WORLDWIDE wwPDB PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 09:16 am GMT

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PDB ID	:	1QJS
Title	:	MAMMALIAN BLOOD SERUM HAEMOPEXIN GLYCOSYLATED-NATIVE PROTEIN AND IN COMPLEX WITH ITS LIGAND HAEM
Authors	:	Paoli, M.; Baker, H.M.; Morgan, W.T.; Smith, A.; Baker, E.N.
Deposited on	:	1999-07-01
Resolution	:	2.90 Å(reported)

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 2.90 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	Percentile Ranks	Value
Clashscore		14
Ramachandran outliers		1.0%
Sidechain outliers		9.8%
RSRZ outliers		20.2%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
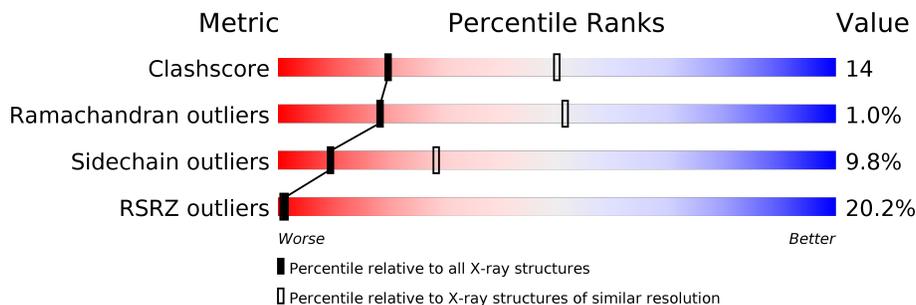
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	112137	1807 (2.90-2.90)
Ramachandran outliers	110173	1768 (2.90-2.90)
Sidechain outliers	110143	1770 (2.90-2.90)
RSRZ outliers	101464	1596 (2.90-2.90)

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 <=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	460	12% — 62% / 21% / 5% / 11%
1	B	460	23% — 60% / 23% / 5% / 11%

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
2	HEM	B	500	-	-	X	X
3	PO4	B	501	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	CL	B	511	-	-	-	X
5	NA	A	512	-	-	-	X
5	NA	B	513	-	-	-	X

2 Entry composition ⓘ

There are 5 unique types of molecules in this entry. The entry contains 6686 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 HEMOPEXIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	408	Total	C	N	O	S	0	0	0
			3289	2102	579	592	16			
1	B	408	Total	C	N	O	S	0	0	0
			3289	2102	579	592	16			

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).
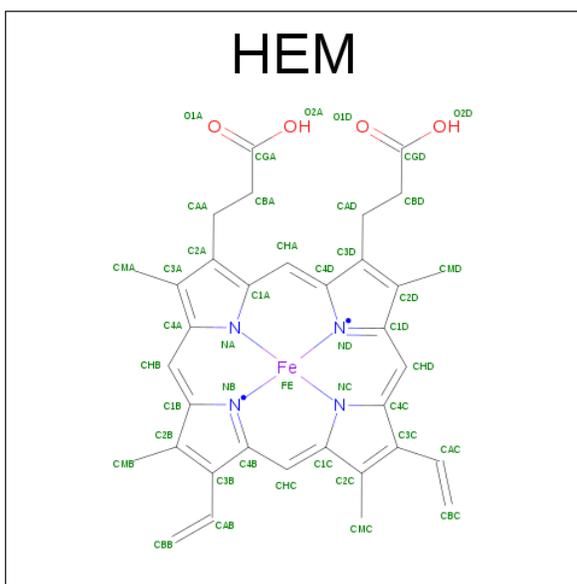
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).

PO4

O3

O⁻

O2 O⁻ — P = O O1

P

O⁻

O4
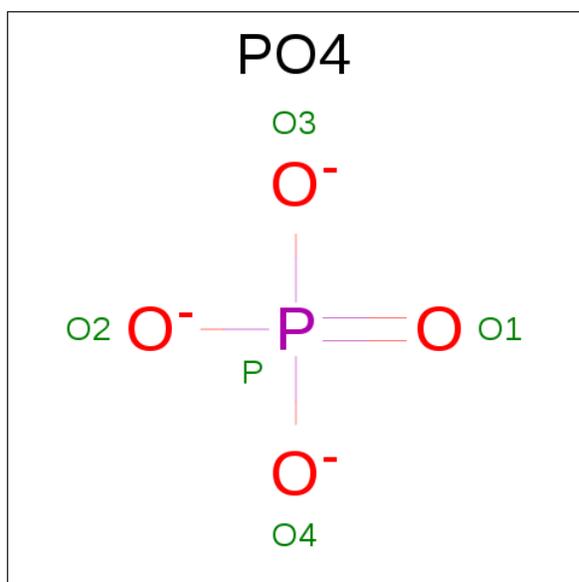
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 5	O 4	P 1	0	0
3	B	1	Total 5	O 4	P 1	0	0

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	2	Total 2	Cl 2	0	0
4	A	2	Total 2	Cl 2	0	0

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	4	Total 4	Na 4	0	0
5	A	4	Total 4	Na 4	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: HEMOPEXIN

Chain A:

- Molecule 1: HEMOPEXIN

Chain B:

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	103.90Å 69.90Å 151.81Å 90.00° 108.16° 90.00°	Depositor
Resolution (Å)	20.00 – 2.90 19.90 – 2.96	Depositor EDS
% Data completeness (in resolution range)	97.5 (20.00-2.90) 96.3 (19.90-2.96)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	2.10 (at 2.98Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.255 , 0.312 0.338 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å^2)	59.9	Xtriage
Anisotropy	0.478	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 23.9	EDS
L-test for twinning[2]	$<|L|> = 0.48, <L^2> = 0.32$	Xtriage
Estimated twinning fraction	0.019 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.78	EDS
Total number of atoms	6686	wwPDB-VP
Average B, all atoms (Å^2)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.39% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]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, PO4, CL, NA

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	0.74	2/3400 (0.1%)	1.39	27/4624 (0.6%)
1	B	0.71	4/3400 (0.1%)	1.28	28/4624 (0.6%)
All	All	0.72	6/6800 (0.1%)	1.33	55/9248 (0.6%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	435	HIS	N-CA	-19.25	1.07	1.46
1	B	435	HIS	N-CA	-10.09	1.26	1.46
1	A	434	THR	C-N	-9.07	1.13	1.34
1	B	434	THR	CA-C	-8.59	1.30	1.52
1	B	434	THR	C-N	-6.05	1.20	1.34

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	434	THR	O-C-N	29.98	170.66	122.70
1	A	434	THR	CA-C-N	-25.70	60.66	117.20
1	A	434	THR	C-N-CA	9.55	145.57	121.70
1	B	126	CYS	CA-CB-SG	-9.34	97.19	114.00
1	A	126	CYS	CA-CB-SG	-9.23	97.39	114.00

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	3289	0	3120	93	0
1	B	3289	0	3121	110	12
2	A	43	0	30	7	0
2	B	43	0	30	24	0
3	A	5	0	0	1	0
3	B	5	0	0	2	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
5	A	4	0	0	0	0
5	B	4	0	0	0	0
All	All	6686	0	6301	185	12

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 14.

The worst 5 of 185 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:A:434:THR:HG23	1:A:435:HIS:CB	1.24	1.65
1:A:434:THR:CG2	1:A:435:HIS:HB3	1.54	1.37
1:A:434:THR:CG2	1:A:435:HIS:CB	2.04	1.30
1:A:411:HIS:CE1	1:B:100:LYS:NZ	2.04	1.25
1:A:411:HIS:HE1	1:B:100:LYS:NZ	1.39	1.15

The worst 5 of 12 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:118:PHE:CZ	1:B:312:ASN:CG[4_556]	1.31	0.89
1:B:51:PHE:CE1	1:B:156:GLU:O[4_556]	1.44	0.76
1:B:118:PHE:CE1	1:B:312:ASN:ND2[4_556]	1.73	0.47
1:B:118:PHE:CZ	1:B:312:ASN:OD1[4_556]	1.80	0.40
1:B:118:PHE:CE2	1:B:312:ASN:CB[4_556]	1.88	0.32

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	404/460 (88%)	370 (92%)	30 (7%)	4 (1%)	18	51
1	B	404/460 (88%)	369 (91%)	31 (8%)	4 (1%)	18	51
All	All	808/920 (88%)	739 (92%)	61 (8%)	8 (1%)	18	51

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	101	ASN
1	A	296	ASP
1	B	101	ASN
1	B	296	ASP
1	A	55	SER

5.3.2 Protein sidechains ⓘ

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	352/393 (90%)	317 (90%)	35 (10%)	9	28
1	B	352/393 (90%)	318 (90%)	34 (10%)	9	29
All	All	704/786 (90%)	635 (90%)	69 (10%)	9	28

5 of 69 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	410	ARG

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Mol	Chain	Res	Type
1	B	56	HIS
1	B	376	VAL
1	A	411	HIS
1	B	26	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	411	HIS
1	B	26	GLN
1	B	243	ASN
1	A	243	ASN
1	B	142	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 16 ligands modelled in this entry, 12 are monoatomic - leaving 4 for Mogul analysis.

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
2	HEM	A	500	1	28,50,50	1.87	7 (25%)	17,82,82	1.90	5 (29%)
3	PO4	A	501	-	4,4,4	1.47	0	6,6,6	1.33	1 (16%)
2	HEM	B	500	1	28,50,50	1.49	4 (14%)	17,82,82	3.53	10 (58%)
3	PO4	B	501	-	4,4,4	1.48	0	6,6,6	1.33	1 (16%)

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
2	HEM	A	500	1	-	0/6/54/54	0/0/8/8
3	PO4	A	501	-	-	0/0/0/0	0/0/0/0
2	HEM	B	500	1	-	0/6/54/54	0/0/8/8
3	PO4	B	501	-	-	0/0/0/0	0/0/0/0

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	500	HEM	C3B-CAB	-5.82	1.36	1.47
2	A	500	HEM	C3C-CAC	-3.47	1.40	1.47
2	A	500	HEM	C1C-NC	-3.34	1.32	1.36
2	A	500	HEM	C4D-ND	-3.12	1.33	1.36
2	A	500	HEM	C4C-NC	-2.85	1.33	1.36

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	500	HEM	C4A-C3A-C2A	-4.31	104.00	107.00
2	B	500	HEM	C4A-C3A-C2A	-4.25	104.04	107.00
2	B	500	HEM	CMD-C2D-C3D	-3.42	118.49	124.94
2	A	500	HEM	C4C-C3C-C2C	-2.86	104.90	106.90
2	B	500	HEM	C3C-C4C-NC	-2.55	106.12	110.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 34 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	HEM	7	0
3	A	501	PO4	1	0
2	B	500	HEM	24	0
3	B	501	PO4	2	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6   Fit of model and data ⓘ

6.1   Protein, DNA and RNA chains ⓘ

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, 95th 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(Å²)	Q<0.9
1	A	408/460 (88%)	1.03	57 (13%)	3	2	19, 39, 59, 70	0
1	B	408/460 (88%)	1.52	108 (26%)	1	0	18, 38, 59, 68	0
All	All	816/920 (88%)	1.27	165 (20%)	1	1	18, 38, 59, 70	0

The worst 5 of 165 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	341	GLY	9.9
1	B	101	ASN	7.2
1	A	217	HIS	7.2
1	A	101	ASN	7.0
1	A	423	GLN	6.9

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

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

6.3   Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4   Ligands ⓘ

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, 95th 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.

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
5	NA	A	512	1/1	0.78	0.48	4.18	33,33,33,33	0
4	CL	B	511	1/1	0.45	0.51	3.61	26,26,26,26	0
2	HEM	B	500	43/43	0.58	0.65	3.34	14,30,39,40	0
3	PO4	A	501	5/5	0.84	0.31	1.82	18,19,20,20	5
3	PO4	B	501	5/5	0.76	0.40	1.72	18,19,20,20	5
5	NA	B	513	1/1	0.37	0.41	1.34	32,32,32,32	0
4	CL	B	521	1/1	0.83	0.31	0.28	20,20,20,20	0
4	CL	A	521	1/1	0.84	0.23	0.26	20,20,20,20	0
5	NA	B	523	1/1	0.91	0.27	-0.15	27,27,27,27	0
5	NA	A	522	1/1	0.67	0.23	-0.47	26,26,26,26	0
5	NA	A	513	1/1	0.17	0.23	-0.60	32,32,32,32	0
2	HEM	A	500	43/43	0.89	0.23	-0.67	23,33,49,60	0
5	NA	B	512	1/1	0.49	0.25	-0.84	33,33,33,33	0
4	CL	A	511	1/1	0.90	0.16	-1.56	26,26,26,26	0
5	NA	A	523	1/1	0.89	0.15	-1.67	27,27,27,27	0
5	NA	B	522	1/1	0.58	0.17	-3.44	26,26,26,26	0

6.5 Other polymers ⓘ

There are no such residues in this entry.