



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 07:11 AM GMT

PDB ID : 2ZX9  
Title : alpha-L-fucosidase complexed with inhibitor, B4  
Authors : Wu, H.-J.; Ko, T.-P.; Ho, C.-W.; Lin, C.-H.; Wang, A.H.-J.  
Deposited on : 2008-12-22  
Resolution : 2.62 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](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 (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

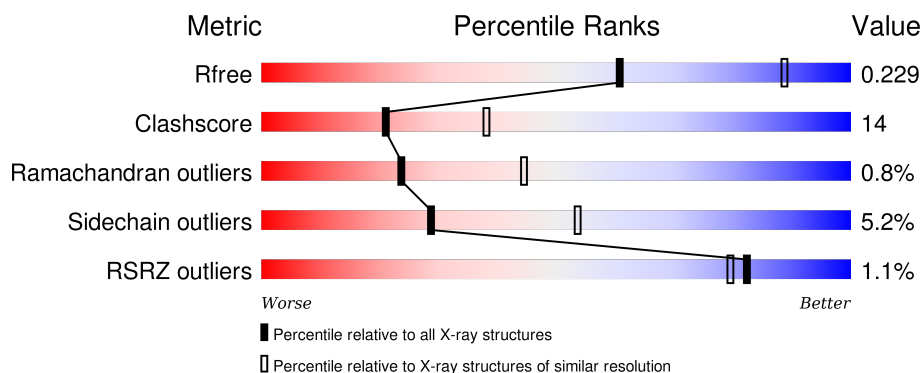
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.62 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	2700 (2.64-2.60)
Clashscore	102246	3065 (2.64-2.60)
Ramachandran outliers	100387	3015 (2.64-2.60)
Sidechain outliers	100360	3015 (2.64-2.60)
RSRZ outliers	91569	2706 (2.64-2.60)

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	455	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 25%, green 70%, grey 4%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> <span>%</span> <span>70%</span> <span>25%</span> <span>• •</span> </div> </div>
1	B	455	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 28%, green 66%, grey 4%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> <span>%</span> <span>66%</span> <span>28%</span> <span>• •</span> </div> </div>

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
2	ZX9	A	901	-	-	X	-

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7739 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.

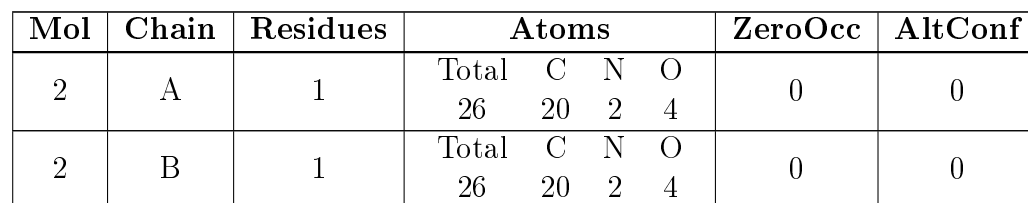
- Molecule 1 is a protein called Alpha-L-fucosidase, putative.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	442	Total	C	N	O	S	0	0	0
			3648	2377	600	663	8			
1	B	442	Total	C	N	O	S	0	0	0
			3648	2377	600	663	8			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	450	HIS	-	EXPRESSION TAG	UNP Q9WYE2
A	451	HIS	-	EXPRESSION TAG	UNP Q9WYE2
A	452	HIS	-	EXPRESSION TAG	UNP Q9WYE2
A	453	HIS	-	EXPRESSION TAG	UNP Q9WYE2
A	454	HIS	-	EXPRESSION TAG	UNP Q9WYE2
A	455	HIS	-	EXPRESSION TAG	UNP Q9WYE2
B	450	HIS	-	EXPRESSION TAG	UNP Q9WYE2
B	451	HIS	-	EXPRESSION TAG	UNP Q9WYE2
B	452	HIS	-	EXPRESSION TAG	UNP Q9WYE2
B	453	HIS	-	EXPRESSION TAG	UNP Q9WYE2
B	454	HIS	-	EXPRESSION TAG	UNP Q9WYE2
B	455	HIS	-	EXPRESSION TAG	UNP Q9WYE2

- Molecule 2 is (2S)-2-CYCLOPENTYL-2-PHENYL-N-{[(2R,3R,4R,5R,6S)-3,4,5-TRIHYDROXY-6-METHYLPYPERIDIN-2-YL]METHYL}ETHANAMIDE (three-letter code: ZX9) (formula: C<sub>20</sub>H<sub>30</sub>N<sub>2</sub>O<sub>4</sub>).

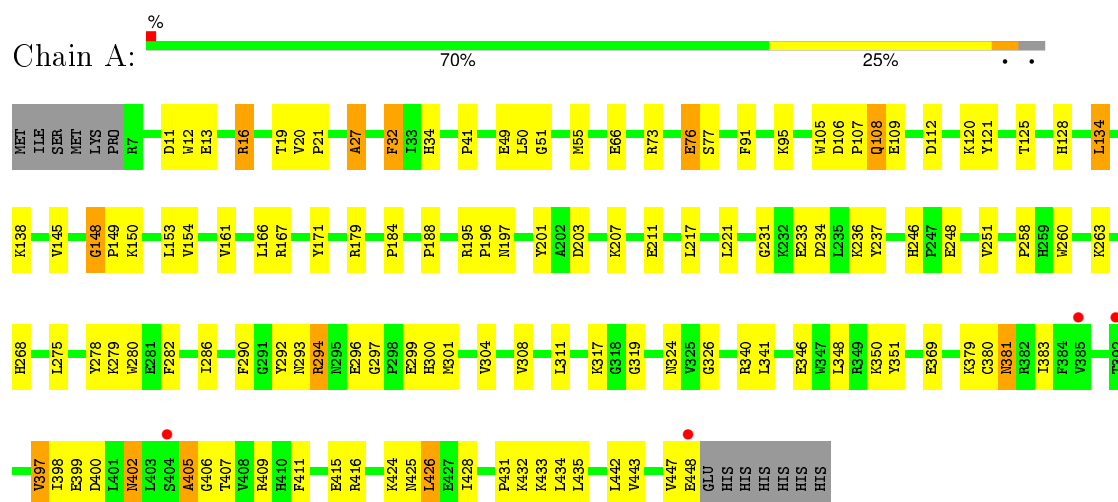


- | Mol | Chain | Residues | Atoms              | ZeroOcc | AltConf |
|-----|-------|----------|--------------------|---------|---------|
| 3   | A     | 191      | Total O<br>191 191 | 0       | 0       |
| 3   | B     | 200      | Total O<br>200 200 | 0       | 0       |

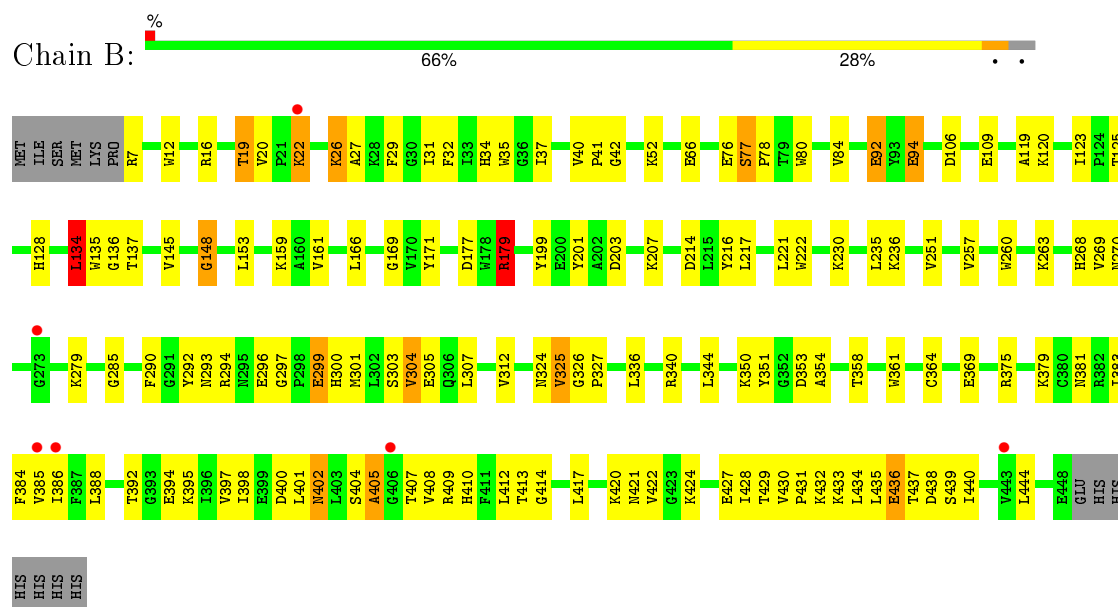
### 3 Residue-property plots

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: Alpha-L-fucosidase, putative



- Molecule 1: Alpha-L-fucosidase, putative



## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	180.81Å 180.81Å 169.72Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	25.45 – 2.62 25.45 – 2.62	Depositor EDS
% Data completeness (in resolution range)	95.3 (25.45-2.62) 95.2 (25.45-2.62)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.80 (at 2.60Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.162 , 0.227 0.162 , 0.229	Depositor DCC
$R_{free}$ test set	1516 reflections (4.96%)	DCC
Wilson B-factor (Å <sup>2</sup> )	37.2	Xtriage
Anisotropy	0.059	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 50.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 30644 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7739	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.40% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZX9

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	1/3768 (0.0%)	0.97	5/5120 (0.1%)
1	B	0.99	1/3768 (0.0%)	0.98	7/5120 (0.1%)
All	All	1.00	2/7536 (0.0%)	0.98	12/10240 (0.1%)

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	2
1	B	0	1
All	All	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	94	GLU	CG-CD	5.40	1.60	1.51
1	A	76	GLU	CG-CD	5.01	1.59	1.51

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	179	ARG	NE-CZ-NH1	-8.70	115.95	120.30
1	B	179	ARG	NE-CZ-NH2	7.28	123.94	120.30
1	A	179	ARG	NE-CZ-NH2	6.03	123.32	120.30
1	B	179	ARG	CG-CD-NE	5.74	123.85	111.80
1	A	27	ALA	N-CA-C	-5.64	95.76	111.00

There are no chirality outliers.



All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	201	TYR	Sidechain
1	A	237	TYR	Sidechain
1	B	201	TYR	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	3648	0	3512	105	0
1	B	3648	0	3512	101	0
2	A	26	0	30	10	0
2	B	26	0	30	5	0
3	A	191	0	0	4	0
3	B	200	0	0	1	1
All	All	7739	0	7084	207	1

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 14.

The worst 5 of 207 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)
2:B:902:ZX9:HAJ	2:B:902:ZX9:HAN	1.23	1.09
2:A:901:ZX9:HAJ	2:A:901:ZX9:HAN	1.36	1.03
1:A:297:GLY:H	1:A:300:HIS:HD2	1.05	0.98
1:B:350:LYS:NZ	1:B:439:SER:HB2	1.87	0.90
2:B:902:ZX9:HAJ	2:B:902:ZX9:CAN	2.03	0.89

All (1) 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)
3:B:602:HOH:O	3:B:602:HOH:O[3_555]	1.63	0.57

## 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	440/455 (97%)	411 (93%)	25 (6%)	4 (1%)	21	41
1	B	440/455 (97%)	405 (92%)	32 (7%)	3 (1%)	26	49
All	All	880/910 (97%)	816 (93%)	57 (6%)	7 (1%)	24	44

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	405	ALA
1	B	405	ALA
1	B	148	GLY
1	A	406	GLY
1	A	258	PRO

### 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	382/395 (97%)	364 (95%)	18 (5%)	32	59
1	B	382/395 (97%)	360 (94%)	22 (6%)	25	47
All	All	764/790 (97%)	724 (95%)	40 (5%)	29	53

5 of 40 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	19	THR

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Mol	Chain	Res	Type
1	B	37	ILE
1	B	402	ASN
1	B	26	LYS
1	B	66	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	381	ASN
1	B	300	HIS
1	A	402	ASN
1	A	108	GLN
1	A	425	ASN

### 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	ZX9	A	901	-	27,28,28	0.39	0	26,39,39	1.33	4 (15%)
2	ZX9	B	902	-	27,28,28	0.37	0	26,39,39	1.37	4 (15%)

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	ZX9	A	901	-	-	0/16/44/44	0/3/3/3
2	ZX9	B	902	-	-	0/16/44/44	0/3/3/3

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	901	ZX9	CAK-CAM-CAX	-3.49	96.26	105.10
2	B	902	ZX9	CAY-CAO-NAP	-3.47	103.19	112.84
2	B	902	ZX9	CAL-CAN-CAX	-3.08	97.31	105.10
2	A	901	ZX9	CAY-CAO-NAP	-2.59	105.62	112.84
2	A	901	ZX9	CAI-CAS-CAZ	-2.53	116.43	120.84

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	901	ZX9	10	0
2	B	902	ZX9	5	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, 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	442/455 (97%)	-0.57	4 (0%) 85 83	18, 34, 60, 91	0
1	B	442/455 (97%)	-0.48	6 (1%) 78 73	20, 36, 61, 75	0
All	All	884/910 (97%)	-0.53	10 (1%) 82 79	18, 35, 61, 91	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	448	GLU	3.9
1	B	406	GLY	2.9
1	B	385	VAL	2.8
1	A	385	VAL	2.6
1	A	392	THR	2.5

### 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( $\text{\AA}^2$ )	Q<0.9
2	ZX9	A	901	26/26	0.84	0.23	1.27	29,48,57,58	0
2	ZX9	B	902	26/26	0.88	0.18	0.78	27,48,58,58	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.