

Full wwPDB X-ray Structure Validation Report (i)

Mar 18, 2025 – 12:14 pm GMT

PDB ID : 9EPG

Title : DtpAa Y389F 24 fs 10 microjoules XFEL Pulse Data Collection

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Deposited on : 2024-03-18

Resolution : 1.33 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 : 3.0

buster-report : 1.1.7 (2018)

Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)

CCP4 : 9.0.003 (Gargrove)

Density-Fitness : 1.0.11

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

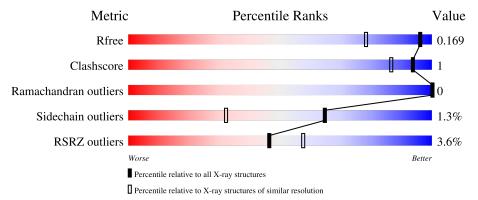
Validation Pipeline (wwPDB-VP) : 2.41

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 1.33 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	164625	1904 (1.36-1.32)
Clashscore	180529	2038 (1.36-1.32)
Ramachandran outliers	177936	2016 (1.36-1.32)
Sidechain outliers	177891	2016 (1.36-1.32)
RSRZ outliers	164620	1903 (1.36-1.32)

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	373	92%	
1	В	373	93%	



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 6234 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.

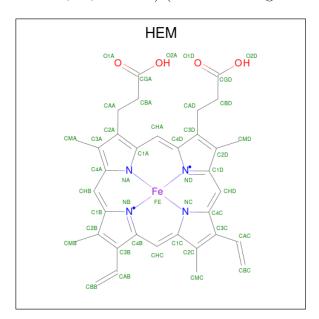
• Molecule 1 is a protein called Deferrochelatase.

	\mathbf{Mol}	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
Ī	1	Λ	362	Total	С	N	О	S	0	7	0
	1	1 A	302	2818	1776	521	516	5	0		
	1	D	363	Total	С	N	О	S	0	4	0
	1	Ъ	303	2797	1764	513	515	5	0		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	due Modelled Actual		Comment	Reference
A	389	PHE	TYR	engineered mutation	UNP A0A7U9DT46
В	389	PHE	TYR	engineered mutation	UNP A0A7U9DT46

• Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: C₃₄H₃₂FeN₄O₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues		At	oms			ZeroOcc	AltConf
2	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0



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

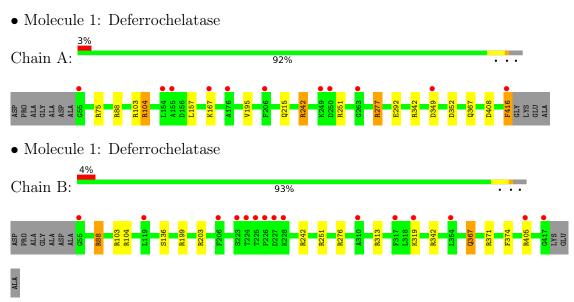
• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	250	Total O 250 250	0	0
3	В	282	Total O 283 283	0	1



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.





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	72.72Å 68.20Å 74.60Å	Donogitor
a, b, c, α , β , γ	90.00° 105.60° 90.00°	Depositor
Resolution (Å)	35.05 - 1.33	Depositor
Resolution (A)	35.05 - 1.33	EDS
% Data completeness	100.0 (35.05-1.33)	Depositor
(in resolution range)	100.0 (35.05-1.33)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.29 (at 1.33Å)	Xtriage
Refinement program	REFMAC 5.8.0419	Depositor
D.D.	0.153 , 0.169	Depositor
R, R_{free}	0.153 , 0.169	DCC
R_{free} test set	7962 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	17.4	Xtriage
Anisotropy	0.028	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.39, 34.4	EDS
L-test for twinning ²	$< L > = 0.49, < L^2> = 0.32$	Xtriage
Estimated twinning fraction	0.016 for l,-k,h	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6234	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.69% 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

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		RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.59	0/2907	0.97	9/3941 (0.2%)	
1	В	0.60	0/2877	1.02	$12/3902 \ (0.3\%)$	
All	All	0.59	0/5784	1.00	21/7843 (0.3%)	

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 maintenain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	9
1	В	0	5
All	All	0	14

There are no bond length outliers.

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	В	251	ARG	NE-CZ-NH2	-10.14	115.23	120.30
1	В	251	ARG	NE-CZ-NH1	9.65	125.12	120.30
1	В	88[A]	ARG	NE-CZ-NH2	-8.60	116.00	120.30
1	В	88[B]	ARG	NE-CZ-NH2	-8.60	116.00	120.30
1	В	371	ARG	NE-CZ-NH1	-7.87	116.37	120.30
1	В	276	ARG	NE-CZ-NH2	-7.71	116.44	120.30
1	В	251	ARG	CD-NE-CZ	7.68	134.35	123.60
1	В	88[A]	ARG	CD-NE-CZ	7.60	134.24	123.60
1	В	88[B]	ARG	CD-NE-CZ	7.60	134.24	123.60
1	A	251	ARG	NE-CZ-NH2	-7.18	116.71	120.30
1	A	242	ARG	NE-CZ-NH1	-6.99	116.80	120.30
1	A	251	ARG	NE-CZ-NH1	6.67	123.63	120.30



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Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	416	PHE	CA-C-O	-5.84	107.83	120.10
1	A	342	ARG	NE-CZ-NH1	5.62	123.11	120.30
1	В	203	ARG	NE-CZ-NH2	-5.60	117.50	120.30
1	A	103	ARG	NE-CZ-NH2	-5.53	117.54	120.30
1	A	104[A]	ARG	NE-CZ-NH2	-5.34	117.63	120.30
1	A	104[B]	ARG	NE-CZ-NH2	-5.34	117.63	120.30
1	A	352	ASP	CB-CG-OD2	-5.27	113.56	118.30
1	В	342	ARG	NE-CZ-NH1	5.21	122.90	120.30
1	В	103	ARG	CG-CD-NE	-5.16	100.97	111.80

There are no chirality outliers.

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	\mathbf{Group}	
1	A	104[A]	ARG	Sidechain	
1	A	104[B]	ARG	Sidechain	
1	A	242	ARG	Sidechain	
1	A	277[A]	ARG	Sidechain	
1	A	277[B]	ARG	Sidechain	
1	A	75[A]	ARG	Sidechain	
1	A	75[B]	ARG	Sidechain	
1	A	88[A]	ARG	Sidechain	
1	A	88[B]	ARG	Sidechain	
1	В	104	ARG	Sidechain	
1	В	242	ARG	Sidechain	
1	В	313	ARG	Sidechain	
1	В	88[A]	ARG	Sidechain	
1	В	88[B]	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)	H(added)	Clashes	Symm-Clashes
1	A	2818	0	2778	5	0
1	В	2797	0	2747	7	0
2	A	43	0	30	2	0
2	В	43	0	30	1	0



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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	250	0	0	3	0
3	В	283	0	0	3	0
All	All	6234	0	5585	15	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 1.

All (15) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
	120022 2	$\operatorname{distance}\left(\mathrm{\AA}\right)$	overlap (Å)
1:B:405:ARG:NH1	3:B:601:HOH:O	1.95	0.98
1:A:292[A]:GLU:HG3	3:A:778:HOH:O	1.89	0.72
1:A:277[A]:ARG:NH2	1:A:349:ASP:OD2	2.36	0.59
1:B:367:GLN:HE21	1:B:374:PHE:H	1.52	0.56
1:A:416:PHE:C	3:A:603:HOH:O	2.47	0.53
1:B:367:GLN:HE22	1:B:374:PHE:HB2	1.75	0.51
1:A:215:GLN:OE1	1:A:277[B]:ARG:HD3	2.10	0.50
1:B:367:GLN:NE2	1:B:374:PHE:H	2.10	0.48
1:A:195:VAL:HG23	3:A:792:HOH:O	2.16	0.46
1:B:136[B]:SER:OG	3:B:602:HOH:O	2.17	0.46
1:B:405:ARG:NH1	3:B:607:HOH:O	2.49	0.44
2:A:501:HEM:HBB2	2:A:501:HEM:HMB2	2.00	0.43
1:B:405:ARG:HD3	1:B:405:ARG:HA	1.83	0.41
2:B:501:HEM:HBB2	2:B:501:HEM:HMB2	2.03	0.41
2:A:501:HEM:HBB2	2:A:501:HEM:CMB	2.52	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	Percentiles	
1	A	367/373~(98%)	360 (98%)	7 (2%)	0	100	100	
1	В	365/373~(98%)	360 (99%)	5 (1%)	0	100	100	
All	All	732/746 (98%)	720 (98%)	12 (2%)	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	284/282 (101%)	280 (99%)	4 (1%)	62 30	
1	В	281/282 (100%)	278 (99%)	3 (1%)	70 39	
All	All	565/564 (100%)	558 (99%)	7 (1%)	65 36	

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	157	LEU
1	A	167	LYS
1	A	367	GLN
1	A	408	ASP
1	В	199	ARG
1	В	319	LYS
1	В	367	GLN

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

Mol	Chain	Res	Type
1	В	367	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

2 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	Trme	oe Chain	Dag	Link	Bond lengths			Bond angles		
MIOI	Type	Chain	Res		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HEM	В	501	1,3	41,50,50	1.48	6 (14%)	45,82,82	1.64	8 (17%)
2	HEM	A	501	1,3	41,50,50	1.39	5 (12%)	45,82,82	1.57	7 (15%)

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.

N	Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
	2	HEM	В	501	1,3	-	4/12/54/54	-
	2	HEM	A	501	1,3	-	4/12/54/54	-

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\mathring{A})$	Ideal(Å)
2	A	501	HEM	C1B-NB	-4.56	1.32	1.40
2	В	501	HEM	C1B-NB	-4.01	1.33	1.40
2	В	501	HEM	C3C-C2C	-3.30	1.35	1.40
2	A	501	HEM	C4D-ND	-2.76	1.35	1.40
2	В	501	HEM	O2A-CGA	-2.73	1.21	1.30
2	В	501	HEM	C4B-NB	-2.63	1.33	1.38



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Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(ext{\AA})$
2	A	501	HEM	C1A-NA	2.29	1.40	1.36
2	В	501	HEM	O2D-CGD	-2.24	1.23	1.30
2	A	501	HEM	C1D-ND	-2.24	1.34	1.38
2	В	501	HEM	C4D-ND	-2.19	1.36	1.40
2	A	501	HEM	CHB-C1B	2.15	1.40	1.35

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\mathbf{Ideal}(^o)$
2	В	501	HEM	C1B-NB-C4B	5.26	110.50	105.07
2	A	501	HEM	C1B-NB-C4B	4.68	109.91	105.07
2	В	501	HEM	C4B-CHC-C1C	3.41	127.06	122.56
2	В	501	HEM	CBA-CAA-C2A	3.33	118.31	112.62
2	A	501	HEM	CHC-C4B-NB	3.16	127.86	124.43
2	A	501	HEM	CHB-C1B-NB	3.16	128.28	124.38
2	A	501	HEM	CMA-C3A-C4A	-3.05	123.77	128.46
2	В	501	HEM	CHC-C4B-NB	2.85	127.53	124.43
2	В	501	HEM	CMC-C2C-C3C	2.71	129.76	124.68
2	A	501	HEM	CMA-C3A-C2A	2.57	129.78	124.94
2	В	501	HEM	CHA-C4D-ND	2.35	127.28	124.38
2	В	501	HEM	CMA-C3A-C2A	2.26	129.21	124.94
2	В	501	HEM	CMA-C3A-C4A	-2.26	124.98	128.46
2	A	501	HEM	O2A-CGA-CBA	2.26	121.28	114.03
2	A	501	HEM	CAD-C3D-C4D	2.17	128.45	124.66

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	В	501	HEM	CAD-CBD-CGD-O1D
2	A	501	HEM	CAD-CBD-CGD-O2D
2	A	501	HEM	CAD-CBD-CGD-O1D
2	В	501	HEM	CAD-CBD-CGD-O2D
2	A	501	HEM	CAA-CBA-CGA-O2A
2	A	501	HEM	CAA-CBA-CGA-O1A
2	В	501	HEM	CAA-CBA-CGA-O2A
2	В	501	HEM	CAA-CBA-CGA-O1A

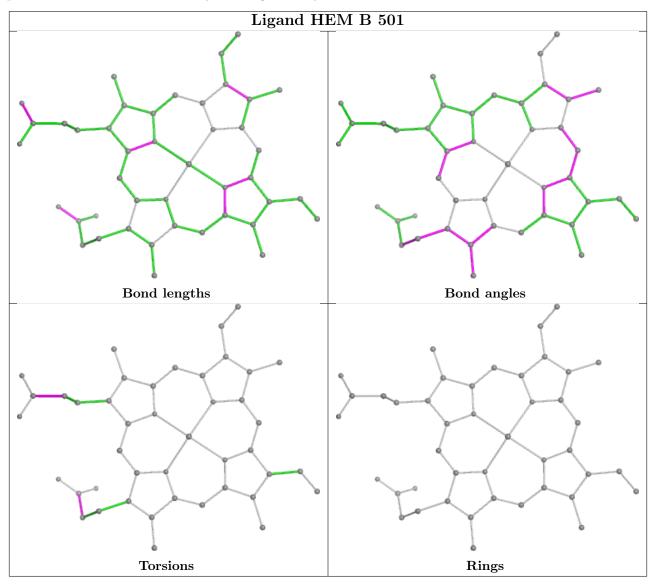
There are no ring outliers.

2 monomers are involved in 3 short contacts:

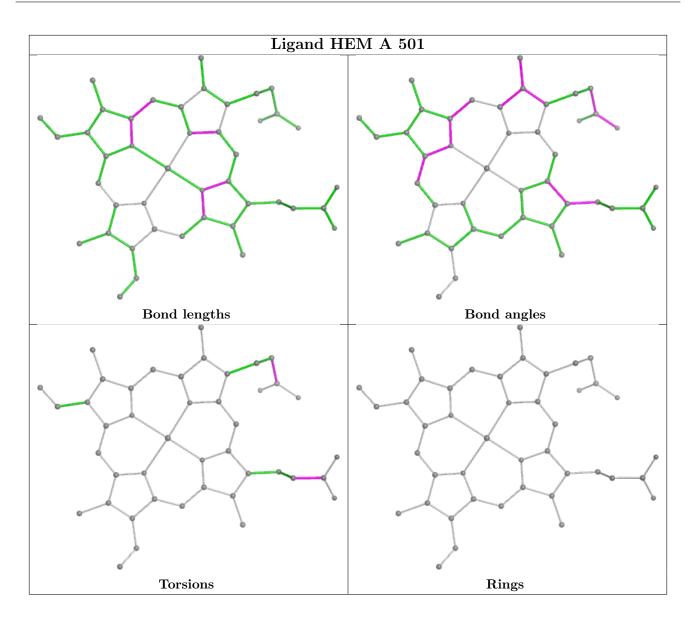


Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	501	HEM	1	0
2	A	501	HEM	2	0

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	<RSRZ $>$	$\# \mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	A	362/373~(97%)	0.29	11 (3%) 52 63	9, 18, 34, 47	7 (1%)
1	В	363/373 (97%)	0.22	15 (4%) 42 52	9, 17, 34, 50	4 (1%)
All	All	725/746 (97%)	0.25	26 (3%) 46 57	9, 17, 34, 50	11 (1%)

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	55	GLY	4.5
1	В	224	THR	3.5
1	В	354	LEU	3.3
1	A	250	ASP	3.1
1	В	417	GLY	3.1
1	В	319	LYS	3.0
1	A	176	ALA	3.0
1	В	226	PRO	3.0
1	A	206	PHE	2.9
1	В	119	LEU	2.8
1	A	416	PHE	2.8
1	В	206	PHE	2.7
1	A	349	ASP	2.6
1	В	405	ARG	2.5
1	В	228	LYS	2.5
1	В	223	SER	2.4
1	В	225	THR	2.4
1	В	227	ASP	2.4
1	A	167	LYS	2.2
1	A	155	ALA	2.2
1	A	55	GLY	2.2
1	A	154	LEU	2.1
1	A	263	GLY	2.1
1	В	317	PHE	2.1



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Mol	Chain	Res	Type	RSRZ
1	A	249	LYS	2.1
1	В	310	ALA	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.

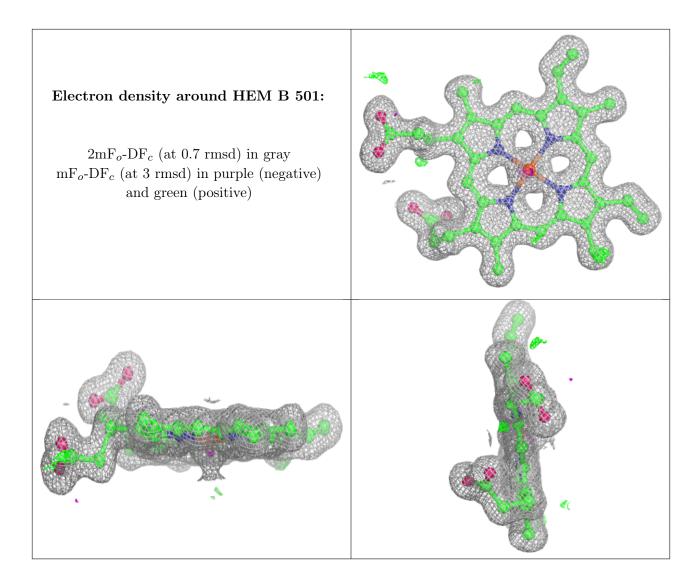
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
2	HEM	A	501	43/43	0.99	0.04	10,12,15,18	0
2	HEM	В	501	43/43	0.99	0.04	11,12,15,16	0

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 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)





6.5 Other polymers (i)

There are no such residues in this entry.

