

wwPDB X-ray Structure Validation Summary Report (i)

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PDB ID : 4P3T

Title: Crystal structure of the bacterial A1408C-mutant ribosomal decoding site

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Deposited on : 2014-03-10

Resolution : 1.60 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

https://www.wwpdb.org/validation/2017/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: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.13.1

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Refmac: 5.8.0158

CCP4 : 7.0.044 (Gargrove) oteins) : Engh & Huber (2001)

Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

Validation Pipeline (wwPDB-VP) : 2.13.1

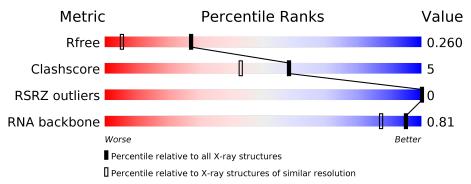
RNA backbone

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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.



3102

 Metric
 Whole archive (#Entries) Similar resolution $(\#\text{Entries}, \text{ resolution range}(\mathring{\textbf{A}}))$
 R_{free} 130704
 3398 (1.60-1.60)

 Clashscore
 141614
 3665 (1.60-1.60)

 RSRZ outliers
 127900
 3321 (1.60-1.60)

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 >=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 <=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.

1015 (2.36-0.86)

Mol	Chain	Length	Quality of chain						
1	A	23	83%	17%	_				
1	В	23	57%	39% •	_				



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1120 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 RNA chain called 5'-D(*UP*UP*GP*CP*GP*UP*CP*CP*CP*GP*(5BU) P*CP*GP*AP*AP*AP*GP*UP*CP*GP*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
1	A	23	Total 485		C 217				0	0	0
1	В	23	Total 485		C 217			P 22	0	0	0

• Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	76	Total O 76 76	0	0
2	В	74	Total O 74 74	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: 5'-D(*UP*UP*GP*CP*GP*UP*CP*CP*CP*GP*(5BU)P*CP*GP*AP*CP*GP*AP*CP*GP*AP*CP*GP*AP*CP*GP*C)-3'



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	33.44Å 40.48Å 41.27Å	Depositor
a, b, c, α , β , γ	90.00° 103.07° 90.00°	Depositor
Resolution (Å)	20.00 - 1.60	Depositor
resolution (A)	28.52 - 1.60	EDS
% Data completeness	98.4 (20.00-1.60)	Depositor
(in resolution range)	98.4 (28.52-1.60)	EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	4.33 (at 1.60Å)	Xtriage
Refinement program	CNS	Depositor
P. P.	0.248 , 0.271	Depositor
R, R_{free}	0.238 , 0.260	DCC
R_{free} test set	1430 reflections (10.15%)	wwPDB-VP
Wilson B-factor (Å ²)	23.0	Xtriage
Anisotropy	0.078	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.41, 58.5	EDS
L-test for twinning ²	$ < L > = 0.52, < L^2> = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	1120	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 11.21% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $< L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

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: 5BU

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		
MIOI	Chain	RMSZ	# Z >5	RMSZ	# Z >5	
1	A	0.33	0/517	0.70	0/804	
1	В	0.30	0/517	0.77	0/804	
All	All	0.32	0/1034	0.74	0/1608	

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	485	0	249	1	0
1	В	485	0	249	6	0
2	A	76	0	0	0	0
2	В	74	0	0	2	0
All	All	1120	0	498	7	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.

The worst 5 of 7 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$egin{array}{c} ext{Clash} \ ext{overlap } (ext{Å}) \end{array}$
1:B:40:A:N7	2:B:174:HOH:O	2.27	0.67
1:A:20:U:H2'	1:A:21:C:C6	2.44	0.53
1:B:45:G:O2'	1:B:46:C:H5'	2.14	0.48
1:B:33:G:H2'	1:B:34:5BU:H6	1.96	0.48
1:B:29:U:H2'	1:B:30:C:O4'	2.15	0.47

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

There are no protein molecules in this entry.

5.3.2 Protein sidechains (i)

There are no protein molecules in this entry.

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	$22/23 \ (95\%)$	1 (4%)	0
1	В	$22/23 \ (95\%)$	0	0
All	All	44/46 (95%)	1 (2%)	0

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	17	A

There are no RNA pucker outliers to report.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

2 non-standard protein/DNA/RNA residues 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	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Chain	Res	Link	Bo	nd leng	$ ag{ths}$	В	ond ang	les
WIOI	Туре	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2														
1	5BU	В	34	1	15,22,23	1.47	3 (20%)	17,32,35	3.93	3 (17%)														
1	5BU	A	11	1	15,22,23	1.32	3 (20%)	17,32,35	3.96	2 (11%)														

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
1	5BU	В	34	1	-	0/5/25/26	0/2/2/2
1	5BU	A	11	1	_	0/5/25/26	0/2/2/2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	${f Observed(\AA)}$	$\operatorname{Ideal}(ext{\AA})$
1	В	34	5BU	C4-C5	3.86	1.43	1.38
1	A	11	5BU	C4-N3	3.21	1.38	1.33
1	В	34	5BU	C4-N3	2.95	1.38	1.33
1	A	11	5BU	C4-C5	2.65	1.41	1.38
1	A	11	5BU	C6-C5	-2.54	1.34	1.39

All (5) bond angle outliers are listed below:

Mol	Chain	${f Res}$	Type	ype Atoms		$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
1	A	11	5BU	C4-N3-C2	14.05	127.00	115.14
1	В	34	5BU	C4-N3-C2	13.93	126.90	115.14
1	В	34	5BU	C5-C4-N3	-7.57	114.58	123.64
1	A	11	5BU	C5-C4-N3	-7.56	114.59	123.64
1	В	34	5BU	C5-C6-N1	2.05	122.62	119.97

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:



Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	В	34	5BU	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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^{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 $>$	$\#\mathrm{RSRZ}{>}2$		$\mathbf{Z}\mathbf{>}2$	$OWAB(A^2)$	$\mathbf{Q}{<}0.9$
1	A	$22/23\ (95\%)$	0.01	0	100	100	18, 33, 47, 48	0
1	В	$22/23 \ (95\%)$	0.21	0	100	100	19, 36, 45, 48	0
All	All	44/46 (95%)	0.11	0	100	100	18, 36, 47, 48	0

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains (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^{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	\mathbf{Res}	Atoms	RSCC	RSR	${f B-factors}({f A}^2)$	Q<0.9
1	5BU	В	34	21/22	0.96	0.09	32,33,40,42	0
1	5BU	A	11	21/22	0.99	0.09	17,22,25,27	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.

