



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:22 PM GMT

PDB ID : 1K0Y
Title : X-ray Crystallographic Analyses of Symmetrical Allosteric Effectors of Hemoglobin. Compounds Designed to Link Primary and Secondary Binding Sites
Authors : Safo, M.K.; Boyiri, T.; Burnett, J.C.; Danso-Danquah, R.; Moure, C.M.; Joshi, G.S.; Abraham, D.J.
Deposited on : 2001-09-21
Resolution : 1.87 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

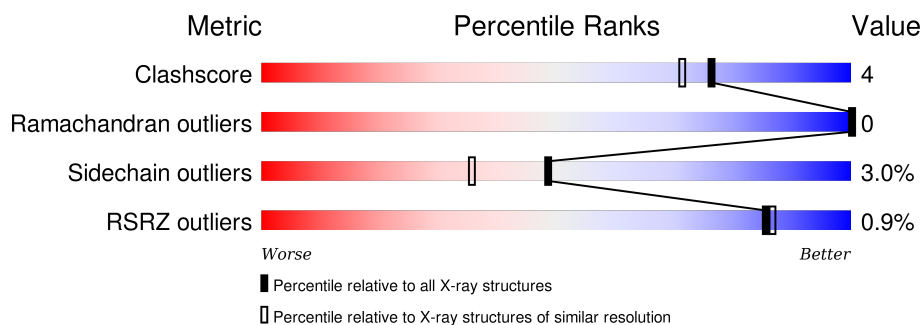
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.87 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	7778 (1.90-1.86)
Ramachandran outliers	100387	7691 (1.90-1.86)
Sidechain outliers	100360	7692 (1.90-1.86)
RSRZ outliers	91569	6979 (1.90-1.86)

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	141	<div> <div></div> <div>94%6%</div> </div>
1	C	141	<div> <div></div> <div>95%5%</div> </div>
2	B	146	<div> <div></div> <div>93%5%.</div> </div>
2	D	146	<div> <div></div> <div>92%8%.</div> </div>

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
3	SO4	B	1400	-	-	-	X
3	SO4	D	1300	-	-	-	X
5	CNO	D	801	-	-	-	X
5	CNO	D	802	-	-	-	X

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 4903 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 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	141	Total	C	N	O	S	0	0	0
			1069	685	187	194	3			
1	C	141	Total	C	N	O	S	0	0	0
			1069	685	187	194	3			

- Molecule 2 is a protein called hemoglobin beta chain.

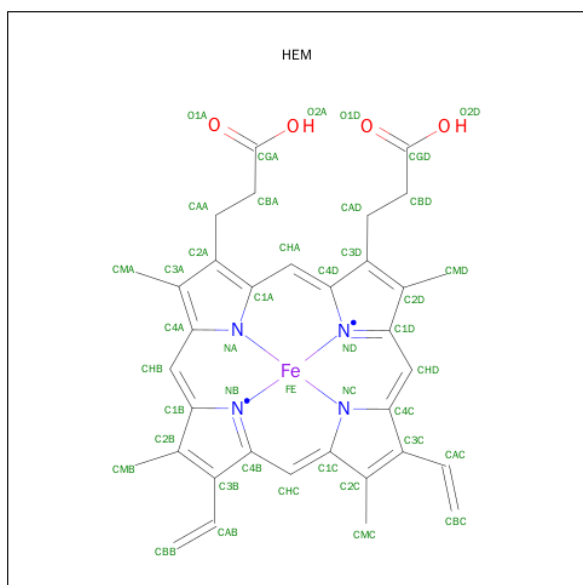
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	146	Total	C	N	O	S	0	0	0
			1123	724	195	201	3			
2	D	146	Total	C	N	O	S	0	0	0
			1123	724	195	201	3			

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



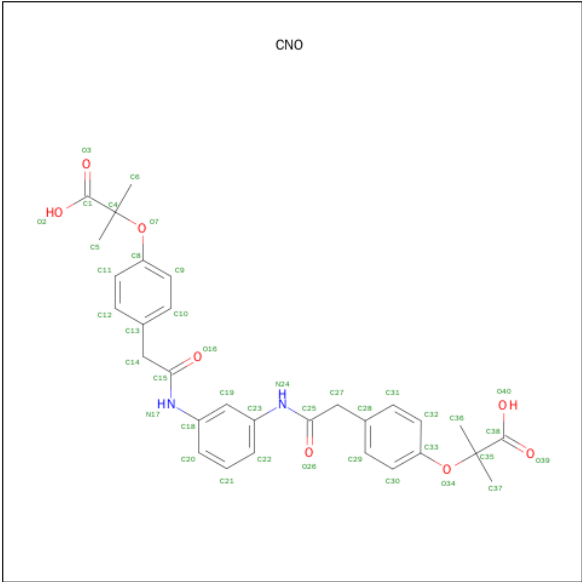
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	1	Total O S 5 4 1	0	0
3	B	1	Total O S 5 4 1	0	0

- Molecule 4 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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

- Molecule 5 is 2-{4-[(3{2-[4-(1-CARBOXY-1-METHYL-ETHOXY)-PHENYL]-ACETYLAMINO}-PHENYL-CARBAMOYL)-METHYL]-PHENOXY}-2-METHYL-PROPIONIC ACID (three-letter code: CNO) (formula: $C_{30}H_{32}N_2O_8$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	D	1	Total	C	N	O	0	0
			40	30	2	8		
5	D	1	Total	C	N	O	0	0
			40	30	2	8		

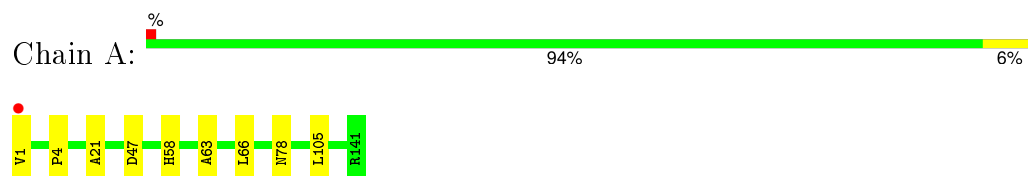
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	70	Total	O	0	0
			70	70		
6	B	56	Total	O	0	0
			56	56		
6	C	71	Total	O	0	0
			71	71		
6	D	60	Total	O	0	0
			60	60		

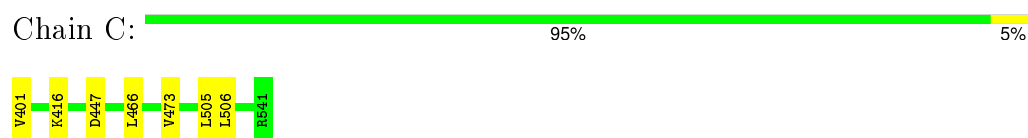
3 Residue-property plots [i](#)

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.

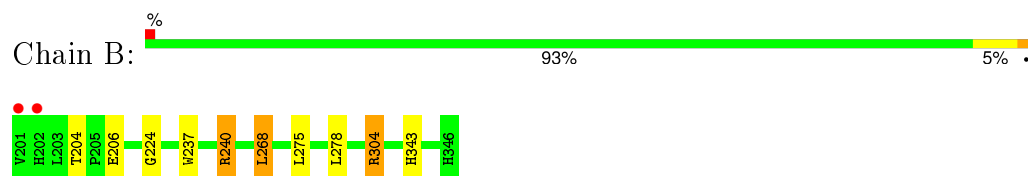
- Molecule 1: hemoglobin alpha chain



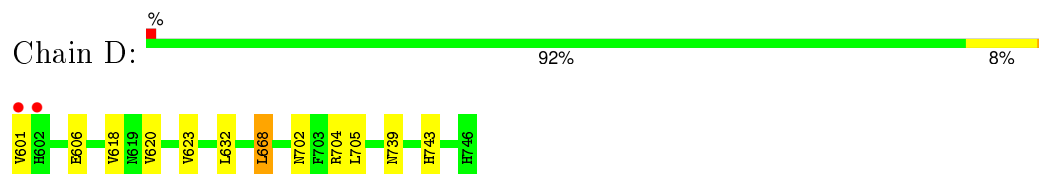
- Molecule 1: hemoglobin alpha chain



- Molecule 2: hemoglobin beta chain



- Molecule 2: hemoglobin beta chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	63.28Å 83.79Å 53.80Å 90.00° 99.33° 90.00°	Depositor
Resolution (Å)	53.00 – 1.87 53.09 – 1.87	Depositor EDS
% Data completeness (in resolution range)	100.0 (53.00-1.87) 92.9 (53.09-1.87)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.16 (at 1.87Å)	Xtriage
Refinement program	X-PLOR 3.843	Depositor
R, R_{free}	0.163 , 0.189 0.163 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	21.8	Xtriage
Anisotropy	0.115	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 48.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 80799 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	4903	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.74% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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, SO4, CNO

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	0.80	0/1097	0.61	1/1491 (0.1%)
1	C	0.85	0/1097	0.66	1/1491 (0.1%)
2	B	0.85	2/1153 (0.2%)	0.63	0/1566
2	D	0.85	1/1153 (0.1%)	0.62	0/1566
All	All	0.84	3/4500 (0.1%)	0.63	2/6114 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	240	ARG	NE-CZ	8.35	1.44	1.33
2	B	304	ARG	NE-CZ	6.38	1.41	1.33
2	D	704	ARG	NE-CZ	5.26	1.39	1.33

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	47	ASP	N-CA-C	-5.43	96.34	111.00
1	C	447	ASP	N-CA-C	-5.38	96.48	111.00

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	1069	0	1073	5	0
1	C	1069	0	1070	1	0
2	B	1123	0	1115	9	0
2	D	1123	0	1115	8	0
3	B	5	0	0	0	0
3	D	5	0	0	0	0
4	A	43	0	30	0	0
4	B	43	0	30	0	0
4	C	43	0	30	0	0
4	D	43	0	30	1	0
5	D	80	0	60	13	0
6	A	70	0	0	4	0
6	B	56	0	0	1	0
6	C	71	0	0	3	0
6	D	60	0	0	5	0
All	All	4903	0	4553	35	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 4.

All (35) 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)
5:D:801:CNO:H362	5:D:801:CNO:H30C	1.57	0.85
5:D:802:CNO:H362	5:D:802:CNO:H32C	1.59	0.83
5:D:801:CNO:C36	5:D:801:CNO:H30C	2.11	0.81
2:D:739:ASN:HB3	6:D:1070:HOH:O	1.88	0.74
5:D:802:CNO:C36	5:D:802:CNO:H32C	2.20	0.70
2:D:705:LEU:HA	6:D:1072:HOH:O	1.94	0.67
5:D:802:CNO:H362	5:D:802:CNO:C32	2.29	0.61
2:D:705:LEU:HD23	6:D:1072:HOH:O	1.99	0.61
1:A:21:ALA:HB1	1:A:63:ALA:HB1	1.85	0.58
5:D:801:CNO:O16	5:D:801:CNO:H19C	2.04	0.57
2:B:304:ARG:HB2	2:B:304:ARG:NH1	2.20	0.57
5:D:801:CNO:O26	5:D:801:CNO:H22C	2.05	0.55
1:C:401:VAL:N	6:C:1058:HOH:O	2.39	0.55
1:A:1:VAL:N	6:A:906:HOH:O	2.40	0.54
2:D:702:ASN:HB3	4:D:748:HEM:HMC1	1.90	0.54
1:A:58:HIS:HD2	6:A:933:HOH:O	1.89	0.54
5:D:801:CNO:H362	5:D:801:CNO:C30	2.34	0.53
2:B:304:ARG:HH21	5:D:802:CNO:H30C	1.74	0.52
2:D:620:VAL:HG13	2:D:668:LEU:HB3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:224:GLY:HA2	2:B:268:LEU:HG	1.92	0.51
2:B:343:HIS:HB2	6:B:1086:HOH:O	2.11	0.50
5:D:802:CNO:C32	5:D:802:CNO:C36	2.90	0.50
5:D:802:CNO:H11C	5:D:802:CNO:C1	2.42	0.49
2:D:618:VAL:HG13	2:D:623:VAL:HG21	1.97	0.47
5:D:802:CNO:H22C	5:D:802:CNO:O26	2.15	0.46
2:D:601:VAL:HG12	6:D:1068:HOH:O	2.14	0.46
2:B:237:TRP:HD1	2:B:240:ARG:HH11	1.63	0.46
2:B:240:ARG:HD2	6:C:1149:HOH:O	2.16	0.45
2:D:743:HIS:HB3	6:D:940:HOH:O	2.18	0.44
2:B:240:ARG:CD	6:C:1149:HOH:O	2.67	0.42
1:A:4:PRO:HD2	6:A:1006:HOH:O	2.19	0.42
2:B:204:THR:OG1	2:B:206:GLU:HG2	2.19	0.42
5:D:801:CNO:H11C	5:D:801:CNO:C1	2.49	0.42
1:A:58:HIS:HE1	6:A:935:HOH:O	2.01	0.42
2:B:304:ARG:HB2	2:B:304:ARG:HH11	1.84	0.41

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	139/141 (99%)	137 (99%)	2 (1%)	0	100	100
1	C	139/141 (99%)	136 (98%)	3 (2%)	0	100	100
2	B	144/146 (99%)	142 (99%)	2 (1%)	0	100	100
2	D	144/146 (99%)	142 (99%)	2 (1%)	0	100	100
All	All	566/574 (99%)	557 (98%)	9 (2%)	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	113/113 (100%)	110 (97%)	3 (3%)	52	40
1	C	113/113 (100%)	108 (96%)	5 (4%)	35	20
2	B	118/118 (100%)	115 (98%)	3 (2%)	55	44
2	D	118/118 (100%)	115 (98%)	3 (2%)	55	44
All	All	462/462 (100%)	448 (97%)	14 (3%)	48	36

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	66	LEU
1	A	78	ASN
1	A	105	LEU
2	B	268	LEU
2	B	275	LEU
2	B	278	LEU
1	C	416	LYS
1	C	466	LEU
1	C	473	VAL
1	C	505	LEU
1	C	506	LEU
2	D	606	GLU
2	D	632	LEU
2	D	668	LEU

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	58	HIS
2	B	339	ASN
1	C	450	HIS
2	D	663	HIS

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 ⓘ

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
4	HEM	A	143	1	30,50,50	2.75	13 (43%)	24,82,82	2.27	7 (29%)
3	SO4	B	1400	-	4,4,4	0.91	0	6,6,6	0.23	0
4	HEM	B	348	2	30,50,50	2.78	14 (46%)	24,82,82	2.41	9 (37%)
4	HEM	C	543	1	30,50,50	3.15	13 (43%)	24,82,82	2.35	7 (29%)
3	SO4	D	1300	-	4,4,4	0.83	0	6,6,6	0.40	0
4	HEM	D	748	2	30,50,50	2.95	12 (40%)	24,82,82	2.24	7 (29%)
5	CNO	D	801	-	36,42,42	1.69	6 (16%)	52,60,60	1.15	5 (9%)
5	CNO	D	802	-	36,42,42	1.26	3 (8%)	52,60,60	0.96	2 (3%)

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
4	HEM	A	143	1	-	0/10/54/54	0/0/8/8

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SO4	B	1400	-	-	0/0/0/0	0/0/0/0
4	HEM	B	348	2	-	0/10/54/54	0/0/8/8
4	HEM	C	543	1	-	0/10/54/54	0/0/8/8
3	SO4	D	1300	-	-	0/0/0/0	0/0/0/0
4	HEM	D	748	2	-	0/10/54/54	0/0/8/8
5	CNO	D	801	-	-	0/26/38/38	0/3/3/3
5	CNO	D	802	-	-	0/26/38/38	0/3/3/3

All (61) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	543	HEM	C3B-C4B	-9.66	1.43	1.51
4	D	748	HEM	C3B-C4B	-8.01	1.44	1.51
4	C	543	HEM	C2D-C3D	-6.64	1.34	1.54
4	D	748	HEM	C3C-CAC	-6.52	1.39	1.51
4	B	348	HEM	C2D-C3D	-6.13	1.36	1.54
4	D	748	HEM	C2D-C3D	-6.10	1.36	1.54
4	A	143	HEM	C2D-C3D	-5.41	1.38	1.54
4	A	143	HEM	C3B-CAB	-5.37	1.41	1.51
4	B	348	HEM	C3D-C4D	-4.98	1.45	1.51
4	D	748	HEM	C3B-CAB	-4.87	1.42	1.51
4	A	143	HEM	C3C-CAC	-4.71	1.42	1.51
4	C	543	HEM	C3B-CAB	-4.71	1.42	1.51
5	D	801	CNO	C30-C29	-4.67	1.30	1.38
4	B	348	HEM	C3C-CAC	-4.66	1.42	1.51
4	A	143	HEM	C3D-C4D	-4.58	1.45	1.51
4	C	543	HEM	C3D-C4D	-4.45	1.45	1.51
4	B	348	HEM	C3B-C4B	-4.40	1.47	1.51
4	C	543	HEM	C3C-CAC	-4.25	1.43	1.51
4	B	348	HEM	C3B-CAB	-3.76	1.44	1.51
4	C	543	HEM	C2C-C1C	-3.68	1.45	1.52
5	D	801	CNO	C14-C13	-3.40	1.45	1.51
4	D	748	HEM	C3D-C4D	-3.22	1.47	1.51
4	A	143	HEM	C2C-C1C	-3.20	1.46	1.52
4	A	143	HEM	C3B-C4B	-3.11	1.49	1.51
4	D	748	HEM	C2C-C1C	-2.80	1.47	1.52
4	D	748	HEM	C2B-C1B	-2.15	1.44	1.51
4	B	348	HEM	C2D-C1D	-2.01	1.45	1.51
4	B	348	HEM	CHD-C4C	2.04	1.41	1.36
4	B	348	HEM	CHC-C1C	2.07	1.41	1.36
4	A	143	HEM	FE-NB	2.17	2.09	1.97
4	C	543	HEM	FE-NB	2.18	2.09	1.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	801	CNO	O34-C35	2.20	1.48	1.45
4	D	748	HEM	CBB-CAB	2.46	1.43	1.29
4	C	543	HEM	CBB-CAB	2.49	1.43	1.29
5	D	802	CNO	O7-C8	2.55	1.48	1.40
4	B	348	HEM	FE-ND	2.77	2.12	1.97
5	D	801	CNO	O7-C8	2.77	1.49	1.40
4	D	748	HEM	CBC-CAC	2.79	1.45	1.29
4	C	543	HEM	FE-NC	2.80	2.06	1.95
4	A	143	HEM	CBC-CAC	2.81	1.45	1.29
4	C	543	HEM	CHC-C1C	2.88	1.43	1.36
4	A	143	HEM	CBB-CAB	2.93	1.46	1.29
5	D	802	CNO	C30-C29	2.97	1.44	1.38
4	B	348	HEM	CBB-CAB	3.18	1.47	1.29
4	A	143	HEM	C4C-NC	3.27	1.40	1.36
4	D	748	HEM	C4C-NC	3.31	1.40	1.36
4	D	748	HEM	C1C-NC	3.45	1.40	1.36
4	B	348	HEM	CBC-CAC	3.46	1.49	1.29
5	D	801	CNO	C32-C31	3.50	1.45	1.38
5	D	802	CNO	O34-C33	3.60	1.51	1.40
4	C	543	HEM	C4C-NC	3.72	1.40	1.36
4	C	543	HEM	CBC-CAC	3.73	1.50	1.29
4	A	143	HEM	CHC-C1C	3.82	1.45	1.36
4	B	348	HEM	FE-NC	3.84	2.10	1.95
4	C	543	HEM	C1C-NC	4.10	1.41	1.36
4	A	143	HEM	C1C-NC	4.14	1.41	1.36
4	D	748	HEM	FE-NC	4.20	2.12	1.95
4	B	348	HEM	C4C-NC	4.63	1.41	1.36
4	B	348	HEM	C1C-NC	4.71	1.41	1.36
5	D	801	CNO	O34-C33	4.74	1.55	1.40
4	A	143	HEM	FE-NC	5.21	2.16	1.95

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	348	HEM	CMA-C3A-C4A	-2.90	123.56	128.36
5	D	801	CNO	C27-C28-C29	-2.20	117.56	120.86
5	D	801	CNO	C32-C31-C28	-2.18	118.05	121.04
4	D	748	HEM	C3C-CAC-CBC	-2.06	121.29	124.46
4	B	348	HEM	C4B-CHC-C1C	2.01	129.18	125.82
5	D	802	CNO	C31-C32-C33	2.02	122.29	119.74
4	A	143	HEM	C3B-C4B-CHC	2.04	126.03	123.16
4	C	543	HEM	C3C-CAC-CBC	2.04	127.59	124.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	802	CNO	C4-O7-C8	2.19	124.84	121.04
5	D	801	CNO	C4-O7-C8	2.22	124.88	121.04
4	A	143	HEM	CMD-C2D-C3D	2.59	125.80	114.35
4	B	348	HEM	CMD-C2D-C3D	2.60	125.87	114.35
4	C	543	HEM	CMD-C2D-C3D	2.72	126.36	114.35
5	D	801	CNO	C35-O34-C33	2.72	125.75	121.04
4	D	748	HEM	CMD-C2D-C3D	2.85	126.94	114.35
4	B	348	HEM	C2D-C3D-C4D	2.98	106.55	101.50
4	B	348	HEM	C3B-CAB-CBB	3.07	129.16	124.46
5	D	801	CNO	C29-C30-C33	3.20	123.78	119.74
4	D	748	HEM	C2D-C3D-C4D	3.24	106.99	101.50
4	C	543	HEM	CAD-C3D-C2D	3.25	122.57	113.22
4	B	348	HEM	CAD-C3D-C4D	3.43	124.55	112.47
4	D	748	HEM	CAD-C3D-C2D	3.47	123.19	113.22
4	A	143	HEM	CAD-C3D-C4D	3.87	126.10	112.47
4	A	143	HEM	C2D-C3D-C4D	4.00	108.29	101.50
4	D	748	HEM	CMB-C2B-C3B	4.27	127.19	116.53
4	A	143	HEM	CAD-C3D-C2D	4.28	125.52	113.22
4	C	543	HEM	CMC-C2C-C3C	4.29	127.24	116.53
4	C	543	HEM	CAD-C3D-C4D	4.42	128.06	112.47
4	A	143	HEM	CMC-C2C-C3C	4.45	127.65	116.53
4	C	543	HEM	C2D-C3D-C4D	4.61	109.32	101.50
4	B	348	HEM	CMC-C2C-C3C	4.77	128.44	116.53
4	D	748	HEM	CAD-C3D-C4D	4.90	129.76	112.47
4	A	143	HEM	CMB-C2B-C3B	4.91	128.80	116.53
4	B	348	HEM	CMB-C2B-C3B	4.99	128.98	116.53
4	D	748	HEM	CMC-C2C-C3C	5.03	129.07	116.53
4	B	348	HEM	CAD-C3D-C2D	5.33	128.55	113.22
4	C	543	HEM	CMB-C2B-C3B	5.69	130.74	116.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	748	HEM	1	0
5	D	801	CNO	6	0
5	D	802	CNO	7	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	141/141 (100%)	-0.16	1 (0%) 89 89	11, 18, 31, 39	0
1	C	141/141 (100%)	-0.26	0 100 100	11, 17, 32, 41	0
2	B	146/146 (100%)	-0.08	2 (1%) 78 80	12, 19, 36, 58	0
2	D	146/146 (100%)	-0.04	2 (1%) 78 80	12, 20, 39, 51	0
All	All	574/574 (100%)	-0.13	5 (0%) 85 87	11, 18, 35, 58	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	202	HIS	4.8
2	B	201	VAL	3.9
2	D	602	HIS	3.4
1	A	1	VAL	2.7
2	D	601	VAL	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 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
5	CNO	D	802	40/40	0.79	0.44	11.72	26,37,50,54	40
5	CNO	D	801	40/40	0.85	0.37	9.03	26,35,45,46	40
3	SO4	B	1400	5/5	0.78	0.50	6.21	75,76,79,80	0
3	SO4	D	1300	5/5	0.77	0.27	3.30	65,65,69,69	0
4	HEM	C	543	43/43	0.96	0.09	-0.04	12,15,29,36	0
4	HEM	A	143	43/43	0.96	0.09	-0.08	12,17,27,35	0
4	HEM	D	748	43/43	0.97	0.09	-0.09	14,17,39,44	0
4	HEM	B	348	43/43	0.96	0.10	-0.21	12,14,23,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.