



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 22, 2020 – 09:00 AM BST

PDB ID : 4EGM  
Title : The X-ray crystal structure of CYP199A4 in complex with 4-ethylbenzoic acid  
Authors : Zhou, W.; Bell, S.G.; Yang, W.; Zhou, R.M.; Tan, A.B.H.; Wong, L.-L.  
Deposited on : 2012-03-31  
Resolution : 2.91 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](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 : 2.13.1  
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) : 2.13.1

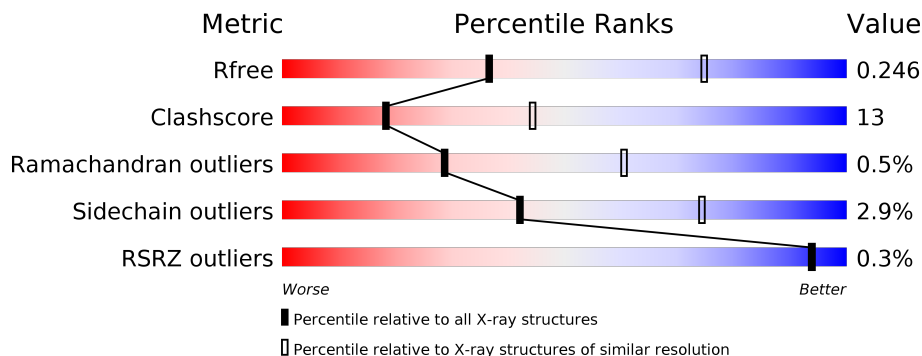
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*





The reported resolution of this entry is 2.91 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	2307 (2.94-2.90)
Clashscore	141614	2531 (2.94-2.90)
Ramachandran outliers	138981	2462 (2.94-2.90)
Sidechain outliers	138945	2464 (2.94-2.90)
RSRZ outliers	127900	2248 (2.94-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	 75% 19% . .
1	B	410	 75% 20% . .
1	C	410	 76% 19% . .
1	D	410	 75% 19% . .

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:

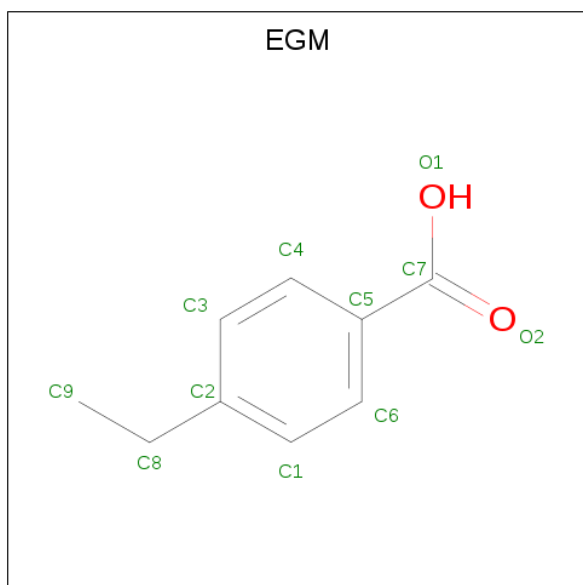
Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	SO4	D	505	-	-	X	-



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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-ethylbenzoic acid (three-letter code: EGM) (formula:  $C_9H_{10}O_2$ ).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	C O	0	0
			11	9 2		
3	B	1	Total	C O	0	0
			11	9 2		
3	C	1	Total	C O	0	0
			11	9 2		
3	D	1	Total	C O	0	0
			11	9 2		

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

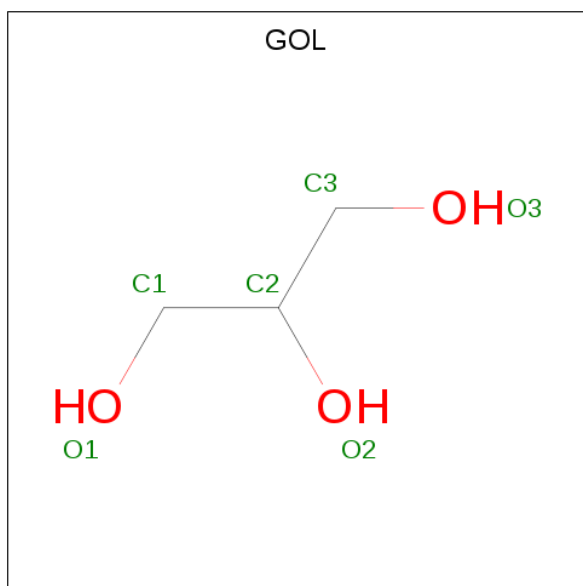
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Cl	0	0
			1	1		
4	A	1	Total	Cl	0	0
			1	1		
4	D	1	Total	Cl	0	0
			1	1		

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

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



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	C	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<sub>4</sub>S).



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	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	C	1	Total	O	S	0	0
			5	4	1		
6	D	1	Total	O	S	0	0
			5	4	1		
6	D	1	Total	O	S	0	0
			5	4	1		
6	D	1	Total	O	S	0	0
			5	4	1		

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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	61	Total	O	0	0
			61	61		
7	B	65	Total	O	0	0
			65	65		
7	C	58	Total	O	0	0
			58	58		
7	D	46	Total	O	0	0
			46	46		

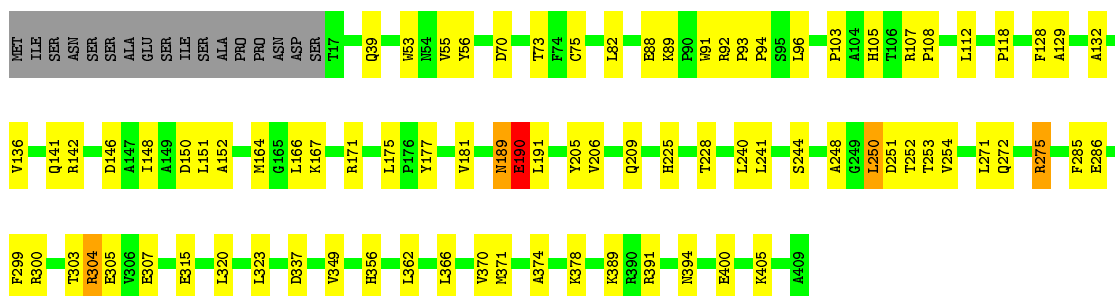


### 3 Residue-property plots [i](#)


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.

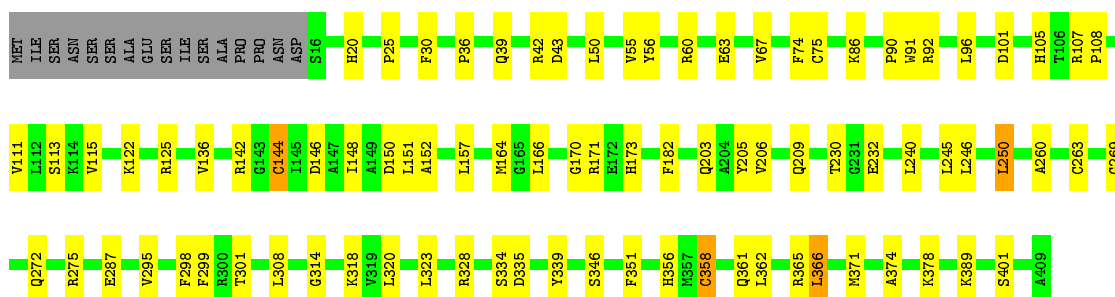
- Molecule 1: Cytochrome P450

Chain A: 




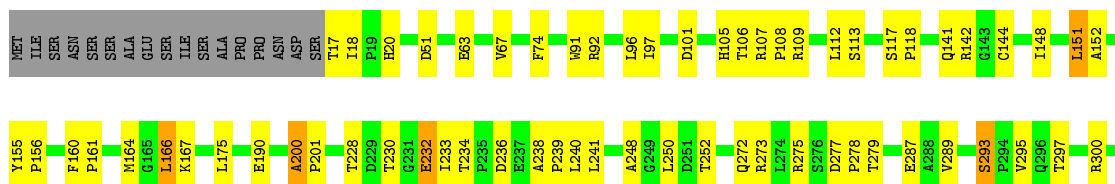
- Molecule 1: Cytochrome P450

Chain B: 



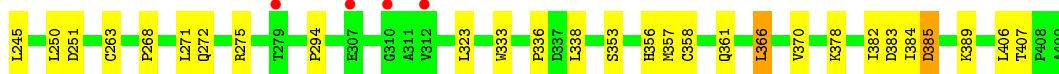
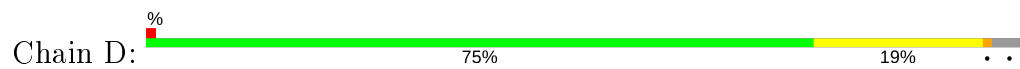
- Molecule 1: Cytochrome P450

Chain C: 





● Molecule 1: Cytochrome P450



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	106.86Å 143.28Å 172.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.57 – 2.91 41.57 – 2.91	Depositor EDS
% Data completeness (in resolution range)	99.3 (41.57-2.91) 98.9 (41.57-2.91)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.28 (at 2.90Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.182 , 0.249 0.185 , 0.246	Depositor DCC
$R_{free}$ test set	2970 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	41.8	Xtrriage
Anisotropy	0.447	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 28.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	12651	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	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 51.12 % 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 5.8696e-05. 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, HEM, SO4, EGM, 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	0.84	2/3093 (0.1%)	0.85	2/4209 (0.0%)
1	B	0.80	1/3108 (0.0%)	0.83	1/4229 (0.0%)
1	C	0.78	1/3102 (0.0%)	0.82	1/4221 (0.0%)
1	D	0.82	4/3093 (0.1%)	0.84	1/4209 (0.0%)
All	All	0.81	8/12396 (0.1%)	0.84	5/16868 (0.0%)

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	D	0	1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	190	GLU	CB-CG	7.25	1.66	1.52
1	D	169	GLU	CB-CG	6.49	1.64	1.52
1	B	144	CYS	CB-SG	6.33	1.93	1.82
1	D	169	GLU	CG-CD	6.27	1.61	1.51
1	A	190	GLU	CG-CD	6.14	1.61	1.51

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	250	LEU	CA-CB-CG	5.67	128.34	115.30
1	B	308	LEU	CA-CB-CG	5.50	127.95	115.30
1	D	338	LEU	CA-CB-CG	5.15	127.15	115.30
1	A	304	ARG	NE-CZ-NH2	5.14	122.87	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	166	LEU	CA-CB-CG	5.04	126.89	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	105	HIS	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	3021	0	2993	93	0
1	B	3033	0	3006	81	0
1	C	3027	0	2999	63	0
1	D	3021	0	2993	87	0
2	A	43	0	30	1	0
2	B	43	0	30	7	0
2	C	43	0	30	5	0
2	D	43	0	30	3	0
3	A	11	0	9	1	0
3	B	11	0	9	1	0
3	C	11	0	9	1	0
3	D	11	0	9	0	0
4	A	1	0	0	0	0
4	B	1	0	0	1	0
4	C	1	0	0	0	0
4	D	1	0	0	1	0
5	A	6	0	8	0	0
5	B	6	0	8	2	0
5	C	6	0	8	3	0
5	D	6	0	8	1	0
6	A	20	0	0	0	0
6	B	15	0	0	1	0
6	C	20	0	0	1	0
6	D	20	0	0	2	0
7	A	61	0	0	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	65	0	0	3	0
7	C	58	0	0	5	0
7	D	46	0	0	4	0
All	All	12651	0	12179	326	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 13.

The worst 5 of 326 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:A:129:ALA:HA	1:A:370:VAL:CG2	1.69	1.21
1:A:175:LEU:HD21	1:A:250:LEU:HD11	1.26	1.16
1:D:223:CYS:HB2	7:D:638:HOH:O	1.45	1.15
1:A:96:LEU:HD23	1:A:240:LEU:HG	1.34	1.03
1:A:175:LEU:CD2	1:A:250:LEU:HD11	1.90	1.00

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%)	371 (95%)	18 (5%)	2 (0%)	29	60
1	B	393/410 (96%)	374 (95%)	18 (5%)	1 (0%)	41	70
1	C	392/410 (96%)	371 (95%)	19 (5%)	2 (0%)	29	60
1	D	391/410 (95%)	368 (94%)	20 (5%)	3 (1%)	19	49
All	All	1567/1640 (96%)	1484 (95%)	75 (5%)	8 (0%)	29	60

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	167	LYS
1	A	189	ASN
1	D	385	ASP
1	D	148	ILE
1	A	171	ARG

### 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%)	312 (98%)	7 (2%)	52 80
1	B	321/334 (96%)	312 (97%)	9 (3%)	43 75
1	C	320/334 (96%)	309 (97%)	11 (3%)	37 69
1	D	319/334 (96%)	309 (97%)	10 (3%)	40 72
All	All	1279/1336 (96%)	1242 (97%)	37 (3%)	42 74

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	106	THR
1	C	232	GLU
1	D	366	LEU
1	C	142	ARG
1	C	151	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	272	GLN
1	C	168	GLN
1	D	272	GLN
1	B	283	ASN
1	C	20	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

### 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 31 ligands modelled in this entry, 4 are monoatomic - leaving 27 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	EGM	D	502	-	9,11,11	2.17	1 (11%)	11,14,14	1.12	0
2	HEM	B	501	1	27,50,50	2.08	8 (29%)	17,82,82	1.71	3 (17%)
2	HEM	A	501	1	27,50,50	2.10	7 (25%)	17,82,82	1.82	5 (29%)
6	SO4	A	507	-	4,4,4	0.18	0	6,6,6	0.48	0
6	SO4	B	506	-	4,4,4	0.17	0	6,6,6	0.48	0
6	SO4	D	508	-	4,4,4	0.24	0	6,6,6	0.31	0
3	EGM	C	502	-	9,11,11	1.15	1 (11%)	11,14,14	1.03	0
5	GOL	C	504	-	5,5,5	0.42	0	5,5,5	0.61	0
3	EGM	B	502	-	9,11,11	1.15	1 (11%)	11,14,14	0.84	0
6	SO4	A	508	-	4,4,4	0.25	0	6,6,6	0.58	0
6	SO4	B	507	-	4,4,4	0.19	0	6,6,6	0.34	0
6	SO4	A	506	-	4,4,4	0.08	0	6,6,6	0.46	0
6	SO4	B	505	-	4,4,4	0.20	0	6,6,6	0.69	0
6	SO4	C	505	-	4,4,4	0.16	0	6,6,6	0.57	0
2	HEM	D	501	1	27,50,50	2.08	6 (22%)	17,82,82	1.83	4 (23%)
6	SO4	C	506	-	4,4,4	0.17	0	6,6,6	0.26	0



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	SO4	C	508	-	4,4,4	0.21	0	6,6,6	0.58	0
6	SO4	D	507	-	4,4,4	0.19	0	6,6,6	0.32	0
6	SO4	D	506	-	4,4,4	0.14	0	6,6,6	0.30	0
2	HEM	C	501	1	27,50,50	2.27	5 (18%)	17,82,82	1.96	7 (41%)
6	SO4	D	505	-	4,4,4	0.21	0	6,6,6	0.31	0
3	EGM	A	502	-	9,11,11	2.62	1 (11%)	11,14,14	1.07	1 (9%)
5	GOL	A	504	-	5,5,5	0.58	0	5,5,5	0.50	0
6	SO4	C	507	-	4,4,4	0.28	0	6,6,6	0.46	0
5	GOL	B	504	-	5,5,5	0.42	0	5,5,5	0.77	0
6	SO4	A	505	-	4,4,4	0.35	0	6,6,6	0.89	0
5	GOL	D	504	-	5,5,5	0.40	0	5,5,5	0.52	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	EGM	A	502	-	-	0/2/6/6	0/1/1/1
3	EGM	D	502	-	-	0/2/6/6	0/1/1/1
5	GOL	C	504	-	-	2/4/4/4	-
2	HEM	D	501	1	-	0/6/54/54	-
2	HEM	B	501	1	-	0/6/54/54	-
3	EGM	B	502	-	-	0/2/6/6	0/1/1/1
2	HEM	A	501	1	-	0/6/54/54	-
5	GOL	A	504	-	-	2/4/4/4	-
5	GOL	B	504	-	-	2/4/4/4	-
3	EGM	C	502	-	-	0/2/6/6	0/1/1/1
2	HEM	C	501	1	-	0/6/54/54	-
5	GOL	D	504	-	-	0/4/4/4	-

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	502	EGM	C5-C7	7.71	1.54	1.47
3	D	502	EGM	C5-C7	6.07	1.53	1.47
2	C	501	HEM	C3C-C2C	-5.88	1.32	1.40
2	A	501	HEM	C3D-C2D	5.50	1.54	1.37
2	C	501	HEM	C3B-C2B	-5.32	1.33	1.40

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	501	HEM	CBD-CAD-C3D	-3.97	105.16	112.48
2	A	501	HEM	CBD-CAD-C3D	-3.86	105.36	112.48
2	B	501	HEM	CBD-CAD-C3D	-3.66	105.74	112.48
2	C	501	HEM	CAA-CBA-CGA	-3.62	106.59	112.67
2	C	501	HEM	CBA-CAA-C2A	3.46	118.86	112.49

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	504	GOL	O1-C1-C2-C3
5	B	504	GOL	O1-C1-C2-C3
5	A	504	GOL	C1-C2-C3-O3
5	B	504	GOL	O1-C1-C2-O2
5	A	504	GOL	O2-C2-C3-O3

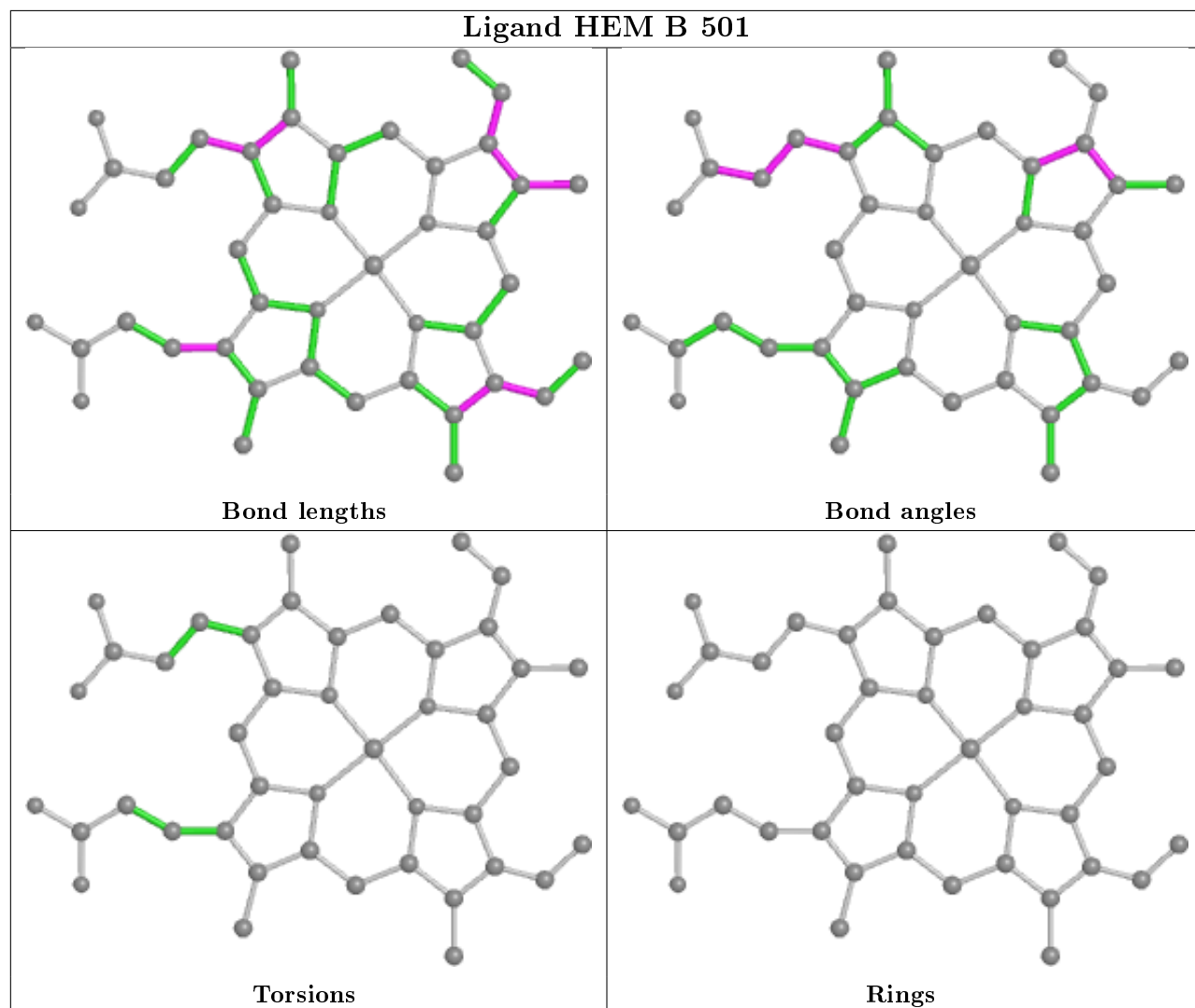
There are no ring outliers.

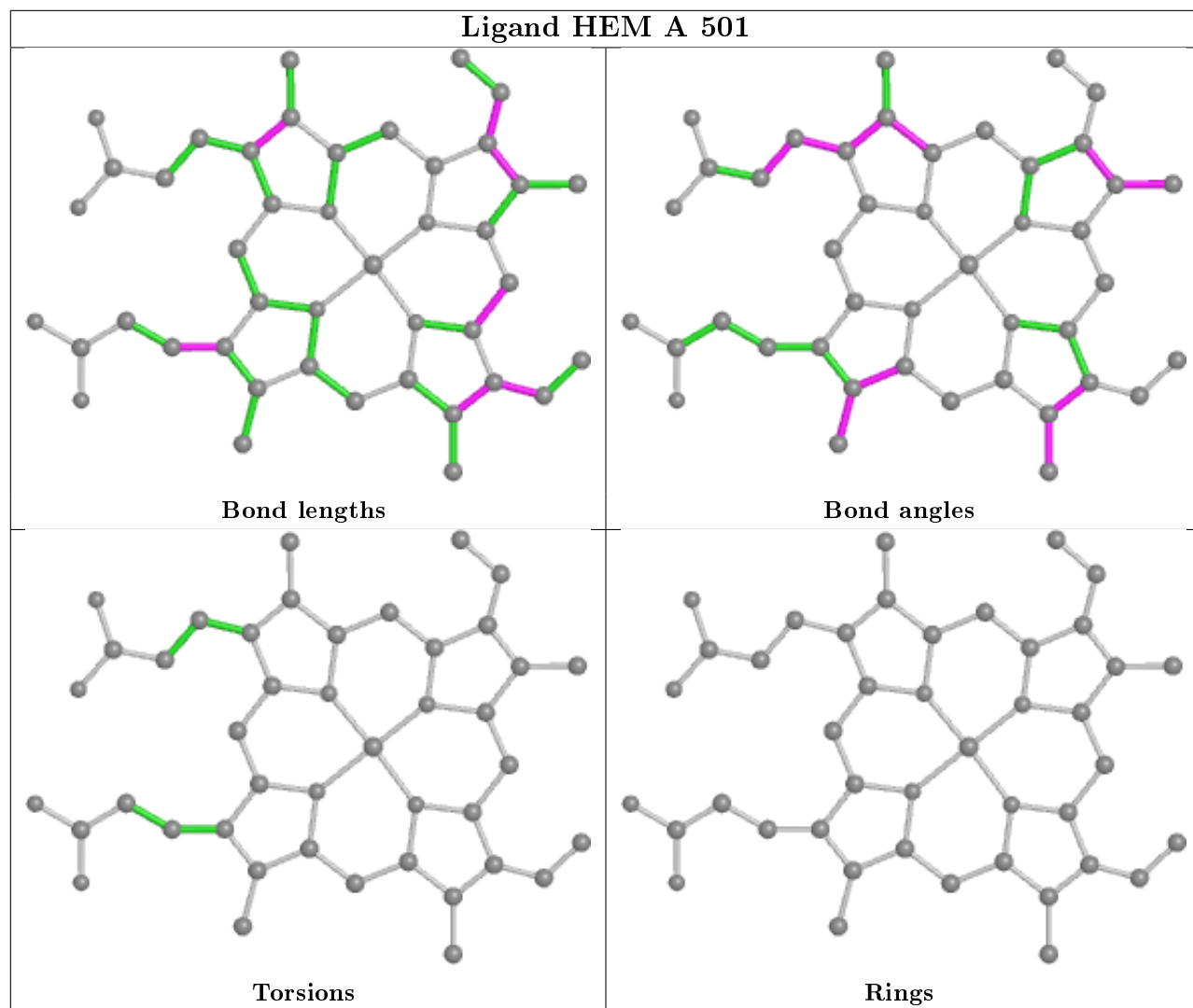
13 monomers are involved in 26 short contacts:

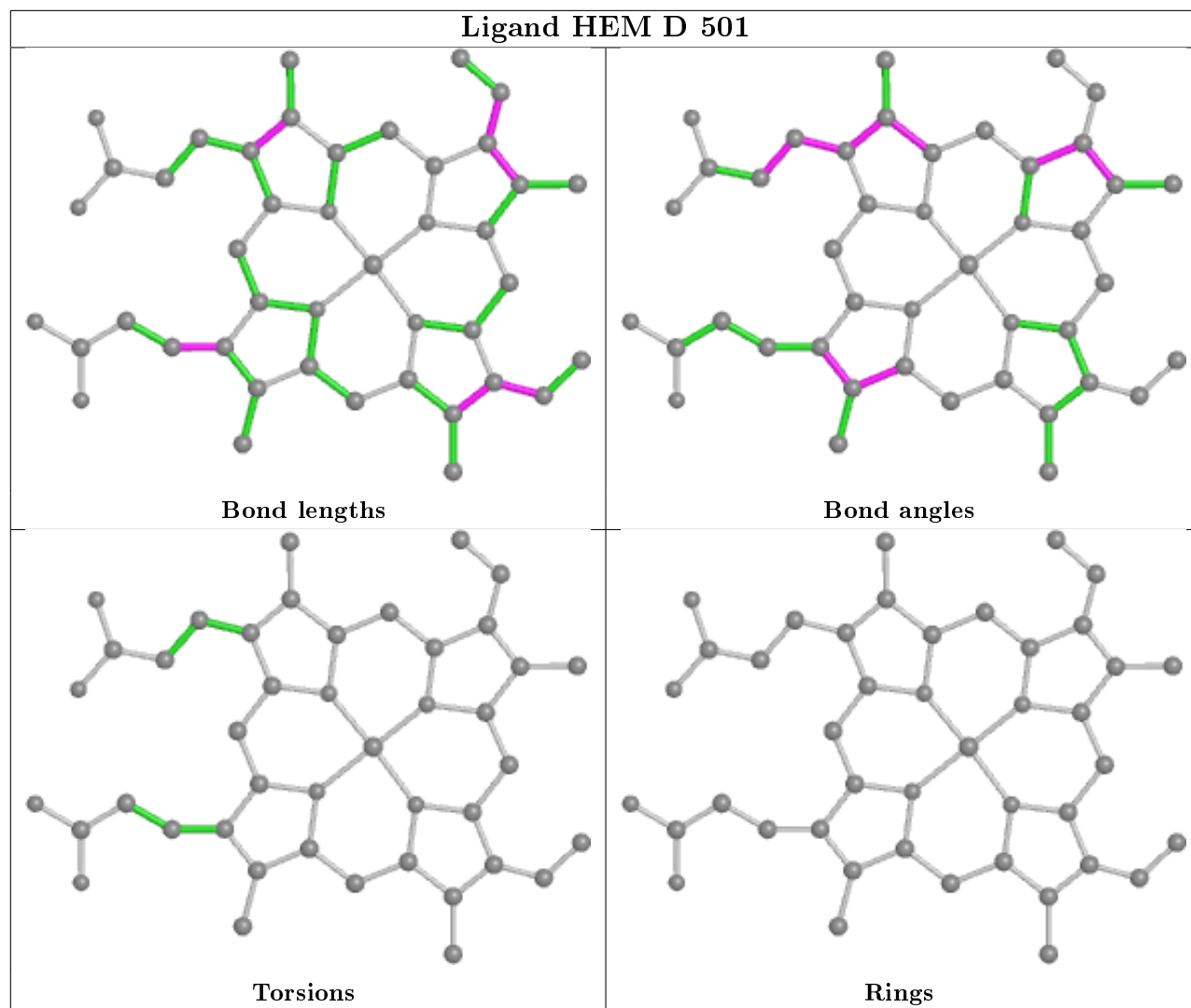
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	HEM	7	0
2	A	501	HEM	1	0
6	B	506	SO4	1	0
3	C	502	EGM	1	0
5	C	504	GOL	3	0
3	B	502	EGM	1	0
6	C	505	SO4	1	0
2	D	501	HEM	3	0
2	C	501	HEM	5	0
6	D	505	SO4	2	0
3	A	502	EGM	1	0
5	B	504	GOL	2	0
5	D	504	GOL	1	0

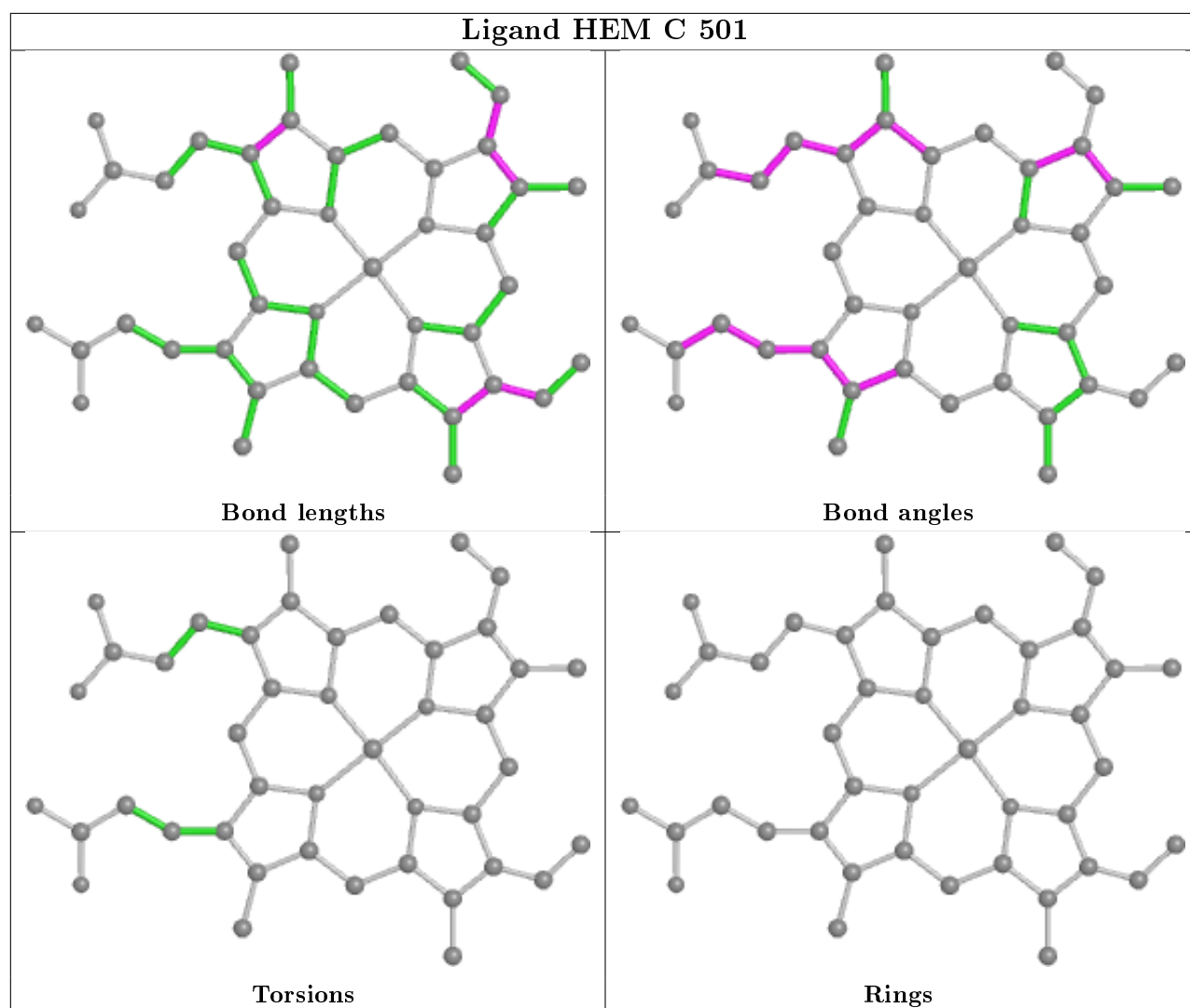
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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%)	-0.59	0	100   100	20, 32, 43, 49	0
1	B	394/410 (96%)	-0.56	0	100   100	22, 33, 45, 55	0
1	C	393/410 (95%)	-0.40	0	100   100	25, 37, 48, 56	0
1	D	393/410 (95%)	-0.26	5 (1%)	77   77	25, 41, 56, 70	0
All	All	1573/1640 (95%)	-0.45	5 (0%)	94   94	20, 35, 50, 70	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	279	THR	2.5
1	D	307	GLU	2.4
1	D	213	PRO	2.3
1	D	310	GLY	2.1
1	D	312	VAL	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 monosaccharides in this entry.

### 6.4 Ligands [i](#)

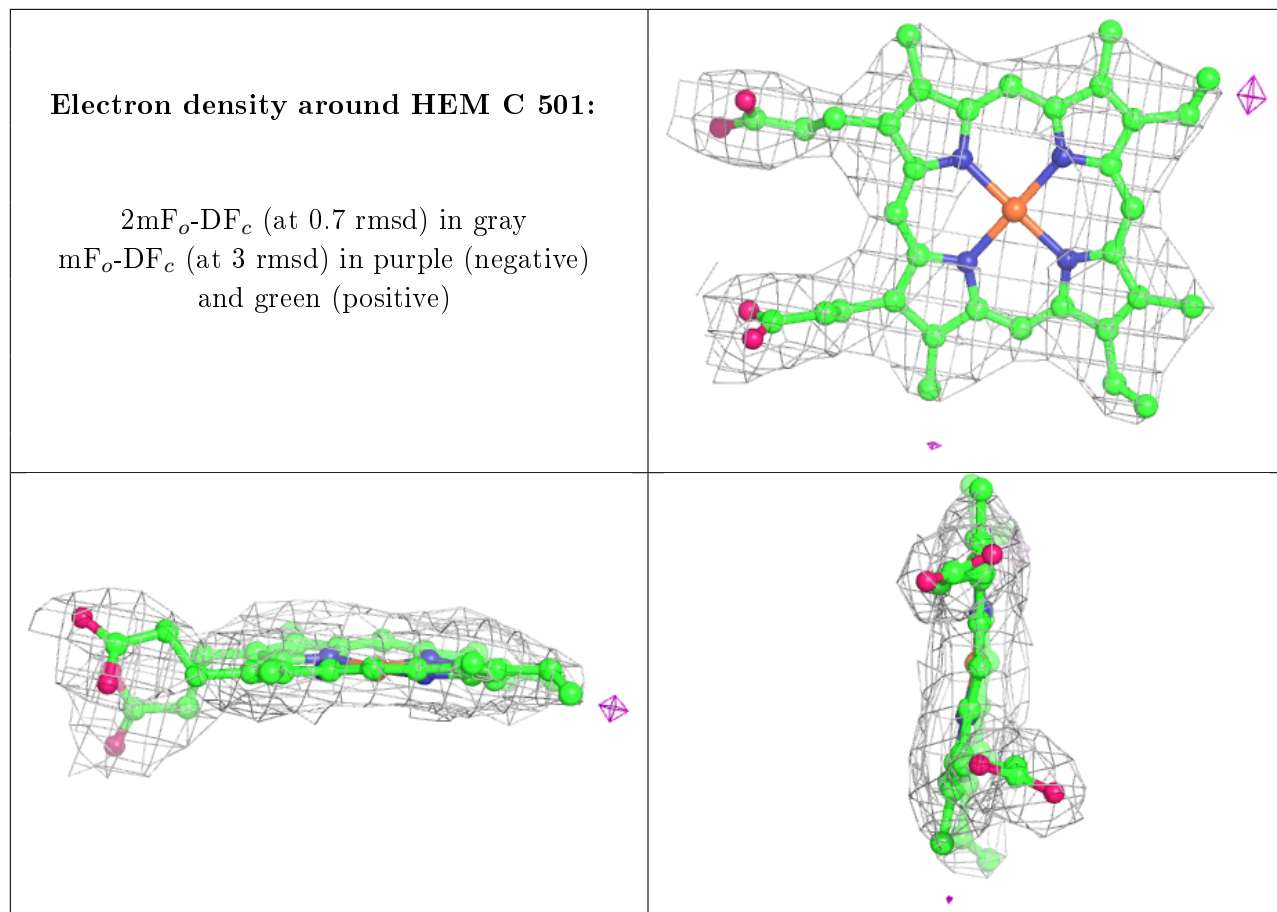
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

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
6	SO4	C	507	5/5	0.79	0.33	86,87,87,88	0
6	SO4	A	508	5/5	0.85	0.35	97,98,99,99	0
6	SO4	D	507	5/5	0.88	0.43	107,108,109,109	0
6	SO4	A	507	5/5	0.89	0.27	98,99,99,100	0
6	SO4	D	506	5/5	0.90	0.40	87,88,89,89	0
6	SO4	C	506	5/5	0.91	0.37	87,87,88,88	0
6	SO4	B	506	5/5	0.93	0.47	101,101,102,103	0
4	CL	C	503	1/1	0.93	0.12	53,53,53,53	0
6	SO4	A	506	5/5	0.93	0.42	91,91,91,91	0
5	GOL	D	504	6/6	0.94	0.16	45,48,51,52	0
6	SO4	B	507	5/5	0.95	0.13	66,66,67,67	0
5	GOL	B	504	6/6	0.95	0.20	40,44,46,46	0
4	CL	B	503	1/1	0.95	0.10	38,38,38,38	0
5	GOL	C	504	6/6	0.95	0.14	33,36,38,39	0
5	GOL	A	504	6/6	0.96	0.21	39,40,43,43	0
6	SO4	B	505	5/5	0.97	0.12	56,58,59,59	0
6	SO4	D	505	5/5	0.97	0.14	61,61,63,63	0
3	EGM	A	502	11/11	0.97	0.13	24,26,31,34	0
4	CL	A	503	1/1	0.97	0.07	33,33,33,33	0
4	CL	D	503	1/1	0.97	0.25	46,46,46,46	0
3	EGM	C	502	11/11	0.97	0.14	23,24,28,31	0
6	SO4	C	505	5/5	0.98	0.10	32,33,35,36	0
2	HEM	C	501	43/43	0.98	0.17	22,26,31,37	0
2	HEM	D	501	43/43	0.98	0.19	26,29,33,34	0
3	EGM	D	502	11/11	0.98	0.13	19,20,24,25	0
6	SO4	C	508	5/5	0.98	0.11	43,45,48,50	0
6	SO4	D	508	5/5	0.98	0.11	54,54,55,55	0
6	SO4	A	505	5/5	0.98	0.09	33,35,36,36	0
3	EGM	B	502	11/11	0.98	0.12	18,20,24,25	0
2	HEM	B	501	43/43	0.99	0.13	16,22,27,29	0
2	HEM	A	501	43/43	0.99	0.11	20,27,30,32	0

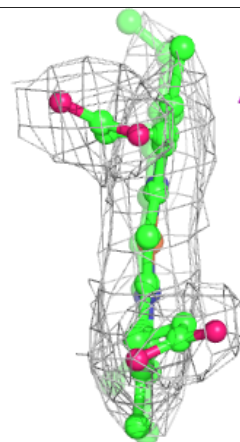
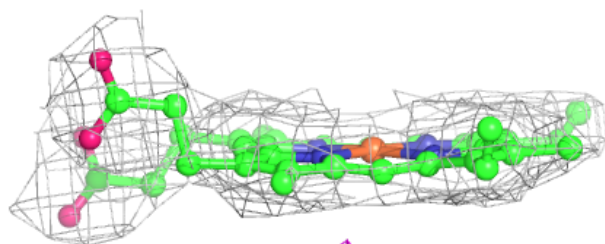
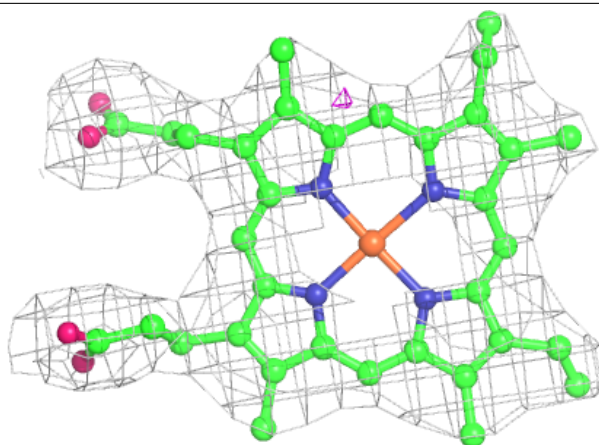
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



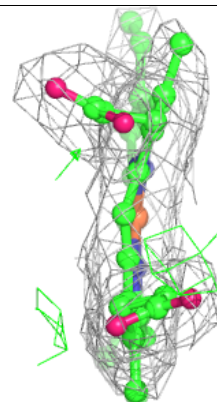
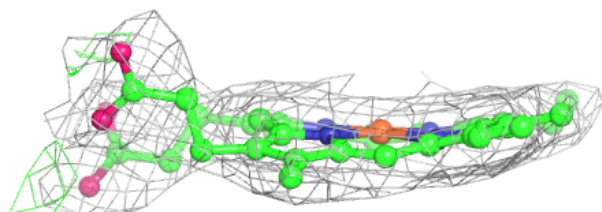
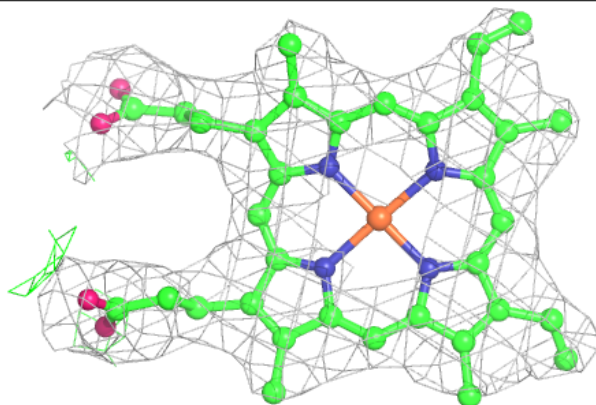


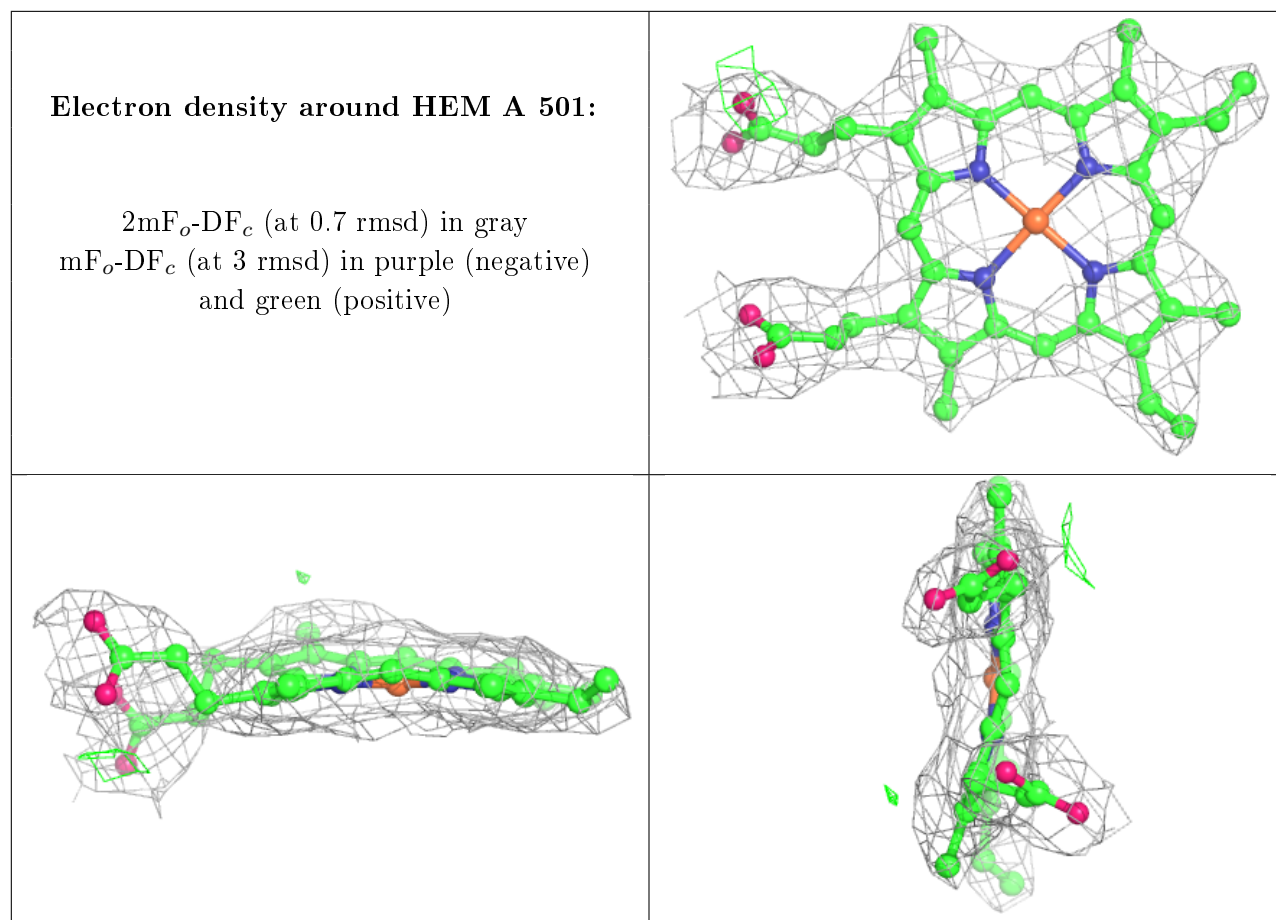
**Electron density around HEM D 501:**

$2mF_o-DF_c$  (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 [i](#)

There are no such residues in this entry.