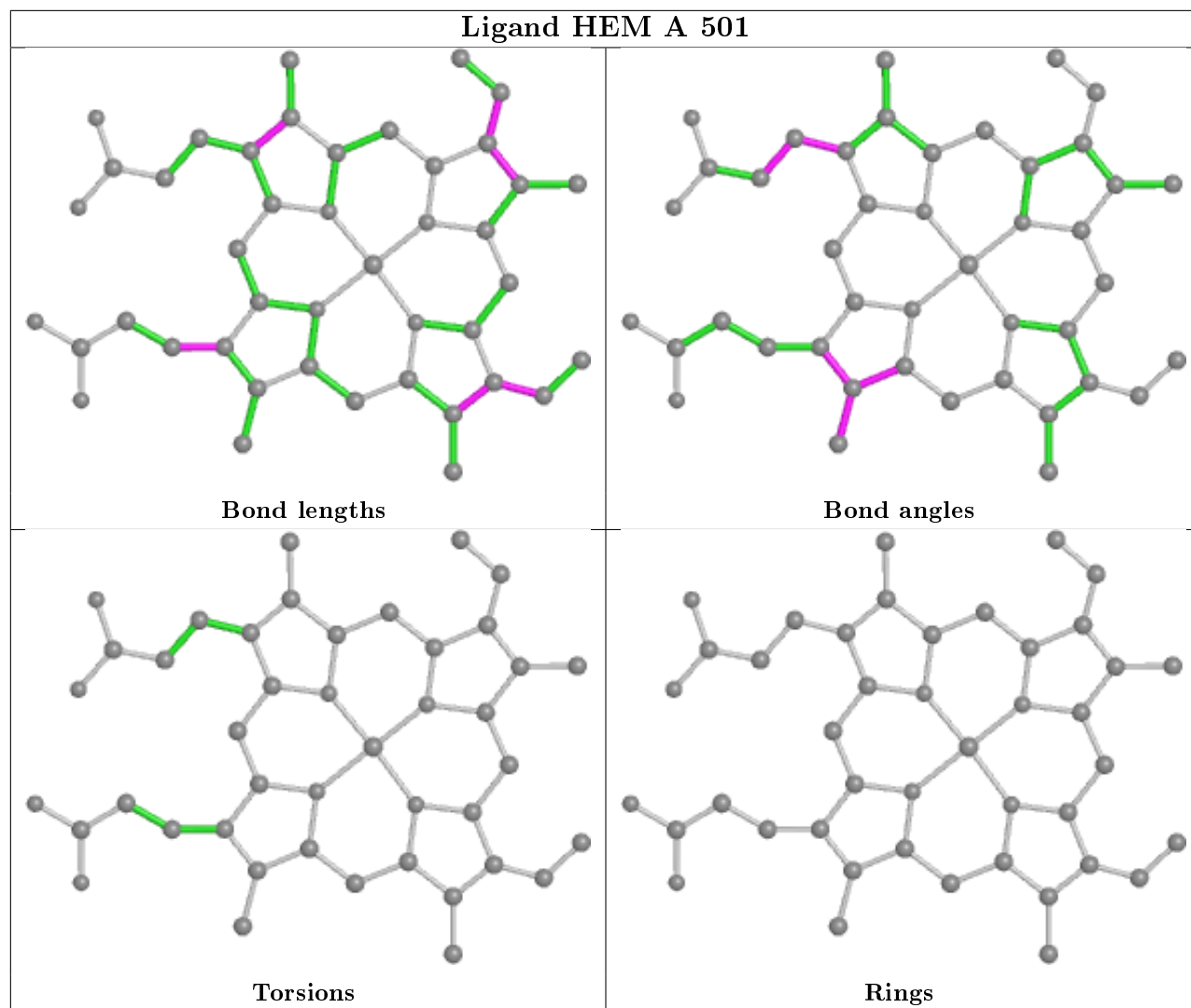
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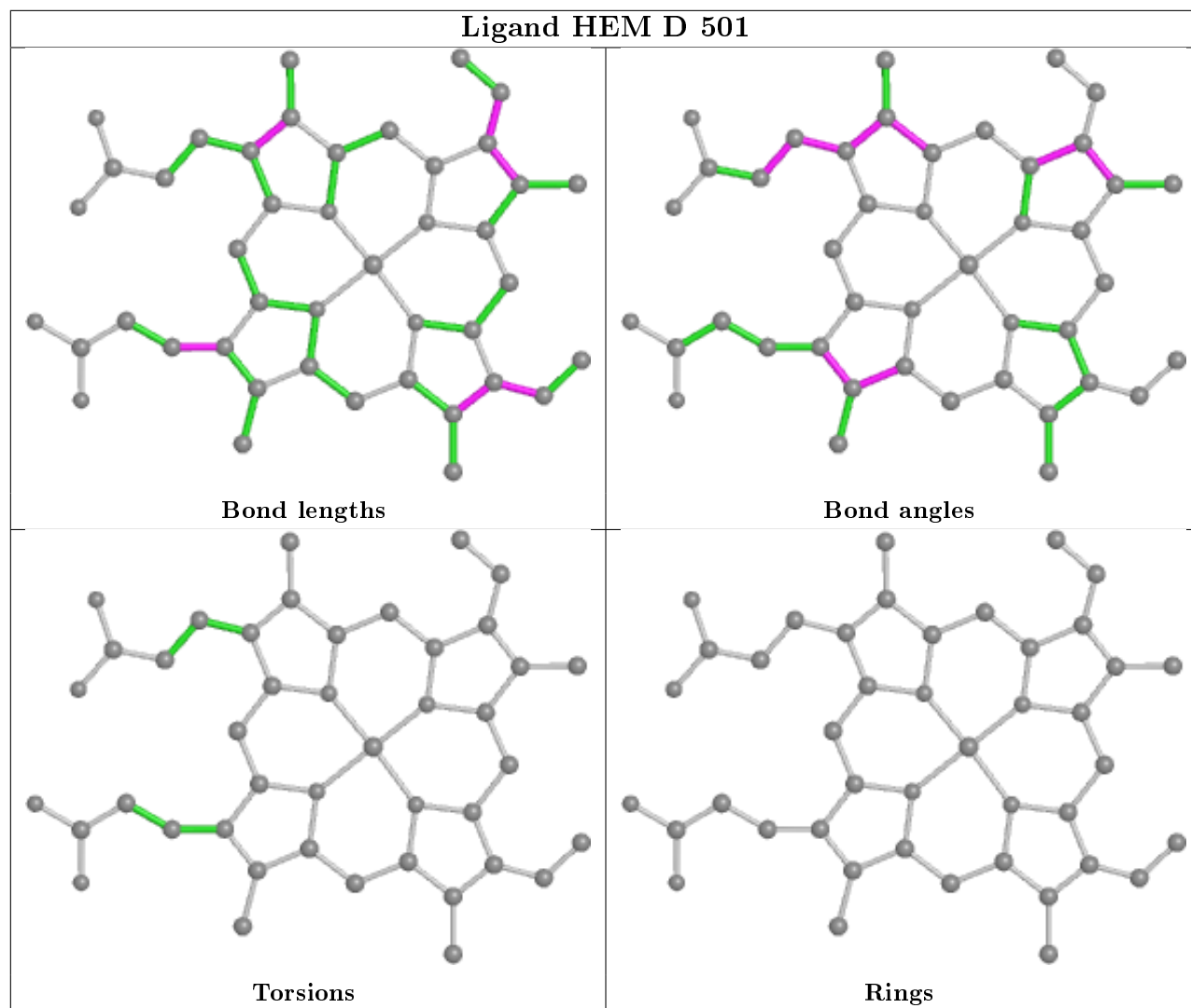
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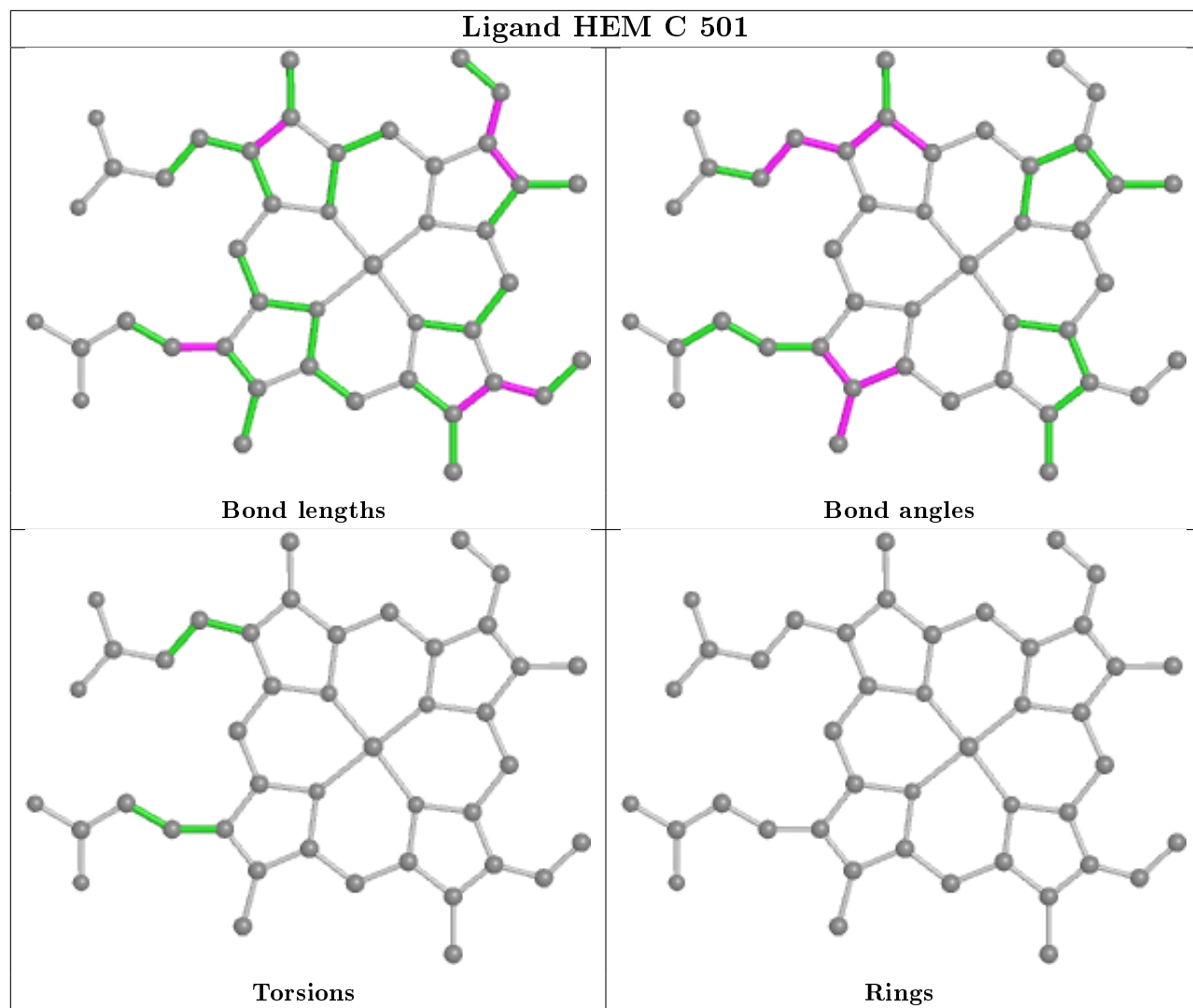
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	501	HEM	7	0
3	B	503	8ZX	1	0
3	A	503	8ZX	1	0
2	B	501	HEM	6	0
3	B	502	8ZX	3	0
3	C	502	8ZX	2	0
3	D	502	8ZX	1	0

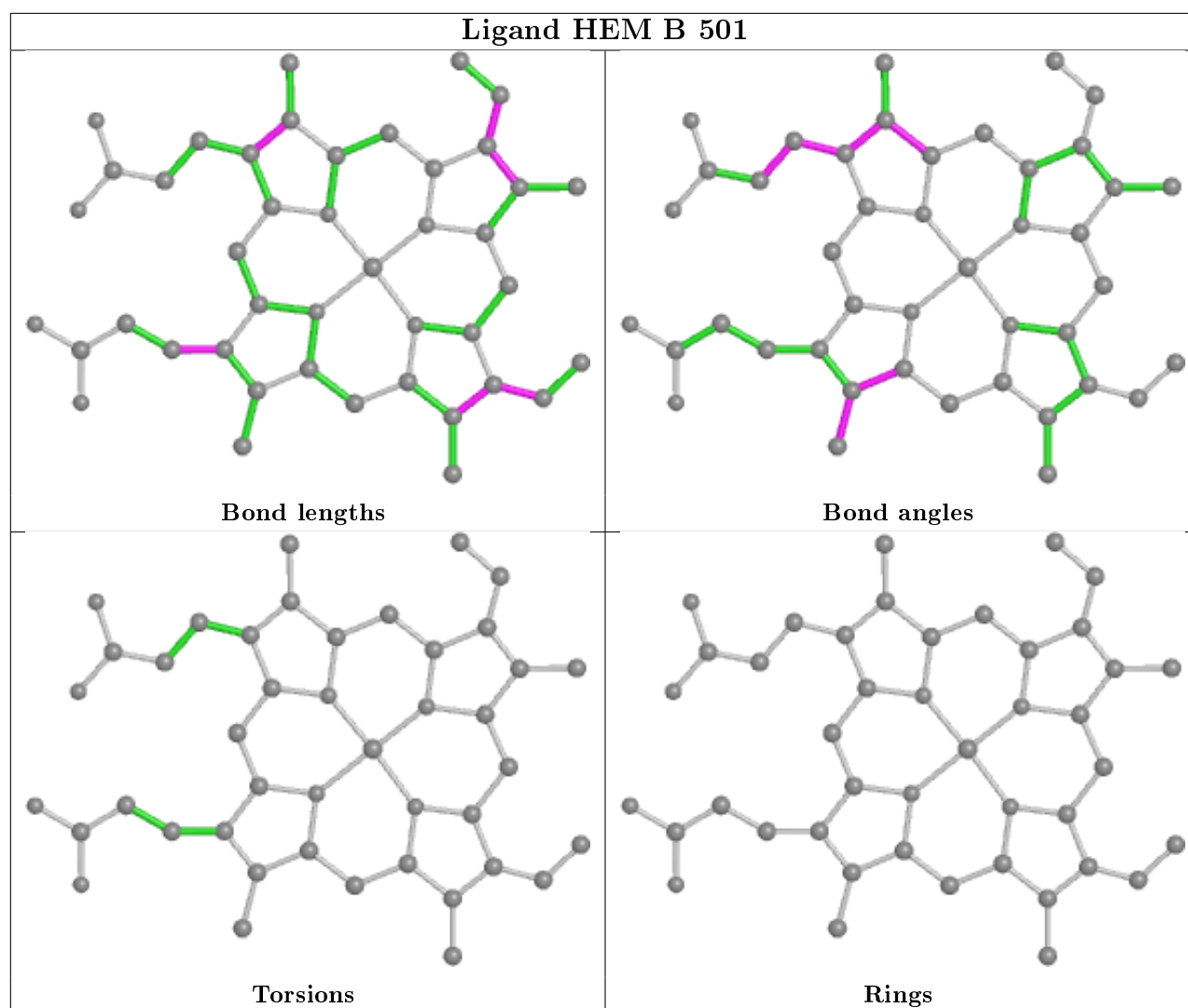
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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, 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	393/410 (95%)	-0.02	1 (0%) 94 96	25, 37, 50, 68	0
1	B	393/410 (95%)	-0.07	0 100 100	27, 38, 52, 70	0
1	C	393/410 (95%)	-0.00	11 (2%) 53 60	34, 46, 63, 82	0
1	D	393/410 (95%)	0.24	18 (4%) 32 39	34, 51, 69, 86	0
All	All	1572/1640 (95%)	0.04	30 (1%) 66 73	25, 43, 63, 86	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	382	ILE	5.1
1	D	169	GLU	4.2
1	D	91	TRP	3.7
1	D	158	SER	3.5
1	C	91	TRP	3.5
1	A	409	ALA	3.5
1	D	196	ILE	3.2
1	D	198	ARG	3.1
1	D	197	GLU	2.9
1	D	93	PRO	2.9
1	D	210	CYS	2.8
1	D	200	ALA	2.7
1	C	199	SER	2.7
1	C	197	GLU	2.6
1	C	280	LEU	2.6
1	D	206	VAL	2.5
1	C	196	ILE	2.5
1	D	170	GLY	2.5
1	D	199	SER	2.5
1	D	165	GLY	2.5
1	C	200	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	246	LEU	2.3
1	C	372	LEU	2.2
1	C	93	PRO	2.2
1	D	208	GLU	2.2
1	C	89	LYS	2.1
1	C	203	GLN	2.1
1	D	203	GLN	2.1
1	C	207	ASN	2.0
1	D	409	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
5	GOL	D	505	6/6	0.48	0.30	53,56,67,68	0
4	CL	D	503	1/1	0.64	0.19	75,75,75,75	0
6	SO4	B	511	5/5	0.82	0.35	53,65,86,87	0
3	8ZX	B	502	11/11	0.82	0.22	37,44,54,58	0
3	8ZX	B	504	11/11	0.83	0.18	49,53,59,64	0
3	8ZX	B	503	11/11	0.83	0.23	41,50,55,57	0
3	8ZX	A	504	11/11	0.83	0.21	45,51,59,62	0
6	SO4	B	510	5/5	0.84	0.22	64,70,86,92	0
5	GOL	C	505	6/6	0.84	0.32	55,62,65,75	0
3	8ZX	A	502	11/11	0.86	0.23	27,37,46,50	0
5	GOL	A	506	6/6	0.87	0.17	39,43,48,48	0
5	GOL	B	506	6/6	0.87	0.21	41,44,46,47	0
5	GOL	B	507	6/6	0.88	0.26	46,49,58,61	0
3	8ZX	C	502	11/11	0.88	0.34	46,51,56,59	0

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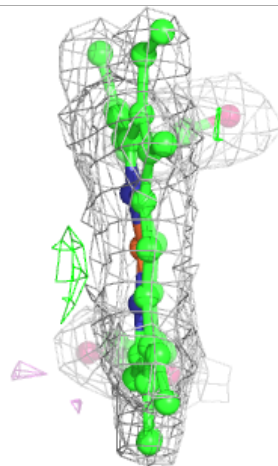
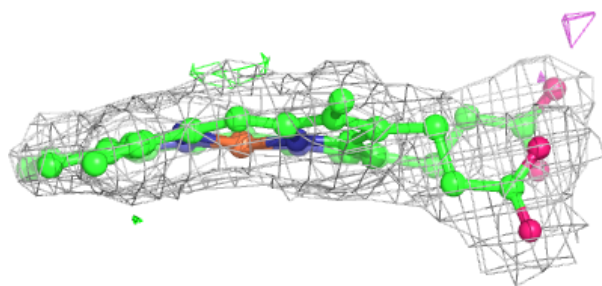
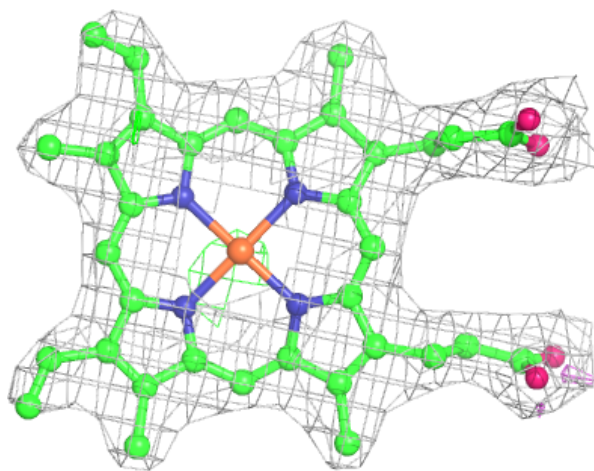
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	GOL	D	504	6/6	0.90	0.11	45,48,55,59	0
4	CL	C	503	1/1	0.91	0.16	71,71,71,71	0
3	8ZX	D	502	11/11	0.91	0.26	46,47,53,56	0
6	SO4	A	511	5/5	0.92	0.30	57,62,75,80	0
3	8ZX	A	503	11/11	0.92	0.15	43,47,54,54	0
6	SO4	C	508	5/5	0.92	0.26	65,68,89,93	0
6	SO4	B	508	5/5	0.93	0.12	53,58,65,66	0
6	SO4	A	510	5/5	0.93	0.13	58,62,74,87	0
4	CL	B	505	1/1	0.93	0.09	63,63,63,63	0
6	SO4	A	508	5/5	0.94	0.13	56,60,62,66	0
6	SO4	A	512	5/5	0.95	0.34	55,58,68,69	0
5	GOL	C	504	6/6	0.95	0.17	39,45,47,52	0
6	SO4	C	507	5/5	0.96	0.19	65,66,81,82	0
6	SO4	A	507	5/5	0.97	0.09	45,48,53,57	0
4	CL	A	505	1/1	0.97	0.15	45,45,45,45	0
2	HEM	C	501	43/43	0.98	0.14	30,38,41,43	0
2	HEM	D	501	43/43	0.98	0.11	31,41,45,47	0
6	SO4	A	509	5/5	0.98	0.10	35,45,57,58	0
2	HEM	B	501	43/43	0.98	0.16	23,31,35,36	0
6	SO4	C	506	5/5	0.99	0.13	41,49,55,64	0
6	SO4	B	509	5/5	0.99	0.14	38,46,53,55	0
2	HEM	A	501	43/43	0.99	0.17	23,29,32,36	0
6	SO4	D	506	5/5	0.99	0.12	53,53,65,68	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 C 501:**

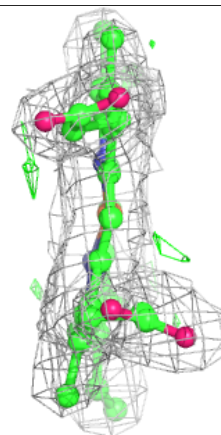
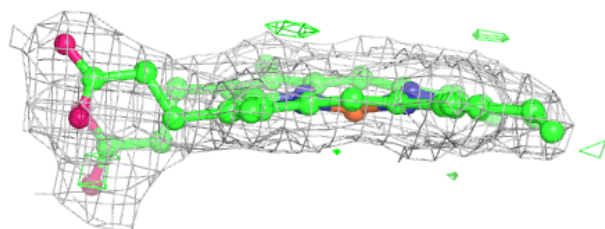
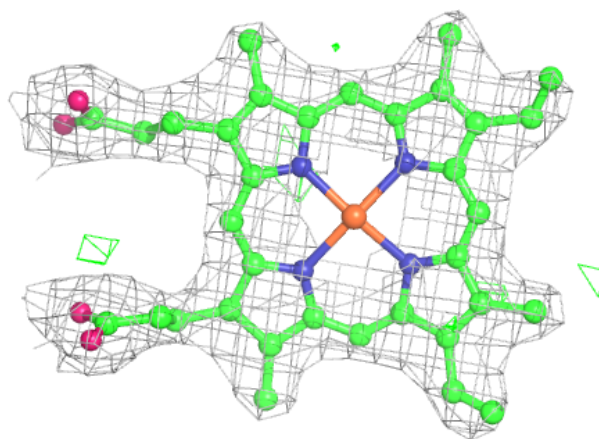
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





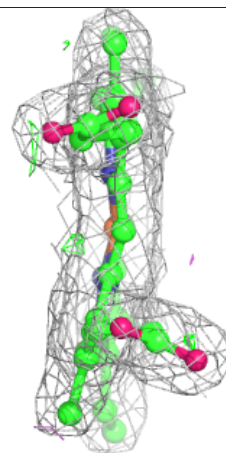
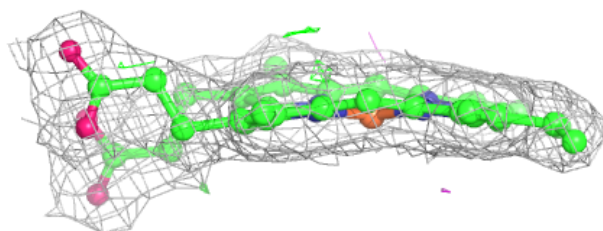
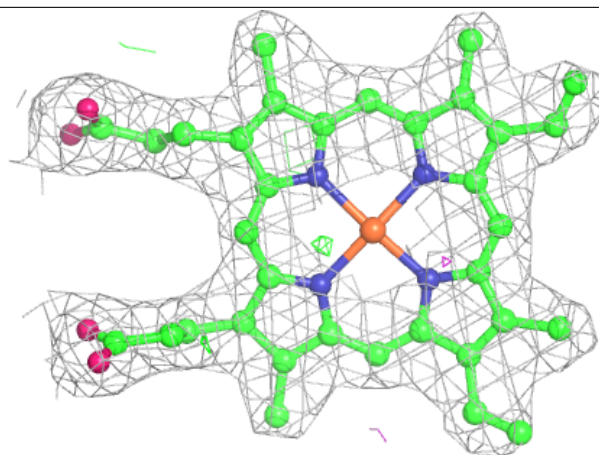
**Electron density around HEM D 501:**

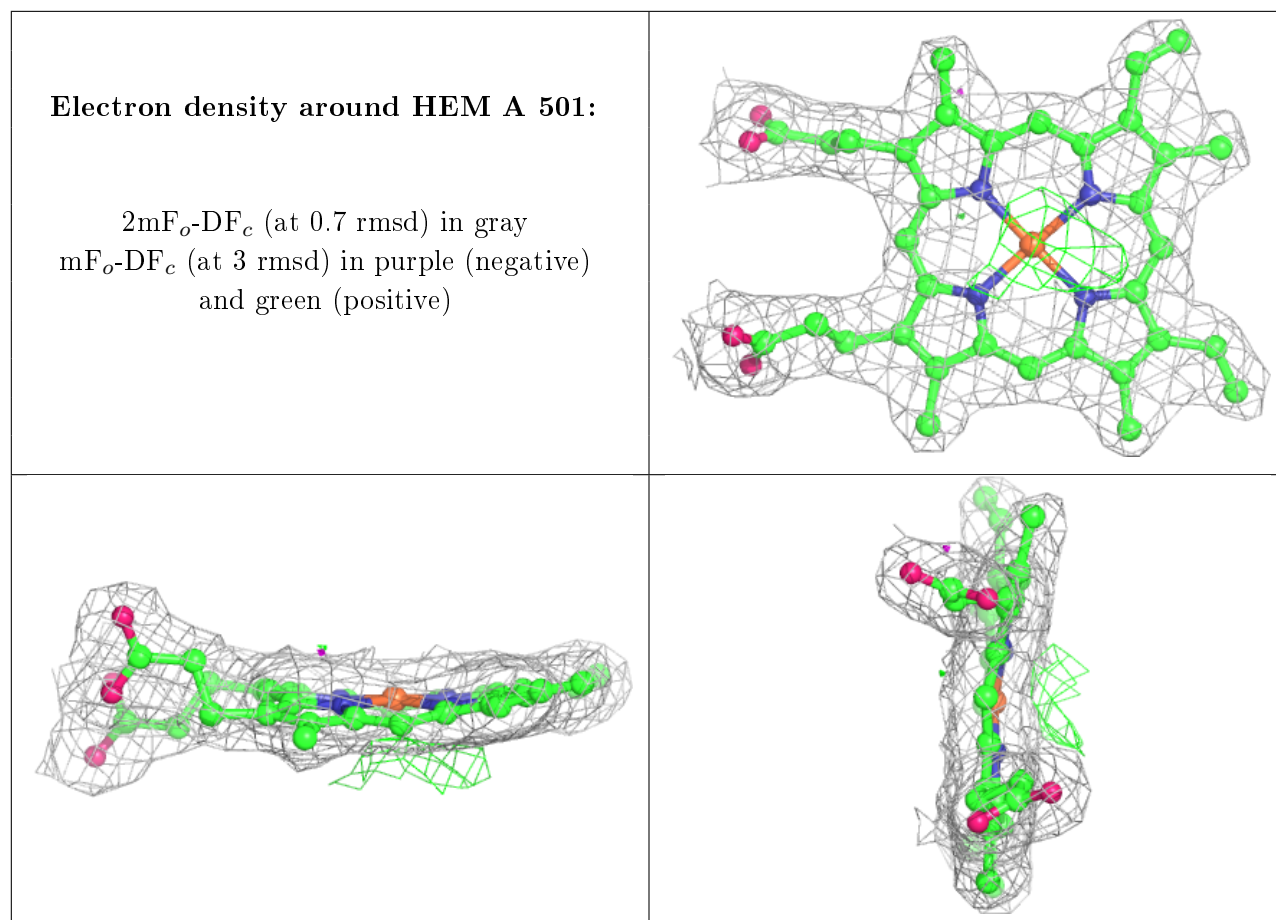
$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**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.