Full wwPDB X-ray Structure Validation Report (i)

May 29, 2024 – 01:15 PM EDT

PDB ID	:	1PBX
Title	:	HAEMOGLOBIN OF THE ANTARCTIC FISH PAGOTHENIA BERNACCHII: AMINO ACID SEQUENCE, OXYGEN EQUILIBRIA AND CRYSTAL STRUCTURE OF ITS CARBONMONOXY DERIVATIVE
Authors	:	Fermi, G.
Deposited on	:	1991-11-04
Resolution	:	2.50 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

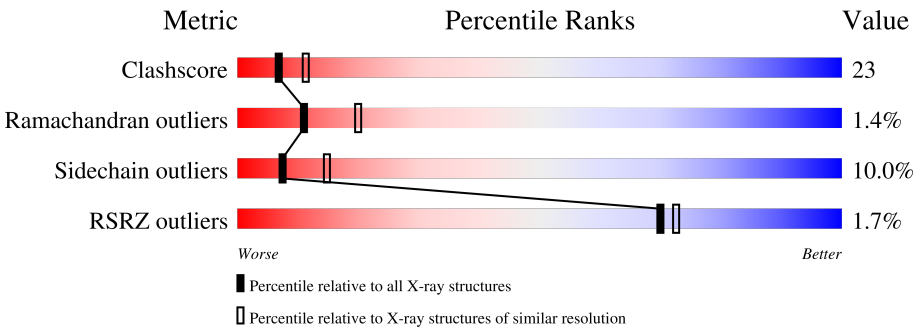
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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% 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	143	48% 35% 10% 6%
2	B	146	3% 50% 30% 17% •

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 2360 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.

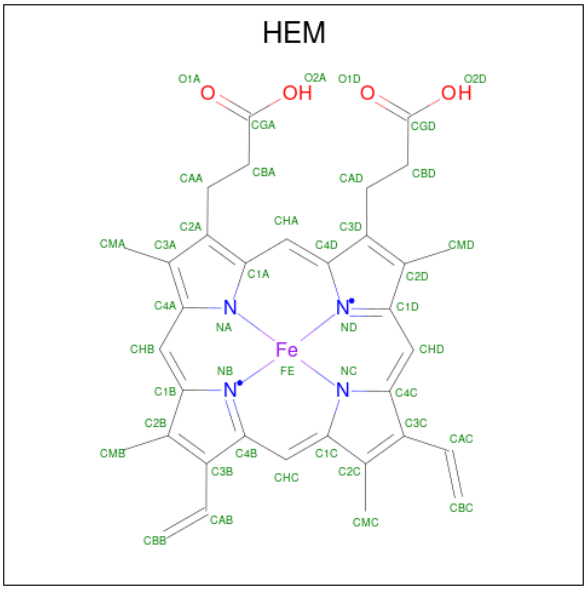
- Molecule 1 is a protein called HEMOGLOBIN (CARBONMONOXY) (ALPHA CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	143	1104	710	190	199	5	0	0	0

- Molecule 2 is a protein called HEMOGLOBIN (CARBONMONOXY) (BETA CHAIN).

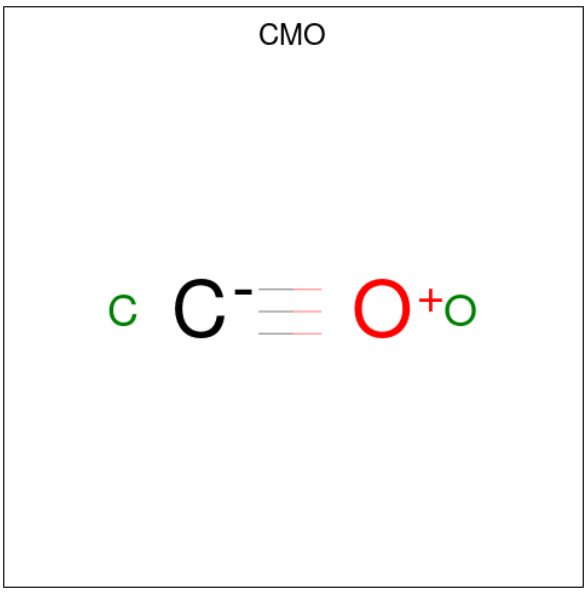
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	146	1138	726	196	211	5	0	0	0

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

- Molecule 4 is CARBON MONOXIDE (three-letter code: CMO) (formula: CO).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
4	A	1	2	1	1	0	0
4	B	1	2	1	1	0	0

- Molecule 5 is water.

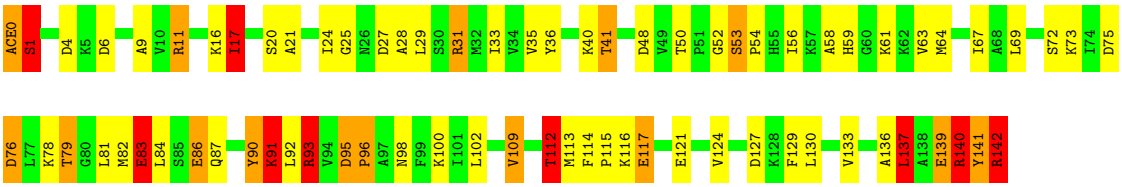
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	15	15	15	0	0
5	B	13	13	13	0	0

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 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.

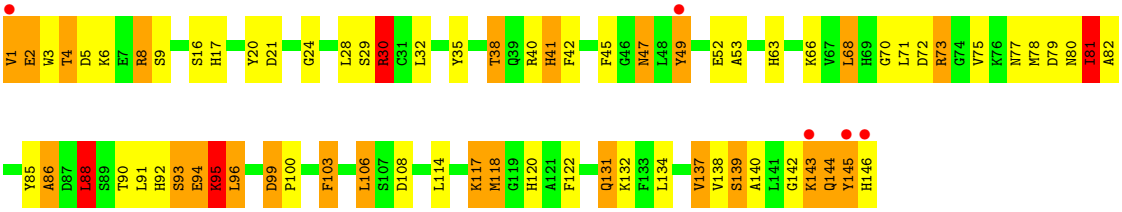
- Molecule 1: HEMOGLOBIN (CARBONMONOXY) (ALPHA CHAIN)

Chain A: 48% 35% 10% 6%



- Molecule 2: HEMOGLOBIN (CARBONMONOXY) (BETA CHAIN)

Chain B: 3% 50% 30% 17%



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	91.38Å 88.54Å 55.34Å 90.00° 97.16° 90.00°	Depositor
Resolution (Å)	10.00 – 2.50 9.96 – 2.50	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-2.50) 91.2 (9.96-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	6.04 (at 2.50Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.178 , (Not available) 0.172 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	24.7	Xtriage
Anisotropy	0.338	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 54.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	2360	wwPDB-VP
Average B, all atoms (Å^2)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.17% of the height of the origin peak. No significant pseudotranslation is detected.*

[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, ACE, CMO

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	2/1127 (0.2%)	2.53	65/1523 (4.3%)
2	B	1.13	2/1164 (0.2%)	2.40	59/1576 (3.7%)
All	All	1.13	4/2291 (0.2%)	2.46	124/3099 (4.0%)

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	A	0	3
2	B	0	2
All	All	0	5

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	29	SER	CB-OG	-5.33	1.35	1.42
1	A	130	LEU	C-O	5.09	1.33	1.23
1	A	83	GLU	CD-OE1	5.08	1.31	1.25
2	B	9	SER	CB-OG	5.08	1.48	1.42

All (124) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	73	ARG	NE-CZ-NH1	22.16	131.38	120.30
1	A	140	ARG	NE-CZ-NH1	19.56	130.08	120.30
1	A	140	ARG	NE-CZ-NH2	-19.54	110.53	120.30
2	B	8	ARG	NE-CZ-NH2	-18.88	110.86	120.30
1	A	48	ASP	CB-CG-OD2	-13.86	105.82	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	121	GLU	OE1-CD-OE2	-13.59	106.99	123.30
1	A	90	TYR	CB-CG-CD1	-13.57	112.86	121.00
1	A	142	ARG	NE-CZ-NH1	12.78	126.69	120.30
2	B	40	ARG	NE-CZ-NH1	12.26	126.43	120.30
1	A	27	ASP	CB-CG-OD2	11.71	128.84	118.30
1	A	17	ILE	CA-CB-CG2	11.66	134.22	110.90
1	A	93	ARG	NE-CZ-NH1	11.65	126.13	120.30
1	A	76	ASP	CB-CG-OD2	-11.53	107.92	118.30
1	A	40	LYS	CA-CB-CG	11.32	138.31	113.40
1	A	141	TYR	CB-CG-CD2	-10.87	114.48	121.00
1	A	95	ASP	CB-CG-OD2	-10.52	108.83	118.30
2	B	73	ARG	CA-CB-CG	9.92	135.22	113.40
1	A	11	ARG	NE-CZ-NH2	-9.87	115.36	120.30
2	B	8	ARG	NH1-CZ-NH2	9.73	130.11	119.40
2	B	99	ASP	CB-CG-OD2	-9.58	109.68	118.30
1	A	93	ARG	NE-CZ-NH2	-9.42	115.59	120.30
2	B	108	ASP	CB-CG-OD1	9.15	126.54	118.30
2	B	73	ARG	NE-CZ-NH2	-8.87	115.86	120.30
2	B	21	ASP	CB-CG-OD2	8.86	126.27	118.30
2	B	81	ILE	CB-CG1-CD1	8.70	138.26	113.90
2	B	108	ASP	CB-CG-OD2	-8.56	110.59	118.30
1	A	109	VAL	CA-CB-CG2	8.47	123.61	110.90
2	B	4	THR	N-CA-CB	8.28	126.03	110.30
2	B	131	GLN	CG-CD-OE1	8.13	137.87	121.60
2	B	30	ARG	NE-CZ-NH1	-7.92	116.34	120.30
2	B	2	GLU	CA-CB-CG	-7.89	96.04	113.40
1	A	75	ASP	CB-CG-OD1	7.86	125.38	118.30
1	A	76	ASP	CB-CG-OD1	7.81	125.33	118.30
2	B	40	ARG	NH1-CZ-NH2	-7.70	110.93	119.40
1	A	112	THR	CA-CB-CG2	7.65	123.11	112.40
1	A	31	ARG	NE-CZ-NH1	-7.56	116.52	120.30
1	A	6	ASP	CB-CG-OD2	-7.35	111.69	118.30
2	B	114	LEU	CB-CG-CD2	-7.32	98.56	111.00
1	A	16	LYS	C-N-CA	7.23	139.78	121.70
2	B	82	ALA	CA-C-O	-7.21	104.95	120.10
1	A	52	GLY	C-N-CA	7.15	139.56	121.70
2	B	2	GLU	OE1-CD-OE2	7.13	131.86	123.30
1	A	41	THR	OG1-CB-CG2	6.87	125.80	110.00
2	B	99	ASP	CB-CG-OD1	6.86	124.47	118.30
2	B	5	ASP	CB-CG-OD2	-6.83	112.15	118.30
2	B	82	ALA	CA-C-N	6.80	132.16	117.20
2	B	20	TYR	C-N-CA	6.80	138.69	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	95	LYS	C-N-CA	6.73	138.53	121.70
1	A	1	SER	N-CA-CB	6.69	120.53	110.50
1	A	142	ARG	CD-NE-CZ	6.66	132.93	123.60
1	A	90	TYR	CB-CA-C	6.66	123.72	110.40
1	A	48	ASP	CB-CG-OD1	6.65	124.28	118.30
1	A	78	LYS	CB-CG-CD	6.62	128.82	111.60
2	B	77	ASN	CB-CG-OD1	-6.57	108.46	121.60
1	A	142	ARG	NE-CZ-NH2	-6.56	117.02	120.30
1	A	72	SER	N-CA-CB	6.48	120.23	110.50
1	A	137	LEU	CA-CB-CG	6.43	130.09	115.30
1	A	0	ACE	O-C-N	-6.41	112.44	122.70
1	A	121	GLU	CG-CD-OE2	6.38	131.07	118.30
2	B	68	LEU	CB-CG-CD2	-6.38	100.15	111.00
1	A	72	SER	CA-C-O	-6.32	106.83	120.10
2	B	142	GLY	C-N-CA	6.29	137.44	121.70
2	B	49	TYR	CB-CA-C	6.28	122.97	110.40
2	B	131	GLN	CB-CA-C	6.27	122.94	110.40
1	A	31	ARG	CD-NE-CZ	-6.22	114.89	123.60
1	A	139	GLU	OE1-CD-OE2	6.21	130.75	123.30
2	B	137	VAL	CA-CB-CG1	6.20	120.20	110.90
2	B	72	ASP	CB-CG-OD2	-6.15	112.77	118.30
1	A	82	MET	CA-CB-CG	6.13	123.72	113.30
2	B	40	ARG	CD-NE-CZ	6.12	132.17	123.60
1	A	117	GLU	CG-CD-OE2	6.11	130.52	118.30
2	B	30	ARG	CD-NE-CZ	-6.10	115.06	123.60
1	A	124	VAL	CB-CA-C	-6.05	99.90	111.40
2	B	16	SER	CB-CA-C	6.04	121.58	110.10
2	B	73	ARG	NH1-CZ-NH2	-6.04	112.75	119.40
1	A	11	ARG	O-C-N	5.99	132.28	122.70
1	A	141	TYR	CB-CG-CD1	5.97	124.58	121.00
2	B	93	SER	CA-C-N	5.92	130.22	117.20
2	B	86	ALA	N-CA-CB	-5.92	101.82	110.10
1	A	96	PRO	N-CD-CG	-5.88	94.38	103.20
1	A	27	ASP	OD1-CG-OD2	-5.86	112.16	123.30
2	B	86	ALA	C-N-CA	5.85	136.33	121.70
1	A	72	SER	CB-CA-C	-5.84	99.00	110.10
1	A	95	ASP	CB-CG-OD1	5.83	123.55	118.30
1	A	91	LYS	CA-CB-CG	5.76	126.07	113.40
1	A	86	GLU	CA-CB-CG	5.76	126.06	113.40
1	A	9	ALA	CB-CA-C	5.75	118.72	110.10
1	A	4	ASP	CB-CG-OD2	-5.73	113.14	118.30
1	A	90	TYR	CB-CG-CD2	5.72	124.43	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	139	SER	N-CA-CB	5.69	119.04	110.50
2	B	94	GLU	CA-C-N	5.67	129.68	117.20
2	B	103	PHE	CB-CG-CD2	5.65	124.76	120.80
1	A	127	ASP	CB-CG-OD2	5.65	123.39	118.30
1	A	52	GLY	CA-C-O	5.61	130.69	120.60
1	A	109	VAL	CG1-CB-CG2	-5.57	102.00	110.90
2	B	88	LEU	O-C-N	5.55	131.57	122.70
2	B	138	VAL	CA-CB-CG1	5.53	119.19	110.90
2	B	118	MET	CA-C-O	-5.45	108.65	120.10
2	B	120	HIS	CA-CB-CG	-5.45	104.33	113.60
1	A	90	TYR	CG-CD2-CE2	-5.44	116.95	121.30
2	B	118	MET	CA-C-N	5.42	127.05	116.20
2	B	53	ALA	CB-CA-C	5.38	118.17	110.10
1	A	11	ARG	NH1-CZ-NH2	5.35	125.28	119.40
1	A	35	VAL	O-C-N	-5.34	114.15	122.70
2	B	106	LEU	CB-CG-CD2	-5.34	101.92	111.00
1	A	142	ARG	CA-CB-CG	5.28	125.02	113.40
2	B	41	HIS	CA-C-O	-5.27	109.03	120.10
2	B	52	GLU	CB-CG-CD	5.23	128.31	114.20
2	B	134	LEU	N-CA-CB	-5.22	99.95	110.40
2	B	145	TYR	N-CA-CB	5.22	120.00	110.60
2	B	80	ASN	CB-CA-C	5.21	120.82	110.40
1	A	48	ASP	O-C-N	5.18	130.99	122.70
2	B	75	VAL	CG1-CB-CG2	-5.16	102.64	110.90
1	A	33	ILE	N-CA-CB	-5.16	98.94	110.80
1	A	72	SER	O-C-N	5.15	130.95	122.70
2	B	66	LYS	CA-CB-CG	-5.14	102.09	113.40
1	A	41	THR	CB-CA-C	-5.13	97.74	111.60
2	B	117	LYS	CG-CD-CE	5.08	127.15	111.90
2	B	134	LEU	CB-CG-CD1	-5.07	102.38	111.00
2	B	17	HIS	CA-CB-CG	-5.05	105.02	113.60
1	A	40	LYS	CD-CE-NZ	5.04	123.29	111.70
1	A	11	ARG	CB-CG-CD	-5.04	98.51	111.60
1	A	93	ARG	CD-NE-CZ	5.04	130.65	123.60
2	B	72	ASP	OD1-CG-OD2	5.02	132.84	123.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	11	ARG	Sidechain
1	A	142	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	A	93	ARG	Sidechain
2	B	30	ARG	Sidechain
2	B	73	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	A	1104	0	1136	42	0
2	B	1138	0	1119	59	0
3	A	43	0	30	6	0
3	B	43	0	30	10	0
4	A	2	0	0	0	0
4	B	2	0	0	1	0
5	A	15	0	0	0	0
5	B	13	0	0	3	0
All	All	2360	0	2315	108	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 23.

All (108) 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:0:ACE:O	1:A:1:SER:HB3	1.61	0.99
3:B:148:HEM:HBB2	3:B:148:HEM:HHC	1.44	0.95
2:B:35:TYR:O	2:B:38:THR:HB	1.70	0.92
2:B:32:LEU:HD23	2:B:38:THR:CG2	2.02	0.89
3:B:148:HEM:HHD	3:B:148:HEM:HBC2	1.58	0.86
3:B:148:HEM:HHC	3:B:148:HEM:CBB	2.08	0.83
1:A:102:LEU:HD23	3:A:144:HEM:HBB2	1.60	0.82
2:B:91:LEU:O	2:B:96:LEU:HB2	1.81	0.79
2:B:32:LEU:HD23	2:B:38:THR:HG23	1.67	0.77
2:B:41:HIS:CD2	3:B:148:HEM:HBC1	2.20	0.76
2:B:78:MET:O	2:B:81:ILE:HD12	1.84	0.76
3:A:144:HEM:HBB2	3:A:144:HEM:HHC	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:93:SER:HB3	2:B:145:TYR:HD2	1.51	0.73
3:B:148:HEM:HBB2	3:B:148:HEM:CHC	2.12	0.72
1:A:0:ACE:O	1:A:1:SER:CB	2.32	0.71
1:A:63:VAL:HG12	1:A:64:MET:CE	2.24	0.67
1:A:129:PHE:O	1:A:133:VAL:HG23	1.94	0.67
1:A:76:ASP:OD2	1:A:79:THR:HG23	1.95	0.66
1:A:102:LEU:HD23	3:A:144:HEM:CBB	2.25	0.66
1:A:17:ILE:HD13	1:A:17:ILE:N	2.10	0.66
2:B:81:ILE:CD1	2:B:81:ILE:H	2.08	0.66
2:B:81:ILE:H	2:B:81:ILE:HD13	1.60	0.66
1:A:36:TYR:OH	2:B:131:GLN:NE2	2.28	0.65
1:A:86:GLU:OE1	1:A:140:ARG:NH1	2.29	0.64
2:B:81:ILE:HD13	5:B:472:HOH:O	1.96	0.64
2:B:41:HIS:HD2	3:B:148:HEM:HBC1	1.62	0.64
2:B:85:TYR:CD1	2:B:88:LEU:HD23	2.34	0.63
1:A:20:SER:O	1:A:24:ILE:HG13	2.00	0.62
1:A:29:LEU:HD11	1:A:59:HIS:HD2	1.65	0.62
2:B:140:ALA:HA	2:B:143:LYS:HD3	1.82	0.62
2:B:94:GLU:HG2	2:B:145:TYR:CE2	2.36	0.60
2:B:94:GLU:N	2:B:145:TYR:HE2	2.01	0.59
1:A:114:PHE:HB3	1:A:117:GLU:OE1	2.04	0.57
1:A:21:ALA:O	1:A:64:MET:HG3	2.04	0.57
1:A:50:THR:O	1:A:53:SER:HB3	2.04	0.57
1:A:17:ILE:N	1:A:17:ILE:CD1	2.65	0.57
2:B:81:ILE:CD1	5:B:472:HOH:O	2.52	0.56
2:B:1:VAL:CG2	2:B:2:GLU:H	2.17	0.56
1:A:58:ALA:O	1:A:61:LYS:HB3	2.06	0.56
2:B:63:HIS:NE2	4:B:149:CMO:C	2.69	0.55
2:B:1:VAL:HG13	2:B:132:LYS:NZ	2.22	0.54
2:B:93:SER:HB3	2:B:145:TYR:CD2	2.38	0.54
2:B:93:SER:CB	2:B:145:TYR:HD2	2.19	0.53
2:B:8:ARG:HH22	2:B:79:ASP:CG	2.12	0.53
2:B:32:LEU:HD23	2:B:38:THR:HG22	1.88	0.53
1:A:112:THR:HG22	1:A:113:MET:HG3	1.90	0.52
2:B:85:TYR:HD1	2:B:88:LEU:HD23	1.75	0.52
2:B:106:LEU:HD23	3:B:148:HEM:HBB2	1.91	0.51
2:B:41:HIS:CD2	3:B:148:HEM:CBC	2.92	0.51
2:B:93:SER:CB	2:B:145:TYR:CD2	2.94	0.50
2:B:68:LEU:HD12	2:B:71:LEU:HD12	1.94	0.50
2:B:1:VAL:CG2	2:B:2:GLU:N	2.75	0.50
2:B:1:VAL:HG22	2:B:2:GLU:N	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1:VAL:HG22	2:B:2:GLU:O	2.11	0.50
2:B:8:ARG:HD2	5:B:453:HOH:O	2.12	0.49
2:B:42:PHE:O	2:B:45:PHE:HB2	2.12	0.49
2:B:139:SER:O	2:B:143:LYS:HB3	2.12	0.49
2:B:94:GLU:HB2	2:B:145:TYR:OH	2.13	0.48
1:A:69:LEU:O	1:A:73:LYS:HG2	2.14	0.48
1:A:17:ILE:HD12	1:A:17:ILE:HA	1.31	0.47
1:A:114:PHE:N	1:A:115:PRO:CD	2.77	0.47
2:B:4:THR:O	2:B:8:ARG:HG3	2.13	0.47
1:A:31:ARG:HH11	1:A:31:ARG:HD3	1.49	0.47
2:B:94:GLU:HB2	2:B:145:TYR:CE2	2.49	0.47
3:B:148:HEM:HBC2	3:B:148:HEM:CHD	2.34	0.46
1:A:61:LYS:HB2	1:A:61:LYS:HE3	1.63	0.46
2:B:88:LEU:HD12	2:B:88:LEU:HA	1.47	0.46
1:A:84:LEU:HB3	1:A:137:LEU:HD11	1.98	0.46
2:B:24:GLY:CA	2:B:68:LEU:HD22	2.44	0.46
2:B:3:TRP:CE3	2:B:132:LYS:HE2	2.51	0.46
2:B:70:GLY:O	2:B:85:TYR:OH	2.21	0.46
3:A:144:HEM:HBB2	3:A:144:HEM:CHC	2.38	0.45
2:B:3:TRP:CZ3	2:B:132:LYS:HE2	2.50	0.45
2:B:85:TYR:HD1	2:B:88:LEU:CD2	2.29	0.45
1:A:95:ASP:HA	1:A:96:PRO:HD2	1.66	0.45
2:B:92:HIS:HB3	2:B:103:PHE:HZ	1.81	0.45
2:B:1:VAL:HG22	2:B:2:GLU:H	1.81	0.45
1:A:53:SER:HA	1:A:54:PRO:HD3	1.73	0.45
2:B:30:ARG:HH11	2:B:30:ARG:HD3	1.48	0.45
2:B:86:ALA:HA	2:B:143:LYS:NZ	2.32	0.44
1:A:98:ASN:HB3	3:A:144:HEM:HBC2	2.00	0.44
2:B:32:LEU:HA	2:B:38:THR:HG22	2.00	0.44
2:B:85:TYR:CD1	2:B:88:LEU:CD2	3.01	0.44
1:A:81:LEU:HD22	1:A:84:LEU:HD12	1.99	0.44
2:B:8:ARG:NH2	2:B:79:ASP:OD2	2.48	0.43
2:B:99:ASP:CG	2:B:100:PRO:HD2	2.39	0.43
1:A:136:ALA:O	1:A:139:GLU:HB2	2.17	0.43
1:A:64:MET:HE2	1:A:67:ILE:HG12	1.99	0.43
2:B:1:VAL:HG13	2:B:132:LYS:HZ1	1.82	0.43
2:B:94:GLU:CB	2:B:145:TYR:CE2	3.01	0.43
1:A:63:VAL:HG12	1:A:64:MET:HE2	1.98	0.43
2:B:118:MET:HB2	2:B:122:PHE:HB2	2.00	0.42
1:A:25:GLY:O	1:A:29:LEU:HB2	2.20	0.42
3:A:144:HEM:HBC2	3:A:144:HEM:HMC1	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:LEU:O	1:A:93:ARG:C	2.57	0.42
1:A:56:ILE:HA	1:A:56:ILE:HD13	1.77	0.42
1:A:28:ALA:N	1:A:109:VAL:HG21	2.35	0.42
1:A:76:ASP:OD2	1:A:79:THR:CG2	2.66	0.41
1:A:87:GLN:HG3	1:A:91:LYS:HD3	2.01	0.41
1:A:96:PRO:HD3	1:A:141:TYR:CZ	2.55	0.41
1:A:109:VAL:O	1:A:112:THR:HB	2.20	0.41
1:A:96:PRO:HD3	1:A:141:TYR:OH	2.20	0.41
2:B:63:HIS:CE1	3:B:148:HEM:HBD2	2.56	0.41
1:A:83:GLU:H	1:A:83:GLU:HG3	1.25	0.41
2:B:144:GLN:H	2:B:144:GLN:HG3	1.69	0.41
1:A:90:TYR:C	1:A:90:TYR:CD1	2.94	0.41
2:B:95:LYS:HB2	2:B:95:LYS:HE3	1.85	0.41
2:B:47:ASN:OD1	2:B:49:TYR:HB3	2.22	0.40

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	A	141/143 (99%)	130 (92%)	9 (6%)	2 (1%)	11	20
2	B	144/146 (99%)	138 (96%)	4 (3%)	2 (1%)	11	20
All	All	285/289 (99%)	268 (94%)	13 (5%)	4 (1%)	11	20

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	53	SER
2	B	143	LYS
1	A	1	SER
2	B	47	ASN

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	119/119 (100%)	108 (91%)	11 (9%)	9 18
2	B	120/120 (100%)	107 (89%)	13 (11%)	6 12
All	All	239/239 (100%)	215 (90%)	24 (10%)	7 15

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	ILE
1	A	41	THR
1	A	79	THR
1	A	83	GLU
1	A	91	LYS
1	A	100	LYS
1	A	112	THR
1	A	116	LYS
1	A	137	LEU
1	A	140	ARG
1	A	142	ARG
2	B	1	VAL
2	B	6	LYS
2	B	28	LEU
2	B	38	THR
2	B	81	ILE
2	B	88	LEU
2	B	90	THR
2	B	95	LYS
2	B	96	LEU
2	B	117	LYS
2	B	137	VAL
2	B	144	GLN
2	B	146	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	ASN
1	A	38	GLN
1	A	55	HIS
1	A	59	HIS
1	A	87	GLN
1	A	98	ASN
2	B	41	HIS
2	B	80	ASN
2	B	144	GLN

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 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	$\#\|Z\| > 2$
4	CMO	B	149	3	0,1,1	-	-	-		
4	CMO	A	145	3	0,1,1	-	-	-		
3	HEM	B	148	4,2	41,50,50	1.64	6 (14%)	45,82,82	2.34	18 (40%)
3	HEM	A	144	4,1	41,50,50	1.64	8 (19%)	45,82,82	3.19	15 (33%)

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	B	148	4,2	-	2/12/54/54	-
3	HEM	A	144	4,1	-	5/12/54/54	-

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	148	HEM	C3C-C2C	-5.20	1.33	1.40
3	A	144	HEM	C3C-C2C	-5.11	1.33	1.40
3	B	148	HEM	C3C-CAC	3.49	1.55	1.47
3	B	148	HEM	C4A-NA	3.04	1.42	1.36
3	A	144	HEM	CMD-C2D	2.92	1.57	1.50
3	A	144	HEM	C3C-CAC	2.80	1.53	1.47
3	B	148	HEM	CAB-C3B	2.62	1.54	1.47
3	A	144	HEM	C4A-NA	2.55	1.41	1.36
3	A	144	HEM	CMA-C3A	2.53	1.56	1.51
3	B	148	HEM	CMD-C2D	2.42	1.55	1.50
3	A	144	HEM	O1A-CGA	2.32	1.29	1.22
3	A	144	HEM	CBA-CGA	2.23	1.55	1.50
3	B	148	HEM	O1A-CGA	2.16	1.29	1.22
3	A	144	HEM	CAB-C3B	2.15	1.53	1.47

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	144	HEM	CBA-CAA-C2A	14.40	137.19	112.62
3	A	144	HEM	O2A-CGA-O1A	5.94	138.09	123.30
3	A	144	HEM	C4B-CHC-C1C	5.61	129.97	122.56
3	A	144	HEM	C4B-C3B-C2B	5.57	111.54	107.11
3	B	148	HEM	CMA-C3A-C4A	-5.33	120.27	128.46
3	B	148	HEM	C4D-ND-C1D	5.05	110.29	105.07
3	B	148	HEM	CHA-C4D-ND	5.01	130.57	124.38
3	A	144	HEM	O1A-CGA-CBA	-4.86	107.46	123.08
3	A	144	HEM	CHB-C1B-NB	4.68	130.16	124.38
3	A	144	HEM	CHC-C4B-C3B	4.51	131.47	124.57
3	B	148	HEM	C2C-C3C-C4C	4.14	109.79	106.90
3	B	148	HEM	O2D-CGD-O1D	3.77	132.69	123.30
3	A	144	HEM	O2D-CGD-O1D	-3.66	114.17	123.30
3	B	148	HEM	C3D-C4D-ND	-3.60	106.16	110.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	148	HEM	C2D-C1D-ND	-3.55	105.63	109.88
3	A	144	HEM	CHC-C4B-NB	-3.52	120.60	124.43
3	B	148	HEM	CAD-CBD-CGD	-3.44	106.20	113.60
3	B	148	HEM	C4C-CHD-C1D	3.37	127.00	122.56
3	B	148	HEM	CMA-C3A-C2A	3.05	130.69	124.94
3	B	148	HEM	C4A-C3A-C2A	2.91	109.02	107.00
3	A	144	HEM	CAB-C3B-C2B	-2.84	119.24	128.60
3	A	144	HEM	CMC-C2C-C3C	2.63	129.60	124.68
3	B	148	HEM	O1D-CGD-CBD	-2.57	114.81	123.08
3	A	144	HEM	CBB-CAB-C3B	-2.54	114.96	127.62
3	A	144	HEM	CHB-C1B-C2B	-2.42	120.02	126.72
3	A	144	HEM	C3B-C2B-C1B	-2.40	104.70	106.49
3	B	148	HEM	CBA-CAA-C2A	2.34	116.62	112.62
3	B	148	HEM	C4B-CHC-C1C	2.30	125.59	122.56
3	B	148	HEM	O1A-CGA-CBA	-2.27	115.79	123.08
3	B	148	HEM	C3B-C2B-C1B	2.27	108.17	106.49
3	B	148	HEM	CHD-C1D-ND	2.20	126.82	124.43
3	A	144	HEM	O2D-CGD-CBD	2.16	120.96	114.03
3	B	148	HEM	CBB-CAB-C3B	-2.05	117.42	127.62

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	144	HEM	C1A-C2A-CAA-CBA
3	A	144	HEM	C3A-C2A-CAA-CBA
3	A	144	HEM	C2A-CAA-CBA-CGA
3	A	144	HEM	CAA-CBA-CGA-O1A
3	B	148	HEM	CAD-CBD-CGD-O2D
3	A	144	HEM	CAA-CBA-CGA-O2A
3	B	148	HEM	CAD-CBD-CGD-O1D

There are no ring outliers.

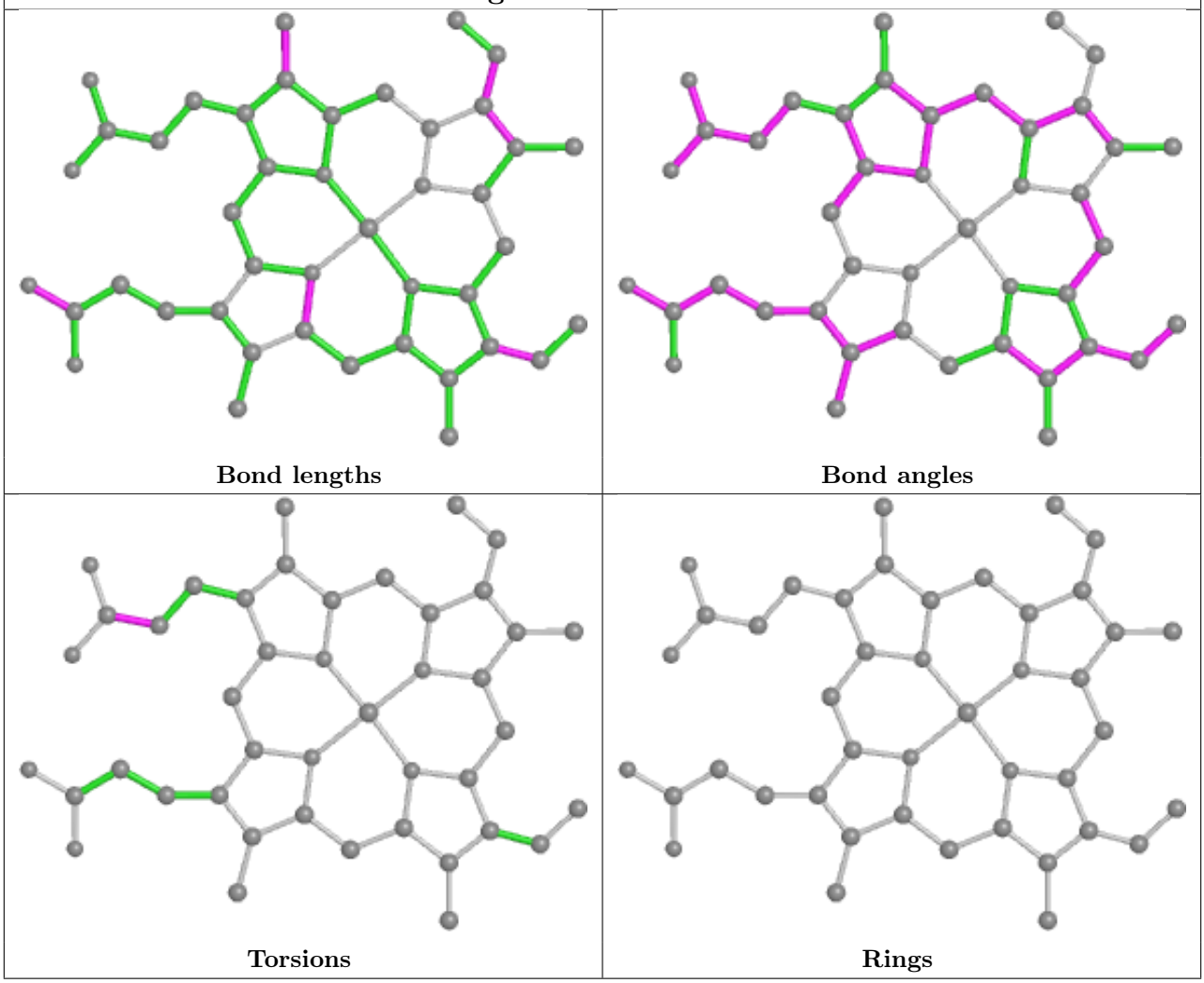
3 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	149	CMO	1	0
3	B	148	HEM	10	0
3	A	144	HEM	6	0

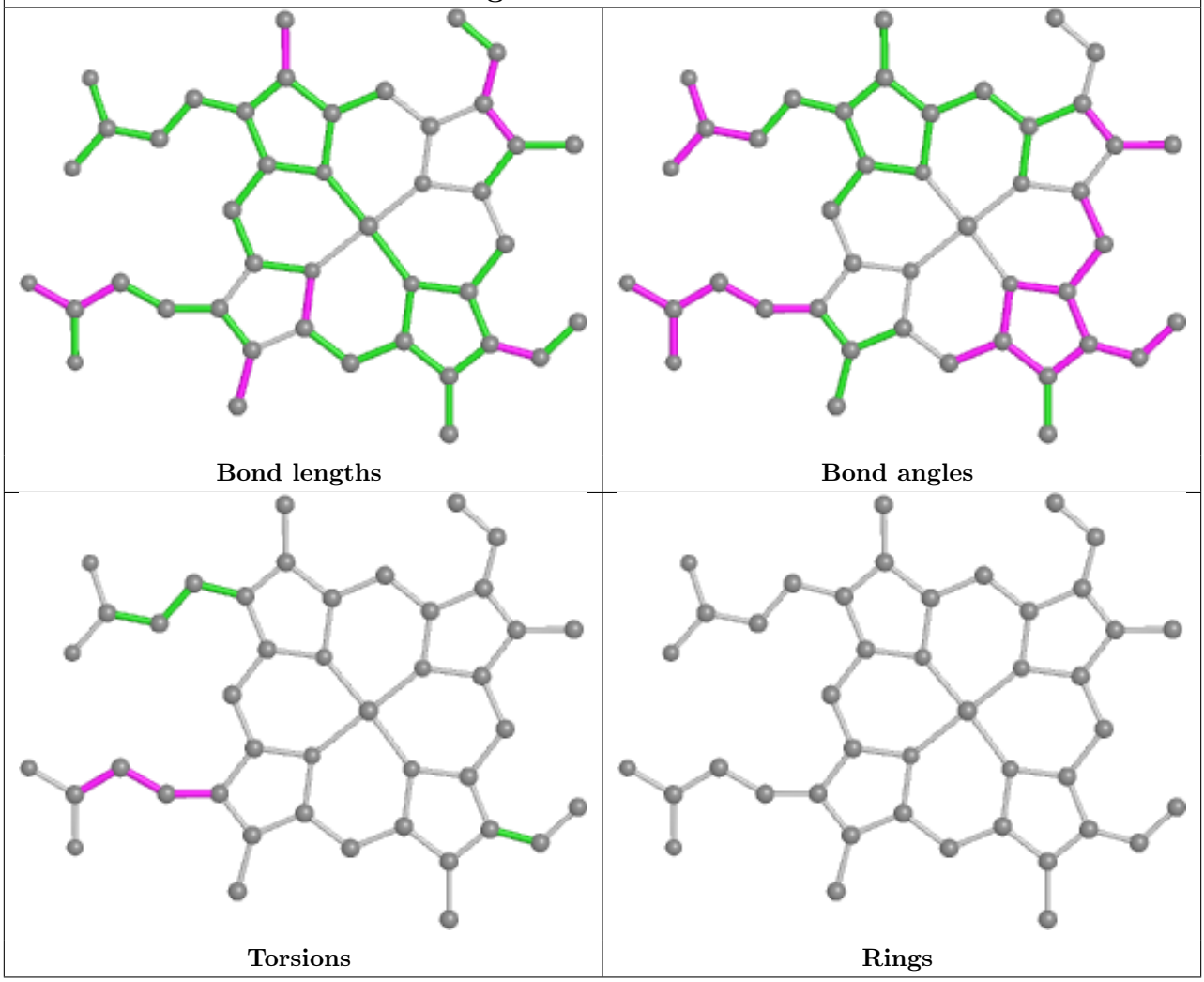
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

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 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.

Ligand HEM B 148



Ligand HEM A 144



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)

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	142/143 (99%)	-1.02	0 100 100	12, 25, 46, 53	0
2	B	146/146 (100%)	-0.61	5 (3%) 45 48	11, 32, 58, 92	0
All	All	288/289 (99%)	-0.81	5 (1%) 70 72	11, 28, 55, 92	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	1	VAL	6.3
2	B	145	TYR	4.8
2	B	49	TYR	3.8
2	B	146	HIS	2.2
2	B	143	LYS	2.2

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 monosaccharides in this entry.

6.4 Ligands (i)

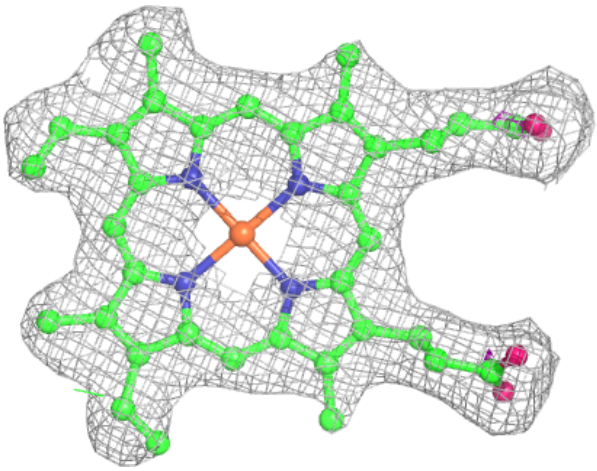
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

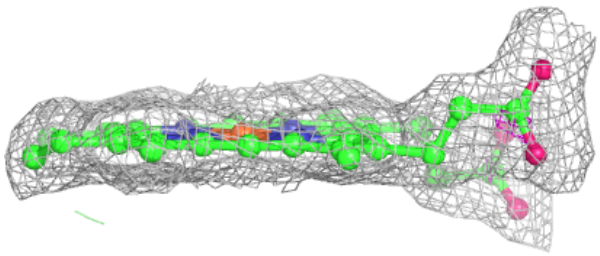
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	HEM	B	148	43/43	0.94	0.12	25,33,50,52	0
3	HEM	A	144	43/43	0.96	0.11	16,22,46,54	0
4	CMO	B	149	2/2	0.98	0.15	40,40,40,44	0
4	CMO	A	145	2/2	0.99	0.09	38,38,38,42	0

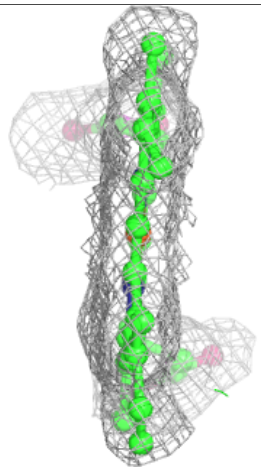
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around HEM B 148:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)

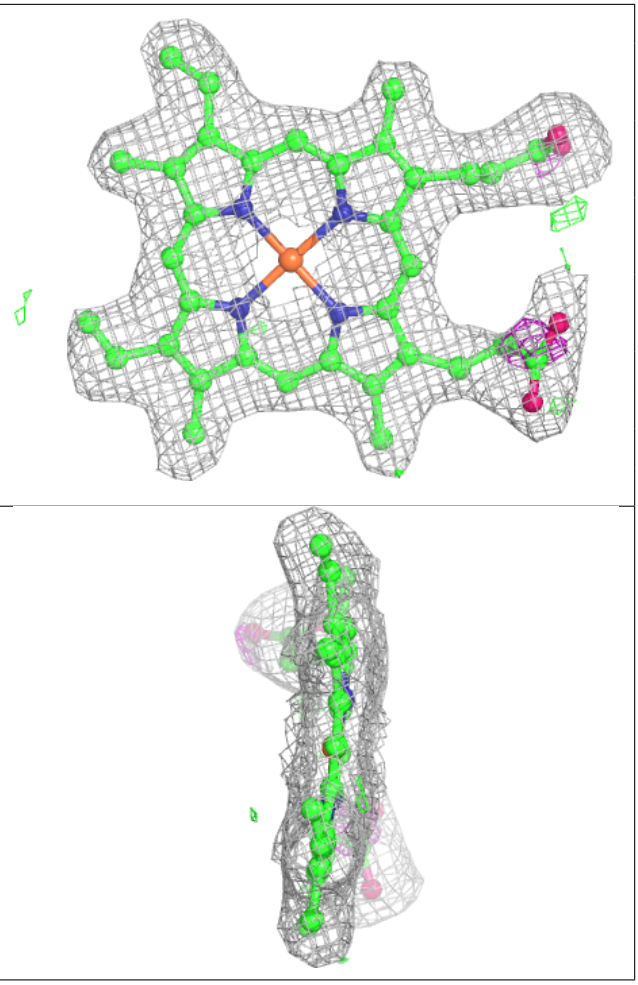






Electron density around HEM A 144:

$2mF_o$-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 (i)

There are no such residues in this entry.