

Full wwPDB X-ray Structure Validation Report (i)

Aug 6, 2023 – 02:43 PM EDT

PDB ID : 1LA6

Title : The crystal structure of Trematomus newnesi hemoglobin in a partial

hemichrome state

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Deposited on : 2002-03-28

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)

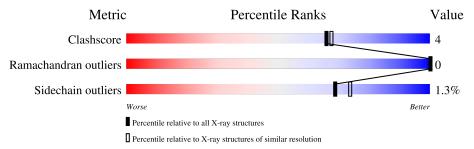
Validation Pipeline (wwPDB-VP) : 2.35

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	143	92%	8% •
2	В	146	82%	8% • 10%



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 2311 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.

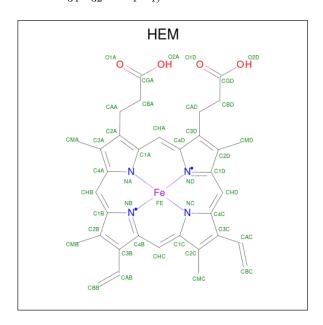
• Molecule 1 is a protein called Hemoglobin alpha-1 chain.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	143	Total	C 71.4	N 102	0	S	0	1	0
1	A	143	Total 1112	C 714	N 192	201	S 5	0	1	

• Molecule 2 is a protein called Hemoglobin beta-1/2 chain.

\mathbf{Mol}	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	В	132	Total 1042	C 663	N 176	O 196	S 7	0	3	0

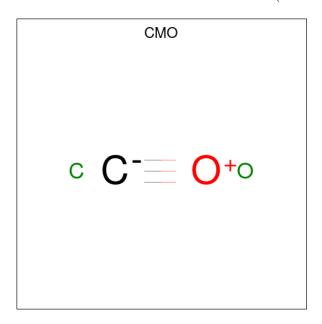
• Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf			
2	Λ	1	Total	С	Fe	N	О	0	0		
3 A	1	43	34	1	4	4	0	0			
2	D	1	Total	С	Fe	N	О	0	0		
3	D	В		43	34	1	4	4			



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



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total 2	C 1	O 1	0	0

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	42	Total O 42 42	0	0
5	В	27	Total O 27 27	0	0

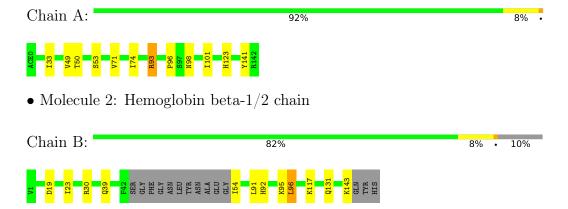


3 Residue-property plots (i)

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: Hemoglobin alpha-1 chain





4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	C 1 2 1	Depositor	
Cell constants	89.85Å 88.19Å 55.14Å	Depositor	
a, b, c, α , β , γ	90.00° 97.79° 90.00°	Depositor	
Resolution (Å)	12.00 - 2.00	Depositor	
% Data completeness	(Not available) (12.00-2.00)	Depositor	
(in resolution range)	(1700 available) (12.00 2.00)	Беровног	
R_{merge}	0.08	Depositor	
R_{sym}	(Not available)	Depositor	
Refinement program	X-PLOR 3.1	Depositor	
R, R_{free}	0.179 , 0.212	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	2311	wwPDB-VP	
Average B, all atoms (Å ²)	32.0	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, CMO, ACE

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	0.42	0/1138	0.58	0/1536	
2	В	0.43	0/1075	0.60	0/1454	
All	All	0.42	0/2213	0.59	0/2990	

There are no bond length outliers.

There are no bond angle outliers.

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	1112	0	1148	7	0
2	В	1042	0	1026	12	0
3	A	43	0	30	0	0
3	В	43	0	30	1	0
4	A	2	0	0	0	0
5	A	42	0	0	0	0
5	В	27	0	0	1	0
All	All	2311	0	2234	18	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 4.



All (18) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} ({\rm \AA}) \end{array}$	Clash overlap (Å)
2:B:23:ILE:HD11	2:B:117:LYS:HD2	1.40	1.03
2:B:19:ASP:H	2:B:117:LYS:NZ	1.95	0.64
2:B:92:HIS:HA	2:B:96:LEU:HB2	1.79	0.63
2:B:19:ASP:H	2:B:117:LYS:HZ1	1.52	0.58
2:B:131[B]:GLN:HG2	5:B:262:HOH:O	2.04	0.57
2:B:91:LEU:HG	2:B:96:LEU:HD22	1.88	0.56
2:B:91:LEU:HD11	2:B:95:LYS:HD3	1.91	0.52
2:B:91:LEU:CD1	2:B:95:LYS:HD3	2.44	0.47
1:A:123:HIS:ND1	2:B:30:ARG:HD3	2.29	0.47
2:B:143:LYS:HE2	2:B:143:LYS:HB3	1.76	0.46
1:A:93:ARG:HH11	1:A:93:ARG:HB3	1.81	0.45
1:A:98:ASN:HD22	1:A:101:ILE:HD12	1.82	0.45
2:B:39:GLN:NE2	2:B:54:ILE:HD11	2.32	0.45
1:A:49:VAL:HG12	1:A:49:VAL:O	2.18	0.44
1:A:71:VAL:O	1:A:74:ILE:HB	2.18	0.44
2:B:92:HIS:CE1	3:B:147:HEM:NA	2.86	0.43
1:A:50:THR:O	1:A:53:SER:HB3	2.18	0.43
1:A:96:PRO:HD3	1:A:141:TYR:CE1	2.55	0.42

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	ntiles
1	A	142/143~(99%)	140 (99%)	2 (1%)	0	100	100
2	В	$131/146\ (90\%)$	129 (98%)	2 (2%)	0	100	100
All	All	$273/289 \ (94\%)$	269 (98%)	4 (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	Analysed Rotameric Outliers		Percentiles		
1	A	122/121 (101%)	120 (98%)	2 (2%)	62	67	
2	В	114/121 (94%)	113 (99%)	1 (1%)	78	83	
All	All	236/242 (98%)	233 (99%)	3 (1%)	69	74	

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	ILE
1	A	93	ARG
2	В	96	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	98	ASN
1	A	103	ASN

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)

3 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).

Mal	Trms	Chain	Res Link		Bond lengths			Bond angles		
MIOI	Type	Chain	Res	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
3	HEM	A	143	4,1	41,50,50	1.47	9 (21%)	45,82,82	1.55	9 (20%)
3	HEM	В	147	2	41,50,50	1.69	10 (24%)	45,82,82	1.50	7 (15%)
4	CMO	A	144	3	0,1,1	-	-	-		

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
3	HEM	A	143	4,1	-	3/12/54/54	-
3	HEM	В	147	2	-	4/12/54/54	-

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(A)
3	В	147	HEM	C3C-CAC	-4.68	1.38	1.47
3	В	147	HEM	CBB-CAB	3.82	1.49	1.30
3	В	147	HEM	C2C-C1C	3.41	1.50	1.42
3	A	143	HEM	CBB-CAB	3.08	1.45	1.30
3	A	143	HEM	C3C-CAC	-3.05	1.41	1.47
3	A	143	HEM	CBC-CAC	2.92	1.48	1.29
3	A	143	HEM	CAA-C2A	-2.90	1.47	1.52
3	A	143	HEM	C2C-C1C	2.57	1.48	1.42
3	В	147	HEM	CAB-C3B	-2.56	1.40	1.47
3	A	143	HEM	CAB-C3B	-2.52	1.40	1.47
3	В	147	HEM	C3B-C4B	2.49	1.49	1.44
3	В	147	HEM	C4A-NA	2.47	1.41	1.36
3	В	147	HEM	FE-NB	2.34	2.08	1.96
3	В	147	HEM	C3C-C2C	-2.32	1.37	1.40

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Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	$\operatorname{Ideal}(ext{\AA})$
3	В	147	HEM	CHA-C4D	2.30	1.40	1.35
3	В	147	HEM	CBC-CAC	2.29	1.44	1.29
3	A	143	HEM	C3B-C4B	2.23	1.49	1.44
3	A	143	HEM	CHA-C4D	2.20	1.40	1.35
3	A	143	HEM	C2A-C3A	-2.09	1.31	1.37

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}(^{o})$
3	В	147	HEM	C4B-CHC-C1C	4.67	128.72	122.56
3	A	143	HEM	C4B-C3B-C2B	-3.85	104.06	107.11
3	A	143	HEM	C3B-C2B-C1B	3.30	108.94	106.49
3	A	143	HEM	CBA-CAA-C2A	-3.24	107.09	112.62
3	В	147	HEM	CAB-C3B-C2B	-3.15	118.22	128.60
3	A	143	HEM	C4B-CHC-C1C	3.03	126.56	122.56
3	В	147	HEM	CBA-CAA-C2A	-2.71	108.00	112.62
3	A	143	HEM	CAB-C3B-C2B	-2.68	119.77	128.60
3	В	147	HEM	CMB-C2B-C1B	2.64	129.07	125.04
3	В	147	HEM	C2B-C1B-NB	2.64	112.96	109.84
3	A	143	HEM	C4C-CHD-C1D	2.59	125.98	122.56
3	В	147	HEM	C1B-NB-C4B	-2.39	102.60	105.07
3	В	147	HEM	C4C-CHD-C1D	2.35	125.66	122.56
3	A	143	HEM	C2D-C1D-ND	2.30	112.64	109.88
3	A	143	HEM	C4A-C3A-C2A	-2.09	105.54	107.00
3	A	143	HEM	CAB-C3B-C4B	2.06	134.08	124.47

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	143	HEM	C4B-C3B-CAB-CBB
3	В	147	HEM	CAA-CBA-CGA-O1A
3	A	143	HEM	CAD-CBD-CGD-O1D
3	В	147	HEM	CAD-CBD-CGD-O1D
3	В	147	HEM	CAD-CBD-CGD-O2D
3	A	143	HEM	CAD-CBD-CGD-O2D
3	В	147	HEM	CAA-CBA-CGA-O2A

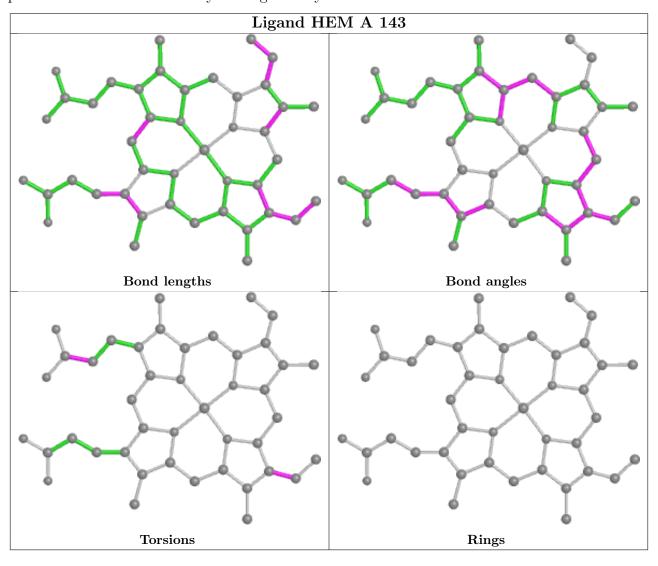
There are no ring outliers.

1 monomer is involved in 1 short contact:

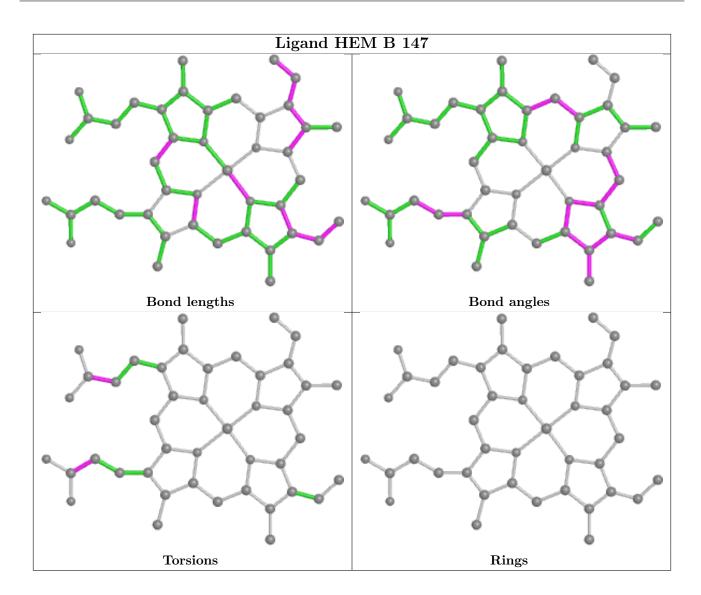


Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	В	147	HEM	1	0

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 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)

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.

