



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:23 AM GMT

PDB ID : 2CVC  
Title : Crystal structure of High-Molecular Weight Cytochrome c from *Desulfovibrio vulgaris* (Hildenborough)  
Authors : Suto, K.; Sato, M.; Shibata, N.; Kitamura, M.; Morimoto, Y.; Takayama, Y.; Ozawa, K.; Akutsu, H.; Higuchi, Y.; Yasuoka, N.  
Deposited on : 2005-06-02  
Resolution : 2.00 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

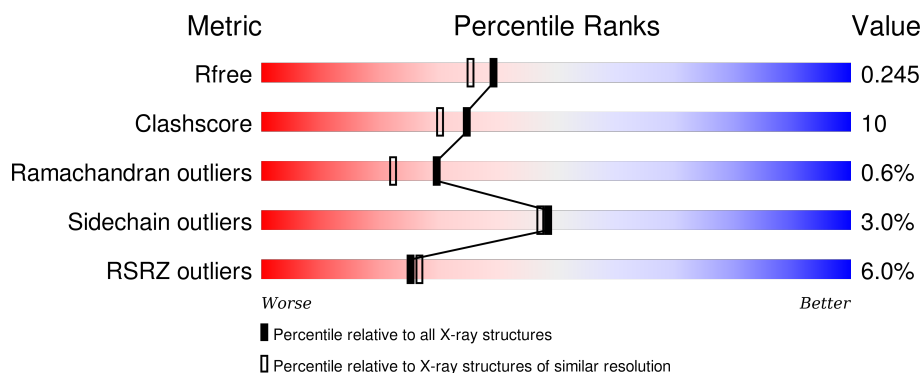
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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))
$R_{free}$	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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  $\geq 3$ , 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	545	<div> <div>6%</div> <div>76%</div> <div>14%</div> <div>8%</div> </div>

## 2 Entry composition i

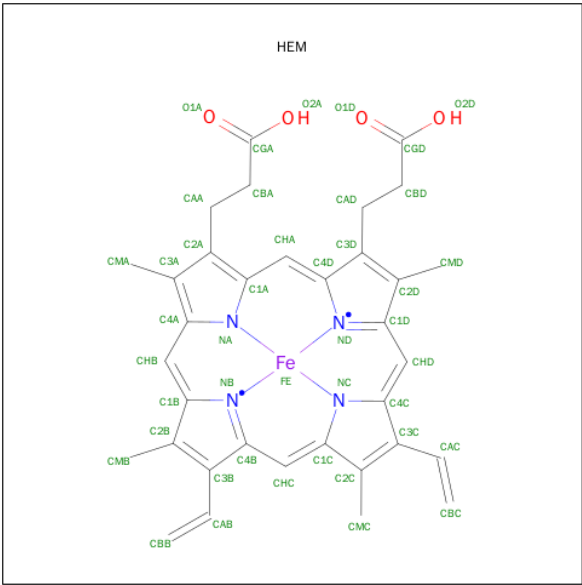
There are 3 unique types of molecules in this entry. The entry contains 4940 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 High-molecular-weight cytochrome c precursor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	500	Total	C	N	O	S	0	0	0
			3779	2322	714	699	44			

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

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

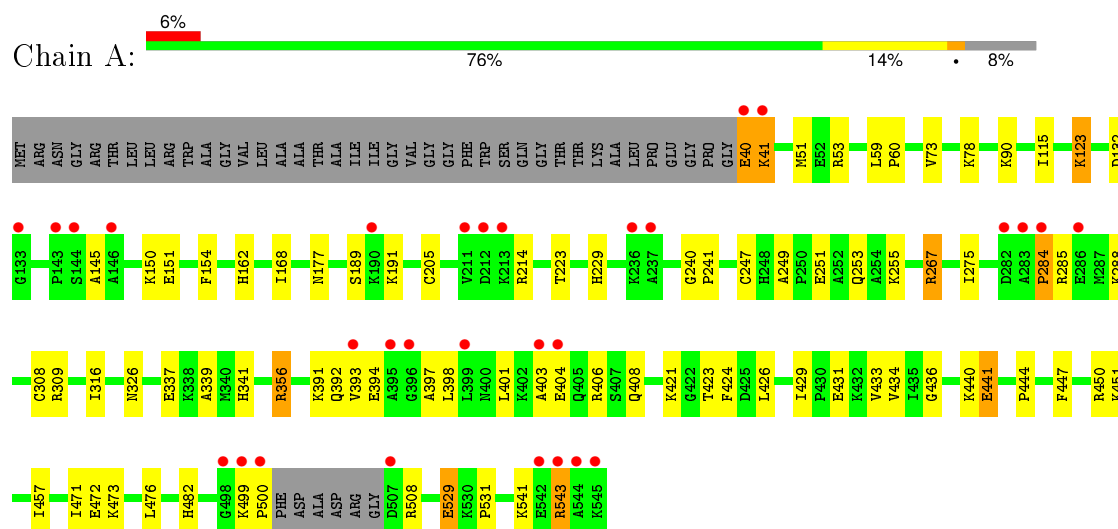
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	473	Total	O	0	0
			473	473		

### 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: High-molecular-weight cytochrome c precursor



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 62	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	108.67Å 108.67Å 103.89Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.35 – 2.00 29.35 – 1.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (29.35-2.00) 99.3 (29.35-1.80)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.57 (at 1.80Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.200 , 0.243 0.200 , 0.245	Depositor DCC
$R_{free}$ test set	4713 reflections (11.14%)	DCC
Wilson B-factor (Å <sup>2</sup> )	35.1	Xtriage
Anisotropy	0.212	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 42.2	EDS
Estimated twinning fraction	0.044 for h,-h-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 63946 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4940	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.20% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality

### 5.1 Standard geometry

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.27	0/3860	0.46	0/5196

There are no bond length outliers.

There are no bond angle outliers.

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	3779	0	3714	79	0
2	A	688	0	480	26	0
3	A	473	0	0	10	0
All	All	4940	0	4194	86	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 10.

All (86) 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:356:ARG:HH21	1:A:356:ARG:HG3	1.42	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:GLU:HG3	2:A:1007:HEM:O1D	1.83	0.78
1:A:309:ARG:HG3	2:A:1004:HEM:O1A	1.90	0.72
1:A:41:LYS:HD2	1:A:41:LYS:O	1.90	0.71
1:A:90:LYS:HE3	1:A:223:THR:HG21	1.78	0.66
1:A:356:ARG:NH2	1:A:356:ARG:HG3	2.12	0.65
1:A:177:ASN:HB2	3:A:1099:HOH:O	1.96	0.64
1:A:151:GLU:HG3	2:A:1007:HEM:CGD	2.28	0.64
1:A:499:LYS:H	1:A:500:PRO:HA	1.62	0.64
2:A:1006:HEM:HBC2	2:A:1006:HEM:CMC	2.29	0.62
1:A:403:ALA:HA	1:A:406:ARG:HD3	1.81	0.62
1:A:309:ARG:HG3	2:A:1004:HEM:CGA	2.31	0.61
1:A:431:GLU:HA	1:A:450:ARG:HB2	1.82	0.61
1:A:73:VAL:HG13	1:A:78:LYS:HB2	1.81	0.60
1:A:499:LYS:N	1:A:500:PRO:HA	2.17	0.60
1:A:531:PRO:HD3	2:A:1015:HEM:HAA1	1.84	0.60
1:A:267:ARG:NH2	3:A:1093:HOH:O	2.35	0.59
1:A:341:HIS:HE1	2:A:1012:HEM:NA	1.99	0.59
2:A:1015:HEM:HHA	2:A:1015:HEM:HBA1	1.85	0.59
1:A:151:GLU:HG2	3:A:1188:HOH:O	2.04	0.58
1:A:154:PHE:HB2	2:A:1004:HEM:HBD1	1.86	0.57
2:A:1006:HEM:HBC2	2:A:1006:HEM:HMC2	1.86	0.57
1:A:339:ALA:HA	2:A:1009:HEM:HMA3	1.87	0.57
1:A:241:PRO:HG2	1:A:247:CYS:SG	2.44	0.56
1:A:436:GLY:HA3	1:A:444:PRO:HB3	1.86	0.56
1:A:441:GLU:HG2	3:A:1344:HOH:O	2.05	0.56
1:A:40:GLU:O	1:A:145:ALA:HB1	2.05	0.56
1:A:499:LYS:HE2	3:A:1339:HOH:O	2.06	0.55
1:A:73:VAL:CG1	1:A:78:LYS:HB2	2.36	0.55
1:A:398:LEU:N	1:A:398:LEU:HD22	2.22	0.55
1:A:341:HIS:HE1	2:A:1012:HEM:C1A	2.27	0.53
1:A:189:SER:HB2	1:A:191:LYS:HE3	1.89	0.53
1:A:267:ARG:HD3	1:A:267:ARG:O	2.10	0.52
1:A:249:ALA:HB1	1:A:251:GLU:OE2	2.10	0.52
1:A:404:GLU:O	1:A:408:GLN:HG3	2.09	0.52
1:A:426:LEU:HD21	1:A:457:ILE:HD12	1.91	0.52
1:A:337:GLU:HG2	3:A:1317:HOH:O	2.10	0.51
1:A:398:LEU:HA	1:A:401:LEU:HD13	1.91	0.51
1:A:541:LYS:HE2	3:A:1461:HOH:O	2.10	0.51
1:A:391:LYS:HG3	1:A:392:GLN:HG3	1.93	0.51
1:A:205:CYS:O	1:A:214:ARG:HD2	2.11	0.50
1:A:275:ILE:HG22	2:A:1012:HEM:HBD1	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:531:PRO:HD3	2:A:1015:HEM:CAA	2.41	0.50
1:A:59:LEU:HB3	1:A:60:PRO:HD2	1.93	0.50
2:A:1002:HEM:CMC	2:A:1002:HEM:HBC2	2.42	0.50
1:A:499:LYS:HB3	1:A:500:PRO:C	2.33	0.49
1:A:508:ARG:HG2	2:A:1014:HEM:C3D	2.48	0.49
1:A:398:LEU:C	1:A:401:LEU:HD13	2.34	0.48
2:A:1010:HEM:HBD2	3:A:1046:HOH:O	2.13	0.48
1:A:431:GLU:HA	1:A:450:ARG:CB	2.43	0.48
1:A:326:ASN:HB2	3:A:1228:HOH:O	2.13	0.48
1:A:162:HIS:HB3	2:A:1004:HEM:HBC2	1.95	0.48
1:A:308:CYS:SG	2:A:1004:HEM:HBA1	2.55	0.47
1:A:168:ILE:HG22	1:A:177:ASN:OD1	2.14	0.47
1:A:90:LYS:HE3	1:A:223:THR:CG2	2.43	0.47
1:A:531:PRO:HD3	2:A:1015:HEM:C2A	2.50	0.47
1:A:451:LYS:HE3	2:A:1015:HEM:O2D	2.15	0.46
1:A:337:GLU:HG3	1:A:341:HIS:HD1	1.79	0.46
1:A:433:VAL:HG13	1:A:447:PHE:HB3	1.96	0.46
2:A:1010:HEM:HBC2	2:A:1010:HEM:CMC	2.46	0.46
1:A:356:ARG:CG	1:A:356:ARG:NH2	2.79	0.46
1:A:406:ARG:HD3	3:A:1301:HOH:O	2.15	0.46
1:A:115:ILE:HG21	1:A:132:ASP:HB3	1.98	0.46
1:A:543:ARG:HG3	1:A:543:ARG:HH11	1.81	0.45
1:A:398:LEU:HA	1:A:401:LEU:CD1	2.47	0.45
1:A:423:THR:HG22	1:A:424:PHE:N	2.31	0.45
1:A:229:HIS:CE1	1:A:240:GLY:HA3	2.53	0.44
1:A:255:LYS:O	1:A:255:LYS:HG2	2.17	0.43
1:A:393:VAL:HA	1:A:398:LEU:HD23	1.99	0.43
1:A:123:LYS:HG2	1:A:123:LYS:H	1.59	0.43
1:A:251:GLU:CD	1:A:251:GLU:H	2.21	0.43
1:A:150:LYS:HD2	1:A:253:GLN:OE1	2.19	0.43
1:A:316:ILE:HD13	2:A:1008:HEM:HMB1	2.00	0.42
2:A:1015:HEM:HMB1	2:A:1016:HEM:HAC	2.01	0.42
1:A:423:THR:OG1	1:A:476:LEU:HD12	2.20	0.42
1:A:499:LYS:N	1:A:500:PRO:CA	2.83	0.42
1:A:429:ILE:HG21	2:A:1013:HEM:HBB2	2.01	0.42
1:A:284:PRO:HA	1:A:285:ARG:HA	1.92	0.41
1:A:397:ALA:HB3	1:A:398:LEU:HD22	2.03	0.41
1:A:434:VAL:HG13	1:A:434:VAL:O	2.21	0.41
1:A:421:LYS:O	1:A:473:LYS:HD3	2.21	0.40
1:A:356:ARG:HD2	1:A:356:ARG:HA	1.92	0.40
1:A:115:ILE:HG12	2:A:1003:HEM:HBC2	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:529:GLU:OE1	1:A:529:GLU:HA	2.21	0.40
1:A:436:GLY:CA	1:A:444:PRO:HB3	2.52	0.40
1:A:471:ILE:HG13	1:A:472:GLU:HG3	2.04	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	496/545 (91%)	470 (95%)	23 (5%)	3 (1%)	30	22

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	440	LYS
1	A	284	PRO
1	A	543	ARG

### 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	405/435 (93%)	393 (97%)	12 (3%)	48	47

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	GLU
1	A	41	LYS
1	A	51	MET
1	A	53	ARG
1	A	123	LYS
1	A	267	ARG
1	A	288	LYS
1	A	356	ARG
1	A	394	GLU
1	A	441	GLU
1	A	482	HIS
1	A	529	GLU

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	306	ASN
1	A	326	ASN
1	A	400	ASN
1	A	405	GLN
1	A	443	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](#)

16 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	HEM	A	1001	1	30,50,50	3.89	13 (43%)	24,82,82	3.45	8 (33%)
2	HEM	A	1002	1	30,50,50	3.94	14 (46%)	24,82,82	3.49	10 (41%)
2	HEM	A	1003	1	30,50,50	3.83	14 (46%)	24,82,82	3.67	11 (45%)
2	HEM	A	1004	1	30,50,50	3.88	15 (50%)	24,82,82	3.57	11 (45%)
2	HEM	A	1005	1	30,50,50	4.08	14 (46%)	24,82,82	3.53	12 (50%)
2	HEM	A	1006	1	30,50,50	3.96	12 (40%)	24,82,82	3.45	12 (50%)
2	HEM	A	1007	1	30,50,50	3.95	12 (40%)	24,82,82	3.63	11 (45%)
2	HEM	A	1008	1	30,50,50	4.04	13 (43%)	24,82,82	3.44	12 (50%)
2	HEM	A	1009	1	30,50,50	3.82	13 (43%)	24,82,82	3.61	10 (41%)
2	HEM	A	1010	1	30,50,50	4.34	14 (46%)	24,82,82	3.60	11 (45%)
2	HEM	A	1011	1	30,50,50	3.81	13 (43%)	24,82,82	3.48	9 (37%)
2	HEM	A	1012	1	30,50,50	4.17	13 (43%)	24,82,82	3.52	9 (37%)
2	HEM	A	1013	1	30,50,50	4.19	14 (46%)	24,82,82	3.53	10 (41%)
2	HEM	A	1014	1	30,50,50	4.02	14 (46%)	24,82,82	3.55	11 (45%)
2	HEM	A	1015	1	30,50,50	4.32	14 (46%)	24,82,82	2.33	7 (29%)
2	HEM	A	1016	1	30,50,50	3.88	13 (43%)	24,82,82	3.55	10 (41%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEM	A	1001	1	-	0/10/54/54	0/0/8/8
2	HEM	A	1002	1	-	0/10/54/54	0/0/8/8
2	HEM	A	1003	1	-	0/10/54/54	0/0/8/8
2	HEM	A	1004	1	-	0/10/54/54	0/0/8/8
2	HEM	A	1005	1	-	0/10/54/54	0/0/8/8
2	HEM	A	1006	1	-	0/10/54/54	0/0/8/8
2	HEM	A	1007	1	-	0/10/54/54	0/0/8/8
2	HEM	A	1008	1	-	0/10/54/54	0/0/8/8
2	HEM	A	1009	1	-	0/10/54/54	0/0/8/8
2	HEM	A	1010	1	-	0/10/54/54	0/0/8/8

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEM	A	1011	1	-	0/10/54/54	0/0/8/8
2	HEM	A	1012	1	-	0/10/54/54	0/0/8/8
2	HEM	A	1013	1	-	0/10/54/54	0/0/8/8
2	HEM	A	1014	1	-	0/10/54/54	0/0/8/8
2	HEM	A	1015	1	-	0/10/54/54	0/0/8/8
2	HEM	A	1016	1	-	0/10/54/54	0/0/8/8

All (215) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1010	HEM	C3B-C4B	-15.76	1.37	1.51
2	A	1012	HEM	C3B-C4B	-15.26	1.38	1.51
2	A	1013	HEM	C3B-C4B	-14.95	1.38	1.51
2	A	1008	HEM	C3B-C4B	-14.40	1.39	1.51
2	A	1001	HEM	C3B-C4B	-14.24	1.39	1.51
2	A	1015	HEM	C3B-C4B	-14.00	1.39	1.51
2	A	1014	HEM	C3B-C4B	-13.99	1.39	1.51
2	A	1002	HEM	C3B-C4B	-13.98	1.39	1.51
2	A	1005	HEM	C3B-C4B	-13.70	1.39	1.51
2	A	1006	HEM	C3B-C4B	-13.61	1.39	1.51
2	A	1007	HEM	C3B-C4B	-13.53	1.39	1.51
2	A	1011	HEM	C3B-C4B	-13.18	1.40	1.51
2	A	1004	HEM	C3B-C4B	-13.15	1.40	1.51
2	A	1009	HEM	C3B-C4B	-12.86	1.40	1.51
2	A	1016	HEM	C3B-C4B	-12.46	1.40	1.51
2	A	1003	HEM	C3B-C4B	-12.21	1.40	1.51
2	A	1010	HEM	C3D-C4D	-10.61	1.37	1.51
2	A	1013	HEM	C3D-C4D	-10.49	1.38	1.51
2	A	1015	HEM	C3D-C4D	-10.41	1.38	1.51
2	A	1007	HEM	C3D-C4D	-10.20	1.38	1.51
2	A	1005	HEM	C3D-C4D	-10.12	1.38	1.51
2	A	1014	HEM	C3D-C4D	-9.91	1.38	1.51
2	A	1008	HEM	C3D-C4D	-9.80	1.39	1.51
2	A	1012	HEM	C3D-C4D	-9.78	1.39	1.51
2	A	1003	HEM	C3D-C4D	-9.58	1.39	1.51
2	A	1016	HEM	C3D-C4D	-9.41	1.39	1.51
2	A	1006	HEM	C3D-C4D	-9.39	1.39	1.51
2	A	1009	HEM	C3D-C4D	-9.32	1.39	1.51
2	A	1002	HEM	C3D-C4D	-9.05	1.39	1.51
2	A	1004	HEM	C3D-C4D	-8.74	1.40	1.51
2	A	1011	HEM	C3D-C4D	-8.32	1.40	1.51
2	A	1001	HEM	C3D-C4D	-8.26	1.41	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1016	HEM	C2C-C1C	-7.86	1.37	1.52
2	A	1012	HEM	C2C-C1C	-7.67	1.38	1.52
2	A	1011	HEM	C2C-C1C	-7.67	1.38	1.52
2	A	1004	HEM	C2C-C1C	-7.14	1.39	1.52
2	A	1006	HEM	C2C-C1C	-7.05	1.39	1.52
2	A	1005	HEM	C2C-C1C	-6.96	1.39	1.52
2	A	1014	HEM	C2C-C1C	-6.92	1.39	1.52
2	A	1013	HEM	C2C-C1C	-6.86	1.39	1.52
2	A	1001	HEM	C2C-C1C	-6.83	1.39	1.52
2	A	1003	HEM	C2C-C1C	-6.73	1.39	1.52
2	A	1007	HEM	C2C-C1C	-6.67	1.39	1.52
2	A	1002	HEM	C2C-C1C	-6.60	1.40	1.52
2	A	1009	HEM	C2C-C1C	-6.48	1.40	1.52
2	A	1015	HEM	C2C-C1C	-6.35	1.40	1.52
2	A	1010	HEM	C2C-C1C	-6.27	1.40	1.52
2	A	1008	HEM	C2C-C1C	-6.18	1.40	1.52
2	A	1015	HEM	C3B-CAB	-6.14	1.39	1.51
2	A	1015	HEM	C3C-CAC	-6.07	1.39	1.51
2	A	1006	HEM	C2D-C3D	-5.63	1.37	1.54
2	A	1008	HEM	C2D-C3D	-5.60	1.37	1.54
2	A	1005	HEM	C2D-C3D	-5.36	1.38	1.54
2	A	1016	HEM	C2D-C3D	-5.28	1.38	1.54
2	A	1015	HEM	C2D-C3D	-5.23	1.38	1.54
2	A	1009	HEM	C2D-C3D	-5.09	1.39	1.54
2	A	1001	HEM	C2D-C3D	-5.06	1.39	1.54
2	A	1010	HEM	C2D-C3D	-4.99	1.39	1.54
2	A	1014	HEM	C2D-C3D	-4.98	1.39	1.54
2	A	1004	HEM	C2D-C3D	-4.97	1.39	1.54
2	A	1003	HEM	C2D-C3D	-4.86	1.40	1.54
2	A	1002	HEM	C2D-C3D	-4.73	1.40	1.54
2	A	1011	HEM	C2D-C3D	-4.72	1.40	1.54
2	A	1013	HEM	C2D-C3D	-4.71	1.40	1.54
2	A	1007	HEM	C2D-C3D	-4.62	1.40	1.54
2	A	1012	HEM	C2D-C3D	-4.57	1.40	1.54
2	A	1010	HEM	C2B-C1B	-4.45	1.37	1.51
2	A	1010	HEM	C2D-C1D	-4.37	1.37	1.51
2	A	1015	HEM	C2D-C1D	-4.25	1.37	1.51
2	A	1013	HEM	C2B-C1B	-4.24	1.38	1.51
2	A	1005	HEM	C2B-C1B	-4.14	1.38	1.51
2	A	1007	HEM	C2B-C1B	-4.09	1.38	1.51
2	A	1008	HEM	C2B-C1B	-4.03	1.38	1.51
2	A	1009	HEM	C2D-C1D	-3.99	1.38	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1005	HEM	C2D-C1D	-3.98	1.38	1.51
2	A	1002	HEM	C2D-C1D	-3.92	1.39	1.51
2	A	1015	HEM	C2B-C1B	-3.92	1.39	1.51
2	A	1012	HEM	C2D-C1D	-3.91	1.39	1.51
2	A	1003	HEM	C2B-C1B	-3.90	1.39	1.51
2	A	1011	HEM	C2B-C1B	-3.89	1.39	1.51
2	A	1007	HEM	C2D-C1D	-3.84	1.39	1.51
2	A	1012	HEM	C2B-C1B	-3.83	1.39	1.51
2	A	1004	HEM	C2B-C1B	-3.82	1.39	1.51
2	A	1016	HEM	C2B-C1B	-3.81	1.39	1.51
2	A	1011	HEM	C2D-C1D	-3.77	1.39	1.51
2	A	1004	HEM	C2D-C1D	-3.75	1.39	1.51
2	A	1016	HEM	C2D-C1D	-3.73	1.39	1.51
2	A	1002	HEM	C2B-C1B	-3.70	1.39	1.51
2	A	1001	HEM	C2B-C1B	-3.66	1.39	1.51
2	A	1009	HEM	C2B-C1B	-3.64	1.39	1.51
2	A	1006	HEM	C2D-C1D	-3.63	1.39	1.51
2	A	1008	HEM	C2D-C1D	-3.62	1.40	1.51
2	A	1013	HEM	C2D-C1D	-3.61	1.40	1.51
2	A	1003	HEM	C2D-C1D	-3.59	1.40	1.51
2	A	1014	HEM	C2D-C1D	-3.56	1.40	1.51
2	A	1014	HEM	C2B-C1B	-3.35	1.40	1.51
2	A	1006	HEM	C2B-C1B	-3.33	1.41	1.51
2	A	1002	HEM	C1C-NC	-3.26	1.31	1.36
2	A	1010	HEM	C4C-NC	-3.24	1.32	1.36
2	A	1001	HEM	C2D-C1D	-3.09	1.41	1.51
2	A	1004	HEM	C1C-NC	-3.09	1.32	1.36
2	A	1006	HEM	C1C-NC	-2.99	1.32	1.36
2	A	1015	HEM	C4C-NC	-2.93	1.32	1.36
2	A	1016	HEM	C4C-NC	-2.65	1.32	1.36
2	A	1005	HEM	C1C-NC	-2.53	1.32	1.36
2	A	1012	HEM	C4C-NC	-2.42	1.33	1.36
2	A	1015	HEM	C1C-NC	-2.42	1.33	1.36
2	A	1013	HEM	C1C-NC	-2.37	1.33	1.36
2	A	1008	HEM	C1C-NC	-2.27	1.33	1.36
2	A	1014	HEM	C4C-NC	-2.19	1.33	1.36
2	A	1010	HEM	C1C-NC	-2.14	1.33	1.36
2	A	1013	HEM	C4C-NC	-2.14	1.33	1.36
2	A	1003	HEM	C4C-NC	-2.07	1.33	1.36
2	A	1004	HEM	C4C-NC	-2.02	1.33	1.36
2	A	1007	HEM	C1C-NC	-2.01	1.33	1.36
2	A	1013	HEM	CHC-C1C	2.00	1.41	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1007	HEM	CHD-C4C	2.00	1.41	1.36
2	A	1010	HEM	FE-NB	2.01	2.08	1.97
2	A	1011	HEM	CHC-C1C	2.02	1.41	1.36
2	A	1010	HEM	CHC-C1C	2.05	1.41	1.36
2	A	1009	HEM	CHC-C1C	2.06	1.41	1.36
2	A	1014	HEM	CHC-C1C	2.09	1.41	1.36
2	A	1010	HEM	CHD-C4C	2.10	1.41	1.36
2	A	1001	HEM	CHD-C4C	2.18	1.41	1.36
2	A	1001	HEM	CHC-C1C	2.21	1.41	1.36
2	A	1002	HEM	CHC-C1C	2.24	1.41	1.36
2	A	1014	HEM	CHD-C4C	2.26	1.41	1.36
2	A	1004	HEM	CHD-C4C	2.28	1.41	1.36
2	A	1009	HEM	CHD-C4C	2.30	1.41	1.36
2	A	1012	HEM	CHD-C4C	2.35	1.41	1.36
2	A	1011	HEM	CHD-C4C	2.35	1.41	1.36
2	A	1004	HEM	CHC-C1C	2.36	1.42	1.36
2	A	1003	HEM	CHC-C1C	2.37	1.42	1.36
2	A	1012	HEM	FE-NB	2.38	2.10	1.97
2	A	1002	HEM	FE-ND	2.41	2.10	1.97
2	A	1003	HEM	CHD-C4C	2.43	1.42	1.36
2	A	1013	HEM	CHD-C4C	2.46	1.42	1.36
2	A	1002	HEM	CHD-C4C	2.50	1.42	1.36
2	A	1008	HEM	CHC-C1C	2.52	1.42	1.36
2	A	1013	HEM	FE-ND	2.52	2.10	1.97
2	A	1015	HEM	FE-NB	2.54	2.10	1.97
2	A	1011	HEM	FE-NB	2.56	2.11	1.97
2	A	1016	HEM	CHC-C1C	2.56	1.42	1.36
2	A	1005	HEM	CHD-C4C	2.58	1.42	1.36
2	A	1005	HEM	FE-NB	2.58	2.11	1.97
2	A	1008	HEM	FE-NB	2.60	2.11	1.97
2	A	1006	HEM	FE-ND	2.65	2.11	1.97
2	A	1007	HEM	FE-ND	2.70	2.11	1.97
2	A	1009	HEM	FE-ND	2.72	2.11	1.97
2	A	1012	HEM	FE-ND	2.73	2.11	1.97
2	A	1008	HEM	FE-ND	2.73	2.11	1.97
2	A	1004	HEM	FE-NB	2.84	2.12	1.97
2	A	1005	HEM	CHC-C1C	2.84	1.43	1.36
2	A	1016	HEM	FE-NB	2.84	2.12	1.97
2	A	1014	HEM	FE-NB	2.85	2.12	1.97
2	A	1003	HEM	FE-ND	2.91	2.12	1.97
2	A	1016	HEM	FE-ND	2.92	2.12	1.97
2	A	1005	HEM	FE-ND	2.92	2.12	1.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1004	HEM	FE-ND	2.95	2.13	1.97
2	A	1014	HEM	FE-ND	2.97	2.13	1.97
2	A	1001	HEM	FE-NB	2.99	2.13	1.97
2	A	1015	HEM	CBC-CAC	3.06	1.47	1.29
2	A	1001	HEM	FE-ND	3.13	2.14	1.97
2	A	1011	HEM	FE-ND	3.13	2.14	1.97
2	A	1015	HEM	CBB-CAB	3.18	1.47	1.29
2	A	1002	HEM	FE-NB	3.20	2.14	1.97
2	A	1006	HEM	FE-NB	3.22	2.14	1.97
2	A	1002	HEM	FE-NC	3.25	2.08	1.95
2	A	1006	HEM	FE-NC	3.29	2.08	1.95
2	A	1003	HEM	FE-NB	3.32	2.15	1.97
2	A	1009	HEM	FE-NB	3.36	2.15	1.97
2	A	1011	HEM	FE-NC	3.38	2.09	1.95
2	A	1012	HEM	FE-NC	3.41	2.09	1.95
2	A	1009	HEM	FE-NC	3.59	2.09	1.95
2	A	1001	HEM	FE-NC	3.60	2.10	1.95
2	A	1008	HEM	FE-NC	3.64	2.10	1.95
2	A	1016	HEM	FE-NC	3.81	2.10	1.95
2	A	1004	HEM	FE-NC	3.95	2.11	1.95
2	A	1007	HEM	FE-NC	3.99	2.11	1.95
2	A	1014	HEM	FE-NC	4.05	2.11	1.95
2	A	1006	HEM	CBC-CAC	4.12	1.53	1.29
2	A	1010	HEM	CBB-CAB	4.12	1.53	1.29
2	A	1008	HEM	CBC-CAC	4.12	1.53	1.29
2	A	1009	HEM	CBB-CAB	4.14	1.53	1.29
2	A	1012	HEM	CBC-CAC	4.15	1.53	1.29
2	A	1001	HEM	CBB-CAB	4.15	1.53	1.29
2	A	1014	HEM	CBB-CAB	4.15	1.53	1.29
2	A	1009	HEM	CBC-CAC	4.16	1.53	1.29
2	A	1007	HEM	CBB-CAB	4.16	1.53	1.29
2	A	1001	HEM	CBC-CAC	4.16	1.53	1.29
2	A	1002	HEM	CBC-CAC	4.18	1.53	1.29
2	A	1007	HEM	CBC-CAC	4.18	1.53	1.29
2	A	1004	HEM	CBC-CAC	4.18	1.53	1.29
2	A	1016	HEM	CBB-CAB	4.18	1.53	1.29
2	A	1002	HEM	CBB-CAB	4.18	1.53	1.29
2	A	1008	HEM	CBB-CAB	4.19	1.53	1.29
2	A	1016	HEM	CBC-CAC	4.20	1.53	1.29
2	A	1005	HEM	CBC-CAC	4.20	1.53	1.29
2	A	1014	HEM	CBC-CAC	4.20	1.53	1.29
2	A	1005	HEM	CBB-CAB	4.21	1.53	1.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1013	HEM	CBC-CAC	4.21	1.53	1.29
2	A	1003	HEM	CBB-CAB	4.21	1.53	1.29
2	A	1011	HEM	CBC-CAC	4.23	1.53	1.29
2	A	1010	HEM	CBC-CAC	4.24	1.53	1.29
2	A	1006	HEM	CBB-CAB	4.24	1.53	1.29
2	A	1011	HEM	CBB-CAB	4.25	1.53	1.29
2	A	1003	HEM	CBC-CAC	4.25	1.53	1.29
2	A	1004	HEM	CBB-CAB	4.25	1.53	1.29
2	A	1013	HEM	CBB-CAB	4.26	1.53	1.29
2	A	1012	HEM	CBB-CAB	4.26	1.53	1.29
2	A	1005	HEM	FE-NC	4.26	2.12	1.95
2	A	1003	HEM	FE-NC	4.46	2.13	1.95
2	A	1013	HEM	FE-NC	4.64	2.14	1.95
2	A	1015	HEM	FE-NC	5.08	2.15	1.95
2	A	1010	HEM	FE-NC	5.42	2.17	1.95

All (164) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1007	HEM	C3B-CAB-CBB	-9.60	109.72	124.46
2	A	1002	HEM	C3B-CAB-CBB	-9.56	109.79	124.46
2	A	1016	HEM	C3B-CAB-CBB	-9.51	109.87	124.46
2	A	1014	HEM	C3B-CAB-CBB	-9.50	109.88	124.46
2	A	1009	HEM	C3C-CAC-CBC	-9.50	109.89	124.46
2	A	1004	HEM	C3B-CAB-CBB	-9.47	109.94	124.46
2	A	1013	HEM	C3C-CAC-CBC	-9.42	110.01	124.46
2	A	1003	HEM	C3B-CAB-CBB	-9.41	110.02	124.46
2	A	1005	HEM	C3B-CAB-CBB	-9.40	110.03	124.46
2	A	1010	HEM	C3B-CAB-CBB	-9.38	110.07	124.46
2	A	1003	HEM	C3C-CAC-CBC	-9.31	110.18	124.46
2	A	1001	HEM	C3B-CAB-CBB	-9.30	110.20	124.46
2	A	1009	HEM	C3B-CAB-CBB	-9.29	110.20	124.46
2	A	1007	HEM	C3C-CAC-CBC	-9.25	110.27	124.46
2	A	1011	HEM	C3C-CAC-CBC	-9.24	110.28	124.46
2	A	1005	HEM	C3C-CAC-CBC	-9.24	110.28	124.46
2	A	1011	HEM	C3B-CAB-CBB	-9.23	110.30	124.46
2	A	1012	HEM	C3B-CAB-CBB	-9.19	110.36	124.46
2	A	1014	HEM	C3C-CAC-CBC	-9.15	110.42	124.46
2	A	1008	HEM	C3B-CAB-CBB	-9.15	110.42	124.46
2	A	1004	HEM	C3C-CAC-CBC	-9.10	110.49	124.46
2	A	1006	HEM	C3B-CAB-CBB	-9.08	110.53	124.46
2	A	1001	HEM	C3C-CAC-CBC	-9.05	110.58	124.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1013	HEM	C3B-CAB-CBB	-9.00	110.65	124.46
2	A	1012	HEM	C3C-CAC-CBC	-8.99	110.67	124.46
2	A	1010	HEM	C3C-CAC-CBC	-8.88	110.83	124.46
2	A	1016	HEM	C3C-CAC-CBC	-8.88	110.84	124.46
2	A	1008	HEM	C3C-CAC-CBC	-8.80	110.96	124.46
2	A	1002	HEM	C3C-CAC-CBC	-8.62	111.24	124.46
2	A	1006	HEM	C3C-CAC-CBC	-8.46	111.48	124.46
2	A	1010	HEM	CAA-C2A-C1A	-2.78	123.99	127.01
2	A	1005	HEM	CAA-C2A-C1A	-2.36	124.45	127.01
2	A	1006	HEM	C3B-C4B-CHC	2.03	126.02	123.16
2	A	1008	HEM	C2C-C1C-CHC	2.04	126.78	123.68
2	A	1010	HEM	C4B-CHC-C1C	2.06	129.27	125.82
2	A	1008	HEM	C4B-CHC-C1C	2.08	129.30	125.82
2	A	1013	HEM	C3B-C4B-CHC	2.16	126.20	123.16
2	A	1011	HEM	C3B-C4B-CHC	2.18	126.23	123.16
2	A	1001	HEM	CMD-C2D-C3D	2.21	124.11	114.35
2	A	1004	HEM	C3B-C4B-CHC	2.23	126.31	123.16
2	A	1013	HEM	C2D-C3D-C4D	2.23	105.29	101.50
2	A	1006	HEM	CMD-C2D-C3D	2.27	124.37	114.35
2	A	1005	HEM	C1D-CHD-C4C	2.27	129.62	125.82
2	A	1014	HEM	C3B-C4B-CHC	2.27	126.36	123.16
2	A	1004	HEM	C2D-C3D-C4D	2.34	105.47	101.50
2	A	1006	HEM	CAA-C2A-C1A	2.35	129.56	127.01
2	A	1008	HEM	CMD-C2D-C3D	2.40	124.95	114.35
2	A	1003	HEM	C2D-C3D-C4D	2.44	105.64	101.50
2	A	1008	HEM	C3B-C4B-CHC	2.46	126.63	123.16
2	A	1005	HEM	C2D-C3D-C4D	2.47	105.69	101.50
2	A	1009	HEM	C3B-C4B-CHC	2.48	126.66	123.16
2	A	1007	HEM	C4B-CHC-C1C	2.53	130.06	125.82
2	A	1005	HEM	C2C-C1C-CHC	2.54	127.54	123.68
2	A	1002	HEM	C2D-C3D-C4D	2.55	105.83	101.50
2	A	1006	HEM	C4B-CHC-C1C	2.57	130.12	125.82
2	A	1013	HEM	CMD-C2D-C3D	2.58	125.75	114.35
2	A	1012	HEM	CAA-C2A-C1A	2.59	129.82	127.01
2	A	1016	HEM	C2D-C3D-C4D	2.62	105.94	101.50
2	A	1007	HEM	C1D-CHD-C4C	2.64	130.24	125.82
2	A	1005	HEM	C4B-CHC-C1C	2.66	130.27	125.82
2	A	1005	HEM	CMD-C2D-C3D	2.67	126.15	114.35
2	A	1014	HEM	C4B-CHC-C1C	2.71	130.36	125.82
2	A	1007	HEM	C2D-C3D-C4D	2.73	106.13	101.50
2	A	1002	HEM	C4B-CHC-C1C	2.74	130.40	125.82
2	A	1008	HEM	C1D-CHD-C4C	2.79	130.48	125.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1015	HEM	CMD-C2D-C3D	2.79	126.70	114.35
2	A	1008	HEM	C2D-C3D-C4D	2.80	106.25	101.50
2	A	1003	HEM	C1D-CHD-C4C	2.81	130.52	125.82
2	A	1002	HEM	C1D-CHD-C4C	2.83	130.56	125.82
2	A	1004	HEM	C1D-CHD-C4C	2.84	130.56	125.82
2	A	1016	HEM	C3B-C4B-CHC	2.86	127.19	123.16
2	A	1010	HEM	C2D-C3D-C4D	2.87	106.37	101.50
2	A	1011	HEM	C4B-CHC-C1C	2.89	130.65	125.82
2	A	1010	HEM	C1D-CHD-C4C	2.91	130.69	125.82
2	A	1014	HEM	CMD-C2D-C3D	2.94	127.37	114.35
2	A	1015	HEM	C4B-CHC-C1C	2.98	130.80	125.82
2	A	1009	HEM	C2D-C3D-C4D	2.98	106.55	101.50
2	A	1016	HEM	C4B-CHC-C1C	2.98	130.81	125.82
2	A	1003	HEM	CMD-C2D-C3D	3.02	127.72	114.35
2	A	1014	HEM	C1D-CHD-C4C	3.02	130.88	125.82
2	A	1016	HEM	CMD-C2D-C3D	3.05	127.82	114.35
2	A	1007	HEM	C3B-C4B-CHC	3.05	127.45	123.16
2	A	1009	HEM	CMD-C2D-C3D	3.05	127.86	114.35
2	A	1011	HEM	CMD-C2D-C3D	3.06	127.89	114.35
2	A	1003	HEM	C3B-C4B-CHC	3.06	127.48	123.16
2	A	1007	HEM	CMD-C2D-C3D	3.12	128.16	114.35
2	A	1015	HEM	C2D-C3D-C4D	3.13	106.81	101.50
2	A	1003	HEM	C4B-CHC-C1C	3.14	131.08	125.82
2	A	1004	HEM	CMD-C2D-C3D	3.15	128.28	114.35
2	A	1004	HEM	C4B-CHC-C1C	3.18	131.13	125.82
2	A	1011	HEM	CMC-C2C-C3C	3.18	124.47	116.53
2	A	1010	HEM	CMD-C2D-C3D	3.19	128.45	114.35
2	A	1002	HEM	CMD-C2D-C3D	3.19	128.46	114.35
2	A	1006	HEM	C2D-C3D-C4D	3.19	106.91	101.50
2	A	1014	HEM	C2D-C3D-C4D	3.21	106.95	101.50
2	A	1012	HEM	CMD-C2D-C3D	3.23	128.65	114.35
2	A	1014	HEM	CAD-C3D-C4D	3.34	124.26	112.47
2	A	1006	HEM	C1D-CHD-C4C	3.40	131.50	125.82
2	A	1007	HEM	CAD-C3D-C4D	3.53	124.91	112.47
2	A	1012	HEM	CAD-C3D-C4D	3.55	124.98	112.47
2	A	1016	HEM	CAD-C3D-C4D	3.60	125.17	112.47
2	A	1003	HEM	CAD-C3D-C4D	3.64	125.32	112.47
2	A	1001	HEM	C1D-CHD-C4C	3.65	131.92	125.82
2	A	1009	HEM	CMC-C2C-C3C	3.76	125.91	116.53
2	A	1002	HEM	CAD-C3D-C4D	3.81	125.90	112.47
2	A	1002	HEM	CMB-C2B-C3B	3.85	126.14	116.53
2	A	1009	HEM	C4B-CHC-C1C	3.86	132.28	125.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1008	HEM	CAD-C3D-C4D	3.87	126.11	112.47
2	A	1012	HEM	C1D-CHD-C4C	3.87	132.29	125.82
2	A	1006	HEM	CAD-C3D-C2D	3.95	124.58	113.22
2	A	1013	HEM	CMB-C2B-C3B	3.96	126.42	116.53
2	A	1010	HEM	CAD-C3D-C4D	3.98	126.49	112.47
2	A	1004	HEM	CAD-C3D-C4D	4.02	126.63	112.47
2	A	1013	HEM	CAD-C3D-C4D	4.03	126.69	112.47
2	A	1004	HEM	CMB-C2B-C3B	4.13	126.84	116.53
2	A	1015	HEM	CAD-C3D-C4D	4.15	127.09	112.47
2	A	1005	HEM	CMC-C2C-C3C	4.24	127.11	116.53
2	A	1014	HEM	CMB-C2B-C3B	4.29	127.24	116.53
2	A	1009	HEM	CAD-C3D-C4D	4.29	127.61	112.47
2	A	1003	HEM	CMC-C2C-C3C	4.30	127.26	116.53
2	A	1001	HEM	CMC-C2C-C3C	4.30	127.27	116.53
2	A	1005	HEM	CAD-C3D-C2D	4.31	125.59	113.22
2	A	1012	HEM	CMC-C2C-C3C	4.32	127.32	116.53
2	A	1009	HEM	CAD-C3D-C2D	4.39	125.83	113.22
2	A	1005	HEM	CMB-C2B-C3B	4.43	127.58	116.53
2	A	1015	HEM	CAD-C3D-C2D	4.48	126.10	113.22
2	A	1008	HEM	CMC-C2C-C3C	4.53	127.84	116.53
2	A	1011	HEM	CAD-C3D-C4D	4.54	128.49	112.47
2	A	1006	HEM	CAD-C3D-C4D	4.54	128.50	112.47
2	A	1005	HEM	CAD-C3D-C4D	4.60	128.71	112.47
2	A	1001	HEM	CAD-C3D-C2D	4.60	126.45	113.22
2	A	1012	HEM	CMB-C2B-C3B	4.62	128.05	116.53
2	A	1006	HEM	CMB-C2B-C3B	4.65	128.14	116.53
2	A	1007	HEM	CMC-C2C-C3C	4.68	128.20	116.53
2	A	1014	HEM	CMC-C2C-C3C	4.69	128.23	116.53
2	A	1004	HEM	CMC-C2C-C3C	4.79	128.49	116.53
2	A	1001	HEM	CMB-C2B-C3B	4.79	128.49	116.53
2	A	1015	HEM	CMB-C2B-C3B	4.80	128.50	116.53
2	A	1016	HEM	CMC-C2C-C3C	4.80	128.51	116.53
2	A	1001	HEM	CAD-C3D-C4D	4.81	129.43	112.47
2	A	1008	HEM	CMB-C2B-C3B	4.82	128.56	116.53
2	A	1010	HEM	CAD-C3D-C2D	4.83	127.09	113.22
2	A	1016	HEM	CMB-C2B-C3B	4.90	128.76	116.53
2	A	1013	HEM	C1D-CHD-C4C	4.92	134.04	125.82
2	A	1007	HEM	CMB-C2B-C3B	4.93	128.84	116.53
2	A	1011	HEM	CAD-C3D-C2D	4.93	127.39	113.22
2	A	1010	HEM	CMB-C2B-C3B	4.96	128.91	116.53
2	A	1008	HEM	CAD-C3D-C2D	5.01	127.62	113.22
2	A	1006	HEM	CMC-C2C-C3C	5.02	129.07	116.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1004	HEM	CAD-C3D-C2D	5.11	127.90	113.22
2	A	1013	HEM	CMC-C2C-C3C	5.14	129.36	116.53
2	A	1013	HEM	CAD-C3D-C2D	5.15	128.01	113.22
2	A	1015	HEM	CMC-C2C-C3C	5.15	129.39	116.53
2	A	1002	HEM	CAD-C3D-C2D	5.23	128.26	113.22
2	A	1002	HEM	CMC-C2C-C3C	5.31	129.78	116.53
2	A	1014	HEM	CAD-C3D-C2D	5.41	128.76	113.22
2	A	1016	HEM	CAD-C3D-C2D	5.44	128.86	113.22
2	A	1003	HEM	CAD-C3D-C2D	5.45	128.89	113.22
2	A	1007	HEM	CAD-C3D-C2D	5.47	128.95	113.22
2	A	1009	HEM	CMB-C2B-C3B	5.50	130.25	116.53
2	A	1011	HEM	CMB-C2B-C3B	5.73	130.83	116.53
2	A	1010	HEM	CMC-C2C-C3C	5.79	130.99	116.53
2	A	1003	HEM	CMB-C2B-C3B	5.85	131.14	116.53
2	A	1012	HEM	CAD-C3D-C2D	5.89	130.14	113.22

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

13 monomers are involved in 26 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1002	HEM	1	0
2	A	1003	HEM	1	0
2	A	1004	HEM	5	0
2	A	1006	HEM	2	0
2	A	1007	HEM	2	0
2	A	1008	HEM	1	0
2	A	1009	HEM	1	0
2	A	1010	HEM	2	0
2	A	1012	HEM	3	0
2	A	1013	HEM	1	0
2	A	1014	HEM	1	0
2	A	1015	HEM	6	0
2	A	1016	HEM	1	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

### 6.1 Protein, DNA and RNA chains

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	500/545 (91%)	-0.03	30 (6%) 25 27	25, 39, 75, 105	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	283	ALA	9.0
1	A	144	SER	7.9
1	A	544	ALA	7.7
1	A	543	ARG	7.0
1	A	545	LYS	6.6
1	A	500	PRO	5.5
1	A	284	PRO	5.4
1	A	403	ALA	5.1
1	A	499	LYS	5.0
1	A	393	VAL	4.6
1	A	395	ALA	4.1
1	A	211	VAL	3.7
1	A	40	GLU	3.6
1	A	282	ASP	3.2
1	A	507	ASP	3.0
1	A	212	ASP	2.9
1	A	286	GLU	2.8
1	A	404	GLU	2.8
1	A	396	GLY	2.7
1	A	498	GLY	2.6
1	A	143	PRO	2.5
1	A	41	LYS	2.5
1	A	146	ALA	2.4
1	A	236	LYS	2.4
1	A	133	GLY	2.3
1	A	237	ALA	2.3
1	A	190	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	542	GLU	2.1
1	A	399	LEU	2.0
1	A	213	LYS	2.0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	HEM	A	1010	43/43	0.96	0.12	0.87	18,29,59,77	0
2	HEM	A	1001	43/43	0.98	0.12	0.66	20,28,37,40	0
2	HEM	A	1013	43/43	0.94	0.14	0.47	23,42,64,76	0
2	HEM	A	1012	43/43	0.98	0.11	0.39	18,27,36,44	0
2	HEM	A	1015	43/43	0.94	0.15	0.33	24,35,76,89	0
2	HEM	A	1008	43/43	0.98	0.10	0.15	18,29,41,47	0
2	HEM	A	1011	43/43	0.97	0.10	0.07	22,28,38,58	0
2	HEM	A	1002	43/43	0.98	0.10	-0.05	21,29,40,50	0
2	HEM	A	1006	43/43	0.97	0.09	-0.06	20,30,44,49	0
2	HEM	A	1016	43/43	0.96	0.12	-0.09	24,33,44,49	0
2	HEM	A	1014	43/43	0.95	0.11	-0.16	25,38,59,72	0
2	HEM	A	1009	43/43	0.97	0.09	-0.25	19,33,50,65	0
2	HEM	A	1007	43/43	0.98	0.10	-0.30	20,29,43,56	0
2	HEM	A	1005	43/43	0.98	0.08	-0.52	21,30,50,72	0
2	HEM	A	1004	43/43	0.98	0.08	-0.68	22,31,41,61	0
2	HEM	A	1003	43/43	0.97	0.08	-0.78	17,30,37,42	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.