



Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 09:49 am BST

PDB ID : 1MNI
Title : ALTERATION OF AXIAL COORDINATION BY PROTEIN ENGINEERING IN MYOGLOBIN. BIS-IMIDAZOLE LIGATION IN THE HIS64-->VAL(SLASH)VAL68-->HIS DOUBLE MUTANT
Authors : Krzywda, S.; Wilkinson, A.J.
Deposited on : 1995-01-11
Resolution : 2.07 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

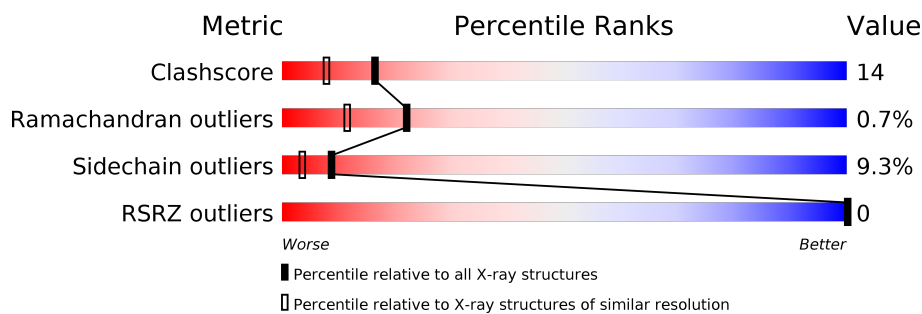
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.07 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	141614	2801 (2.08-2.04)
Ramachandran outliers	138981	2768 (2.08-2.04)
Sidechain outliers	138945	2768 (2.08-2.04)
RSRZ outliers	127900	2646 (2.08-2.04)

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 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 $\leq 5\%$. 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 2679 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.

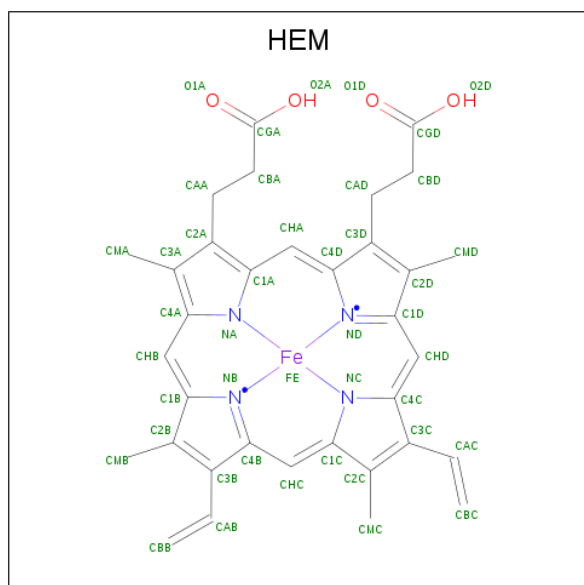
- Molecule 1 is a protein called MYOGLOBIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	153	Total	C	N	O	S	13	0	0
			1196	764	208	221	3			
1	B	153	Total	C	N	O	S	13	0	0
			1196	764	208	221	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	HIS	VAL	CONFLICT	UNP P02189
B	64	VAL	HIS	CONFLICT	UNP P02189
B	68	HIS	VAL	CONFLICT	UNP P02189

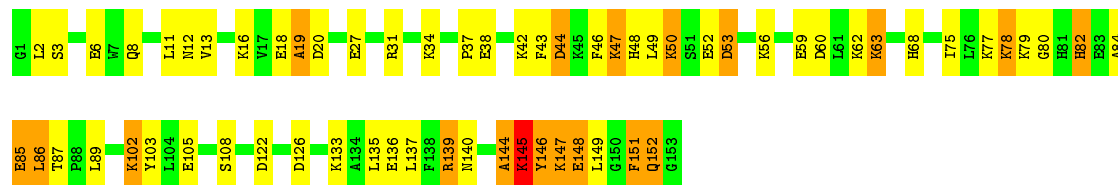
- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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	98	Total 98	O 98	0	0
3	B	103	Total 103	O 103	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	I 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	124.49Å 42.28Å 92.27Å 90.00° 92.62° 90.00°	Depositor
Resolution (Å)	10.00 – 2.07 12.62 – 2.06	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-2.07) 87.4 (12.62-2.06)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.39 (at 2.06Å)	Xtriage
Refinement program	PROLSQ	Depositor
R, R_{free}	0.175 , (Not available) 0.171 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	26.0	Xtriage
Anisotropy	0.245	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 87.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.207 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2679	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 100.00 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 0.0000e+00. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical 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 ⓘ

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	1.13	1/1221 (0.1%)	2.24	41/1637 (2.5%)
1	B	0.90	0/1221	2.25	53/1637 (3.2%)
All	All	1.02	1/2442 (0.0%)	2.24	94/3274 (2.9%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	151	PHE	C-N	-24.60	0.77	1.34

All (94) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	31	ARG	NE-CZ-NH1	27.44	134.02	120.30
1	A	31	ARG	NE-CZ-NH2	-21.49	109.56	120.30
1	B	31	ARG	NE-CZ-NH2	-20.88	109.86	120.30
1	A	139	ARG	NE-CZ-NH1	16.82	128.71	120.30
1	A	139	ARG	NE-CZ-NH2	-14.49	113.05	120.30
1	A	151	PHE	O-C-N	-14.31	99.81	122.70
1	B	31	ARG	NE-CZ-NH1	13.28	126.94	120.30
1	B	139	ARG	NE-CZ-NH2	-12.83	113.89	120.30
1	B	86	LEU	CB-CA-C	10.21	129.59	110.20
1	A	151	PHE	C-N-CA	9.53	145.52	121.70
1	B	146	TYR	CB-CG-CD1	9.44	126.66	121.00
1	A	126	ASP	CB-CG-OD1	9.29	126.66	118.30
1	A	109	GLU	OE1-CD-OE2	9.15	134.28	123.30
1	B	53	ASP	CB-CG-OD2	-8.89	110.30	118.30
1	B	44	ASP	CB-CG-OD1	8.74	126.17	118.30
1	B	151	PHE	CA-C-O	8.67	138.31	120.10
1	A	59	GLU	OE1-CD-OE2	8.50	133.50	123.30
1	B	85	GLU	CG-CD-OE1	8.03	134.37	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	148	GLU	OE1-CD-OE2	7.87	132.74	123.30
1	A	53	ASP	CB-CG-OD2	-7.65	111.42	118.30
1	A	153	GLY	CA-C-O	-7.42	107.25	120.60
1	A	146	TYR	CB-CG-CD1	7.41	125.45	121.00
1	A	71	ALA	N-CA-CB	7.41	120.47	110.10
1	B	152	GLN	CB-CG-CD	7.41	130.85	111.60
1	B	151	PHE	O-C-N	-7.30	111.02	122.70
1	B	43	PHE	O-C-N	7.25	134.29	122.70
1	B	48	HIS	CA-CB-CG	6.95	125.42	113.60
1	B	34	LYS	CD-CE-NZ	6.93	127.65	111.70
1	B	108	SER	O-C-N	-6.90	111.66	122.70
1	A	27	GLU	OE1-CD-OE2	-6.89	115.03	123.30
1	A	122	ASP	CB-CG-OD2	-6.85	112.14	118.30
1	A	85	GLU	CG-CD-OE1	6.83	131.97	118.30
1	B	60	ASP	CB-CG-OD2	-6.75	112.23	118.30
1	B	6	GLU	CG-CD-OE1	6.72	131.74	118.30
1	B	102	LYS	CB-CG-CD	6.54	128.61	111.60
1	B	84	ALA	O-C-N	6.54	133.16	122.70
1	B	86	LEU	CA-CB-CG	6.45	130.14	115.30
1	B	85	GLU	OE1-CD-OE2	-6.39	115.63	123.30
1	A	93	HIS	CA-CB-CG	-6.28	102.92	113.60
1	B	122	ASP	CB-CG-OD1	-6.22	112.70	118.30
1	B	20	ASP	CB-CG-OD1	6.21	123.89	118.30
1	A	139	ARG	CD-NE-CZ	6.21	132.30	123.60
1	A	128	GLN	CG-CD-OE1	-6.20	109.20	121.60
1	B	146	TYR	CB-CG-CD2	-6.09	117.34	121.00
1	A	85	GLU	CG-CD-OE2	-6.08	106.13	118.30
1	A	140	ASN	CB-CG-ND2	6.07	131.26	116.70
1	A	148	GLU	CA-CB-CG	6.07	126.75	113.40
1	B	13	VAL	CA-CB-CG1	6.03	119.95	110.90
1	A	27	GLU	CG-CD-OE1	5.99	130.29	118.30
1	B	126	ASP	CB-CG-OD2	-5.95	112.94	118.30
1	B	103	TYR	CB-CG-CD1	-5.93	117.44	121.00
1	B	103	TYR	O-C-N	5.90	132.14	122.70
1	B	38	GLU	CA-CB-CG	5.85	126.28	113.40
1	A	152	GLN	O-C-N	5.82	133.09	123.20
1	B	68	HIS	CA-CB-CG	-5.78	103.77	113.60
1	B	75	ILE	CB-CG1-CD1	-5.74	97.82	113.90
1	B	60	ASP	CB-CG-OD1	5.74	123.46	118.30
1	B	44	ASP	CB-CG-OD2	-5.71	113.16	118.30
1	A	146	TYR	CB-CG-CD2	-5.70	117.58	121.00
1	B	149	LEU	CB-CG-CD1	-5.68	101.35	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	6	GLU	CG-CD-OE2	-5.67	106.97	118.30
1	B	78	LYS	CB-CA-C	-5.65	99.10	110.40
1	A	108	SER	CA-C-O	5.64	131.95	120.10
1	B	82	HIS	N-CA-CB	-5.56	100.59	110.60
1	A	152	GLN	CA-CB-CG	-5.55	101.18	113.40
1	A	71	ALA	CA-C-N	5.49	129.27	117.20
1	B	137	LEU	O-C-N	-5.46	113.96	122.70
1	B	86	LEU	CA-C-N	5.38	129.04	117.20
1	A	31	ARG	CD-NE-CZ	5.32	131.04	123.60
1	A	140	ASN	CB-CG-OD1	-5.32	110.97	121.60
1	B	59	GLU	CA-CB-CG	5.27	125.00	113.40
1	A	105	GLU	CB-CA-C	-5.27	99.86	110.40
1	B	3	SER	O-C-N	-5.25	114.30	122.70
1	A	35	GLY	CA-C-N	5.25	128.74	117.20
1	A	108	SER	O-C-N	-5.22	114.35	122.70
1	A	151	PHE	CA-C-N	5.19	128.63	117.20
1	B	86	LEU	N-CA-CB	-5.19	100.03	110.40
1	A	34	LYS	N-CA-CB	5.18	119.93	110.60
1	B	139	ARG	NE-CZ-NH1	5.18	122.89	120.30
1	B	140	ASN	O-C-N	-5.17	114.42	122.70
1	B	37	PRO	O-C-N	5.12	130.89	122.70
1	B	151	PHE	C-N-CA	5.11	134.47	121.70
1	A	54	GLU	OE1-CD-OE2	-5.09	117.19	123.30
1	B	86	LEU	O-C-N	-5.09	114.55	122.70
1	A	86	LEU	CA-CB-CG	-5.09	103.59	115.30
1	B	80	GLY	CA-C-O	-5.07	111.48	120.60
1	A	72	LEU	O-C-N	-5.05	114.62	123.20
1	B	19	ALA	N-CA-CB	5.04	117.15	110.10
1	B	145	LYS	CB-CG-CD	5.03	124.68	111.60
1	A	50	LYS	CD-CE-NZ	5.03	123.26	111.70
1	B	148	GLU	CB-CA-C	5.03	120.45	110.40
1	B	144	ALA	CB-CA-C	-5.02	102.57	110.10
1	A	35	GLY	CA-C-O	-5.02	111.57	120.60
1	A	11	LEU	CA-CB-CG	-5.00	103.79	115.30

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	1196	0	1204	35	0
1	B	1196	0	1204	31	0
2	A	43	0	30	3	0
2	B	43	0	30	2	0
3	A	98	0	0	6	0
3	B	103	0	0	5	1
All	All	2679	0	2468	70	1

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.

All (70) 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:12:ASN:HB3	3:A:183:HOH:O	1.27	1.31
1:B:145:LYS:HB2	1:B:145:LYS:NZ	1.63	1.11
1:B:145:LYS:HB2	1:B:145:LYS:HZ3	1.24	0.94
1:A:78:LYS:HE2	1:A:78:LYS:HA	1.52	0.92
1:A:36:HIS:HD2	3:A:176:HOH:O	1.55	0.87
1:B:145:LYS:HB2	1:B:145:LYS:HZ2	1.43	0.83
1:A:27:GLU:HG3	1:A:118:LYS:NZ	1.97	0.80
2:B:154:HEM:HMC1	2:B:154:HEM:HBC2	1.64	0.79
1:B:82:HIS:HA	1:B:85:GLU:OE1	1.82	0.78
1:B:145:LYS:CB	1:B:145:LYS:NZ	2.36	0.76
1:A:16:LYS:N	1:A:16:LYS:HD2	1.99	0.75
2:A:154:HEM:HMC1	2:A:154:HEM:HBC2	1.71	0.72
1:A:102:LYS:HD2	1:A:106:PHE:CZ	2.24	0.72
1:B:145:LYS:CB	1:B:145:LYS:HZ3	2.00	0.71
1:A:27:GLU:HG2	3:A:221:HOH:O	1.92	0.70
1:A:95:THR:O	1:A:98:LYS:CE	2.40	0.70
1:A:95:THR:O	1:A:98:LYS:HE3	1.92	0.69
2:B:154:HEM:CMC	2:B:154:HEM:HBC2	2.22	0.69
1:A:102:LYS:HE3	1:A:103:TYR:HE1	1.57	0.69
1:A:102:LYS:HE3	1:A:103:TYR:CE1	2.30	0.66
1:A:95:THR:C	1:A:98:LYS:HE3	2.16	0.65
1:B:62:LYS:NZ	3:B:180:HOH:O	2.30	0.65
1:B:146:TYR:CD2	1:B:151:PHE:HD1	2.16	0.63
1:B:102:LYS:HG3	1:B:105:GLU:OE2	1.99	0.63
1:A:95:THR:HG22	1:A:151:PHE:CZ	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:154:HEM:CMC	2:A:154:HEM:HBC2	2.30	0.61
1:A:78:LYS:CA	1:A:78:LYS:HE2	2.25	0.61
1:B:145:LYS:CB	1:B:145:LYS:HZ2	2.05	0.60
1:B:44:ASP:HA	1:B:47:LYS:HE2	1.82	0.60
1:A:27:GLU:HG3	1:A:118:LYS:HZ3	1.68	0.59
1:A:144:ALA:HA	1:A:147:LYS:HE3	1.85	0.59
1:A:105:GLU:HA	1:A:139:ARG:HD3	1.85	0.58
1:B:146:TYR:CD2	1:B:151:PHE:CD1	2.93	0.57
1:A:34:LYS:HG3	3:A:220:HOH:O	2.06	0.54
1:B:52:GLU:HG2	1:B:56:LYS:HZ2	1.73	0.53
1:A:46:PHE:CZ	1:A:61:LEU:HA	2.45	0.52
1:A:36:HIS:CD2	3:A:176:HOH:O	2.43	0.51
1:B:145:LYS:CG	3:B:193:HOH:O	2.58	0.51
1:B:2:LEU:HD11	1:B:133:LYS:HB3	1.93	0.51
1:A:44:ASP:OD1	1:A:47:LYS:HE2	2.12	0.50
1:B:145:LYS:HG3	3:B:193:HOH:O	2.11	0.49
1:A:87:THR:OG1	1:A:145:LYS:HE3	2.13	0.49
1:A:18:GLU:OE2	1:A:77:LYS:NZ	2.41	0.49
1:B:12:ASN:HB3	3:B:238:HOH:O	2.12	0.49
1:B:146:TYR:HD2	1:B:151:PHE:HD1	1.61	0.47
1:B:144:ALA:HA	1:B:147:LYS:HE2	1.96	0.47
1:B:146:TYR:CE2	1:B:151:PHE:CE1	3.03	0.47
1:A:44:ASP:OD1	1:A:47:LYS:CE	2.63	0.47
1:B:46:PHE:HB3	1:B:49:LEU:HD12	1.98	0.46
1:A:102:LYS:HG3	1:A:103:TYR:HD1	1.81	0.45
1:B:50:LYS:HE3	1:B:50:LYS:HB3	1.86	0.45
1:A:52:GLU:OE1	3:A:220:HOH:O	2.21	0.45
1:A:89:LEU:HD21	2:A:154:HEM:HMB2	1.98	0.45
1:A:24:HIS:NE2	1:A:119:HIS:NE2	2.52	0.45
1:B:18:GLU:OE2	1:B:77:LYS:NZ	2.38	0.45
1:A:49:LEU:HD13	1:A:55:MET:HA	1.98	0.45
1:B:78:LYS:HG3	1:B:82:HIS:HA	1.98	0.45
1:B:146:TYR:HE2	1:B:151:PHE:HE1	1.65	0.44
1:A:85:GLU:N	1:A:85:GLU:CD	2.71	0.43
1:A:13:VAL:HG22	1:A:131:MET:CE	2.48	0.42
1:B:19:ALA:HB1	3:B:239:HOH:O	2.18	0.42
1:B:135:LEU:O	1:B:139:ARG:HG3	2.20	0.42
1:B:87:THR:HA	1:B:145:LYS:HD2	2.01	0.42
1:A:102:LYS:HG3	1:A:103:TYR:N	2.33	0.42
1:B:63:LYS:N	1:B:63:LYS:HD3	2.35	0.42
1:A:135:LEU:HA	1:A:135:LEU:HD23	1.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:11:LEU:CD1	1:B:79:LYS:HE3	2.51	0.41
1:A:44:ASP:HA	1:A:47:LYS:HG3	2.04	0.40
1:A:9:LEU:HD23	1:A:9:LEU:HA	1.82	0.40
1:B:42:LYS:HD3	1:B:42:LYS:HA	1.95	0.40

All (1) 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)
3:B:160:HOH:O	3:B:237:HOH:O[2_645]	2.14	0.06

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	151/153 (99%)	146 (97%)	4 (3%)	1 (1%)	22	11
1	B	151/153 (99%)	147 (97%)	3 (2%)	1 (1%)	22	11
All	All	302/306 (99%)	293 (97%)	7 (2%)	2 (1%)	22	11

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	152	GLN
1	B	152	GLN

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	124/124 (100%)	114 (92%)	10 (8%)	11	5
1	B	124/124 (100%)	111 (90%)	13 (10%)	7	2
All	All	248/248 (100%)	225 (91%)	23 (9%)	9	3

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	LYS
1	A	34	LYS
1	A	42	LYS
1	A	48	HIS
1	A	78	LYS
1	A	83	GLU
1	A	85	GLU
1	A	100	PRO
1	A	109	GLU
1	A	152	GLN
1	B	8	GLN
1	B	16	LYS
1	B	27	GLU
1	B	47	LYS
1	B	50	LYS
1	B	53	ASP
1	B	63	LYS
1	B	86	LEU
1	B	89	LEU
1	B	136	GLU
1	B	145	LYS
1	B	147	LYS
1	B	148	GLU

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	128	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	B	154	1	27,50,50	2.24	10 (37%)	17,82,82	2.87	8 (47%)
2	HEM	A	154	1	27,50,50	2.22	9 (33%)	17,82,82	2.14	6 (35%)

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	B	154	1	-	0/6/54/54	-
2	HEM	A	154	1	-	0/6/54/54	-

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	154	HEM	C3C-C2C	-5.37	1.32	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	154	HEM	C3C-CAC	5.03	1.58	1.47
2	B	154	HEM	C3B-C2B	-4.47	1.34	1.40
2	A	154	HEM	C3B-C2B	-4.30	1.34	1.40
2	B	154	HEM	C3C-C2C	-4.12	1.34	1.40
2	A	154	HEM	CAA-C2A	4.08	1.58	1.52
2	B	154	HEM	C3B-CAB	3.75	1.55	1.47
2	A	154	HEM	C3C-CAC	3.60	1.55	1.47
2	A	154	HEM	C3B-CAB	3.40	1.54	1.47
2	B	154	HEM	CAA-C2A	3.33	1.56	1.52
2	A	154	HEM	CMA-C3A	2.83	1.57	1.51
2	A	154	HEM	C1D-CHD	-2.54	1.33	1.41
2	A	154	HEM	CMB-C2B	2.38	1.57	1.51
2	B	154	HEM	CMC-C2C	2.31	1.57	1.51
2	B	154	HEM	C1D-CHD	-2.23	1.34	1.41
2	B	154	HEM	CAD-C3D	2.12	1.55	1.52
2	A	154	HEM	CAD-C3D	2.06	1.55	1.52
2	B	154	HEM	C4A-NA	2.05	1.40	1.36
2	B	154	HEM	CMB-C2B	2.02	1.56	1.51

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	154	HEM	CBD-CAD-C3D	-7.34	98.95	112.48
2	A	154	HEM	CBD-CAD-C3D	-5.24	102.83	112.48
2	B	154	HEM	CMA-C3A-C4A	-3.84	122.57	128.46
2	B	154	HEM	CAD-CBD-CGD	-3.62	106.59	112.67
2	A	154	HEM	CMA-C3A-C4A	-3.44	123.18	128.46
2	B	154	HEM	CMA-C3A-C2A	3.25	131.06	124.94
2	B	154	HEM	CMD-C2D-C1D	-3.12	123.67	128.46
2	A	154	HEM	CMD-C2D-C1D	-3.08	123.73	128.46
2	B	154	HEM	CMB-C2B-C3B	3.00	130.29	124.68
2	B	154	HEM	CMD-C2D-C3D	2.84	130.29	124.94
2	A	154	HEM	CMD-C2D-C3D	2.71	130.05	124.94
2	B	154	HEM	C4C-C3C-C2C	2.56	108.69	106.90
2	A	154	HEM	CAA-CBA-CGA	2.20	116.36	112.67
2	A	154	HEM	CMA-C3A-C2A	2.08	128.87	124.94

There are no chirality outliers.

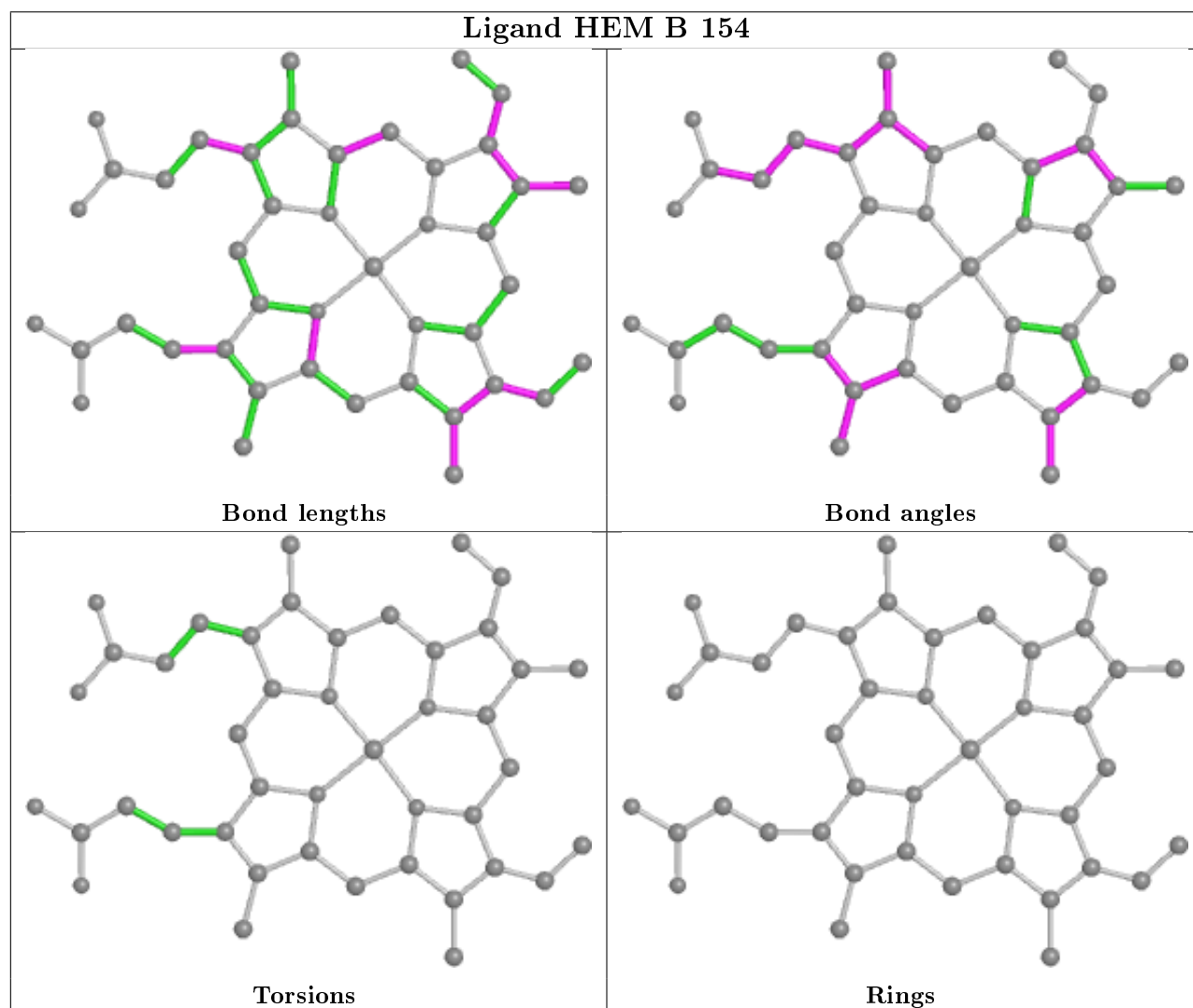
There are no torsion outliers.

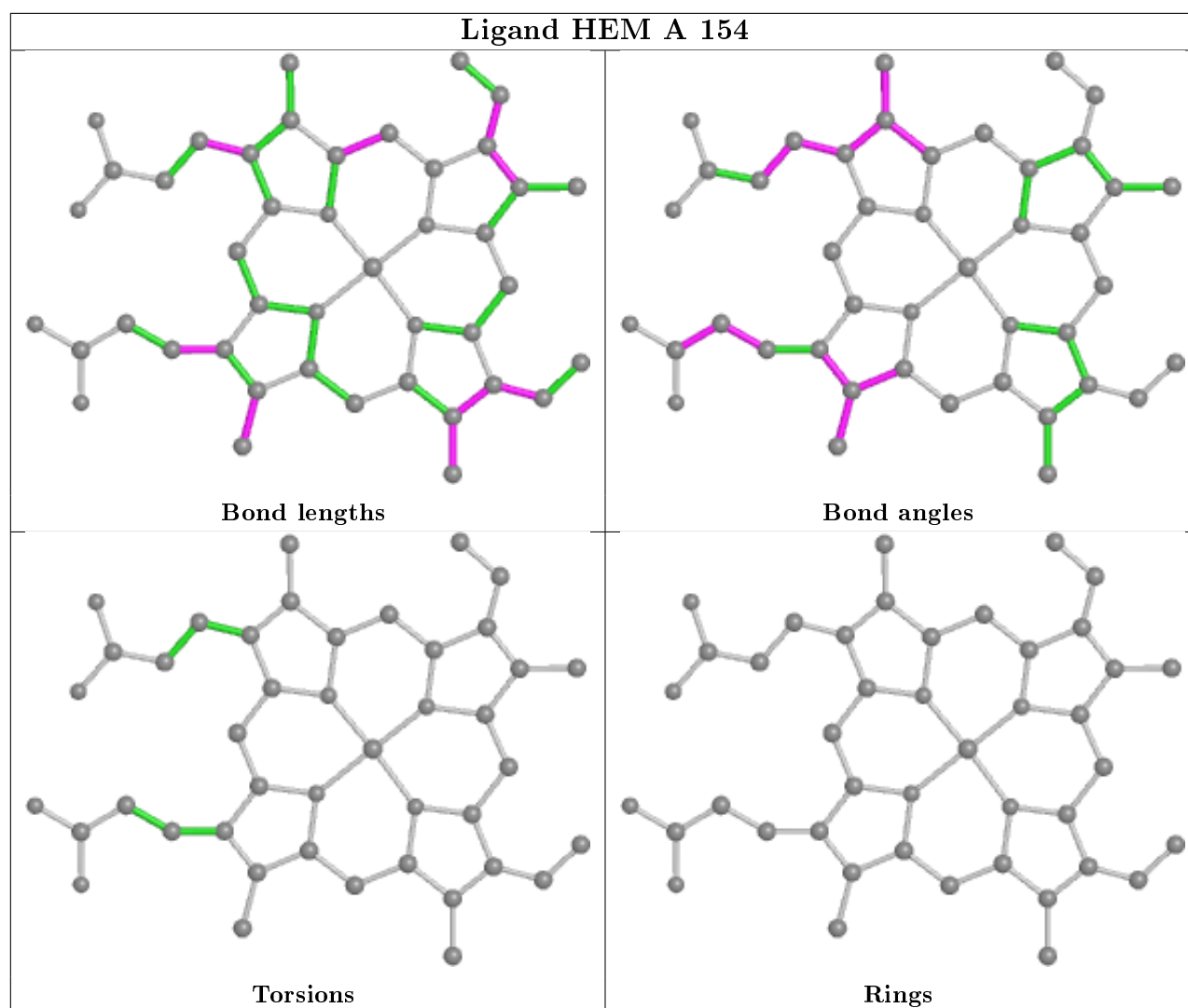
There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	154	HEM	2	0
2	A	154	HEM	3	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 than 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 any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	151:PHE	C	152:GLN	N	0.77

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%)	-0.74	0 100 100	12, 27, 51, 71	0
1	B	151/153 (98%)	-0.80	0 100 100	14, 27, 49, 63	0
All	All	302/306 (98%)	-0.77	0 100 100	12, 27, 50, 71	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](#)

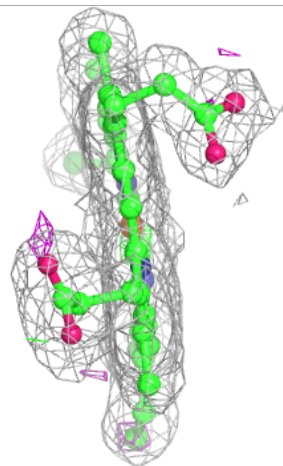
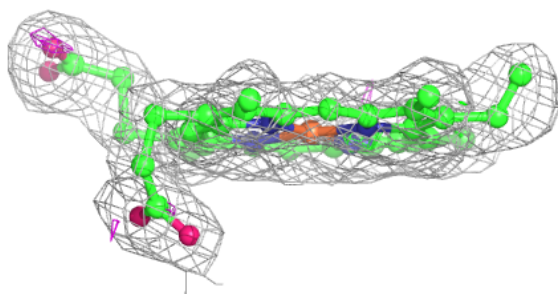
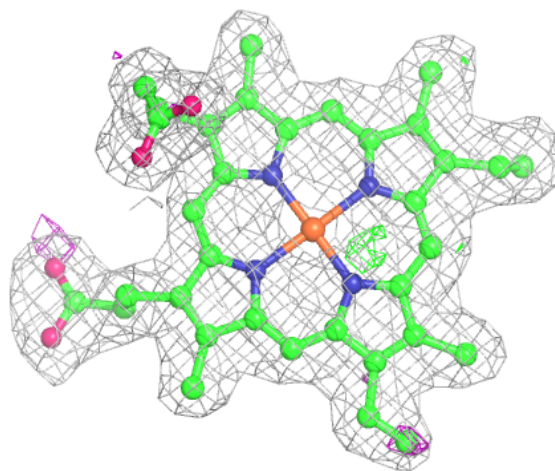
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	HEM	B	154	43/43	0.98	0.07	16,18,26,28	0
2	HEM	A	154	43/43	0.98	0.07	18,20,27,32	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

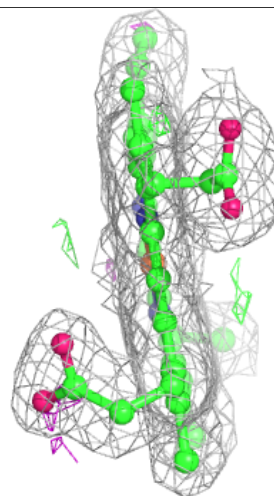
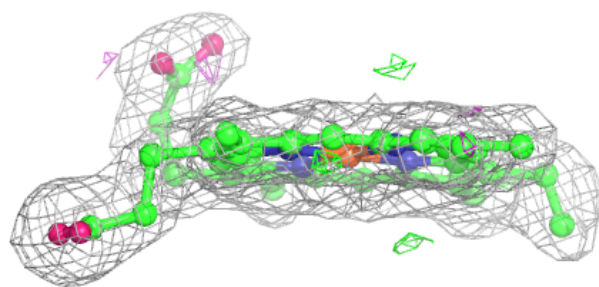
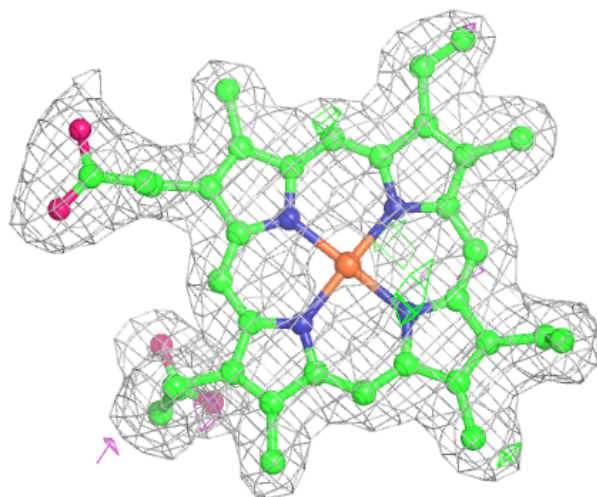
Electron density around HEM B 154:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM A 154:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers ⓘ

There are no such residues in this entry.