



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jul 29, 2025 – 02:16 PM JST

PDB ID : 9JQM / pdb\_00009jqm  
Title : X-ray structure of cytochrome P450 OleT from *Lacicoccus alkaliphilus* in complex with icosanoic acid  
Authors : Phaisan, S.; Phintha, A.; Trisrivirat, D.; Charoenpol, A.; Tanaka, H.; Kurisu, G.; Watthaisong, P.; Sucharitakul, J.; Chaiken, P.  
Deposited on : 2024-09-27  
Resolution : 2.44 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.

The types of validation reports are described at

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

---

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

MolProbity	:	4-5-2 with Phenix2.0rc1
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.45.1



Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	GOL	A	505	-	-	X	-
4	GOL	B	505	-	X	X	-

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7629 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

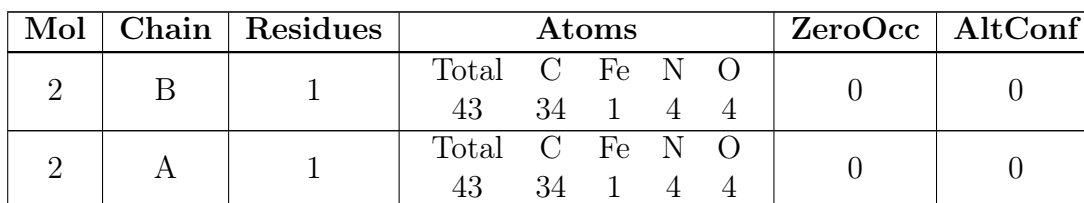
- Molecule 1 is a protein called Fatty-acid peroxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	428	Total	C	N	O	S	0	0	0
			3465	2210	603	634	18			
1	A	427	Total	C	N	O	S	0	0	0
			3441	2192	598	633	18			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	425	LEU	-	expression tag	UNP A0A1M7CBV6
B	426	GLU	-	expression tag	UNP A0A1M7CBV6
B	427	HIS	-	expression tag	UNP A0A1M7CBV6
B	428	HIS	-	expression tag	UNP A0A1M7CBV6
B	429	HIS	-	expression tag	UNP A0A1M7CBV6
B	430	HIS	-	expression tag	UNP A0A1M7CBV6
B	431	HIS	-	expression tag	UNP A0A1M7CBV6
B	432	HIS	-	expression tag	UNP A0A1M7CBV6
A	425	LEU	-	expression tag	UNP A0A1M7CBV6
A	426	GLU	-	expression tag	UNP A0A1M7CBV6
A	427	HIS	-	expression tag	UNP A0A1M7CBV6
A	428	HIS	-	expression tag	UNP A0A1M7CBV6
A	429	HIS	-	expression tag	UNP A0A1M7CBV6
A	430	HIS	-	expression tag	UNP A0A1M7CBV6
A	431	HIS	-	expression tag	UNP A0A1M7CBV6
A	432	HIS	-	expression tag	UNP A0A1M7CBV6

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ) (labeled as "Ligand of Interest" by depositor).



- # DCR
- 
- Chemical structure of Dodecanedioic acid (DCR) is shown, featuring a zigzag chain of 12 carbon atoms (C1 to C12) and two carboxylic acid groups (OH and O).

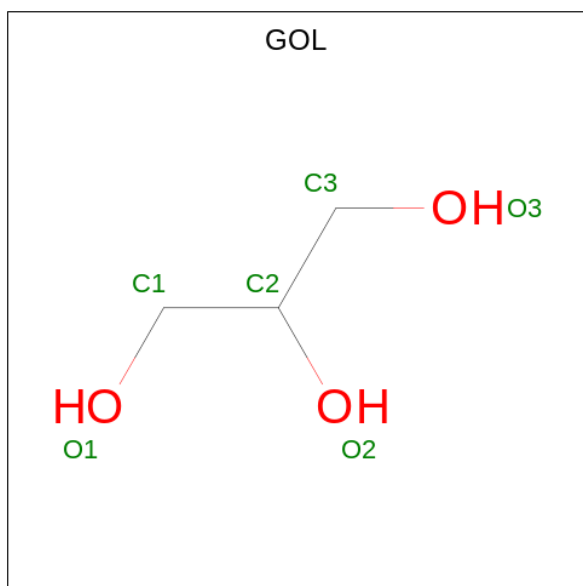
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			22	20	2		

*Continued on next page...*

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			22	20	2		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula:  $C_3H_8O_3$ ).



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

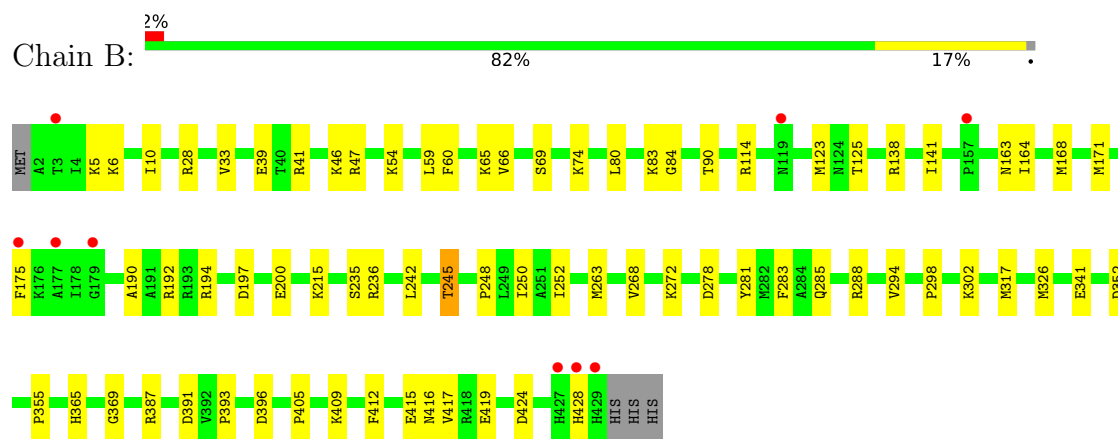
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	291	Total	O	0	0
			291	291		
5	A	266	Total	O	0	0
			266	266		

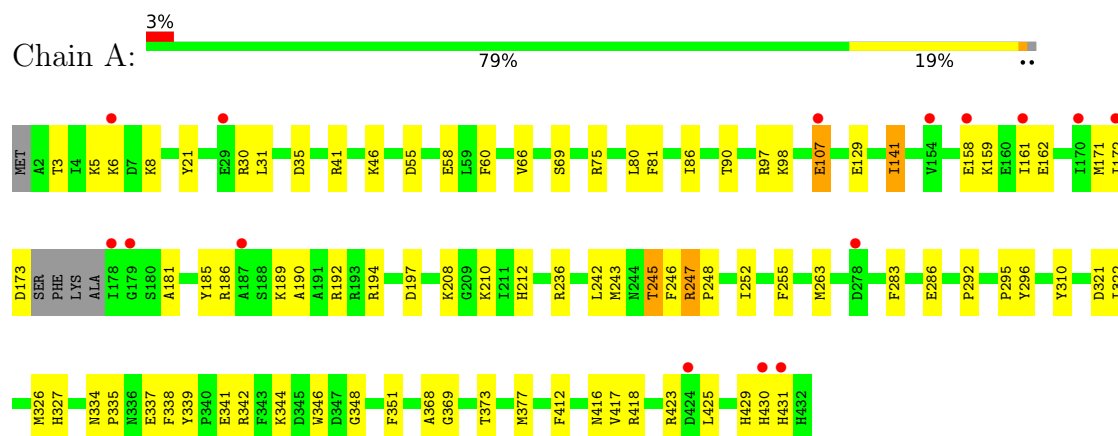
### 3 Residue-property plots [i](#)

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: Fatty-acid peroxygenase



#### • Molecule 1: Fatty-acid peroxygenase



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	82.80Å 188.86Å 198.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.63 – 2.44 42.63 – 2.44	Depositor EDS
% Data completeness (in resolution range)	99.0 (42.63-2.44) 98.8 (42.63-2.44)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.08 (at 2.45Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, $R_{free}$	0.182 , 0.230 0.182 , 0.229	Depositor DCC
$R_{free}$ test set	2895 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	70.6	Xtriage
Anisotropy	0.173	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 63.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.018 for -h,-l,-k	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7629	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% 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, GOL, DCR

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	0.38	0/3521	0.59	3/4754 (0.1%)
1	B	0.37	0/3547	0.54	0/4787
All	All	0.37	0/7068	0.57	3/9541 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	246	PHE	CA-C-N	-6.66	111.77	120.09
1	A	246	PHE	C-N-CA	-6.66	111.77	120.09
1	A	107	GLU	CA-CB-CG	5.16	124.42	114.10

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	3441	0	3349	70	2
1	B	3465	0	3399	54	0
2	A	43	0	30	7	0
2	B	43	0	30	9	0
3	A	22	0	39	4	0
3	B	22	0	39	4	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	18	0	23	5	0
4	B	18	0	24	6	0
5	A	266	0	0	6	1
5	B	291	0	0	8	0
All	All	7629	0	6933	131	3

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 9.

The worst 5 of 131 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:247:ARG:HH21	3:A:502:DCR:H2A	1.45	0.80
1:A:416:ASN:HA	4:A:505:GOL:H32	1.64	0.79
1:B:5:LYS:HD2	1:B:33:VAL:HG12	1.67	0.76
1:B:83:LYS:HE3	1:B:84:GLY:H	1.51	0.74
1:A:30:ARG:HG2	1:A:30:ARG:HH11	1.55	0.71

All (3) 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:212:HIS:O	1:A:418:ARG:NH2[8_565]	2.08	0.12
5:A:817:HOH:O	5:A:817:HOH:O[7_556]	2.11	0.09
1:A:107:GLU:OE2	1:A:430:HIS:NE2[8_565]	2.19	0.01

## 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	423/432 (98%)	407 (96%)	15 (4%)	1 (0%)	44 53

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	426/432 (99%)	409 (96%)	16 (4%)	1 (0%)	44	53
All	All	849/864 (98%)	816 (96%)	31 (4%)	2 (0%)	44	53

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	412	PHE
1	A	412	PHE

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	357/373 (96%)	354 (99%)	3 (1%)	79	87
1	B	362/373 (97%)	360 (99%)	2 (1%)	84	90
All	All	719/746 (96%)	714 (99%)	5 (1%)	81	89

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	245	THR
1	B	428	HIS
1	A	141	ILE
1	A	245	THR
1	A	247	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	402	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 oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

10 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	$\# Z  > 2$
4	GOL	A	504	-	5,5,5	0.78	0	5,5,5	1.04	0
3	DCR	B	502	-	21,21,21	0.70	1 (4%)	21,21,21	0.97	0
4	GOL	B	503	-	5,5,5	0.93	0	5,5,5	0.99	0
3	DCR	A	502	-	21,21,21	0.69	0	21,21,21	0.70	0
2	HEM	B	501	1	41,50,50	1.59	6 (14%)	45,82,82	1.91	13 (28%)
2	HEM	A	501	1	41,50,50	1.68	6 (14%)	45,82,82	1.75	11 (24%)
4	GOL	B	505	-	5,5,5	1.56	2 (40%)	5,5,5	0.63	0
4	GOL	A	505	-	5,5,5	0.96	0	5,5,5	0.98	0
4	GOL	A	503	-	5,5,5	1.16	1 (20%)	5,5,5	1.00	0
4	GOL	B	504	-	5,5,5	0.88	0	5,5,5	1.01	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
4	GOL	A	504	-	-	2/4/4/4	-
3	DCR	B	502	-	-	7/19/19/19	-
4	GOL	B	503	-	-	1/4/4/4	-
3	DCR	A	502	-	-	10/19/19/19	-
2	HEM	B	501	1	-	4/12/54/54	-
2	HEM	A	501	1	-	2/12/54/54	-
4	GOL	B	505	-	-	4/4/4/4	-
4	GOL	A	505	-	-	2/4/4/4	-
4	GOL	A	503	-	-	0/4/4/4	-
4	GOL	B	504	-	-	4/4/4/4	-

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	HEM	C3C-C2C	-5.38	1.32	1.40
2	B	501	HEM	C3C-C2C	-4.49	1.34	1.40
2	A	501	HEM	FE-ND	3.45	2.13	1.96
2	A	501	HEM	C3C-CAC	3.38	1.54	1.47
2	B	501	HEM	C3C-CAC	3.32	1.54	1.47

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	HEM	C4C-CHD-C1D	4.26	128.19	122.56
2	A	501	HEM	C4C-CHD-C1D	4.17	128.06	122.56
2	B	501	HEM	C1B-NB-C4B	3.99	109.19	105.07
2	B	501	HEM	CHC-C4B-C3B	3.82	130.42	124.57
2	A	501	HEM	CHC-C4B-C3B	3.63	130.13	124.57

There are no chirality outliers.

5 of 36 torsion outliers are listed below:

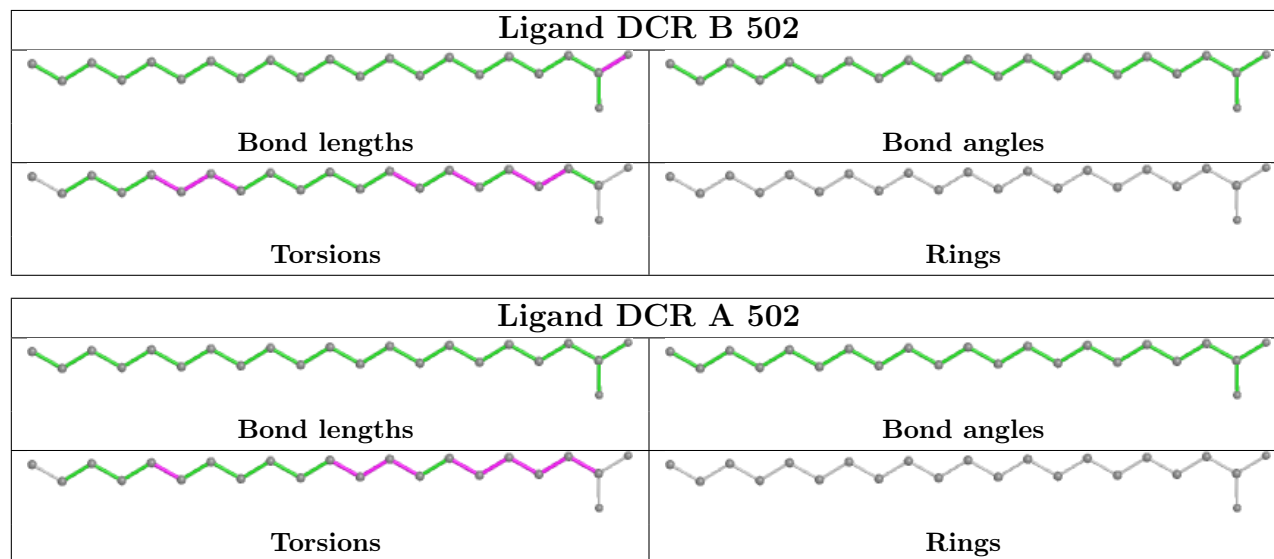
Mol	Chain	Res	Type	Atoms
4	B	504	GOL	C1-C2-C3-O3
4	B	505	GOL	C1-C2-C3-O3
4	A	504	GOL	O1-C1-C2-C3
3	B	502	DCR	C2-C3-C4-C5
3	A	502	DCR	C2-C3-C4-C5

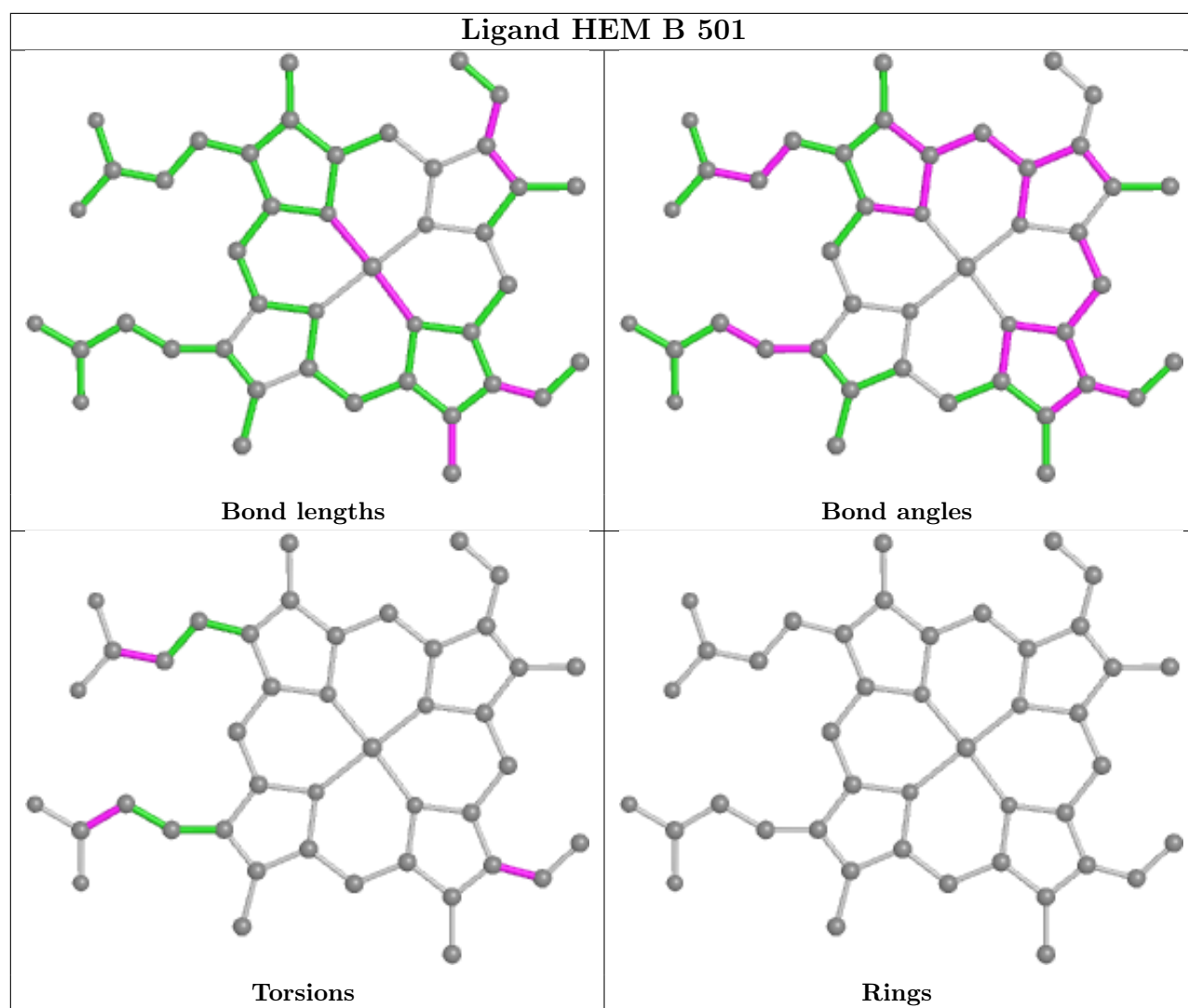
There are no ring outliers.

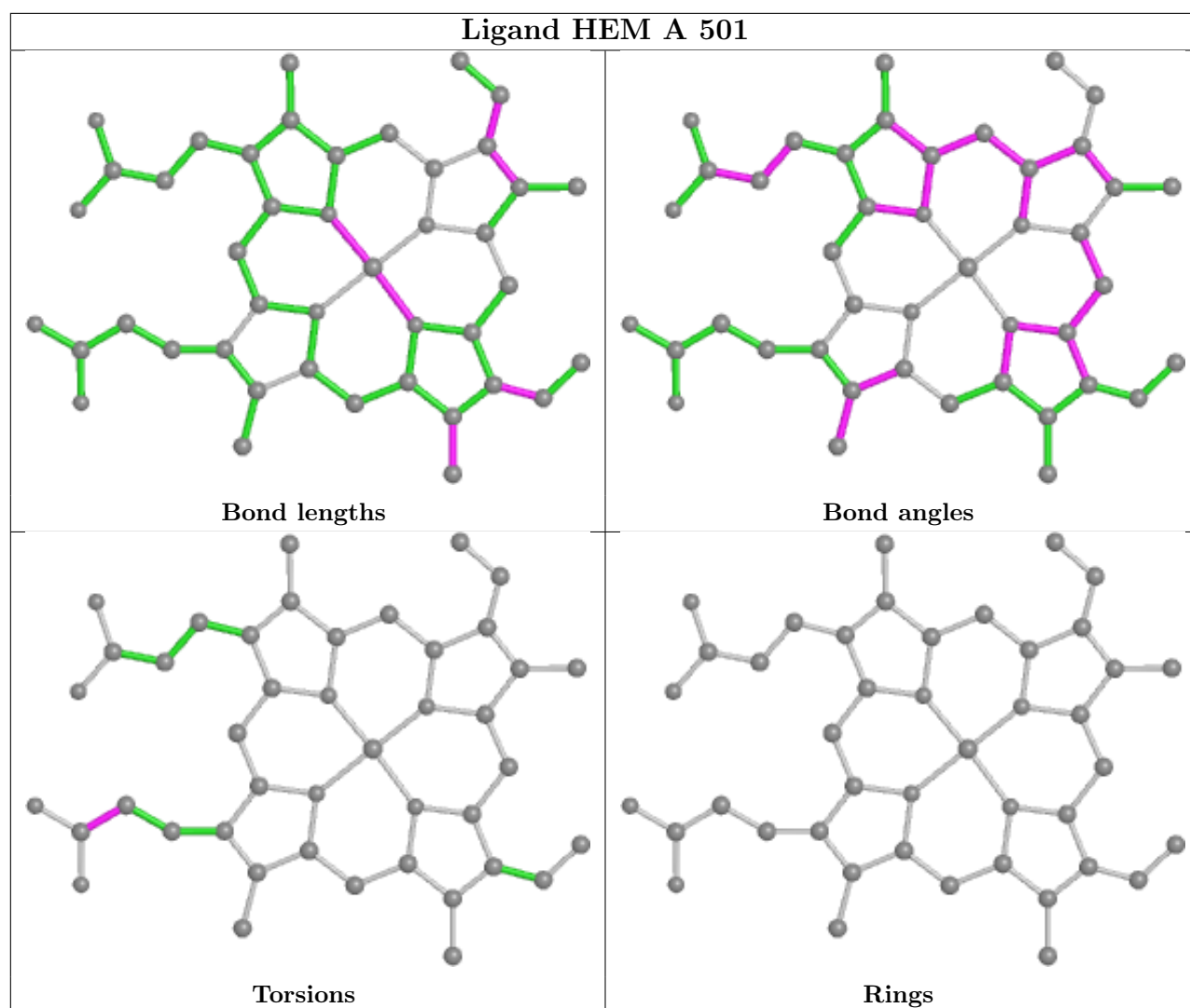
7 monomers are involved in 34 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	502	DCR	4	0
3	A	502	DCR	4	0
2	B	501	HEM	9	0
2	A	501	HEM	7	0
4	B	505	GOL	4	0
4	A	505	GOL	5	0
4	B	504	GOL	2	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	427/432 (98%)	0.08	15 (3%) 47 47	53, 73, 95, 113	0
1	B	428/432 (99%)	-0.13	9 (2%) 63 65	50, 66, 82, 104	0
All	All	855/864 (98%)	-0.02	24 (2%) 55 56	50, 69, 92, 113	0

The worst 5 of 24 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	161	ILE	4.6
1	B	427	HIS	3.8
1	B	175	PHE	3.3
1	A	179	GLY	3.3
1	A	172	ILE	3.0

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

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

### 6.3 Carbohydrates [i](#)

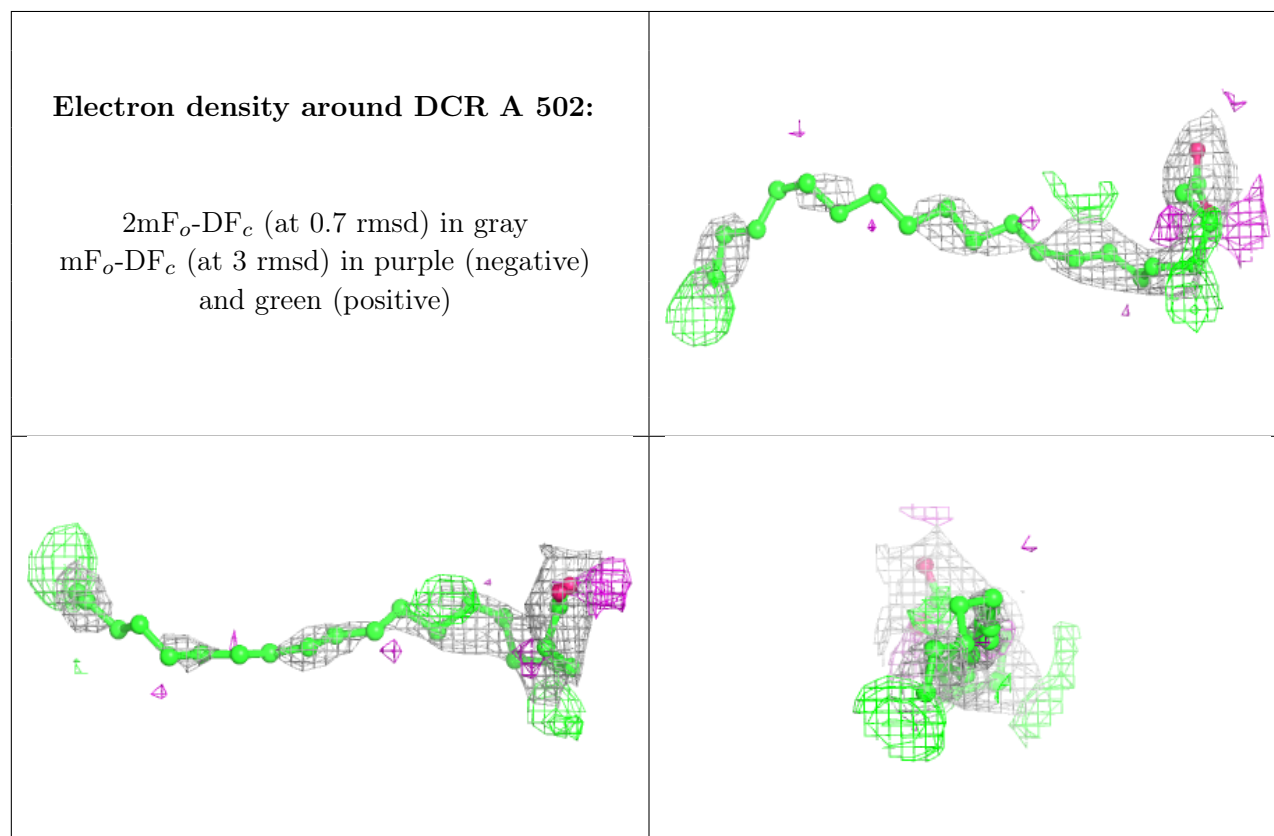
There are no oligosaccharides in this entry.

### 6.4 Ligands [i](#)

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

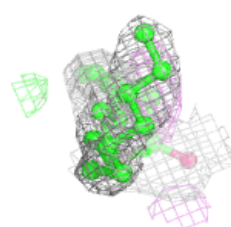
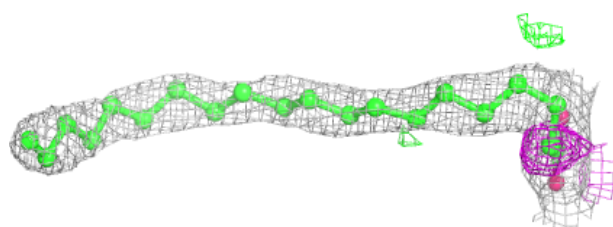
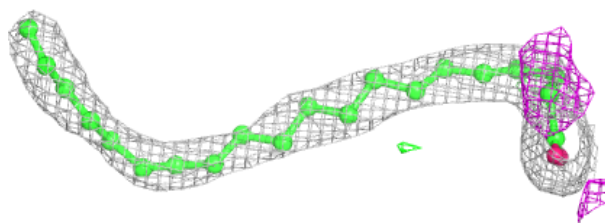
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	GOL	B	505	6/6	0.84	0.14	69,74,76,81	0
4	GOL	A	505	6/6	0.85	0.11	75,75,81,86	0
3	DCR	A	502	22/22	0.89	0.22	66,79,86,88	0
4	GOL	B	504	6/6	0.89	0.13	73,76,81,84	0
4	GOL	A	504	6/6	0.91	0.11	82,84,84,88	0
3	DCR	B	502	22/22	0.94	0.16	58,66,71,74	0
4	GOL	B	503	6/6	0.97	0.09	66,68,71,73	0
4	GOL	A	503	6/6	0.97	0.07	69,73,75,81	0
2	HEM	B	501	43/43	0.98	0.07	47,54,63,66	0
2	HEM	A	501	43/43	0.98	0.07	50,58,66,67	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.



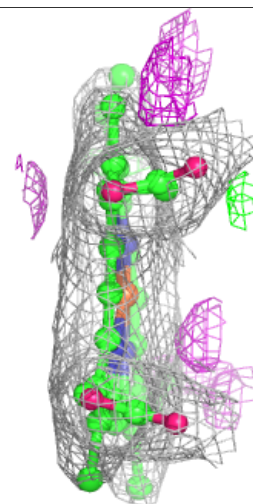
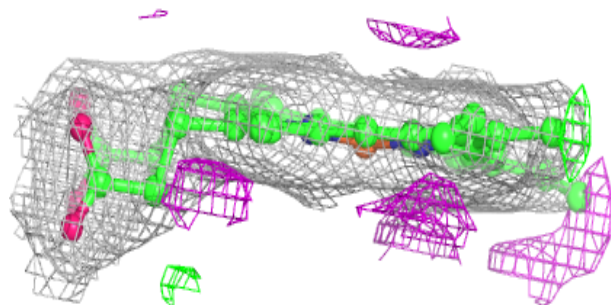
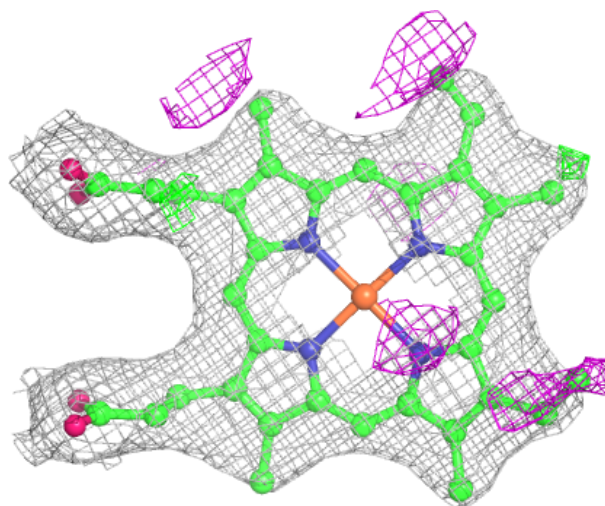
**Electron density around DCR B 502:**

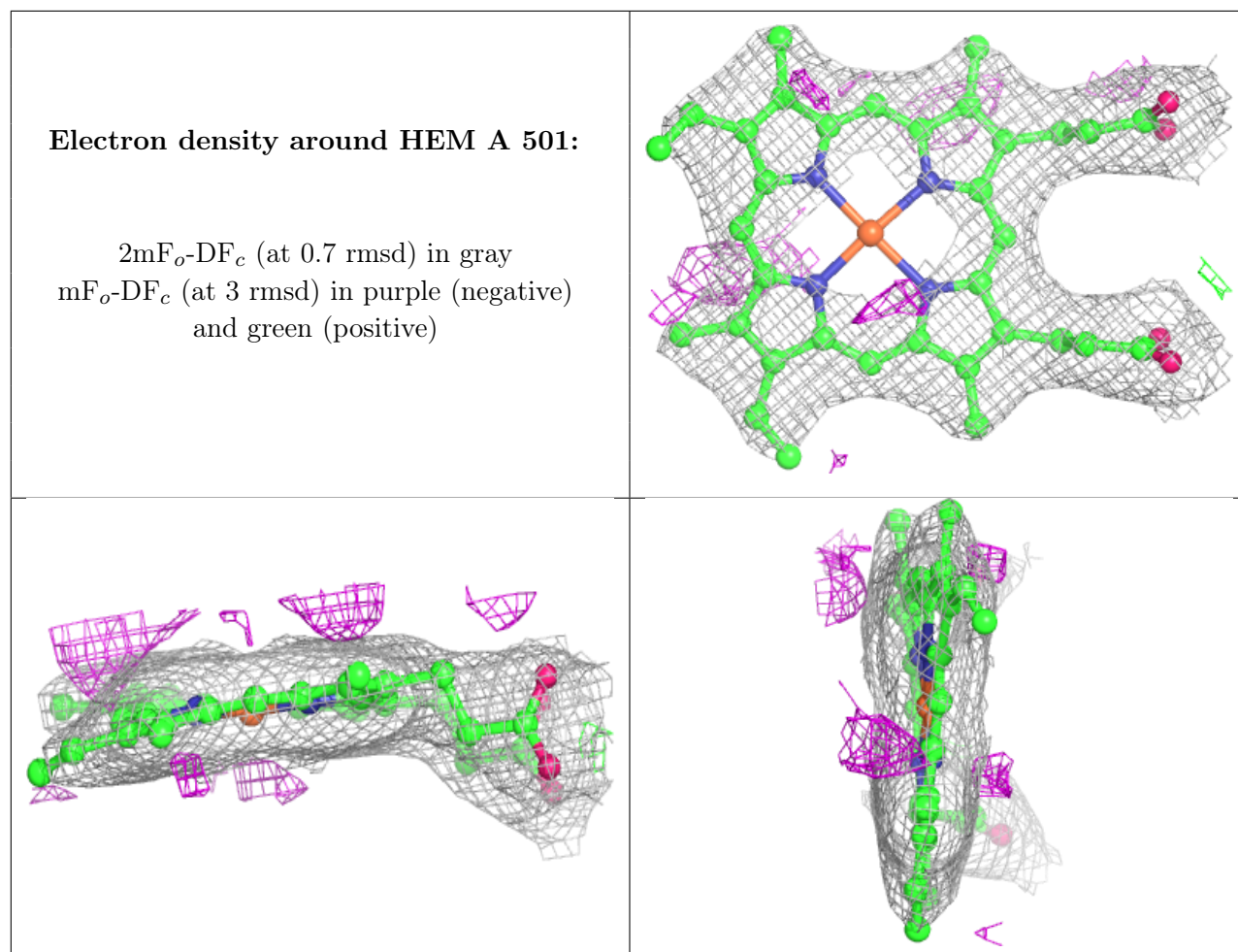
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**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.