



# Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 04:50 PM GMT

PDB ID : 1GCV  
Title : DEOXY FORM HEMOGLOBIN FROM MUSTELUS GRISEUS  
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Deposited on : 2000-08-08  
Resolution : 2.00 Å(reported)

This is a full wwPDB validation 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/ValidationPDFNotes.html>

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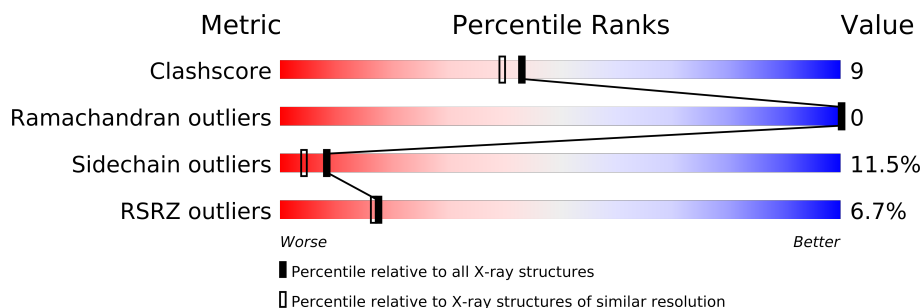
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

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))
Clashscore	79885	6188 (2.00-2.00)
Ramachandran outliers	78287	6102 (2.00-2.00)
Sidechain outliers	78261	6100 (2.00-2.00)
RSRZ outliers	66119	4890 (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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	140	
1	C	140	
2	B	136	
2	D	136	

## 2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 4722 atoms, of which 0 are hydrogen and 0 are deuterium.

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	140	Total	C	N	O	S	0	0	0
			1075	683	185	201	6			
1	C	140	Total	C	N	O	S	0	0	0
			1075	683	185	201	6			

- Molecule 2 is a protein called HEMOGLOBIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	136	Total	C	N	O	S	0	0	0
			1126	723	193	205	5			
2	D	136	Total	C	N	O	S	0	0	0
			1126	723	193	205	5			

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



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	47	Total 47	O 47	0	0
4	B	40	Total 40	O 40	0	0
4	C	34	Total 34	O 34	0	0
4	D	27	Total 27	O 27	0	0

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

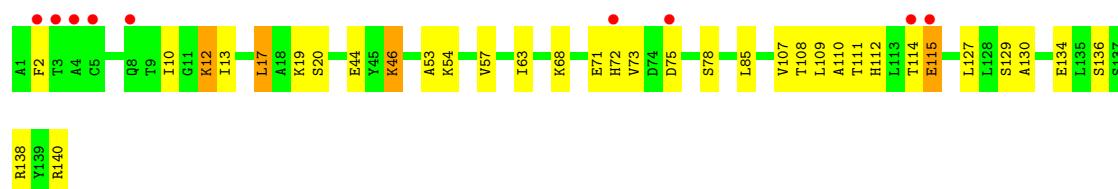
- Molecule 1: HEMOGLOBIN

Chain A: 



- Molecule 1: HEMOGLOBIN

Chain C: 



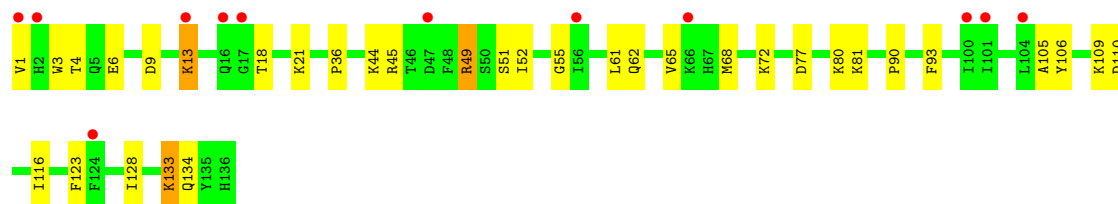
- Molecule 2: HEMOGLOBIN

Chain B: 



- Molecule 2: HEMOGLOBIN

Chain D: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	57.68Å 90.55Å 61.45Å 90.00° 98.45° 90.00°	Depositor
Resolution (Å)	10.00 – 2.00 27.03 – 2.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-2.00) 98.8 (27.03-2.00)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, $R_{free}$	0.181 , 0.223 0.191 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	27.1	Xtriage
Anisotropy	0.080	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.46 , 58.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 41723 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	4722	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.69% of the height of the origin peak. No significant pseudotranslation is detected.*

## 5 Model quality

### 5.1 Standard geometry

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	0.34	0/1097	0.55	0/1484
1	C	0.34	0/1097	0.54	0/1484
2	B	0.36	0/1155	0.57	0/1560
2	D	0.36	0/1155	0.54	0/1560
All	All	0.35	0/4504	0.55	0/6088

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1075	0	1085	23	0
1	C	1075	0	1085	18	0
2	B	1126	0	1105	23	0
2	D	1126	0	1105	24	0
3	A	43	0	30	0	0
3	B	43	0	30	2	0
3	C	43	0	30	0	0
3	D	43	0	30	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	47	0	0	0	0
4	B	40	0	0	1	0
4	C	34	0	0	0	0
4	D	27	0	0	2	0
All	All	4722	0	4500	80	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 9.

All (80) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:138:ARG:HH11	1:A:138:ARG:HG2	1.39	0.87
1:C:46:LYS:H	1:C:46:LYS:HE3	1.51	0.74
2:B:124:PHE:O	2:B:128:ILE:HG12	1.89	0.73
2:B:72:LYS:HD3	2:B:133:LYS:NZ	2.05	0.70
1:A:15:GLN:HA	1:A:15:GLN:HE21	1.56	0.69
1:C:111:THR:HG22	2:D:105:ALA:HB1	1.79	0.65
1:A:98:PHE:HB2	1:A:99:PRO:HD3	1.78	0.65
2:D:9:ASP:O	2:D:13:LYS:HB2	1.96	0.64
1:A:31:ARG:HD3	2:B:117:GLN:OE1	1.99	0.63
1:C:68:LYS:O	1:C:72:HIS:HD2	1.83	0.62
2:D:3:TRP:HH2	2:D:123:PHE:HA	1.64	0.62
1:A:140:ARG:HB3	2:D:36:PRO:HG3	1.81	0.61
1:A:120:THR:O	1:A:124:VAL:HG23	2.02	0.59
2:B:9:ASP:O	2:B:13:LYS:HB2	2.02	0.59
2:D:49:ARG:HD2	2:D:51:SER:OG	2.03	0.59
1:A:138:ARG:HH11	1:A:138:ARG:CG	2.13	0.59
2:D:80:LYS:HG3	2:D:134:GLN:HG3	1.85	0.58
1:C:17:LEU:HD11	1:C:109:LEU:HD21	1.86	0.57
2:D:61:LEU:O	2:D:65:VAL:HG23	2.05	0.56
1:A:138:ARG:NH1	1:A:138:ARG:HG2	2.15	0.56
2:B:11:ILE:HD13	2:B:68:MET:HE1	1.87	0.56
1:A:115:GLU:O	1:A:115:GLU:HG3	2.05	0.56
1:C:115:GLU:HG3	1:C:115:GLU:O	2.05	0.55
2:B:13:LYS:HE3	2:B:13:LYS:HA	1.89	0.55
2:D:49:ARG:HG2	2:D:52:ILE:H	1.71	0.55
2:B:90:PRO:HD3	2:B:135:TYR:CE1	2.42	0.55
2:D:45:ARG:CZ	2:D:45:ARG:HB2	2.37	0.55
2:B:93:PHE:HB3	2:B:128:ILE:HD12	1.89	0.54
2:B:72:LYS:HD3	2:B:133:LYS:HZ1	1.72	0.54
1:C:85:LEU:HD21	1:C:138:ARG:CZ	2.38	0.53
1:A:13:ILE:HD13	1:A:124:VAL:CG2	2.39	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:D:49:ARG:HG2	2:D:52:ILE:HB	1.91	0.52
2:D:128:ILE:HD13	4:D:1102:HOH:O	2.10	0.51
1:C:107:VAL:O	1:C:111:THR:HG23	2.12	0.50
1:C:111:THR:HB	2:D:109:LYS:O	2.12	0.50
1:C:85:LEU:HD21	1:C:138:ARG:NH2	2.28	0.48
2:D:49:ARG:CG	2:D:52:ILE:H	2.26	0.48
1:A:133:GLN:HG3	1:A:134:GLU:N	2.27	0.47
1:A:9:THR:HG22	1:A:13:ILE:HD12	1.97	0.47
2:D:49:ARG:HG2	2:D:52:ILE:CB	2.44	0.47
1:A:108:THR:O	1:A:112:HIS:HD2	1.97	0.47
2:B:3:TRP:HH2	2:B:123:PHE:HA	1.78	0.47
2:D:128:ILE:HG21	4:D:1102:HOH:O	2.15	0.46
2:B:72:LYS:HD3	2:B:133:LYS:CE	2.45	0.46
2:D:90:PRO:HA	2:D:93:PHE:CE1	2.50	0.46
2:B:11:ILE:HD13	2:B:68:MET:CE	2.46	0.46
2:B:86:LEU:HD22	3:B:137:HEM:HAD2	1.97	0.46
2:B:6:GLU:OE2	2:B:115:HIS:HE1	1.99	0.46
1:A:138:ARG:NH1	1:A:138:ARG:CG	2.73	0.46
1:A:13:ILE:HD11	1:A:120:THR:HG23	1.97	0.45
1:C:53:ALA:O	1:C:57:VAL:HG23	2.16	0.45
2:B:4:THR:OG1	2:B:7:GLU:HG3	2.18	0.44
2:B:61:LEU:O	2:B:65:VAL:HG23	2.17	0.44
1:C:111:THR:CG2	2:D:105:ALA:HB1	2.46	0.44
2:D:133:LYS:HD3	2:D:133:LYS:HA	1.50	0.44
1:A:13:ILE:HD11	1:A:120:THR:CG2	2.47	0.44
2:D:21:LYS:HG3	2:D:55:GLY:HA2	1.98	0.44
2:B:11:ILE:CD1	2:B:68:MET:HE1	2.48	0.44
2:B:41:TYR:CE1	2:B:88:VAL:HA	2.53	0.43
1:A:88:GLY:HA2	1:A:139:TYR:CE1	2.53	0.43
1:C:108:THR:O	1:C:112:HIS:HD2	2.02	0.43
1:C:110:ALA:O	2:D:106:TYR:HA	2.18	0.43
1:C:2:PHE:CE2	1:C:10:ILE:HD11	2.53	0.43
2:B:109:LYS:HB3	2:B:110:ASP:H	1.55	0.43
1:C:130:ALA:O	1:C:134:GLU:HG2	2.19	0.43
2:B:81:LYS:O	2:B:85:ASP:HB2	2.19	0.43
1:A:38:GLY:HA3	2:D:90:PRO:CG	2.50	0.42
2:B:45:ARG:NE	3:B:137:HEM:HBD1	2.35	0.41
1:A:84:ALA:CB	1:A:138:ARG:HD3	2.50	0.41
1:C:63:ILE:HA	1:C:63:ILE:HD13	1.88	0.41
1:A:13:ILE:HD13	1:A:124:VAL:HG22	2.03	0.41
2:B:80:LYS:HG3	2:B:134:GLN:HG3	2.02	0.41
1:A:76:LEU:HD23	1:A:76:LEU:HA	1.92	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:140:ARG:HB3	2:D:36:PRO:CG	2.51	0.41
2:D:13:LYS:HE3	2:D:13:LYS:HA	2.03	0.41
2:B:72:LYS:HE2	4:B:1044:HOH:O	2.20	0.40
1:C:12:LYS:HG2	1:C:13:ILE:N	2.36	0.40
1:C:2:PHE:HZ	1:C:127:LEU:HA	1.86	0.40
1:A:56:GLN:HB3	1:A:56:GLN:HE21	1.72	0.40
2:D:116:ILE:HD13	2:D:116:ILE:HA	1.95	0.40

There are no symmetry-related clashes.

## 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	138/140 (99%)	133 (96%)	5 (4%)	0	100	100
1	C	138/140 (99%)	134 (97%)	4 (3%)	0	100	100
2	B	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
2	D	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
All	All	544/552 (99%)	526 (97%)	18 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	116/116 (100%)	105 (90%)	11 (10%)	12	7
1	C	116/116 (100%)	100 (86%)	16 (14%)	5	2

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	124/124 (100%)	110 (89%)	14 (11%)	9	4
2	D	124/124 (100%)	110 (89%)	14 (11%)	9	4
All	All	480/480 (100%)	425 (88%)	55 (12%)	8	4

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	CYS
1	A	8	GLN
1	A	15	GLN
1	A	46	LYS
1	A	78	SER
1	A	115	GLU
1	A	119	ASP
1	A	133	GLN
1	A	135	LEU
1	A	138	ARG
1	A	140	ARG
2	B	13	LYS
2	B	16	GLN
2	B	33	LYS
2	B	44	LYS
2	B	49	ARG
2	B	68	MET
2	B	70	ASP
2	B	73	THR
2	B	76	LYS
2	B	81	LYS
2	B	85	ASP
2	B	108	ARG
2	B	109	LYS
2	B	133	LYS
1	C	12	LYS
1	C	17	LEU
1	C	19	LYS
1	C	20	SER
1	C	44	GLU
1	C	46	LYS
1	C	54	LYS
1	C	71	GLU
1	C	73	VAL

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Mol	Chain	Res	Type
1	C	75	ASP
1	C	78	SER
1	C	114	THR
1	C	115	GLU
1	C	129	SER
1	C	136	SER
1	C	140	ARG
2	D	1	VAL
2	D	4	THR
2	D	6	GLU
2	D	13	LYS
2	D	18	THR
2	D	44	LYS
2	D	49	ARG
2	D	62	GLN
2	D	68	MET
2	D	72	LYS
2	D	77	ASP
2	D	81	LYS
2	D	110	ASP
2	D	133	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	GLN
1	A	56	GLN
1	A	97	ASN
2	B	16	GLN
2	B	67	HIS
2	B	87	HIS
2	B	115	HIS
1	C	8	GLN
1	C	36	HIS
1	C	72	HIS
2	D	53	HIS
2	D	115	HIS

### 5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

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	141	1	49,50,50	2.45	14 (28%)	46,82,82	1.46	9 (19%)
3	HEM	B	137	2	49,50,50	1.94	14 (28%)	46,82,82	1.46	6 (13%)
3	HEM	C	141	1	49,50,50	3.14	22 (44%)	46,82,82	1.24	6 (13%)
3	HEM	D	137	2	49,50,50	2.33	11 (22%)	46,82,82	1.54	9 (19%)

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	141	1	-	0/14/114/114	0/0/8/8
3	HEM	B	137	2	-	0/14/114/114	0/0/8/8
3	HEM	C	141	1	-	0/14/114/114	0/0/8/8
3	HEM	D	137	2	-	0/14/114/114	0/0/8/8

All (61) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	141	HEM	C3D-C4D	12.82	1.47	1.44
3	D	137	HEM	C3D-C4D	10.37	1.47	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	141	HEM	C2D-C1D	9.76	1.47	1.44
3	A	141	HEM	C2B-C1B	8.88	1.46	1.44
3	A	141	HEM	C3D-C4D	7.79	1.46	1.44
3	B	137	HEM	C3D-C4D	5.83	1.46	1.44
3	D	137	HEM	C3B-C2B	-5.13	1.34	1.43
3	C	141	HEM	C4A-C3A	5.09	1.46	1.40
3	C	141	HEM	C3B-C2B	-4.61	1.35	1.43
3	A	141	HEM	C3D-C2D	-4.53	1.35	1.43
3	B	137	HEM	C3D-C2D	-4.47	1.35	1.43
3	D	137	HEM	C4A-C3A	4.30	1.45	1.40
3	C	141	HEM	C4C-NC	4.29	1.44	1.38
3	D	137	HEM	C3D-C2D	-4.00	1.36	1.43
3	C	141	HEM	C3D-C2D	-3.91	1.36	1.43
3	B	137	HEM	C3B-C4B	3.85	1.49	1.44
3	D	137	HEM	C3C-C2C	-3.83	1.37	1.43
3	B	137	HEM	CHA-C4D	3.82	1.41	1.35
3	C	141	HEM	CHA-C4D	3.68	1.41	1.35
3	A	141	HEM	C3C-C2C	-3.66	1.37	1.43
3	B	137	HEM	C3C-C2C	-3.63	1.37	1.43
3	A	141	HEM	CHA-C4D	3.44	1.40	1.35
3	C	141	HEM	CHC-C1C	3.43	1.42	1.36
3	A	141	HEM	C4A-C3A	3.35	1.44	1.40
3	D	137	HEM	C3B-C4B	3.34	1.48	1.44
3	C	141	HEM	C3C-C2C	-3.22	1.38	1.43
3	A	141	HEM	C3B-C2B	-3.20	1.38	1.43
3	A	141	HEM	C2D-C1D	3.18	1.45	1.44
3	B	137	HEM	C4A-C3A	3.13	1.44	1.40
3	A	141	HEM	CHB-C1B	3.12	1.40	1.35
3	C	141	HEM	CHB-C1B	2.95	1.40	1.35
3	B	137	HEM	CHC-C1C	2.92	1.41	1.36
3	C	141	HEM	C1A-C2A	2.74	1.48	1.43
3	C	141	HEM	C4A-NA	2.73	1.41	1.36
3	B	137	HEM	C3B-C2B	-2.70	1.39	1.43
3	C	141	HEM	C3B-C4B	2.53	1.47	1.44
3	D	137	HEM	C4A-NA	2.48	1.41	1.36
3	D	137	HEM	CHA-C4D	2.43	1.39	1.35
3	C	141	HEM	C1D-ND	2.43	1.43	1.37
3	A	141	HEM	C3B-C4B	2.38	1.47	1.44
3	C	141	HEM	FE-NC	2.36	2.06	1.97
3	A	141	HEM	C4A-NA	2.35	1.41	1.36
3	C	141	HEM	FE-NA	2.33	2.02	1.92
3	D	137	HEM	CHC-C1C	2.32	1.40	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	137	HEM	CMB-C2B	2.26	1.54	1.47
3	B	137	HEM	C4A-NA	2.23	1.40	1.36
3	C	141	HEM	C1A-NA	2.23	1.40	1.36
3	C	141	HEM	C1C-NC	2.22	1.41	1.38
3	B	137	HEM	CBB-CAB	2.20	1.41	1.28
3	A	141	HEM	FE-NA	2.19	2.01	1.92
3	C	141	HEM	CBC-CAC	2.13	1.41	1.28
3	D	137	HEM	CBC-CAC	2.12	1.41	1.28
3	B	137	HEM	CBC-CAC	2.08	1.40	1.28
3	C	141	HEM	C2C-C1C	2.07	1.49	1.43
3	B	137	HEM	C1C-NC	2.07	1.41	1.38
3	C	141	HEM	CMB-C2B	2.05	1.53	1.47
3	D	137	HEM	CHD-C4C	2.05	1.40	1.36
3	A	141	HEM	CBC-CAC	2.04	1.40	1.28
3	C	141	HEM	CBB-CAB	2.03	1.40	1.28
3	A	141	HEM	CMD-C2D	2.01	1.53	1.47
3	B	137	HEM	CMC-C2C	2.00	1.53	1.47

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	137	HEM	C3B-C4B-NB	-5.28	110.22	114.00
3	D	137	HEM	C3B-C4B-NB	-4.79	110.57	114.00
3	C	141	HEM	C3B-C4B-NB	-4.15	111.03	114.00
3	A	141	HEM	C3B-C4B-NB	-3.59	111.43	114.00
3	A	141	HEM	C3A-C4A-NA	3.49	112.04	109.41
3	D	137	HEM	C3A-C4A-NA	3.39	111.97	109.41
3	D	137	HEM	C4A-CHB-C1B	-3.29	123.14	127.47
3	B	137	HEM	C4A-CHB-C1B	-3.04	123.47	127.47
3	A	141	HEM	CBA-CAA-C2A	-2.93	107.52	112.69
3	A	141	HEM	C4A-CHB-C1B	-2.81	123.77	127.47
3	D	137	HEM	C4A-NA-C1A	-2.77	103.11	106.76
3	A	141	HEM	CBD-CAD-C3D	-2.76	108.34	114.37
3	B	137	HEM	CBA-CAA-C2A	-2.76	107.83	112.69
3	B	137	HEM	C3A-C4A-NA	2.64	111.41	109.41
3	D	137	HEM	C1A-CHA-C4D	-2.62	124.02	127.47
3	C	141	HEM	C4A-CHB-C1B	-2.57	124.08	127.47
3	D	137	HEM	CBD-CAD-C3D	-2.53	108.85	114.37
3	A	141	HEM	C4A-NA-C1A	-2.53	103.43	106.76
3	B	137	HEM	C1A-CHA-C4D	-2.46	124.23	127.47
3	D	137	HEM	C1B-NB-C4B	-2.35	102.76	105.16
3	A	141	HEM	C1A-CHA-C4D	-2.34	124.39	127.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	137	HEM	C4A-NA-C1A	-2.24	103.81	106.76
3	D	137	HEM	CAD-C3D-C4D	2.11	128.32	124.53
3	C	141	HEM	C4C-NC-C1C	-2.07	103.38	105.53
3	C	141	HEM	CBD-CAD-C3D	-2.07	109.86	114.37
3	D	137	HEM	C3A-C4A-CHB	-2.05	122.11	126.00
3	C	141	HEM	C3A-C4A-NA	2.03	110.95	109.41
3	C	141	HEM	C4A-NA-C1A	-2.03	104.09	106.76
3	A	141	HEM	C4C-NC-C1C	-2.03	103.43	105.53
3	A	141	HEM	C4A-C3A-C2A	-2.02	105.59	107.00

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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, 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	140/140 (100%)	0.38	11 (7%) 13 12	14, 23, 47, 60	0
1	C	140/140 (100%)	0.33	9 (6%) 19 18	16, 25, 55, 69	0
2	B	136/136 (100%)	0.30	5 (3%) 39 39	14, 24, 42, 51	0
2	D	136/136 (100%)	0.56	12 (8%) 10 9	14, 29, 57, 70	0
All	All	552/552 (100%)	0.39	37 (6%) 17 17	14, 25, 51, 70	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	5	CYS	5.2
2	D	2	HIS	4.5
2	D	16	GLN	4.2
1	A	109	LEU	3.6
1	A	5	CYS	3.5
2	B	17	GLY	3.4
2	D	1	VAL	3.3
1	A	44	GLU	3.3
1	A	105	ILE	3.2
2	D	101	ILE	3.2
2	B	18	THR	3.2
1	C	2	PHE	3.0
2	D	47	ASP	3.0
1	C	3	THR	2.9
2	D	66	LYS	2.8
1	A	1	ALA	2.8
1	C	8	GLN	2.8
2	B	70	ASP	2.8
1	C	72	HIS	2.8
1	C	114	THR	2.7
2	D	17	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	115	GLU	2.6
2	D	100	ILE	2.6
2	D	104	LEU	2.6
1	A	114	THR	2.5
1	A	75	ASP	2.4
1	C	4	ALA	2.4
2	D	124	PHE	2.3
2	D	56	ILE	2.3
2	B	14	THR	2.3
1	A	4	ALA	2.2
1	C	75	ASP	2.2
1	A	133	GLN	2.2
2	D	13	LYS	2.2
1	C	115	GLU	2.1
1	A	107	VAL	2.1
2	B	102	VAL	2.1

## 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, 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	HEM	C	141	43/43	0.15	1.05	17,20,40,47	0
3	HEM	B	137	43/43	0.16	0.93	17,24,45,52	0
3	HEM	D	137	43/43	0.15	-0.11	16,21,36,40	0
3	HEM	A	141	43/43	0.12	-0.21	13,19,43,46	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.