



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 06:25 PM GMT

PDB ID : 2NZL  
Title : Crystal structure of human hydroxyacid oxidase 1  
Authors : Ugochukwu, E.; Kavanagh, K.; Pilka, E.; Berridge, G.; Debreczeni, J.E.; Papa-grigoriou, E.; Turnbull, A.; Niesen, F.; Gileadi, O.; Von Delft, F.; Sundstrom, M.; Arrowsmith, C.H.; Weigelt, J.; Edwards, A.; Oppermann, U.; Structural Genomics Consortium (SGC)  
Deposited on : 2006-11-24  
Resolution : 1.35 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026982  
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) : rb-20026982

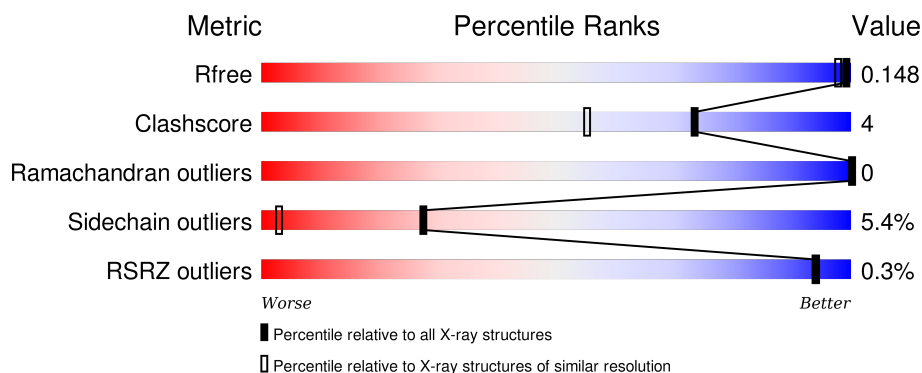
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*


The reported resolution of this entry is 1.35 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	2199 (1.40-1.32)
Clashscore	102246	2337 (1.40-1.32)
Ramachandran outliers	100387	2280 (1.40-1.32)
Sidechain outliers	100360	2279 (1.40-1.32)
RSRZ outliers	91569	2199 (1.40-1.32)

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  $\geq 3$ , 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	392	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2824 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 Hydroxyacid oxidase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	339	2632	1691	448	480	13	0	12	0

There are 22 discrepancies between the modelled and reference sequences:

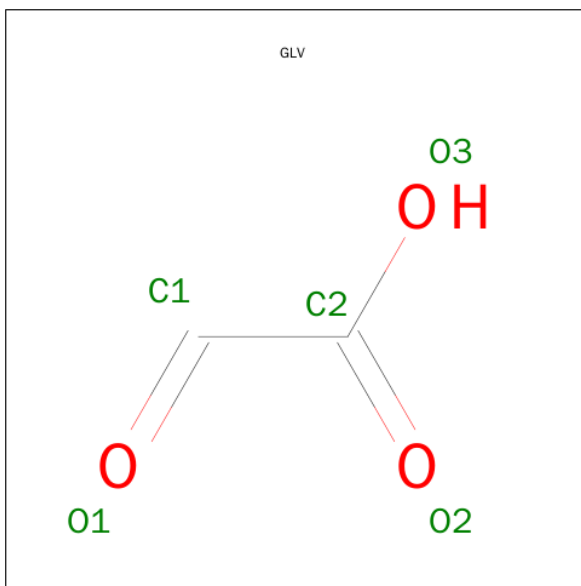
Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	CLONING ARTIFACT	UNP Q9UJM8
A	-20	HIS	-	EXPRESSION TAG	UNP Q9UJM8
A	-19	HIS	-	EXPRESSION TAG	UNP Q9UJM8
A	-18	HIS	-	EXPRESSION TAG	UNP Q9UJM8
A	-17	HIS	-	EXPRESSION TAG	UNP Q9UJM8
A	-16	HIS	-	EXPRESSION TAG	UNP Q9UJM8
A	-15	HIS	-	EXPRESSION TAG	UNP Q9UJM8
A	-14	SER	-	CLONING ARTIFACT	UNP Q9UJM8
A	-13	SER	-	CLONING ARTIFACT	UNP Q9UJM8
A	-12	GLY	-	CLONING ARTIFACT	UNP Q9UJM8
A	-11	VAL	-	CLONING ARTIFACT	UNP Q9UJM8
A	-10	ASP	-	CLONING ARTIFACT	UNP Q9UJM8
A	-9	LEU	-	CLONING ARTIFACT	UNP Q9UJM8
A	-8	GLY	-	CLONING ARTIFACT	UNP Q9UJM8
A	-7	THR	-	CLONING ARTIFACT	UNP Q9UJM8
A	-6	GLU	-	CLONING ARTIFACT	UNP Q9UJM8
A	-5	ASN	-	CLONING ARTIFACT	UNP Q9UJM8
A	-4	LEU	-	CLONING ARTIFACT	UNP Q9UJM8
A	-3	TYR	-	CLONING ARTIFACT	UNP Q9UJM8
A	-2	PHE	-	CLONING ARTIFACT	UNP Q9UJM8
A	-1	GLN	-	CLONING ARTIFACT	UNP Q9UJM8
A	0	SER	-	CLONING ARTIFACT	UNP Q9UJM8

- Molecule 2 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C<sub>17</sub>H<sub>21</sub>N<sub>4</sub>O<sub>9</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

- Molecule 3 is GLYOXYLIC ACID (three-letter code: GLV) (formula:  $C_2H_2O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			5	2	3		

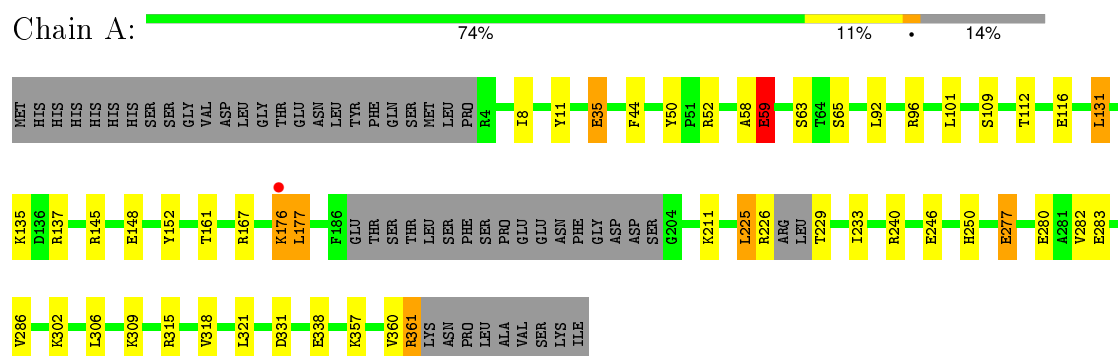
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	156	Total 156	O 156	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: Hydroxyacid oxidase 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 4	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	97.29Å 97.29Å 79.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	26.06 – 1.35 26.06 – 1.35	Depositor EDS
% Data completeness (in resolution range)	(Not available) (26.06-1.35) 98.2 (26.06-1.35)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.04 (at 1.35Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, $R_{free}$	0.126 , 0.155 0.132 , 0.148	Depositor DCC
$R_{free}$ test set	4008 reflections (5.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	12.5	Xtriage
Anisotropy	0.425	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 45.2	EDS
Estimated twinning fraction	0.410 for -k,-h,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.38$ , $\langle L^2 \rangle = 0.20$	Xtriage
Outliers	0 of 81283 reflections	Xtriage
$F_o, F_c$ correlation	0.98	EDS
Total number of atoms	2824	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.00% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FMN, GLV

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	3.86	8/2712 (0.3%)	2.13	34/3674 (0.9%)

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	1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	35[A]	GLU	CD-OE1	70.83	2.03	1.25
1	A	35[B]	GLU	CD-OE1	70.83	2.03	1.25
1	A	59[A]	GLU	CD-OE2	70.62	2.03	1.25
1	A	59[B]	GLU	CD-OE2	70.62	2.03	1.25
1	A	59[A]	GLU	CD-OE1	70.05	2.02	1.25
1	A	59[B]	GLU	CD-OE1	70.05	2.02	1.25
1	A	35[A]	GLU	CD-OE2	69.41	2.02	1.25
1	A	35[B]	GLU	CD-OE2	69.41	2.02	1.25

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	59[A]	GLU	OE1-CD-OE2	-48.46	65.15	123.30
1	A	59[B]	GLU	OE1-CD-OE2	-48.46	65.15	123.30
1	A	35[A]	GLU	OE1-CD-OE2	-47.52	66.27	123.30
1	A	35[B]	GLU	OE1-CD-OE2	-47.52	66.27	123.30
1	A	59[A]	GLU	CG-CD-OE1	-9.82	98.66	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	59[B]	GLU	CG-CD-OE1	-9.82	98.66	118.30
1	A	35[A]	GLU	CG-CD-OE1	-9.78	98.74	118.30
1	A	35[B]	GLU	CG-CD-OE1	-9.78	98.74	118.30
1	A	35[A]	GLU	CG-CD-OE2	-9.55	99.21	118.30
1	A	35[B]	GLU	CG-CD-OE2	-9.55	99.21	118.30
1	A	59[A]	GLU	CG-CD-OE2	-9.50	99.30	118.30
1	A	59[B]	GLU	CG-CD-OE2	-9.50	99.30	118.30
1	A	361	ARG	NE-CZ-NH1	9.42	125.01	120.30
1	A	167	ARG	NE-CZ-NH2	-8.83	115.89	120.30
1	A	137	ARG	NE-CZ-NH1	8.67	124.63	120.30
1	A	152	TYR	CB-CG-CD1	8.19	125.91	121.00
1	A	96	ARG	NE-CZ-NH1	-7.98	116.31	120.30
1	A	361	ARG	NE-CZ-NH2	-7.63	116.48	120.30
1	A	361	ARG	CD-NE-CZ	7.55	134.17	123.60
1	A	167	ARG	CG-CD-NE	6.75	125.98	111.80
1	A	240	ARG	NE-CZ-NH1	-6.61	116.99	120.30
1	A	137	ARG	NE-CZ-NH2	-6.57	117.02	120.30
1	A	116	GLU	C-N-CA	6.18	137.16	121.70
1	A	52	ARG	CD-NE-CZ	6.14	132.19	123.60
1	A	96	ARG	CD-NE-CZ	6.09	132.13	123.60
1	A	131	LEU	CA-CB-CG	5.70	128.41	115.30
1	A	283	GLU	OE1-CD-OE2	-5.70	116.46	123.30
1	A	96	ARG	NE-CZ-NH2	5.39	123.00	120.30
1	A	44	PHE	CB-CG-CD2	-5.39	117.03	120.80
1	A	277	GLU	OE1-CD-OE2	-5.30	116.94	123.30
1	A	225	LEU	CA-CB-CG	5.21	127.27	115.30
1	A	338	GLU	OE1-CD-OE2	5.07	129.39	123.30
1	A	109	SER	C-N-CA	5.03	134.28	121.70
1	A	240	ARG	NE-CZ-NH2	5.01	122.80	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	59[A]	GLU	Sidechain

## 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	2632	0	2676	22	0
2	A	31	0	19	0	0
3	A	5	0	1	0	0
4	A	156	0	0	0	0
All	All	2824	0	2696	22	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 4.

All (22) 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:315:ARG:O	1:A:318:VAL:HG22	1.92	0.69
1:A:135:LYS:HE3	1:A:211:LYS:O	2.03	0.59
1:A:145:ARG:HD3	1:A:148:GLU:OE2	2.03	0.59
1:A:302:LYS:O	1:A:306:LEU:HD23	2.03	0.59
1:A:229:THR:CG2	1:A:233[A]:ILE:HD11	2.36	0.56
1:A:357:LYS:HD2	1:A:357:LYS:O	2.11	0.51
1:A:11:TYR:OH	1:A:331:ASP:OD1	2.30	0.47
1:A:306:LEU:CD2	1:A:360:VAL:HG21	2.46	0.46
1:A:50:TYR:CE2	1:A:361:ARG:HB2	2.50	0.46
1:A:65:SER:O	1:A:309:LYS:HE3	2.16	0.46
1:A:246:GLU:O	1:A:250:HIS:HD2	2.00	0.45
1:A:176[B]:LYS:HG2	1:A:177:LEU:O	2.17	0.45
1:A:306:LEU:HD22	1:A:360:VAL:HG21	1.99	0.44
1:A:246:GLU:OE1	1:A:250:HIS:NE2	2.50	0.44
1:A:176[B]:LYS:NZ	1:A:177:LEU:O	2.50	0.43
1:A:161:THR:O	1:A:161:THR:HG22	2.19	0.42
1:A:282:VAL:CG1	1:A:286:VAL:HG22	2.50	0.41

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	345/392 (88%)	337 (98%)	8 (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	273/328 (83%)	257 (94%)	16 (6%)	24	2

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ILE
1	A	59[A]	GLU
1	A	59[B]	GLU
1	A	63	SER
1	A	92	LEU
1	A	101	LEU
1	A	112	THR
1	A	131	LEU
1	A	176[A]	LYS
1	A	176[B]	LYS
1	A	177	LEU
1	A	225	LEU
1	A	226	ARG
1	A	277	GLU
1	A	280	GLU
1	A	321	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 molecules 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 ⓘ

2 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	FMN	A	501	-	32,33,33	1.32	5 (15%)	34,50,50	2.44	8 (23%)
3	GLV	A	601	-	1,4,4	0.84	0	0,4,4	0.00	-

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	FMN	A	501	-	-	0/18/18/18	0/3/3/3
3	GLV	A	601	-	-	0/0/2/2	0/0/0/0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	FMN	C9A-C5A	-2.92	1.36	1.42
2	A	501	FMN	C8-C7	-2.66	1.33	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	FMN	C2-N1	-2.37	1.33	1.38
2	A	501	FMN	C4A-N5	2.10	1.36	1.33
2	A	501	FMN	O2'-C2'	2.24	1.48	1.43

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	FMN	N3-C2-N1	-4.71	119.76	127.69
2	A	501	FMN	C4A-C4-N3	-4.52	117.61	123.52
2	A	501	FMN	C9-C8-C7	-2.75	114.59	119.97
2	A	501	FMN	O5'-P-O1P	-2.73	100.23	107.08
2	A	501	FMN	C1'-N10-C9A	2.33	121.53	118.83
2	A	501	FMN	C8-C9-C9A	2.37	127.51	119.18
2	A	501	FMN	C5A-C9A-N10	4.36	120.85	117.58
2	A	501	FMN	C4-N3-C2	9.18	122.82	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	339/392 (86%)	-0.33	1 (0%) 94 94	9, 16, 27, 36	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	176[A]	LYS	2.3

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	FMN	A	501	31/31	0.98	0.07	0.63	9,15,19,25	0
3	GLV	A	601	5/5	0.96	0.07	0.38	19,19,25,29	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.