



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:16 AM GMT

PDB ID : 2CJ0
Title : CHLOROPEROXIDASE COMPLEXED WITH NITRATE
Authors : Kuhnel, K.; Blankenfeldt, W.; Turner, J.; Schlichting, I.
Deposited on : 2006-03-26
Resolution : 1.75 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

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

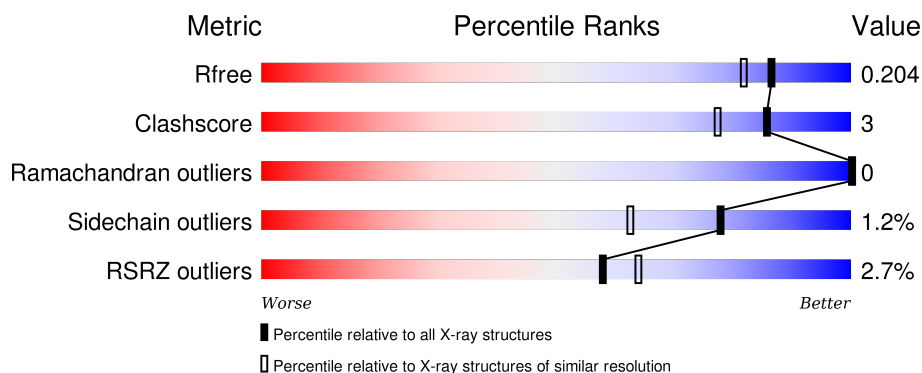
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

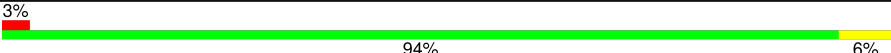
The reported resolution of this entry is 1.75 Å.

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	1609 (1.76-1.76)
Clashscore	102246	1730 (1.76-1.76)
Ramachandran outliers	100387	1711 (1.76-1.76)
Sidechain outliers	100360	1711 (1.76-1.76)
RSRZ outliers	91569	1610 (1.76-1.76)

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	299	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
8	EDO	A	1322	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
9	NO3	A	1323	-	X	-	X

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 3003 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 CHLOROPEROXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	299	Total	C	N	O	S	0	5	0
			2360	1493	391	470	6			

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mn	0	0
			1	1		

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



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

- Molecule 4 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	2	Total	C	N	O	0	0
			28	16	2	10		
5	A	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 6 is SUGAR (ALPHA-D-MANNOSE) (three-letter code: MAN) (formula: $C_6H_{12}O_6$).

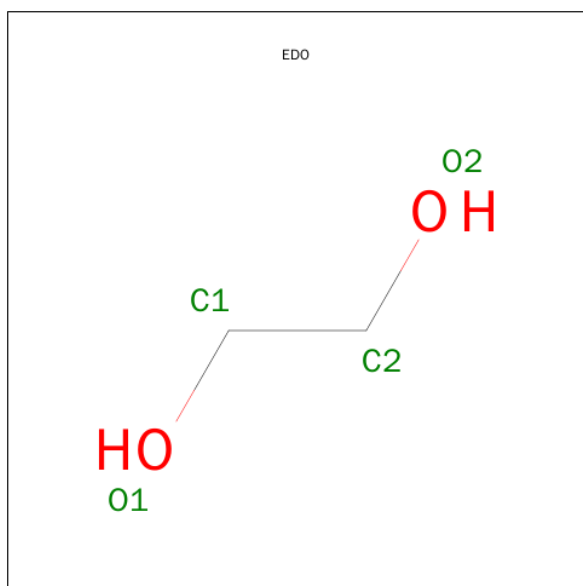


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			11	6	5		
6	A	1	Total	C	O	0	0
			11	6	5		
6	A	1	Total	C	O	0	0
			11	6	5		
6	A	1	Total	C	O	0	0
			11	6	5		
6	A	1	Total	C	O	0	0
			11	6	5		
6	A	1	Total	C	O	0	0
			11	6	5		
6	A	1	Total	C	O	0	0
			11	6	5		
6	A	1	Total	C	O	0	0
			11	6	5		

- Molecule 7 is a polymer of unknown type called SUGAR (2-MER).

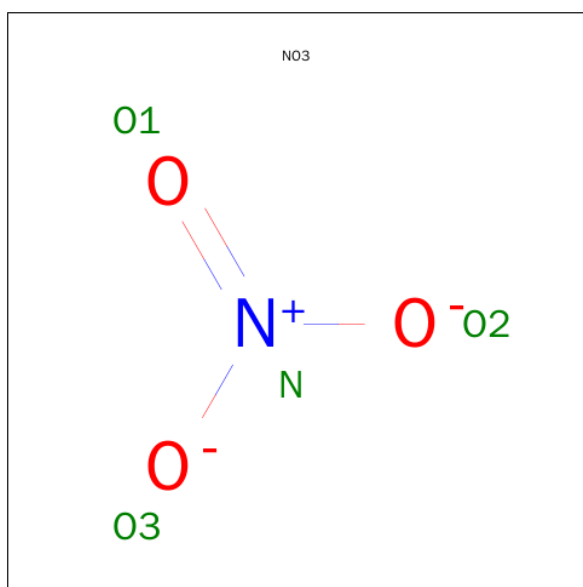
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	2	Total	C	O	0	0
			22	12	10		

- Molecule 8 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 9 is NITRATE ION (three-letter code: NO3) (formula: NO_3).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	N	O	0	0
			4	1	3		

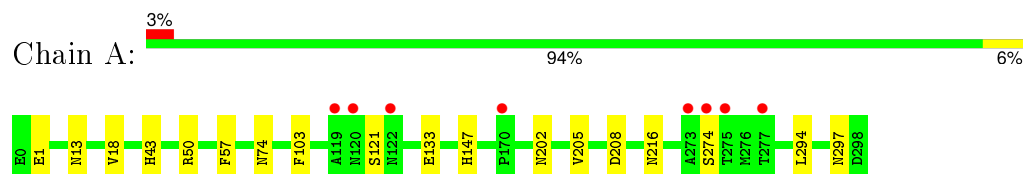
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	359	Total	O	0	0
			359	359		

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 ($\text{RSRZ} > 2$). 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: CHLOROPEROXIDASE



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	56.90Å 150.63Å 100.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.74 – 1.75 19.74 – 1.75	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.74-1.75) 99.4 (19.74-1.75)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.29 (at 1.76Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.173 , 0.207 0.171 , 0.204	Depositor DCC
R_{free} test set	2185 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	18.7	Xtriage
Anisotropy	0.667	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 52.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 43690 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3003	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.23% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, MN, NO3, EDO, HEM, PCA, MAN

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	0.61	0/2426	0.63	1/3328 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	208	ASP	CB-CG-OD1	5.07	122.86	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	2360	0	2160	11	1
2	A	1	0	0	0	0
3	A	43	0	30	4	0
4	A	14	0	13	0	0
5	A	56	0	50	0	0
6	A	132	0	120	0	0
7	A	22	0	19	0	0
8	A	12	0	18	1	0
9	A	4	0	0	0	0
10	A	359	0	0	4	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	3003	0	2410	14	2

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 3.

All (14) 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:1[A]:GLU:H	1:A:297:ASN:ND2	1.93	0.67
1:A:1[B]:GLU:H	1:A:297:ASN:ND2	1.95	0.64
1:A:18:VAL:O	1:A:43[A]:HIS:HE1	1.83	0.61
1:A:216:ASN:HB3	1:A:294:LEU:HD11	1.83	0.60
1:A:74:ASN:HD22	8:A:1322:EDO:H11	1.77	0.50
1:A:147:HIS:HA	1:A:205:VAL:O	2.14	0.48
3:A:1300:HEM:HBC2	3:A:1300:HEM:HMC1	1.99	0.45
3:A:1300:HEM:HBC2	3:A:1300:HEM:CMC	2.46	0.44
3:A:1300:HEM:HBB2	3:A:1300:HEM:HMB2	2.00	0.43
1:A:43[B]:HIS:HE1	10:A:2088:HOH:O	2.02	0.42
1:A:43[A]:HIS:CD2	10:A:2087:HOH:O	2.71	0.42
1:A:57:PHE:CE1	3:A:1300:HEM:HMC2	2.55	0.41
1:A:50:ARG:HB2	10:A:2105:HOH:O	2.21	0.41
1:A:13[B]:ASN:ND2	10:A:2036:HOH:O	2.54	0.40

All (2) 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)
10:A:2108:HOH:O	10:A:2159:HOH:O[4_555]	2.06	0.14
1:A:133:GLU:OE2	1:A:202[B]:ASN:OD1[8_555]	2.17	0.03

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	302/299 (101%)	295 (98%)	7 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	256/251 (102%)	253 (99%)	3 (1%)	78	62

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	103	PHE
1	A	121	SER
1	A	274	SER

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	55	ASN
1	A	59	ASN
1	A	122	ASN
1	A	284	ASN
1	A	297	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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$
1	PCA	A	0	1	7,8,9	1.45	1 (14%)	9,10,12	1.41	1 (11%)

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
1	PCA	A	0	1	-	0/0/11/13	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	0	PCA	CD-N	3.55	1.45	1.33

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	0	PCA	CA-N-CD	-2.67	104.85	113.81

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates ⓘ

6 carbohydrates 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	$\# Z > 2$
5	NAG	A	1302	1,5	14,14,15	0.63	0	15,19,21	0.85	1 (6%)
5	NAG	A	1303	5	14,14,15	0.43	0	15,19,21	1.20	2 (13%)
5	NAG	A	1304	1,5	14,14,15	0.67	0	15,19,21	0.82	0
5	NAG	A	1305	5	14,14,15	0.51	0	15,19,21	0.77	0
7	MAN	A	1317	1,7	11,11,12	0.50	0	14,15,17	0.82	0
7	MAN	A	1318	7	11,11,12	0.68	0	14,15,17	1.11	1 (7%)

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
5	NAG	A	1302	1,5	-	0/6/23/26	0/1/1/1
5	NAG	A	1303	5	-	0/6/23/26	0/1/1/1
5	NAG	A	1304	1,5	-	0/6/23/26	0/1/1/1
5	NAG	A	1305	5	-	0/6/23/26	0/1/1/1
7	MAN	A	1317	1,7	-	0/2/19/22	0/1/1/1
7	MAN	A	1318	7	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1303	NAG	C3-C4-C5	2.14	113.93	110.20
7	A	1318	MAN	C1-O5-C5	2.28	115.14	112.25
5	A	1302	NAG	C1-O5-C5	2.39	115.28	112.25
5	A	1303	NAG	C1-O5-C5	2.77	115.76	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.6 Ligand geometry

Of 19 ligands modelled in this entry, 1 is monoatomic - leaving 18 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
3	HEM	A	1300	1,2	30,50,50	2.18	10 (33%)	24,82,82	2.42	9 (37%)
4	NAG	A	1301	1	14,14,15	0.45	0	15,19,21	0.68	0
6	MAN	A	1306	1	11,11,12	0.51	0	14,15,17	0.97	1 (7%)
6	MAN	A	1307	1	11,11,12	0.69	0	14,15,17	0.97	1 (7%)
6	MAN	A	1308	1	11,11,12	0.54	0	14,15,17	0.75	0
6	MAN	A	1309	1	11,11,12	0.64	0	14,15,17	1.06	1 (7%)
6	MAN	A	1310	1	11,11,12	0.59	0	14,15,17	1.12	1 (7%)
6	MAN	A	1311	1	11,11,12	0.75	0	14,15,17	1.32	2 (14%)
6	MAN	A	1312	1	11,11,12	0.53	0	14,15,17	1.16	2 (14%)
6	MAN	A	1313	1	11,11,12	0.57	0	14,15,17	1.28	1 (7%)
6	MAN	A	1314	1	11,11,12	0.56	0	14,15,17	1.26	2 (14%)
6	MAN	A	1315	1	11,11,12	0.51	0	14,15,17	1.42	1 (7%)
6	MAN	A	1316	1	11,11,12	0.58	0	14,15,17	0.98	1 (7%)
6	MAN	A	1319	1	11,11,12	0.54	0	14,15,17	1.07	1 (7%)
8	EDO	A	1320	-	3,3,3	0.54	0	2,2,2	0.41	0
8	EDO	A	1321	-	3,3,3	0.55	0	2,2,2	0.10	0
8	EDO	A	1322	-	3,3,3	0.40	0	2,2,2	0.56	0
9	NO3	A	1323	-	3,3,3	3.18	3 (100%)	3,3,3	0.40	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
3	HEM	A	1300	1,2	-	0/10/54/54	0/0/8/8
4	NAG	A	1301	1	-	0/6/23/26	0/1/1/1
6	MAN	A	1306	1	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	MAN	A	1307	1	-	0/2/19/22	0/1/1/1
6	MAN	A	1308	1	-	0/2/19/22	0/1/1/1
6	MAN	A	1309	1	-	0/2/19/22	0/1/1/1
6	MAN	A	1310	1	-	0/2/19/22	0/1/1/1
6	MAN	A	1311	1	-	0/2/19/22	0/1/1/1
6	MAN	A	1312	1	-	0/2/19/22	0/1/1/1
6	MAN	A	1313	1	-	0/2/19/22	0/1/1/1
6	MAN	A	1314	1	-	0/2/19/22	0/1/1/1
6	MAN	A	1315	1	-	0/2/19/22	0/1/1/1
6	MAN	A	1316	1	-	0/2/19/22	0/1/1/1
6	MAN	A	1319	1	-	0/2/19/22	0/1/1/1
8	EDO	A	1320	-	-	0/1/1/1	0/0/0/0
8	EDO	A	1321	-	-	0/1/1/1	0/0/0/0
8	EDO	A	1322	-	-	0/1/1/1	0/0/0/0
9	NO3	A	1323	-	-	0/0/0/0	0/0/0/0

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1300	HEM	C3B-C4B	-6.20	1.46	1.51
3	A	1300	HEM	C3D-C4D	-5.47	1.44	1.51
3	A	1300	HEM	C2C-C1C	-3.51	1.45	1.52
3	A	1300	HEM	C2B-C1B	-2.18	1.44	1.51
3	A	1300	HEM	C2D-C1D	-2.08	1.45	1.51
3	A	1300	HEM	FE-ND	2.08	2.08	1.97
3	A	1300	HEM	C3C-CAC	2.35	1.55	1.51
3	A	1300	HEM	CAA-C2A	2.46	1.56	1.52
9	A	1323	NO3	O2-N	2.72	1.39	1.25
9	A	1323	NO3	O3-N	2.84	1.40	1.25
3	A	1300	HEM	C1C-NC	2.92	1.39	1.36
3	A	1300	HEM	FE-NC	3.53	2.09	1.95
9	A	1323	NO3	O1-N	3.84	1.40	1.24

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1300	HEM	CAA-C2A-C1A	-3.17	123.56	127.01
6	A	1311	MAN	O5-C1-C2	-2.80	106.32	110.86
3	A	1300	HEM	C3B-C4B-NB	-2.22	107.39	111.63
6	A	1319	MAN	C3-C4-C5	2.06	113.80	110.20
6	A	1316	MAN	C1-O5-C5	2.15	114.98	112.25
3	A	1300	HEM	C2D-C3D-C4D	2.18	105.20	101.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1307	MAN	C1-C2-C3	2.19	112.13	109.54
6	A	1314	MAN	C1-C2-C3	2.19	112.13	109.54
3	A	1300	HEM	C3B-C4B-CHC	2.23	126.31	123.16
6	A	1312	MAN	C1-O5-C5	2.44	115.35	112.25
6	A	1306	MAN	C1-O5-C5	2.46	115.37	112.25
6	A	1312	MAN	C1-C2-C3	2.64	112.67	109.54
6	A	1311	MAN	C1-C2-C3	2.91	112.98	109.54
6	A	1309	MAN	C1-O5-C5	3.02	116.09	112.25
3	A	1300	HEM	CMD-C2D-C3D	3.16	128.31	114.35
6	A	1310	MAN	C1-C2-C3	3.20	113.32	109.54
6	A	1314	MAN	C1-O5-C5	3.35	116.49	112.25
6	A	1313	MAN	C1-O5-C5	4.23	117.62	112.25
3	A	1300	HEM	CMC-C2C-C3C	4.36	127.43	116.53
3	A	1300	HEM	CAD-C3D-C4D	4.38	127.92	112.47
6	A	1315	MAN	C1-O5-C5	4.64	118.13	112.25
3	A	1300	HEM	CAD-C3D-C2D	4.75	126.88	113.22
3	A	1300	HEM	CMB-C2B-C3B	5.15	129.39	116.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1300	HEM	4	0
8	A	1322	EDO	1	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	298/299 (99%)	-0.03	8 (2%) 58 64	11, 17, 32, 44	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	275	THR	6.1
1	A	119	ALA	4.2
1	A	120	ASN	4.2
1	A	274	SER	4.0
1	A	122	ASN	3.7
1	A	273	ALA	2.9
1	A	277	THR	2.1
1	A	170	PRO	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
1	PCA	A	0	8/9	0.97	0.10	-	15,16,16,16	0

6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains.

The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
5	NAG	A	1303	14/15	0.90	0.12	1.02	18,23,32,34	0
5	NAG	A	1304	14/15	0.95	0.07	-0.74	15,18,19,25	0
5	NAG	A	1302	14/15	0.97	0.05	-1.10	17,19,22,22	0
5	NAG	A	1305	14/15	0.85	0.33	-	32,37,39,41	0
7	MAN	A	1318	11/12	0.85	0.28	-	41,43,44,47	0
7	MAN	A	1317	11/12	0.90	0.23	-	34,39,42,42	0

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
8	EDO	A	1322	4/4	0.91	0.19	16.65	38,38,38,38	0
9	NO3	A	1323	4/4	0.97	0.11	2.78	22,22,23,23	0
6	MAN	A	1311	11/12	0.78	0.16	1.79	42,44,46,47	0
2	MN	A	1299	1/1	0.98	0.12	1.44	18,18,18,18	0
8	EDO	A	1321	4/4	0.94	0.13	0.90	16,21,24,24	0
6	MAN	A	1312	11/12	0.89	0.10	-0.11	30,32,33,33	0
6	MAN	A	1307	11/12	0.95	0.10	-0.38	20,21,22,22	0
6	MAN	A	1308	11/12	0.97	0.07	-0.69	14,16,17,17	0
8	EDO	A	1320	4/4	0.97	0.07	-0.72	19,22,22,23	0
6	MAN	A	1313	11/12	0.88	0.11	-0.72	35,37,39,43	0
3	HEM	A	1300	43/43	0.98	0.07	-0.77	9,11,13,14	0
6	MAN	A	1306	11/12	0.94	0.10	-	26,31,33,34	0
4	NAG	A	1301	14/15	0.89	0.15	-	26,28,33,35	0
6	MAN	A	1319	11/12	0.70	0.26	-	37,43,45,47	0
6	MAN	A	1309	11/12	0.87	0.20	-	28,32,34,35	0
6	MAN	A	1310	11/12	0.74	0.28	-	45,49,51,51	0
6	MAN	A	1314	11/12	0.68	0.31	-	46,50,51,52	0
6	MAN	A	1316	11/12	0.80	0.33	-	41,46,48,49	0
6	MAN	A	1315	11/12	0.68	0.47	-	47,52,54,55	0

6.5 Other polymers

There are no such residues in this entry.