

Full wwPDB X-ray Structure Validation Report (i)

Oct 23, 2021 – 03:02 PM EDT

PDB ID	:	1F65
Title	:	CRYSTAL STRUCTURE OF OXY SPERM WHALE MYOGLOBIN MU-
		TANT $Y(B10)Q(E7)R(E10)$
Authors	:	Brunori, M.; Cutruzzola, F.; Savino, C.; Travaglini-Allocatelli, C.; Vallone,
		B.; Gibson, Q.H.
Deposited on	:	2000-06-20
Resolution	:	1.70 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.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 following versions of software and data (see references (1)) were used in the production of this report:

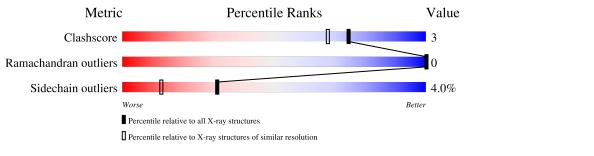
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 1.70 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	$(\# {\rm Entries})$	$(\# { m Entries}, { m resolution} { m range}({ m \AA}))$
Clashscore	141614	4695(1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)

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	А	154	84%	14%	•••



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 1454 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.

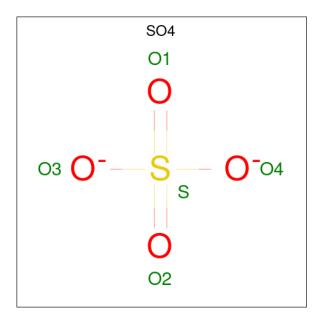
• Molecule 1 is a protein called MYOGLOBIN.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	А	154	Total 1232	C 792	N 220	0 217	${ m S} { m 3}$	25	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP P02185
А	29	TYR	LEU	engineered mutation	UNP P02185
А	64	GLN	HIS	engineered mutation	UNP P02185
А	67	ARG	THR	engineered mutation	UNP P02185

• Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	А	1	Total 5	0 4	S 1	0	0

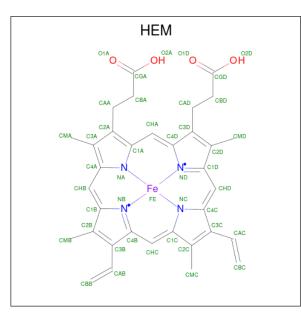
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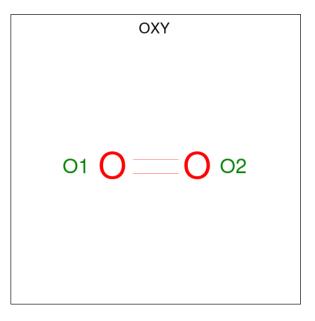
Mol	Chain	Residues	Ato	\mathbf{ms}		ZeroOcc	AltConf
2	А	1	Total 5	0 4	S 1	0	0

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



Mol	Chain	Residues		Ate	\mathbf{oms}			ZeroOcc	AltConf
3	А	1	Total 43	С 34	Fe 1	N 4	0 4	0	0

• Molecule 4 is OXYGEN MOLECULE (three-letter code: OXY) (formula: O_2).





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

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	167	Total O 167 167	0	0

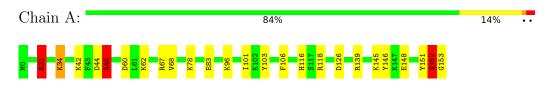


3 Residue-property plots (i)

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 6	Depositor
Cell constants	90.33Å 90.33Å 45.24Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	14.80 - 1.70	Depositor
% Data completeness	95.0 (14.80-1.70)	Depositor
(in resolution range)	55.0 (14.00-1.10)	Depositor
R_{merge}	0.08	Depositor
R _{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.180 , 0.230	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1454	wwPDB-VP
Average B, all atoms $(Å^2)$	14.0	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, SO4, OXY

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	Bo	Bond lengths		ond angles
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	1.45	3/1260~(0.2%)	2.12	30/1689~(1.8%)

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	А	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	Ideal(Å)
1	А	152	GLN	CG-CD	37.77	2.38	1.51
1	А	45	ARG	CD-NE	-13.00	1.24	1.46
1	А	62	LYS	CD-CE	-6.11	1.35	1.51

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	118	ARG	NE-CZ-NH2	31.40	136.00	120.30
1	А	152	GLN	CG-CD-OE1	-25.82	69.96	121.60
1	А	118	ARG	NE-CZ-NH1	-25.52	107.54	120.30
1	А	45	ARG	CG-CD-NE	19.64	153.03	111.80
1	А	45	ARG	CD-NE-CZ	16.95	147.32	123.60
1	А	152	GLN	CG-CD-NE2	13.61	149.36	116.70
1	А	31	ARG	NE-CZ-NH2	-10.64	114.98	120.30
1	А	146	TYR	CB-CG-CD1	10.64	127.39	121.00
1	А	31	ARG	NE-CZ-NH1	10.19	125.40	120.30
1	А	146	TYR	CB-CG-CD2	-9.80	115.12	121.00

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Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	103	TYR	CB-CG-CD2	-9.67	115.20	121.00
1	А	152	GLN	CB-CG-CD	-9.64	86.54	111.60
1	А	118	ARG	CD-NE-CZ	8.40	135.37	123.60
1	А	60	ASP	CB-CG-OD1	8.38	125.84	118.30
1	А	34	LYS	CD-CE-NZ	7.20	128.26	111.70
1	А	126	ASP	CB-CG-OD2	-7.09	111.92	118.30
1	А	67	ARG	NE-CZ-NH1	6.96	123.78	120.30
1	А	67	ARG	CD-NE-CZ	-6.81	114.06	123.60
1	А	106	PHE	CB-CG-CD2	-6.56	116.21	120.80
1	А	60	ASP	CB-CG-OD2	-6.47	112.48	118.30
1	А	148	GLU	OE1-CD-OE2	-6.20	115.86	123.30
1	А	139	ARG	NE-CZ-NH2	-5.51	117.54	120.30
1	А	42	LYS	O-C-N	-5.38	114.08	122.70
1	А	139	ARG	NE-CZ-NH1	5.34	122.97	120.30
1	А	68	VAL	CA-CB-CG2	-5.25	103.03	110.90
1	А	83	GLU	OE1-CD-OE2	-5.14	117.14	123.30
1	А	106	PHE	CB-CG-CD1	5.12	124.39	120.80
1	А	118	ARG	CG-CD-NE	5.08	122.47	111.80
1	А	44	ASP	CB-CG-OD2	-5.04	113.77	118.30
1	А	34	LYS	CA-CB-CG	5.02	124.44	113.40

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There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	А	152	GLN	Sidechain
1	А	45	ARG	Sidechain

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	А	1232	0	1258	7	0
2	А	10	0	0	0	0
3	А	43	0	30	1	0
4	А	2	0	0	0	0
5	А	167	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	1454	0	1288	8	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 3.

All (8) 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:200:HEM:HMC2	3:A:200:HEM:HBC2	1.75	0.69
1:A:31:ARG:HA	1:A:34:LYS:HE2	1.79	0.64
1:A:101:ILE:HG12	1:A:153:GLY:OXT	2.09	0.52
1:A:151:TYR:CE2	1:A:153:GLY:HA3	2.48	0.49
1:A:31:ARG:HD2	5:A:461:HOH:O	2.14	0.47
1:A:116:HIS:HE1	5:A:455:HOH:O	2.01	0.43
1:A:145:LYS:HD2	1:A:145:LYS:HA	1.91	0.41
1:A:151:TYR:CZ	1:A:153:GLY:HA3	2.56	0.41

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	А	152/154~(99%)	150 (99%)	2(1%)	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 side chain 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	А	126/126~(100%)	121 (96%)	5 (4%)	31 13

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	31	ARG
1	А	45	ARG
1	А	78	LYS
1	А	96	LYS
1	А	152	GLN

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

Mol	Chain	Res	Type
1	А	116	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)

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



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
3	HEM	А	200	1,4	$27,\!50,\!50$	1.96	7 (25%)	17,82,82	2.21	5 (29%)
2	SO4	А	413	-	4,4,4	1.08	0	$6,\!6,\!6$	0.85	0
4	OXY	А	201	3	1,1,1	0.09	0	-		
2	SO4	А	414	-	4,4,4	0.66	0	$6,\!6,\!6$	0.83	0

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).

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	А	200	1,4	-	0/6/54/54	-

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
3	А	200	HEM	C3C-C2C	-4.71	1.33	1.40
3	А	200	HEM	C3B-C2B	-4.43	1.34	1.40
3	А	200	HEM	C3C-CAC	3.46	1.54	1.47
3	А	200	HEM	C3B-CAB	2.79	1.53	1.47
3	А	200	HEM	CAD-C3D	2.70	1.57	1.52
3	А	200	HEM	CMB-C2B	2.09	1.56	1.51
3	А	200	HEM	CMD-C2D	2.01	1.55	1.51

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
3	А	200	HEM	CBD-CAD-C3D	-5.92	101.56	112.48
3	А	200	HEM	CMD-C2D-C1D	-3.87	122.52	128.46
3	А	200	HEM	CMD-C2D-C3D	2.41	129.48	124.94
3	А	200	HEM	CMC-C2C-C3C	2.07	128.55	124.68
3	А	200	HEM	CMA-C3A-C4A	-2.05	125.31	128.46

There are no chirality outliers.

There are no torsion outliers.

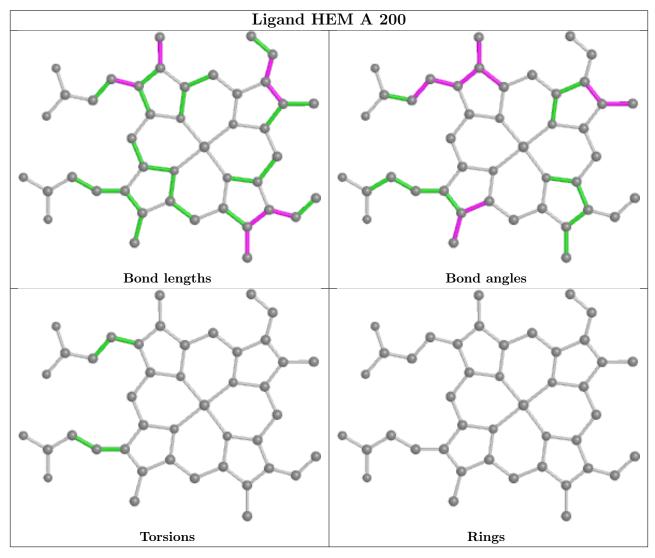
There are no ring outliers.

1 monomer is involved in 1 short contact:



	Mol	Chain	Res	Type	Clashes	Symm-Clashes
Γ	3	А	200	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 sufficient 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.

