



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2018 – 02:35 pm GMT

PDB ID : 3HQ7
Title : CcpA from *G. sulfurreducens*, G94K/K97Q/R100I variant
Authors : Hoffmann, M.; Seidel, J.; Einsle, O.
Deposited on : 2009-06-05
Resolution : 2.31 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : trunk31020
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk31020

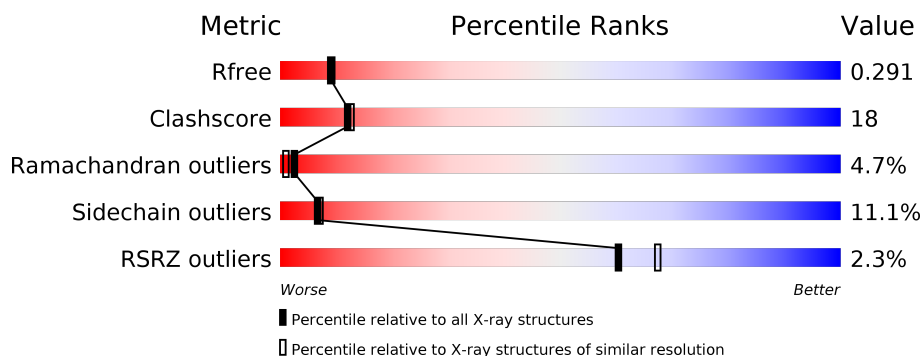
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.31 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}	111664	5225 (2.34-2.30)
Clashscore	122126	5849 (2.34-2.30)
Ramachandran outliers	120053	5790 (2.34-2.30)
Sidechain outliers	120020	5789 (2.34-2.30)
RSRZ outliers	108989	5109 (2.34-2.30)

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	345	<div> <div>2%</div> <div>54%</div> <div>25%</div> <div>8%</div> <div>12%</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2557 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 Cytochrome c551 peroxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	304	2287	1465	388	425	9	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	94	LYS	GLY	ENGINEERED	UNP Q749D0
A	97	GLN	LYS	ENGINEERED	UNP Q749D0
A	100	ILE	ARG	ENGINEERED	UNP Q749D0

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

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

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ca		
			1	1	0	0

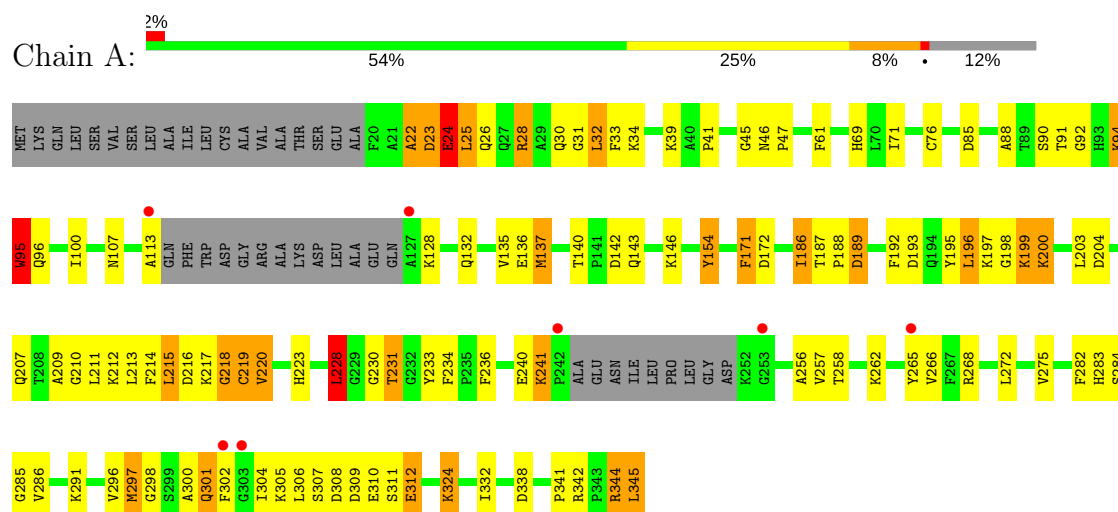
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	183	Total	O		
			183	183	0	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Cytochrome c551 peroxidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	99.30Å 99.35Å 78.22Å 89.97° 89.98° 90.00°	Depositor
Resolution (Å)	70.00 – 2.31 49.65 – 2.31	Depositor EDS
% Data completeness (in resolution range)	99.8 (70.00-2.31) 99.7 (49.65-2.31)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.15	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.23 (at 2.32Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.209 , 0.294 0.207 , 0.291	Depositor DCC
R_{free} test set	906 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	36.2	Xtriage
Anisotropy	0.142	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 61.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2557	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.59% 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, 0.333 respectively for untwinned datasets, and 0.375, 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, CA

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	1.49	5/2341 (0.2%)	1.29	13/3177 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	154	TYR	CE1-CZ	6.24	1.46	1.38
1	A	100	ILE	CA-CB	5.61	1.67	1.54
1	A	61	PHE	CE2-CZ	5.42	1.47	1.37
1	A	95	TRP	CB-CG	5.41	1.59	1.50
1	A	171	PHE	CE1-CZ	5.05	1.47	1.37

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	342	ARG	NE-CZ-NH2	-12.45	114.08	120.30
1	A	342	ARG	NE-CZ-NH1	11.66	126.13	120.30
1	A	172	ASP	CB-CG-OD1	-8.94	110.25	118.30
1	A	28	ARG	NE-CZ-NH1	6.92	123.76	120.30
1	A	297	MET	CG-SD-CE	-6.37	90.01	100.20
1	A	228	LEU	CB-CG-CD2	6.03	121.24	111.00
1	A	32	LEU	CA-CB-CG	5.95	128.98	115.30
1	A	332	ILE	CA-CB-CG1	-5.53	100.49	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	85	ASP	CB-CG-OD1	5.52	123.27	118.30
1	A	344	ARG	NE-CZ-NH2	-5.28	117.66	120.30
1	A	345	LEU	CA-CB-CG	5.11	127.05	115.30
1	A	338	ASP	CB-CG-OD1	5.09	122.88	118.30
1	A	344	ARG	NE-CZ-NH1	5.01	122.80	120.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	218	GLY	Peptide
1	A	230	GLY	Peptide
1	A	311	SER	Peptide
1	A	344	ARG	Peptide
1	A	45	GLY	Peptide

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	2287	0	2298	85	0
2	A	86	0	60	10	0
3	A	1	0	0	1	0
4	A	183	0	0	14	0
All	All	2557	0	2358	87	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 18.

All (87) 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:76:CYS:SG	2:A:401:HEM:CAC	2.27	1.22
1:A:193:ASP:O	1:A:197:LYS:HG3	1.45	1.17
1:A:214:PHE:O	1:A:219:CYS:HB2	1.62	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:CYS:SG	2:A:401:HEM:CBC	2.50	0.99
1:A:146:LYS:HD3	1:A:341:PRO:HG3	1.56	0.88
1:A:216:ASP:OD1	4:A:496:HOH:O	1.92	0.87
1:A:220:VAL:HG22	1:A:220:VAL:O	1.75	0.83
1:A:285:GLY:O	4:A:470:HOH:O	1.99	0.80
1:A:113:ALA:HB1	1:A:268:ARG:HD3	1.65	0.79
1:A:302:PHE:CE1	2:A:402:HEM:HBC2	2.20	0.76
1:A:76:CYS:SG	2:A:401:HEM:C3C	2.79	0.75
1:A:107:ASN:HD21	1:A:187:THR:H	1.38	0.72
1:A:233:TYR:CE2	1:A:268:ARG:HB2	2.23	0.72
1:A:192:PHE:CZ	1:A:196:LEU:HD21	2.26	0.71
1:A:22:ALA:O	1:A:24:GLU:HB3	1.91	0.70
1:A:28:ARG:NH2	4:A:496:HOH:O	1.99	0.67
1:A:113:ALA:CB	1:A:268:ARG:HD3	2.25	0.66
1:A:26:GLN:NE2	1:A:198:GLY:O	2.30	0.65
1:A:71:ILE:HD11	4:A:387:HOH:O	1.96	0.64
3:A:403:CA:CA	4:A:468:HOH:O	1.72	0.64
1:A:90:SER:HB2	2:A:401:HEM:HBC2	1.79	0.64
1:A:300:ALA:O	1:A:302:PHE:N	2.33	0.62
1:A:213:LEU:O	1:A:217:LYS:HG3	2.01	0.61
1:A:28:ARG:HG3	1:A:32:LEU:HD11	1.83	0.60
1:A:46:ASN:N	1:A:47:PRO:CD	2.65	0.59
1:A:220:VAL:O	1:A:220:VAL:CG2	2.49	0.59
1:A:113:ALA:CB	1:A:268:ARG:CD	2.81	0.58
1:A:22:ALA:HB1	1:A:200:LYS:HD3	1.86	0.58
1:A:256:ALA:HA	1:A:296:VAL:HG13	1.84	0.58
1:A:69:HIS:HD2	4:A:383:HOH:O	1.86	0.58
1:A:186:ILE:HG13	1:A:188:PRO:HD3	1.86	0.58
1:A:195:TYR:HA	1:A:199:LYS:O	2.05	0.56
1:A:28:ARG:NH1	4:A:496:HOH:O	2.39	0.56
1:A:217:LYS:O	1:A:304:ILE:HD11	2.06	0.56
1:A:132:GLN:O	1:A:136:GLU:HG3	2.07	0.55
1:A:241:LYS:HB2	4:A:531:HOH:O	2.08	0.54
1:A:94:LYS:HG2	1:A:137:MET:HG2	1.89	0.54
1:A:113:ALA:HB2	1:A:268:ARG:HD2	1.89	0.53
1:A:113:ALA:HB2	1:A:268:ARG:CD	2.39	0.53
1:A:298:GLY:HA2	1:A:304:ILE:CG2	2.39	0.53
1:A:140:THR:OG1	1:A:142:ASP:HB3	2.09	0.52
1:A:28:ARG:HG3	1:A:32:LEU:CD1	2.40	0.52
1:A:204:ASP:C	1:A:204:ASP:OD1	2.48	0.51
1:A:231:THR:HG22	4:A:356:HOH:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:PHE:HB3	1:A:236:PHE:HD1	1.76	0.50
1:A:146:LYS:HD3	1:A:341:PRO:CG	2.35	0.50
1:A:113:ALA:HA	1:A:233:TYR:OH	2.12	0.50
1:A:211:LEU:O	1:A:214:PHE:HB3	2.13	0.48
1:A:189:ASP:N	1:A:189:ASP:OD1	2.40	0.48
1:A:28:ARG:O	1:A:31:GLY:N	2.40	0.48
1:A:26:GLN:HG3	1:A:195:TYR:CZ	2.49	0.48
1:A:231:THR:HG21	4:A:358:HOH:O	2.13	0.48
1:A:33:PHE:CD2	1:A:228:LEU:HD22	2.49	0.47
1:A:41:PRO:O	4:A:422:HOH:O	2.20	0.47
1:A:203:LEU:HA	1:A:207:GLN:HE21	1.78	0.47
1:A:223:HIS:HE1	2:A:402:HEM:ND	2.01	0.47
1:A:272:LEU:O	1:A:275:VAL:HG12	2.14	0.47
1:A:215:LEU:O	1:A:218:GLY:N	2.28	0.47
1:A:298:GLY:HA2	1:A:304:ILE:HG22	1.95	0.47
1:A:46:ASN:N	1:A:47:PRO:HD3	2.31	0.46
1:A:217:LYS:NZ	1:A:305:LYS:O	2.37	0.46
1:A:113:ALA:HB1	1:A:268:ARG:CD	2.39	0.46
1:A:25:LEU:O	1:A:28:ARG:HB3	2.16	0.45
1:A:88:ALA:HB3	4:A:407:HOH:O	2.16	0.45
1:A:306:LEU:HD23	1:A:306:LEU:HA	1.78	0.45
1:A:301:GLN:H	1:A:301:GLN:HG2	1.66	0.45
1:A:143:GLN:HE22	1:A:341:PRO:HB3	1.81	0.45
1:A:135:VAL:HG11	1:A:171:PHE:CE1	2.52	0.44
1:A:90:SER:HB2	2:A:401:HEM:CBC	2.46	0.44
1:A:215:LEU:O	1:A:216:ASP:C	2.56	0.44
1:A:91:THR:HA	1:A:96:GLN:HE22	1.82	0.44
1:A:188:PRO:O	1:A:324:LYS:HG2	2.18	0.44
1:A:71:ILE:CD1	4:A:387:HOH:O	2.63	0.43
1:A:282:PHE:O	1:A:284:SER:N	2.52	0.43
1:A:92:GLY:HA3	2:A:401:HEM:C3C	2.53	0.43
1:A:233:TYR:HB3	1:A:266:VAL:HB	2.02	0.42
1:A:188:PRO:O	1:A:324:LYS:CG	2.67	0.41
2:A:401:HEM:HMC1	2:A:401:HEM:HAC	1.85	0.41
1:A:257:VAL:HG12	1:A:258:THR:N	2.35	0.41
1:A:241:LYS:HE3	1:A:241:LYS:HB3	1.38	0.41
1:A:214:PHE:CE1	1:A:219:CYS:HB3	2.56	0.41
1:A:95:TRP:CD1	1:A:95:TRP:C	2.95	0.41
1:A:236:PHE:CD1	2:A:402:HEM:HBC1	2.56	0.41
1:A:34:LYS:HB3	1:A:34:LYS:HE2	1.82	0.41
1:A:143:GLN:HG3	4:A:491:HOH:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:307:SER:N	1:A:310:GLU:OE1	2.36	0.40
1:A:307:SER:OG	1:A:310:GLU:HG3	2.20	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	298/345 (86%)	259 (87%)	25 (8%)	14 (5%)	2 1

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	219	CYS
1	A	301	GLN
1	A	22	ALA
1	A	23	ASP
1	A	24	GLU
1	A	30	GLN
1	A	240	GLU
1	A	283	HIS
1	A	209	ALA
1	A	210	GLY
1	A	215	LEU
1	A	312	GLU
1	A	231	THR
1	A	220	VAL

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	244/277 (88%)	217 (89%)	27 (11%)	7 7

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	ASP
1	A	24	GLU
1	A	25	LEU
1	A	39	LYS
1	A	94	LYS
1	A	95	TRP
1	A	128	LYS
1	A	137	MET
1	A	154	TYR
1	A	186	ILE
1	A	189	ASP
1	A	196	LEU
1	A	199	LYS
1	A	200	LYS
1	A	212	LYS
1	A	228	LEU
1	A	241	LYS
1	A	262	LYS
1	A	265	TYR
1	A	286	VAL
1	A	291	LYS
1	A	297	MET
1	A	308	ASP
1	A	309	ASP
1	A	312	GLU
1	A	324	LYS
1	A	345	LEU

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	69	HIS
1	A	107	ASN
1	A	143	GLN
1	A	194	GLN
1	A	207	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](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

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	401	1	27,50,50	2.41	9 (33%)	17,82,82	2.56	8 (47%)
2	HEM	A	402	1	27,50,50	2.41	11 (40%)	17,82,82	2.15	7 (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	401	1	-	0/6/54/54	0/0/8/8
2	HEM	A	402	1	-	0/6/54/54	0/0/8/8

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	HEM	C3C-C2C	-5.16	1.33	1.40
2	A	402	HEM	C3C-C2C	-4.11	1.34	1.40
2	A	401	HEM	C3B-C2B	-3.47	1.35	1.40
2	A	402	HEM	C3B-C2B	-2.23	1.37	1.40
2	A	402	HEM	CMC-C2C	2.06	1.56	1.51
2	A	402	HEM	CMA-C3A	2.11	1.55	1.51
2	A	402	HEM	CAA-C2A	2.22	1.55	1.52
2	A	402	HEM	C1C-C2C	2.39	1.48	1.42
2	A	402	HEM	CMD-C2D	2.50	1.56	1.51
2	A	401	HEM	CMC-C2C	2.68	1.57	1.51
2	A	401	HEM	C1A-NA	2.91	1.42	1.36
2	A	401	HEM	CMA-C3A	3.26	1.58	1.51
2	A	402	HEM	C1D-ND	3.35	1.43	1.36
2	A	401	HEM	CAA-C2A	3.73	1.58	1.52
2	A	401	HEM	C3C-CAC	3.93	1.55	1.47
2	A	401	HEM	C3D-C2D	4.63	1.51	1.37
2	A	401	HEM	C3B-CAB	4.86	1.57	1.47
2	A	402	HEM	C3B-CAB	4.98	1.57	1.47
2	A	402	HEM	C3C-CAC	5.29	1.58	1.47
2	A	402	HEM	C3D-C2D	5.86	1.55	1.37

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	402	HEM	CMA-C3A-C4A	-4.69	121.25	128.46
2	A	401	HEM	CMA-C3A-C4A	-4.29	121.87	128.46
2	A	401	HEM	CBA-CAA-C2A	-2.96	106.82	112.48
2	A	402	HEM	C1D-C2D-C3D	-2.40	105.33	107.00
2	A	402	HEM	CAD-CBD-CGD	-2.38	108.59	112.66
2	A	401	HEM	C3B-C4B-NB	-2.33	106.20	109.21
2	A	402	HEM	CAA-CBA-CGA	-2.32	108.70	112.66
2	A	402	HEM	C3C-C4C-NC	-2.26	106.67	110.94
2	A	401	HEM	C3C-C4C-NC	-2.20	106.78	110.94
2	A	401	HEM	CMA-C3A-C2A	2.33	129.34	124.94
2	A	401	HEM	C4A-C3A-C2A	2.55	108.77	107.00
2	A	402	HEM	CMB-C2B-C3B	2.90	130.15	124.88
2	A	401	HEM	CMB-C2B-C3B	3.07	130.47	124.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	402	HEM	CMA-C3A-C2A	3.71	131.93	124.94
2	A	401	HEM	CAA-CBA-CGA	6.49	123.75	112.66

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	HEM	7	0
2	A	402	HEM	3	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q < 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	304/345 (88%)	0.08	7 (2%) 60 67	18, 37, 66, 80	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	113	ALA	4.7
1	A	265	TYR	4.5
1	A	302	PHE	3.5
1	A	127	ALA	3.3
1	A	242	PRO	3.0
1	A	253	GLY	2.8
1	A	303	GLY	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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	HEM	A	402	43/43	0.97	0.18	24,48,53,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	HEM	A	401	43/43	0.98	0.15	21,27,49,53	0
3	CA	A	403	1/1	0.99	0.17	19,19,19,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.