



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 04:43 AM GMT

PDB ID : 2NW7
Title : Crystal Structure of Tryptophan 2,3-dioxygenase (TDO) from *Xanthomonas campestris* in complex with ferric heme. Northeast Structural Genomics Target XcR13
Authors : Forouhar, F.; Anderson, J.L.R.; Mowat, C.G.; Hussain, A.; Bruckmann, C.; Thackray, S.J.; Seetharaman, J.; Tucker, T.; Ho, C.K.; Ma, L.C.; Cunningham, K.; Janjua, H.; Zhao, L.; Xiao, R.; Liu, J.; Baran, M.C.; Acton, T.B.; Rost, B.; Montelione, G.T.; Chapman, S.K.; Tong, L.; Northeast Structural Genomics Consortium (NESG)
Deposited on : 2006-11-14
Resolution : 2.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

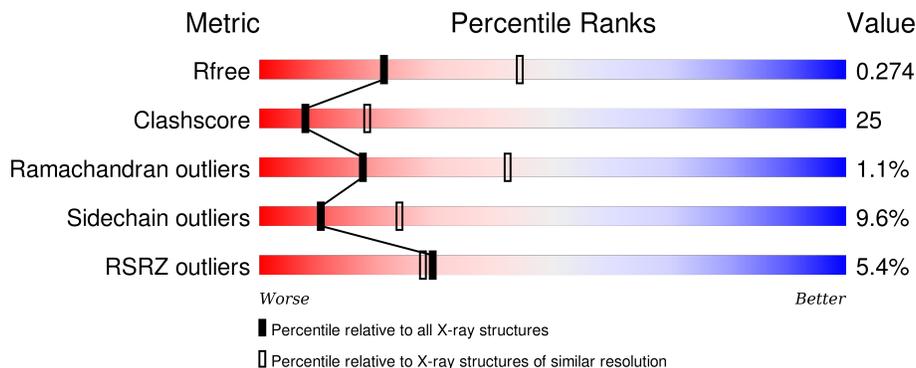
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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	306	
1	B	306	
1	C	306	
1	D	306	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 8957 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 Tryptophan 2,3-dioxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	259	2158	1387	380	384	7	0	0	0
1	B	259	2158	1387	380	384	7	0	0	0
1	C	259	2158	1387	380	384	7	0	0	0
1	D	260	2169	1393	384	385	7	0	0	0

There are 32 discrepancies between the modelled and reference sequences:

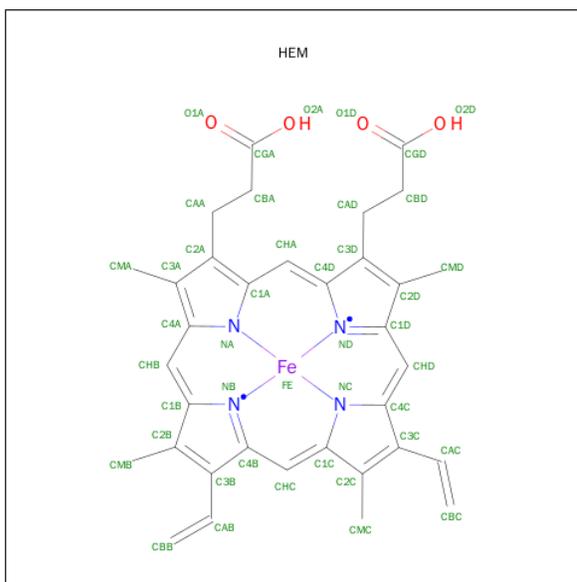
Chain	Residue	Modelled	Actual	Comment	Reference
A	299	LEU	-	CLONING ARTIFACT	UNP Q8PDA8
A	300	GLU	-	CLONING ARTIFACT	UNP Q8PDA8
A	301	HIS	-	CLONING ARTIFACT	UNP Q8PDA8
A	302	HIS	-	CLONING ARTIFACT	UNP Q8PDA8
A	303	HIS	-	CLONING ARTIFACT	UNP Q8PDA8
A	304	HIS	-	CLONING ARTIFACT	UNP Q8PDA8
A	305	HIS	-	CLONING ARTIFACT	UNP Q8PDA8
A	306	HIS	-	CLONING ARTIFACT	UNP Q8PDA8
B	299	LEU	-	CLONING ARTIFACT	UNP Q8PDA8
B	300	GLU	-	CLONING ARTIFACT	UNP Q8PDA8
B	301	HIS	-	CLONING ARTIFACT	UNP Q8PDA8
B	302	HIS	-	CLONING ARTIFACT	UNP Q8PDA8
B	303	HIS	-	CLONING ARTIFACT	UNP Q8PDA8
B	304	HIS	-	CLONING ARTIFACT	UNP Q8PDA8
B	305	HIS	-	CLONING ARTIFACT	UNP Q8PDA8
B	306	HIS	-	CLONING ARTIFACT	UNP Q8PDA8
C	299	LEU	-	CLONING ARTIFACT	UNP Q8PDA8
C	300	GLU	-	CLONING ARTIFACT	UNP Q8PDA8
C	301	HIS	-	CLONING ARTIFACT	UNP Q8PDA8
C	302	HIS	-	CLONING ARTIFACT	UNP Q8PDA8
C	303	HIS	-	CLONING ARTIFACT	UNP Q8PDA8

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Chain	Residue	Modelled	Actual	Comment	Reference
C	304	HIS	-	CLONING ARTIFACT	UNP Q8PDA8
C	305	HIS	-	CLONING ARTIFACT	UNP Q8PDA8
C	306	HIS	-	CLONING ARTIFACT	UNP Q8PDA8
D	299	LEU	-	CLONING ARTIFACT	UNP Q8PDA8
D	300	GLU	-	CLONING ARTIFACT	UNP Q8PDA8
D	301	HIS	-	CLONING ARTIFACT	UNP Q8PDA8
D	302	HIS	-	CLONING ARTIFACT	UNP Q8PDA8
D	303	HIS	-	CLONING ARTIFACT	UNP Q8PDA8
D	304	HIS	-	CLONING ARTIFACT	UNP Q8PDA8
D	305	HIS	-	CLONING ARTIFACT	UNP Q8PDA8
D	306	HIS	-	CLONING ARTIFACT	UNP Q8PDA8

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).

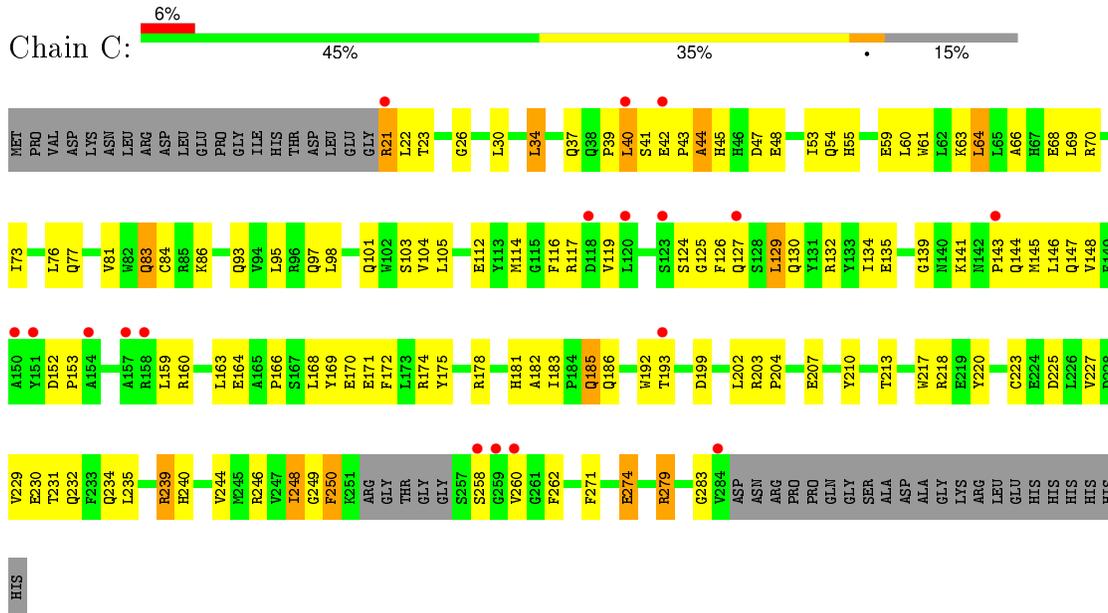


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	D	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

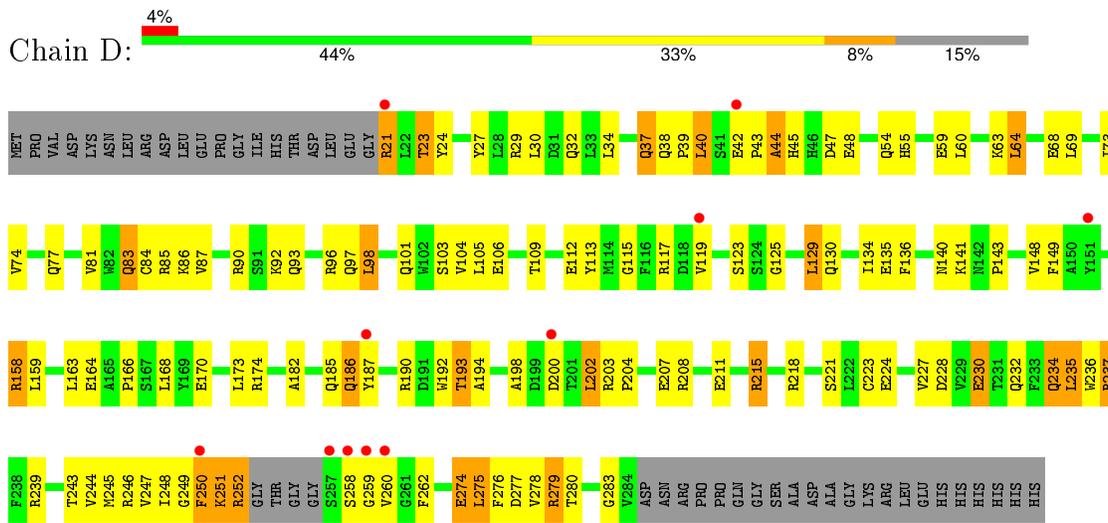
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	28	Total 28	O 28	0	0
3	B	44	Total 44	O 44	0	0
3	C	37	Total 37	O 37	0	0
3	D	33	Total 33	O 33	0	0

• Molecule 1: Tryptophan 2,3-dioxygenase



• Molecule 1: Tryptophan 2,3-dioxygenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	88.94Å 109.36Å 125.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.43 – 2.70 46.43 – 2.60	Depositor EDS
% Data completeness (in resolution range)	72.0 (46.43-2.70) 85.5 (46.43-2.60)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.12 (at 2.61Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.257 , 0.263 0.273 , 0.274	Depositor DCC
R_{free} test set	3034 reflections (11.37%)	DCC
Wilson B-factor (Å ²)	31.5	Xtrriage
Anisotropy	0.794	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 48.4	EDS
Estimated twinning fraction	No twinning to report.	Xtrriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtrriage
Outliers	5 of 37786 reflections (0.013%)	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	8957	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 77.38 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 8.6044e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: 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	0.44	0/2213	0.60	0/2999
1	B	0.45	0/2213	0.59	0/2999
1	C	0.43	0/2213	0.58	0/2999
1	D	0.46	0/2224	0.60	0/3013
All	All	0.44	0/8863	0.59	0/12010

There are no bond length outliers.

There are no bond angle outliers.

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	2158	0	2117	133	0
1	B	2158	0	2117	118	0
1	C	2158	0	2117	116	0
1	D	2169	0	2130	119	0
2	A	43	0	30	4	0
2	B	43	0	30	2	0
2	C	43	0	30	9	0
2	D	43	0	30	9	0
3	A	28	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	44	0	0	5	0
3	C	37	0	0	2	0
3	D	33	0	0	2	0
All	All	8957	0	8601	436	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 25.

The worst 5 of 436 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:D:105:LEU:HD23	1:D:243:THR:HG21	1.45	0.98
1:A:143:PRO:HG3	1:A:193:THR:HG22	1.43	0.97
1:C:250:PHE:HA	1:C:260:VAL:HG11	1.47	0.96
2:D:401:HEM:HBC2	2:D:401:HEM:HHD	1.45	0.96
1:C:83:GLN:H	1:C:83:GLN:HE21	0.99	0.96

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	255/306 (83%)	241 (94%)	12 (5%)	2 (1%)	24	51
1	B	255/306 (83%)	242 (95%)	12 (5%)	1 (0%)	39	69
1	C	255/306 (83%)	237 (93%)	14 (6%)	4 (2%)	12	30
1	D	256/306 (84%)	233 (91%)	19 (7%)	4 (2%)	12	30
All	All	1021/1224 (83%)	953 (93%)	57 (6%)	11 (1%)	17	42

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	182	ALA
1	D	251	LYS
1	C	144	GLN
1	C	248	ILE
1	B	182	ALA

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	229/267 (86%)	208 (91%)	21 (9%)	11	25
1	B	229/267 (86%)	206 (90%)	23 (10%)	9	22
1	C	229/267 (86%)	212 (93%)	17 (7%)	17	39
1	D	230/267 (86%)	203 (88%)	27 (12%)	7	15
All	All	917/1068 (86%)	829 (90%)	88 (10%)	10	24

5 of 88 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	272	PHE
1	C	70	ARG
1	D	235	LEU
1	B	274	GLU
1	C	21	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	234	GLN
1	C	45	HIS
1	D	185	GLN
1	B	240	HIS
1	C	32	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](#)

4 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	HEM	A	401	1	30,50,50	2.43	13 (43%)	24,82,82	2.70	9 (37%)
2	HEM	B	401	1	30,50,50	2.41	13 (43%)	24,82,82	2.69	9 (37%)
2	HEM	C	401	1	30,50,50	2.37	11 (36%)	24,82,82	2.69	9 (37%)
2	HEM	D	401	1	30,50,50	2.38	12 (40%)	24,82,82	2.70	9 (37%)

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	-	0/10/54/54	0/0/8/8
2	HEM	B	401	1	-	0/10/54/54	0/0/8/8
2	HEM	C	401	1	-	0/10/54/54	0/0/8/8
2	HEM	D	401	1	-	0/10/54/54	0/0/8/8

The worst 5 of 49 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	HEM	C2D-C3D	-5.95	1.36	1.54
2	D	401	HEM	C2D-C3D	-5.95	1.36	1.54
2	A	401	HEM	C2D-C3D	-5.94	1.36	1.54
2	C	401	HEM	C2D-C3D	-5.92	1.36	1.54
2	C	401	HEM	C3D-C4D	-5.30	1.44	1.51

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	HEM	CAD-CBD-CGD	2.35	122.58	113.02
2	B	401	HEM	CAD-CBD-CGD	2.35	122.59	113.02
2	A	401	HEM	CAD-CBD-CGD	2.35	122.59	113.02
2	D	401	HEM	CAD-CBD-CGD	2.36	122.63	113.02
2	B	401	HEM	CMD-C2D-C3D	2.69	126.23	114.35

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	HEM	4	0
2	B	401	HEM	2	0
2	C	401	HEM	9	0
2	D	401	HEM	9	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	259/306 (84%)	0.35	17 (6%) 22 20	18, 35, 61, 78	0
1	B	259/306 (84%)	0.07	10 (3%) 43 43	16, 30, 53, 63	0
1	C	259/306 (84%)	0.37	18 (6%) 20 18	16, 36, 62, 71	0
1	D	260/306 (84%)	0.15	11 (4%) 40 39	18, 29, 52, 63	0
All	All	1037/1224 (84%)	0.23	56 (5%) 29 28	16, 32, 58, 78	0

The worst 5 of 56 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	146	LEU	5.6
1	A	127	GLN	4.7
1	D	257	SER	4.7
1	C	42	GLU	4.5
1	D	119	VAL	4.3

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, 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(\AA^2)	Q<0.9
2	HEM	C	401	43/43	0.86	0.27	0.89	45,52,61,64	0
2	HEM	D	401	43/43	0.90	0.25	0.75	30,39,50,56	0
2	HEM	A	401	43/43	0.90	0.22	0.25	32,42,48,52	0
2	HEM	B	401	43/43	0.90	0.21	0.19	25,36,41,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.