

Full wwPDB X-ray Structure Validation Report (i)

Aug 20, 2020 – 04:27 PM BST

PDB ID	:	4FEP
Title	:	Crystal structure of the $ m A24U/U25A/A46G/C74U$ mutant xpt-pbuX guanine
		riboswitch aptamer domain in complex with 2,6-diaminopurine
Authors	:	Stoddard, C.D.; Trausch, J.J.; Widmann, J.; Marcano, J.; Knight, R.; Batey,
		R.T.
Deposited on		
Resolution	:	1.65 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* 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:

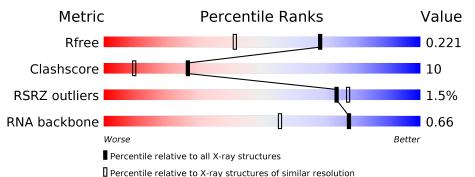
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	$7.0.044 (\mathrm{Gargrove})$
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

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 1.65 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.



Whole archive Similar resolution Metric (#Entries) (#Entries, resolution range(A))1307041827 (1.66 - 1.66) \mathbf{R}_{free} Clashscore 141614 1931 (1.66-1.66) **RSRZ** outliers 127900 1791 (1.66-1.66) RNA backbone 3102 1011 (2.36-0.96)

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.

Mol	Chain	Length	Quality of chair	n	
1	В	67	% 64%	34%	•

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	\mathbf{Res}	Chirality	Geometry	Clashes	Electron density
3	NCO	В	109	-	-	-	Х



2 Entry composition (i)

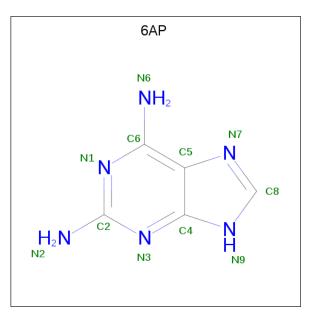
There are 4 unique types of molecules in this entry. The entry contains 2068 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

 $\bullet\,$ Molecule 1 is a RNA chain called A24U/U25A/A46G/C74U mutant of the B. subtilis xpt-pbuX guanine riboswitch aptamer domain.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	В	67	Total 1423	C 637	N 252	O 468	Р 66	0	0	0

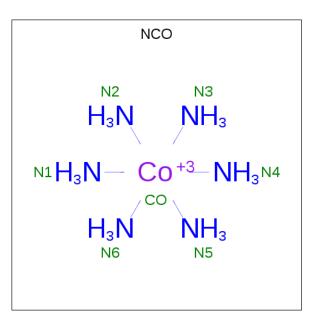
• Molecule 2 is 9H-PURINE-2,6-DIAMINE (three-letter code: 6AP) (formula: $C_5H_6N_6$).



Mol	Chain	Residues			ZeroOcc	AltConf	
2	В	1	Total 11	С 5	N 6	0	0

• Molecule 3 is COBALT HEXAMMINE(III) (three-letter code: NCO) (formula: CoH₁₈N₆).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	В	1	TotalCoN716	0	0
3	В	1	TotalCoN716	0	0
3	В	1	TotalCoN716	0	0
3	В	1	TotalCoN716	0	0
3	В	1	TotalCoN716	0	0
3	В	1	Total Co N 7 1 6	0	0
3	В	1	Total Co N 7 1 6	0	0
3	В	1	TotalCoN716	0	0
3	В	1	TotalCoN716	0	0

• Molecule 4 is water.

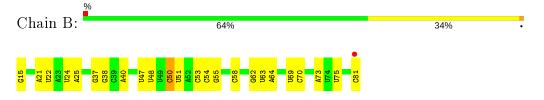
ľ	Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
	4	В	571	Total O 571 571	0	0



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.

 \bullet Molecule 1: A24U/U25A/A46G/C74U mutant of the B. subtilis xpt-pbuX guanine riboswitch aptamer domain





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	133.07\AA 35.25\AA 41.85\AA	Depositor
a, b, c, α , β , γ	90.00° 91.40° 90.00°	Depositor
Resolution (Å)	40.00 - 1.65	Depositor
Resolution (A)	26.35 - 1.65	EDS
% Data completeness	(Not available) $(40.00-1.65)$	Depositor
(in resolution range)	87.9(26.35 - 1.65)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$0.79 ({\rm at} 1.65{ m \AA})$	Xtriage
Refinement program	CNS	Depositor
D D .	0.179 , 0.229	Depositor
R, R_{free}	0.171 , 0.221	DCC
R_{free} test set	2059 reflections $(9.25%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	12.9	Xtriage
Anisotropy	0.616	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.28 , 44.2	EDS
L-test for twinning ²	$< L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	0.026 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2068	wwPDB-VP
Average B, all atoms $(Å^2)$	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 9.05% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



 $^{^1 {\}rm Intensities}$ 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: 6AP, NCO

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).

Mal	Chain	Bond	lengths	Bond angles		
	Iol Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	В	0.28	0/1590	0.68	0/2476	

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	В	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	В	38	G	Sidechain

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	В	1423	0	722	23	0
2	В	11	0	6	0	0

Continued on next page...



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 10.

All (23) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom 1	Atom 9	Interatomic	Clash
Atom-1	Atom-2	${ m distance}~({ m \AA})$	overlap (Å)
1:B:62:G:H4'	4:B:1159:HOH:O	1.74	0.88
1:B:63:U:H5'	4:B:1159:HOH:O	2.00	0.61
1:B:21:A:H2'	1:B:22:U:H2'	1.83	0.60
1:B:47:U:H3'	4:B:1165:HOH:O	2.07	0.55
1:B:25:A:H5"	4:B:822:HOH:O	2.10	0.51
1:B:81:C:H4'	4:B:1021:HOH:O	2.10	0.51
1:B:75:U:H4'	4:B:966:HOH:O	2.09	0.51
1:B:58:C:H3'	4:B:958:HOH:O	2.11	0.50
1:B:50:C:H5"	4:B:1001:HOH:O	2.12	0.50
1:B:40:A:H4'	4:B:953:HOH:O	2.13	0.49
1:B:24:U:H2'	1:B:54:C:C4	2.48	0.48
1:B:37:G:H5"	4:B:973:HOH:O	2.12	0.48
1:B:54:C:H3'	4:B:971:HOH:O	2.14	0.47
1:B:55:G:H5"	4:B:998:HOH:O	2.14	0.47
1:B:63:U:H6	4:B:1159:HOH:O	2.01	0.44
1:B:15:G:H5'	4:B:1046:HOH:O	2.18	0.43
1:B:15:G:H8	1:B:15:G:HO5'	1.65	0.43
1:B:64:A:H3'	4:B:1061:HOH:O	2.19	0.42
1:B:24:U:H4'	4:B:1080:HOH:O	2.19	0.42
1:B:51:U:H1'	4:B:966:HOH:O	2.19	0.42
1:B:69:U:H2'	1:B:70:C:C6	2.55	0.42
1:B:48:U:H4'	4:B:1165:HOH:O	2.19	0.41
1:B:53:C:H1'	4:B:1080:HOH:O	2.21	0.40

There are no symmetry-related clashes.



Chain Non-H H(model) H(added) Clashes Symm-Clashes Mol В 3 63 0 0 0 0 4 В 571 0 0 19 0 All All 0 2068072823

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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	В	66/67~(98%)	2(3%)	0

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	В	50	С
1	В	73	А

There are no RNA pucker outliers to report.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

10 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



Mol	Tune	Chain	Res	Link	Bo	ond leng	ths	Bond angles		
	Type	Chain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ $ $ $# Z > 2 $	
3	NCO	В	107	-	6,6,6	0.08	0	-		
3	NCO	В	103	-	6,6,6	0.07	0	-		
3	NCO	В	102	-	$6,\!6,\!6$	0.10	0	-		
3	NCO	В	109	-	6,6,6	0.05	0	-		
3	NCO	В	105	-	6,6,6	0.20	0	-		
2	6AP	В	101	-	10,12,12	1.12	1 (10%)	9,17,17	2.64 4 (44%)	
3	NCO	В	108	-	6,6,6	0.05	0	-		
3	NCO	В	106	-	6,6,6	0.04	0	-		
3	NCO	В	110	-	6,6,6	0.05	0	-		
3	NCO	В	104	-	6,6,6	0.12	0	-		

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).

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	6AP	В	101	-	-	-	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(\operatorname{\AA})$
2	В	101	6AP	C2-N2	2.51	1.38	1.33

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
2	В	101	6AP	C2-N3-C4	4.83	120.87	115.36
2	В	101	6AP	N3-C2-N1	-4.30	121.48	127.22
2	В	101	6AP	C5-C6-N1	-3.10	118.97	121.01
2	В	101	6AP	C4-C5-N7	-2.13	107.18	109.40

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^{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 $>$	$\#RSRZ{>}2$		$OWAB(Å^2)$	Q<0.9	
1	В	67/67~(100%)	-0.30	1 (1%)	73	77	10, 17, 46, 71	0

All (1) RSRZ outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	RSRZ
1	В	81	С	2.8

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 monosaccharides 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^{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	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	$Q{<}0.9$
3	NCO	В	109	7/7	0.49	0.45	$123,\!123,\!123,\!123$	0
3	NCO	В	103	7/7	0.93	0.18	24,24,26,26	0
3	NCO	В	107	7/7	0.93	0.22	27, 28, 28, 29	0
3	NCO	В	106	7/7	0.93	0.21	$37,\!37,\!38,\!39$	0
2	6AP	В	101	11/11	0.95	0.11	$14,\!15,\!16,\!16$	0
3	NCO	В	110	7/7	0.98	0.14	$15,\!15,\!18,\!18$	7

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	Q<0.9
3	NCO	В	108	7/7	0.99	0.07	$25,\!26,\!27,\!27$	0
3	NCO	В	105	7/7	0.99	0.07	$9,\!11,\!14,\!14$	0
3	NCO	В	102	7/7	0.99	0.08	$14,\!15,\!17,\!18$	0
3	NCO	В	104	7/7	0.99	0.12	15, 16, 18, 19	0

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6.5 Other polymers (i)

There are no such residues in this entry.

