



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 07:27 AM GMT

PDB ID : 4N4L
Title : Kuenenia stuttgartiensis hydroxylamine oxidoreductase soaked in hydrazine
Authors : Maalcke, W.J.; Dietl, A.; Marritt, S.J.; Butt, J.N.; Jetten, M.S.M.; Keltjens, J.T.; Barends, T.R.M.B.; Kartal, B.
Deposited on : 2013-10-08
Resolution : 1.90 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

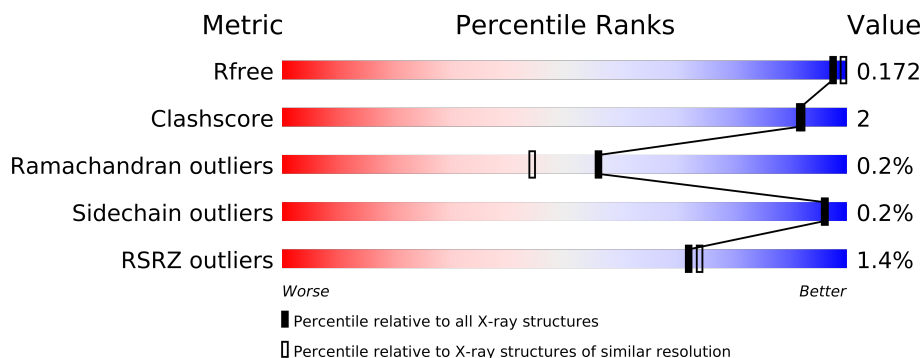
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.90 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}	66092	3684 (1.90-1.90)
Clashscore	79885	4465 (1.90-1.90)
Ramachandran outliers	78287	4413 (1.90-1.90)
Sidechain outliers	78261	4414 (1.90-1.90)
RSRZ outliers	66119	3686 (1.90-1.90)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	500	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	PO4	A	601	-	X
2	PO4	A	602	-	X
2	PO4	A	603	-	X
2	PO4	A	604	-	X
3	EDO	A	605	-	X
3	EDO	A	608	-	X
3	EDO	A	610	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
3	EDO	A	611	-	X
4	HZN	A	612	-	X

2 Entry composition i

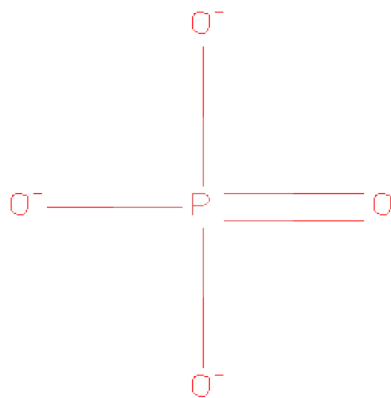
There are 8 unique types of molecules in this entry. The entry contains 4785 atoms, of which 0 are hydrogen and 0 are deuterium.

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 hydroxylamine oxidoreductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	497	Total	C	N	O	S	0	3	0
			3962	2492	706	733	31			

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



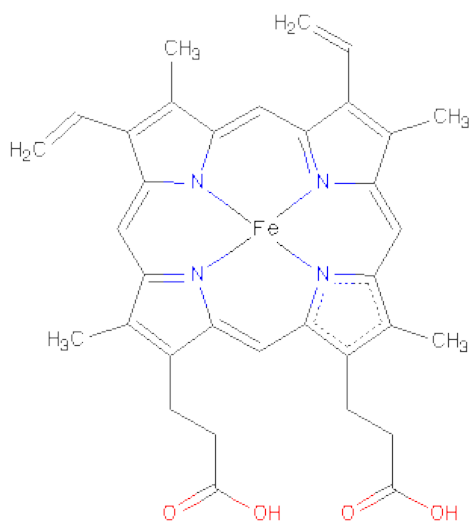
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is HYDRAZINE (three-letter code: HZN) (formula: H_4N_2).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total N 2 2	0	0

- Molecule 5 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



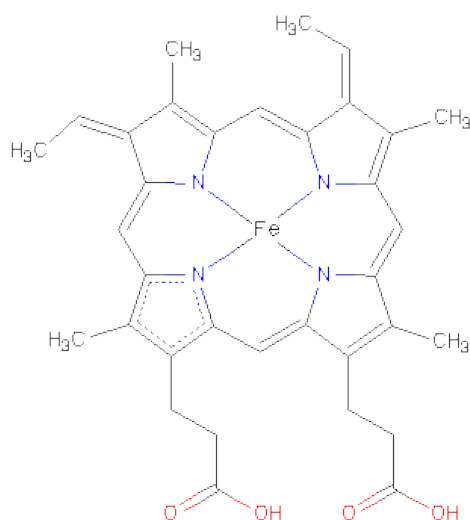
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C Fe N O 43 34 1 4 4	0	0
5	A	1	Total C Fe N O 43 34 1 4 4	0	0

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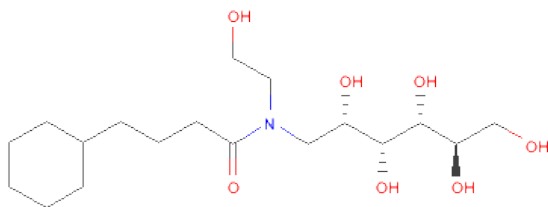
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
5	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
5	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
5	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
5	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 6 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



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

- Molecule 7 is 1-[(4-CYCLOHEXYLBUTANOYL)(2-HYDROXYETHYL)AMINO]-1-DEOXY-D-GLUCITOL (three-letter code: HG1) (formula: $C_{18}H_{35}NO_7$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			12	10	1	1		

- Molecule 8 is water.

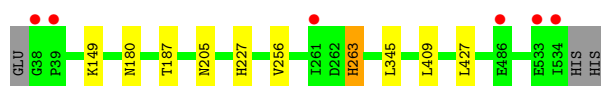
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	417	Total	O	0	0
			417	417		

3 Residue-property plots

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: hydroxylamine oxidoreductase

Chain A: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	130.00Å 130.00Å 130.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.96 – 1.90 45.96 – 1.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (45.96-1.90) 100.0 (45.96-1.90)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.47 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.148 , 0.163 0.155 , 0.172	Depositor DCC
R_{free} test set	2786 reflections (5.07%)	DCC
Wilson B-factor (Å ²)	19.0	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 30.2	EDS
Estimated twinning fraction	0.035 for l,-k,h	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 57701 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4785	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.42% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, HZN, EDO, HG1, HEC, 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	0.34	0/4080	0.54	0/5521

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3962	0	3755	8	0
2	A	20	0	0	2	0
3	A	28	0	42	0	0
4	A	2	0	0	1	0
5	A	301	0	210	2	0
6	A	43	0	30	7	0
7	A	12	0	17	0	0
8	A	417	0	0	5	0
All	All	4785	0	4054	16	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 2.

All (16) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:A:616:HEC:HBC1	8:A:729:HOH:O	1.78	0.82
6:A:616:HEC:HBC3	6:A:616:HEC:HMC1	1.69	0.73
6:A:616:HEC:HBB3	6:A:616:HEC:HMB1	1.72	0.70
2:A:604:PO4:O1	8:A:734:HOH:O	2.16	0.63
1:A:263:HIS:NE2	4:A:612:HZN:N2	2.48	0.61
1:A:256:VAL:HG12	8:A:729:HOH:O	2.01	0.60
1:A:149:LYS:HE2	8:A:1006:HOH:O	2.07	0.53
1:A:180:ASN:HB2	1:A:187:THR:HG21	1.97	0.47
1:A:205:ASN:O	6:A:616:HEC:HHB	2.15	0.46
6:A:616:HEC:CBC	6:A:616:HEC:HMC1	2.41	0.46
1:A:227:HIS:CE1	6:A:616:HEC:NA	2.85	0.44
6:A:616:HEC:HAD2	5:A:618:HEM:HBD2	1.99	0.44
1:A:345:LEU:HD13	1:A:345:LEU:C	2.37	0.44
1:A:427:LEU:C	1:A:427:LEU:HD13	2.38	0.43
5:A:613:HEM:HBC2	5:A:613:HEM:CMC	2.49	0.42
2:A:604:PO4:O2	8:A:741:HOH:O	2.22	0.41

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	498/500 (100%)	486 (98%)	11 (2%)	1 (0%)	56	44

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	263	HIS

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	416/416 (100%)	415 (100%)	1 (0%)	96 96

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	409	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

21 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	PO4	A	601	-	4,4,4	0.39	0	6,6,6	0.31	0
2	PO4	A	602	-	4,4,4	0.44	0	6,6,6	0.31	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PO4	A	603	-	4,4,4	0.36	0	6,6,6	0.32	0
2	PO4	A	604	-	4,4,4	0.38	0	6,6,6	0.31	0
3	EDO	A	605	-	3,3,3	0.65	0	2,2,2	0.12	0
3	EDO	A	606	-	3,3,3	0.57	0	2,2,2	0.21	0
3	EDO	A	607	-	3,3,3	0.52	0	2,2,2	0.37	0
3	EDO	A	608	-	3,3,3	0.50	0	2,2,2	0.17	0
3	EDO	A	609	-	3,3,3	0.54	0	2,2,2	0.25	0
3	EDO	A	610	-	3,3,3	0.47	0	2,2,2	0.45	0
3	EDO	A	611	-	3,3,3	0.55	0	2,2,2	0.19	0
4	HZN	A	612	6	1,1,1	0.18	0	0,0,0	0.00	-
5	HEM	A	613	1	49,50,50	2.04	11 (22%)	46,82,82	2.04	9 (19%)
5	HEM	A	614	1	49,50,50	2.17	13 (26%)	46,82,82	2.00	9 (19%)
5	HEM	A	615	1	49,50,50	2.06	13 (26%)	46,82,82	2.06	8 (17%)
6	HEC	A	616	1,4	50,50,50	3.68	23 (46%)	56,82,82	3.09	24 (42%)
5	HEM	A	617	1	49,50,50	2.01	10 (20%)	46,82,82	2.03	10 (21%)
5	HEM	A	618	1	49,50,50	2.15	13 (26%)	46,82,82	1.94	7 (15%)
5	HEM	A	619	1	49,50,50	1.98	11 (22%)	46,82,82	2.25	10 (21%)
5	HEM	A	620	1	49,50,50	2.08	11 (22%)	46,82,82	1.88	6 (13%)
7	HG1	A	621	-	12,12,26	0.22	0	14,14,33	0.63	0

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	PO4	A	601	-	-	0/0/0/0	0/0/0/0
2	PO4	A	602	-	-	0/0/0/0	0/0/0/0
2	PO4	A	603	-	-	0/0/0/0	0/0/0/0
2	PO4	A	604	-	-	0/0/0/0	0/0/0/0
3	EDO	A	605	-	-	0/1/1/1	0/0/0/0
3	EDO	A	606	-	-	0/1/1/1	0/0/0/0
3	EDO	A	607	-	-	0/1/1/1	0/0/0/0
3	EDO	A	608	-	-	0/1/1/1	0/0/0/0
3	EDO	A	609	-	-	0/1/1/1	0/0/0/0
3	EDO	A	610	-	-	0/1/1/1	0/0/0/0
3	EDO	A	611	-	-	0/1/1/1	0/0/0/0
4	HZN	A	612	6	-	0/0/0/0	0/0/0/0
5	HEM	A	613	1	-	0/14/114/114	0/0/8/8
5	HEM	A	614	1	-	0/14/114/114	0/0/8/8
5	HEM	A	615	1	-	0/14/114/114	0/0/8/8

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	HEC	A	616	1,4	-	0/10/54/54	0/0/8/8
5	HEM	A	617	1	-	0/14/114/114	0/0/8/8
5	HEM	A	618	1	-	0/14/114/114	0/0/8/8
5	HEM	A	619	1	-	0/14/114/114	0/0/8/8
5	HEM	A	620	1	-	0/14/114/114	0/0/8/8
7	HG1	A	621	-	-	0/6/14/39	0/1/1/1

All (105) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	616	HEC	C3B-C4B	10.17	1.54	1.41
6	A	616	HEC	C3C-C4C	8.19	1.51	1.41
6	A	616	HEC	C4C-NC	8.16	1.48	1.37
6	A	616	HEC	C1A-NA	8.04	1.48	1.37
6	A	616	HEC	C1C-C2C	7.24	1.49	1.40
6	A	616	HEC	C3B-CAB	6.58	1.49	1.35
6	A	616	HEC	C3C-CAC	6.35	1.48	1.35
6	A	616	HEC	C4B-NB	6.31	1.46	1.37
6	A	616	HEC	C4B-CHC	6.08	1.57	1.38
5	A	619	HEM	C3B-C2B	-5.91	1.33	1.43
5	A	617	HEM	C3B-C2B	-5.71	1.33	1.43
5	A	614	HEM	C3B-C2B	-5.70	1.33	1.43
5	A	614	HEM	C3C-C2C	-5.61	1.33	1.43
5	A	620	HEM	C3B-C2B	-5.54	1.34	1.43
5	A	618	HEM	C3B-C2B	-5.52	1.34	1.43
5	A	613	HEM	C3B-C2B	-5.50	1.34	1.43
5	A	615	HEM	C3B-C2B	-5.49	1.34	1.43
5	A	620	HEM	C3C-C2C	-5.48	1.34	1.43
5	A	617	HEM	C3C-C2C	-5.41	1.34	1.43
5	A	618	HEM	C3C-C2C	-5.38	1.34	1.43
5	A	615	HEM	C3C-C2C	-5.33	1.34	1.43
5	A	619	HEM	C3C-C2C	-5.31	1.34	1.43
5	A	613	HEM	C3C-C2C	-5.11	1.34	1.43
5	A	618	HEM	C3D-C2D	5.08	1.52	1.43
5	A	620	HEM	C3D-C2D	4.98	1.52	1.43
5	A	613	HEM	C3D-C2D	4.97	1.52	1.43
6	A	616	HEC	C1D-C2D	4.85	1.46	1.40
6	A	616	HEC	C1B-C2B	4.84	1.46	1.40
5	A	614	HEM	C3D-C2D	4.82	1.52	1.43
5	A	615	HEM	C3C-CAC	4.81	1.55	1.40
5	A	615	HEM	C3D-C2D	4.81	1.52	1.43
5	A	617	HEM	C3D-C2D	4.76	1.52	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	620	HEM	C3C-CAC	4.73	1.55	1.40
5	A	619	HEM	C3D-C2D	4.73	1.52	1.43
5	A	613	HEM	C3C-CAC	4.70	1.55	1.40
5	A	614	HEM	C3C-CAC	4.66	1.55	1.40
5	A	619	HEM	C3C-CAC	4.65	1.55	1.40
5	A	618	HEM	C3C-CAC	4.52	1.54	1.40
5	A	618	HEM	C3B-CAB	4.51	1.54	1.40
5	A	617	HEM	C3C-CAC	4.49	1.54	1.40
5	A	615	HEM	C3B-CAB	4.44	1.54	1.40
5	A	618	HEM	C2D-C1D	-4.39	1.43	1.44
5	A	613	HEM	C4A-C3A	4.38	1.45	1.40
5	A	617	HEM	C3B-CAB	4.37	1.54	1.40
5	A	620	HEM	C4A-C3A	4.32	1.45	1.40
5	A	620	HEM	C3B-CAB	4.31	1.54	1.40
5	A	613	HEM	C3B-CAB	4.30	1.53	1.40
5	A	619	HEM	C3B-CAB	4.17	1.53	1.40
5	A	614	HEM	C3B-CAB	4.12	1.53	1.40
5	A	614	HEM	C3D-C4D	3.97	1.45	1.44
5	A	619	HEM	C4A-C3A	3.83	1.44	1.40
5	A	614	HEM	C4A-C3A	3.82	1.44	1.40
5	A	615	HEM	C4A-C3A	3.74	1.44	1.40
5	A	618	HEM	C4A-C3A	3.68	1.44	1.40
5	A	614	HEM	C2B-C1B	3.65	1.45	1.44
5	A	617	HEM	C4A-C3A	3.58	1.44	1.40
5	A	620	HEM	FE-NA	3.31	2.06	1.92
6	A	616	HEC	C1A-C2A	3.26	1.54	1.43
6	A	616	HEC	CBD-CGD	3.17	1.58	1.50
6	A	616	HEC	C1C-CHC	3.10	1.48	1.39
5	A	613	HEM	FE-NA	3.07	2.05	1.92
6	A	616	HEC	C1A-CHA	3.02	1.47	1.38
6	A	616	HEC	C4D-ND	2.97	1.42	1.36
5	A	618	HEM	FE-NA	2.81	2.04	1.92
6	A	616	HEC	O1A-CGA	2.70	1.31	1.22
6	A	616	HEC	C4C-CHD	2.57	1.46	1.38
6	A	616	HEC	C1D-ND	2.57	1.41	1.36
5	A	615	HEM	FE-NA	2.54	2.03	1.92
5	A	617	HEM	CMB-C2B	2.52	1.55	1.47
5	A	617	HEM	FE-NA	2.48	2.03	1.92
5	A	619	HEM	CMB-C2B	2.47	1.55	1.47
5	A	614	HEM	FE-NA	2.47	2.03	1.92
5	A	614	HEM	CMD-C2D	2.46	1.55	1.47
5	A	618	HEM	CMC-C2C	2.45	1.55	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	613	HEM	CMB-C2B	2.44	1.55	1.47
5	A	620	HEM	CMB-C2B	2.42	1.54	1.47
5	A	615	HEM	CMD-C2D	2.42	1.54	1.47
6	A	616	HEC	C4D-C3D	2.42	1.47	1.43
5	A	617	HEM	CMD-C2D	2.42	1.54	1.47
5	A	613	HEM	CMD-C2D	2.41	1.54	1.47
5	A	615	HEM	FE-NC	2.39	2.06	1.97
5	A	614	HEM	CMB-C2B	2.38	1.54	1.47
5	A	620	HEM	CMC-C2C	2.38	1.54	1.47
5	A	619	HEM	CMC-C2C	2.38	1.54	1.47
5	A	614	HEM	CMC-C2C	2.37	1.54	1.47
5	A	617	HEM	CMC-C2C	2.36	1.54	1.47
5	A	613	HEM	CMC-C2C	2.35	1.54	1.47
5	A	614	HEM	FE-NC	2.35	2.06	1.97
5	A	618	HEM	CMB-C2B	2.34	1.54	1.47
5	A	615	HEM	CMB-C2B	2.31	1.54	1.47
5	A	615	HEM	CMC-C2C	2.29	1.54	1.47
5	A	620	HEM	CMD-C2D	2.28	1.54	1.47
5	A	615	HEM	C2D-C1D	-2.28	1.44	1.44
5	A	620	HEM	C2D-C1D	2.24	1.45	1.44
6	A	616	HEC	C3C-C2C	-2.21	1.37	1.41
5	A	619	HEM	FE-ND	2.20	2.05	1.97
5	A	613	HEM	FE-ND	2.17	2.05	1.97
5	A	618	HEM	CMD-C2D	2.17	1.54	1.47
5	A	618	HEM	C3D-C4D	2.15	1.45	1.44
6	A	616	HEC	C1C-NC	-2.15	1.32	1.36
5	A	615	HEM	C3D-C4D	2.12	1.45	1.44
5	A	619	HEM	CMD-C2D	2.10	1.53	1.47
5	A	619	HEM	FE-NC	2.03	2.05	1.97
6	A	616	HEC	O2A-CGA	-2.03	1.23	1.30
5	A	618	HEM	CHB-C1B	2.01	1.38	1.35

All (83) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	616	HEC	C4B-CHC-C1C	-9.40	115.10	127.47
5	A	619	HEM	C3B-C4B-NB	-9.23	107.40	114.00
5	A	614	HEM	C3B-C4B-NB	-8.70	107.78	114.00
6	A	616	HEC	C2A-C1A-NA	-8.62	103.17	109.64
5	A	618	HEM	C3B-C4B-NB	-8.45	107.95	114.00
5	A	620	HEM	C3B-C4B-NB	-8.27	108.08	114.00
5	A	617	HEM	C3B-C4B-NB	-8.23	108.11	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	613	HEM	C3B-C4B-NB	-8.15	108.17	114.00
5	A	615	HEM	C3B-C4B-NB	-8.08	108.22	114.00
6	A	616	HEC	C4A-CHB-C1B	-6.97	118.29	127.47
5	A	619	HEM	C4D-ND-C1D	6.33	111.64	105.16
5	A	613	HEM	C4D-ND-C1D	5.73	111.03	105.16
5	A	615	HEM	C4D-ND-C1D	5.65	110.94	105.16
6	A	616	HEC	O2A-CGA-O1A	-5.64	108.95	123.30
5	A	614	HEM	C4D-ND-C1D	5.54	110.83	105.16
5	A	618	HEM	C4D-ND-C1D	5.53	110.82	105.16
6	A	616	HEC	CBC-CAC-C3C	-5.14	113.97	128.44
5	A	620	HEM	C4D-ND-C1D	5.13	110.41	105.16
6	A	616	HEC	C3C-C4C-NC	-5.13	104.11	111.52
5	A	617	HEM	CBD-CAD-C3D	-5.09	103.27	114.37
6	A	616	HEC	C3B-C4B-NB	-4.97	104.34	111.52
5	A	617	HEM	C4D-ND-C1D	4.91	110.18	105.16
6	A	616	HEC	C4C-CHD-C1D	-4.86	121.08	127.47
5	A	615	HEM	CBA-CAA-C2A	-4.63	104.53	112.69
6	A	616	HEC	CBB-CAB-C3B	-4.61	115.47	128.44
6	A	616	HEC	C1A-CHA-C4D	-4.50	121.55	127.47
6	A	616	HEC	CMB-C2B-C1B	-4.47	121.75	128.62
5	A	613	HEM	CBA-CAA-C2A	-4.09	105.49	112.69
5	A	619	HEM	C2D-C1D-ND	-3.74	108.51	112.93
5	A	615	HEM	CBD-CAD-C3D	-3.58	106.57	114.37
6	A	616	HEC	CMC-C2C-C1C	-3.49	123.25	128.62
5	A	619	HEM	CBA-CAA-C2A	-3.49	106.55	112.69
5	A	619	HEM	CBD-CAD-C3D	-3.44	106.86	114.37
5	A	619	HEM	CHD-C1D-ND	3.37	127.39	124.58
6	A	616	HEC	CMC-C2C-C3C	3.30	129.36	125.72
5	A	614	HEM	CHD-C1D-ND	3.20	127.24	124.58
5	A	613	HEM	C2D-C1D-ND	-3.20	109.16	112.93
5	A	617	HEM	CHD-C1D-ND	3.10	127.16	124.58
5	A	615	HEM	C2D-C1D-ND	-3.08	109.30	112.93
5	A	620	HEM	C2D-C1D-ND	-3.06	109.32	112.93
6	A	616	HEC	CAA-C2A-C3A	-3.03	120.34	129.00
5	A	615	HEM	CHD-C1D-ND	3.01	127.09	124.58
5	A	614	HEM	C2D-C1D-ND	-2.98	109.41	112.93
6	A	616	HEC	CMB-C2B-C3B	2.96	128.99	125.72
5	A	619	HEM	C1B-NB-C4B	2.91	108.14	105.16
5	A	618	HEM	C1B-NB-C4B	2.89	108.12	105.16
5	A	617	HEM	C2D-C1D-ND	-2.88	109.52	112.93
6	A	616	HEC	CAA-CBA-CGA	-2.88	104.22	113.47
6	A	616	HEC	C2D-C1D-ND	-2.79	107.30	109.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	618	HEM	CMA-C3A-C4A	-2.75	124.39	128.62
5	A	614	HEM	C1B-NB-C4B	2.73	107.95	105.16
5	A	618	HEM	C2D-C1D-ND	-2.56	109.91	112.93
5	A	618	HEM	CHD-C1D-ND	2.54	126.69	124.58
5	A	614	HEM	CMA-C3A-C4A	-2.53	124.72	128.62
5	A	619	HEM	C4A-CHB-C1B	-2.53	124.14	127.47
5	A	620	HEM	CMA-C3A-C4A	-2.52	124.74	128.62
5	A	617	HEM	CMA-C3A-C4A	-2.51	124.77	128.62
6	A	616	HEC	CAA-C2A-C1A	2.49	129.15	124.67
5	A	613	HEM	CHD-C1D-ND	2.42	126.60	124.58
6	A	616	HEC	CBA-CAA-C2A	-2.42	107.83	112.35
5	A	613	HEM	C1B-NB-C4B	2.40	107.61	105.16
5	A	615	HEM	C1B-NB-C4B	2.34	107.55	105.16
5	A	617	HEM	CBA-CAA-C2A	-2.34	108.58	112.69
6	A	616	HEC	O2A-CGA-CBA	2.32	122.41	114.22
5	A	620	HEM	C1B-NB-C4B	2.31	107.53	105.16
5	A	617	HEM	C1B-NB-C4B	2.31	107.53	105.16
5	A	613	HEM	C4C-NC-C1C	2.31	107.93	105.53
6	A	616	HEC	CMA-C3A-C2A	2.26	129.21	124.94
6	A	616	HEC	C4A-C3A-C2A	2.24	108.32	106.89
5	A	617	HEM	CAD-C3D-C4D	2.22	128.53	124.53
5	A	613	HEM	CBD-CAD-C3D	-2.22	109.53	114.37
5	A	620	HEM	C4C-NC-C1C	2.22	107.84	105.53
5	A	613	HEM	CAD-C3D-C4D	2.20	128.48	124.53
6	A	616	HEC	C3D-C4D-ND	-2.19	106.69	109.73
5	A	614	HEM	CAD-C3D-C4D	2.17	128.42	124.53
5	A	617	HEM	C4C-NC-C1C	2.15	107.77	105.53
5	A	614	HEM	CHC-C4B-NB	2.13	126.36	124.58
5	A	614	HEM	C3A-C4A-NA	-2.09	107.83	109.41
5	A	619	HEM	CMA-C3A-C4A	-2.09	125.41	128.62
5	A	619	HEM	C1A-CHA-C4D	-2.06	124.76	127.47
6	A	616	HEC	C2C-C1C-NC	2.03	110.94	109.41
5	A	618	HEM	CAD-C3D-C4D	2.02	128.17	124.53
5	A	615	HEM	O2A-CGA-CBA	2.00	121.29	114.22

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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, 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	497/500 (99%)	-0.35	6 (1%) 75 78	12, 17, 27, 37	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	38	GLY	6.4
1	A	534	ILE	5.2
1	A	39	PRO	2.9
1	A	486	GLU	2.3
1	A	533	GLU	2.3
1	A	261	ILE	2.1

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	PO4	A	604	5/5	0.64	79.82	129,129,129,129	1
3	EDO	A	610	4/4	0.23	10.36	39,40,40,40	0
2	PO4	A	602	5/5	0.12	7.57	22,22,24,25	0
3	EDO	A	611	4/4	0.17	6.97	44,44,44,44	0
4	HZN	A	612	2/2	0.29	5.50	19,19,19,22	0
2	PO4	A	603	5/5	0.10	3.77	19,20,20,21	5
3	EDO	A	608	4/4	0.19	3.56	22,25,25,25	0
2	PO4	A	601	5/5	0.09	3.43	23,23,24,25	0
3	EDO	A	605	4/4	0.08	2.09	15,16,17,17	0
7	HG1	A	621	12/26	0.14	1.94	38,38,42,42	0
3	EDO	A	606	4/4	0.17	1.39	25,26,27,27	0
5	HEM	A	618	43/43	0.09	1.12	10,12,16,18	0
3	EDO	A	609	4/4	0.08	0.78	20,22,23,23	0
5	HEM	A	620	43/43	0.08	0.70	10,12,14,15	0
5	HEM	A	614	43/43	0.07	0.47	13,14,14,15	0
5	HEM	A	619	43/43	0.09	0.27	10,11,14,16	0
3	EDO	A	607	4/4	0.12	0.24	30,32,33,34	0
5	HEM	A	615	43/43	0.08	-0.00	13,14,16,17	0
6	HEC	A	616	43/43	0.09	-0.03	12,15,21,25	0
5	HEM	A	617	43/43	0.07	-0.08	11,12,14,16	0
5	HEM	A	613	43/43	0.06	-0.53	13,15,17,20	0

6.5 Other polymers ⓘ

There are no such residues in this entry.