



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:54 PM GMT

PDB ID : 1MNK
Title : INTERACTIONS AMONG RESIDUES CD3, E7, E10 AND E11 IN MYOGLOBINS: ATTEMPTS TO SIMULATE THE O₂ AND CO BINDING PROPERTIES OF APLYSIA MYOGLOBIN
Authors : Krzywda, S.; Wilkinson, A.J.
Deposited on : 1995-01-11
Resolution : 2.20 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
<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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

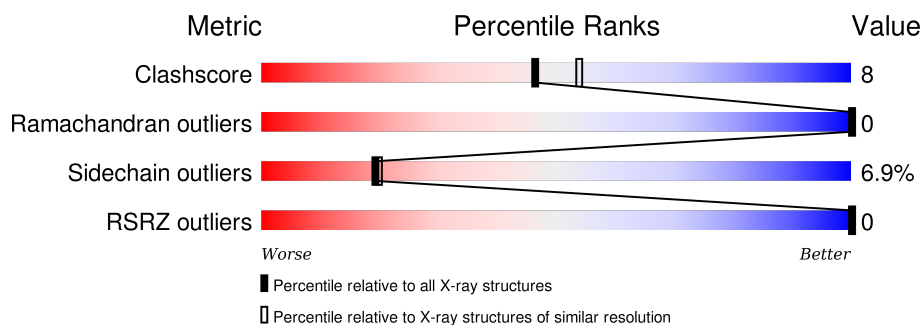
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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.

Mol	Chain	Length	Quality of chain
1	A	153	
1	B	153	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2651 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	151	Total	C	N	O	S	0	0	0
			1180	755	203	219	3			
1	B	151	Total	C	N	O	S	0	0	0
			1180	755	203	219	3			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	64	VAL	HIS	CONFLICT	UNP P02189
A	68	THR	VAL	CONFLICT	UNP P02189
B	64	VAL	HIS	CONFLICT	UNP P02189
B	68	THR	VAL	CONFLICT	UNP P02189

- 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 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

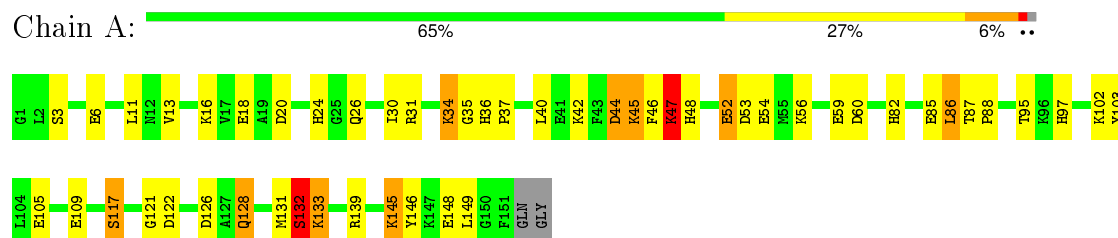
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	90	Total 90	O 90	1	0
3	B	115	Total 115	O 115	1	0

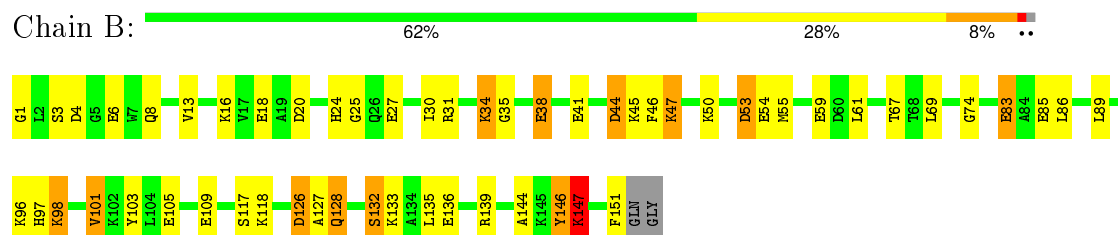
3 Residue-property plots [i](#)

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



• Molecule 1: MYOGLOBIN



4 Data and refinement statistics

Property	Value	Source
Space group	I 21	Depositor
Cell constants a, b, c, α , β , γ	125.26 Å 42.49 Å 92.37 Å 90.00° 92.29° 90.00°	Depositor
Resolution (Å)	10.00 – 2.20 19.81 – 2.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-2.20) 93.4 (19.81-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	ARP/WARP, PROLSQ	Depositor
R, R_{free}	0.164 , (Not available) 0.159 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	(Not available)	Xtriage
Anisotropy	(Not available)	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 108.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ¹	$\langle L \rangle =$ (Not available), $\langle L^2 \rangle =$ (Not available)	Xtriage
Outliers	(Not available)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2651	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *(Not available)*

¹Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

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	1.00	1/1204 (0.1%)	2.25	59/1615 (3.7%)
1	B	1.00	0/1204	2.27	58/1615 (3.6%)
All	All	1.00	1/2408 (0.0%)	2.26	117/3230 (3.6%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	54	GLU	CD-OE1	-5.25	1.19	1.25

All (117) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	31	ARG	NE-CZ-NH2	-21.45	109.57	120.30
1	B	139	ARG	NE-CZ-NH2	-17.78	111.41	120.30
1	B	31	ARG	NE-CZ-NH1	14.12	127.36	120.30
1	A	139	ARG	NE-CZ-NH2	-13.18	113.71	120.30
1	B	139	ARG	NE-CZ-NH1	12.90	126.75	120.30
1	B	146	TYR	CB-CG-CD2	-12.22	113.67	121.00
1	A	109	GLU	OE1-CD-OE2	11.24	136.79	123.30
1	A	59	GLU	OE1-CD-OE2	11.24	136.78	123.30
1	A	105	GLU	OE1-CD-OE2	10.86	136.34	123.30
1	A	44	ASP	CB-CG-OD1	10.57	127.81	118.30
1	A	6	GLU	CG-CD-OE1	10.17	138.65	118.30
1	B	53	ASP	CB-CG-OD1	9.81	127.13	118.30
1	B	20	ASP	CB-CG-OD1	9.09	126.48	118.30
1	A	47	LYS	C-N-CA	9.08	144.39	121.70
1	A	6	GLU	CG-CD-OE2	-8.64	101.02	118.30
1	B	109	GLU	OE1-CD-OE2	8.58	133.60	123.30
1	A	60	ASP	CB-CG-OD1	8.29	125.76	118.30
1	A	53	ASP	CB-CG-OD2	-8.26	110.87	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	31	ARG	NE-CZ-NH1	8.26	124.43	120.30
1	B	117	SER	CB-CA-C	-8.16	94.59	110.10
1	B	117	SER	N-CA-CB	8.11	122.66	110.50
1	B	6	GLU	CG-CD-OE1	8.03	134.35	118.30
1	A	148	GLU	CA-CB-CG	8.01	131.03	113.40
1	B	126	ASP	CB-CG-OD1	7.93	125.43	118.30
1	A	34	LYS	CA-CB-CG	7.92	130.82	113.40
1	B	146	TYR	CB-CG-CD1	7.91	125.75	121.00
1	A	35	GLY	CA-C-O	-7.69	106.76	120.60
1	B	85	GLU	CG-CD-OE1	7.66	133.62	118.30
1	A	20	ASP	CB-CG-OD1	7.62	125.16	118.30
1	A	48	HIS	CA-CB-CG	-7.57	100.74	113.60
1	B	126	ASP	CB-CG-OD2	-7.53	111.53	118.30
1	A	30	ILE	O-C-N	-7.52	110.66	122.70
1	A	44	ASP	CB-CG-OD2	-7.47	111.58	118.30
1	A	52	GLU	CG-CD-OE1	7.44	133.19	118.30
1	A	126	ASP	CB-CG-OD1	7.30	124.87	118.30
1	A	24	HIS	CA-C-N	7.26	130.72	116.20
1	A	133	LYS	CD-CE-NZ	7.14	128.12	111.70
1	B	53	ASP	CB-CG-OD2	-7.07	111.93	118.30
1	B	54	GLU	OE1-CD-OE2	-6.87	115.06	123.30
1	A	103	TYR	CB-CG-CD1	6.82	125.09	121.00
1	A	85	GLU	CG-CD-OE1	6.81	131.92	118.30
1	A	24	HIS	O-C-N	-6.76	111.71	123.20
1	B	69	LEU	O-C-N	6.73	133.46	122.70
1	A	132	SER	N-CA-CB	-6.72	100.42	110.50
1	A	117	SER	CB-CA-C	-6.71	97.34	110.10
1	B	89	LEU	CB-CA-C	6.70	122.92	110.20
1	A	109	GLU	CG-CD-OE2	-6.64	105.02	118.30
1	B	127	ALA	CB-CA-C	6.59	119.98	110.10
1	B	59	GLU	CG-CD-OE1	-6.58	105.14	118.30
1	A	18	GLU	CG-CD-OE1	6.50	131.29	118.30
1	A	18	GLU	CG-CD-OE2	-6.47	105.36	118.30
1	A	31	ARG	NE-CZ-NH2	-6.44	117.08	120.30
1	B	45	LYS	N-CA-CB	-6.41	99.06	110.60
1	B	18	GLU	CG-CD-OE2	-6.41	105.48	118.30
1	A	24	HIS	C-N-CA	6.40	135.74	122.30
1	B	27	GLU	OE1-CD-OE2	6.31	130.87	123.30
1	A	103	TYR	CB-CG-CD2	-6.23	117.26	121.00
1	B	67	THR	CA-CB-CG2	6.19	121.07	112.40
1	A	122	ASP	CB-CG-OD2	-6.17	112.75	118.30
1	A	131	MET	CA-C-O	6.15	133.02	120.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	35	GLY	CA-C-O	-6.13	109.56	120.60
1	A	52	GLU	CG-CD-OE2	-6.00	106.30	118.30
1	B	86	LEU	CB-CG-CD2	-5.98	100.83	111.00
1	A	121	GLY	O-C-N	-5.90	113.26	122.70
1	B	6	GLU	CG-CD-OE2	-5.89	106.51	118.30
1	B	67	THR	CA-CB-OG1	-5.88	96.64	109.00
1	A	59	GLU	CG-CD-OE2	-5.85	106.59	118.30
1	A	42	LYS	CB-CA-C	-5.85	98.69	110.40
1	A	35	GLY	CA-C-N	5.84	130.04	117.20
1	B	74	GLY	O-C-N	-5.83	113.38	122.70
1	A	40	LEU	CB-CG-CD2	-5.82	101.11	111.00
1	B	38	GLU	CG-CD-OE2	-5.82	106.67	118.30
1	A	85	GLU	CG-CD-OE2	-5.79	106.73	118.30
1	A	102	LYS	CB-CA-C	-5.75	98.90	110.40
1	B	128	GLN	OE1-CD-NE2	5.74	135.11	121.90
1	A	26	GLN	CG-CD-OE1	-5.73	110.15	121.60
1	B	3	SER	N-CA-CB	-5.71	101.94	110.50
1	B	105	GLU	OE1-CD-OE2	5.66	130.09	123.30
1	B	135	LEU	CB-CG-CD2	-5.65	101.40	111.00
1	A	128	GLN	CG-CD-OE1	-5.63	110.33	121.60
1	A	3	SER	O-C-N	-5.60	113.74	122.70
1	A	139	ARG	NH1-CZ-NH2	5.59	125.55	119.40
1	B	101	VAL	CA-C-N	5.54	129.39	117.20
1	A	60	ASP	CB-CG-OD2	-5.54	113.32	118.30
1	A	117	SER	N-CA-CB	5.52	118.78	110.50
1	B	133	LYS	CB-CG-CD	-5.52	97.25	111.60
1	A	146	TYR	CB-CG-CD1	5.52	124.31	121.00
1	B	89	LEU	N-CA-CB	-5.51	99.39	110.40
1	B	101	VAL	O-C-N	-5.48	113.93	122.70
1	B	103	TYR	CB-CG-CD2	-5.47	117.72	121.00
1	A	132	SER	CB-CA-C	5.47	120.50	110.10
1	B	24	HIS	C-N-CA	5.47	133.78	122.30
1	B	86	LEU	CB-CA-C	5.45	120.56	110.20
1	B	132	SER	CA-CB-OG	-5.45	96.50	111.20
1	B	85	GLU	CG-CD-OE2	-5.44	107.42	118.30
1	B	44	ASP	CB-CG-OD2	-5.43	113.41	118.30
1	B	147	LYS	CA-CB-CG	5.41	125.30	113.40
1	B	53	ASP	CB-CA-C	5.41	121.21	110.40
1	B	139	ARG	CB-CA-C	-5.40	99.59	110.40
1	B	83	GLU	OE1-CD-OE2	-5.38	116.84	123.30
1	A	46	PHE	CA-C-O	-5.36	108.85	120.10
1	B	25	GLY	CA-C-O	5.34	130.21	120.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	136	GLU	OE1-CD-OE2	5.34	129.70	123.30
1	A	95	THR	CA-CB-CG2	5.33	119.86	112.40
1	B	47	LYS	C-N-CA	5.32	134.99	121.70
1	B	1	GLY	O-C-N	5.29	131.16	122.70
1	A	45	LYS	CB-CA-C	-5.24	99.92	110.40
1	A	54	GLU	OE1-CD-OE2	-5.24	117.02	123.30
1	B	118	LYS	CA-C-O	-5.23	109.12	120.10
1	B	101	VAL	CB-CA-C	5.16	121.20	111.40
1	A	3	SER	N-CA-CB	-5.15	102.77	110.50
1	A	11	LEU	CA-C-O	-5.15	109.28	120.10
1	A	148	GLU	CG-CD-OE2	-5.11	108.08	118.30
1	B	54	GLU	CG-CD-OE1	5.10	128.50	118.30
1	B	128	GLN	CG-CD-OE1	-5.08	111.43	121.60
1	A	30	ILE	CA-C-N	5.05	128.31	117.20
1	B	83	GLU	CB-CG-CD	5.00	127.71	114.20

There are no chirality outliers.

There are no planarity outliers.

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	1180	0	1193	18	0
1	B	1180	0	1194	17	0
2	A	43	0	30	1	0
2	B	43	0	30	2	0
3	A	90	0	0	8	0
3	B	115	0	0	9	0
All	All	2651	0	2447	37	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 8.

All (37) 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:13:VAL:HG13	3:A:232:HOH:O	1.51	1.08
1:A:13:VAL:HG22	3:A:232:HOH:O	1.66	0.95
1:B:126:ASP:HB2	3:B:161:HOH:O	1.73	0.88
1:B:128:GLN:HG2	3:B:197:HOH:O	1.78	0.84
1:A:13:VAL:CG2	3:A:232:HOH:O	2.29	0.77
1:A:13:VAL:CB	3:A:232:HOH:O	2.31	0.76
1:B:128:GLN:CG	3:B:197:HOH:O	2.39	0.70
1:B:38:GLU:HG3	3:B:258:HOH:O	1.92	0.69
1:B:144:ALA:HA	1:B:147:LYS:HE3	1.77	0.66
1:A:13:VAL:HA	3:A:232:HOH:O	1.99	0.62
1:A:128:GLN:HB3	3:A:241:HOH:O	1.99	0.61
1:A:47:LYS:HA	1:A:47:LYS:NZ	2.15	0.61
1:B:13:VAL:HG23	3:B:224:HOH:O	2.03	0.58
1:A:52:GLU:HG2	1:A:56:LYS:HE2	1.86	0.57
2:B:154:HEM:HMC1	2:B:154:HEM:HBC2	1.86	0.57
1:A:82:HIS:O	1:A:86:LEU:HB2	2.10	0.51
2:B:154:HEM:CMC	2:B:154:HEM:HBC2	2.39	0.51
1:A:47:LYS:HA	1:A:47:LYS:HZ3	1.75	0.50
1:B:128:GLN:HB3	3:B:197:HOH:O	2.13	0.47
1:A:97:HIS:NE2	2:A:154:HEM:O1A	2.40	0.47
1:B:128:GLN:CB	3:B:197:HOH:O	2.63	0.46
1:A:128:GLN:O	1:A:132:SER:HB3	2.15	0.46
1:B:46:PHE:CZ	1:B:61:LEU:HA	2.52	0.45
1:B:146:TYR:CD2	1:B:151:PHE:HD2	2.34	0.45
1:B:4:ASP:O	1:B:8:GLN:HG2	2.17	0.45
1:A:87:THR:HB	1:A:88:PRO:HD3	1.99	0.45
1:A:36:HIS:N	1:A:37:PRO:HD3	2.32	0.44
1:B:97:HIS:C	1:B:98:LYS:HG2	2.38	0.44
1:A:13:VAL:CG1	3:A:232:HOH:O	2.19	0.44
1:B:41:GLU:HG3	3:B:217:HOH:O	2.16	0.44
1:B:30:ILE:O	1:B:34:LYS:HB2	2.17	0.43
1:B:83:GLU:HG3	3:B:236:HOH:O	2.19	0.43
1:A:45:LYS:HE3	3:A:222:HOH:O	2.19	0.43
1:A:44:ASP:O	1:A:47:LYS:HG2	2.19	0.42
1:B:44:ASP:HA	1:B:47:LYS:HG3	2.01	0.42
1:B:30:ILE:HG12	1:B:55:MET:HB3	2.02	0.41
1:A:145:LYS:O	1:A:149:LEU:HG	2.21	0.41

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	149/153 (97%)	144 (97%)	5 (3%)	0	100	100
1	B	149/153 (97%)	146 (98%)	3 (2%)	0	100	100
All	All	298/306 (97%)	290 (97%)	8 (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	123/124 (99%)	115 (94%)	8 (6%)	21	23
1	B	123/124 (99%)	114 (93%)	9 (7%)	17	18
All	All	246/248 (99%)	229 (93%)	17 (7%)	19	20

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	LYS
1	A	34	LYS
1	A	47	LYS
1	A	86	LEU
1	A	117	SER
1	A	132	SER
1	A	133	LYS
1	A	145	LYS

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Mol	Chain	Res	Type
1	B	16	LYS
1	B	34	LYS
1	B	50	LYS
1	B	53	ASP
1	B	96	LYS
1	B	98	LYS
1	B	101	VAL
1	B	132	SER
1	B	147	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	91	GLN
1	B	12	ASN
1	B	91	GLN
1	B	140	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 ⓘ

2 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	$\# Z > 2$
2	HEM	A	154	1,3	30,50,50	2.67	10 (33%)	24,82,82	3.38	14 (58%)
2	HEM	B	154	1,3	30,50,50	2.66	7 (23%)	24,82,82	3.88	13 (54%)

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	154	1,3	-	0/10/54/54	0/0/8/8
2	HEM	B	154	1,3	-	0/10/54/54	0/0/8/8

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	154	HEM	C3B-C4B	-7.92	1.44	1.51
2	B	154	HEM	C3B-C4B	-7.67	1.45	1.51
2	B	154	HEM	C2D-C3D	-7.10	1.33	1.54
2	A	154	HEM	C2D-C3D	-6.88	1.33	1.54
2	B	154	HEM	C3D-C4D	-6.50	1.43	1.51
2	A	154	HEM	C3D-C4D	-4.98	1.45	1.51
2	A	154	HEM	C2C-C1C	-3.49	1.46	1.52
2	B	154	HEM	C2C-C1C	-3.05	1.46	1.52
2	A	154	HEM	C2B-C1B	-2.56	1.43	1.51
2	B	154	HEM	C4C-NC	2.22	1.38	1.36
2	A	154	HEM	C4C-NC	2.29	1.38	1.36
2	B	154	HEM	C3C-CAC	2.57	1.56	1.51
2	A	154	HEM	C3B-CAB	2.77	1.56	1.51
2	A	154	HEM	CAA-C2A	3.01	1.57	1.52
2	A	154	HEM	C3C-CAC	3.03	1.57	1.51
2	B	154	HEM	C1C-NC	3.18	1.39	1.36
2	A	154	HEM	C1C-NC	3.20	1.40	1.36

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	154	HEM	C3B-CAB-CBB	-8.02	112.16	124.46
2	A	154	HEM	C3B-CAB-CBB	-7.67	112.69	124.46
2	B	154	HEM	C3C-CAC-CBC	-5.64	115.80	124.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	154	HEM	CAA-C2A-C1A	-5.29	121.26	127.01
2	B	154	HEM	CBD-CAD-C3D	-4.89	99.34	113.55
2	B	154	HEM	CMA-C3A-C4A	-4.76	120.48	128.36
2	A	154	HEM	CBD-CAD-C3D	-4.27	101.11	113.55
2	A	154	HEM	C3C-CAC-CBC	-4.09	118.19	124.46
2	A	154	HEM	CMA-C3A-C4A	-3.07	123.28	128.36
2	A	154	HEM	CAA-C2A-C1A	-2.62	124.17	127.01
2	A	154	HEM	C3B-C4B-NB	-2.22	107.39	111.63
2	A	154	HEM	CAD-C3D-C4D	2.09	119.83	112.47
2	A	154	HEM	CAA-CBA-CGA	2.14	116.67	112.75
2	A	154	HEM	CBA-CAA-C2A	2.39	116.81	112.53
2	B	154	HEM	CAD-C3D-C4D	2.68	121.91	112.47
2	B	154	HEM	CMA-C3A-C2A	2.99	131.48	125.24
2	A	154	HEM	CMD-C2D-C3D	3.70	130.74	114.35
2	B	154	HEM	CAA-CBA-CGA	4.20	120.44	112.75
2	B	154	HEM	CMD-C2D-C3D	4.30	133.37	114.35
2	B	154	HEM	CAD-C3D-C2D	4.66	126.62	113.22
2	A	154	HEM	CMC-C2C-C3C	5.27	129.67	116.53
2	A	154	HEM	C2D-C3D-C4D	5.33	110.53	101.50
2	A	154	HEM	CMB-C2B-C3B	5.39	129.99	116.53
2	B	154	HEM	C2D-C3D-C4D	5.61	111.01	101.50
2	A	154	HEM	CAD-C3D-C2D	5.61	129.36	113.22
2	B	154	HEM	CMC-C2C-C3C	6.01	131.53	116.53
2	B	154	HEM	CMB-C2B-C3B	6.10	131.77	116.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	154	HEM	1	0
2	B	154	HEM	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 [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, 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(Å ²)	Q<0.9
1	A	151/153 (98%)	-0.84	0 100 100	9, 23, 50, 63	0
1	B	151/153 (98%)	-0.82	0 100 100	10, 24, 49, 64	0
All	All	302/306 (98%)	-0.83	0 100 100	9, 24, 49, 64	0

There are no RSRZ outliers to report.

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, 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.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	HEM	B	154	43/43	0.97	0.08	-0.17	13,18,27,33	0
2	HEM	A	154	43/43	0.97	0.08	-0.33	15,18,25,30	0

6.5 Other polymers

There are no such residues in this entry.