



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 23, 2024 – 03:21 pm GMT

PDB ID : 8RE3  
Title : Crystal Structure determination of Dye-decolorizing Peroxidase (DyP) mutant M190G from *Deinococcus radiodurans*  
Authors : Salgueiro, B.A.; Frade, K.; Frazao, C.; Matias, P.; Moe, E.  
Deposited on : 2023-12-10  
Resolution : 1.51 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)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
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) : 2.36

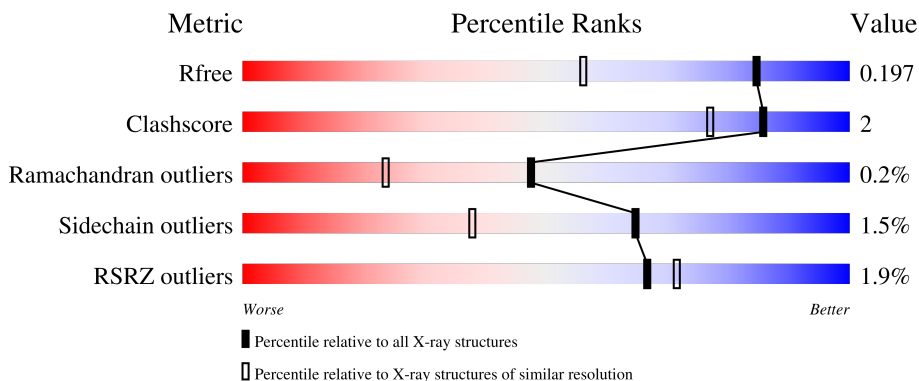
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.51 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	4009 (1.54-1.50)
Clashscore	141614	4249 (1.54-1.50)
Ramachandran outliers	138981	4148 (1.54-1.50)
Sidechain outliers	138945	4146 (1.54-1.50)
RSRZ outliers	127900	3943 (1.54-1.50)

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	445	
1	B	445	

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 14736 atoms, of which 6966 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 Peroxidase, putative.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	445	Total 6963	C 2236	H 3444	N 612	O 663	S 8	0	2	0
1	B	445	Total 6990	C 2243	H 3462	N 615	O 661	S 9	0	4	0

There are 4 discrepancies between the modelled and reference sequences:

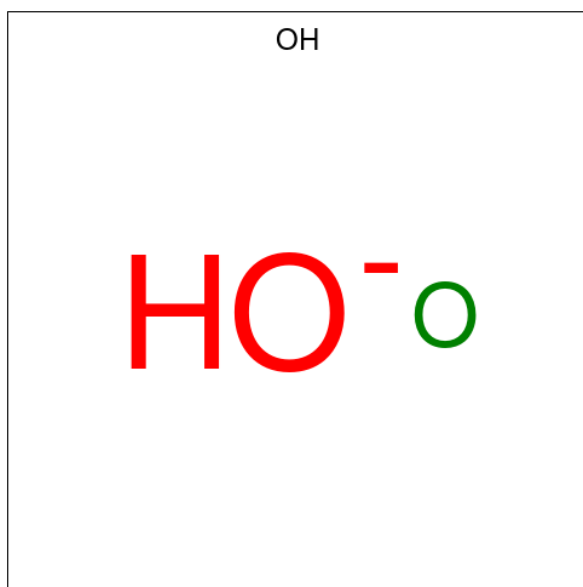
Chain	Residue	Modelled	Actual	Comment	Reference
A	162	GLY	GLU	conflict	UNP Q9RZ08
A	190	GLY	MET	engineered mutation	UNP Q9RZ08
B	162	GLY	GLU	conflict	UNP Q9RZ08
B	190	GLY	MET	engineered mutation	UNP Q9RZ08

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



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

- Molecule 3 is HYDROXIDE ION (three-letter code: OH) (formula: HO).



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

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

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

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

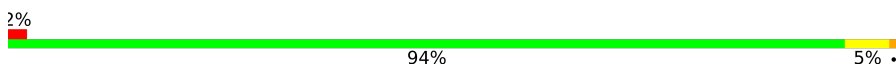
- Molecule 6 is water.

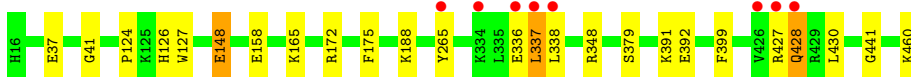
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	312	Total O 312 312	0	0
6	B	317	Total O 317 317	0	0

### 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.

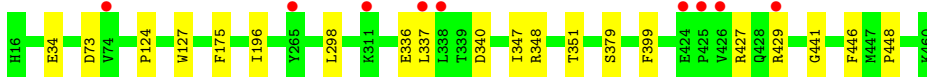
- Molecule 1: Peroxidase, putative

Chain A: 



- Molecule 1: Peroxidase, putative

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	82.09Å 97.70Å 116.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	74.74 – 1.51 74.74 – 1.51	Depositor EDS
% Data completeness (in resolution range)	66.5 (74.74-1.51) 67.2 (74.74-1.51)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.36 (at 1.51Å)	Xtrriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, $R_{free}$	0.167 , 0.195 0.169 , 0.197	Depositor DCC
$R_{free}$ test set	4849 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	18.2	Xtrriage
Anisotropy	0.075	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.41 , 44.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	14736	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	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 42.61 % 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 1.9892e-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: OH, CL, CA, HEM

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	0.50	0/3618	0.69	2/4900 (0.0%)
1	B	0.50	0/3628	0.69	0/4913
All	All	0.50	0/7246	0.69	2/9813 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	148[A]	GLU	CA-CB-CG	5.68	125.89	113.40
1	A	148[B]	GLU	CA-CB-CG	5.68	125.89	113.40

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	3519	3444	3451	13	0
1	B	3528	3462	3465	11	0
2	A	43	30	30	3	0
2	B	43	30	30	4	0
3	A	2	0	0	1	0
3	B	2	0	0	1	0
4	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	1	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	312	0	0	3	0
6	B	317	0	0	2	0
All	All	7770	6966	6976	31	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 2.

All (31) 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)
2:A:501:HEM:HBB2	2:A:501:HEM:HHC	1.73	0.70
1:A:158:GLU:OE2	1:A:172:ARG:NH1	2.30	0.64
1:A:430:LEU:HD23	1:A:430:LEU:N	2.13	0.62
3:B:502:OH:O	3:B:503:OH:O	2.20	0.60
2:B:501:HEM:HBC2	2:B:501:HEM:HHD	1.86	0.58
1:B:340:ASP:OD2	6:B:601:HOH:O	2.17	0.58
1:A:336:GLU:OE1	6:A:601:HOH:O	2.18	0.56
1:B:348:ARG:HD3	2:B:501:HEM:C4A	2.41	0.56
1:B:336:GLU:O	1:B:337:LEU:HB2	2.06	0.56
1:A:392:GLU:OE1	6:A:602:HOH:O	2.19	0.53
1:A:265:TYR:CD1	1:A:428:GLN:HG2	2.44	0.53
2:A:501:HEM:HBC2	2:A:501:HEM:HMC1	1.91	0.53
1:A:126:HIS:HB2	6:A:671:HOH:O	2.08	0.52
1:A:348:ARG:HD3	2:A:501:HEM:C1D	2.45	0.52
1:B:34[B]:GLU:OE2	6:B:602:HOH:O	2.18	0.51
1:A:336:GLU:O	1:A:337:LEU:HB2	2.10	0.50
2:B:501:HEM:HMB2	2:B:501:HEM:HBB2	1.93	0.49
1:B:427:ARG:CZ	1:B:429:ARG:HD2	2.44	0.48
1:B:298:LEU:C	1:B:298:LEU:HD23	2.37	0.45
2:B:501:HEM:HBB2	2:B:501:HEM:CMB	2.47	0.44
1:B:124:PRO:HA	1:B:127:TRP:CD1	2.52	0.44
3:A:502:OH:O	3:A:503:OH:O	2.36	0.43
1:B:196:ILE:HD11	1:B:347:ILE:HD11	2.00	0.43
1:A:265:TYR:HD1	1:A:428:GLN:HG2	1.83	0.42
1:A:41:GLY:HA3	1:A:175:PHE:CZ	2.55	0.42
1:B:175:PHE:CD1	1:B:351:THR:HB	2.55	0.42
1:A:37:GLU:OE2	1:A:188:LYS:NZ	2.54	0.41
1:B:446:PHE:O	1:B:448:PRO:HD3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:127:TRP:CD2	1:A:441:GLY:HA2	2.56	0.41
1:A:124:PRO:HA	1:A:127:TRP:CD1	2.56	0.40
1:B:127:TRP:CD2	1:B:441:GLY:HA2	2.57	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	445/445 (100%)	436 (98%)	7 (2%)	2 (0%)	34 13
1	B	446/445 (100%)	437 (98%)	9 (2%)	0	100 100
All	All	891/890 (100%)	873 (98%)	16 (2%)	2 (0%)	47 23

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	338	LEU
1	A	337	LEU

### 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	368/366 (100%)	359 (98%)	9 (2%)	49 19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	369/366 (101%)	366 (99%)	3 (1%)	81	65
All	All	737/732 (101%)	725 (98%)	12 (2%)	65	35

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	148[A]	GLU
1	A	148[B]	GLU
1	A	165	LYS
1	A	379	SER
1	A	391	LYS
1	A	399	PHE
1	A	427	ARG
1	A	428	GLN
1	A	460	LYS
1	B	73	ASP
1	B	379	SER
1	B	399	PHE

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](#)

Of 10 ligands modelled in this entry, 4 are modelled with single atom and 4 are monoatomic - leaving 2 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
2	HEM	A	501	3,1	41,50,50	1.61	7 (17%)	45,82,82	1.39	5 (11%)
2	HEM	B	501	3,1	41,50,50	1.48	6 (14%)	45,82,82	1.40	9 (20%)

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
2	HEM	A	501	3,1	-	5/12/54/54	-
2	HEM	B	501	3,1	-	4/12/54/54	-

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	HEM	C3C-C2C	-4.47	1.34	1.40
2	A	501	HEM	C3C-C2C	-4.29	1.34	1.40
2	A	501	HEM	C3C-CAC	3.45	1.54	1.47
2	A	501	HEM	CAB-C3B	3.27	1.56	1.47
2	B	501	HEM	C3C-CAC	3.14	1.54	1.47
2	A	501	HEM	CAA-C2A	2.76	1.56	1.52
2	B	501	HEM	CAA-C2A	2.64	1.55	1.52
2	A	501	HEM	C2C-C1C	2.36	1.47	1.42
2	B	501	HEM	CAB-C3B	2.34	1.53	1.47
2	A	501	HEM	CAD-C3D	2.31	1.57	1.51
2	B	501	HEM	CMC-C2C	2.23	1.56	1.51
2	B	501	HEM	CMB-C2B	2.20	1.55	1.50
2	A	501	HEM	CMC-C2C	2.11	1.56	1.51

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	HEM	C4B-CHC-C1C	4.43	128.41	122.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	HEM	C4A-C3A-C2A	3.82	109.65	107.00
2	B	501	HEM	CHC-C4B-NB	3.64	128.38	124.43
2	A	501	HEM	CMA-C3A-C4A	-2.70	124.32	128.46
2	B	501	HEM	CMD-C2D-C1D	-2.62	121.04	125.04
2	B	501	HEM	CMC-C2C-C3C	2.56	129.47	124.68
2	A	501	HEM	C1B-NB-C4B	2.44	107.59	105.07
2	B	501	HEM	C2C-C3C-C4C	2.24	108.46	106.90
2	B	501	HEM	O2D-CGD-CBD	2.23	121.21	114.03
2	B	501	HEM	C4C-CHD-C1D	2.23	125.50	122.56
2	B	501	HEM	CMA-C3A-C4A	-2.17	125.14	128.46
2	B	501	HEM	C4B-CHC-C1C	2.09	125.32	122.56
2	B	501	HEM	O1D-CGD-CBD	-2.09	116.36	123.08
2	A	501	HEM	C4C-CHD-C1D	2.05	125.26	122.56

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	HEM	CAD-CBD-CGD-O1D
2	A	501	HEM	CAD-CBD-CGD-O2D
2	B	501	HEM	CAD-CBD-CGD-O1D
2	B	501	HEM	CAD-CBD-CGD-O2D
2	A	501	HEM	CAA-CBA-CGA-O2A
2	B	501	HEM	CAA-CBA-CGA-O2A
2	A	501	HEM	CAA-CBA-CGA-O1A
2	A	501	HEM	C4B-C3B-CAB-CBB
2	B	501	HEM	CAA-CBA-CGA-O1A

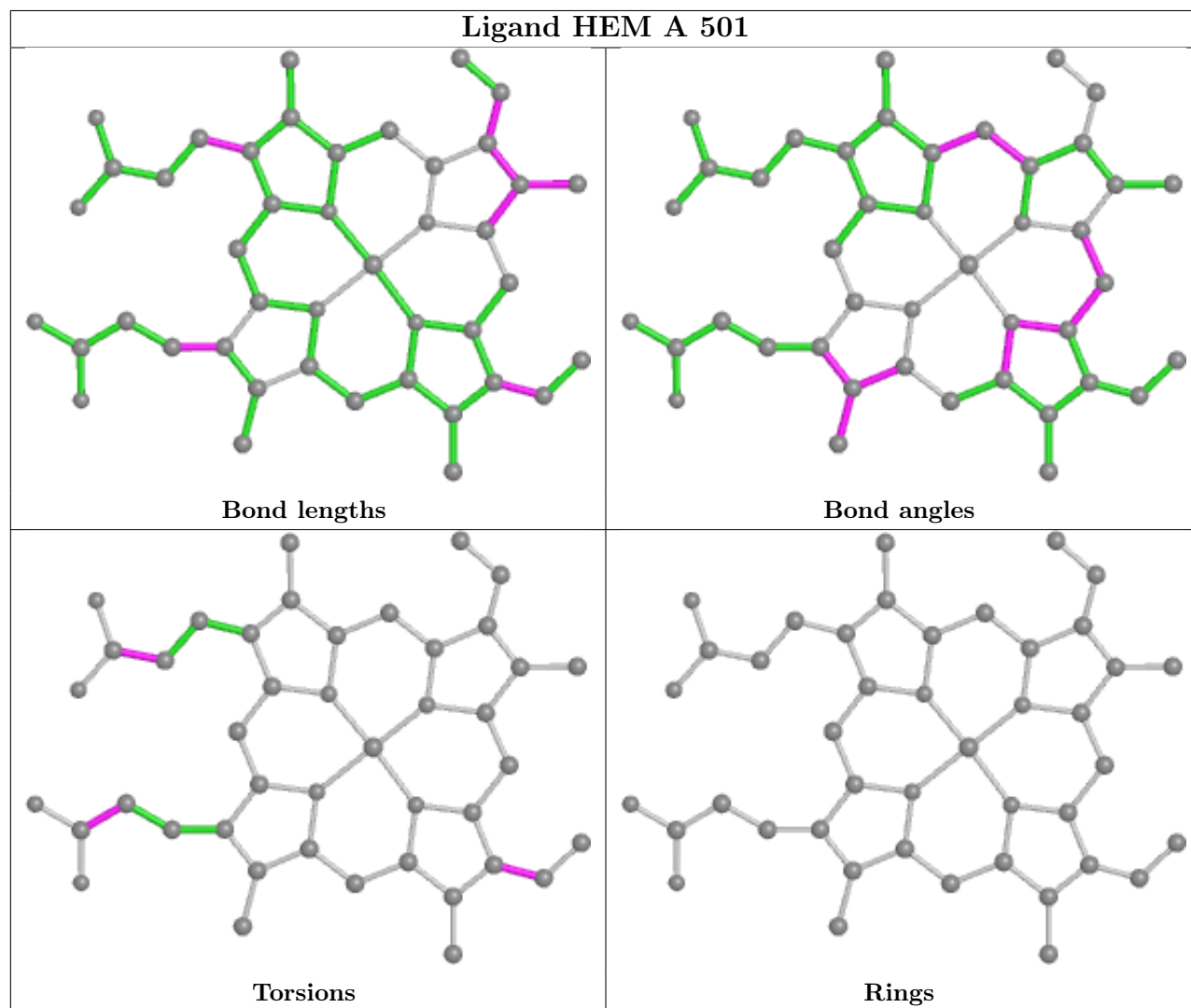
There are no ring outliers.

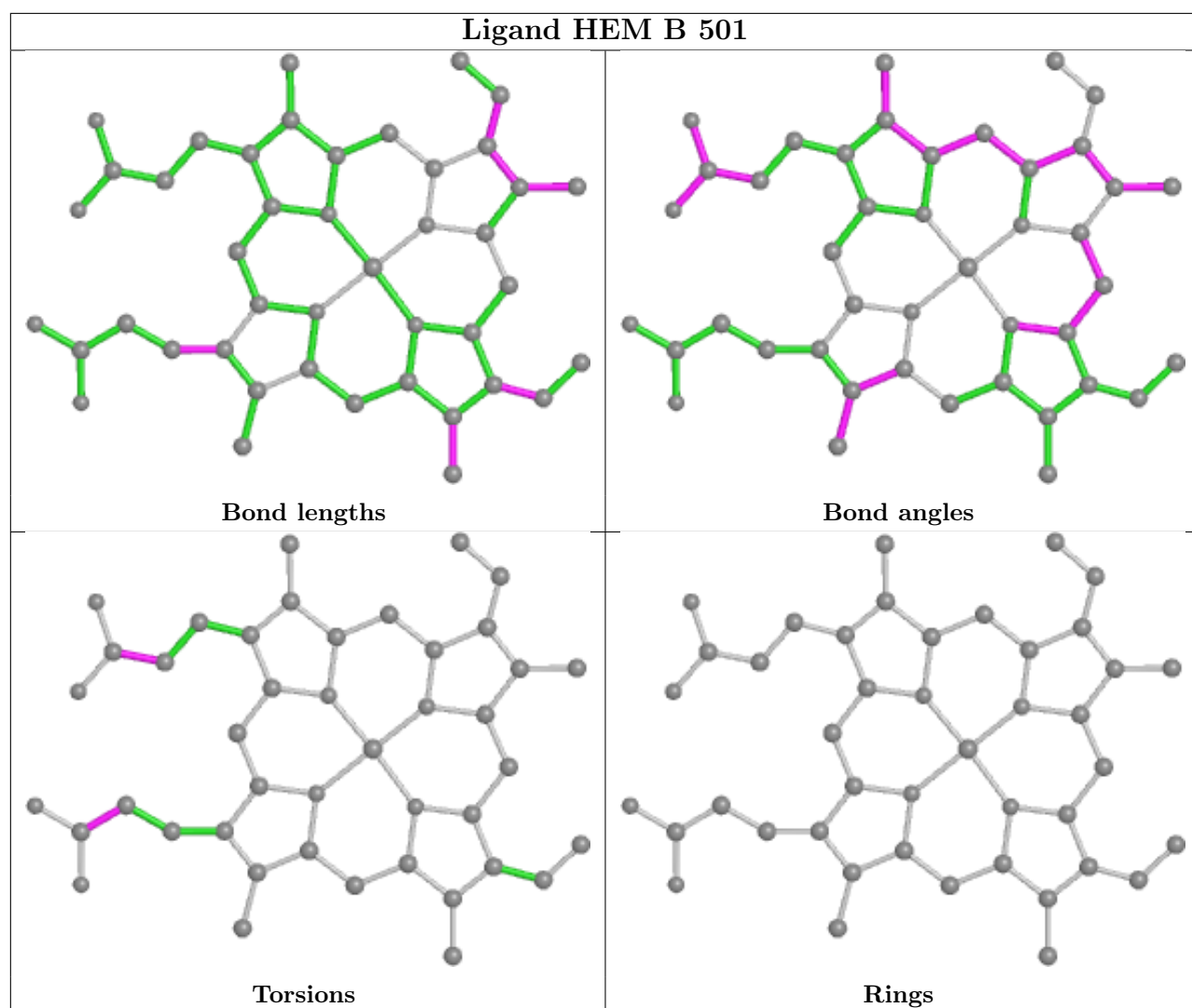
2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	HEM	3	0
2	B	501	HEM	4	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	445/445 (100%)	-0.12	8 (1%) 68 73	13, 24, 46, 72	1 (0%)
1	B	445/445 (100%)	-0.15	9 (2%) 65 70	11, 22, 40, 73	0
All	All	890/890 (100%)	-0.13	17 (1%) 66 71	11, 23, 45, 73	1 (0%)

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	338	LEU	7.6
1	B	337	LEU	7.4
1	A	338	LEU	4.8
1	A	426	VAL	3.3
1	B	424	GLU	2.9
1	B	265	TYR	2.8
1	B	425	PRO	2.8
1	A	265	TYR	2.8
1	A	336	GLU	2.6
1	B	74	VAL	2.4
1	B	426	VAL	2.4
1	A	428	GLN	2.4
1	B	429	ARG	2.3
1	A	337	LEU	2.3
1	B	311	LYS	2.3
1	A	427	ARG	2.1
1	A	334	LYS	2.1

### 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

There are no monosaccharides in this entry.

### 6.4 Ligands

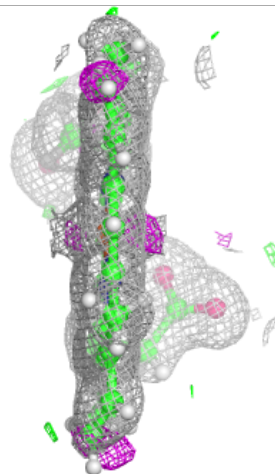
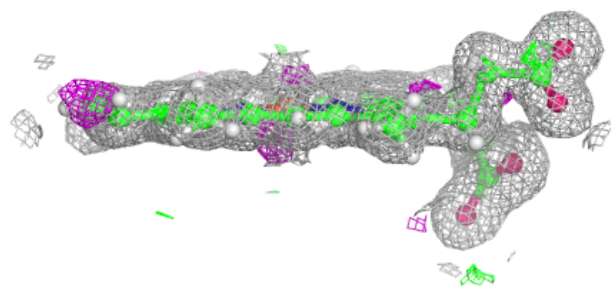
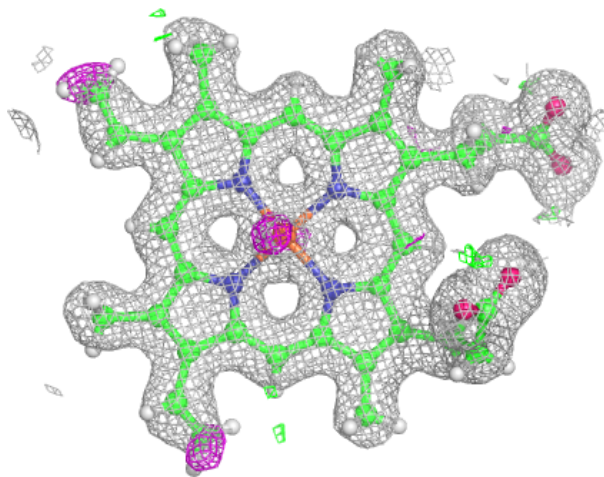
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

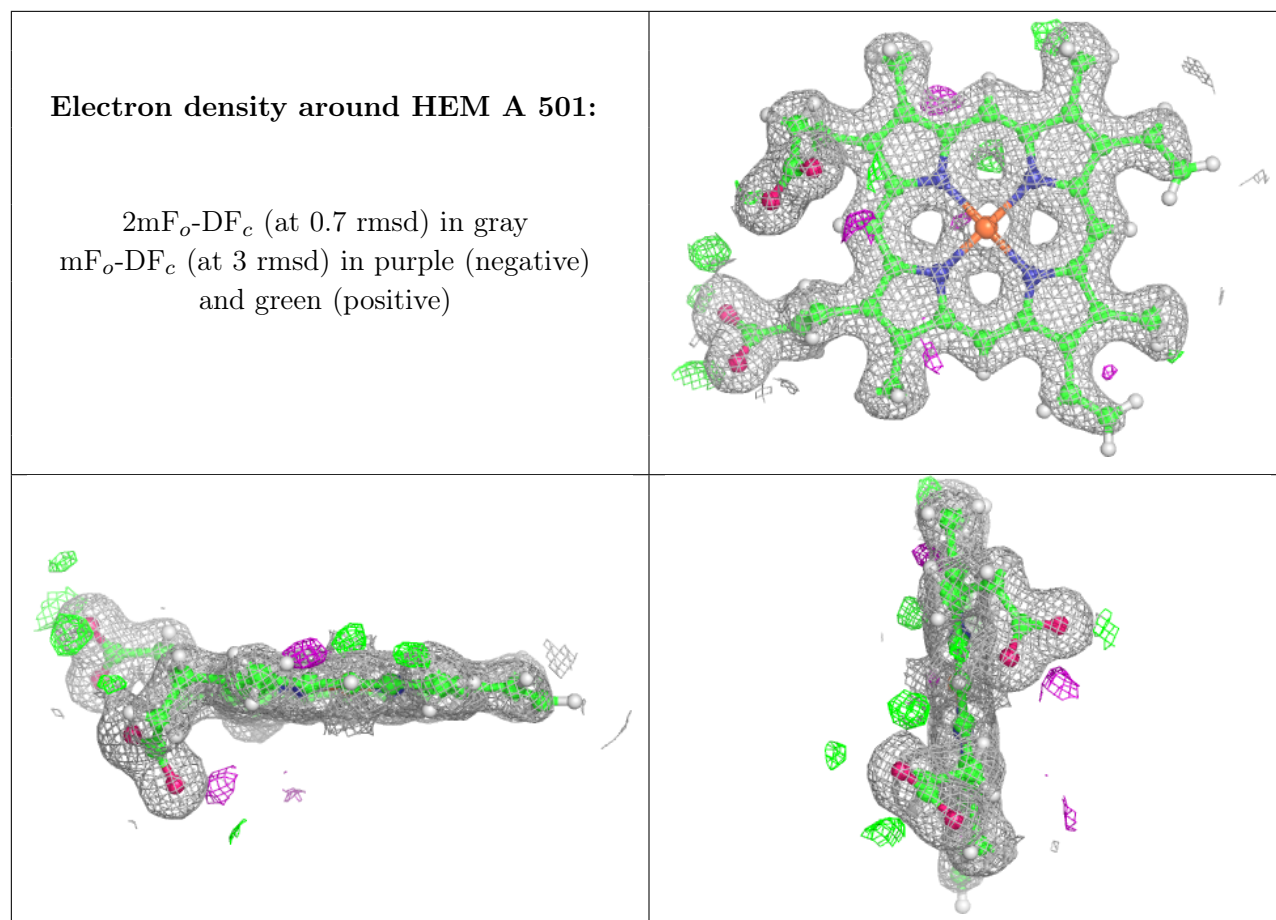
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	OH	B	502	1/1	0.91	0.11	19,19,19,19	0
3	OH	B	503	1/1	0.91	0.12	28,28,28,28	0
3	OH	A	502	1/1	0.97	0.07	20,20,20,20	0
3	OH	A	503	1/1	0.97	0.07	26,26,26,26	0
5	CA	A	505	1/1	0.98	0.06	21,21,21,21	0
2	HEM	B	501	43/43	0.99	0.08	13,18,24,28	0
4	CL	A	504	1/1	0.99	0.06	22,22,22,22	0
4	CL	B	504	1/1	0.99	0.05	25,25,25,25	0
2	HEM	A	501	43/43	0.99	0.07	13,19,22,23	6
5	CA	B	505	1/1	1.00	0.07	17,17,17,17	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 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.