Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 02:20 PM GMT

PDB ID	:	3WXO
Title	:	Crystal structure of isoniazid bound KatG catalase peroxidase from Synechococcus elongatus PCC7942
Authors	:	Wada, K.; Tada, T.; Kamachi, S.
Deposited on	:	2014-08-04
Resolution	:	2.12 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

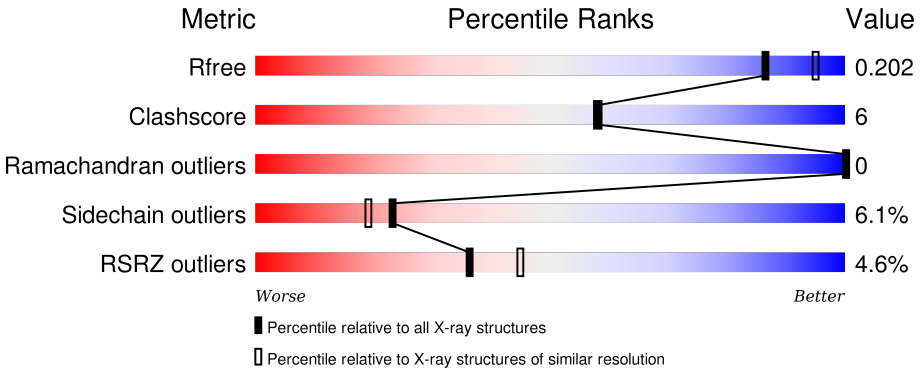
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 2.12 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	4587 (2.14-2.10)
Clashscore	102246	5132 (2.14-2.10)
Ramachandran outliers	100387	5080 (2.14-2.10)
Sidechain outliers	100360	5081 (2.14-2.10)
RSRZ outliers	91569	4597 (2.14-2.10)

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 <=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	710	5% 85% 12%

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
3	NIZ	A	802	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NIZ	A	803	-	-	-	X
3	NIZ	A	804	-	-	-	X

2 Entry composition

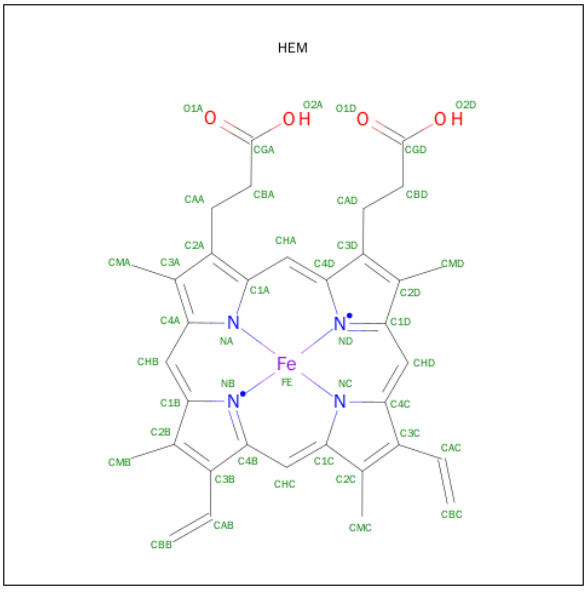
There are 5 unique types of molecules in this entry. The entry contains 6159 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Catalase-peroxidase.

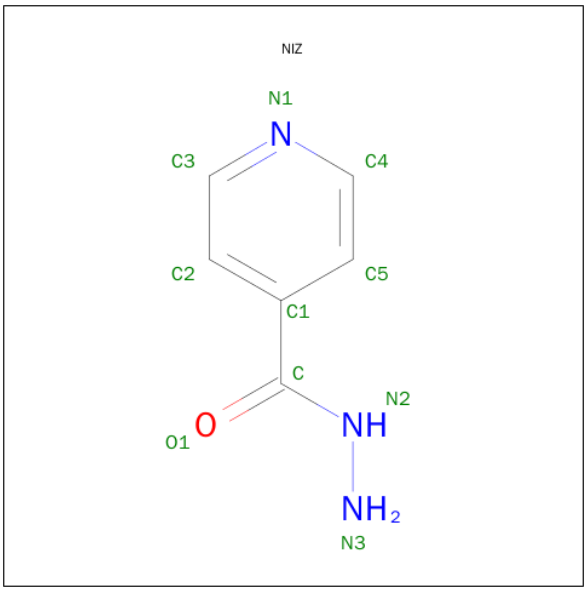
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	710	5595	3531	984	1061	19	0	2	0

- 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

- Molecule 3 is PYRIDINE-4-CARBOHYDRAZIDE (three-letter code: NIZ) (formula: $C_6H_7N_3O$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 10 6 3 1	0	0
3	A	1	Total C N O 10 6 3 1	0	0
3	A	1	Total C N O 10 6 3 1	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	4	Total Na 4 4	0	0

- Molecule 5 is water.

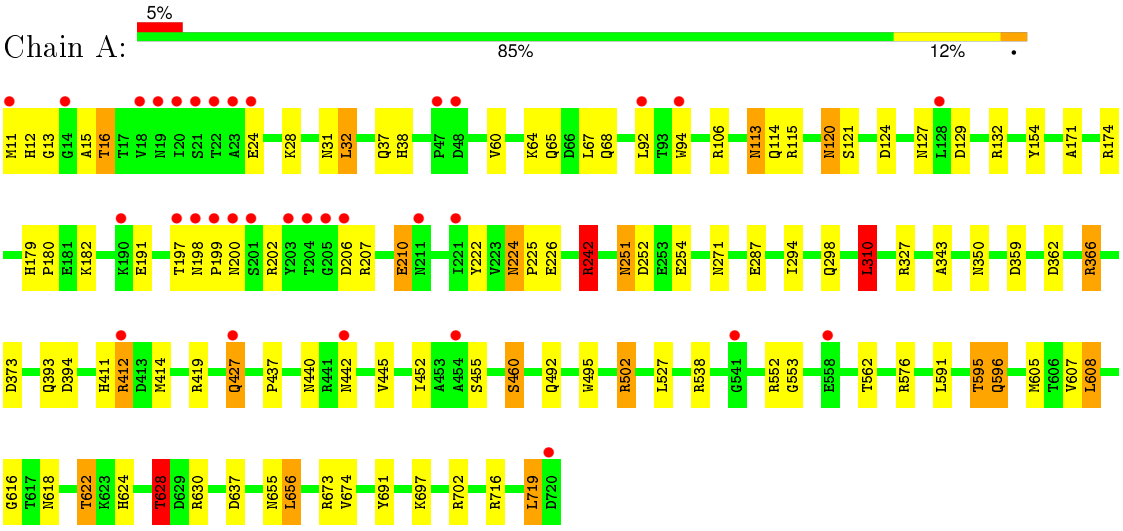
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	487	Total O 487 487	0	0

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 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: Catalase-peroxidase

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	108.65Å 108.65Å 202.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.09 – 2.12 35.09 – 2.12	Depositor EDS
% Data completeness (in resolution range)	94.8 (35.09-2.12) 94.8 (35.09-2.12)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.87 (at 2.12Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.158 , 0.197 0.168 , 0.202	Depositor DCC
R_{free} test set	3356 reflections (5.36%)	DCC
Wilson B-factor (Å^2)	32.4	Xtriage
Anisotropy	0.065	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.40 , 46.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Outliers	0 of 65957 reflections	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	6159	wwPDB-VP
Average B, all atoms (Å^2)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.17% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: NIZ, HEM, NA

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	1.01	3/5748 (0.1%)	1.13	28/7828 (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	3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	13	GLY	C-O	7.21	1.35	1.23
1	A	576	ARG	CD-NE	-5.89	1.36	1.46
1	A	287	GLU	CD-OE1	5.41	1.31	1.25

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	576	ARG	NE-CZ-NH2	-21.91	109.34	120.30
1	A	242	ARG	NE-CZ-NH2	-18.37	111.11	120.30
1	A	242	ARG	NE-CZ-NH1	17.86	129.23	120.30
1	A	576	ARG	NE-CZ-NH1	17.63	129.12	120.30
1	A	412[A]	ARG	NE-CZ-NH2	-11.88	114.36	120.30
1	A	412[B]	ARG	NE-CZ-NH2	-11.88	114.36	120.30
1	A	414	MET	CG-SD-CE	10.26	116.62	100.20
1	A	327	ARG	NE-CZ-NH2	-9.56	115.52	120.30
1	A	412[A]	ARG	NE-CZ-NH1	8.68	124.64	120.30
1	A	412[B]	ARG	NE-CZ-NH1	8.68	124.64	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	502	ARG	NE-CZ-NH2	-8.68	115.96	120.30
1	A	502	ARG	NE-CZ-NH1	8.68	124.64	120.30
1	A	327	ARG	NE-CZ-NH1	7.57	124.09	120.30
1	A	242	ARG	CD-NE-CZ	7.46	134.05	123.60
1	A	628	THR	CB-CA-C	-6.89	93.01	111.60
1	A	202	ARG	NE-CZ-NH2	-6.65	116.97	120.30
1	A	608	LEU	CB-CG-CD1	6.46	121.98	111.00
1	A	576	ARG	CD-NE-CZ	6.42	132.59	123.60
1	A	419	ARG	NE-CZ-NH1	6.41	123.50	120.30
1	A	394	ASP	CB-CG-OD2	-6.30	112.63	118.30
1	A	552	ARG	NE-CZ-NH2	-5.92	117.34	120.30
1	A	32	LEU	CB-CG-CD1	5.87	120.97	111.00
1	A	115	ARG	NE-CZ-NH2	5.76	123.18	120.30
1	A	538	ARG	NE-CZ-NH1	5.75	123.18	120.30
1	A	576	ARG	CG-CD-NE	-5.69	99.85	111.80
1	A	366	ARG	NE-CZ-NH2	-5.34	117.63	120.30
1	A	174	ARG	NE-CZ-NH2	5.30	122.95	120.30
1	A	310	LEU	CA-CB-CG	5.15	127.14	115.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	15	ALA	Peptide
1	A	210	GLU	Peptide
1	A	242	ARG	Sidechain

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	5595	0	5384	66	0
2	A	43	0	30	0	0
3	A	30	0	21	3	0
4	A	4	0	0	0	0
5	A	487	0	0	6	0
All	All	6159	0	5435	66	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 6.

All (66) 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:114:GLN:HE21	1:A:132:ARG:HH11	1.19	0.87
1:A:591:LEU:O	1:A:595:THR:HG23	1.80	0.81
1:A:427:GLN:HE21	1:A:427:GLN:H	1.36	0.73
1:A:106:ARG:HH21	1:A:596:GLN:HE21	1.40	0.69
1:A:38:HIS:H	1:A:179:HIS:HE1	1.44	0.65
1:A:412[B]:ARG:CG	1:A:412[B]:ARG:HH11	2.10	0.65
1:A:171:ALA:H	1:A:411:HIS:HE1	1.45	0.64
1:A:242:ARG:HD3	1:A:252:ASP:OD1	1.97	0.63
1:A:492:GLN:HG2	1:A:495:TRP:CZ3	2.34	0.62
1:A:251:ASN:C	1:A:251:ASN:HD22	2.01	0.61
1:A:94:TRP:HZ3	1:A:222:TYR:HH	1.49	0.61
1:A:224:ASN:HD22	1:A:226:GLU:H	1.48	0.61
1:A:114:GLN:HE21	1:A:132:ARG:NH1	1.96	0.58
1:A:595:THR:HG21	1:A:605:MET:SD	2.44	0.57
1:A:179:HIS:HD2	1:A:180:PRO:O	1.86	0.57
1:A:412[B]:ARG:HG2	1:A:412[B]:ARG:HH11	1.69	0.57
1:A:618:ASN:OD1	1:A:622:THR:HG22	2.06	0.56
1:A:224:ASN:ND2	1:A:226:GLU:H	2.04	0.55
1:A:702:ARG:NH2	5:A:1087:HOH:O	2.39	0.55
1:A:251:ASN:ND2	1:A:254:GLU:H	2.05	0.54
1:A:106:ARG:HH21	1:A:596:GLN:NE2	2.06	0.53
1:A:37:GLN:NE2	1:A:182:LYS:H	2.07	0.52
1:A:37:GLN:HE22	1:A:182:LYS:H	1.56	0.52
1:A:628:THR:HG21	5:A:994:HOH:O	2.09	0.52
1:A:38:HIS:H	1:A:179:HIS:CE1	2.26	0.52
1:A:171:ALA:H	1:A:411:HIS:CE1	2.25	0.51
1:A:452:ILE:O	1:A:455:SER:OG	2.22	0.51
1:A:224:ASN:HD22	1:A:224:ASN:C	2.15	0.50
1:A:460:SER:HB2	1:A:616:GLY:O	2.11	0.50
1:A:198:ASN:OD1	1:A:199:PRO:O	2.29	0.50
1:A:618:ASN:ND2	5:A:999:HOH:O	2.42	0.49
1:A:697:LYS:HE3	5:A:1157:HOH:O	2.12	0.49
1:A:591:LEU:O	1:A:595:THR:CG2	2.59	0.49
1:A:310:LEU:HD22	1:A:343:ALA:HB1	1.95	0.48
1:A:655:ASN:ND2	1:A:673:ARG:H	2.12	0.48
1:A:127:ASN:HA	1:A:129:ASP:OD1	2.14	0.48
1:A:199:PRO:O	1:A:200:ASN:HB2	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:294:ILE:HD12	3:A:802:NIZ:C5	2.45	0.47
1:A:113:ASN:HD22	1:A:114:GLN:N	2.11	0.47
1:A:628:THR:HG23	1:A:637:ASP:OD2	2.15	0.47
1:A:502:ARG:HD3	5:A:1151:HOH:O	2.14	0.47
1:A:622:THR:HG23	1:A:624:HIS:H	1.79	0.47
1:A:716:ARG:HB3	1:A:719:LEU:HD22	1.96	0.46
1:A:120:ASN:HD22	1:A:121:SER:N	2.13	0.46
1:A:92:LEU:HD12	1:A:114:GLN:HE22	1.81	0.46
1:A:294:ILE:HD12	3:A:802:NIZ:H5	1.97	0.46
1:A:607:VAL:CG1	1:A:691:TYR:CZ	3.00	0.45
1:A:114:GLN:NE2	1:A:132:ARG:HH11	2.01	0.44
1:A:65:GLN:HE21	1:A:65:GLN:HB2	1.55	0.44
1:A:492:GLN:HG2	1:A:495:TRP:CH2	2.52	0.44
1:A:60:VAL:HG12	1:A:64:LYS:HD2	2.00	0.44
1:A:366:ARG:NH1	5:A:1183:HOH:O	2.50	0.44
1:A:628:THR:CG2	1:A:637:ASP:OD2	2.66	0.43
1:A:628:THR:HG22	1:A:630:ARG:H	1.84	0.43
1:A:624:HIS:CE1	1:A:656:LEU:HD21	2.54	0.43
1:A:271:ASN:HD21	3:A:804:NIZ:H6	1.66	0.43
1:A:251:ASN:C	1:A:251:ASN:ND2	2.71	0.42
1:A:437:PRO:O	1:A:553:GLY:HA3	2.20	0.42
1:A:12:HIS:NE2	1:A:16:THR:HG21	2.36	0.41
1:A:628:THR:CG2	1:A:630:ARG:H	2.33	0.41
1:A:628:THR:HG22	1:A:630:ARG:HG2	2.02	0.40
1:A:445:VAL:HG13	1:A:527:LEU:HD21	2.03	0.40
1:A:591:LEU:HD22	1:A:674:VAL:HG13	2.02	0.40
1:A:359:ASP:HB3	1:A:362:ASP:O	2.22	0.40
1:A:224:ASN:HD22	1:A:225:PRO:N	2.19	0.40
1:A:440:ASN:ND2	1:A:442:ASN:H	2.19	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	710/710 (100%)	690 (97%)	20 (3%)	0	100 100

There are no Ramachandran outliers to report.

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	575/573 (100%)	540 (94%)	35 (6%)	23 19

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	MET
1	A	16	THR
1	A	24	GLU
1	A	28	LYS
1	A	31	ASN
1	A	32	LEU
1	A	67	LEU
1	A	68	GLN
1	A	113	ASN
1	A	120	ASN
1	A	124	ASP
1	A	154	TYR
1	A	191	GLU
1	A	197	THR
1	A	206	ASP
1	A	207	ARG
1	A	210	GLU
1	A	224	ASN
1	A	242	ARG
1	A	251	ASN
1	A	298	GLN
1	A	310	LEU
1	A	350	ASN

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Mol	Chain	Res	Type
1	A	373	ASP
1	A	393	GLN
1	A	427	GLN
1	A	460	SER
1	A	562	THR
1	A	595	THR
1	A	596	GLN
1	A	608	LEU
1	A	622	THR
1	A	628	THR
1	A	656	LEU
1	A	719	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	ASN
1	A	37	GLN
1	A	65	GLN
1	A	68	GLN
1	A	113	ASN
1	A	114	GLN
1	A	120	ASN
1	A	125	ASN
1	A	179	HIS
1	A	224	ASN
1	A	251	ASN
1	A	317	HIS
1	A	393	GLN
1	A	411	HIS
1	A	427	GLN
1	A	440	ASN
1	A	535	GLN
1	A	572	HIS
1	A	596	GLN
1	A	655	ASN
1	A	666	GLN

5.3.3 RNA

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 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	801	1,5	30,50,50	2.46	10 (33%)	24,82,82	2.35	9 (37%)
3	NIZ	A	802	-	10,10,10	1.58	1 (10%)	12,12,12	2.00	5 (41%)
3	NIZ	A	803	-	10,10,10	0.70	0	12,12,12	1.53	2 (16%)
3	NIZ	A	804	-	10,10,10	1.02	0	12,12,12	1.53	5 (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	801	1,5	-	0/10/54/54	0/0/8/8
3	NIZ	A	802	-	-	0/6/6/6	0/1/1/1
3	NIZ	A	803	-	-	0/6/6/6	0/1/1/1
3	NIZ	A	804	-	-	0/6/6/6	0/1/1/1

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	HEM	C2D-C3D	-6.64	1.34	1.54
2	A	801	HEM	C3B-C4B	-6.46	1.46	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	HEM	C2C-C1C	-4.23	1.44	1.52
2	A	801	HEM	C3D-C4D	-3.78	1.46	1.51
2	A	801	HEM	C2B-C1B	-3.35	1.40	1.51
2	A	801	HEM	C3B-CAB	-2.86	1.46	1.51
2	A	801	HEM	C1C-NC	-2.75	1.32	1.36
2	A	801	HEM	CMA-C3A	-2.49	1.46	1.51
2	A	801	HEM	CMD-C2D	-2.34	1.47	1.53
2	A	801	HEM	FE-NC	2.96	2.07	1.95
3	A	802	NIZ	C-N2	3.35	1.36	1.33

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	802	NIZ	C5-C4-N1	-3.92	116.81	123.64
3	A	802	NIZ	O1-C-N2	-2.68	119.31	122.46
3	A	804	NIZ	O1-C-N2	-2.52	119.50	122.46
2	A	801	HEM	CMA-C3A-C4A	-2.49	124.25	128.36
2	A	801	HEM	CAA-CBA-CGA	-2.35	108.44	112.75
2	A	801	HEM	C3B-C4B-NB	-2.34	107.16	111.63
3	A	804	NIZ	C5-C4-N1	-2.29	119.66	123.64
3	A	804	NIZ	C2-C3-N1	-2.04	120.08	123.64
3	A	803	NIZ	C3-N1-C4	2.04	121.75	116.83
2	A	801	HEM	C2C-C1C-CHC	2.29	127.17	123.68
3	A	804	NIZ	C3-N1-C4	2.29	122.37	116.83
3	A	802	NIZ	C4-C5-C1	2.42	121.58	119.06
3	A	804	NIZ	C1-C-N2	2.45	119.02	116.30
3	A	802	NIZ	C3-N1-C4	2.61	123.13	116.83
2	A	801	HEM	CMB-C2B-C3B	2.96	123.93	116.53
3	A	802	NIZ	C1-C-N2	3.20	119.85	116.30
2	A	801	HEM	CBD-CAD-C3D	3.31	123.19	113.55
3	A	803	NIZ	C1-C-N2	3.49	120.18	116.30
2	A	801	HEM	CAD-C3D-C4D	4.80	129.42	112.47
2	A	801	HEM	CAD-C3D-C2D	5.19	128.13	113.22
2	A	801	HEM	CMC-C2C-C3C	5.22	129.56	116.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	802	NIZ	2	0
3	A	804	NIZ	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	710/710 (100%)	-0.18	33 (4%) 36 45	23, 34, 60, 113	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	199	PRO	7.2
1	A	23	ALA	6.3
1	A	720	ASP	5.5
1	A	200	ASN	5.4
1	A	11	MET	5.2
1	A	204	THR	4.6
1	A	206	ASP	4.4
1	A	197	THR	4.1
1	A	20	ILE	3.8
1	A	19	ASN	3.7
1	A	211	ASN	3.3
1	A	198	ASN	3.0
1	A	14	GLY	2.9
1	A	92	LEU	2.8
1	A	22	THR	2.8
1	A	442	ASN	2.8
1	A	128	LEU	2.7
1	A	21	SER	2.7
1	A	18	VAL	2.6
1	A	24	GLU	2.6
1	A	205	GLY	2.6
1	A	190	LYS	2.6
1	A	221	ILE	2.4
1	A	48	ASP	2.3
1	A	412[A]	ARG	2.3
1	A	454	ALA	2.3
1	A	427	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	201	SER	2.2
1	A	47	PRO	2.2
1	A	94	TRP	2.1
1	A	203	TYR	2.1
1	A	558	GLU	2.1
1	A	541	GLY	2.1

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^{th} 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
3	NIZ	A	804	10/10	0.85	0.35	10.99	55,64,71,77	0
3	NIZ	A	802	10/10	0.94	0.16	2.85	37,47,48,49	0
3	NIZ	A	803	10/10	0.79	0.22	2.56	70,77,86,87	0
2	HEM	A	801	43/43	0.99	0.20	1.38	22,26,28,31	0
4	NA	A	806	1/1	0.99	0.05	-1.21	29,29,29,29	0
4	NA	A	805	1/1	0.99	0.07	-2.60	28,28,28,28	0
4	NA	A	808	1/1	0.85	0.11	-	34,34,34,34	0
4	NA	A	807	1/1	0.93	0.08	-	47,47,47,47	0

6.5 Other polymers (i)

There are no such residues in this entry.