



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 13, 2017 – 04:03 pm GMT

PDB ID : 1GBU
Title : DEOXY (BETA-(C93A,C112G)) HUMAN HEMOGLOBIN
Authors : Vasquez, G.B.; Ji, X.; Fronticelli, C.; Gilliland, G.L.
Deposited on : 1996-01-04
Resolution : 1.80 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

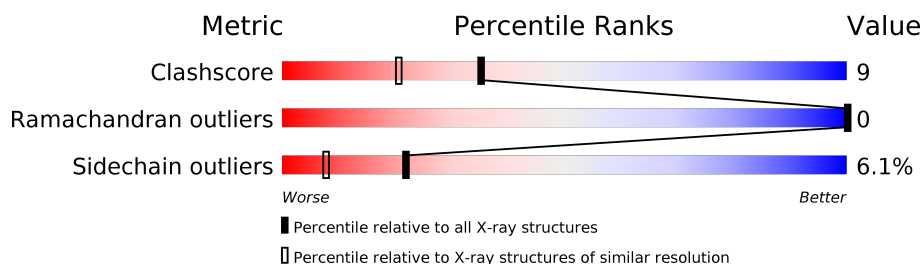
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	112137	5742 (1.80-1.80)
Ramachandran outliers	110173	5676 (1.80-1.80)
Sidechain outliers	110143	5675 (1.80-1.80)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	141	
1	C	141	
2	B	146	
2	D	146	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	B	147	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5012 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	141	Total	C	N	O	S	0	0	0
			1069	685	187	194	3			
1	C	141	Total	C	N	O	S	0	0	0
			1069	685	187	194	3			

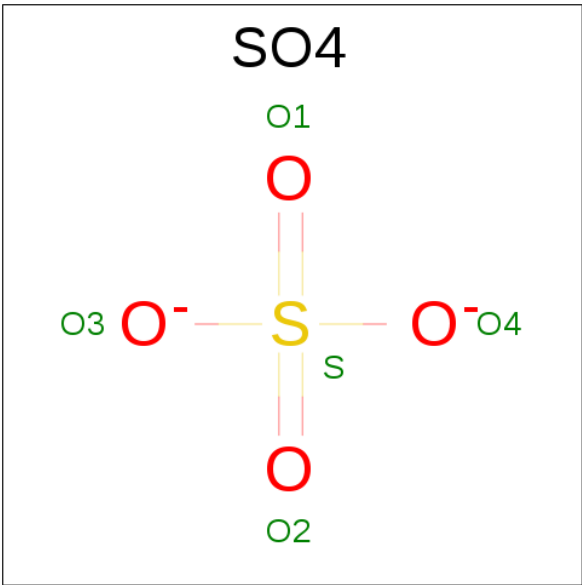
- Molecule 2 is a protein called HEMOGLOBIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	146	Total	C	N	O	S	0	0	0
			1120	723	195	201	1			
2	D	146	Total	C	N	O	S	0	0	0
			1120	723	195	201	1			

There are 4 discrepancies between the modelled and reference sequences:

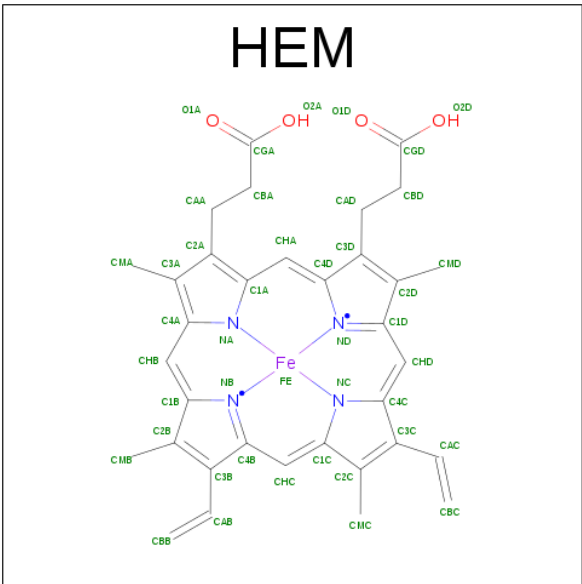
Chain	Residue	Modelled	Actual	Comment	Reference
B	93	ALA	CYS	ENGINEERED	UNP P68871
B	112	GLY	CYS	ENGINEERED	UNP P68871
D	93	ALA	CYS	ENGINEERED	UNP P68871
D	112	GLY	CYS	ENGINEERED	UNP P68871

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	D	1	Total	O	S		0	0
			5	4	1			
3	B	1	Total	O	S		0	0
			5	4	1			

- Molecule 4 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: C₃₄H₃₂FeN₄O₄).



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

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

- Molecule 5 is water.

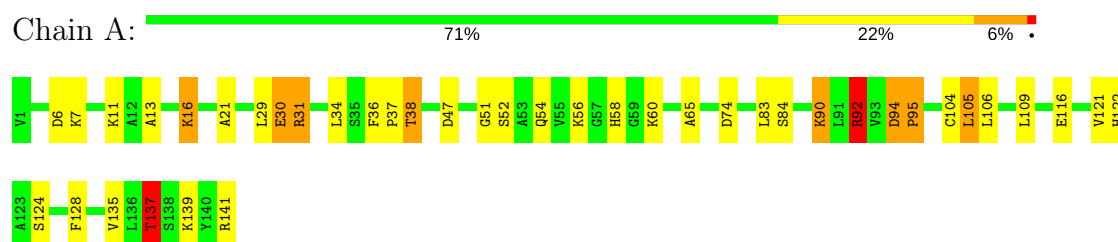
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	122	Total 122	O 122	0	0
5	B	94	Total 94	O 94	0	0
5	C	125	Total 125	O 125	0	0
5	D	111	Total 111	O 111	0	0

3 Residue-property plots [i](#)

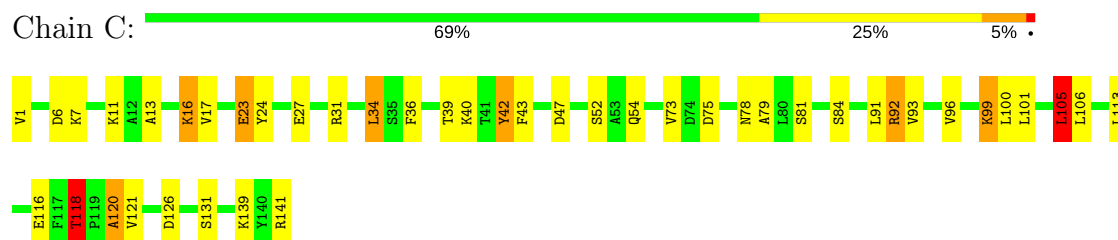
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

Note EDS was not executed.

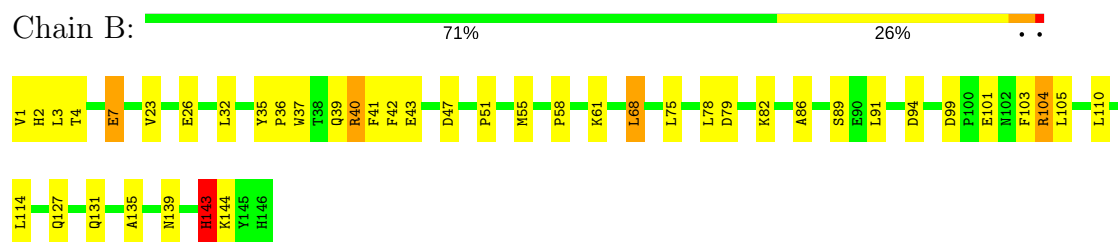
• Molecule 1: HEMOGLOBIN



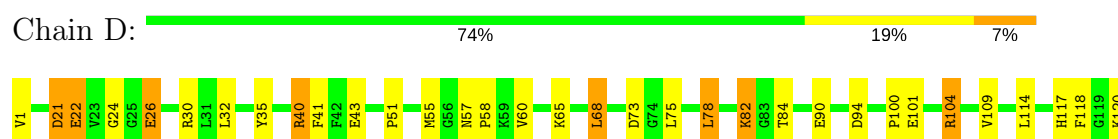
• Molecule 1: HEMOGLOBIN

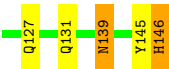


• Molecule 2: HEMOGLOBIN



• Molecule 2: HEMOGLOBIN





4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	63.02Å 82.94Å 53.83Å 90.00° 99.16° 90.00°	Depositor
Resolution (Å)	6.00 – 1.80	Depositor
% Data completeness (in resolution range)	82.7 (6.00-1.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
Refinement program	GPRLSA, PROLSQ	Depositor
R, R_{free}	0.167 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5012	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, SO4

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	1.14	0/1097	1.97	32/1491 (2.1%)
1	C	1.23	2/1097 (0.2%)	2.01	31/1491 (2.1%)
2	B	1.14	0/1150	1.81	25/1562 (1.6%)
2	D	1.17	0/1150	1.89	28/1562 (1.8%)
All	All	1.17	2/4494 (0.0%)	1.92	116/6106 (1.9%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	D	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	141	ARG	CZ-NH2	6.91	1.42	1.33
1	C	40	LYS	N-CA	5.29	1.56	1.46

The worst 5 of 116 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	141	ARG	NE-CZ-NH1	18.53	129.56	120.30
1	A	92	ARG	NE-CZ-NH2	-16.04	112.28	120.30
1	C	92	ARG	NE-CZ-NH2	-13.95	113.32	120.30
1	A	141	ARG	NE-CZ-NH2	-13.15	113.72	120.30
2	D	40	ARG	NE-CZ-NH1	13.08	126.84	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	92	ARG	Sidechain
2	D	40	ARG	Sidechain

5.2 Too-close contacts

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	1069	0	1073	17	0
1	C	1069	0	1073	29	0
2	B	1120	0	1116	26	0
2	D	1120	0	1116	14	0
3	B	5	0	0	2	0
3	D	5	0	0	0	0
4	A	43	0	30	2	0
4	B	43	0	30	2	0
4	C	43	0	30	0	0
4	D	43	0	30	3	0
5	A	122	0	0	2	0
5	B	94	0	0	2	0
5	C	125	0	0	4	0
5	D	111	0	0	2	0
All	All	5012	0	4498	84	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 9.

The worst 5 of 84 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)
1:C:118:THR:HG22	1:C:121:VAL:H	1.29	0.96
1:C:113:LEU:HB3	1:C:116:GLU:HG2	1.54	0.89
2:D:104:ARG:H	2:D:104:ARG:HD2	1.49	0.77
2:D:24:GLY:HA2	2:D:68:LEU:HD13	1.70	0.73
2:D:104:ARG:HD2	2:D:104:ARG:N	2.04	0.72

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	Percentiles	
1	A	139/141 (99%)	134 (96%)	5 (4%)	0	100	100
1	C	139/141 (99%)	137 (99%)	2 (1%)	0	100	100
2	B	144/146 (99%)	142 (99%)	2 (1%)	0	100	100
2	D	144/146 (99%)	143 (99%)	1 (1%)	0	100	100
All	All	566/574 (99%)	556 (98%)	10 (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	113/113 (100%)	105 (93%)	8 (7%)	17	5
1	C	113/113 (100%)	106 (94%)	7 (6%)	21	7
2	B	116/116 (100%)	113 (97%)	3 (3%)	51	36
2	D	116/116 (100%)	106 (91%)	10 (9%)	12	3
All	All	458/458 (100%)	430 (94%)	28 (6%)	22	8

5 of 28 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	16	LYS
1	C	105	LEU
2	D	120	LYS
1	C	23	GLU
1	C	99	LYS

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

Mol	Chain	Res	Type
1	A	9	ASN
2	B	2	HIS
2	B	146	HIS
2	D	19	ASN
2	D	117	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

6 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	HEM	A	142	1	28,50,50	2.56	9 (32%)	17,82,82	2.25	8 (47%)
3	SO4	B	147	-	4,4,4	0.75	0	6,6,6	0.26	0
4	HEM	B	148	2	28,50,50	2.13	8 (28%)	17,82,82	2.36	5 (29%)
4	HEM	C	142	1	28,50,50	2.38	12 (42%)	17,82,82	2.36	7 (41%)
3	SO4	D	147	-	4,4,4	0.72	0	6,6,6	0.34	0
4	HEM	D	148	2	28,50,50	2.13	7 (25%)	17,82,82	2.72	8 (47%)

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
4	HEM	A	142	1	-	0/6/54/54	0/0/8/8
3	SO4	B	147	-	-	0/0/0/0	0/0/0/0
4	HEM	B	148	2	-	0/6/54/54	0/0/8/8
4	HEM	C	142	1	-	0/6/54/54	0/0/8/8
3	SO4	D	147	-	-	0/0/0/0	0/0/0/0
4	HEM	D	148	2	-	0/6/54/54	0/0/8/8

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	142	HEM	C3B-C2B	-5.88	1.32	1.40
4	A	142	HEM	C3C-C2C	-5.51	1.33	1.40
4	C	142	HEM	C3B-C2B	-5.47	1.33	1.40
4	D	148	HEM	C3B-C2B	-5.33	1.33	1.40
4	B	148	HEM	C3B-C2B	-5.01	1.33	1.40

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	142	HEM	CMD-C2D-C1D	-4.25	121.94	128.46
4	D	148	HEM	CMD-C2D-C1D	-4.17	122.05	128.46
4	B	148	HEM	CMD-C2D-C1D	-4.03	122.26	128.46
4	B	148	HEM	CMA-C3A-C4A	-3.91	122.46	128.46
4	A	142	HEM	CMD-C2D-C1D	-3.88	122.50	128.46

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	142	HEM	2	0
3	B	147	SO4	2	0
4	B	148	HEM	2	0
4	D	148	HEM	3	0

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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.