

Full wwPDB X-ray Structure Validation Report (i)

Jan 30, 2024 - 04:44 PM EST

PDB ID	:	1G0B
Title	:	CARBONMONOXY LIGANDED EQUINE HEMOGLOBIN PH 8.5
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Deposited on		
Resolution	:	1.90 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:

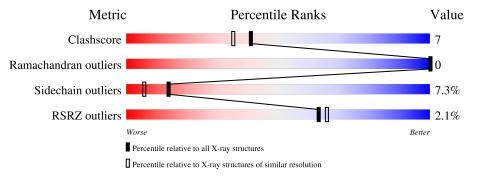
Xtriage (Phenix) EDS buster-report Percentile statistics Refmac CCP4 Ideal geometry (proteins) Ideal geometry (DNA, RNA)	:::::::::::::::::::::::::::::::::::::::	20191225.v01 (using entries in the PDB archive December 25th 2019) 5.8.0158 7.0.044 (Gargrove) Engh & Huber (2001) Parkinson et al. (1996)
Ideal geometry (DNA, RNA) Validation Pipeline (wwPDB-VP)		Parkinson et al. (1996) 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 1.90 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	А	141	83%	13%	
2	В	146	3% 82%	16%	•



1G0B

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 2365 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 HEMOGLOBIN ALPHA CHAIN.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	А	141	Total 1069	C 684	N 187	O 196	$\frac{S}{2}$	3	0	0

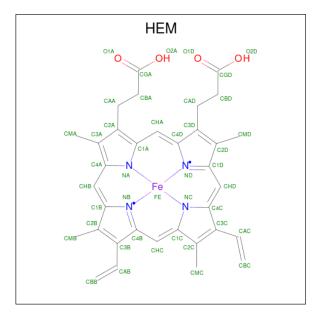
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	82	ASP	ASN	SEE REMARK 999	UNP P01958
А	85	ASN	ASP	SEE REMARK 999	UNP P01958

• Molecule 2 is a protein called HEMOGLOBIN BETA CHAIN.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	В	146	Total 1134	C 728	N 200	O 204	${S \over 2}$	11	0	0

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





Mol	Chain	Residues		Ate	oms			ZeroOcc	AltConf
2	Δ	1	Total	С	Fe	Ν	Ο	0	0
5	3 A	1	43	34	1	4	4	0	0
2	р	1	Total	С	Fe	Ν	Ο	0	0
3	D	1	43	34	1	4	4	0	0

• Molecule 4 is CARBON MONOXIDE (three-letter code: CMO) (formula: CO).

СМО	
c C-= O+ 0	

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 2 & 1 & 1 \end{array}$	0	0
4	В	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 2 & 1 & 1 \end{array}$	0	0

• Molecule 5 is water.

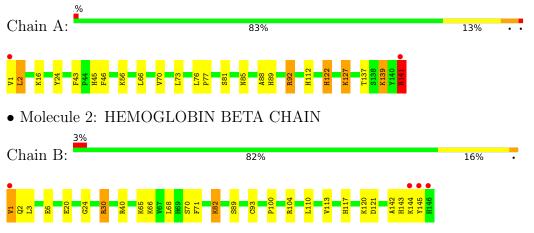
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	32	Total O 32 32	0	0
5	В	40	Total O 40 40	0	0



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: HEMOGLOBIN ALPHA CHAIN





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	108.80Å 63.20Å 54.60Å	Depositor
a, b, c, α , β , γ	90.00° 110.70° 90.00°	Depositor
Resolution (Å)	8.00 – 1.90	Depositor
Resolution (A)	33.98 - 1.90	EDS
% Data completeness	99.4 (8.00-1.90)	Depositor
(in resolution range)	95.8 (33.98-1.90)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.49 (at 1.91 \text{\AA})$	Xtriage
Refinement program	PROLSQ	Depositor
D D.	0.178 , (Not available)	Depositor
R, R_{free}	0.170 , (Not available)	DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor $(Å^2)$	20.8	Xtriage
Anisotropy	0.100	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.34,72.1	EDS
L-test for twinning ²	$ < L >=0.48, < L^2>=0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2365	wwPDB-VP
Average B, all atoms $(Å^2)$	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.89% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



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: CMO, 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	Chain Bond		Bond angles	
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.69	0/1096	1.13	3/1487~(0.2%)
2	В	0.73	0/1162	1.16	3/1572~(0.2%)
All	All	0.71	0/2258	1.15	6/3059~(0.2%)

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	А	0	2
2	В	0	1
All	All	0	3

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	92	ARG	NE-CZ-NH1	8.39	124.50	120.30
1	А	141	ARG	NE-CZ-NH2	-7.63	116.48	120.30
2	В	30	ARG	NE-CZ-NH1	6.72	123.66	120.30
2	В	143	HIS	CA-CB-CG	-6.29	102.91	113.60
1	А	141	ARG	NE-CZ-NH1	6.19	123.39	120.30
2	В	121	ASP	CB-CG-OD2	-5.83	113.05	118.30

There are no chirality outliers.

All (3) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
1	А	141	ARG	Sidechain
1	А	92	ARG	Sidechain
2	В	40	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	А	1069	0	1073	17	2
2	В	1134	0	1124	15	0
3	А	43	0	30	1	0
3	В	43	0	30	1	0
4	А	2	0	0	0	0
4	В	2	0	0	0	0
5	А	32	0	0	1	0
5	В	40	0	0	0	2
All	All	2365	0	2257	32	2

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 7.

All (32) 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:B:1:VAL:HG13	2:B:3:LEU:HD13	1.63	0.80
2:B:82:LYS:HE3	2:B:82:LYS:H	1.55	0.71
1:A:89:HIS:HB2	1:A:139:LYS:HD3	1.81	0.63
3:B:147:HEM:HMC2	3:B:147:HEM:HBC2	1.82	0.62
1:A:43:PHE:HB3	1:A:46:PHE:HB2	1.83	0.60
1:A:45:HIS:H	1:A:45:HIS:CD2	2.20	0.59
2:B:20:GLU:OE1	2:B:65:LYS:NZ	2.37	0.58
2:B:100:PRO:HG3	2:B:145:TYR:CD2	2.40	0.57
2:B:1:VAL:CG1	2:B:3:LEU:HD13	2.32	0.56
1:A:1:VAL:HG13	1:A:2:LEU:HG	1.91	0.52
1:A:1:VAL:HB	5:A:172:HOH:O	2.12	0.50
1:A:137:THR:C	1:A:141:ARG:HH22	2.16	0.49
1:A:88:ALA:HB3	1:A:139:LYS:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89:HIS:HB2	1:A:139:LYS:CE	2.42	0.49
2:B:142:ALA:O	2:B:145:TYR:HB2	2.11	0.49
1:A:89:HIS:HB2	1:A:139:LYS:CD	2.44	0.48
2:B:82:LYS:HE3	2:B:82:LYS:N	2.25	0.48
3:A:142:HEM:HBA2	3:A:142:HEM:HHA	1.95	0.47
2:B:24:GLY:HA2	2:B:68:LEU:HD23	1.96	0.47
1:A:2:LEU:HD23	1:A:127:LYS:HB3	1.95	0.47
1:A:76:LEU:N	1:A:77:PRO:CD	2.77	0.46
1:A:24:TYR:OH	1:A:112:HIS:HB3	2.16	0.46
1:A:137:THR:OG1	1:A:141:ARG:NH2	2.49	0.46
1:A:122:HIS:HD2	2:B:30:ARG:HH11	1.65	0.45
2:B:113:VAL:O	2:B:117:HIS:HD2	2.00	0.45
1:A:66:LEU:O	1:A:70:VAL:HG23	2.19	0.43
2:B:82:LYS:H	2:B:82:LYS:CE	2.29	0.42
1:A:1:VAL:HG12	1:A:73:LEU:O	2.20	0.42
2:B:89:SER:OG	2:B:144:LYS:HG2	2.20	0.41
2:B:120:LYS:HA	2:B:120:LYS:HE2	2.02	0.41
2:B:65:LYS:O	2:B:65:LYS:HD3	2.20	0.41
1:A:122:HIS:CD2	2:B:30:ARG:HH11	2.39	0.40

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All (2) 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:16:LYS:NZ	5:B:181:HOH:O[4_546]	1.24	0.96
1:A:16:LYS:CE	5:B:181:HOH:O[4_546]	1.85	0.35

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	Percentile	s
1	А	139/141~(99%)	138 (99%)	1 (1%)	0	100 100	

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	<i>,</i>	Analysed	Favoured	Allowed	Outliers	Percen	tiles
2	В	144/146~(99%)	139 (96%)	5~(4%)	0	100	100
All	All	283/287~(99%)	277 (98%)	6(2%)	0	100	100

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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	Percen	ntiles
1	А	115/115~(100%)	108 (94%)	7 (6%)	18	9
2	В	118/118 (100%)	108 (92%)	10 (8%)	10	4
All	All	233/233~(100%)	216~(93%)	17 (7%)	14	6

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	2	LEU
1	А	56	LYS
1	А	81	SER
1	А	85	ASN
1	А	122	HIS
1	А	127	LYS
1	А	139	LYS
2	В	1	VAL
2	В	2	GLN
2	В	6	GLU
2	В	66	LYS
2	В	70	SER
2	В	71	PHE
2	В	82	LYS
2	В	93	CYS
2	В	104	ARG
2	В	110	LEU



Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	9	ASN
1	А	45	HIS
1	А	122	HIS
2	В	76	HIS
2	В	143	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)

4 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	ol Type Chain Res	Chain	Dec	Link	Bond lengths			Bond angles		
		nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
4	CMO	В	148	3	$0,\!1,\!1$	-	-	-		
4	CMO	А	143	3	0,1,1	-	-	-		
3	HEM	В	147	2,4	41,50,50	1.54	5 (12%)	45,82,82	1.24	5 (11%)
3	HEM	А	142	4,1	41,50,50	1.44	5 (12%)	45,82,82	1.67	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



[Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
ľ	3	HEM	В	147	2,4	-	4/12/54/54	-
	3	HEM	А	142	4,1	-	6/12/54/54	-

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
3	В	147	HEM	C3C-C2C	-4.77	1.33	1.40
3	А	142	HEM	C3C-C2C	-4.31	1.34	1.40
3	В	147	HEM	C3C-CAC	3.43	1.54	1.47
3	А	142	HEM	C3C-CAC	3.30	1.54	1.47
3	В	147	HEM	CAA-C2A	2.82	1.56	1.52
3	В	147	HEM	CAB-C3B	2.55	1.54	1.47
3	В	147	HEM	CMD-C2D	2.52	1.56	1.50
3	А	142	HEM	CAB-C3B	2.41	1.54	1.47
3	А	142	HEM	C3B-C2B	-2.23	1.32	1.37
3	А	142	HEM	CMB-C2B	2.10	1.55	1.50

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$Ideal(^{o})$
3	А	142	HEM	CBA-CAA-C2A	4.83	120.87	112.62
3	А	142	HEM	CMA-C3A-C4A	-4.39	121.71	128.46
3	А	142	HEM	C4C-CHD-C1D	3.33	126.95	122.56
3	В	147	HEM	CMC-C2C-C3C	3.20	130.66	124.68
3	А	142	HEM	CMA-C3A-C2A	3.01	130.62	124.94
3	А	142	HEM	C4B-CHC-C1C	2.91	126.39	122.56
3	А	142	HEM	O2A-CGA-O1A	2.76	130.18	123.30
3	В	147	HEM	O1D-CGD-CBD	-2.68	114.47	123.08
3	А	142	HEM	CMB-C2B-C1B	-2.59	121.10	125.04
3	В	147	HEM	CMA-C3A-C4A	-2.55	124.55	128.46
3	А	142	HEM	O1A-CGA-CBA	-2.46	115.16	123.08
3	В	147	HEM	CAA-CBA-CGA	2.28	120.15	113.76
3	А	142	HEM	CMC-C2C-C3C	2.21	128.82	124.68
3	В	147	HEM	O2D-CGD-O1D	2.18	128.72	123.30

There are no chirality outliers.

All (10) torsion outliers are listed below:



Mol	Chain	Res	Type	Atoms
3	А	142	HEM	C1A-C2A-CAA-CBA
3	А	142	HEM	C3A-C2A-CAA-CBA
3	В	147	HEM	CAD-CBD-CGD-O1D
3	А	142	HEM	CAA-CBA-CGA-O1A
3	А	142	HEM	CAA-CBA-CGA-O2A
3	В	147	HEM	CAD-CBD-CGD-O2D
3	В	147	HEM	CAA-CBA-CGA-O2A
3	В	147	HEM	CAA-CBA-CGA-O1A
3	А	142	HEM	CAD-CBD-CGD-O2D
3	А	142	HEM	CAD-CBD-CGD-O1D

There are no ring outliers.

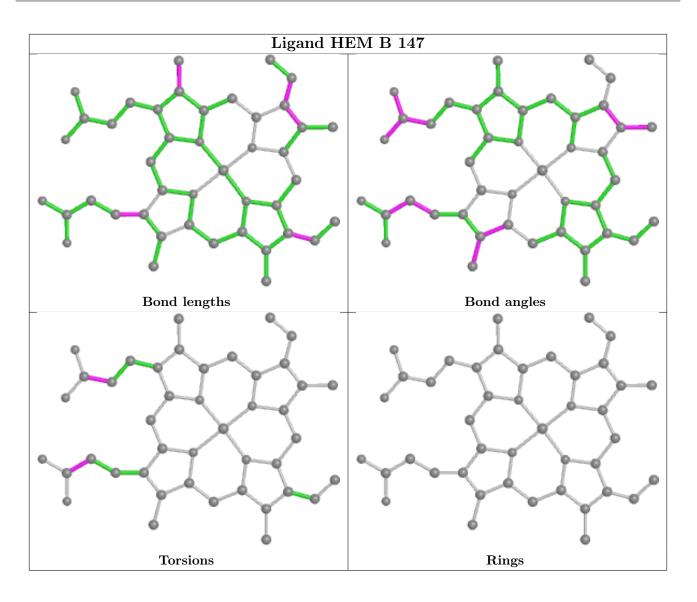
2 monomers are involved in 2 short contacts:

Mo	Chain	Res	Type	Clashes	Symm-Clashes
3	В	147	HEM	1	0
3	А	142	HEM	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 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 sufficient the outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

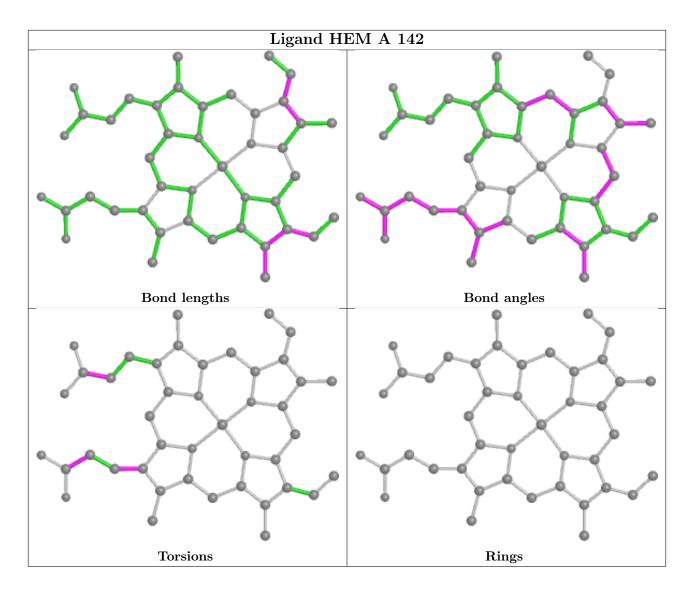












5.7 Other polymers (i)

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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q < 0.9
1	А	141/141 (100%)	-0.38	2 (1%) 75 77	9, 18, 44, 90	1 (0%)
2	В	146/146~(100%)	-0.42	4 (2%) 54 57	9, 19, 53, 87	3 (2%)
All	All	287/287~(100%)	-0.40	6 (2%) 63 66	9, 19, 52, 90	4 (1%)

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	1	VAL	6.9
2	В	1	VAL	3.6
2	В	145	TYR	2.9
1	А	141	ARG	2.8
2	В	144	LYS	2.3
2	В	146	HIS	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.

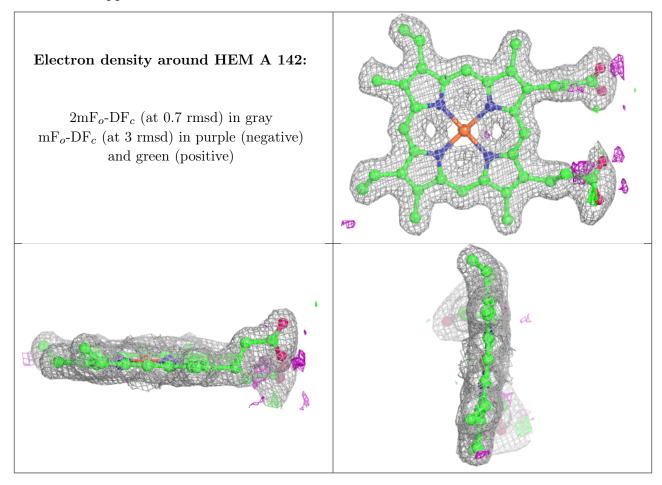
6.4 Ligands (i)

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.

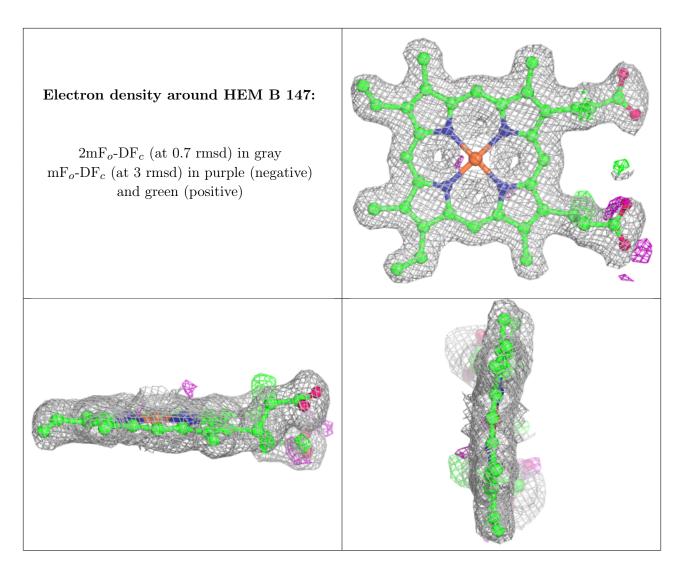


Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
3	HEM	А	142	43/43	0.98	0.08	10, 16, 43, 54	0
3	HEM	В	147	43/43	0.98	0.09	7,16,47,51	0
4	CMO	А	143	2/2	0.99	0.06	7,7,7,13	0
4	CMO	В	148	2/2	0.99	0.06	18,18,18,20	0

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.

