



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:25 PM GMT

PDB ID : 1OUU
Title : CARBONMONOXY TROUT HEMOGLOBIN I
Authors : Tame, J.; Wilson, J.
Deposited on : 1996-06-21
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
<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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

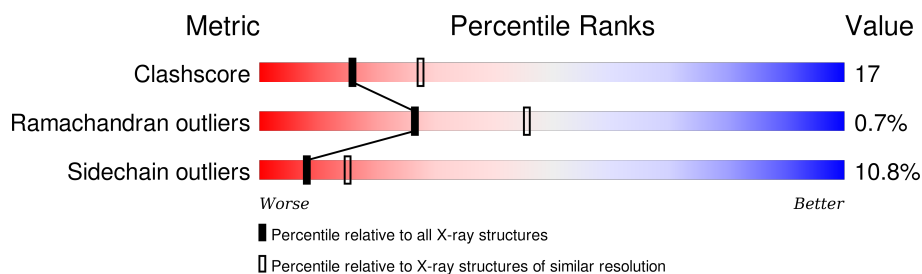
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (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 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	143	 65% 29% 6% •
1	C	143	 67% 28% • •
2	B	146	 55% 37% 8%
2	D	146	 64% 30% 6%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	CMO	A	144	-	-	X	-
4	CMO	C	144	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4717 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 I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	143	Total	C	N	O	S	0	0	0
			1066	690	181	191	4			
1	C	143	Total	C	N	O	S	0	0	0
			1066	690	181	191	4			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ASP	DELETION	UNP P02019
A	?	-	LYS	DELETION	UNP P02019
C	?	-	ASP	DELETION	UNP P02019
C	?	-	LYS	DELETION	UNP P02019

- Molecule 2 is a protein called HEMOGLOBIN I.

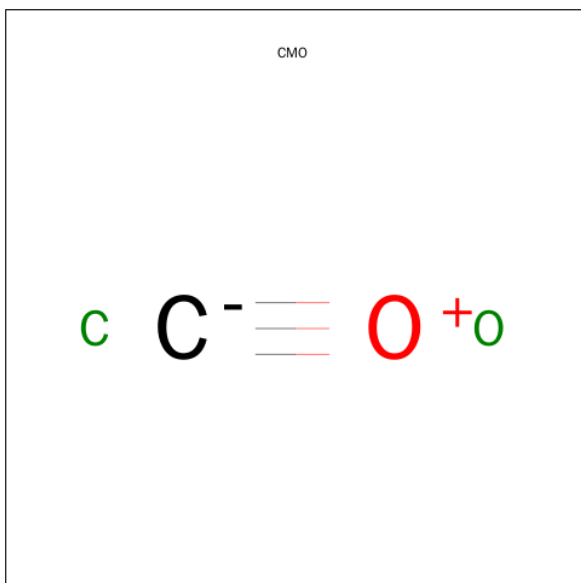
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	146	Total	C	N	O	S	0	0	0
			1121	729	187	200	5			
2	D	146	Total	C	N	O	S	0	0	0
			1121	729	187	200	5			

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



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

- Molecule 5 is water.

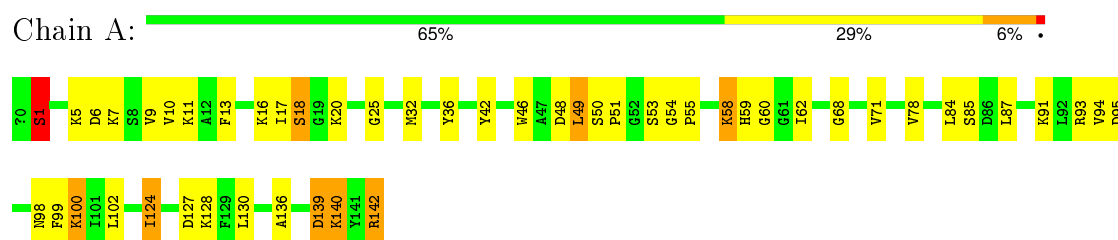
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	52	Total O 52 52	0	0
5	B	29	Total O 29 29	0	0
5	C	50	Total O 50 50	0	0
5	D	32	Total O 32 32	0	0

3 Residue-property plots [i](#)

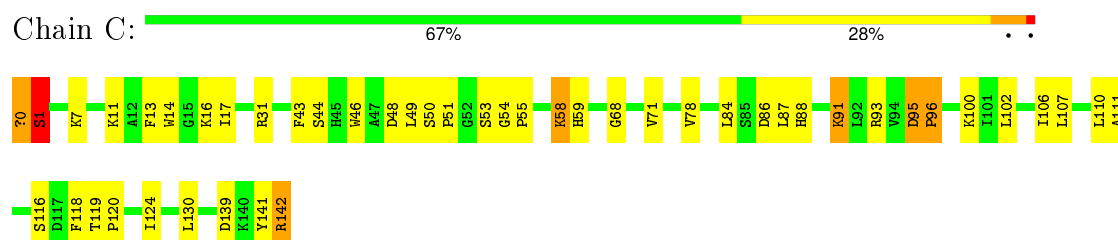
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

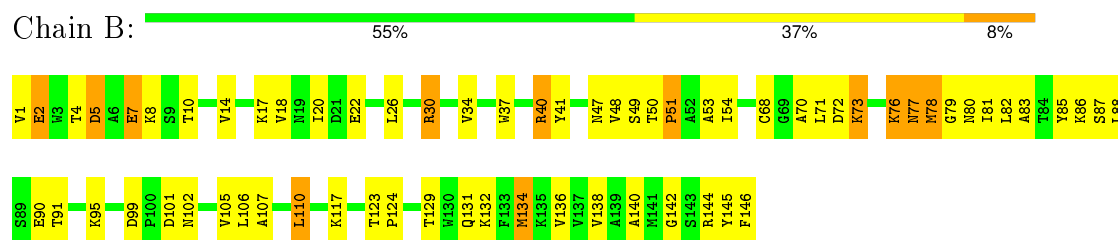
• Molecule 1: HEMOGLOBIN I



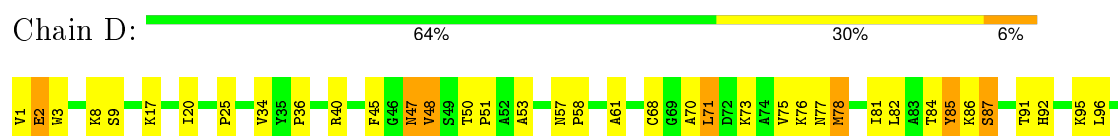
• Molecule 1: HEMOGLOBIN I



• Molecule 2: HEMOGLOBIN I



• Molecule 2: HEMOGLOBIN I



R104	Y105	L106	A107	D108	V109	L110
A116	T123	P124	T129	K132	F133	M134
K135	A140	R144	Y145	F146		

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.20 Å 79.80 Å 122.90 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.50	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-2.50)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.162 , 0.286	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4717	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CMO, HEM, ACE

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	0.72	0/1089	1.36	5/1472 (0.3%)
1	C	0.71	0/1089	1.37	10/1472 (0.7%)
2	B	0.75	0/1148	1.46	9/1560 (0.6%)
2	D	0.75	0/1148	1.51	8/1560 (0.5%)
All	All	0.73	0/4474	1.43	32/6064 (0.5%)

There are no bond length outliers.

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	85	TYR	CB-CG-CD1	10.44	127.26	121.00
2	B	30	ARG	CD-NE-CZ	9.79	137.30	123.60
2	D	110	LEU	CA-CB-CG	8.60	135.07	115.30
2	D	47	ASN	C-N-CA	8.16	142.11	121.70
2	D	47	ASN	CA-C-O	7.57	136.00	120.10
1	A	93	ARG	NE-CZ-NH2	-7.41	116.59	120.30
1	C	31	ARG	CD-NE-CZ	6.78	133.09	123.60
2	B	85	TYR	CB-CG-CD1	6.66	125.00	121.00
2	B	5	ASP	CB-CG-OD1	6.49	124.14	118.30
1	A	1	SER	N-CA-CB	6.28	119.92	110.50
2	B	41	TYR	CB-CG-CD1	-6.27	117.24	121.00
2	D	85	TYR	CB-CG-CD2	-6.17	117.30	121.00
1	A	142	ARG	NE-CZ-NH1	6.16	123.38	120.30
1	C	1	SER	N-CA-CB	6.10	119.65	110.50
2	D	108	ASP	CB-CG-OD1	5.96	123.67	118.30
1	C	95	ASP	CB-CG-OD1	5.96	123.66	118.30
1	C	142	ARG	NE-CZ-NH1	5.73	123.16	120.30
1	A	93	ARG	NE-CZ-NH1	5.68	123.14	120.30
2	B	41	TYR	CB-CG-CD2	5.64	124.38	121.00
1	C	0	ACE	C-N-CA	5.46	135.35	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	144	ARG	NE-CZ-NH1	-5.45	117.57	120.30
1	C	86	ASP	CB-CA-C	-5.37	99.67	110.40
1	C	142	ARG	CD-NE-CZ	5.34	131.08	123.60
1	C	93	ARG	NE-CZ-NH1	-5.34	117.63	120.30
2	B	134	MET	CA-CB-CG	5.24	122.20	113.30
1	A	127	ASP	CB-CG-OD2	5.16	122.95	118.30
2	B	110	LEU	CA-CB-CG	5.16	127.17	115.30
1	C	31	ARG	NE-CZ-NH1	5.13	122.86	120.30
2	D	48	VAL	N-CA-CB	-5.07	100.35	111.50
2	B	51	PRO	N-CA-CB	5.06	109.37	103.30
1	C	96	PRO	O-C-N	-5.04	114.63	123.20
2	B	105	VAL	CA-CB-CG1	5.03	118.44	110.90

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	1066	0	1092	33	0
1	C	1066	0	1092	35	0
2	B	1121	0	1141	48	0
2	D	1121	0	1140	43	0
3	A	43	0	30	5	0
3	B	43	0	30	5	0
3	C	43	0	30	4	0
3	D	43	0	30	2	0
4	A	2	0	0	2	0
4	B	2	0	0	0	0
4	C	2	0	0	2	0
4	D	2	0	0	0	0
5	A	52	0	0	1	0
5	B	29	0	0	1	0
5	C	50	0	0	1	0
5	D	32	0	0	0	0
All	All	4717	0	4585	155	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 17.

All (155) 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)
2:D:1:VAL:HG22	2:D:2:GLU:H	1.39	0.88
2:D:70:ALA:HA	2:D:73:LYS:HE3	1.65	0.79
2:D:92:HIS:HA	2:D:96:LEU:HD12	1.65	0.79
2:D:50:THR:HB	2:D:51:PRO:HD2	1.67	0.75
2:B:20:ILE:HG23	2:B:68:CYS:HB2	1.71	0.72
2:B:132:LYS:O	2:B:136:VAL:HG23	1.88	0.72
2:B:20:ILE:HD12	2:B:20:ILE:H	1.54	0.71
1:A:58:LYS:HE2	1:A:59:HIS:N	2.04	0.71
2:D:1:VAL:HG22	2:D:2:GLU:N	2.06	0.71
1:A:48:ASP:HB3	1:A:53:SER:HB2	1.73	0.70
1:A:59:HIS:HE2	4:A:144:CMO:C	2.04	0.70
2:D:20:ILE:HG13	2:D:68:CYS:HB3	1.74	0.70
2:B:48:VAL:HG13	2:B:54:ILE:HG12	1.74	0.70
2:D:50:THR:H	2:D:53:ALA:HB3	1.59	0.67
2:D:73:LYS:O	2:D:77:ASN:HB2	1.95	0.67
2:D:87:SER:O	2:D:91:THR:HG23	1.94	0.67
2:B:1:VAL:HG11	2:B:132:LYS:HE2	1.76	0.66
1:A:7:LYS:O	1:A:11:LYS:HG3	1.97	0.64
2:B:106:LEU:HD22	3:B:148:HEM:CBB	2.26	0.64
2:D:71:LEU:O	2:D:75:VAL:HG23	1.97	0.64
1:C:58:LYS:HE2	1:C:59:HIS:N	2.13	0.64
1:C:7:LYS:O	1:C:11:LYS:HG3	1.99	0.63
1:A:85:SER:HB3	1:A:140:LYS:HG2	1.81	0.63
3:A:143:HEM:HMC2	3:A:143:HEM:HBC2	1.81	0.63
1:A:48:ASP:HB3	1:A:53:SER:CB	2.30	0.61
1:C:111:ALA:HB1	2:D:116:ALA:HB2	1.81	0.61
2:D:50:THR:HB	2:D:51:PRO:CD	2.30	0.61
2:B:14:VAL:O	2:B:18:VAL:HG23	2.00	0.61
2:B:70:ALA:HA	2:B:73:LYS:NZ	2.16	0.60
2:B:146:PHE:CE2	2:D:1:VAL:HB	2.37	0.60
3:B:148:HEM:HBA1	3:B:148:HEM:HHA	1.84	0.60
2:D:70:ALA:HA	2:D:73:LYS:CE	2.33	0.59
1:A:1:SER:HB2	1:C:139:ASP:OD1	2.02	0.59
2:B:72:ASP:O	2:B:76:LYS:HD2	2.03	0.59
2:D:1:VAL:CG2	2:D:2:GLU:H	2.13	0.58
1:C:119:THR:HB	1:C:120:PRO:CD	2.33	0.58
1:C:87:LEU:HA	1:C:91:LYS:HE2	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:119:THR:HB	1:C:120:PRO:HD2	1.85	0.57
1:A:128:LYS:HD2	1:C:142:ARG:HG3	1.87	0.57
3:A:143:HEM:HBC2	3:A:143:HEM:CMC	2.34	0.57
1:C:13:PHE:O	1:C:17:ILE:HG23	2.05	0.57
3:B:148:HEM:CBA	3:B:148:HEM:HHA	2.35	0.57
1:A:50:SER:HB2	1:A:51:PRO:HD2	1.86	0.56
2:B:4:THR:O	2:B:8:LYS:HG3	2.04	0.56
1:C:0:ACE:H3	5:C:148:HOH:O	2.05	0.56
1:C:124:ILE:CD1	2:D:34:VAL:HA	2.35	0.56
2:B:136:VAL:HG22	2:D:146:PHE:CE1	2.41	0.55
1:C:124:ILE:HD13	2:D:34:VAL:HA	1.89	0.55
2:B:73:LYS:O	2:B:77:ASN:HB2	2.07	0.55
2:D:8:LYS:HA	2:D:78:MET:HE1	1.88	0.55
2:B:78:MET:HA	2:B:81:ILE:HD11	1.88	0.54
2:D:106:LEU:HD22	3:D:148:HEM:CBB	2.38	0.54
1:C:59:HIS:HE2	4:C:144:CMO:C	2.21	0.53
1:A:59:HIS:NE2	4:A:144:CMO:O	2.39	0.53
1:C:14:TRP:CZ3	1:C:17:ILE:HD11	2.44	0.52
2:D:47:ASN:O	2:D:53:ALA:HB1	2.10	0.52
1:C:106:ILE:O	1:C:110:LEU:HG	2.09	0.52
1:A:5:LYS:O	1:A:9:VAL:HG23	2.10	0.51
2:D:25:PRO:HB3	2:D:61:ALA:HA	1.92	0.51
1:A:98:ASN:HB3	3:A:143:HEM:HBC2	1.93	0.51
1:C:48:ASP:HB3	1:C:53:SER:HB2	1.92	0.51
2:D:106:LEU:HD22	3:D:148:HEM:HBB2	1.91	0.51
2:B:50:THR:HB	2:B:51:PRO:CD	2.41	0.51
2:B:70:ALA:O	2:B:73:LYS:HG3	2.11	0.50
1:C:84:LEU:HD22	1:C:88:HIS:HE1	1.77	0.50
1:C:102:LEU:HD23	3:C:143:HEM:HAB	1.94	0.50
3:C:143:HEM:HBC2	3:C:143:HEM:HMC1	1.94	0.50
2:B:77:ASN:O	2:B:79:GLY:N	2.44	0.49
2:D:82:LEU:HD23	2:D:140:ALA:HA	1.93	0.49
1:C:96:PRO:HG3	1:C:141:TYR:CE2	2.46	0.49
1:A:87:LEU:HD12	1:A:91:LYS:HB2	1.94	0.49
2:B:146:PHE:O	2:D:135:LYS:HE3	2.13	0.49
1:A:46:TRP:HB2	1:A:49:LEU:HD21	1.95	0.49
1:A:124:ILE:HG12	2:B:34:VAL:HA	1.93	0.49
2:B:1:VAL:HG22	2:B:2:GLU:H	1.76	0.48
2:B:47:ASN:HD22	2:B:53:ALA:HB1	1.78	0.48
1:A:62:ILE:HD12	5:A:160:HOH:O	2.12	0.48
2:B:7:GLU:O	2:B:10:THR:HB	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:VAL:HA	1:A:136:ALA:HB1	1.95	0.48
2:D:8:LYS:HG2	2:D:78:MET:CE	2.44	0.48
2:D:45:PHE:N	2:D:45:PHE:CD1	2.82	0.47
2:D:78:MET:HA	2:D:81:ILE:HD11	1.94	0.47
1:C:84:LEU:HD22	1:C:88:HIS:CE1	2.49	0.47
1:C:107:LEU:HD22	1:C:118:PHE:HZ	1.79	0.47
2:B:70:ALA:HA	2:B:73:LYS:HZ2	1.79	0.47
1:A:46:TRP:HE3	1:A:49:LEU:HD22	1.80	0.46
2:B:107:ALA:HA	2:B:134:MET:HE2	1.98	0.46
3:B:148:HEM:HBA1	3:B:148:HEM:CHA	2.44	0.46
2:B:47:ASN:HD22	2:B:53:ALA:CB	2.28	0.46
2:D:84:THR:HG22	2:D:85:TYR:HD1	1.79	0.46
2:B:50:THR:HB	2:B:51:PRO:HD2	1.97	0.46
2:D:82:LEU:CD2	2:D:140:ALA:HA	2.46	0.46
2:D:45:PHE:N	2:D:45:PHE:HD1	2.14	0.46
2:D:3:TRP:CH2	2:D:132:LYS:HG2	2.50	0.46
1:C:43:PHE:O	1:C:49:LEU:HD21	2.16	0.46
2:B:70:ALA:HA	2:B:73:LYS:HZ3	1.81	0.45
1:A:99:PHE:HB2	1:A:100:LYS:HE3	1.97	0.45
2:D:8:LYS:HG2	2:D:78:MET:HE2	1.97	0.45
2:B:134:MET:O	2:B:138:VAL:HG23	2.16	0.45
2:B:50:THR:O	2:B:54:ILE:HG13	2.17	0.45
2:B:82:LEU:HA	2:B:82:LEU:HD23	1.89	0.45
2:B:99:ASP:OD1	2:B:101:ASP:HB2	2.17	0.45
1:A:25:GLY:HA3	1:A:60:GLY:O	2.15	0.45
2:B:123:THR:HB	2:B:124:PRO:HD2	1.99	0.45
1:A:42:TYR:CE1	1:A:94:VAL:HA	2.52	0.45
2:B:142:GLY:HA2	2:B:145:TYR:CD1	2.52	0.44
2:D:123:THR:HB	2:D:124:PRO:HD2	1.98	0.44
2:B:82:LEU:HD23	2:B:140:ALA:HA	1.98	0.44
2:B:82:LEU:CD2	2:B:140:ALA:HA	2.47	0.44
2:B:22:GLU:O	2:B:26:LEU:HG	2.18	0.44
1:C:87:LEU:HD12	1:C:91:LYS:HB2	2.00	0.44
2:D:86:LYS:HA	2:D:86:LYS:HD3	1.71	0.44
2:D:25:PRO:HG3	2:D:61:ALA:O	2.18	0.43
1:C:54:GLY:N	1:C:55:PRO:CD	2.80	0.43
1:C:68:GLY:O	1:C:71:VAL:HB	2.17	0.43
2:B:5:ASP:HA	2:B:8:LYS:HE2	2.01	0.43
1:A:102:LEU:HD23	3:A:143:HEM:HAB	2.01	0.43
2:B:77:ASN:OD1	2:B:80:ASN:HB2	2.18	0.43
2:B:1:VAL:HG22	2:B:2:GLU:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:17:ILE:O	1:A:18:SER:C	2.57	0.43
1:A:32:MET:O	1:A:36:TYR:HB2	2.19	0.43
1:A:54:GLY:N	1:A:55:PRO:HD2	2.34	0.43
1:C:91:LYS:HD3	1:C:91:LYS:N	2.33	0.42
2:B:102:ASN:HB3	3:B:148:HEM:HMC1	2.00	0.42
3:C:143:HEM:HBC2	3:C:143:HEM:CMC	2.49	0.42
1:A:94:VAL:HG12	1:A:95:ASP:O	2.20	0.42
2:B:80:ASN:HB3	2:B:83:ALA:HB3	2.02	0.42
1:C:124:ILE:HG12	2:D:34:VAL:HG22	2.01	0.42
1:A:139:ASP:OD1	1:C:1:SER:HB2	2.19	0.42
3:A:143:HEM:HBD2	3:A:143:HEM:HHA	2.01	0.42
2:D:57:ASN:HA	2:D:58:PRO:HD3	1.66	0.42
2:D:92:HIS:CA	2:D:96:LEU:HD12	2.43	0.42
1:C:59:HIS:NE2	4:C:144:CMO:O	2.45	0.42
2:B:82:LEU:HD22	2:B:86:LYS:HE2	2.01	0.42
2:B:87:SER:HA	2:B:90:GLU:HB2	2.02	0.41
2:B:86:LYS:HD3	2:B:86:LYS:HA	1.65	0.41
1:A:6:ASP:O	1:A:10:VAL:HG23	2.20	0.41
1:C:50:SER:HA	1:C:51:PRO:HD3	1.93	0.41
2:B:47:ASN:O	2:B:53:ALA:HB1	2.21	0.41
1:C:46:TRP:HB2	1:C:49:LEU:HD21	2.01	0.41
2:B:91:THR:HG21	5:B:154:HOH:O	2.20	0.41
2:B:87:SER:O	2:B:91:THR:HG23	2.21	0.41
1:A:100:LYS:HZ2	1:A:100:LYS:HG2	1.71	0.41
1:A:68:GLY:O	1:A:71:VAL:HB	2.20	0.41
1:C:95:ASP:HA	1:C:96:PRO:HD3	1.87	0.41
1:A:142:ARG:HB3	2:D:36:PRO:HG2	2.02	0.41
2:D:82:LEU:HA	2:D:82:LEU:HD23	1.91	0.41
2:D:84:THR:HG22	2:D:85:TYR:CD1	2.55	0.41
1:A:54:GLY:N	1:A:55:PRO:CD	2.84	0.41
1:C:107:LEU:HD22	1:C:118:PHE:CZ	2.56	0.41
1:C:102:LEU:HD23	3:C:143:HEM:CAB	2.51	0.41
2:B:37:TRP:O	2:B:40:ARG:HG2	2.21	0.41
2:D:107:ALA:HA	2:D:134:MET:HE2	2.03	0.41
1:C:58:LYS:HE2	1:C:59:HIS:CA	2.51	0.40
1:A:13:PHE:HA	1:A:16:LYS:HG3	2.02	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	141/143 (99%)	136 (96%)	4 (3%)	1 (1%)	26	46
1	C	141/143 (99%)	137 (97%)	3 (2%)	1 (1%)	26	46
2	B	144/146 (99%)	139 (96%)	4 (3%)	1 (1%)	26	46
2	D	144/146 (99%)	138 (96%)	5 (4%)	1 (1%)	26	46
All	All	570/578 (99%)	550 (96%)	16 (3%)	4 (1%)	26	46

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	78	MET
1	C	1	SER
1	A	1	SER
2	D	78	MET

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	110/110 (100%)	99 (90%)	11 (10%)	9	18
1	C	110/110 (100%)	102 (93%)	8 (7%)	17	32
2	B	117/117 (100%)	100 (86%)	17 (14%)	4	7
2	D	117/117 (100%)	104 (89%)	13 (11%)	8	14
All	All	454/454 (100%)	405 (89%)	49 (11%)	8	15

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	SER
1	A	18	SER
1	A	20	LYS
1	A	49	LEU
1	A	58	LYS
1	A	84	LEU
1	A	100	LYS
1	A	124	ILE
1	A	130	LEU
1	A	139	ASP
1	A	140	LYS
2	B	2	GLU
2	B	7	GLU
2	B	17	LYS
2	B	30	ARG
2	B	40	ARG
2	B	49	SER
2	B	71	LEU
2	B	73	LYS
2	B	76	LYS
2	B	77	ASN
2	B	88	LEU
2	B	95	LYS
2	B	110	LEU
2	B	117	LYS
2	B	129	THR
2	B	131	GLN
2	B	144	ARG
1	C	16	LYS
1	C	44	SER
1	C	58	LYS
1	C	78	VAL
1	C	91	LYS
1	C	100	LYS
1	C	116	SER
1	C	130	LEU
2	D	2	GLU
2	D	9	SER
2	D	17	LYS
2	D	40	ARG
2	D	48	VAL
2	D	71	LEU

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Mol	Chain	Res	Type
2	D	76	LYS
2	D	87	SER
2	D	95	LYS
2	D	104	ARG
2	D	110	LEU
2	D	129	THR
2	D	144	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	98	ASN
2	B	47	ASN
2	B	131	GLN
1	C	38	GLN
2	D	131	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

8 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	143	1,4	30,50,50	2.36	7 (23%)	24,82,82	2.91	12 (50%)
4	CMO	A	144	3	0,1,1	0.00	-	0,0,0	0.00	-
3	HEM	B	148	2,4	30,50,50	2.57	10 (33%)	24,82,82	2.83	10 (41%)
4	CMO	B	149	3	0,1,1	0.00	-	0,0,0	0.00	-
3	HEM	C	143	1,4	30,50,50	2.39	6 (20%)	24,82,82	2.98	11 (45%)
4	CMO	C	144	3	0,1,1	0.00	-	0,0,0	0.00	-
3	HEM	D	148	2,4	30,50,50	2.65	10 (33%)	24,82,82	3.11	11 (45%)
4	CMO	D	149	3	0,1,1	0.00	-	0,0,0	0.00	-

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	143	1,4	-	0/10/54/54	0/0/8/8
4	CMO	A	144	3	-	0/0/0/0	0/0/0/0
3	HEM	B	148	2,4	-	0/10/54/54	0/0/8/8
4	CMO	B	149	3	-	0/0/0/0	0/0/0/0
3	HEM	C	143	1,4	-	0/10/54/54	0/0/8/8
4	CMO	C	144	3	-	0/0/0/0	0/0/0/0
3	HEM	D	148	2,4	-	0/10/54/54	0/0/8/8
4	CMO	D	149	3	-	0/0/0/0	0/0/0/0

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	148	HEM	C3B-C4B	-7.60	1.45	1.51
3	D	148	HEM	C3B-C4B	-7.56	1.45	1.51
3	B	148	HEM	C2D-C3D	-7.29	1.32	1.54
3	D	148	HEM	C2D-C3D	-7.05	1.33	1.54
3	C	143	HEM	C2D-C3D	-6.78	1.34	1.54
3	A	143	HEM	C2D-C3D	-6.78	1.34	1.54
3	A	143	HEM	C3B-C4B	-6.48	1.46	1.51
3	C	143	HEM	C3B-C4B	-5.94	1.46	1.51
3	D	148	HEM	C3D-C4D	-5.66	1.44	1.51
3	C	143	HEM	C3D-C4D	-5.15	1.45	1.51
3	A	143	HEM	C3D-C4D	-4.85	1.45	1.51
3	B	148	HEM	C3D-C4D	-4.73	1.45	1.51
3	B	148	HEM	C2C-C1C	-3.98	1.45	1.52
3	C	143	HEM	C2C-C1C	-3.91	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	148	HEM	C2C-C1C	-3.81	1.45	1.52
3	A	143	HEM	C2C-C1C	-3.14	1.46	1.52
3	B	148	HEM	C2D-C1D	-2.15	1.44	1.51
3	D	148	HEM	C2D-C1D	-2.11	1.44	1.51
3	D	148	HEM	C2B-C1B	-2.06	1.45	1.51
3	A	143	HEM	CAA-C2A	2.01	1.55	1.52
3	B	148	HEM	FE-NC	2.03	2.03	1.95
3	D	148	HEM	FE-NC	2.04	2.03	1.95
3	B	148	HEM	C3C-CAC	2.15	1.55	1.51
3	B	148	HEM	CAA-C2A	2.17	1.55	1.52
3	B	148	HEM	C4C-NC	2.35	1.38	1.36
3	D	148	HEM	C3B-CAB	2.38	1.55	1.51
3	D	148	HEM	C4C-NC	2.76	1.39	1.36
3	B	148	HEM	C1C-NC	2.79	1.39	1.36
3	A	143	HEM	C1C-NC	2.84	1.39	1.36
3	C	143	HEM	C1C-NC	3.24	1.40	1.36
3	A	143	HEM	C4C-NC	3.26	1.40	1.36
3	C	143	HEM	C4C-NC	3.42	1.40	1.36
3	D	148	HEM	C1C-NC	3.58	1.40	1.36

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	143	HEM	CMA-C3A-C4A	-5.45	119.34	128.36
3	D	148	HEM	CMA-C3A-C4A	-5.29	119.61	128.36
3	B	148	HEM	C3B-CAB-CBB	-5.18	116.50	124.46
3	A	143	HEM	CMA-C3A-C4A	-5.05	120.01	128.36
3	C	143	HEM	CAA-C2A-C1A	-3.68	123.02	127.01
3	B	148	HEM	CMA-C3A-C4A	-3.63	122.35	128.36
3	D	148	HEM	C3B-CAB-CBB	-3.61	118.92	124.46
3	A	143	HEM	CAA-C2A-C1A	-3.54	123.16	127.01
3	B	148	HEM	C3C-CAC-CBC	-2.86	120.07	124.46
3	A	143	HEM	C3C-CAC-CBC	-2.51	120.61	124.46
3	A	143	HEM	C3B-C4B-CHC	2.11	126.14	123.16
3	B	148	HEM	CMA-C3A-C2A	2.54	130.56	125.24
3	B	148	HEM	CAD-C3D-C4D	2.66	121.86	112.47
3	A	143	HEM	CAD-C3D-C4D	2.73	122.10	112.47
3	D	148	HEM	CBA-CAA-C2A	2.81	117.57	112.53
3	C	143	HEM	CAD-C3D-C4D	2.84	122.48	112.47
3	D	148	HEM	CAD-C3D-C4D	2.91	122.72	112.47
3	A	143	HEM	CMD-C2D-C3D	3.15	128.29	114.35
3	D	148	HEM	CMA-C3A-C2A	3.18	131.90	125.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	143	HEM	CAA-CBA-CGA	3.31	118.81	112.75
3	A	143	HEM	CAA-CBA-CGA	3.31	118.81	112.75
3	B	148	HEM	CMD-C2D-C3D	3.42	129.48	114.35
3	C	143	HEM	CMD-C2D-C3D	3.45	129.63	114.35
3	D	148	HEM	CMD-C2D-C3D	3.66	130.52	114.35
3	C	143	HEM	CMA-C3A-C2A	3.68	132.94	125.24
3	C	143	HEM	C3B-CAB-CBB	3.76	130.23	124.46
3	C	143	HEM	C2D-C3D-C4D	3.78	107.91	101.50
3	A	143	HEM	CMA-C3A-C2A	3.86	133.30	125.24
3	B	148	HEM	C2D-C3D-C4D	4.19	108.60	101.50
3	D	148	HEM	C2D-C3D-C4D	4.34	108.86	101.50
3	D	148	HEM	CMC-C2C-C3C	4.49	127.73	116.53
3	A	143	HEM	C2D-C3D-C4D	4.50	109.13	101.50
3	B	148	HEM	CMC-C2C-C3C	4.54	127.86	116.53
3	A	143	HEM	CMC-C2C-C3C	4.56	127.92	116.53
3	C	143	HEM	CMB-C2B-C3B	4.60	128.01	116.53
3	D	148	HEM	CMB-C2B-C3B	5.02	129.06	116.53
3	D	148	HEM	CAD-C3D-C2D	5.28	128.41	113.22
3	C	143	HEM	CMC-C2C-C3C	5.35	129.88	116.53
3	A	143	HEM	CAD-C3D-C2D	5.39	128.73	113.22
3	A	143	HEM	CMB-C2B-C3B	5.44	130.10	116.53
3	B	148	HEM	CMB-C2B-C3B	5.46	130.17	116.53
3	B	148	HEM	CAD-C3D-C2D	5.68	129.54	113.22
3	C	143	HEM	CAD-C3D-C2D	5.70	129.59	113.22
3	D	148	HEM	CAA-CBA-CGA	6.64	124.91	112.75

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	143	HEM	5	0
4	A	144	CMO	2	0
3	B	148	HEM	5	0
3	C	143	HEM	4	0
4	C	144	CMO	2	0
3	D	148	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](#)

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.