

Full wwPDB X-ray Structure Validation Report (i)

Mar 25, 2024 – 03:15 pm GMT

PDB ID : 8QZE

Title: Heme-domain BM3 variant 21B3 F87V-A328F

Authors: Opperman, D.J.; Ebrecht, A.C.; Aschenbrenner, J.C.

Deposited on : 2023-10-27

Resolution : 1.87 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
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (1)) 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)

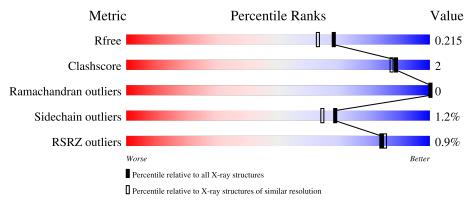
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$

The reported resolution of this entry is 1.87 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	Similar resolution $(\# \text{Entries, resolution range}(\text{\AA}))$
R_{free}	130704	9470 (1.90-1.86)
Clashscore	141614	10282 (1.90-1.86)
Ramachandran outliers	138981	10152 (1.90-1.86)
Sidechain outliers	138945	10152 (1.90-1.86)
RSRZ outliers	127900	9303 (1.90-1.86)

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 >=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 <=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	466	91%	6%	-
1	В	466	94%	•	-



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 7725 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 Bifunctional cytochrome P450/NADPH-P450 reductase.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	454	Total 3679	C 2350	N 626	O 687	S 16	0	2	0
1	В	454	Total 3674	C 2346	N 625	O 687	S 16	0	1	0

There are 26 discrepancies between the modelled and reference sequences:

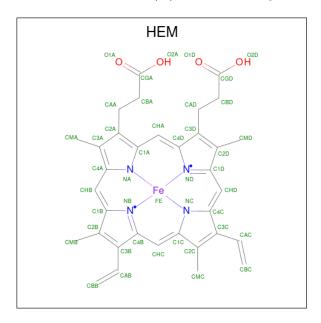
Chain	Residue	Modelled	Actual	Comment	Reference
A	58	VAL	ILE	engineered mutation	UNP P14779
A	87	VAL	PHE	engineered mutation	UNP P14779
A	100	ARG	HIS	engineered mutation	UNP P14779
A	107	LEU	PHE	engineered mutation	UNP P14779
A	135	SER	ALA	engineered mutation	UNP P14779
A	145	VAL	MET	engineered mutation	UNP P14779
A	239	HIS	ASN	engineered mutation	UNP P14779
A	274	THR	SER	engineered mutation	UNP P14779
A	328	PHE	ALA	engineered mutation	UNP P14779
A	434	GLU	LYS	engineered mutation	UNP P14779
A	446	ILE	VAL	engineered mutation	UNP P14779
A	464	LEU	-	expression tag	UNP P14779
A	465	GLU	-	expression tag	UNP P14779
В	58	VAL	ILE	engineered mutation	UNP P14779
В	87	VAL	PHE	engineered mutation	UNP P14779
В	100	ARG	HIS	engineered mutation	UNP P14779
В	107	LEU	PHE	engineered mutation	UNP P14779
В	135	SER	ALA	engineered mutation	UNP P14779
В	145	VAL	MET	engineered mutation	UNP P14779
В	239	HIS	ASN	engineered mutation	UNP P14779
В	274	THR	SER	engineered mutation	UNP P14779
В	328	PHE	ALA	engineered mutation	UNP P14779
В	434	GLU	LYS	engineered mutation	UNP P14779
В	446	ILE	VAL	engineered mutation	UNP P14779
В	464	LEU	-	expression tag	UNP P14779



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Chain	Residue	Modelled	Actual	Comment	Reference
В	465	GLU	-	expression tag	UNP P14779

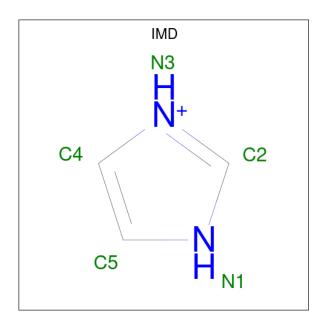
• Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
2	Δ	1	Total	С	Fe	N	О	0	0
	11	1	43	34	1	4	4		U
2	D	1	Total	С	Fe	N	Ο	0	0
	Б	1	43	34	1	4	4	U	U

• Molecule 3 is IMIDAZOLE (three-letter code: IMD) (formula: $C_3H_5N_2$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N 5 3 2	0	0
3	В	1	Total C N 5 3 2	0	0

• Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

• Molecule 5 is water.



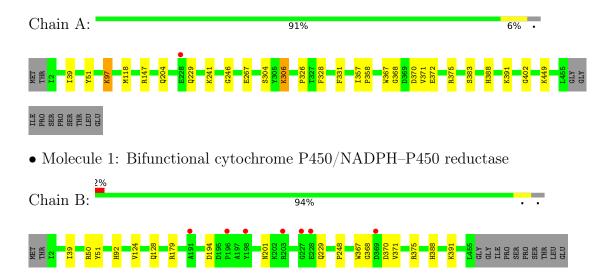
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	164	Total O 164 164	0	0
5	В	106	Total O 106 106	0	0



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: Bifunctional cytochrome P450/NADPH-P450 reductase





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants	125.82Å 127.20Å 64.44Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	89.61 - 1.87	Depositor
rtesolution (A)	89.45 - 1.87	EDS
% Data completeness	100.0 (89.61-1.87)	Depositor
(in resolution range)	99.9 (89.45-1.87)	EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.61 (at 1.87Å)	Xtriage
Refinement program	REFMAC 5.8.0419	Depositor
Ρ. Р.	0.170 , 0.204	Depositor
R, R_{free}	0.181 , 0.215	DCC
R_{free} test set	4364 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	33.5	Xtriage
Anisotropy	0.290	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.38, 45.3	EDS
L-test for twinning ²	$< L > = 0.48, < L^2> = 0.31$	Xtriage
Estimated twinning fraction	0.015 for k,h,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7725	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.70% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

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, IMD

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		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.45	0/3767	0.84	0/5095	
1	В	0.42	0/3758	0.81	2/5083~(0.0%)	
All	All	0.44	0/7525	0.82	2/10178 (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	В	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\mathrm{Ideal}(^{o})$
1	В	50	ARG	NE-CZ-NH2	-6.14	117.23	120.30
1	В	50	ARG	NE-CZ-NH1	5.83	123.22	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	В	179	ARG	Sidechain

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)	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
1	A	3679	0	3654	18	0
1	В	3674	0	3648	10	0
2	A	43	0	30	2	0
2	В	43	0	30	0	0
3	A	5	0	4	0	0
3	В	5	0	4	0	0
4	A	6	0	8	2	0
5	A	164	0	0	3	0
5	В	106	0	0	0	0
All	All	7725	0	7378	28	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 (28) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance } (\text{\AA}) \end{array}$	Clash overlap (Å)
1:A:388:HIS:HA	1:A:391:LYS:HD3	1.79	0.65
1:A:241:LYS:HE2	1:A:246:GLY:O	2.02	0.59
1:A:372:GLU:OE2	5:A:601:HOH:O	2.16	0.58
1:B:388:HIS:HA	1:B:391:LYS:HD3	1.85	0.58
1:B:368:GLY:O	1:B:371:VAL:HG13	2.06	0.56
1:A:118:MET:HE2	5:A:623:HOH:O	2.06	0.56
1:B:367:TRP:HB2	1:B:371:VAL:HG12	1.88	0.56
1:B:201:ASN:HD22	1:B:201:ASN:N	2.04	0.55
1:A:306:LYS:HE2	1:A:306:LYS:H	1.73	0.54
1:A:383:SER:HG	1:B:92:HIS:CE1	2.27	0.53
1:A:147:ARG:HG2	4:A:503:GOL:C1	2.39	0.53
1:A:97:LYS:HB2	5:A:652:HOH:O	2.09	0.52
1:A:304:SER:HB2	1:A:306:LYS:HE3	1.91	0.51
1:A:147:ARG:HG2	4:A:503:GOL:H12	1.94	0.48
1:A:370:ASP:OD2	1:A:375:ARG:NH1	2.44	0.46
1:A:367:TRP:HB2	1:A:371:VAL:HG12	1.98	0.45
1:B:370:ASP:OD2	1:B:375:ARG:NH1	2.47	0.45
1:A:357:ILE:N	1:A:358:PRO:CD	2.80	0.44
2:A:501:HEM:HBB2	2:A:501:HEM:HMB2	2.00	0.44
1:A:368:GLY:O	1:A:371:VAL:HG13	2.19	0.42
1:A:331:PHE:HD1	1:A:357:ILE:HD11	1.84	0.42
1:A:39:ILE:HA	1:A:51:TYR:O	2.19	0.42



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	.,	10	1

Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${ m distance}({ m \AA})$	overlap (Å)
1:B:124:VAL:O	1:B:128:GLN:HG3	2.18	0.42
1:B:388:HIS:HD2	1:B:391:LYS:NZ	2.18	0.42
1:B:39:ILE:HA	1:B:51:TYR:O	2.21	0.41
1:A:326:PRO:HG3	1:A:357:ILE:HG22	2.03	0.41
1:B:201:ASN:N	1:B:201:ASN:ND2	2.68	0.41
1:A:402:GLY:HA3	2:A:501:HEM:C3C	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	Perce	\mathbf{ntiles}
1	A	454/466 (97%)	438 (96%)	16 (4%)	0	100	100
1	В	453/466 (97%)	442 (98%)	11 (2%)	0	100	100
All	All	907/932 (97%)	880 (97%)	27 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	402/410 (98%)	395 (98%)	7 (2%)	60 54
1	В	401/410 (98%)	398 (99%)	3 (1%)	84 83



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Mol	Chain	Analysed Rotameric		Outliers	Percentiles
All	All	803/820 (98%)	793 (99%)	10 (1%)	69 67

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	97	LYS
1	A	204	GLN
1	A	229	GLN
1	A	267	GLU
1	A	306	LYS
1	A	328	PHE
1	A	449	LYS
1	В	194	ASP
1	В	229	GLN
1	В	248	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	95	ASN
1	A	163	ASN
1	A	169	GLN
1	A	186	ASN
1	В	95	ASN
1	В	163	ASN
1	В	189	GLN
1	В	192	ASN
1	В	229	GLN
1	В	388	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)

5 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	Chain	Chain	Chain	Chain	Des	Res Link	Вс	Bond lengths			Bond angles		
MIOI	Type	Chain	nes	Res	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2			
4	GOL	A	503	-	5,5,5	0.23	0	5,5,5	0.83	0					
2	HEM	A	501	1,3	41,50,50	1.67	7 (17%)	45,82,82	1.95	11 (24%)					
3	IMD	В	501	2	3,5,5	0.17	0	4,5,5	0.64	0					
3	IMD	A	502	2	3,5,5	0.17	0	4,5,5	0.57	0					
2	HEM	В	500	1,3	41,50,50	1.43	7 (17%)	45,82,82	1.98	12 (26%)					

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	503	-	-	2/4/4/4	-
2	HEM	A	501	1,3	-	2/12/54/54	-
3	IMD	В	501	2	-	-	0/1/1/1
3	IMD	A	502	2	-	-	0/1/1/1
2	HEM	В	500	1,3	-	0/12/54/54	-

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\mathring{\mathrm{A}})$	Ideal(A)
2	A	501	HEM	C1B-NB	-5.35	1.31	1.40
2	В	500	HEM	C1B-NB	-4.77	1.32	1.40
2	A	501	HEM	C4D-ND	-3.57	1.34	1.40
2	A	501	HEM	C4B-NB	-2.80	1.33	1.38



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Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(ext{\AA})$
2	В	500	HEM	FE-NB	2.60	2.09	1.96
2	A	501	HEM	O2A-CGA	-2.49	1.22	1.30
2	В	500	HEM	C3B-C4B	2.45	1.49	1.44
2	A	501	HEM	C1A-NA	2.39	1.41	1.36
2	В	500	HEM	C4B-NB	-2.24	1.34	1.38
2	В	500	HEM	C1D-ND	-2.21	1.34	1.38
2	A	501	HEM	CHB-C1B	2.18	1.40	1.35
2	В	500	HEM	CHB-C1B	2.16	1.40	1.35
2	В	500	HEM	CHA-C4D	2.09	1.40	1.35
2	A	501	HEM	CHC-C4B	-2.09	1.35	1.41

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
2	A	501	HEM	CHD-C1D-ND	5.19	130.07	124.43
2	В	500	HEM	C1B-NB-C4B	4.64	109.87	105.07
2	A	501	HEM	C1B-NB-C4B	4.49	109.71	105.07
2	В	500	HEM	CHD-C1D-ND	4.42	129.24	124.43
2	В	500	HEM	CHC-C4B-NB	4.26	129.06	124.43
2	A	501	HEM	C4B-C3B-C2B	-3.88	104.03	107.11
2	A	501	HEM	CHD-C1D-C2D	-3.72	119.17	124.98
2	В	500	HEM	C4B-CHC-C1C	3.56	127.26	122.56
2	A	501	HEM	CHC-C4B-NB	3.38	128.11	124.43
2	В	500	HEM	CMA-C3A-C4A	-3.24	123.49	128.46
2	A	501	HEM	C4A-C3A-C2A	3.23	109.25	107.00
2	В	500	HEM	C4B-C3B-C2B	-3.22	104.56	107.11
2	В	500	HEM	CAD-C3D-C4D	2.93	129.77	124.66
2	A	501	HEM	C4B-CHC-C1C	2.92	126.41	122.56
2	A	501	HEM	CAD-C3D-C4D	2.71	129.39	124.66
2	В	500	HEM	CHA-C4D-ND	2.69	127.70	124.38
2	В	500	HEM	O2D-CGD-CBD	2.56	122.25	114.03
2	A	501	HEM	O2A-CGA-CBA	2.50	122.06	114.03
2	A	501	HEM	CMC-C2C-C3C	2.48	129.31	124.68
2	В	500	HEM	CHA-C4D-C3D	-2.35	120.92	125.33
2	В	500	HEM	CBA-CAA-C2A	-2.33	108.65	112.62
2	В	500	HEM	CHD-C1D-C2D	-2.27	121.43	124.98
2	A	501	HEM	C3B-C2B-C1B	2.13	108.06	106.49

There are no chirality outliers.

All (4) torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
4	A	503	GOL	O2-C2-C3-O3
4	A	503	GOL	C1-C2-C3-O3
2	A	501	HEM	CAD-CBD-CGD-O2D
2	A	501	HEM	CAD-CBD-CGD-O1D

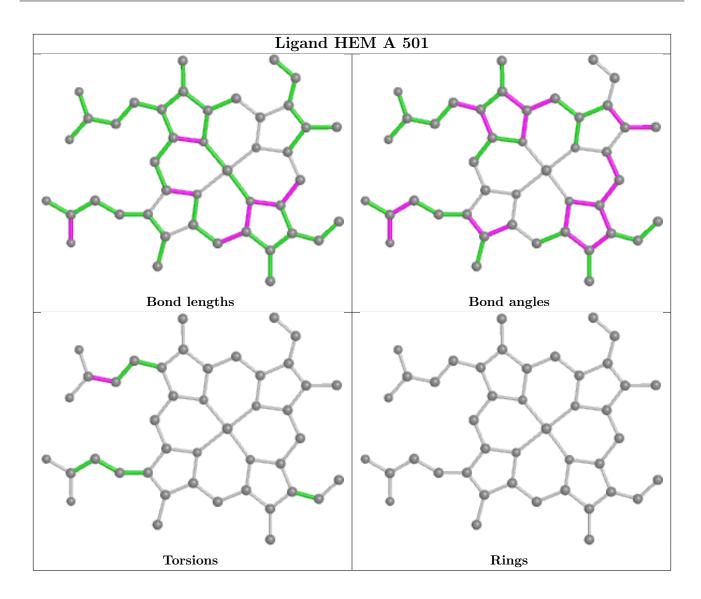
There are no ring outliers.

2 monomers are involved in 4 short contacts:

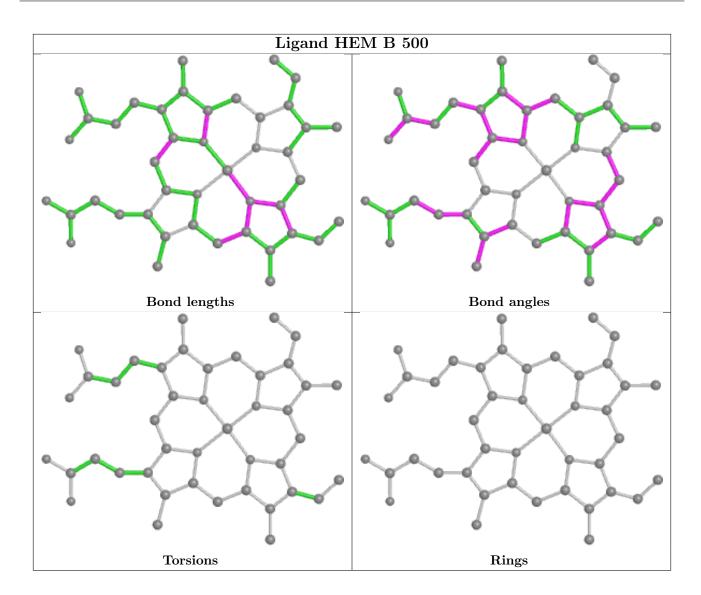
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	503	GOL	2	0
2	A	501	HEM	2	0

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 then 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^{th} 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	$\langle { m RSRZ} \rangle$	$\# \mathbf{RSRZ} > 1$	2	$\mathbf{OWAB}(\mathrm{\AA}^2)$	Q < 0.9
1	A	454/466 (97%)	-0.25	1 (0%) 95	95	26, 35, 56, 88	0
1	В	$454/466 \ (97\%)$	-0.18	7 (1%) 73	75	27, 41, 71, 110	0
All	All	908/932 (97%)	-0.21	8 (0%) 84	85	26, 38, 64, 110	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	227	GLY	4.8
1	В	228	GLU	4.3
1	В	191	ALA	3.4
1	В	196	PRO	3.3
1	В	369	ASP	2.3
1	В	198	TYR	2.2
1	A	228	GLU	2.1
1	В	203	ARG	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)

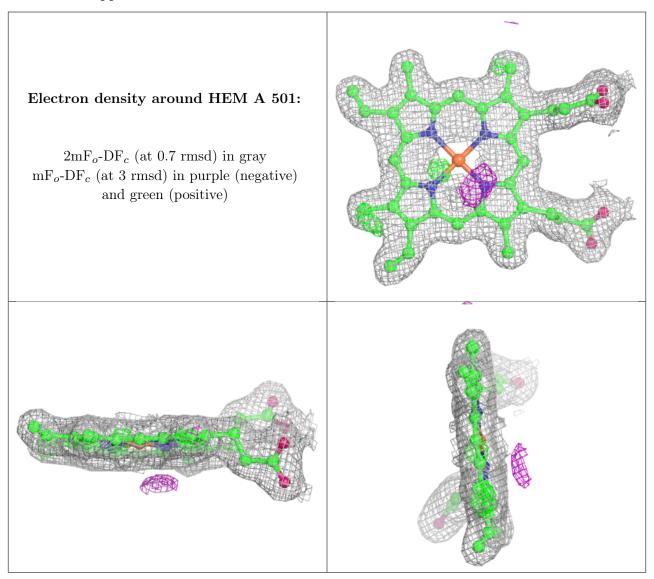
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,



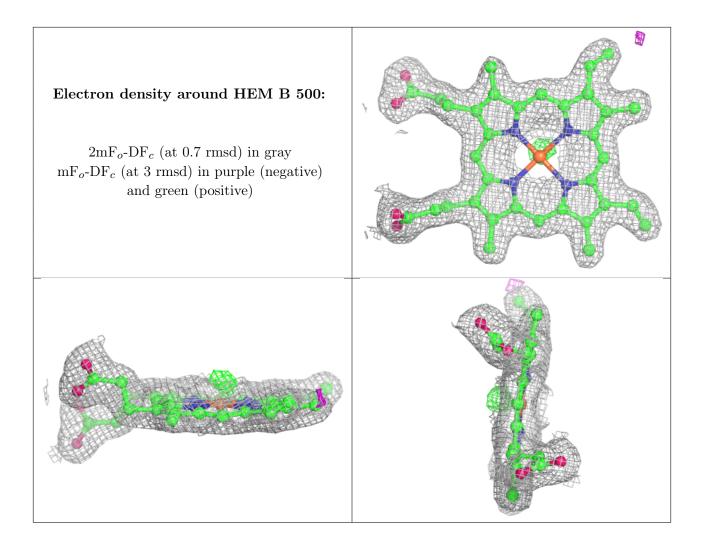
median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
4	GOL	A	503	6/6	0.93	0.15	37,39,47,48	0
3	IMD	A	502	5/5	0.95	0.11	31,33,35,35	0
2	HEM	A	501	43/43	0.99	0.10	22,26,29,31	0
3	IMD	В	501	5/5	0.99	0.07	40,41,47,48	0
2	HEM	В	500	43/43	0.99	0.09	26,30,35,37	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.







6.5 Other polymers (i)

There are no such residues in this entry.

