

wwPDB X-ray Structure Validation Summary Report (i)

Feb 10, 2024 – 10:39 AM EST

PDB ID : 2LH3

Title: X-RAY STRUCTURAL INVESTIGATION OF LEGHEMOGLOBIN. VI.

STRUCTURE OF ACETATE-FERRILEGHEMOGLOBIN AT A RESO-

LUTION OF 2.0 ANGSTROMS (RUSSIAN)

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Deposited on : 1982-04-23

Resolution : 2.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

 $Mol Probity \quad : \quad 4.02b\text{--}467$

Mogul : 1.8.5 (274361), 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

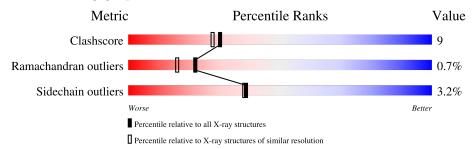


1 Overall quality at a glance (i)

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

The reported resolution of this entry is 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%

Mol	Chain	Length		Quality of chain		
1	A	153	21%	46%	29%	5%



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 1291 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.

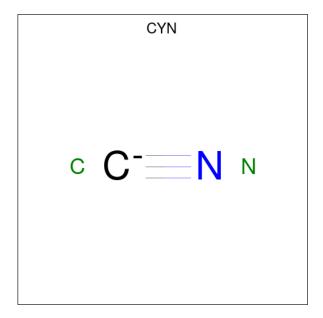
• Molecule 1 is a protein called LEGHEMOGLOBIN (CYANO MET).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	153	Total 1180	C 761	N 193	O 225	S 1	35	1	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Modelled Actual		Reference
A	79	GLU	GLN	conflict	UNP P02240
A	150	ASP	ASN	conflict	UNP P02240

• Molecule 2 is CYANIDE ION (three-letter code: CYN) (formula: CN).

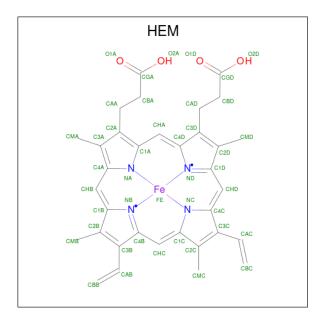


N	/Iol	Chain	Residues	Atoms			ZeroOcc	AltConf
	2	A	1	Total 2	C 1	N 1	0	0

• Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (for-



 $mula:\ C_{34}H_{32}FeN_4O_4\big).$



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

• Molecule 4 is water.

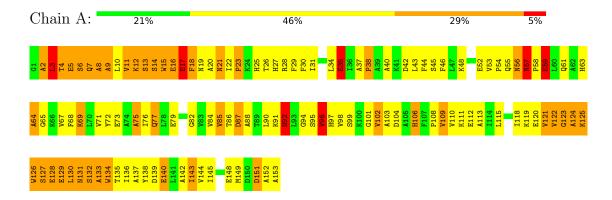
Mol	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
4	A	66	Total O 66 66	0	0



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.

• Molecule 1: LEGHEMOGLOBIN (CYANO MET)





4 Data and refinement statistics (i)

Property	Value	Source
Space group	B 1 1 2	Depositor
Cell constants	93.19Å 38.41Å 52.07Å	Donositon
a, b, c, α , β , γ	90.00° 90.00° 98.90°	Depositor
Resolution (Å)	(Not available) – 2.00	Depositor
Resolution (A)	9.94 - 1.99	EDS
% Data completeness	(Not available) ((Not available)-2.00)	Depositor
(in resolution range)	92.5 (9.94-1.99)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$	-	Xtriage
Refinement program	unknown	Depositor
P. P.	(Not available) , (Not available)	Depositor
R, R_{free}	0.489 , (Not available)	DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	20.4	Xtriage
Anisotropy	0.238	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	1.17, 256.3	EDS
L-test for twinning ¹	$< L > = 0.42, < L^2> = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.51	EDS
Total number of atoms	1291	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 13.59% of the height of the origin peak. No significant pseudotranslation is detected.

Theoretical 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.



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, CYN

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	В	ond lengths	Bond angles		
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	3.23	135/1214 (11.1%)	2.13	41/1648 (2.5%)	

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	9

The worst 5 of 135 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(ext{\AA})$
1	A	95	SER	CB-OG	10.49	1.55	1.42
1	A	138	TYR	CZ-OH	10.07	1.54	1.37
1	A	138	TYR	CB-CG	9.92	1.66	1.51
1	A	112	GLU	CG-CD	9.46	1.66	1.51
1	A	15	TRP	CD2-CE2	9.18	1.52	1.41

The worst 5 of 41 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^o)$
1	A	72	TYR	CB-CG-CD1	-9.85	115.09	121.00
1	A	112	GLU	OE1-CD-OE2	-9.48	111.92	123.30
1	A	28	ARG	NE-CZ-NH2	-8.68	115.96	120.30
1	A	73	GLU	OE1-CD-OE2	-8.09	113.59	123.30
1	A	16	GLU	OE1-CD-OE2	-7.72	114.03	123.30

There are no chirality outliers.

5 of 9 planarity outliers are listed below:



Mol	Chain	Res	Type	Group
1	A	17	GLU	Sidechain
1	A	35	GLU	Sidechain
1	A	42	ASP	Sidechain
1	A	56	ASN	Sidechain
1	A	7	GLN	Sidechain

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5.2 Torsion angles (i)

5.2.1 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	lysed Favoured Allowed		Outliers	Percentiles	
1	A	153/153 (100%)	147 (96%)	5 (3%)	1 (1%)	22	16

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	LEU

5.2.2 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	$127/125\ (102\%)$	123 (97%)	4 (3%)	40	40

All (4) residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	A	21	ASN
1	A	34	LEU
1	A	96	VAL
1	A	151	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	ASN
1	A	25	HIS
1	A	61	GLN
1	A	77	GLN

5.2.3 RNA (i)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.4 Carbohydrates (i)

There are no monosaccharides in this entry.

5.5 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	Trunc	Chain	Dag	Timle	В	ond leng	gths	В	ond ang	gles
MIOI	Type	Chain	nes	Link	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2
3	HEM	A	155	1,2	41,50,50	3.99	27 (65%)	45,82,82	2.25	19 (42%)
2	CYN	A	154	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	155	1,2	-	4/12/54/54	-

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	$Ideal(\AA)$
3	A	155	HEM	C1D-C2D	7.38	1.58	1.44
3	A	155	HEM	C1B-C2B	7.03	1.58	1.44
3	A	155	HEM	C4D-C3D	6.79	1.56	1.45
3	A	155	HEM	FE-NB	6.78	2.30	1.96
3	A	155	HEM	C3B-C4B	6.47	1.57	1.44

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\mathrm{Ideal}(^{o})$
3	A	155	HEM	CMA-C3A-C4A	-5.07	120.67	128.46
3	A	155	HEM	C4C-CHD-C1D	4.78	128.86	122.56
3	A	155	HEM	C4A-C3A-C2A	4.30	109.99	107.00
3	A	155	HEM	C2C-C3C-C4C	3.97	109.67	106.90
3	A	155	HEM	C3C-C4C-NC	-3.43	104.47	110.94

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	155	HEM	CAA-CBA-CGA-O2A
3	A	155	HEM	CAA-CBA-CGA-O1A
3	A	155	HEM	CAD-CBD-CGD-O1D
3	A	155	HEM	CAD-CBD-CGD-O2D

There are no ring outliers.

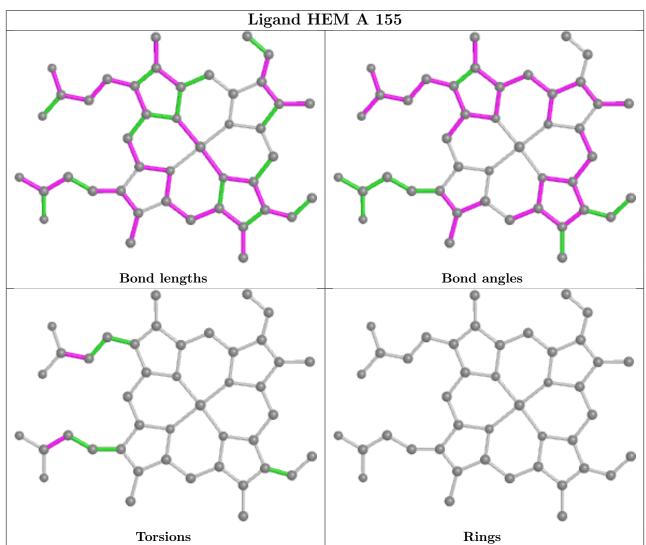
1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	155	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.



5.6 Other polymers (i)

There are no such residues in this entry.



5.7 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)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

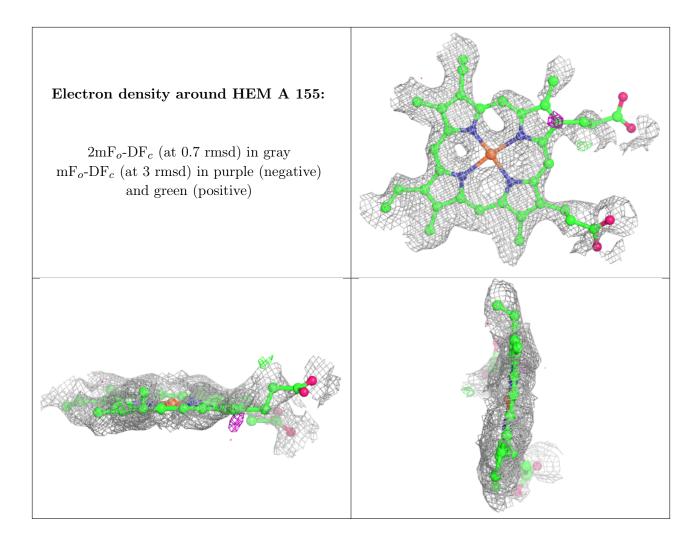
Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

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)

Unable to reproduce the depositors R factor - this section is therefore empty.

