

# Full wwPDB X-ray Structure Validation Report (i)

#### Feb 3, 2024 – 01:38 PM EST

PDB ID : 1LHS

Title : LOGGERHEAD SEA TURTLE MYOGLOBIN (AQUO-MET)

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Deposited on : 1995-02-01

Resolution : 2.00 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.orgA 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 : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : NOT EXECUTED

EDS : NOT EXECUTED

buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

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

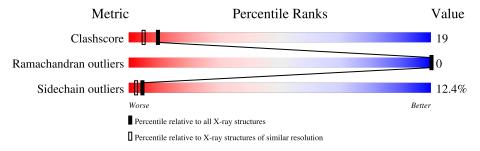
Validation Pipeline (wwPDB-VP) : 2.36

## 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 2.00 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	$(\# \mathrm{Entries})$	$(\#  ext{Entries},  ext{ resolution range}( ext{Å}))$
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain		
1	A	153	63%	30%	6% •



## 2 Entry composition (i)

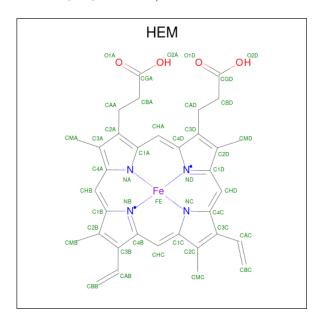
There are 3 unique types of molecules in this entry. The entry contains 1245 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 MYOGLOBIN.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	153	Total 1139	C 736	N 190	O 210	S 3	0	0	0

• Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: C<sub>34</sub>H<sub>32</sub>FeN<sub>4</sub>O<sub>4</sub>).



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

• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	63	Total O 63 63	0	0

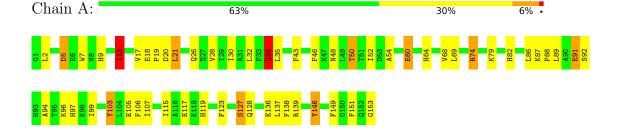


## 3 Residue-property plots (i)

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. 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. 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.

Note EDS was not executed.

• Molecule 1: MYOGLOBIN





# 4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source	
Space group	P 21 21 21	Depositor	
Cell constants	37.50Å 61.10Å 75.20Å	Depositor	
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor	
Resolution (Å)	15.00 - 2.00	Depositor	
% Data completeness	(Not available) (15.00-2.00)	Depositor	
(in resolution range)	(1000 available) (19.00 2.00)		
$R_{merge}$	(Not available)	Depositor	
$R_{sym}$	(Not available)	Depositor	
Refinement program	TNT, X-PLOR 3.1	Depositor	
$R, R_{free}$	0.182 , (Not available)	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	1245	wwPDB-VP	
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP	



## 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).

Mal	Chain	Bo	nd lengths	Во	ond angles
MIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	A	0.92	3/1165 (0.3%)	1.46	14/1577~(0.9%)

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	4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(\text{\AA})$
1	A	21	LEU	C-N	-7.62	1.16	1.34
1	A	94	ALA	C-N	5.33	1.46	1.34
1	A	50	THR	C-N	-5.12	1.22	1.34

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	5	ASP	O-C-N	-10.18	106.41	122.70
1	A	50	THR	N-CA-CB	-9.79	91.70	110.30
1	A	52	ILE	CB-CA-C	-9.49	92.62	111.60
1	A	146	TYR	CB-CG-CD2	-8.71	115.77	121.00
1	A	74	ARG	NE-CZ-NH1	7.27	123.93	120.30
1	A	28	VAL	CG1-CB-CG2	-6.84	99.96	110.90
1	A	103	TYR	CB-CG-CD1	-6.80	116.92	121.00
1	A	146	TYR	CB-CG-CD1	6.48	124.89	121.00
1	A	50	THR	CB-CA-C	5.90	127.53	111.60
1	A	69	LEU	CB-CG-CD1	-5.83	101.10	111.00



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Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	153	GLY	CA-C-O	-5.26	111.13	120.60
1	A	50	THR	O-C-N	-5.25	114.30	122.70
1	A	34	GLN	O-C-N	-5.19	114.39	122.70
1	A	21	LEU	CB-CA-C	5.08	119.85	110.20

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	13	ILE	Mainchain
1	A	34	GLN	Mainchain
1	A	5	ASP	Mainchain
1	A	54	ALA	Mainchain

#### 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	1139	0	1053	43	1
2	A	43	0	30	9	0
3	A	63	0	0	0	1
All	All	1245	0	1083	44	1

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 19.

All (44) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
1100111 1	1100111 2	${f distance}({f A})$	overlap (Å)
1:A:97:HIS:HB2	1:A:99:ILE:HD12	1.47	0.96
1:A:97:HIS:HB2	1:A:99:ILE:CD1	2.07	0.85
1:A:43:PHE:CE1	2:A:155:HEM:HBC2	2.13	0.83
1:A:138:PHE:CZ	2:A:155:HEM:HBB2	2.23	0.74
1:A:43:PHE:HE1	2:A:155:HEM:HBC2	1.53	0.73
1:A:123:PHE:CE2	1:A:128:GLN:HG2	2.26	0.70



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At and 1		Interatomic	Clash	
Atom-1	Atom-2	${\rm distance}(\mathring{\rm A})$	overlap (Å)	
1:A:18:GLU:N	1:A:19:PRO:HD2	2.06	0.70	
1:A:97:HIS:CB	1:A:99:ILE:CD1	2.69	0.70	
1:A:97:HIS:CB	1:A:99:ILE:HD12	2.22	0.65	
1:A:18:GLU:N	1:A:19:PRO:CD	2.63	0.61	
1:A:21:LEU:C	1:A:21:LEU:HD23	2.22	0.60	
1:A:91:GLU:HG3	1:A:149:PHE:CZ	2.36	0.60	
1:A:105:GLU:HB3	1:A:139:ARG:HD3	1.82	0.60	
1:A:115:ILE:HG23	1:A:119:HIS:HD2	1.65	0.59	
1:A:138:PHE:HZ	2:A:155:HEM:HBB2	1.67	0.59	
1:A:87:LYS:CB	1:A:88:PRO:HD3	2.34	0.58	
1:A:138:PHE:CE2	2:A:155:HEM:CBB	2.87	0.58	
1:A:26:GLN:O	1:A:30:ILE:HG13	2.05	0.56	
1:A:2:LEU:HB2	1:A:7:TRP:NE1	2.20	0.56	
1:A:123:PHE:CD2	1:A:128:GLN:HG2	2.42	0.54	
1:A:138:PHE:CE2	2:A:155:HEM:HBB2	2.44	0.52	
1:A:105:GLU:CB	1:A:139:ARG:HD3	2.40	0.52	
1:A:17:VAL:C	1:A:19:PRO:HD2	2.31	0.51	
1:A:87:LYS:CB	1:A:88:PRO:CD	2.89	0.51	
1:A:2:LEU:HD12	1:A:2:LEU:N	2.26	0.50	
1:A:46:PHE:HE1	1:A:60:GLU:HB3	1.74	0.50	
1:A:115:ILE:HG23	1:A:119:HIS:CD2	2.46	0.49	
1:A:13:ILE:HD11	1:A:127:SER:HB2	1.95	0.48	
1:A:138:PHE:CZ	2:A:155:HEM:CBB	2.97	0.47	
1:A:48:ASN:O	1:A:50:THR:N	2.47	0.47	
1:A:97:HIS:HB3	1:A:99:ILE:HD11	1.97	0.46	
1:A:146:TYR:CE2	1:A:151:PHE:HE2	2.34	0.44	
1:A:64:HIS:O	1:A:68:VAL:HG23	2.18	0.44	
1:A:97:HIS:HB3	1:A:99:ILE:CD1	2.46	0.44	
1:A:91:GLU:CG	1:A:149:PHE:CZ	3.00	0.43	
2:A:155:HEM:HHA	2:A:155:HEM:HAA1	1.90	0.42	
1:A:86:LEU:HD23	1:A:86:LEU:HA	1.78	0.42	
1:A:92:SER:O	1:A:96:LYS:HB2	2.19	0.42	
1:A:86:LEU:O	1:A:89:LEU:N	2.50	0.42	
1:A:103:TYR:O	1:A:106:PHE:HB2	2.20	0.42	
1:A:9:HIS:O	1:A:13:ILE:HG12	2.19	0.42	
1:A:32:LEU:HD22	1:A:107:ILE:HD12	2.03	0.41	
1:A:13:ILE:HD11	1:A:127:SER:CB	2.50	0.40	
1:A:99:ILE:HG12	2:A:155:HEM:CAC	2.51	0.40	

All (1) 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		$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$egin{aligned}  ext{Clash} \  ext{overlap } ( ext{Å}) \end{aligned}$
1:A:105:GLU:O	3:A:312:HOH:O[1_545]	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	151/153 (99%)	147 (97%)	4 (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	Analysed Rotameric		Percentiles	
1	A	105/132 (80%)	92 (88%)	13 (12%)	4 2	

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ILE
1	A	20	ASP
1	A	34	GLN
1	A	35	LEU
1	A	60	GLU
1	A	74	ARG
1	A	79	LYS
1	A	82	HIS



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Mol	Chain	Res	Type
1	A	91	GLU
1	A	117	GLU
1	A	127	SER
1	A	136	GLU
1	A	137	LEU

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

Mol	Chain	Res	Type
1	A	119	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)

1 ligand is 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	Res	Link	Bo	ond leng	${ m ths}$	$\mathbf{B}$	ond ang	gles
Moi Type	nes		Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2			
2	HEM	A	155	3,1	41,50,50	1.62	8 (19%)	45,82,82	2.17	14 (31%)		



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	155	3,1	-	8/12/54/54	-

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}( ext{\AA})$
2	A	155	HEM	C3C-C2C	-3.42	1.35	1.40
2	A	155	HEM	CAB-C3B	3.13	1.55	1.47
2	A	155	HEM	CMA-C3A	3.00	1.57	1.51
2	A	155	HEM	CMB-C2B	2.90	1.56	1.50
2	A	155	HEM	C1B-NB	-2.73	1.35	1.40
2	A	155	HEM	CMD-C2D	2.40	1.55	1.50
2	A	155	HEM	C3C-CAC	2.32	1.52	1.47
2	A	155	HEM	C1B-C2B	2.14	1.48	1.44

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
2	A	155	HEM	C4A-C3A-C2A	-6.59	102.41	107.00
2	A	155	HEM	CMA-C3A-C2A	4.68	133.77	124.94
2	A	155	HEM	C2C-C3C-C4C	4.25	109.87	106.90
2	A	155	HEM	C4C-CHD-C1D	4.21	128.12	122.56
2	A	155	HEM	CHC-C4B-C3B	-3.42	119.34	124.57
2	A	155	HEM	CMA-C3A-C4A	-3.22	123.52	128.46
2	A	155	HEM	CHB-C1B-NB	-2.94	120.75	124.38
2	A	155	HEM	CHD-C1D-ND	2.85	127.53	124.43
2	A	155	HEM	CAD-C3D-C2D	-2.59	123.05	127.88
2	A	155	HEM	CHA-C4D-ND	-2.41	121.41	124.38
2	A	155	HEM	CHC-C4B-NB	2.38	127.02	124.43
2	A	155	HEM	O1D-CGD-CBD	-2.35	115.52	123.08
2	A	155	HEM	CAD-C3D-C4D	2.35	128.76	124.66
2	A	155	HEM	CMB-C2B-C3B	-2.03	123.32	128.30

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	155	HEM	C1A-C2A-CAA-CBA



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Mol	Chain	Res	Type	Atoms
2	A	155	HEM	C2B-C3B-CAB-CBB
2	A	155	HEM	C4B-C3B-CAB-CBB
2	A	155	HEM	C3A-C2A-CAA-CBA
2	A	155	HEM	CAD-CBD-CGD-O1D
2	A	155	HEM	CAA-CBA-CGA-O2A
2	A	155	HEM	CAA-CBA-CGA-O1A
2	A	155	HEM	CAD-CBD-CGD-O2D

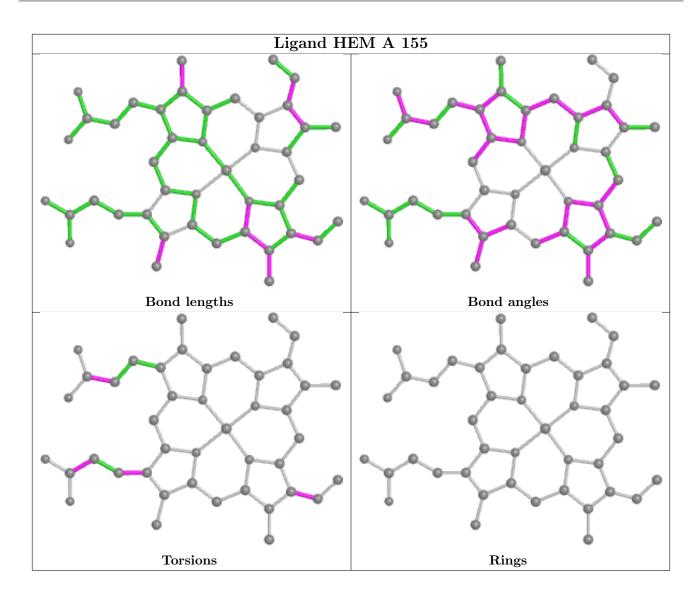
There are no ring outliers.

1 monomer is involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	155	HEM	9	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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	21:LEU	С	22:SER	N	1.16



## 6 Fit of model and data (i)

#### 6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

#### 6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

