



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:43 PM GMT

PDB ID : 1GWS  
Title : HEXADECAHEME HIGH MOLECULAR WEIGHT CYTOCHROME HMC  
FROM DESULFOVIBRIO VULGARIS HILDENBOROUGH  
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Deposited on : 2002-03-25  
Resolution : 2.40 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

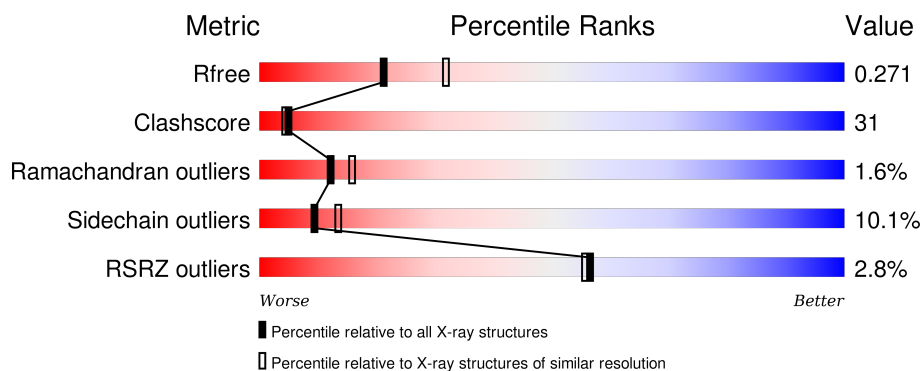
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	

## 2 Entry composition i

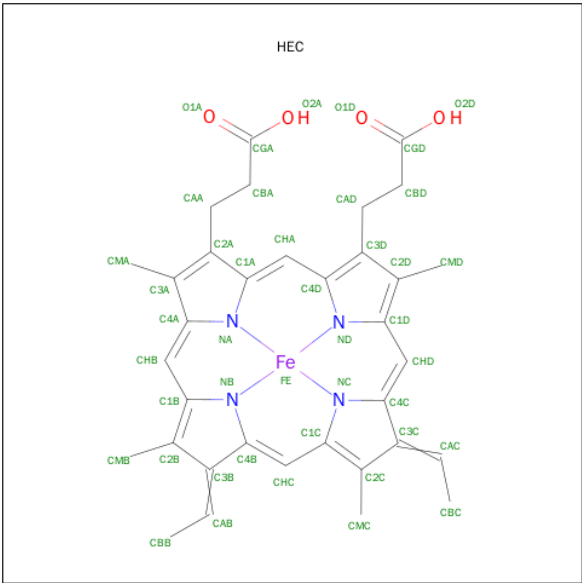
There are 4 unique types of molecules in this entry. The entry contains 4632 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	503	Total	C	N	O	S	0	0	0
			3793	2331	715	703	44			

- Molecule 2 is HEME C (three-letter code: HEC) (formula:  $C_{34}H_{34}FeN_4O_4$ ).



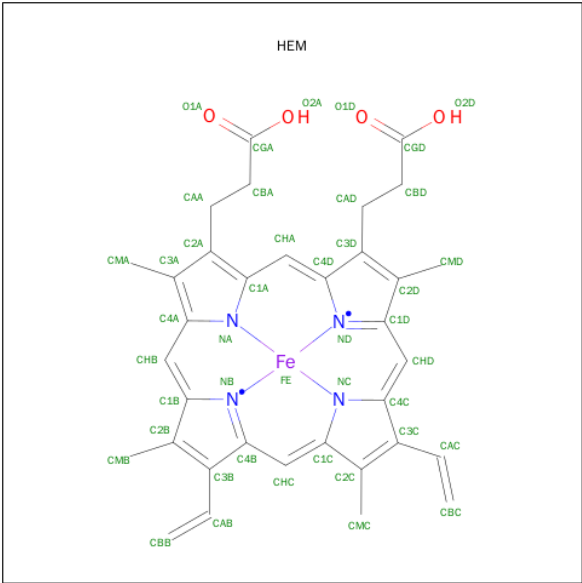
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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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		

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula:  $C_{34}H_{32}FeN_4O_4$ ).



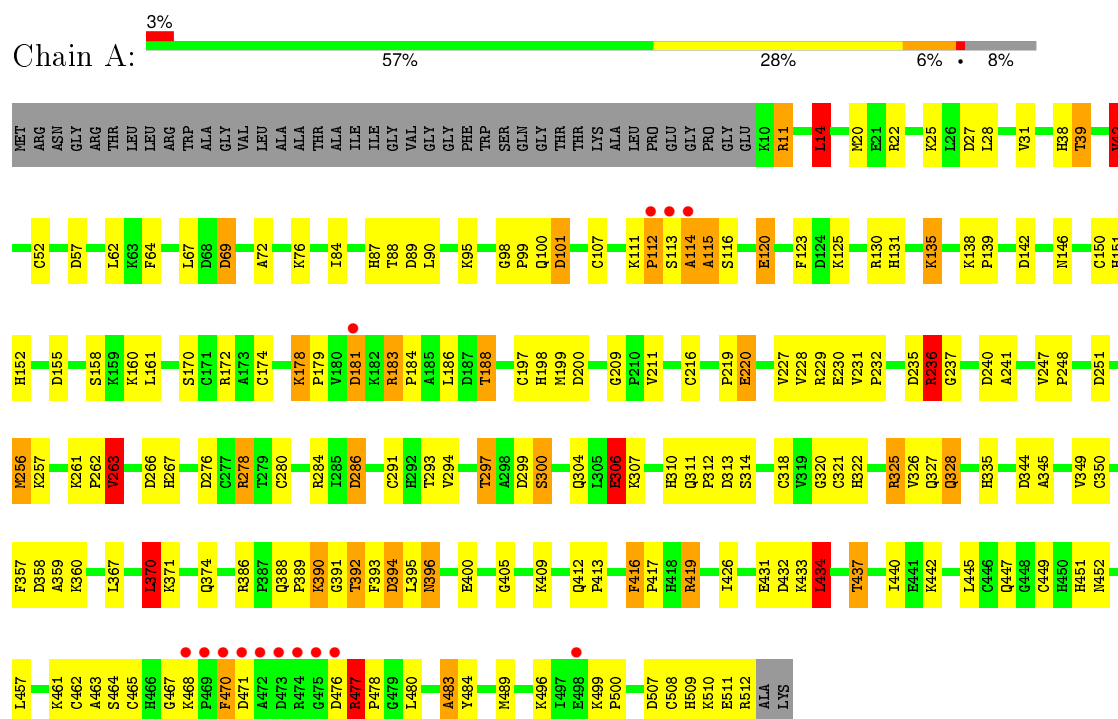
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	151	Total	O	0	0
			151	151		

### 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



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 62	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	108.39Å 108.39Å 102.81Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	33.52 – 2.40 33.54 – 2.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (33.52-2.40) 99.0 (33.54-2.40)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.51 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.0.36	Depositor
R, $R_{free}$	0.201 , 0.276 0.199 , 0.271	Depositor DCC
$R_{free}$ test set	1281 reflections (5.06%)	DCC
Wilson B-factor (Å <sup>2</sup> )	46.9	Xtriage
Anisotropy	0.280	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 35.2	EDS
Estimated twinning fraction	0.044 for h,-h-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 26599 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4632	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% 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, HEC

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	1.16	12/3876 (0.3%)	1.29	34/5221 (0.7%)

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	31	VAL	CB-CG1	6.94	1.67	1.52
1	A	489	MET	SD-CE	-5.97	1.44	1.77
1	A	14	LEU	CG-CD2	5.66	1.72	1.51
1	A	483	ALA	CA-CB	-5.58	1.40	1.52
1	A	306	GLU	CD-OE1	5.56	1.31	1.25
1	A	120	GLU	CG-CD	5.33	1.59	1.51
1	A	328	GLN	CG-CD	5.28	1.63	1.51
1	A	57	ASP	CB-CG	5.24	1.62	1.51
1	A	345	ALA	CA-CB	-5.20	1.41	1.52
1	A	42	VAL	CA-CB	5.12	1.65	1.54
1	A	328	GLN	CB-CG	5.06	1.66	1.52
1	A	241	ALA	CA-CB	5.03	1.63	1.52

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	155	ASP	CB-CG-OD2	9.55	126.89	118.30
1	A	240	ASP	CB-CG-OD2	9.47	126.83	118.30
1	A	394	ASP	CB-CG-OD2	9.06	126.45	118.30
1	A	236	ARG	C-N-CA	-8.73	103.97	122.30
1	A	69	ASP	CB-CG-OD2	8.61	126.05	118.30
1	A	266	ASP	CB-CG-OD2	8.38	125.84	118.30
1	A	358	ASP	CB-CG-OD2	7.77	125.29	118.30
1	A	278	ARG	NE-CZ-NH1	7.64	124.12	120.30
1	A	181	ASP	CB-CG-OD2	7.61	125.15	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	200	ASP	CB-CG-OD2	7.51	125.06	118.30
1	A	313	ASP	CB-CG-OD2	7.46	125.01	118.30
1	A	507	ASP	CB-CG-OD1	6.80	124.42	118.30
1	A	386	ARG	NE-CZ-NH1	-6.55	117.02	120.30
1	A	300	SER	C-N-CA	-6.39	105.72	121.70
1	A	370	LEU	CA-CB-CG	6.08	129.28	115.30
1	A	101	ASP	CB-CG-OD2	6.08	123.77	118.30
1	A	286	ASP	CB-CG-OD2	6.01	123.71	118.30
1	A	89	ASP	CB-CG-OD2	5.93	123.64	118.30
1	A	300	SER	N-CA-C	-5.82	95.29	111.00
1	A	142	ASP	CB-CG-OD2	5.78	123.50	118.30
1	A	199	MET	CG-SD-CE	-5.68	91.11	100.20
1	A	57	ASP	CB-CG-OD1	5.66	123.39	118.30
1	A	276	ASP	CB-CG-OD1	5.57	123.31	118.30
1	A	263	VAL	CG1-CB-CG2	5.45	119.61	110.90
1	A	236	ARG	N-CA-C	-5.40	96.42	111.00
1	A	419	ARG	NE-CZ-NH2	-5.35	117.62	120.30
1	A	130	ARG	NE-CZ-NH1	-5.35	117.63	120.30
1	A	251	ASP	CB-CG-OD2	5.31	123.08	118.30
1	A	470	PHE	N-CA-C	5.29	125.29	111.00
1	A	434	LEU	CA-CB-CG	5.24	127.35	115.30
1	A	11	ARG	NE-CZ-NH1	-5.03	117.78	120.30
1	A	39	THR	N-CA-CB	-5.03	100.75	110.30
1	A	278	ARG	CA-CB-CG	5.03	124.46	113.40
1	A	344	ASP	CB-CG-OD2	5.01	122.81	118.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3793	0	3721	220	0
2	A	516	0	367	95	0
3	A	172	0	120	30	0
4	A	151	0	0	9	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4632	0	4208	267	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 31.

All (267) 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:321:CYS:SG	2:A:610:HEC:CAC	2.10	1.39
1:A:508:CYS:SG	2:A:616:HEC:CAC	2.10	1.39
1:A:449:CYS:SG	2:A:613:HEC:CAC	2.10	1.39
1:A:280:CYS:SG	3:A:608:HEM:CAC	2.12	1.37
1:A:107:CYS:SG	2:A:603:HEC:CAC	2.18	1.31
1:A:52:CYS:SG	2:A:601:HEC:CAC	2.23	1.26
1:A:216:CYS:SG	3:A:607:HEM:CAC	2.26	1.24
1:A:150:CYS:SG	3:A:604:HEM:CAC	2.33	1.17
1:A:465:CYS:SG	2:A:614:HEC:CAC	2.33	1.16
1:A:321:CYS:SG	2:A:610:HEC:HAC	1.86	1.15
1:A:14:LEU:H	1:A:14:LEU:HD22	1.07	1.14
1:A:11:ARG:HB2	1:A:14:LEU:HD11	1.17	1.13
1:A:508:CYS:SG	2:A:616:HEC:HAC	1.87	1.11
1:A:178:LYS:HE3	1:A:179:PRO:HD3	1.33	1.09
1:A:280:CYS:SG	3:A:608:HEM:HAC	1.93	1.04
1:A:174:CYS:SG	2:A:605:HEC:HAC	1.97	1.03
2:A:609:HEC:HBC3	2:A:609:HEC:HMC1	1.40	1.03
1:A:476:ASP:O	1:A:477:ARG:O	1.76	1.02
1:A:216:CYS:SG	3:A:607:HEM:CBC	2.50	0.98
1:A:280:CYS:HG	3:A:608:HEM:CAC	1.73	0.96
1:A:449:CYS:SG	2:A:613:HEC:CBC	2.52	0.95
1:A:135:LYS:HB2	1:A:135:LYS:NZ	1.80	0.95
1:A:14:LEU:CD2	1:A:14:LEU:H	1.76	0.95
1:A:371:LYS:H	1:A:374:GLN:HE21	1.14	0.94
2:A:606:HEC:HBC3	2:A:606:HEC:HMC1	1.50	0.94
2:A:606:HEC:HMB1	2:A:606:HEC:HBB3	1.50	0.93
2:A:615:HEC:HBB3	2:A:615:HEC:HMB1	1.50	0.93
1:A:69:ASP:OD1	4:A:2016:HOH:O	1.88	0.91
1:A:476:ASP:HA	4:A:2126:HOH:O	1.70	0.90
1:A:174:CYS:SG	2:A:605:HEC:CBC	2.60	0.89
2:A:611:HEC:HMB1	2:A:611:HEC:HBB3	1.54	0.88
1:A:449:CYS:SG	2:A:613:HEC:HAC	2.12	0.87
1:A:107:CYS:SG	2:A:603:HEC:CBC	2.62	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:220:GLU:CD	1:A:220:GLU:H	1.76	0.87
1:A:465:CYS:SG	2:A:614:HEC:CBC	2.63	0.87
3:A:607:HEM:HMC1	3:A:607:HEM:HBC2	1.58	0.86
1:A:11:ARG:CB	1:A:14:LEU:HD11	2.05	0.86
1:A:371:LYS:H	1:A:374:GLN:NE2	1.74	0.85
1:A:20:MET:HE3	1:A:72:ALA:O	1.77	0.84
1:A:135:LYS:HB2	1:A:135:LYS:HZ3	1.41	0.84
1:A:174:CYS:O	1:A:183:ARG:HD3	1.78	0.84
1:A:350:CYS:SG	2:A:612:HEC:CBC	2.67	0.83
1:A:465:CYS:SG	2:A:614:HEC:HBC3	2.20	0.82
2:A:611:HEC:HBC3	2:A:611:HEC:HMC1	1.62	0.81
2:A:614:HEC:HBD2	2:A:614:HEC:HHA	1.61	0.81
1:A:14:LEU:N	1:A:14:LEU:HD22	1.91	0.81
1:A:111:LYS:O	1:A:113:SER:N	2.14	0.81
1:A:150:CYS:SG	3:A:604:HEM:HAC	2.22	0.80
1:A:114:ALA:O	1:A:115:ALA:HB3	1.80	0.80
1:A:107:CYS:SG	2:A:603:HEC:C3C	2.71	0.79
1:A:178:LYS:CE	1:A:179:PRO:HD3	2.14	0.78
1:A:256:MET:O	1:A:256:MET:HG2	1.82	0.78
1:A:263:VAL:HG13	2:A:612:HEC:HBD2	1.66	0.77
2:A:603:HEC:HMC1	2:A:603:HEC:HBC3	1.65	0.77
2:A:605:HEC:HBC3	2:A:605:HEC:HMC1	1.66	0.77
1:A:307:LYS:HG3	1:A:311:GLN:NE2	2.00	0.76
1:A:297:THR:HG22	1:A:299:ASP:H	1.50	0.76
1:A:172:ARG:NH1	3:A:604:HEM:O1D	2.18	0.76
2:A:613:HEC:HMB1	2:A:613:HEC:HBB3	1.68	0.76
1:A:38:HIS:O	1:A:42:VAL:HG13	1.87	0.75
2:A:606:HEC:HMC1	2:A:606:HEC:CBC	2.17	0.74
1:A:20:MET:CE	1:A:72:ALA:O	2.36	0.74
1:A:52:CYS:SG	2:A:601:HEC:HAC	2.24	0.74
3:A:608:HEM:CMB	3:A:608:HEM:HBB2	2.17	0.73
1:A:20:MET:HG3	2:A:603:HEC:O1D	1.88	0.73
1:A:280:CYS:SG	3:A:608:HEM:CBC	2.73	0.73
1:A:174:CYS:SG	2:A:605:HEC:C3C	2.76	0.73
1:A:52:CYS:SG	2:A:601:HEC:CBC	2.76	0.73
1:A:216:CYS:SG	3:A:607:HEM:C3C	2.82	0.73
1:A:27:ASP:C	1:A:28:LEU:HD12	2.09	0.73
2:A:609:HEC:HBB3	2:A:609:HEC:HMB1	1.71	0.72
1:A:508:CYS:SG	2:A:616:HEC:CBC	2.77	0.72
1:A:465:CYS:SG	2:A:614:HEC:C3C	2.77	0.72
2:A:609:HEC:CBC	2:A:609:HEC:HMC1	2.20	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:392:THR:HG21	1:A:426:ILE:HD11	1.72	0.72
1:A:172:ARG:HD2	1:A:278:ARG:HD3	1.71	0.71
1:A:197:CYS:SG	2:A:606:HEC:C3C	2.78	0.71
1:A:219:PRO:HD2	1:A:220:GLU:OE1	1.90	0.71
1:A:114:ALA:O	1:A:115:ALA:CB	2.39	0.70
1:A:297:THR:HG22	1:A:299:ASP:N	2.07	0.70
2:A:603:HEC:HBB3	2:A:603:HEC:HMB1	1.74	0.70
1:A:28:LEU:HD12	1:A:28:LEU:N	2.05	0.69
1:A:52:CYS:SG	2:A:601:HEC:C3C	2.81	0.69
2:A:610:HEC:O1A	2:A:610:HEC:HMA2	1.91	0.69
2:A:612:HEC:HMC1	2:A:612:HEC:HBC3	1.75	0.69
1:A:120:GLU:HG3	3:A:607:HEM:CGD	2.23	0.69
1:A:280:CYS:SG	3:A:608:HEM:C3C	2.86	0.69
1:A:476:ASP:OD1	4:A:2126:HOH:O	2.10	0.68
1:A:461:LYS:HZ2	2:A:613:HEC:CGA	2.06	0.68
1:A:449:CYS:SG	2:A:613:HEC:HBC3	2.33	0.68
1:A:350:CYS:SG	2:A:612:HEC:C3C	2.81	0.67
1:A:321:CYS:SG	2:A:610:HEC:CBC	2.82	0.67
1:A:388:GLN:HG3	1:A:389:PRO:HD2	1.75	0.67
1:A:371:LYS:N	1:A:374:GLN:HE21	1.87	0.67
3:A:607:HEM:HBC2	3:A:607:HEM:CMC	2.25	0.66
1:A:183:ARG:O	1:A:183:ARG:CG	2.44	0.66
1:A:107:CYS:SG	2:A:603:HEC:HBC3	2.34	0.65
1:A:508:CYS:SG	2:A:616:HEC:C3C	2.85	0.65
1:A:107:CYS:SG	2:A:603:HEC:HAC	2.30	0.65
2:A:611:HEC:CMB	2:A:611:HEC:HBB3	2.27	0.65
1:A:220:GLU:OE1	1:A:220:GLU:N	2.25	0.64
1:A:360:LYS:NZ	4:A:2094:HOH:O	2.29	0.64
1:A:230:GLU:HG2	1:A:230:GLU:O	1.96	0.64
1:A:321:CYS:SG	2:A:610:HEC:C3C	2.86	0.64
1:A:297:THR:CG2	1:A:299:ASP:H	2.11	0.63
1:A:150:CYS:SG	3:A:604:HEM:C3C	2.92	0.63
1:A:449:CYS:SG	2:A:613:HEC:C3C	2.86	0.63
2:A:615:HEC:HBC3	2:A:615:HEC:HMC1	1.81	0.62
1:A:14:LEU:N	1:A:14:LEU:HD13	2.16	0.61
2:A:613:HEC:HBC3	2:A:613:HEC:HMC1	1.81	0.61
1:A:113:SER:OG	1:A:114:ALA:N	2.33	0.61
1:A:367:LEU:HA	1:A:370:LEU:HD22	1.82	0.61
1:A:412:GLN:HB2	1:A:413:PRO:CD	2.31	0.60
1:A:390:LYS:NZ	1:A:440:ILE:O	2.33	0.60
1:A:88:THR:HA	1:A:100:GLN:HE22	1.65	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:111:LYS:O	1:A:112:PRO:C	2.41	0.59
1:A:437:THR:HG21	2:A:610:HEC:HAA2	1.84	0.59
2:A:612:HEC:O2A	2:A:612:HEC:HMA3	2.03	0.58
1:A:400:GLU:HA	1:A:419:ARG:HB2	1.85	0.58
1:A:135:LYS:CB	1:A:135:LYS:NZ	2.61	0.58
3:A:608:HEM:HMB2	3:A:608:HEM:CBB	2.34	0.58
1:A:412:GLN:HB2	1:A:413:PRO:HD2	1.84	0.58
1:A:178:LYS:HE3	1:A:178:LYS:HA	1.84	0.58
1:A:198:HIS:CE1	1:A:209:GLY:HA3	2.39	0.57
2:A:611:HEC:HBC3	2:A:611:HEC:CMC	2.34	0.57
1:A:52:CYS:HB3	1:A:64:PHE:CE1	2.40	0.57
1:A:465:CYS:HG	2:A:614:HEC:HBC3	1.69	0.57
3:A:602:HEM:HBB2	3:A:602:HEM:CMB	2.34	0.57
3:A:608:HEM:CMB	3:A:608:HEM:CBB	2.83	0.56
1:A:14:LEU:CD2	1:A:14:LEU:N	2.57	0.56
1:A:183:ARG:HG3	1:A:183:ARG:O	2.04	0.56
1:A:325:ARG:CG	1:A:325:ARG:HH11	2.18	0.56
1:A:123:PHE:HB2	3:A:604:HEM:CBD	2.36	0.55
1:A:112:PRO:HA	4:A:2029:HOH:O	2.05	0.55
2:A:603:HEC:HBB3	2:A:603:HEC:CMB	2.35	0.55
1:A:318:CYS:HA	2:A:610:HEC:CHC	2.36	0.55
1:A:219:PRO:CD	1:A:220:GLU:OE1	2.53	0.55
3:A:608:HEM:HMB2	3:A:608:HEM:HBB2	1.87	0.55
1:A:131:HIS:HB3	3:A:604:HEM:HBC2	1.88	0.54
2:A:606:HEC:HMB1	2:A:606:HEC:CBB	2.30	0.54
1:A:11:ARG:O	1:A:116:SER:HA	2.08	0.54
1:A:123:PHE:HB2	3:A:604:HEM:HBD2	1.89	0.54
1:A:230:GLU:O	1:A:232:PRO:HD3	2.08	0.54
1:A:220:GLU:CD	1:A:220:GLU:N	2.55	0.54
1:A:416:PHE:HB2	2:A:615:HEC:HMB2	1.89	0.53
1:A:461:LYS:NZ	2:A:613:HEC:O1A	2.39	0.53
1:A:412:GLN:HG2	1:A:510:LYS:O	2.08	0.53
1:A:310:HIS:HE1	2:A:612:HEC:C1A	2.20	0.53
3:A:602:HEM:HBC2	3:A:602:HEM:CMC	2.39	0.53
1:A:52:CYS:HB3	1:A:64:PHE:CD1	2.44	0.53
1:A:111:LYS:N	1:A:112:PRO:HD2	2.24	0.53
1:A:294:VAL:O	1:A:304:GLN:HB2	2.09	0.53
1:A:197:CYS:SG	2:A:606:HEC:CBC	2.88	0.52
1:A:335:HIS:HE1	2:A:611:HEC:C1A	2.22	0.52
2:A:605:HEC:CBC	2:A:605:HEC:HMC1	2.38	0.52
1:A:392:THR:OG1	1:A:393:PHE:N	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:606:HEC:HMA3	2:A:606:HEC:HBA2	1.92	0.52
1:A:28:LEU:N	1:A:28:LEU:CD1	2.72	0.52
1:A:87:HIS:CE1	1:A:98:GLY:HA3	2.44	0.52
1:A:135:LYS:HE2	4:A:2036:HOH:O	2.10	0.52
1:A:20:MET:HG3	2:A:603:HEC:CGD	2.40	0.51
2:A:613:HEC:HBB3	2:A:613:HEC:CMB	2.38	0.51
1:A:511:GLU:O	1:A:512:ARG:CB	2.58	0.51
2:A:614:HEC:HBD2	2:A:614:HEC:CHA	2.33	0.51
1:A:123:PHE:O	1:A:278:ARG:NH2	2.42	0.51
1:A:357:PHE:O	4:A:2092:HOH:O	2.19	0.51
1:A:230:GLU:O	1:A:230:GLU:CG	2.59	0.51
1:A:509:HIS:HE1	2:A:616:HEC:NB	2.08	0.51
1:A:178:LYS:CE	1:A:178:LYS:HA	2.41	0.50
1:A:433:LYS:O	1:A:437:THR:CG2	2.59	0.50
2:A:615:HEC:HHA	2:A:615:HEC:CBA	2.40	0.50
1:A:150:CYS:SG	3:A:604:HEM:CBC	2.95	0.50
1:A:467:GLY:C	1:A:468:LYS:O	2.47	0.50
2:A:612:HEC:HBB3	2:A:612:HEC:HMB1	1.93	0.50
1:A:395:LEU:HD11	1:A:426:ILE:HD12	1.92	0.50
1:A:499:LYS:HA	1:A:500:PRO:C	2.31	0.49
1:A:314:SER:O	1:A:320:GLY:HA3	2.12	0.49
1:A:84:ILE:HG21	1:A:101:ASP:HB3	1.95	0.49
1:A:174:CYS:SG	2:A:605:HEC:HBC3	2.49	0.49
2:A:606:HEC:CMA	2:A:606:HEC:HBA2	2.43	0.49
1:A:480:LEU:HG	1:A:484:TYR:CE2	2.48	0.49
1:A:120:GLU:HG3	3:A:607:HEM:O2D	2.13	0.49
1:A:325:ARG:HB3	1:A:325:ARG:HH11	1.77	0.48
1:A:322:HIS:CG	1:A:434:LEU:HD11	2.47	0.48
2:A:609:HEC:HMD1	2:A:609:HEC:HBD1	1.94	0.48
1:A:27:ASP:HB3	1:A:28:LEU:HD12	1.96	0.48
1:A:135:LYS:CB	4:A:2035:HOH:O	2.61	0.48
1:A:27:ASP:CB	1:A:28:LEU:HD12	2.43	0.48
1:A:135:LYS:HB2	1:A:135:LYS:HZ2	1.76	0.48
1:A:235:ASP:C	1:A:235:ASP:OD2	2.53	0.48
1:A:11:ARG:O	1:A:14:LEU:HD21	2.14	0.47
1:A:371:LYS:HB2	1:A:374:GLN:HE21	1.79	0.47
1:A:437:THR:CG2	2:A:610:HEC:HAA2	2.44	0.47
1:A:52:CYS:SG	2:A:601:HEC:HBC3	2.55	0.47
1:A:158:SER:O	1:A:160:LYS:HG2	2.14	0.47
1:A:247:VAL:O	1:A:293:THR:HB	2.15	0.47
1:A:248:PRO:HB3	1:A:256:MET:CE	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:311:GLN:HA	1:A:312:PRO:HD3	1.64	0.47
1:A:388:GLN:HG3	1:A:389:PRO:CD	2.43	0.47
1:A:307:LYS:HG3	1:A:311:GLN:HE21	1.74	0.47
1:A:158:SER:HB2	1:A:160:LYS:HE3	1.98	0.46
1:A:235:ASP:OD2	1:A:236:ARG:O	2.34	0.46
1:A:463:ALA:O	1:A:464:SER:C	2.51	0.46
1:A:388:GLN:CG	1:A:389:PRO:CD	2.93	0.46
1:A:367:LEU:HD23	1:A:370:LEU:HD22	1.97	0.46
1:A:227:VAL:HG12	1:A:228:VAL:N	2.30	0.46
1:A:391:GLY:O	1:A:442:LYS:HA	2.15	0.46
1:A:452:ASN:HD22	2:A:614:HEC:CHD	2.30	0.45
2:A:609:HEC:HBD1	2:A:609:HEC:CMD	2.47	0.45
1:A:463:ALA:C	1:A:465:CYS:N	2.67	0.45
1:A:219:PRO:N	1:A:220:GLU:OE1	2.50	0.45
2:A:606:HEC:CMC	2:A:606:HEC:CBC	2.90	0.45
1:A:462:CYS:N	2:A:613:HEC:O2D	2.44	0.45
1:A:267:HIS:CE1	3:A:608:HEM:C4B	3.04	0.45
1:A:464:SER:O	1:A:465:CYS:HB3	2.17	0.44
1:A:405:GLY:HA2	2:A:616:HEC:O1D	2.17	0.44
1:A:170:SER:OG	1:A:172:ARG:HG3	2.18	0.44
1:A:138:LYS:HA	1:A:139:PRO:HD3	1.89	0.44
1:A:307:LYS:HD2	1:A:307:LYS:HA	1.65	0.44
2:A:609:HEC:HBB3	2:A:609:HEC:CMB	2.44	0.44
1:A:262:PRO:HD3	1:A:359:ALA:HB3	1.99	0.44
1:A:267:HIS:HE1	3:A:608:HEM:C4B	2.36	0.44
1:A:90:LEU:HD13	3:A:602:HEM:HMD3	2.00	0.44
1:A:325:ARG:HG3	1:A:325:ARG:HH11	1.83	0.43
2:A:614:HEC:HMC1	2:A:614:HEC:HBC3	2.00	0.43
1:A:291:CYS:O	1:A:297:THR:HB	2.19	0.43
1:A:151:HIS:CD2	3:A:604:HEM:NB	2.87	0.43
1:A:483:ALA:HB1	2:A:614:HEC:CHB	2.48	0.43
1:A:477:ARG:HB2	1:A:478:PRO:HD3	1.98	0.43
1:A:349:VAL:O	1:A:349:VAL:HG12	2.18	0.43
1:A:62:LEU:HD12	1:A:188:THR:HB	2.01	0.43
1:A:198:HIS:NE2	1:A:209:GLY:HA3	2.34	0.43
1:A:125:LYS:HE3	1:A:229:ARG:NH1	2.35	0.42
1:A:299:ASP:C	1:A:300:SER:O	2.54	0.42
1:A:183:ARG:HA	1:A:184:PRO:HD3	1.87	0.42
1:A:304:GLN:HG3	1:A:306:GLU:HG2	2.02	0.42
1:A:227:VAL:CG1	1:A:228:VAL:N	2.82	0.42
1:A:318:CYS:HB3	2:A:610:HEC:C4B	2.46	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:477:ARG:CB	1:A:478:PRO:CD	2.97	0.42
1:A:87:HIS:CE1	1:A:99:PRO:HD2	2.55	0.42
1:A:447:GLN:NE2	4:A:2118:HOH:O	2.52	0.42
1:A:467:GLY:O	1:A:468:LYS:C	2.58	0.42
2:A:610:HEC:HBC3	2:A:610:HEC:HMC1	2.02	0.42
1:A:311:GLN:HB2	1:A:311:GLN:HE21	1.52	0.42
1:A:20:MET:HE1	1:A:72:ALA:O	2.20	0.42
1:A:135:LYS:HG3	1:A:135:LYS:O	2.19	0.42
1:A:183:ARG:HG2	1:A:183:ARG:O	2.17	0.42
2:A:616:HEC:HMC1	2:A:616:HEC:HBC3	2.02	0.41
2:A:615:HEC:CBB	2:A:615:HEC:HMB1	2.30	0.41
1:A:477:ARG:HB2	1:A:478:PRO:CD	2.50	0.41
1:A:248:PRO:HB3	1:A:256:MET:HE2	2.02	0.41
1:A:236:ARG:HB2	1:A:237:GLY:H	1.69	0.41
1:A:367:LEU:HA	1:A:367:LEU:HD23	1.81	0.41
1:A:367:LEU:HD23	1:A:370:LEU:CD2	2.51	0.41
1:A:433:LYS:O	1:A:437:THR:HG22	2.21	0.41
1:A:416:PHE:HA	1:A:417:PRO:HD3	1.87	0.41
1:A:432:ASP:OD2	1:A:434:LEU:N	2.54	0.41
1:A:228:VAL:O	1:A:231:VAL:CG2	2.69	0.41
1:A:261:LYS:HB3	1:A:262:PRO:HD2	2.02	0.41
1:A:325:ARG:HH11	1:A:325:ARG:CB	2.33	0.40
1:A:433:LYS:O	1:A:437:THR:HG23	2.22	0.40
2:A:613:HEC:HBC1	2:A:615:HEC:C2C	2.51	0.40
1:A:452:ASN:HD22	2:A:614:HEC:C1D	2.33	0.40
1:A:152:HIS:CD2	1:A:161:LEU:HD22	2.57	0.40
1:A:299:ASP:O	2:A:609:HEC:HMD3	2.22	0.40
1:A:335:HIS:CE1	2:A:611:HEC:C1A	3.04	0.40
1:A:394:ASP:OD2	1:A:396:ASN:HB2	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:2028:HOH:O	4:A:2136:HOH:O[4_675]	0.64	1.56



## 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	501/545 (92%)	460 (92%)	33 (7%)	8 (2%)	12 16

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	112	PRO
1	A	181	ASP
1	A	257	LYS
1	A	477	ARG
1	A	115	ALA
1	A	114	ALA
1	A	409	LYS
1	A	286	ASP

### 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%)	364 (90%)	41 (10%)	9 13

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	LEU
1	A	22	ARG
1	A	25	LYS

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Mol	Chain	Res	Type
1	A	39	THR
1	A	42	VAL
1	A	67	LEU
1	A	76	LYS
1	A	95	LYS
1	A	135	LYS
1	A	146	ASN
1	A	178	LYS
1	A	183	ARG
1	A	186	LEU
1	A	188	THR
1	A	211	VAL
1	A	220	GLU
1	A	236	ARG
1	A	256	MET
1	A	263	VAL
1	A	284	ARG
1	A	297	THR
1	A	306	GLU
1	A	325	ARG
1	A	326	VAL
1	A	327	GLN
1	A	328	GLN
1	A	370	LEU
1	A	390	LYS
1	A	392	THR
1	A	396	ASN
1	A	416	PHE
1	A	431	GLU
1	A	434	LEU
1	A	437	THR
1	A	445	LEU
1	A	451	HIS
1	A	457	LEU
1	A	470	PHE
1	A	471	ASP
1	A	477	ARG
1	A	496	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	GLN
1	A	100	GLN
1	A	146	ASN
1	A	222	GLN
1	A	282	HIS
1	A	311	GLN
1	A	323	ASN
1	A	346	GLN
1	A	374	GLN
1	A	447	GLN
1	A	452	ASN
1	A	486	GLN
1	A	487	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	HEC	A	601	1	24,50,50	2.70	8 (33%)	19,82,82	2.27	4 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	HEM	A	602	1	30,50,50	2.58	9 (30%)	24,82,82	4.09	10 (41%)
2	HEC	A	603	1	24,50,50	3.09	8 (33%)	19,82,82	3.63	10 (52%)
3	HEM	A	604	1	30,50,50	2.46	5 (16%)	24,82,82	2.99	10 (41%)
2	HEC	A	605	1	24,50,50	2.80	8 (33%)	19,82,82	2.48	3 (15%)
2	HEC	A	606	1	24,50,50	3.06	6 (25%)	19,82,82	2.53	8 (42%)
3	HEM	A	607	1	30,50,50	2.40	7 (23%)	24,82,82	3.50	13 (54%)
3	HEM	A	608	1	30,50,50	2.29	9 (30%)	24,82,82	3.12	10 (41%)
2	HEC	A	609	1	24,50,50	3.11	7 (29%)	19,82,82	3.33	7 (36%)
2	HEC	A	610	1	24,50,50	2.62	12 (50%)	19,82,82	3.18	8 (42%)
2	HEC	A	611	1	24,50,50	3.42	10 (41%)	19,82,82	4.12	9 (47%)
2	HEC	A	612	1	24,50,50	2.58	8 (33%)	19,82,82	2.96	8 (42%)
2	HEC	A	613	1	24,50,50	2.79	10 (41%)	19,82,82	3.15	8 (42%)
2	HEC	A	614	1	24,50,50	2.59	8 (33%)	19,82,82	3.22	7 (36%)
2	HEC	A	615	1	24,50,50	2.67	7 (29%)	19,82,82	3.79	10 (52%)
2	HEC	A	616	1	24,50,50	3.13	9 (37%)	19,82,82	2.66	7 (36%)

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	HEC	A	601	1	-	0/6/54/54	0/0/8/8
3	HEM	A	602	1	-	0/10/54/54	0/0/8/8
2	HEC	A	603	1	-	0/6/54/54	0/0/8/8
3	HEM	A	604	1	-	0/10/54/54	0/0/8/8
2	HEC	A	605	1	-	0/6/54/54	0/0/8/8
2	HEC	A	606	1	-	0/6/54/54	0/0/8/8
3	HEM	A	607	1	-	0/10/54/54	0/0/8/8
3	HEM	A	608	1	-	0/10/54/54	0/0/8/8
2	HEC	A	609	1	-	0/6/54/54	0/0/8/8
2	HEC	A	610	1	-	0/6/54/54	0/0/8/8
2	HEC	A	611	1	-	0/6/54/54	0/0/8/8
2	HEC	A	612	1	-	0/6/54/54	0/0/8/8
2	HEC	A	613	1	-	0/6/54/54	0/0/8/8
2	HEC	A	614	1	-	0/6/54/54	0/0/8/8
2	HEC	A	615	1	-	0/6/54/54	0/0/8/8
2	HEC	A	616	1	-	0/6/54/54	0/0/8/8

All (131) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	609	HEC	C3C-C2C	-11.66	1.28	1.40
3	A	602	HEM	C3B-C4B	-10.22	1.42	1.51
2	A	611	HEC	C3B-C2B	-10.09	1.30	1.40
2	A	606	HEC	C3B-C2B	-9.39	1.30	1.40
3	A	604	HEM	C3B-C4B	-9.34	1.43	1.51
2	A	616	HEC	C3C-C2C	-9.30	1.31	1.40
3	A	607	HEM	C3B-C4B	-9.06	1.43	1.51
2	A	603	HEC	C3C-C2C	-8.92	1.31	1.40
2	A	611	HEC	C3C-C2C	-8.63	1.31	1.40
2	A	613	HEC	C3B-C2B	-8.61	1.31	1.40
2	A	606	HEC	C3C-C2C	-8.12	1.32	1.40
2	A	605	HEC	C3C-C2C	-7.92	1.32	1.40
2	A	603	HEC	C3B-C2B	-7.87	1.32	1.40
3	A	608	HEM	C3B-C4B	-7.77	1.44	1.51
2	A	601	HEC	C3B-C2B	-7.62	1.32	1.40
2	A	612	HEC	C3C-C2C	-7.54	1.32	1.40
2	A	615	HEC	C3B-C2B	-7.28	1.33	1.40
2	A	610	HEC	C3B-C2B	-7.09	1.33	1.40
2	A	614	HEC	C3B-C2B	-6.89	1.33	1.40
2	A	615	HEC	C3C-C2C	-5.87	1.34	1.40
3	A	604	HEM	C3D-C4D	-5.80	1.44	1.51
2	A	601	HEC	C3C-C2C	-5.66	1.34	1.40
2	A	616	HEC	C3B-C2B	-5.65	1.34	1.40
2	A	613	HEC	C3C-C2C	-5.57	1.34	1.40
2	A	605	HEC	C3B-C2B	-5.00	1.35	1.40
3	A	602	HEM	C3D-C4D	-4.94	1.45	1.51
2	A	614	HEC	C3C-C2C	-4.77	1.35	1.40
2	A	612	HEC	C3B-C2B	-4.67	1.35	1.40
2	A	605	HEC	CBB-CAB	-4.59	1.30	1.49
2	A	603	HEC	CBC-CAC	-4.22	1.32	1.49
2	A	614	HEC	CBB-CAB	-4.16	1.32	1.49
2	A	609	HEC	C3B-C2B	-4.15	1.36	1.40
3	A	607	HEM	C2C-C1C	-3.90	1.45	1.52
2	A	616	HEC	CBC-CAC	-3.84	1.33	1.49
2	A	609	HEC	CBC-CAC	-3.78	1.34	1.49
2	A	611	HEC	CBC-CAC	-3.75	1.34	1.49
2	A	612	HEC	CBB-CAB	-3.70	1.34	1.49
2	A	610	HEC	C3C-C2C	-3.63	1.37	1.40
2	A	610	HEC	CBB-CAB	-3.61	1.34	1.49
2	A	613	HEC	CBC-CAC	-3.61	1.34	1.49
2	A	611	HEC	CBB-CAB	-3.59	1.34	1.49
2	A	603	HEC	CBB-CAB	-3.55	1.35	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	606	HEC	CBB-CAB	-3.53	1.35	1.49
2	A	616	HEC	CBB-CAB	-3.48	1.35	1.49
2	A	614	HEC	CBC-CAC	-3.44	1.35	1.49
3	A	604	HEM	C2C-C1C	-3.44	1.46	1.52
3	A	608	HEM	C2C-C1C	-3.36	1.46	1.52
3	A	607	HEM	C3D-C4D	-3.27	1.47	1.51
2	A	605	HEC	CBC-CAC	-3.22	1.36	1.49
2	A	610	HEC	CBC-CAC	-3.15	1.36	1.49
2	A	601	HEC	CBC-CAC	-3.08	1.36	1.49
2	A	612	HEC	CBC-CAC	-3.06	1.37	1.49
2	A	615	HEC	CBC-CAC	-3.04	1.37	1.49
2	A	606	HEC	CBC-CAC	-3.00	1.37	1.49
3	A	602	HEM	C2B-C1B	-2.96	1.42	1.51
3	A	608	HEM	C3D-C4D	-2.94	1.47	1.51
2	A	615	HEC	CBB-CAB	-2.93	1.37	1.49
3	A	602	HEM	C2C-C1C	-2.68	1.47	1.52
3	A	608	HEM	CHD-C4C	-2.66	1.30	1.36
2	A	601	HEC	CBB-CAB	-2.60	1.38	1.49
3	A	604	HEM	C2D-C1D	-2.59	1.43	1.51
2	A	606	HEC	C2A-C3A	-2.51	1.30	1.37
3	A	608	HEM	C2A-C3A	-2.50	1.30	1.37
2	A	616	HEC	C1D-CHD	-2.36	1.33	1.39
3	A	602	HEM	C2D-C1D	-2.32	1.44	1.51
3	A	607	HEM	C2D-C1D	-2.25	1.44	1.51
2	A	612	HEC	C4A-NA	-2.17	1.33	1.36
3	A	608	HEM	CHD-C1D	-2.14	1.32	1.38
2	A	613	HEC	CBB-CAB	-2.12	1.40	1.49
2	A	612	HEC	C1C-CHC	-2.05	1.34	1.39
2	A	610	HEC	CAD-C3D	2.01	1.55	1.52
2	A	615	HEC	C4A-NA	2.02	1.39	1.36
2	A	609	HEC	CMA-C3A	2.03	1.56	1.51
2	A	613	HEC	CMC-C2C	2.03	1.56	1.51
2	A	603	HEC	CMC-C2C	2.03	1.56	1.51
2	A	605	HEC	C4A-NA	2.12	1.39	1.36
2	A	613	HEC	C4B-NB	2.14	1.39	1.36
2	A	614	HEC	CMB-C2B	2.16	1.56	1.51
3	A	607	HEM	C3C-CAC	2.18	1.55	1.51
2	A	610	HEC	CMC-C2C	2.19	1.56	1.51
2	A	613	HEC	CMA-C3A	2.20	1.56	1.51
3	A	608	HEM	C4C-NC	2.23	1.38	1.36
2	A	609	HEC	C4B-NB	2.23	1.39	1.36
2	A	611	HEC	C1A-NA	2.24	1.39	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	613	HEC	CAD-C3D	2.33	1.56	1.52
2	A	601	HEC	CMB-C2B	2.34	1.56	1.51
2	A	614	HEC	CAA-C2A	2.35	1.56	1.52
2	A	610	HEC	C4B-NB	2.41	1.39	1.36
2	A	612	HEC	CMB-C2B	2.41	1.56	1.51
2	A	601	HEC	CAA-C2A	2.45	1.56	1.52
2	A	610	HEC	CAA-C2A	2.52	1.57	1.52
2	A	603	HEC	CMB-C2B	2.54	1.57	1.51
3	A	602	HEM	C3C-CAC	2.55	1.56	1.51
2	A	611	HEC	C4C-NC	2.57	1.40	1.36
2	A	605	HEC	C3C-C4C	2.59	1.48	1.42
2	A	611	HEC	CMD-C2D	2.60	1.57	1.51
3	A	602	HEM	C4C-NC	2.63	1.39	1.36
2	A	610	HEC	C4A-NA	2.73	1.40	1.36
2	A	611	HEC	C4A-NA	2.73	1.40	1.36
2	A	616	HEC	C1A-NA	2.77	1.40	1.36
3	A	602	HEM	CAA-C2A	2.81	1.56	1.52
3	A	607	HEM	CMA-C3A	2.89	1.57	1.51
3	A	608	HEM	C3C-CAC	2.90	1.56	1.51
2	A	610	HEC	C4C-NC	3.03	1.40	1.36
2	A	616	HEC	CMB-C2B	3.03	1.58	1.51
2	A	601	HEC	CMC-C2C	3.15	1.58	1.51
2	A	603	HEC	CAA-C2A	3.16	1.58	1.52
2	A	609	HEC	CAA-C2A	3.21	1.58	1.52
2	A	610	HEC	C3C-C4C	3.22	1.50	1.42
3	A	604	HEM	C3B-CAB	3.26	1.57	1.51
3	A	602	HEM	C1C-NC	3.27	1.40	1.36
2	A	611	HEC	C4B-NB	3.36	1.41	1.36
2	A	613	HEC	C4A-NA	3.53	1.41	1.36
2	A	616	HEC	C4A-NA	3.57	1.41	1.36
2	A	614	HEC	C4C-NC	3.68	1.41	1.36
2	A	605	HEC	C4C-NC	4.08	1.42	1.36
2	A	611	HEC	C3D-C2D	4.16	1.50	1.37
2	A	606	HEC	C3D-C2D	4.21	1.50	1.37
2	A	615	HEC	C3D-C2D	4.28	1.50	1.37
2	A	603	HEC	C3D-C2D	4.30	1.50	1.37
2	A	612	HEC	C3D-C2D	4.39	1.50	1.37
2	A	605	HEC	C3D-C2D	4.42	1.50	1.37
2	A	615	HEC	C4B-NB	4.49	1.42	1.36
2	A	613	HEC	C3D-C2D	4.55	1.51	1.37
2	A	614	HEC	C3D-C2D	4.62	1.51	1.37
3	A	607	HEM	CAA-C2A	4.63	1.59	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	609	HEC	C3D-C2D	4.75	1.51	1.37
3	A	608	HEM	C3B-CAB	4.79	1.60	1.51
2	A	610	HEC	C3D-C2D	4.90	1.52	1.37
2	A	601	HEC	C3D-C2D	5.01	1.52	1.37
2	A	616	HEC	C3D-C2D	5.68	1.54	1.37

All (132) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	HEM	C3B-CAB-CBB	-15.26	101.05	124.46
2	A	614	HEC	CBB-CAB-C3B	-11.22	102.41	127.35
3	A	607	HEM	C3B-CAB-CBB	-11.14	107.36	124.46
3	A	608	HEM	C3B-CAB-CBB	-10.67	108.09	124.46
2	A	603	HEC	CBB-CAB-C3B	-10.41	104.21	127.35
2	A	611	HEC	CAA-CBA-CGA	-8.27	97.59	112.75
2	A	611	HEC	CBB-CAB-C3B	-8.27	108.98	127.35
2	A	605	HEC	CBB-CAB-C3B	-7.96	109.67	127.35
2	A	609	HEC	CAD-CBD-CGD	-7.90	98.26	112.75
2	A	616	HEC	CBB-CAB-C3B	-7.65	110.34	127.35
3	A	604	HEM	C3B-CAB-CBB	-7.60	112.80	124.46
3	A	604	HEM	CBA-CAA-C2A	-7.31	99.42	112.53
2	A	613	HEC	CBB-CAB-C3B	-7.08	111.61	127.35
2	A	609	HEC	CBB-CAB-C3B	-7.05	111.69	127.35
2	A	601	HEC	CBB-CAB-C3B	-6.96	111.88	127.35
2	A	610	HEC	CAA-C2A-C1A	-6.39	120.07	127.01
2	A	611	HEC	CBC-CAC-C3C	-6.23	113.51	127.35
2	A	613	HEC	CBC-CAC-C3C	-6.06	113.89	127.35
2	A	615	HEC	CMC-C2C-C1C	-6.05	118.35	128.36
2	A	612	HEC	CBB-CAB-C3B	-6.03	113.94	127.35
2	A	606	HEC	CBB-CAB-C3B	-5.96	114.12	127.35
2	A	609	HEC	CBC-CAC-C3C	-5.82	114.41	127.35
2	A	612	HEC	CBD-CAD-C3D	-5.80	102.13	112.53
2	A	610	HEC	CBB-CAB-C3B	-5.79	114.48	127.35
2	A	613	HEC	CBA-CAA-C2A	-5.67	102.37	112.53
2	A	603	HEC	CBC-CAC-C3C	-5.45	115.25	127.35
2	A	615	HEC	CBC-CAC-C3C	-5.26	115.67	127.35
2	A	616	HEC	CBD-CAD-C3D	-5.06	103.46	112.53
2	A	612	HEC	CBC-CAC-C3C	-5.03	116.17	127.35
2	A	610	HEC	CMC-C2C-C1C	-4.96	120.16	128.36
2	A	609	HEC	CBD-CAD-C3D	-4.88	103.78	112.53
3	A	607	HEM	C3C-CAC-CBC	-4.84	117.03	124.46
2	A	610	HEC	CBD-CAD-C3D	-4.79	103.95	112.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	613	HEC	CAA-C2A-C1A	-4.76	121.84	127.01
2	A	610	HEC	CBC-CAC-C3C	-4.68	116.95	127.35
2	A	614	HEC	CBD-CAD-C3D	-4.54	104.40	112.53
2	A	605	HEC	CBD-CAD-C3D	-4.50	104.47	112.53
2	A	610	HEC	CBA-CAA-C2A	-4.45	104.55	112.53
2	A	612	HEC	CAA-CBA-CGA	-4.42	104.64	112.75
2	A	615	HEC	CAA-CBA-CGA	-4.38	104.72	112.75
2	A	601	HEC	CMC-C2C-C1C	-4.23	121.37	128.36
2	A	606	HEC	CBD-CAD-C3D	-4.23	104.95	112.53
2	A	611	HEC	CAA-C2A-C3A	-4.16	117.13	129.00
2	A	613	HEC	CMC-C2C-C1C	-4.14	121.52	128.36
2	A	609	HEC	CMC-C2C-C1C	-4.13	121.53	128.36
2	A	603	HEC	CBD-CAD-C3D	-4.13	105.13	112.53
3	A	602	HEM	C3C-CAC-CBC	-4.08	118.20	124.46
2	A	606	HEC	CBC-CAC-C3C	-4.06	118.33	127.35
2	A	605	HEC	CBC-CAC-C3C	-4.02	118.41	127.35
2	A	610	HEC	CMB-C2B-C1B	-3.98	121.78	128.36
2	A	606	HEC	CMB-C2B-C1B	-3.92	121.88	128.36
2	A	614	HEC	CAD-CBD-CGD	-3.88	105.63	112.75
2	A	603	HEC	CAA-CBA-CGA	-3.79	105.79	112.75
2	A	615	HEC	CBB-CAB-C3B	-3.77	118.97	127.35
2	A	616	HEC	CMB-C2B-C1B	-3.63	122.37	128.36
3	A	604	HEM	C3C-CAC-CBC	-3.61	118.91	124.46
3	A	607	HEM	CMA-C3A-C4A	-3.54	122.51	128.36
2	A	612	HEC	CMC-C2C-C1C	-3.51	122.55	128.36
2	A	606	HEC	CAA-CBA-CGA	-3.45	106.42	112.75
3	A	607	HEM	CBD-CAD-C3D	-3.41	103.63	113.55
3	A	608	HEM	C1D-CHD-C4C	-3.40	120.14	125.82
2	A	616	HEC	CBC-CAC-C3C	-3.33	119.95	127.35
3	A	607	HEM	C1D-CHD-C4C	-3.26	120.37	125.82
2	A	614	HEC	CBC-CAC-C3C	-3.26	120.11	127.35
2	A	615	HEC	CAD-C3D-C2D	-3.19	119.89	129.00
3	A	608	HEM	CAA-CBA-CGA	-3.15	106.97	112.75
2	A	606	HEC	CAA-C2A-C1A	-3.12	123.62	127.01
2	A	609	HEC	CMB-C2B-C1B	-3.09	123.26	128.36
2	A	613	HEC	CAA-CBA-CGA	-3.08	107.11	112.75
2	A	614	HEC	CMC-C2C-C1C	-3.07	123.28	128.36
2	A	601	HEC	CBC-CAC-C3C	-3.04	120.59	127.35
2	A	611	HEC	CAD-C3D-C2D	-3.03	120.36	129.00
2	A	615	HEC	CBD-CAD-C3D	-2.92	107.29	112.53
3	A	602	HEM	CBD-CAD-C3D	-2.86	105.24	113.55
2	A	615	HEC	CAA-C2A-C3A	-2.81	120.98	129.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	HEC	CBD-CAD-C3D	-2.77	107.56	112.53
2	A	613	HEC	CMD-C2D-C1D	-2.59	124.08	128.36
2	A	603	HEC	CMC-C2C-C1C	-2.55	124.15	128.36
2	A	603	HEC	CAD-C3D-C2D	-2.31	122.42	129.00
3	A	607	HEM	CAD-CBD-CGD	-2.26	103.80	113.02
2	A	612	HEC	CMB-C2B-C1B	-2.26	124.63	128.36
2	A	614	HEC	CMD-C2D-C1D	-2.25	124.65	128.36
3	A	602	HEM	CMA-C3A-C4A	-2.22	124.70	128.36
2	A	616	HEC	CAA-C2A-C1A	-2.20	124.62	127.01
3	A	604	HEM	C4B-CHC-C1C	-2.14	122.24	125.82
2	A	614	HEC	CAA-C2A-C1A	-2.13	124.69	127.01
2	A	616	HEC	CBA-CAA-C2A	-2.10	108.77	112.53
2	A	606	HEC	CMC-C2C-C1C	-2.04	124.99	128.36
2	A	610	HEC	CAD-C3D-C4D	-2.03	124.80	127.01
3	A	608	HEM	C2D-C3D-C4D	2.05	104.97	101.50
2	A	613	HEC	CMD-C2D-C3D	2.09	129.62	125.24
2	A	603	HEC	CMA-C3A-C2A	2.11	129.65	125.24
3	A	604	HEM	C2D-C3D-C4D	2.17	105.17	101.50
3	A	607	HEM	CMD-C2D-C3D	2.20	124.08	114.35
2	A	611	HEC	CMD-C2D-C1D	2.20	132.01	128.36
3	A	602	HEM	C2D-C3D-C4D	2.23	105.29	101.50
2	A	606	HEC	C4B-C3B-C2B	2.28	108.81	106.35
3	A	604	HEM	CMD-C2D-C3D	2.31	124.55	114.35
2	A	609	HEC	CAD-C3D-C4D	2.36	129.57	127.01
2	A	612	HEC	CMD-C2D-C1D	2.52	132.53	128.36
3	A	607	HEM	C2D-C3D-C4D	2.55	105.82	101.50
3	A	607	HEM	C3B-C4B-CHC	2.65	126.89	123.16
3	A	607	HEM	CMC-C2C-C3C	2.66	123.17	116.53
2	A	616	HEC	CMD-C2D-C3D	2.66	130.80	125.24
2	A	603	HEC	CMD-C2D-C1D	2.82	133.02	128.36
3	A	608	HEM	CMC-C2C-C3C	2.82	123.57	116.53
2	A	603	HEC	C4B-C3B-C2B	2.86	109.44	106.35
3	A	608	HEM	C4B-CHC-C1C	2.89	130.65	125.82
2	A	611	HEC	C4B-C3B-C2B	3.09	109.69	106.35
3	A	602	HEM	CMD-C2D-C3D	3.14	128.25	114.35
3	A	604	HEM	CMB-C2B-C3B	3.18	124.48	116.53
2	A	615	HEC	CAA-C2A-C1A	3.27	130.56	127.01
3	A	608	HEM	CMD-C2D-C3D	3.35	129.17	114.35
3	A	608	HEM	CMB-C2B-C3B	3.52	125.31	116.53
2	A	612	HEC	CAA-C2A-C1A	3.54	130.85	127.01
3	A	607	HEM	CAD-C3D-C2D	3.59	123.54	113.22
3	A	602	HEM	CAD-C3D-C4D	3.62	125.23	112.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	604	HEM	CAD-C3D-C2D	3.67	123.77	113.22
3	A	604	HEM	CMC-C2C-C3C	4.32	127.32	116.53
3	A	608	HEM	CAD-C3D-C2D	4.46	126.03	113.22
3	A	602	HEM	CMC-C2C-C3C	4.55	127.88	116.53
3	A	608	HEM	CAD-C3D-C4D	4.67	128.96	112.47
3	A	607	HEM	CAD-C3D-C4D	5.15	130.64	112.47
3	A	604	HEM	CAD-C3D-C4D	5.27	131.06	112.47
3	A	607	HEM	CMB-C2B-C3B	5.51	130.29	116.53
3	A	602	HEM	CAD-C3D-C2D	5.65	129.47	113.22
2	A	603	HEC	CAD-C3D-C4D	5.67	133.17	127.01
3	A	602	HEM	CMB-C2B-C3B	6.27	132.17	116.53
2	A	611	HEC	CAD-C3D-C4D	6.57	134.14	127.01
2	A	611	HEC	CAA-C2A-C1A	6.98	134.59	127.01
2	A	615	HEC	CAD-CBD-CGD	7.34	126.21	112.75
2	A	615	HEC	CAD-C3D-C4D	8.70	136.46	127.01

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

16 monomers are involved in 125 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	HEC	5	0
3	A	602	HEM	3	0
2	A	603	HEC	10	0
3	A	604	HEM	9	0
2	A	605	HEC	6	0
2	A	606	HEC	9	0
3	A	607	HEM	7	0
3	A	608	HEM	11	0
2	A	609	HEC	7	0
2	A	610	HEC	10	0
2	A	611	HEC	6	0
2	A	612	HEC	7	0
2	A	613	HEC	12	0
2	A	614	HEC	11	0
2	A	615	HEC	6	0
2	A	616	HEC	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, 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	503/545 (92%)	-0.10	14 (2%) 56 55	19, 33, 64, 91	11 (2%)

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	469	PRO	10.7
1	A	470	PHE	9.4
1	A	468	LYS	6.2
1	A	473	ASP	5.6
1	A	474	ARG	5.5
1	A	471	ASP	4.9
1	A	113	SER	4.9
1	A	472	ALA	4.0
1	A	476	ASP	3.7
1	A	114	ALA	3.2
1	A	181	ASP	2.8
1	A	112	PRO	2.4
1	A	475	GLY	2.3
1	A	498	GLU	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	HEC	A	615	43/43	0.94	0.17	0.68	16,23,42,46	0
3	HEM	A	602	43/43	0.98	0.13	0.52	15,21,31,42	0
2	HEC	A	606	43/43	0.97	0.15	0.51	16,24,34,35	0
3	HEM	A	607	43/43	0.97	0.15	0.26	20,26,40,43	0
3	HEM	A	608	43/43	0.98	0.12	0.05	9,21,27,30	0
3	HEM	A	604	43/43	0.98	0.13	0.04	22,27,33,37	0
2	HEC	A	610	43/43	0.97	0.12	0.04	13,21,32,38	0
2	HEC	A	605	43/43	0.96	0.14	-0.03	19,27,41,53	0
2	HEC	A	614	43/43	0.95	0.14	-0.11	17,27,40,44	0
2	HEC	A	613	43/43	0.96	0.14	-0.13	11,25,39,43	0
2	HEC	A	609	43/43	0.97	0.13	-0.17	14,27,50,58	0
2	HEC	A	611	43/43	0.98	0.12	-0.19	13,20,25,28	0
2	HEC	A	616	43/43	0.98	0.12	-0.30	12,25,31,34	0
2	HEC	A	612	43/43	0.98	0.11	-0.43	15,22,29,35	0
2	HEC	A	601	43/43	0.98	0.11	-0.61	6,22,30,42	0
2	HEC	A	603	43/43	0.97	0.11	-0.71	16,22,25,31	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.