



# wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 12:39 AM GMT

PDB ID : 2AB4  
Title : Dissecting the Roles of a Strictly Conserved Tyrosine in Substrate Recognition and Catalysis by Pseudouridine 55 Synthase  
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Deposited on : 2005-07-14  
Resolution : 2.40 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

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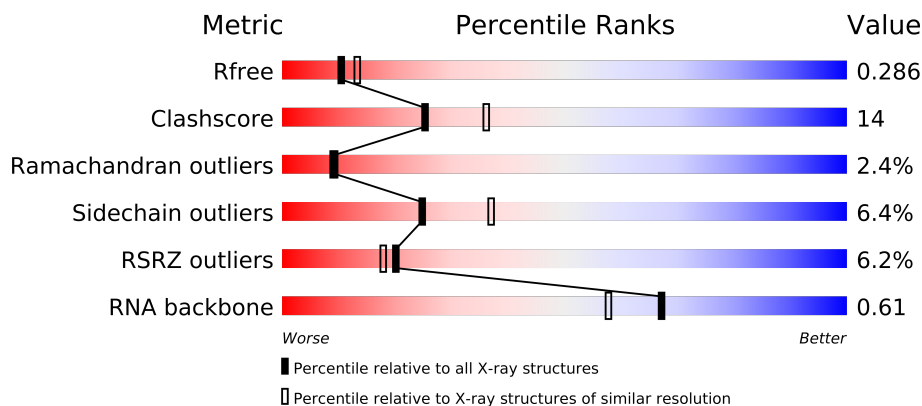
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.40 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))
$R_{free}$	66092	2207 (2.40-2.40)
Clashscore	79885	2789 (2.40-2.40)
Ramachandran outliers	78287	2736 (2.40-2.40)
Sidechain outliers	78261	2737 (2.40-2.40)
RSRZ outliers	66119	2210 (2.40-2.40)
RNA backbone	1838	1029 (3.00-1.80)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	B	20	
2	A	309	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2921 atoms, of which 0 are hydrogen and 0 are deuterium.

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(\*CP\*CP\*AP\*CP\*GP\*GP\*UP\*(FHU)P\*CP\*GP\*AP\*AP\*UP\*CP\*CP\*GP\*UP\*GP\*GP\*C)-3'.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	B	20	Total	C	F	N	O	P	0	0	0
			423	189	1	74	140	19			

- Molecule 2 is a protein called tRNA pseudouridine synthase B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	300	Total	C	N	O	S	0	0	0
			2415	1546	420	439	10			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	67	PHE	TYR	engineered	UNP Q9WZW0
A	296	GLN	ASN	see remark 999	UNP Q9WZW0
A	307	GLN	ASN	see remark 999	UNP Q9WZW0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	62	Total	O	0	0
			62	62		
4	B	20	Total	O	0	0
			20	20		



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	157.87Å 51.87Å 57.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.40 36.94 – 2.40	Depositor EDS
% Data completeness (in resolution range)	86.0 (50.00-2.40) 95.1 (36.94-2.40)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.65 (at 2.39Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.222 , 0.272 0.236 , 0.286	Depositor DCC
$R_{free}$ test set	1438 reflections (8.56%)	DCC
Wilson B-factor (Å <sup>2</sup> )	31.5	Xtriage
Anisotropy	0.851	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 24.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 19120 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	2921	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.62% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>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: FHU, ZN

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	B	0.43	0/447	1.17	8/695 (1.2%)
2	A	0.37	0/2460	0.61	0/3312
All	All	0.38	0/2907	0.74	8/4007 (0.2%)

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(°)
1	B	15	U	N1-C1'-C2'	6.53	122.49	114.00
1	B	15	U	O4'-C1'-N1	6.48	113.39	108.20
1	B	13	A	C4'-C3'-C2'	6.20	108.80	102.60
1	B	14	A	C2'-C3'-O3'	5.62	122.69	113.70
1	B	12	G	N9-C1'-C2'	5.25	120.83	114.00

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	423	0	219	11	0
2	A	2415	0	2473	72	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	1	0	0	0	0
4	A	62	0	0	3	0
4	B	20	0	0	0	0
All	All	2921	0	2692	76	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 14.

The worst 5 of 76 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:149:ILE:HG12	2:A:163:VAL:HG12	1.34	1.08
2:A:103:ILE:HD13	2:A:178:ILE:HG21	1.51	0.92
2:A:247:GLN:HG3	2:A:298:ARG:HE	1.47	0.77
2:A:233:VAL:HG12	2:A:255:GLU:HB2	1.66	0.77
2:A:5:ILE:HD13	2:A:56:ILE:HD11	1.66	0.76

There are no symmetry-related clashes.

## 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
2	A	296/309 (96%)	265 (90%)	24 (8%)	7 (2%)	9 9

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	239	THR
2	A	256	TRP
2	A	244	ASN
2	A	250	LEU
2	A	261	LYS

### 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
2	A	264/273 (97%)	247 (94%)	17 (6%)	25 37

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	236	GLN
2	A	240	LYS
2	A	281	GLU
2	A	218	ARG
2	A	295	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	34	HIS
2	A	93	ASN
2	A	236	GLN
2	A	307	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	B	19/20 (95%)	6 (31%)	3 (15%)

5 of 6 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	B	10	FHU
1	B	11	C
1	B	12	G
1	B	13	A
1	B	14	A

All (3) RNA pucker outliers are listed below:



Mol	Chain	Res	Type
1	B	12	G
1	B	13	A
1	B	14	A

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

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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
1	FHU	B	10	1	21,23,24	2.96	5 (23%)	31,35,38	2.43	8 (25%)

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	FHU	B	10	1	-	0/5/47/48	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	10	FHU	O4-C4	11.02	1.43	1.22
1	B	10	FHU	C4-N3	5.91	1.47	1.37
1	B	10	FHU	C6-N1	2.96	1.47	1.44
1	B	10	FHU	C2-N1	2.28	1.40	1.34
1	B	10	FHU	F5-C5	-2.26	1.33	1.41

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	10	FHU	O4-C4-N3	-7.02	109.69	120.51
1	B	10	FHU	F5-C5-C6	6.09	111.31	102.88
1	B	10	FHU	O4-C4-C5	-5.27	111.92	122.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	10	FHU	N3-C2-N1	3.80	120.38	116.16
1	B	10	FHU	C4-N3-C2	-3.66	120.09	125.99

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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.

## 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	B	20/20 (100%)	0.19	1 (5%) 28 25	22, 33, 79, 81	0
2	A	300/309 (97%)	0.19	19 (6%) 19 18	15, 33, 93, 99	1 (0%)
All	All	320/329 (97%)	0.19	20 (6%) 20 18	15, 33, 92, 99	1 (0%)

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	256	TRP	5.7
2	A	299	VAL	5.4
2	A	295	ARG	4.4
2	A	286	PHE	4.3
2	A	284	SER	3.5

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
1	FHU	B	10	22/23	0.23	1.98	29,31,34,37	0

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands

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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	ZN	A	310	1/1	0.11	-0.70	48,48,48,48	0

## 6.5 Other polymers

There are no such residues in this entry.