



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 13, 2017 – 06:02 pm GMT

PDB ID : 3WYO  
Title : Heterodimeric myoglobin formed by domain swapping  
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Deposited on : 2014-09-04  
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](mailto: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.

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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)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

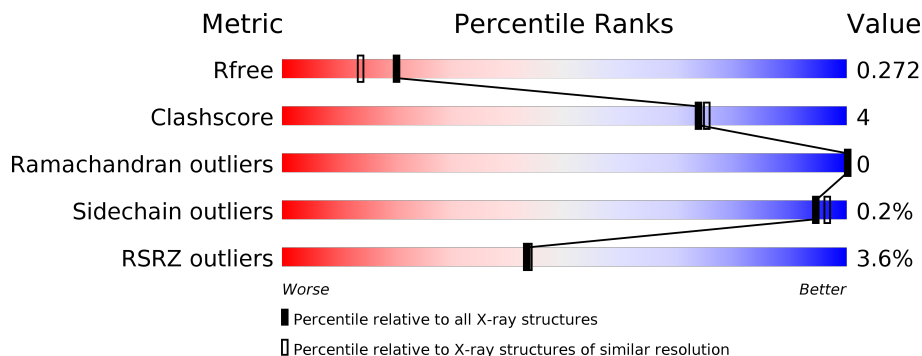
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	100719	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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.

Mol	Chain	Length	Quality of chain
1	A	153	<div> <div>6%</div> <div> <div></div> <div>92%</div> <div>8%</div> </div> </div>
1	C	153	<div> <div>4%</div> <div> <div></div> <div>92%</div> <div>8%</div> </div> </div>
2	B	153	<div> <div>%</div> <div> <div></div> <div>96%</div> <div>•</div> </div> </div>
2	D	153	<div> <div>3%</div> <div> <div></div> <div>94%</div> <div>6%</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5351 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	C	N	O	S	0	1	0
			1210	778	215	215	2			
1	C	153	Total	C	N	O	S	0	1	0
			1209	777	213	217	2			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	64	VAL	HIS	ENGINEERED MUTATION	UNP P68082
A	68	HIS	VAL	ENGINEERED MUTATION	UNP P68082
A	85	LYS	GLU	ENGINEERED MUTATION	UNP P68082
A	141	LYS	ASP	ENGINEERED MUTATION	UNP P68082
C	64	VAL	HIS	ENGINEERED MUTATION	UNP P68082
C	68	HIS	VAL	ENGINEERED MUTATION	UNP P68082
C	85	LYS	GLU	ENGINEERED MUTATION	UNP P68082
C	141	LYS	ASP	ENGINEERED MUTATION	UNP P68082

- Molecule 2 is a protein called Myoglobin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	153	Total	C	N	O	S	0	0	0
			1198	766	208	222	2			
2	D	153	Total	C	N	O	S	0	1	0
			1207	771	209	225	2			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	78	GLU	LYS	ENGINEERED MUTATION	UNP P68082
B	79	ASP	LYS	ENGINEERED MUTATION	UNP P68082
D	78	GLU	LYS	ENGINEERED MUTATION	UNP P68082
D	79	ASP	LYS	ENGINEERED MUTATION	UNP P68082

- # HEM

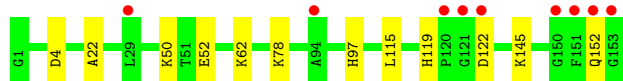
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	94	Total O 94 94	0	0
4	B	128	Total O 128 128	0	0
4	C	46	Total O 46 46	0	0
4	D	87	Total O 87 87	0	0

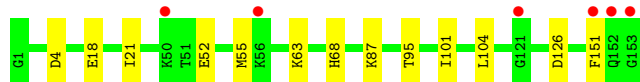
### 3 Residue-property plots [i](#)

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.

#### • Molecule 1: Myoglobin



#### • Molecule 1: Myoglobin



#### • Molecule 2: Myoglobin



#### • Molecule 2: Myoglobin



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.70Å 72.17Å 161.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00 19.44 – 2.00	Depositor EDS
% Data completeness (in resolution range)	91.3 (20.00-2.00) 91.5 (19.44-2.00)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.55 (at 1.99Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, $R_{free}$	0.226 , 0.266 0.232 , 0.272	Depositor DCC
$R_{free}$ test set	1999 reflections (5.11%)	DCC
Wilson B-factor (Å <sup>2</sup> )	24.0	Xtriage
Anisotropy	0.107	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 38.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	5351	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.52% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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.

## 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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.59	0/1238	0.69	1/1659 (0.1%)
1	C	0.60	0/1236	0.74	1/1656 (0.1%)
2	B	0.67	0/1225	0.69	0/1646
2	D	0.66	0/1234	0.67	0/1658
All	All	0.63	0/4933	0.70	2/6619 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4	ASP	CB-CG-OD2	-5.33	113.50	118.30
1	C	126	ASP	CB-CG-OD2	5.24	123.02	118.30

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	1210	0	1234	11	0
1	C	1209	0	1233	10	0
2	B	1198	0	1196	8	0
2	D	1207	0	1201	8	0
3	A	43	0	30	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	43	0	30	1	0
3	C	43	0	30	2	0
3	D	43	0	30	3	0
4	A	94	0	0	1	0
4	B	128	0	0	2	0
4	C	46	0	0	0	0
4	D	87	0	0	2	0
All	All	5351	0	4984	38	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.

The worst 5 of 38 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)
3:A:201:HEM:HBC2	3:A:201:HEM:HMC2	1.68	0.76
3:C:201:HEM:HMC2	3:C:201:HEM:HBC2	1.70	0.73
1:C:4:ASP:OD2	1:C:87:LYS:HD2	1.93	0.69
1:A:152:GLN:HB3	1:C:63:LYS:HD2	1.81	0.62
2:D:52:GLU:HA	2:D:55:MET:HE3	1.83	0.60

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	152/153 (99%)	149 (98%)	3 (2%)	0	100	100
1	C	152/153 (99%)	149 (98%)	3 (2%)	0	100	100
2	B	151/153 (99%)	147 (97%)	4 (3%)	0	100	100
2	D	152/153 (99%)	149 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	607/612 (99%)	594 (98%)	13 (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	124/123 (101%)	123 (99%)	1 (1%)	85	88
1	C	124/123 (101%)	124 (100%)	0	100	100
2	B	123/123 (100%)	123 (100%)	0	100	100
2	D	124/123 (101%)	124 (100%)	0	100	100
All	All	495/492 (101%)	494 (100%)	1 (0%)	94	96

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	82	HIS
2	D	128	GLN
1	C	128	GLN
2	B	9	GLN
2	D	8	GLN

### 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](#)

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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
3	HEM	A	201	1,4	28,50,50	1.15	3 (10%)	17,82,82	1.71	3 (17%)
3	HEM	B	201	1,2	28,50,50	0.91	2 (7%)	17,82,82	1.76	2 (11%)
3	HEM	C	201	1,4	28,50,50	0.82	0	17,82,82	1.83	3 (17%)
3	HEM	D	201	1,2	28,50,50	0.86	1 (3%)	17,82,82	1.57	3 (17%)

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	201	1,4	-	0/6/54/54	0/0/8/8
3	HEM	B	201	1,2	-	0/6/54/54	0/0/8/8
3	HEM	C	201	1,4	-	0/6/54/54	0/0/8/8
3	HEM	D	201	1,2	-	0/6/54/54	0/0/8/8

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	201	HEM	C1B-NB	-3.09	1.33	1.36
3	A	201	HEM	C1B-NB	-3.00	1.33	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	201	HEM	C4D-ND	-2.59	1.33	1.36
3	A	201	HEM	C3B-C2B	-2.41	1.37	1.40
3	B	201	HEM	C1B-NB	-2.23	1.34	1.36

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	201	HEM	CBD-CAD-C3D	-4.82	103.27	112.47
3	C	201	HEM	CBD-CAD-C3D	-4.74	103.42	112.47
3	B	201	HEM	CBD-CAD-C3D	-4.42	104.03	112.47
3	B	201	HEM	CMA-C3A-C4A	-3.54	123.02	128.46
3	D	201	HEM	CMA-C3A-C4A	-2.61	124.45	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
3	A	201	HEM	3	0
3	B	201	HEM	1	0
3	C	201	HEM	2	0
3	D	201	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 [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<sup>th</sup> 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	<RSRZ>	#RSRZ>2		OWAB(Å <sup>2</sup> )	Q<0.9
1	A	153/153 (100%)	0.43	9 (5%)	23 23	14, 32, 63, 109	0
1	C	153/153 (100%)	0.46	6 (3%)	40 40	21, 35, 60, 95	0
2	B	153/153 (100%)	0.13	2 (1%)	77 77	16, 24, 47, 59	0
2	D	153/153 (100%)	0.32	5 (3%)	47 47	17, 31, 57, 82	0
All	All	612/612 (100%)	0.34	22 (3%)	43 44	14, 31, 57, 109	0

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	121	GLY	6.4
1	A	153	GLY	6.4
1	A	151	PHE	5.7
1	C	153	GLY	5.6
2	D	153	GLY	4.5

### 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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	HEM	A	201	43/43	0.95	0.13	-0.48	19,26,34,40	0
3	HEM	C	201	43/43	0.96	0.12	-0.51	17,20,27,35	0
3	HEM	D	201	43/43	0.94	0.13	-0.58	26,32,36,37	0
3	HEM	B	201	43/43	0.97	0.10	-0.70	11,15,23,36	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.