W O R L D W I D E

wwPDB

P R O T E I N   D A T A   B A N K

wwPDB X-ray Structure Validation Summary Report ⓘ

May 25, 2020 – 02:13 am BST

PDB ID	:	1R3E
Title	:	Crystal Structure of tRNA Pseudouridine Synthase TruB and Its RNA Complex: RNA-protein Recognition Through a Combination of Rigid Docking and Induced Fit
Authors	:	Pan, H.; Agarwalla, S.; Moustakas, D.T.; Finer-Moore, J.; Stroud, R.M.
Deposited on	:	2003-10-01
Resolution	:	2.10 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 ⓘ symbol.

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

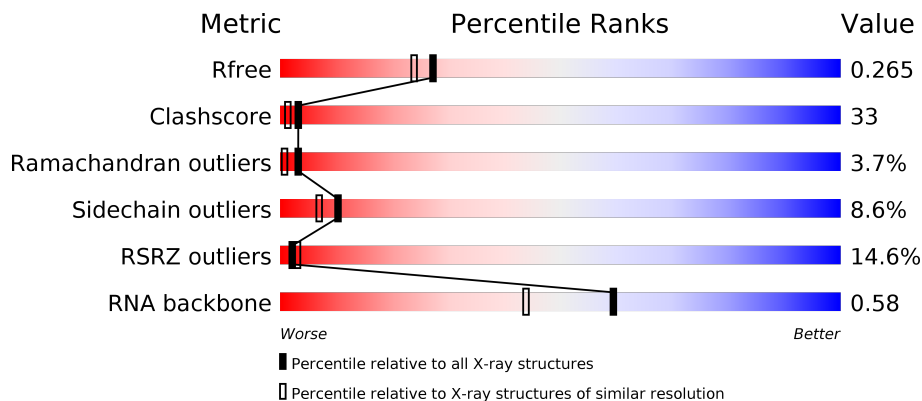|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.10 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	Percentile Ranks	Value
Rfree		0.265
Clashscore		33
Ramachandran outliers		3.7%
Sidechain outliers		8.6%
RSRZ outliers		14.6%
RNA backbone		0.58

Worse — *Better*

■ Percentile relative to all X-ray structures
⧠ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)
RNA backbone	3102	1000 (2.54-1.66)

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 chain
1	C	17	41% 24% 29% 6%
2	D	17	18% / 41% 29% 24% 6%
2	E	17	18% / 41% 29% 29%
3	A	309	15% / 54% 36% 7% ··

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	Res	Chirality	Geometry	Clashes	Electron density
1	FHU	C	410	-	-	X	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3789 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(*CP*UP*GP*UP*GP*UP*(FHU)P*CP*GP*AP*U P*CP*CP*AP*CP*AP*G)-3'.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	F	N	O	P			
1	C	17	357	160	1	60	120	16	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	D	17	355	160	60	119	16	0	0	0
2	E	17	355	160	60	119	16	0	0	0

- Molecule 3 is a protein called tRNA pseudouridine synthase B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	A	305	2459	1573	428	448	10	0	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	C	35	35	35	0	0
4	D	23	23	23	0	0
4	E	19	19	19	0	0
4	A	186	186	186	0	0

3 Residue-property plots ⓘ

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: 5'-R(*CP*UP*GP*UP*GP*UP*(FHU)P*CP*GP*AP*UP*CP*CP*AP*CP*AP*G)-3'

Chain C:

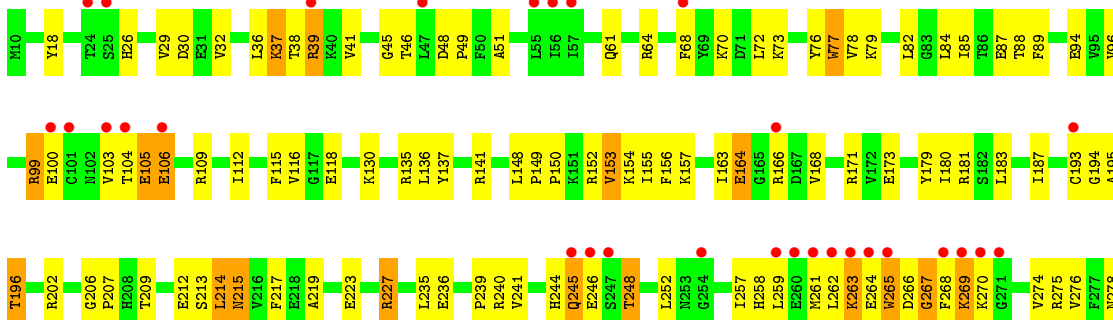- Molecule 2: 5'-R(*CP*UP*GP*UP*GP*UP*UP*CP*GP*AP*UP*CP*CP*AP*CP*AP*G)-3'

Chain D:

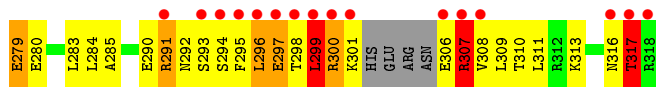- Molecule 2: 5'-R(*CP*UP*GP*UP*GP*UP*UP*CP*GP*AP*UP*CP*CP*AP*CP*AP*G)-3'

Chain E:

- Molecule 3: tRNA pseudouridine synthase B

Chain A:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	98.86Å 159.34Å 44.55Å 90.00° 97.77° 90.00°	Depositor
Resolution (Å)	15.00 – 2.10 39.83 – 2.11	Depositor EDS
% Data completeness (in resolution range)	98.4 (15.00-2.10) 88.3 (39.83-2.11)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	2.66 (at 2.10Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.223 , 0.273 0.221 , 0.265	Depositor DCC
R_{free} test set	1063 reflections (2.75%)	wwPDB-VP
Wilson B-factor (Å^2)	34.7	Xtriage
Anisotropy	0.532	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 75.2	EDS
L-test for twinning[2]	$<|L|> = 0.50$, $<L^2> = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	3789	wwPDB-VP
Average B, all atoms (Å^2)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.88% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical 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.

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

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	C	1.68	1/373 (0.3%)	1.10	2/579 (0.3%)
2	D	0.83	3/395 (0.8%)	1.33	6/613 (1.0%)
2	E	0.37	0/395	0.71	0/613
3	A	0.46	1/2504 (0.0%)	0.76	2/3370 (0.1%)
All	All	0.72	5/3667 (0.1%)	0.88	10/5175 (0.2%)

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	C	0	1
2	D	0	1
All	All	0	2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	410	FHU	O3'-P	30.91	1.98	1.61
2	D	419	A	C2'-O2'	-10.29	1.28	1.41
3	A	77	TRP	NE1-CE2	8.75	1.49	1.37
2	D	419	A	C8-N7	6.56	1.36	1.31
2	D	419	A	C5-C6	-5.55	1.36	1.41

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	410	FHU	P-O3'-C3'	-13.18	103.88	119.70
2	D	419	A	C2-N3-C4	12.54	116.87	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	419	A	C3'-C2'-O2'	-11.47	80.04	113.30
2	D	419	A	C5-C6-N1	9.89	122.64	117.70
2	D	419	A	N1-C2-N3	-8.61	125.00	129.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	408	G	Sidechain
2	D	408	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	C	357	0	185	20	1
2	D	355	0	184	14	0
2	E	355	0	184	16	0
3	A	2459	0	2523	179	0
4	A	186	0	0	11	1
4	C	35	0	0	0	3
4	D	23	0	0	4	0
4	E	19	0	0	1	0
All	All	3789	0	3076	214	5

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 33.

The worst 5 of 214 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:C:410:FHU:O3'	1:C:411:C:P	1.98	1.22
3:A:299:LEU:O	3:A:300:ARG:NE	1.75	1.19
3:A:299:LEU:H	3:A:299:LEU:CD2	1.56	1.15
3:A:29:VAL:HG12	4:A:390:HOH:O	1.45	1.15
3:A:106:GLU:HA	3:A:106:GLU:OE2	1.31	1.09

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:388:HOH:O	4:A:480:HOH:O[2_656]	0.17	2.03
4:C:205:HOH:O	4:C:212:HOH:O[2_656]	0.51	1.69
4:C:133:HOH:O	4:C:247:HOH:O[2_656]	0.65	1.55
4:C:41:HOH:O	4:C:41:HOH:O[2_655]	1.99	0.21
1:C:414:U:N3	1:C:414:U:N3[2_656]	2.17	0.03

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	
3	A	301/309 (97%)	271 (90%)	19 (6%)	11 (4%)	3	1

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	263	LYS
3	A	317	THR
3	A	105	GLU
3	A	245	GLN
3	A	267	GLY

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
3	A	269/273 (98%)	246 (91%)	23 (9%)	10 7

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	227	ARG
3	A	265	TRP
3	A	311	LEU
3	A	248	THR
3	A	269	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
3	A	215	ASN
3	A	292	ASN
3	A	244	HIS
3	A	61	GLN
3	A	226	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	C	16/17 (94%)	5 (31%)	3 (18%)
2	D	16/17 (94%)	5 (31%)	3 (18%)
2	E	16/17 (94%)	5 (31%)	3 (18%)
All	All	48/51 (94%)	15 (31%)	9 (18%)

5 of 15 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	C	409	U
1	C	410	FHU
1	C	411	C
1	C	412	G
1	C	414	U

5 of 9 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	D	410	U

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Mol	Chain	Res	Type
2	E	411	C
2	E	408	G
1	C	415	C
2	D	411	C

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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#$|Z| > 2$	Counts	RMSZ	#$|Z| > 2$
1	FHU	C	410	1	16,23,24	2.22	3 (18%)	19,35,38	2.18	8 (42%)

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	C	410	1	-	0/3/47/48	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	410	FHU	C2-N1	5.12	1.45	1.34
1	C	410	FHU	C4-N3	5.09	1.45	1.37
1	C	410	FHU	C2-N3	4.42	1.45	1.37

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	410	FHU	C5-C4-N3	-5.43	111.02	116.72
1	C	410	FHU	C6-N1-C2	-3.63	117.73	126.45
1	C	410	FHU	C4-N3-C2	-3.55	120.66	126.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	410	FHU	O4-C4-N3	-2.95	115.80	120.50
1	C	410	FHU	C5-C6-N1	2.61	115.30	111.43

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	410	FHU	9	0

5.5 Carbohydrates (i)

There are no carbohydrates 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)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	C	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	410:FHU	O3'	411:C	P	1.98

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, 95th 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(Å²)	Q<0.9
1	C	16/17 (94%)	-0.29	0	100	100	26, 33, 52, 61	0
2	D	17/17 (100%)	0.98	3 (17%)	1	1	46, 63, 152, 161	0
2	E	17/17 (100%)	0.39	3 (17%)	1	1	52, 62, 141, 162	0
3	A	305/309 (98%)	1.11	46 (15%)	2	3	18, 46, 101, 137	2 (0%)
All	All	355/360 (98%)	1.01	52 (14%)	2	3	18, 48, 108, 162	2 (0%)

The worst 5 of 52 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	298	THR	10.1
3	A	299	LEU	9.4
3	A	301	LYS	7.1
2	D	409	U	6.5
2	D	410	U	5.9

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, 95th 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(Å²)	Q<0.9
1	FHU	C	410	22/23	0.86	0.24	25,35,41,49	0

6.3 Carbohydrates (i)

There are no carbohydrates 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.