



# Full wwPDB X-ray Structure Validation Report ⓘ

May 23, 2020 – 03:27 pm BST

PDB ID : 6IDE  
Title : Crystal structure of the Vibrio cholera VqmA-Ligand-DNA complex provides molecular mechanisms for drug design  
Authors : Wu, H.; Li, M.J.; Guo, H.J.; Zhou, H.; Li, B.; Xu, Q.; Xu, C.Y.; Yu, F.; He, J.H.  
Deposited on : 2018-09-09  
Resolution : 2.51 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

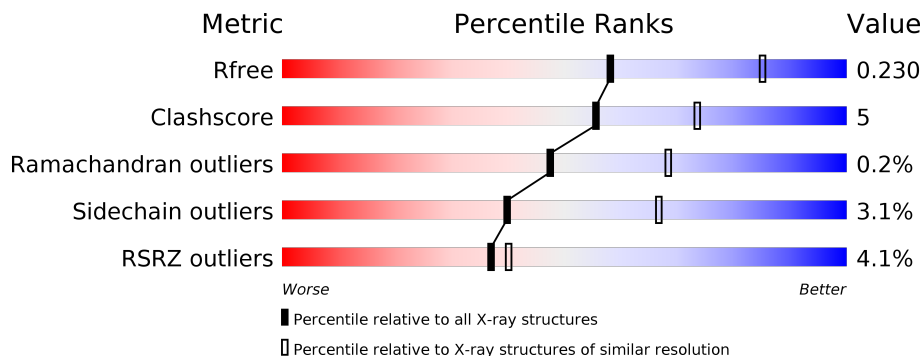
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.51 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))
$R_{free}$	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 respectively. 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	256	 3% 79% 9% 12%
1	B	256	 5% 74% 14% 11%
2	C	18	 67% 33%
3	D	18	 61% 39%

## 2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 4330 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 Transcriptional regulator LuxR family.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	226	Total	C	N	O	S	0	0	0
			1775	1142	307	320	6			
1	B	228	Total	C	N	O	S	0	0	0
			1799	1153	310	330	6			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP A0A0H6WEL7
A	1	LYS	-	expression tag	UNP A0A0H6WEL7
A	247	LEU	-	expression tag	UNP A0A0H6WEL7
A	248	LEU	-	expression tag	UNP A0A0H6WEL7
A	249	GLU	-	expression tag	UNP A0A0H6WEL7
A	250	HIS	-	expression tag	UNP A0A0H6WEL7
A	251	HIS	-	expression tag	UNP A0A0H6WEL7
A	252	HIS	-	expression tag	UNP A0A0H6WEL7
A	253	HIS	-	expression tag	UNP A0A0H6WEL7
A	254	HIS	-	expression tag	UNP A0A0H6WEL7
A	255	HIS	-	expression tag	UNP A0A0H6WEL7
B	0	MET	-	initiating methionine	UNP A0A0H6WEL7
B	1	LYS	-	expression tag	UNP A0A0H6WEL7
B	247	LEU	-	expression tag	UNP A0A0H6WEL7
B	248	LEU	-	expression tag	UNP A0A0H6WEL7
B	249	GLU	-	expression tag	UNP A0A0H6WEL7
B	250	HIS	-	expression tag	UNP A0A0H6WEL7
B	251	HIS	-	expression tag	UNP A0A0H6WEL7
B	252	HIS	-	expression tag	UNP A0A0H6WEL7
B	253	HIS	-	expression tag	UNP A0A0H6WEL7
B	254	HIS	-	expression tag	UNP A0A0H6WEL7
B	255	HIS	-	expression tag	UNP A0A0H6WEL7

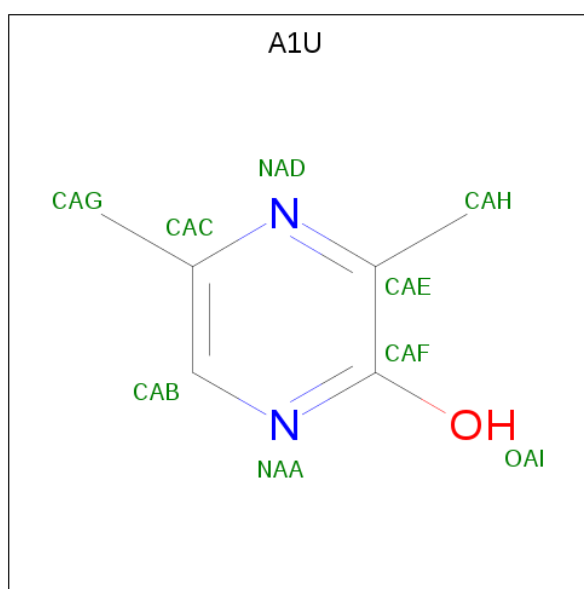
- Molecule 2 is a DNA chain called DNA (5'-D(\*AP\*GP\*GP\*GP\*GP\*GP\*GP\*AP\*AP\*AP\*TP\*CP\*CP\*CP\*CP\*CP\*CP\*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	C	18	367	174	72	104	17	0	0	0

- Molecule 3 is a DNA chain called DNA (5'-D(\*AP\*GP\*GP\*GP\*GP\*GP\*GP\*AP\*TP\*TP\*TP\*CP\*CP\*CP\*CP\*CP\*CP\*CP\*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	D	18	365	174	66	108	17	0	0	0

- Molecule 4 is 3,5-dimethylpyrazin-2-ol (three-letter code: A1U) (formula: C<sub>6</sub>H<sub>8</sub>N<sub>2</sub>O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	9	6	2	1	0	0
4	B	1	9	6	2	1	0	0

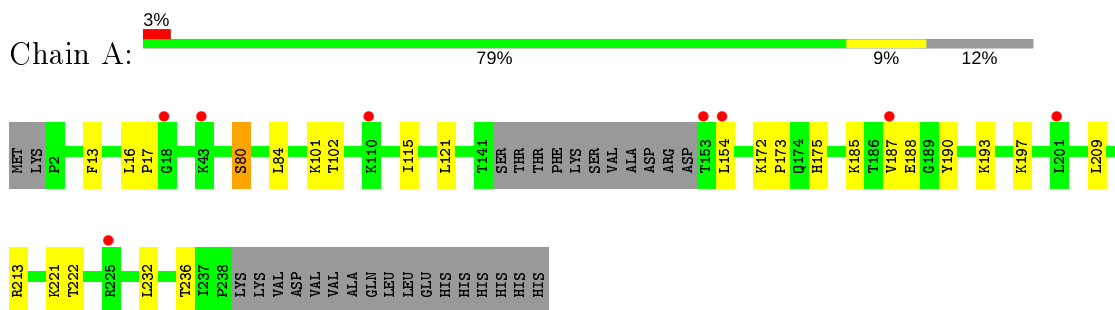
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	6	Total 6 6	0	0

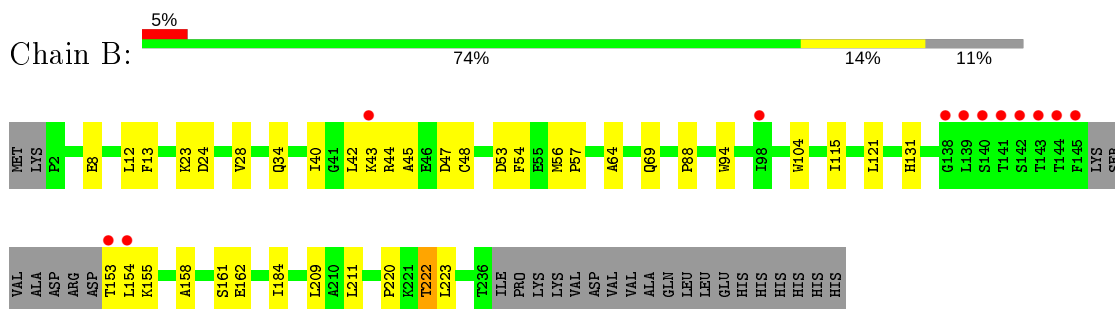
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

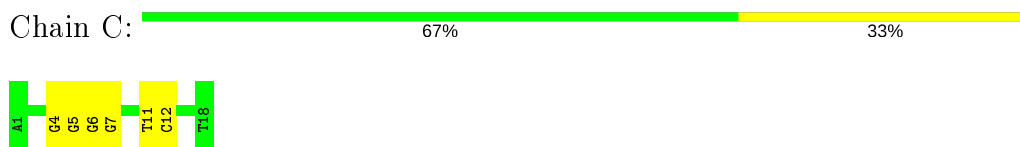
- Molecule 1: Transcriptional regulator LuxR family



- Molecule 1: Transcriptional regulator LuxR family



- Molecule 2: DNA (5'-D(\*AP\*GP\*GP\*GP\*GP\*GP\*GP\*AP\*AP\*AP\*TP\*CP\*CP\*CP\*CP\*CP\*CP\*T)-3')



- Molecule 3: DNA (5'-D(\*AP\*GP\*GP\*GP\*GP\*GP\*GP\*AP\*TP\*TP\*TP\*CP\*CP\*CP\*CP\*CP\*CP\*T)-3')



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	52.78Å 108.98Å 214.32Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.33 – 2.51 43.33 – 2.51	Depositor EDS
% Data completeness (in resolution range)	99.6 (43.33-2.51) 99.6 (43.33-2.51)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.88 (at 2.51Å)	Xtrriage
Refinement program	PHENIX 1.13_2998: ???	Depositor
R, $R_{free}$	0.192 , 0.229 0.192 , 0.230	Depositor DCC
$R_{free}$ test set	1997 reflections (4.63%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	78.3	Xtrriage
Anisotropy	0.466	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 67.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4330	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	96.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.39% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: A1U

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	0.32	0/1817	0.50	0/2461
1	B	0.32	0/1841	0.49	0/2492
2	C	0.57	0/412	0.86	0/634
3	D	0.56	0/408	0.88	0/628
All	All	0.38	0/4478	0.59	0/6215

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	1775	0	1782	13	0
1	B	1799	0	1795	22	0
2	C	367	0	202	4	0
3	D	365	0	204	5	0
4	A	9	0	0	0	0
4	B	9	0	0	0	0
5	A	6	0	0	0	0
All	All	4330	0	3983	42	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 5.

All (42) 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:B:220:PRO:HG2	1:B:223:LEU:HD13	1.66	0.77
1:A:154:LEU:HD13	1:A:213:ARG:HH22	1.53	0.73
1:A:80:SER:HB2	1:A:102:THR:HG22	1.75	0.68
1:B:43:LYS:HG3	1:B:44:ARG:HG3	1.79	0.65
1:B:104:TRP:HB2	1:B:115:ILE:HG13	1.84	0.58
1:B:23:LYS:NZ	1:B:53:ASP:OD2	2.34	0.56
2:C:11:DT:H2'	2:C:12:DC:C6	2.40	0.56
1:B:40:ILE:HG23	1:B:42:LEU:HD13	1.88	0.54
3:D:4:DG:H2''	3:D:5:DG:H5'	1.89	0.54
1:A:173:PRO:HD2	2:C:11:DT:H5''	1.88	0.54
2:C:4:DG:H2''	2:C:5:DG:H5'	1.89	0.54
3:D:3:DG:H2'	3:D:4:DG:H5''	1.89	0.53
1:A:154:LEU:HD13	1:A:213:ARG:NH2	2.24	0.50
1:A:193:LYS:O	1:A:197:LYS:HG2	2.12	0.48
1:A:209:LEU:O	1:A:213:ARG:HG2	2.14	0.48
1:A:16:LEU:HD12	1:A:17:PRO:HD2	1.95	0.48
1:B:56:MET:HG3	1:B:57:PRO:HD2	1.95	0.48
1:B:42:LEU:HD23	1:B:47:ASP:HB2	1.96	0.48
1:A:84:LEU:HB2	1:A:232:LEU:HD11	1.96	0.47
1:B:184:ILE:H	1:B:184:ILE:HD12	1.80	0.47
3:D:16:DC:H2'	3:D:17:DC:C6	2.50	0.47
1:B:40:ILE:HG12	1:B:56:MET:HG2	1.98	0.46
1:A:13:PHE:HD1	1:B:13:PHE:HD1	1.64	0.45
1:B:155:LYS:HA	1:B:155:LYS:HD2	1.69	0.45
1:B:161:SER:HB3	1:B:220:PRO:HB3	1.97	0.45
1:B:54:PHE:CE1	1:B:64:ALA:HB3	2.52	0.45
1:B:153:THR:OG1	1:B:154:LEU:N	2.50	0.44
1:B:131:HIS:HB2	1:B:211:LEU:HD13	1.99	0.44
1:A:101:LYS:HA	1:A:115:ILE:O	2.18	0.43
1:B:42:LEU:HD22	1:B:48:CYS:SG	2.59	0.43
1:B:88:PRO:HG3	1:B:94:TRP:CZ2	2.54	0.43
1:B:158:ALA:O	1:B:162:GLU:HG3	2.17	0.43
1:B:24:ASP:OD1	1:B:28:VAL:HG12	2.17	0.43
3:D:10:DT:H2''	3:D:11:DT:H5''	2.01	0.43
3:D:4:DG:H2''	3:D:5:DG:C8	2.55	0.42
1:A:185:LYS:HD3	1:A:185:LYS:HA	1.88	0.41
1:A:172:LYS:HB2	1:A:172:LYS:HE3	1.91	0.41
1:A:188:GLU:C	1:A:190:TYR:H	2.23	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:34:GLN:HA	1:B:45:ALA:HB2	2.01	0.41
1:B:222:THR:HG23	1:B:223:LEU:HD12	2.03	0.41
2:C:6:DG:H2''	2:C:7:DG:C8	2.56	0.40
1:B:54:PHE:CD1	1:B:64:ALA:HB3	2.56	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	222/256 (87%)	215 (97%)	6 (3%)	1 (0%)	29	48
1	B	224/256 (88%)	219 (98%)	5 (2%)	0	100	100
All	All	446/512 (87%)	434 (97%)	11 (2%)	1 (0%)	47	68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	187	VAL

### 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	190/221 (86%)	184 (97%)	6 (3%)	39	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	194/221 (88%)	188 (97%)	6 (3%)	40	67
All	All	384/442 (87%)	372 (97%)	12 (3%)	40	67

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	80	SER
1	A	121	LEU
1	A	175	HIS
1	A	221	LYS
1	A	222	THR
1	A	236	THR
1	B	8	GLU
1	B	12	LEU
1	B	69	GLN
1	B	121	LEU
1	B	209	LEU
1	B	222	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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](#)

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
4	A1U	B	301	-	8,9,9	1.40	1 (12%)	9,12,12	1.61	2 (22%)
4	A1U	A	301	-	8,9,9	1.41	1 (12%)	9,12,12	1.27	2 (22%)

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
4	A1U	B	301	-	-	-	0/1/1/1
4	A1U	A	301	-	-	-	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	301	A1U	OAI-CAF	2.45	1.40	1.29
4	A	301	A1U	OAI-CAF	2.45	1.40	1.29

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	301	A1U	CAH-CAE-NAD	3.10	121.28	116.49
4	B	301	A1U	CAC-CAB-NAA	-2.44	119.87	123.21
4	A	301	A1U	CAC-CAB-NAA	-2.18	120.23	123.21
4	A	301	A1U	CAH-CAE-NAD	2.14	119.80	116.49

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

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<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	226/256 (88%)	0.31	8 (3%) 44 47	64, 83, 116, 148	0
1	B	228/256 (89%)	0.46	12 (5%) 26 28	63, 90, 129, 160	0
2	C	18/18 (100%)	-0.55	0 100 100	109, 123, 143, 143	0
3	D	18/18 (100%)	-0.22	0 100 100	105, 124, 145, 147	0
All	All	490/548 (89%)	0.33	20 (4%) 37 40	63, 89, 133, 160	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	145	PHE	4.9
1	A	153	THR	4.4
1	B	153	THR	4.3
1	B	43	LYS	4.2
1	B	140	SER	4.0
1	B	141	THR	3.7
1	B	138	GLY	3.6
1	B	139	LEU	3.6
1	B	142	SER	3.5
1	B	143	THR	3.4
1	B	154	LEU	3.3
1	A	154	LEU	3.2
1	A	110	LYS	2.8
1	B	144	THR	2.8
1	B	98	ILE	2.7
1	A	187	VAL	2.4
1	A	201	LEU	2.3
1	A	225	ARG	2.3
1	A	18	GLY	2.2
1	A	43	LYS	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. 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	B-factors(Å <sup>2</sup> )	Q<0.9
4	A1U	B	301	9/9	0.98	0.19	65,70,77,78	0
4	A1U	A	301	9/9	0.98	0.17	58,64,67,73	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.