

Full wwPDB X-ray Structure Validation Report (i)

Aug 15, 2023 – 10:05 AM EDT

PDB ID	:	1X9C
Title	:	An all-RNA Hairpin Ribozyme with mutation U39C
Authors	:	Alam, S.; Grum-Tokars, V.; Krucinska, J.; Kundracik, M.L.; Wedekind, J.E.
Deposited on	:	2004-08-20
Resolution	:	2.19 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

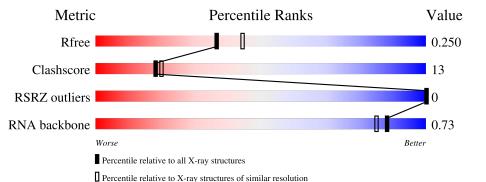
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY\;DIFFRACTION$

The reported resolution of this entry is 2.19 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)
RNA backbone	3102	1032 (2.60-1.80)

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 of 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 chain		
1	А	13	31%	46%	23%)
2	В	12		83%	1	7%
3	С	17	7	1%	29%	
4	D	19	53%		42%	5%



2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 1373 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'-R(*UP*CP*CP*CP*(A2M)P*GP*UP*CP*CP*AP*C P*CP*G)-3'.

Mol	Chain	Residues		Ate	\mathbf{oms}			ZeroOcc	AltConf	Trace
1	А	13	Total 285	C 131	N 47	O 95	Р 12	0	1	0

• Molecule 2 is a RNA chain called 5'-R(*CP*GP*GP*UP*GP*AP*GP*AP*GP*GP*GP*G) -3'.

Mol	Chain	Residues		Ate	oms			ZeroOcc	AltConf	Trace
2	В	12	Total 264	C 118	N 55	O 80	Р 11	0	0	0

• Molecule 3 is a RNA chain called 5'-R(*GP*GP*CP*AP*GP*AP*GP*AP*AP*AP*CP*A P*CP*AP*CP*A)-3'.

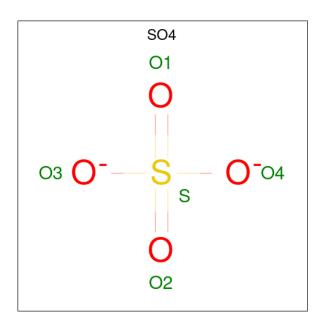
Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
3	С	17	Total 368	C 166	N 77	O 109	Р 16	0	0	0

• Molecule 4 is a RNA chain called 5'-R(*UP*CP*GP*UP*GP*GP*UP*AP*CP*AP*UP*U P*AP*CP*CP*CP*C)-3'.

Mol	Chain	Residues		At	\mathbf{oms}			ZeroOcc	AltConf	Trace
4	D	19	Total 395	C 178	N 65	0 134	Р 18	0	0	0

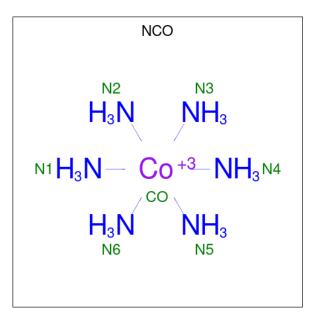
• Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O_4S).





Mol	Chain	Residues	Ato	oms		ZeroOcc	AltConf
5	А	1	Total 5	0 4	S 1	0	0

• Molecule 6 is COBALT HEXAMMINE(III) (three-letter code: NCO) (formula: $CoH_{18}N_6$).



M	ol	Chain	Residues	Atoms	ZeroOcc	AltConf
6		В	1	Total Co N 7 1 6	0	0
6		С	1	Total Co N 7 1 6	0	0

• Molecule 7 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	А	5	$\begin{array}{cc} \text{Total} & \text{O} \\ 5 & 5 \end{array}$	0	0
7	В	10	Total O 10 10	0	0
7	С	10	Total O 10 10	0	0
7	D	17	Total O 17 17	0	0

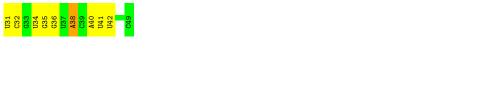


3 Residue-property plots (i)

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'-R(*UP*CP*CP*CP*(A2M)P*GP*UP*CP*CP*AP*CP*CP*G)-3'

Chain A:	31%	46%	23%	-
U1 C2 C3 C3 A5 C9 C8 C8 C8 A10	C11 C12 C13 C13			
• Molecule 2:	5'-R(*CP*GP*GP*	*UP*GP*AP*GP*AI	P*AP*GP*GP*G)-3	,
Chain B:		83%	17%	•
<mark>68 47 62</mark> 113				
• Molecule 3:	5'-R(*GP*GP*CP	*AP*GP*AP*GP*A	P*AP*AP*CP*AP	*CP*AP*CF
Chain C:	71	%	29%	-
615 616 A22 A26 A26 A26 A26 A31				
• Molecule 4: P*C)-3'	5'-R(*UP*CP*GP*	UP*GP*GP*UP*AF	P*CP*AP*UP*UP*.	AP*CP*CP*
Chain D:	53%		42% 5%	6





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants	93.31Å 93.31Å 128.00Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	24.84 - 2.19	Depositor
Resolution (A)	31.49 - 2.20	EDS
% Data completeness	97.9 (24.84-2.19)	Depositor
(in resolution range)	98.0 (31.49-2.20)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	0.04	Depositor
$< I/\sigma(I) > 1$	$3.76 (at 2.20 \text{\AA})$	Xtriage
Refinement program	CNS 1.1	Depositor
D D.	0.249 , 0.263	Depositor
R, R_{free}	0.235 , 0.250	DCC
R_{free} test set	1368 reflections (7.91%)	wwPDB-VP
Wilson B-factor $(Å^2)$	57.9	Xtriage
Anisotropy	0.128	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.27, 42.2	EDS
L-test for twinning ²	$ < L >=0.48, < L^2>=0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	1373	wwPDB-VP
Average B, all atoms $(Å^2)$	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.56% 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.



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: NCO, A2M, SO4 $\,$

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	Bo	nd angles
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.52	0/290	1.26	4/449~(0.9%)
2	В	0.32	0/297	0.60	0/464
3	С	0.33	0/414	0.64	0/645
4	D	0.50	0/439	0.97	4/681~(0.6%)
All	All	0.43	0/1440	0.89	8/2239~(0.4%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}(^{o})$
1	А	5	A2M	P-O3'-C3'	7.45	128.64	119.70
1	А	2	С	O4'-C1'-N1	6.25	113.20	108.20
4	D	38	А	N9-C1'-C2'	5.70	121.41	114.00
1	А	2	С	C4'-C3'-C2'	5.62	108.22	102.60
4	D	41	U	N1-C1'-C2'	5.56	121.23	114.00
1	А	5	A2M	OP2-P-O3'	5.39	117.06	105.20
4	D	36	G	N9-C1'-C2'	5.23	120.80	114.00
4	D	41	U	C2'-C3'-O3'	5.15	121.94	113.70

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	А	285	0	156	17	0
2	В	264	0	133	2	0
3	С	368	0	189	4	0
4	D	395	0	205	4	0
5	А	5	0	0	0	0
6	В	7	0	0	0	0
6	С	7	0	0	1	0
7	А	5	0	0	0	0
7	В	10	0	0	0	0
7	С	10	0	0	0	0
7	D	17	0	0	0	0
All	All	1373	0	683	26	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 13.

All (26) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

A + 1	A + 0	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:A:3:C:H5'	1:A:3:C:H6	1.36	0.91
1:A:2:C:O2'	1:A:3:C:H5"	1.77	0.83
1:A:1[A]:U:HO5'	1:A:1[A]:U:H6	1.31	0.79
1:A:2:C:C2'	1:A:3:C:H5"	2.34	0.58
3:C:15:G:H2'	3:C:16:G:C8	2.38	0.58
6:C:51:NCO:N2	4:D:40:A:OP1	2.36	0.57
1:A:3:C:H5'	1:A:3:C:C6	2.28	0.56
1:A:2:C:HO2'	1:A:3:C:H5"	1.69	0.54
1:A:10:A:H2'	1:A:11:C:C6	2.42	0.54
1:A:1[B]:U:H2'	1:A:2:C:O4'	2.08	0.54
1:A:7:U:O2'	1:A:8:C:H5'	2.08	0.54
4:D:31:U:H2'	4:D:32:C:C6	2.42	0.53
1:A:2:C:C2'	1:A:3:C:C5'	2.88	0.52
4:D:38:A:H5"	4:D:40:A:O4'	2.16	0.46
3:C:25:C:H2'	3:C:26:A:C8	2.51	0.46
1:A:5:A2M:CM'	2:B:8:G:H1	2.28	0.45
1:A:10:A:H2'	1:A:11:C:H6	1.82	0.45
1:A:2:C:H2'	1:A:3:C:H5'	1.99	0.45
1:A:1[A]:U:C3'	1:A:1[A]:U:C6	2.99	0.45
2:B:7:A:H2'	2:B:8:G:O4'	2.17	0.45
1:A:1[A]:U:C6	1:A:1[A]:U:H3'	2.53	0.43
4:D:34:U:O2'	4:D:35:G:H5'	2.19	0.43
1:A:1[A]:U:H6	1:A:1[A]:U:O5'	1.98	0.41

Continued on next page...



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:25:C:H2'	3:C:26:A:H8	1.86	0.41
3:C:15:G:H2'	3:C:16:G:H8	1.84	0.41
1:A:1[A]:U:H2'	1:A:2:C:O4'	2.21	0.40

Continued from previous page...

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	А	12/13~(92%)	2~(16%)	0
2	В	$11/12 \ (91\%)$	0	0
3	С	16/17~(94%)	1 (6%)	0
4	D	18/19~(94%)	1 (5%)	0
All	All	57/61~(93%)	4 (7%)	0

All (4) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	А	3	С
1	А	6	G
3	С	22	А
4	D	42	U

There are no RNA pucker outliers to report.

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

1 non-standard protein/DNA/RNA residue is 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).

Г	Mol	Type	Chain	Res	Link	Bo	ond leng	\mathbf{ths}	В	ond ang	les
	WIOI	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
	1	A2M	А	5	1,2	18,25,26	0.74	0	18,36,39	1.21	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	A2M	А	5	1,2	-	0/5/27/28	0/3/3/3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	5	A2M	O3'-C3'-C2'	2.25	117.55	111.17
1	А	5	A2M	C5-C6-N6	2.23	123.75	120.35

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	А	5	A2M	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.



5.6 Ligand geometry (i)

3 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
5	SO4	А	61	-	4,4,4	0.29	0	$6,\!6,\!6$	0.07	0
6	NCO	В	52	-	$6,\!6,\!6$	1.23	0	-		
6	NCO	С	51	-	$6,\!6,\!6$	0.99	0	-		

There are no bond length outliers.

There are no bond angle outliers.

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
6	С	51	NCO	1	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^{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	$\langle RSRZ \rangle$	#RSRZ>2		Z>2	$OWAB(A^2) Q < 0.9$
1	А	12/13~(92%)	0.16	0	100	100	43, 62, 96, 98 0
2	В	12/12~(100%)	-0.30	0	100	100	44, 61, 87, 88 0
3	С	17/17~(100%)	-0.38	0	100	100	47, 50, 57, 60 0
4	D	19/19~(100%)	-0.36	0	100	100	47, 51, 66, 69 0
All	All	60/61~(98%)	-0.25	0	100	100	43, 54, 88, 98 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	Res	Atoms	RSCC	RSR	$B-factors(Å^2)$	Q < 0.9
1	A2M	A	5	23/24	0.93	0.18	$47,\!53,\!57,\!59$	0

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	Res	Atoms	RSCC	RSR	B-factors(Å ²)	$\mathbf{Q} \! < \! 0.9$
6	NCO	В	52	7/7	0.81	0.54	74,74,75,78	0
5	SO4	А	61	5/5	0.92	0.17	103,103,104,104	0
6	NCO	С	51	7/7	0.94	0.42	44,52,53,53	0

6.5 Other polymers (i)

There are no such residues in this entry.

