



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 25, 2023 – 12:09 pm GMT

PDB ID : 7YXF  
Title : Crystal structure of CYP125 from Mycobacterium tuberculosis in complex with an inhibitor  
Authors : Snee, M.; Katariya, M.; Levy, C.; Leys, D.  
Deposited on : 2022-02-16  
Resolution : 1.85 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.

The types of validation reports are described at

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

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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 : 1.8.4, CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : 2.32.1  
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) : 2.32.1

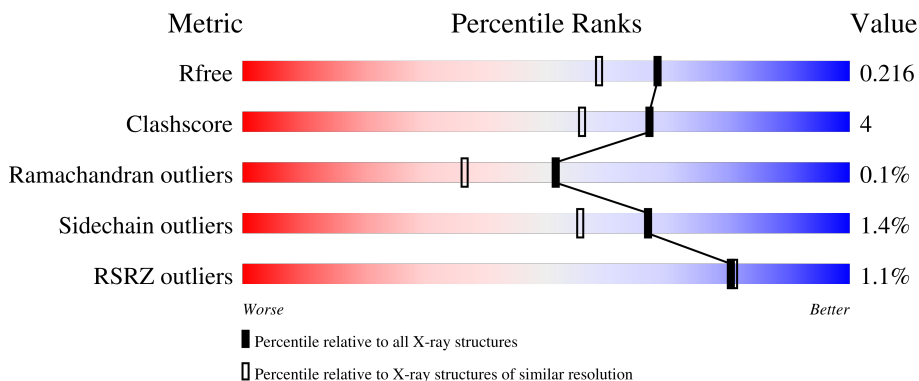
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.85 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	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)
RSRZ outliers	127900	2436 (1.86-1.86)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	418	 88% 10% ..
1	B	418	 3% 91% 6% .
1	C	418	 89% 8% .

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 21092 atoms, of which 9877 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

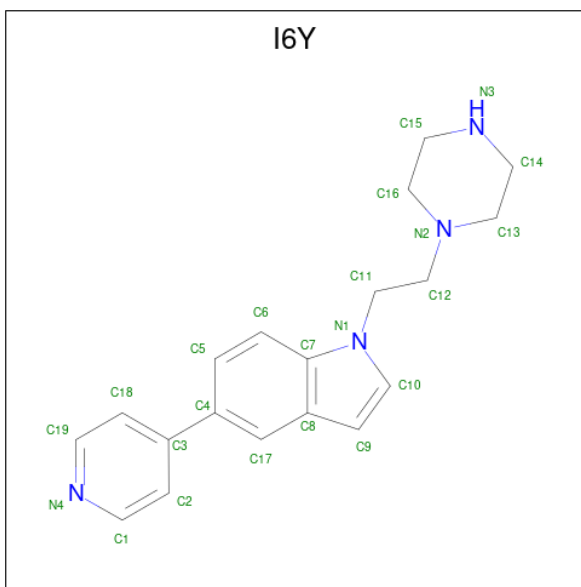
- Molecule 1 is a protein called Steroid C26-monooxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	411	6822	2185	3358	608	654	17	0	52	0
1	B	407	6502	2092	3186	584	622	18	0	30	0
1	C	409	6481	2084	3177	579	624	17	0	21	0

There are 6 discrepancies between the modelled and reference sequences:

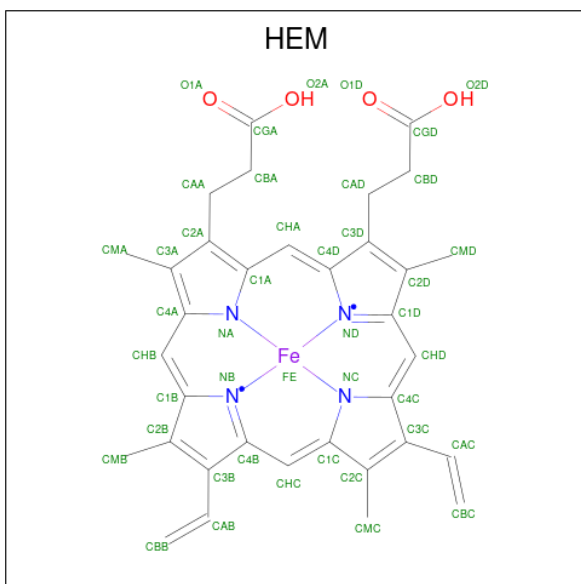
Chain	Residue	Modelled	Actual	Comment	Reference
A	16	ASN	-	expression tag	UNP P9WPP1
A	17	GLY	-	expression tag	UNP P9WPP1
B	16	ASN	-	expression tag	UNP P9WPP1
B	17	GLY	-	expression tag	UNP P9WPP1
C	16	ASN	-	expression tag	UNP P9WPP1
C	17	GLY	-	expression tag	UNP P9WPP1

- Molecule 2 is 1-(2-piperazin-1-ylethyl)-5-pyridin-4-yl-indole (three-letter code: I6Y) (formula: C<sub>19</sub>H<sub>22</sub>N<sub>4</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	N		
2	A	1	Total	C	H	N	0	0
			45	19	22	4		
2	B	1	Total	C	H	N	0	0
			45	19	22	4		
2	C	1	Total	C	H	N	0	0
			45	19	22	4		

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
3	A	1	Total	C	Fe	H	N	O	0	0
			73	34	1	30	4	4		
3	B	1	Total	C	Fe	H	N	O	0	0
			73	34	1	30	4	4		
3	C	1	Total	C	Fe	H	N	O	0	0
			73	34	1	30	4	4		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	413	Total	O	0	0
			413	413		

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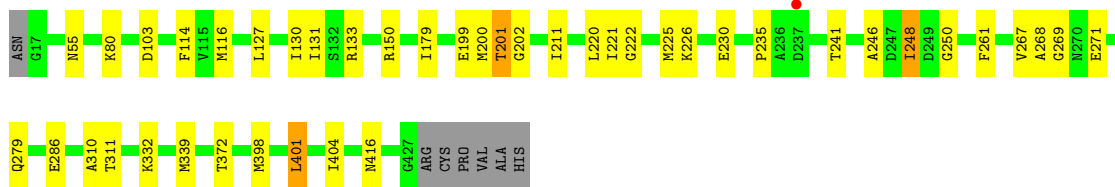
<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
5	B	284	Total 284	O 284	0	0
5	C	206	Total 206	O 206	0	0

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


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

- Molecule 1: Steroid C26-monooxygenase

Chain A:  88% 10% ..




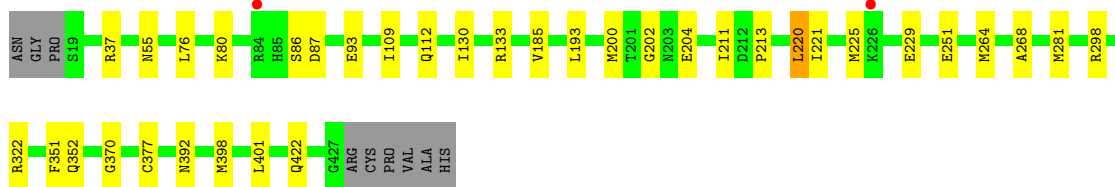
- Molecule 1: Steroid C26-monooxygenase

Chain B:  91% 6% 3%



- Molecule 1: Steroid C26-monooxygenase

Chain C:  89% 8%



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	136.44Å 69.38Å 144.35Å 90.00° 94.29° 90.00°	Depositor
Resolution (Å)	143.95 – 1.85 143.95 – 1.85	Depositor EDS
% Data completeness (in resolution range)	99.6 (143.95-1.85) 92.0 (143.95-1.85)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.99 (at 1.84Å)	Xtrriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, $R_{free}$	0.176 , 0.221 0.171 , 0.216	Depositor DCC
$R_{free}$ test set	5824 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	26.8	Xtrriage
Anisotropy	0.164	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 47.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	21092	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.07% 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, I6Y, SO4

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	0.67	0/3722	0.77	1/5043 (0.0%)
1	B	0.52	0/3518	0.66	0/4768
1	C	0.48	0/3457	0.62	0/4688
All	All	0.56	0/10697	0.69	1/14499 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	339	MET	CG-SD-CE	5.36	108.78	100.20

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	3464	3358	3159	27	1
1	B	3316	3186	3046	19	0
1	C	3304	3177	3096	24	0
2	A	23	22	0	2	0
2	B	23	22	0	0	0
2	C	23	22	0	1	0
3	A	43	30	30	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	43	30	30	2	0
3	C	43	30	30	8	0
4	B	10	0	0	1	0
4	C	20	0	0	0	0
5	A	413	0	0	4	4
5	B	284	0	0	6	0
5	C	206	0	0	7	0
All	All	11215	9877	9391	78	4

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 (78) 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)
3:C:502:HEM:O1A	5:C:601:HOH:O	1.78	1.01
1:C:204:GLU:OE1	5:C:602:HOH:O	1.86	0.92
1:C:200:MET:CE	1:C:220:LEU:HD12	2.11	0.80
1:B:411[A]:ARG:NH1	5:B:602:HOH:O	2.15	0.79
1:B:150:ARG:NH1	5:B:601:HOH:O	2.09	0.78
1:C:86:SER:OG	5:C:603:HOH:O	2.08	0.71
1:C:200:MET:HE1	1:C:220:LEU:HD12	1.72	0.70
3:B:502:HEM:HBC2	3:B:502:HEM:HMC2	1.74	0.70
1:C:112:GLN:NE2	5:C:610:HOH:O	2.27	0.67
1:C:200:MET:HE3	1:C:220:LEU:HD12	1.78	0.66
1:B:133:ARG:O	1:B:136:THR:HG23	1.96	0.65
1:C:281:MET:CE	1:C:401:LEU:HD21	2.27	0.65
3:C:502:HEM:O2A	5:C:604:HOH:O	2.14	0.64
1:C:281:MET:HE1	1:C:401:LEU:HD21	1.82	0.61
1:C:202:GLY:O	5:C:605:HOH:O	2.15	0.59
1:A:150[B]:ARG:HG3	5:A:730:HOH:O	2.03	0.58
1:A:200:MET:HB3	1:A:267:VAL:HG12	1.86	0.57
1:C:211:ILE:HG22	1:C:213:PRO:HD3	1.87	0.56
1:A:130:ILE:O	1:A:133[A]:ARG:HG2	2.05	0.56
3:A:502:HEM:HBC2	3:A:502:HEM:HMC2	1.87	0.56
3:C:502:HEM:HMC1	3:C:502:HEM:HBC2	1.91	0.52
1:C:422[A]:GLN:NE2	5:C:616:HOH:O	2.38	0.51
1:C:370:GLY:HA3	3:C:502:HEM:HBA1	1.93	0.51
3:C:502:HEM:HBC2	3:C:502:HEM:CMC	2.40	0.51
1:A:221:ILE:O	1:A:225:MET:HG3	2.11	0.50
1:B:79:VAL:HG22	1:B:339:MET:HB3	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:246:ALA:N	1:B:252:LYS:HE2	2.26	0.50
3:B:502:HEM:HBC2	3:B:502:HEM:CMC	2.41	0.50
1:A:131:ILE:HD13	1:A:261:PHE:CD1	2.46	0.50
1:A:201[A]:THR:HG23	2:A:501:I6Y:C9	2.41	0.50
1:B:286:GLU:HG3	5:B:748:HOH:O	2.11	0.49
1:A:332:LYS:NZ	5:A:615:HOH:O	2.45	0.49
1:B:286:GLU:OE1	5:B:604:HOH:O	2.20	0.49
1:A:246:ALA:HB1	1:A:250:GLY:HA2	1.95	0.48
1:B:27:ASP:HA	1:B:55:ASN:HD21	1.78	0.48
1:C:185:VAL:HG21	1:C:193:LEU:HD22	1.96	0.47
1:C:109:ILE:O	1:C:112:GLN:HB2	2.15	0.47
1:B:330[B]:GLN:O	5:B:603:HOH:O	2.19	0.47
1:C:298:ARG:HD2	1:C:392:ASN:OD1	2.15	0.46
1:B:93[B]:GLU:HG2	1:B:319:THR:HG21	1.98	0.46
1:B:372:THR:HG23	5:B:829:HOH:O	2.15	0.46
1:C:268:ALA:HA	2:C:501:I6Y:C18	2.45	0.46
1:A:202:GLY:HA3	5:A:794:HOH:O	2.14	0.46
1:A:80:LYS:NZ	1:A:372[A]:THR:OG1	2.49	0.46
1:A:226:LYS:O	1:A:230[A]:GLU:HG3	2.16	0.45
1:C:264[B]:MET:HB3	1:C:264[B]:MET:HE3	1.50	0.45
1:C:76:LEU:CD2	1:C:80:LYS:HD2	2.47	0.45
1:B:142:ARG:HG2	1:B:142:ARG:HH11	1.81	0.44
1:C:225:MET:O	1:C:229:GLU:HG3	2.17	0.44
1:A:310:ALA:O	1:A:311:THR:C	2.57	0.44
1:B:101:LYS:HE2	4:B:503:SO4:O3	2.18	0.43
1:A:279:GLN:HE22	1:A:416:ASN:ND2	2.16	0.43
1:A:235:PRO:HA	1:A:241:THR:HG21	2.01	0.42
1:C:130:ILE:HD11	1:C:251:GLU:HB3	2.01	0.42
1:C:377:CYS:HB2	3:C:502:HEM:NA	2.34	0.42
1:A:235:PRO:HA	1:A:241:THR:CG2	2.50	0.42
1:B:150:ARG:NH1	1:B:150:ARG:HG2	2.34	0.42
1:A:201[A]:THR:HG21	1:A:271:GLU:OE1	2.20	0.42
1:A:179:ILE:HD11	1:A:269:GLY:HA3	2.02	0.41
1:A:114:PHE:CE1	1:B:296[B]:LYS:HG2	2.55	0.41
1:A:268:ALA:HA	2:A:501:I6Y:C18	2.49	0.41
1:A:248:ILE:H	1:A:248:ILE:HG12	1.51	0.41
1:A:199:GLU:HA	1:A:211:ILE:HD13	2.01	0.41
1:A:116[A]:MET:HB3	1:A:127:LEU:HD23	2.02	0.41
1:B:111:VAL:O	1:B:114:PHE:HD2	2.04	0.41
1:B:126[B]:ARG:NH2	1:B:257:GLU:OE1	2.53	0.41
1:A:222:GLY:O	1:A:226:LYS:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:200:MET:HE3	1:A:220:LEU:HD22	2.02	0.41
1:A:398[B]:MET:O	1:A:401[B]:LEU:HD22	2.21	0.41
1:B:310:ALA:O	1:B:311:THR:C	2.60	0.40
1:A:286:GLU:HG2	5:A:837:HOH:O	2.21	0.40
1:C:351:PHE:O	1:C:352:GLN:HB2	2.21	0.40
1:C:221:ILE:O	1:C:225:MET:HG2	2.21	0.40

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:103[A]:ASP:OD2	5:A:945:HOH:O[4_556]	2.07	0.13
5:A:750:HOH:O	5:A:859:HOH:O[4_556]	2.10	0.10
5:A:958:HOH:O	5:A:1004:HOH:O[4_546]	2.14	0.06
5:A:877:HOH:O	5:A:1009:HOH:O[2_556]	2.18	0.02

## 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	461/418 (110%)	452 (98%)	9 (2%)	0	100	100
1	B	433/418 (104%)	424 (98%)	8 (2%)	1 (0%)	47	33
1	C	428/418 (102%)	416 (97%)	12 (3%)	0	100	100
All	All	1322/1254 (105%)	1292 (98%)	29 (2%)	1 (0%)	51	36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	248	ILE

### 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	380/341 (111%)	374 (98%)	6 (2%)	62	49
1	B	357/341 (105%)	354 (99%)	3 (1%)	81	76
1	C	351/341 (103%)	341 (97%)	10 (3%)	43	27
All	All	1088/1023 (106%)	1069 (98%)	19 (2%)	67	47

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	ASN
1	A	201[A]	THR
1	A	201[B]	THR
1	A	248	ILE
1	A	401[A]	LEU
1	A	401[B]	LEU
1	B	19	SER
1	B	55	ASN
1	B	398	MET
1	C	55	ASN
1	C	87	ASP
1	C	93[A]	GLU
1	C	93[B]	GLU
1	C	133[A]	ARG
1	C	133[B]	ARG
1	C	220	LEU
1	C	322	ARG
1	C	398[A]	MET
1	C	398[B]	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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](#)

12 ligands are modelled in this entry.

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	HEM	C	502	2,1	41,50,50	1.47	6 (14%)	45,82,82	1.59	9 (20%)
3	HEM	A	502	2,1	41,50,50	1.79	7 (17%)	45,82,82	1.93	12 (26%)
3	HEM	B	502	2,1	41,50,50	1.60	7 (17%)	45,82,82	1.37	6 (13%)
4	SO4	C	503	-	4,4,4	0.13	0	6,6,6	0.06	0
2	I6Y	A	501	3	26,26,26	0.55	0	31,35,35	0.65	0
2	I6Y	B	501	3	26,26,26	0.54	0	31,35,35	0.62	0
2	I6Y	C	501	3	26,26,26	0.53	0	31,35,35	0.74	1 (3%)
4	SO4	C	506	-	4,4,4	0.12	0	6,6,6	0.11	0
4	SO4	B	504	-	4,4,4	0.13	0	6,6,6	0.16	0
4	SO4	C	504	-	4,4,4	0.11	0	6,6,6	0.29	0
4	SO4	B	503	-	4,4,4	0.18	0	6,6,6	0.27	0
4	SO4	C	505	-	4,4,4	0.13	0	6,6,6	0.07	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	HEM	C	502	2,1	-	0/12/54/54	-
3	HEM	A	502	2,1	-	1/12/54/54	-
3	HEM	B	502	2,1	-	3/12/54/54	-
2	I6Y	A	501	3	-	3/9/17/17	0/4/4/4
2	I6Y	B	501	3	-	1/9/17/17	0/4/4/4
2	I6Y	C	501	3	-	1/9/17/17	1/4/4/4

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	502	HEM	C3C-C2C	-4.46	1.34	1.40
3	A	502	HEM	C3C-C2C	-4.43	1.34	1.40
3	A	502	HEM	CAA-C2A	4.32	1.58	1.52
3	C	502	HEM	C3C-C2C	-4.05	1.34	1.40
3	B	502	HEM	C3C-CAC	3.67	1.55	1.47
3	A	502	HEM	C3C-CAC	3.34	1.54	1.47
3	A	502	HEM	C1A-NA	3.11	1.42	1.36
3	C	502	HEM	C3C-CAC	3.03	1.54	1.47
3	B	502	HEM	C1A-NA	2.66	1.41	1.36
3	C	502	HEM	CAB-C3B	2.58	1.54	1.47
3	B	502	HEM	CMB-C2B	2.57	1.56	1.50
3	A	502	HEM	CMD-C2D	2.40	1.55	1.50
3	B	502	HEM	C1B-NB	-2.40	1.36	1.40
3	C	502	HEM	CAA-C2A	2.28	1.55	1.52
3	B	502	HEM	CAB-C3B	2.18	1.53	1.47
3	A	502	HEM	C1B-NB	-2.10	1.36	1.40
3	A	502	HEM	CMB-C2B	2.09	1.55	1.50
3	C	502	HEM	CMD-C2D	2.04	1.55	1.50
3	C	502	HEM	CHB-C1B	2.01	1.40	1.35
3	B	502	HEM	C4A-CHB	-2.00	1.35	1.41

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	502	HEM	C4A-C3A-C2A	5.97	111.15	107.00
3	A	502	HEM	C1B-NB-C4B	4.56	109.78	105.07
3	C	502	HEM	C1B-NB-C4B	4.16	109.37	105.07
3	C	502	HEM	C4C-CHD-C1D	3.71	127.45	122.56
3	A	502	HEM	C4B-CHC-C1C	3.32	126.94	122.56
3	A	502	HEM	C4D-ND-C1D	3.30	108.48	105.07
3	B	502	HEM	C4C-CHD-C1D	3.22	126.80	122.56
3	B	502	HEM	C1B-NB-C4B	3.08	108.25	105.07
2	C	501	I6Y	C12-C11-N1	3.07	116.03	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	502	HEM	CMC-C2C-C3C	3.01	130.30	124.68
3	C	502	HEM	CMA-C3A-C4A	-2.86	124.07	128.46
3	B	502	HEM	C4D-ND-C1D	2.82	107.99	105.07
3	A	502	HEM	CMC-C2C-C3C	2.78	129.88	124.68
3	A	502	HEM	C3D-C4D-ND	-2.74	107.12	110.17
3	C	502	HEM	C3B-C2B-C1B	2.73	108.51	106.49
3	C	502	HEM	CHC-C4B-NB	2.64	127.30	124.43
3	B	502	HEM	C4A-C3A-C2A	2.60	108.81	107.00
3	A	502	HEM	O1A-CGA-CBA	-2.49	115.09	123.08
3	A	502	HEM	C2D-C1D-ND	-2.48	106.92	109.88
3	A	502	HEM	C1D-C2D-C3D	2.38	109.46	106.96
3	A	502	HEM	CMA-C3A-C4A	-2.36	124.83	128.46
3	C	502	HEM	C2B-C1B-NB	-2.32	107.09	109.84
3	A	502	HEM	CHC-C4B-NB	2.20	126.82	124.43
3	C	502	HEM	C4D-ND-C1D	2.17	107.32	105.07
3	C	502	HEM	CMC-C2C-C3C	2.09	128.58	124.68
3	C	502	HEM	C2C-C3C-C4C	2.08	108.35	106.90
3	B	502	HEM	CMA-C3A-C4A	-2.06	125.29	128.46
3	A	502	HEM	CHD-C1D-ND	2.06	126.67	124.43

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	502	HEM	C3A-C2A-CAA-CBA
3	B	502	HEM	C1A-C2A-CAA-CBA
3	B	502	HEM	C3A-C2A-CAA-CBA
2	C	501	I6Y	C11-C12-N2-C16
2	A	501	I6Y	N1-C11-C12-N2
2	B	501	I6Y	N1-C11-C12-N2
2	A	501	I6Y	C12-C11-N1-C10
3	B	502	HEM	CAD-CBD-CGD-O2D
2	A	501	I6Y	C12-C11-N1-C7

All (1) ring outliers are listed below:

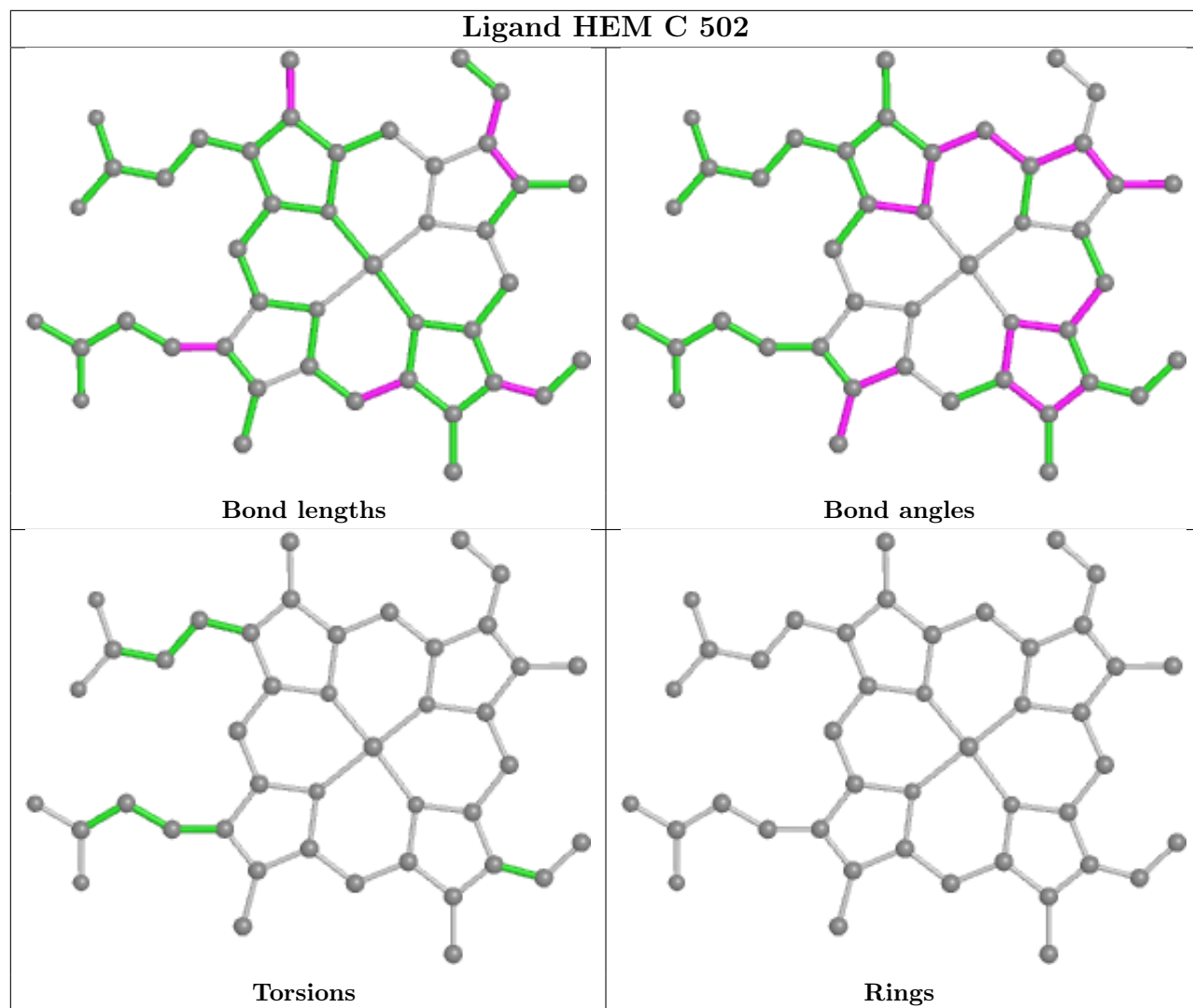
Mol	Chain	Res	Type	Atoms
2	C	501	I6Y	C13-C14-C15-C16-N2-N3

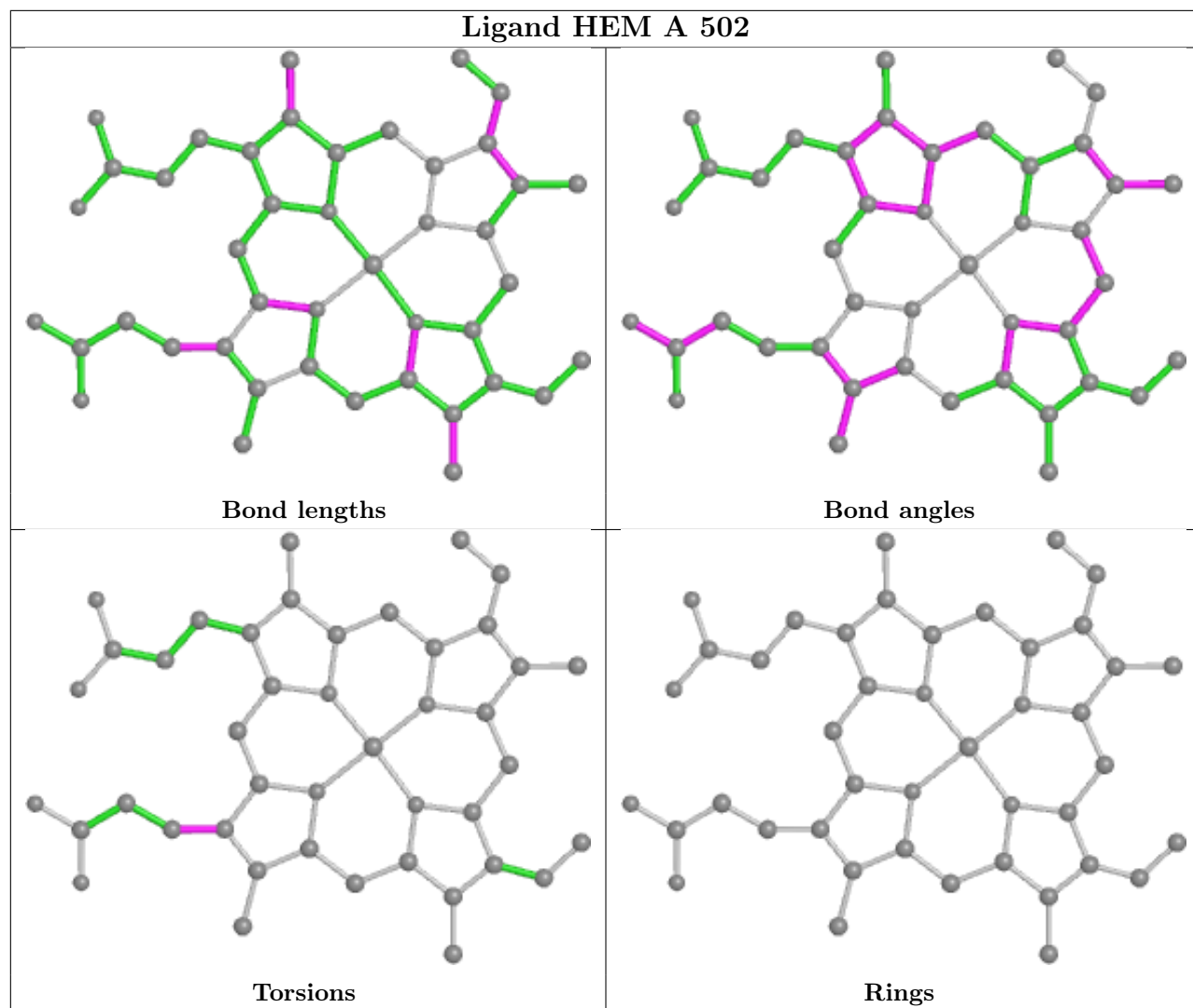
6 monomers are involved in 15 short contacts:

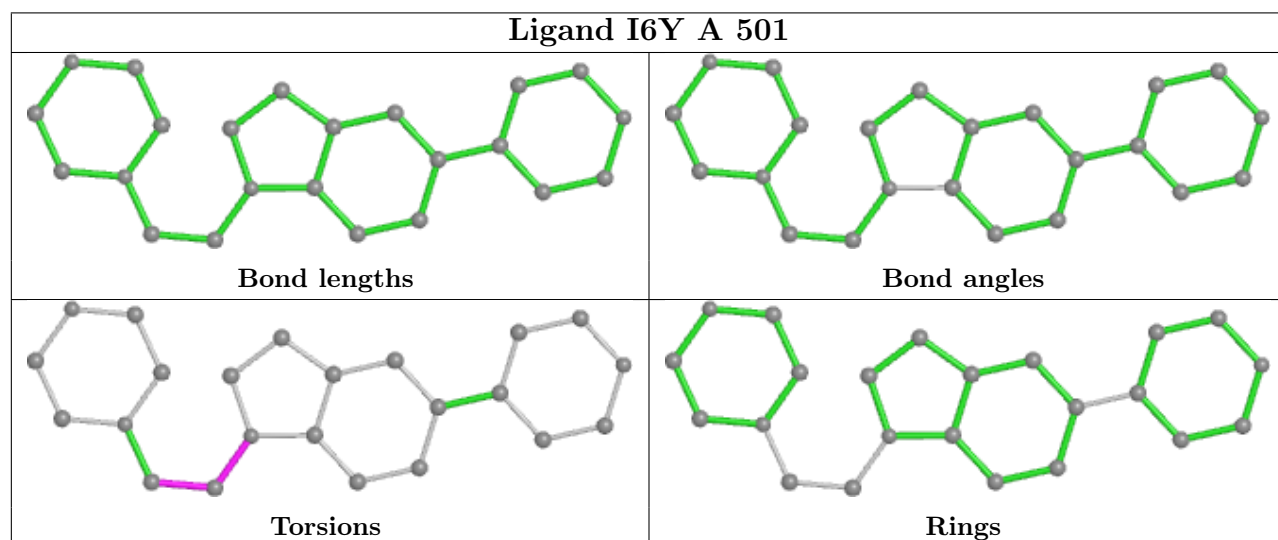
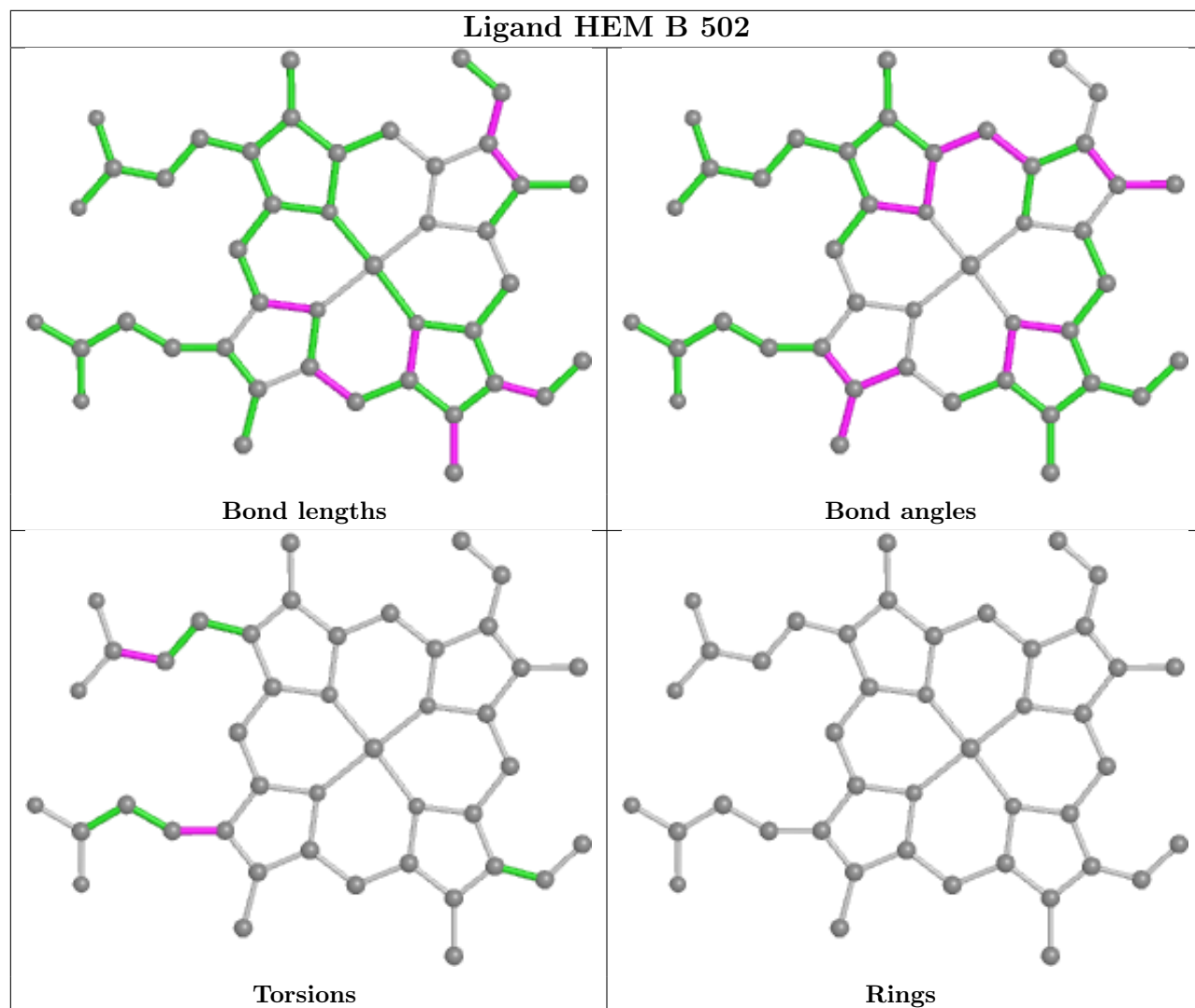


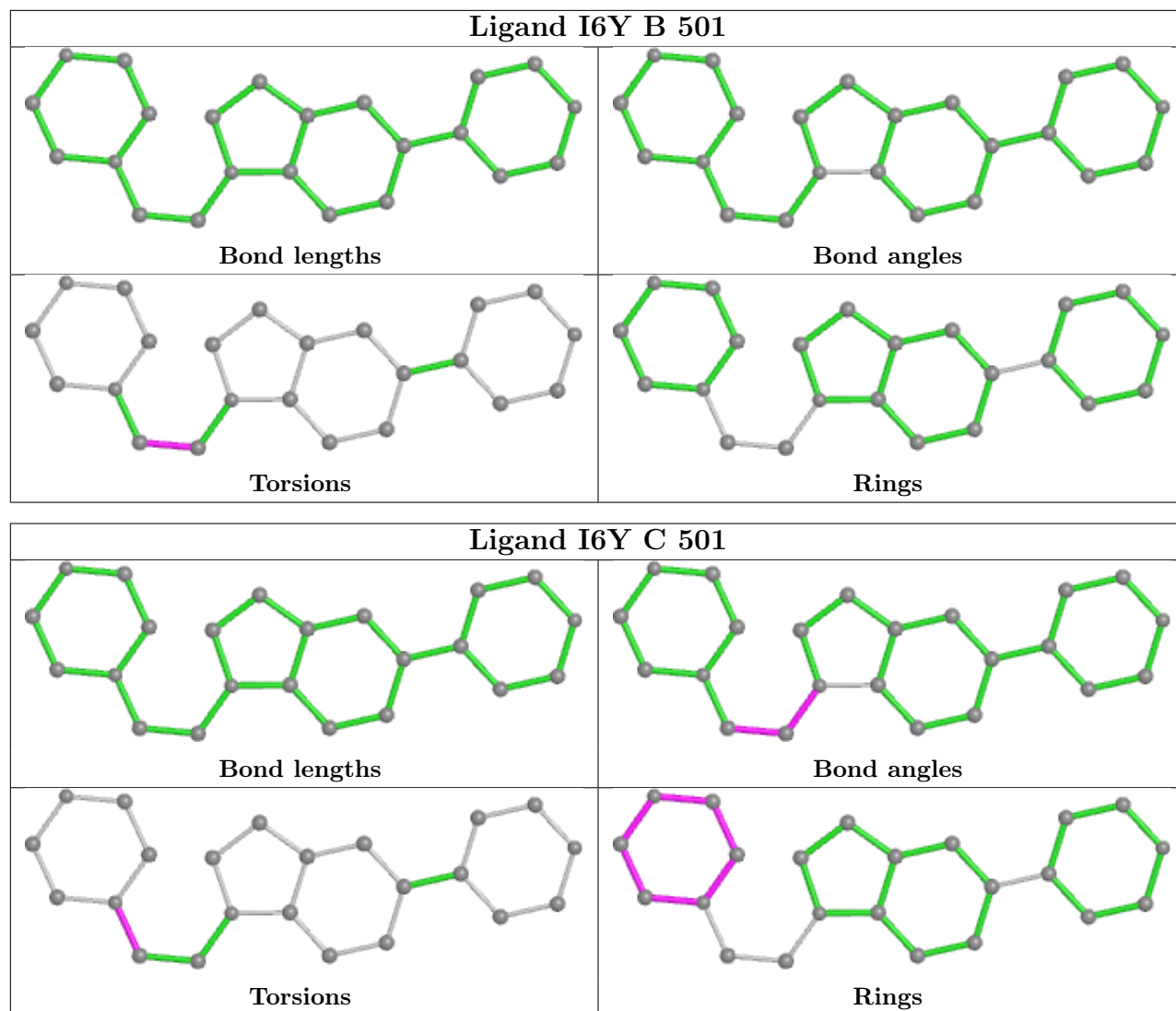
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	502	HEM	8	0
3	A	502	HEM	1	0
3	B	502	HEM	2	0
2	A	501	I6Y	2	0
2	C	501	I6Y	1	0
4	B	503	SO4	1	0

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	411/418 (98%)	-0.02	1 (0%) 95 94	16, 26, 53, 99	0
1	B	407/418 (97%)	0.03	11 (2%) 54 53	23, 39, 82, 120	0
1	C	409/418 (97%)	-0.00	2 (0%) 91 91	28, 43, 69, 95	0
All	All	1227/1254 (97%)	0.00	14 (1%) 80 81	16, 37, 68, 120	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	248	ILE	6.2
1	B	250	GLY	3.6
1	B	249	ASP	2.9
1	B	253	LEU	2.8
1	A	237	ASP	2.6
1	B	232	ALA	2.5
1	B	243	LEU	2.4
1	B	233	LYS	2.3
1	B	246	ALA	2.2
1	C	84	ARG	2.2
1	B	235	PRO	2.1
1	B	240	VAL	2.1
1	B	203	ASN	2.1
1	C	226	LYS	2.0

### 6.2 Non-standard residues in protein, DNA, RNA chains

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](#)

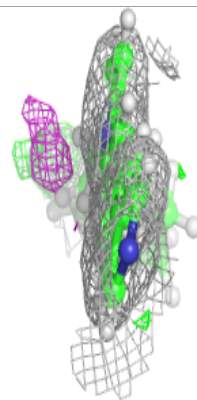
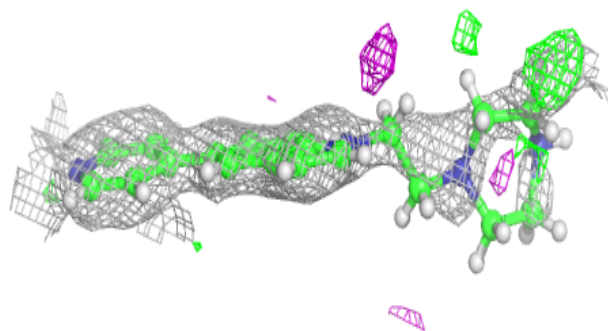
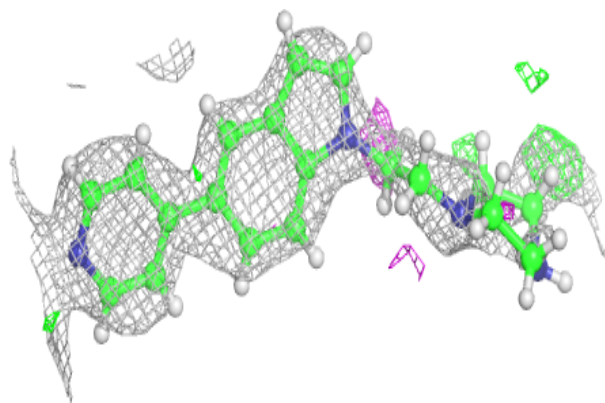
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
4	SO4	C	506	5/5	0.78	0.17	89,96,121,133	0
4	SO4	C	503	5/5	0.84	0.15	83,87,111,137	0
2	I6Y	C	501	23/23	0.87	0.19	33,55,79,91	45
4	SO4	C	505	5/5	0.89	0.21	78,78,107,108	0
2	I6Y	A	501	23/23	0.90	0.17	20,42,93,100	0
4	SO4	B	503	5/5	0.92	0.29	83,94,96,98	0
2	I6Y	B	501	23/23	0.93	0.13	29,48,95,115	0
4	SO4	C	504	5/5	0.94	0.13	63,70,79,91	0
4	SO4	B	504	5/5	0.96	0.11	66,66,77,83	0
3	HEM	A	502	43/43	0.98	0.11	15,20,27,32	0
3	HEM	B	502	43/43	0.98	0.10	25,31,46,48	0
3	HEM	C	502	43/43	0.98	0.10	28,37,48,59	0

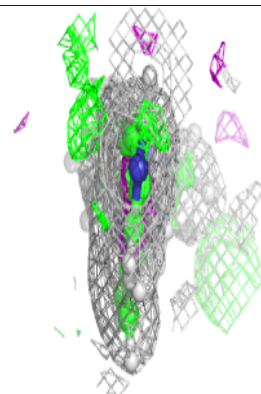
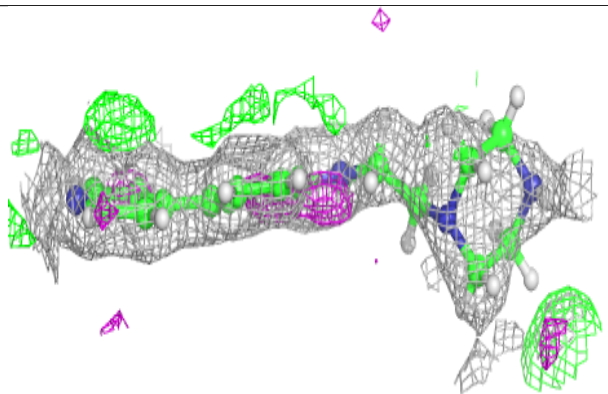
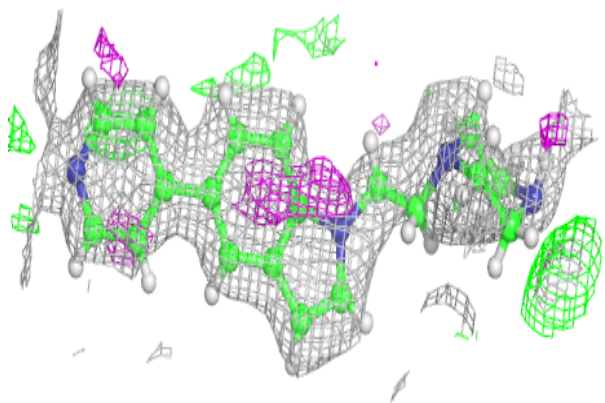
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around I6Y 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 I6Y A 501:**

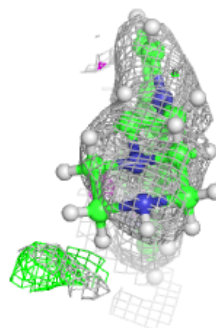
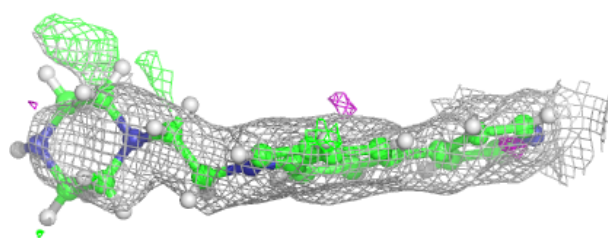
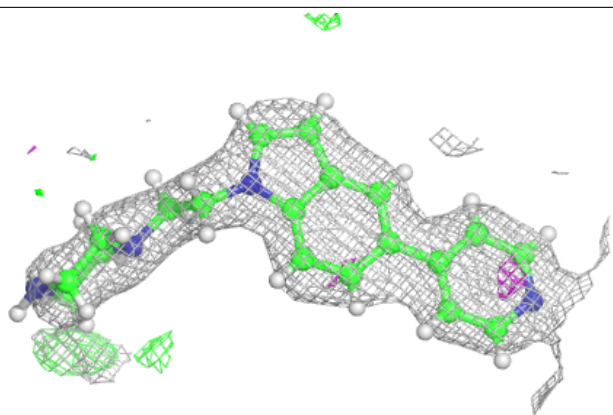
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





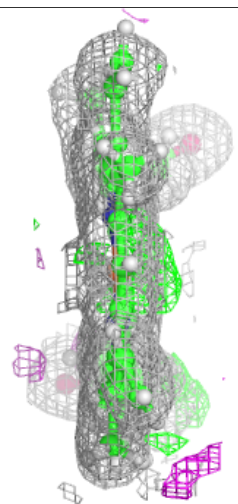
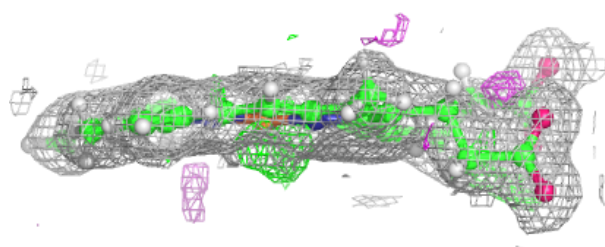
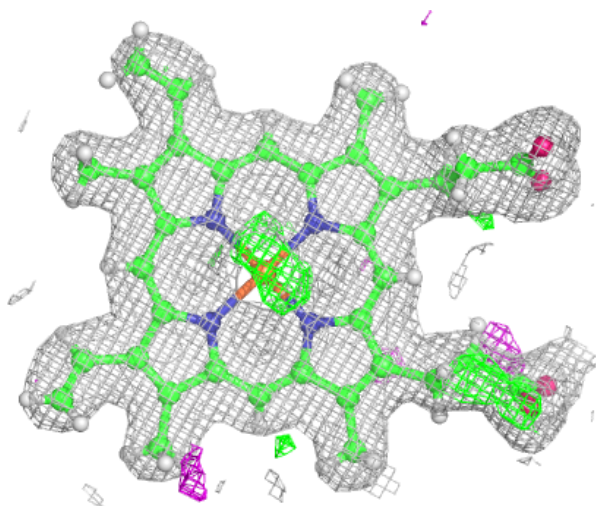
**Electron density around I6Y B 501:**

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



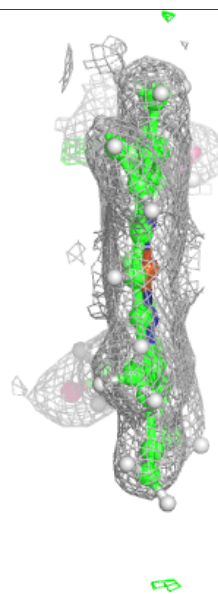
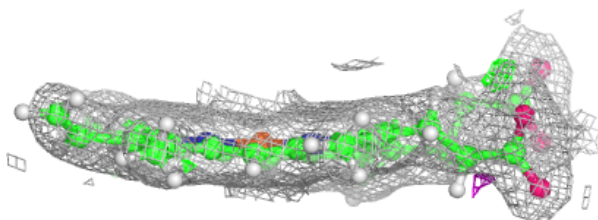
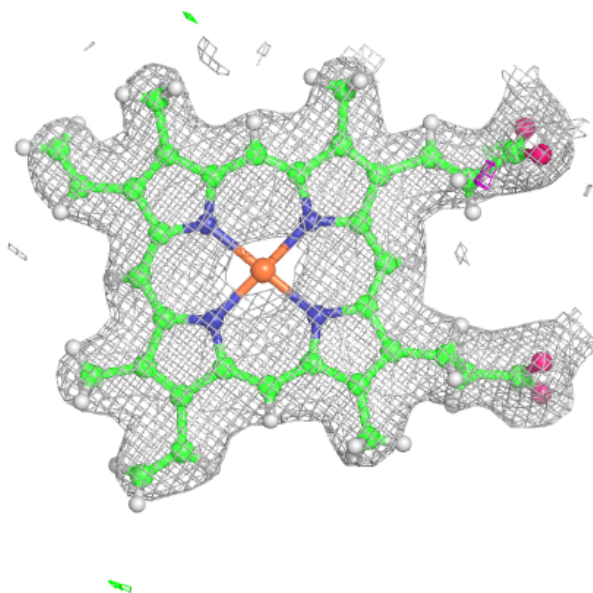
**Electron density around HEM A 502:**

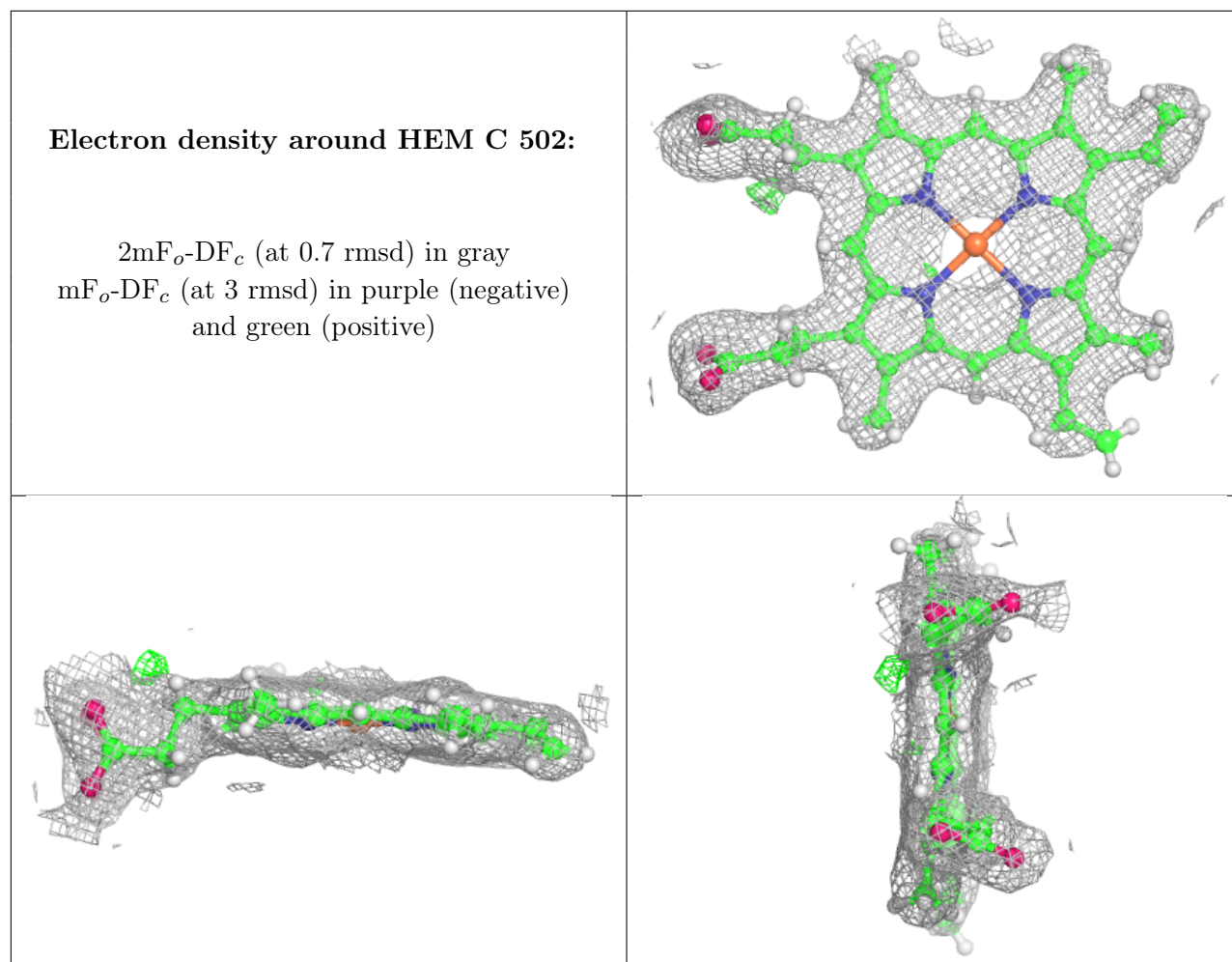
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around HEM B 502:**

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





## 6.5 Other polymers [i](#)

There are no such residues in this entry.