



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 06:18 PM UTC

PDB ID : 2NQP / pdb_00002nqp
Title : Crystal structure of pseudouridine synthase TruA in complex with leucyl tRNA
Authors : Hur, S.; Stroud, R.M.
Deposited on : 2006-10-31
Resolution : 3.50 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

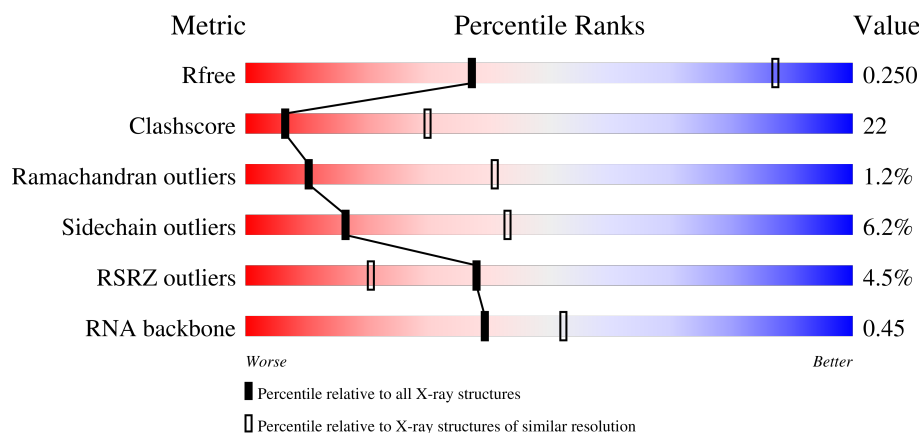
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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}	180053	1085 (3.54-3.46)
Clashscore	190562	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)
RNA backbone	3983	1010 (3.98-3.02)

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 $\leq 5\%$. 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	F	87	40% 22% 46% 13% • 18%
2	A	270	50% 44% • •
2	B	270	% 55% 39% • •
2	C	270	4% 53% 42% • •

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Mol	Chain	Length	Quality of chain
2	D	270	% 49% 44%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9765 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 transfer RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	F	71	Total	C	N	O	P	21	0	0
			1441	636	256	480	69			

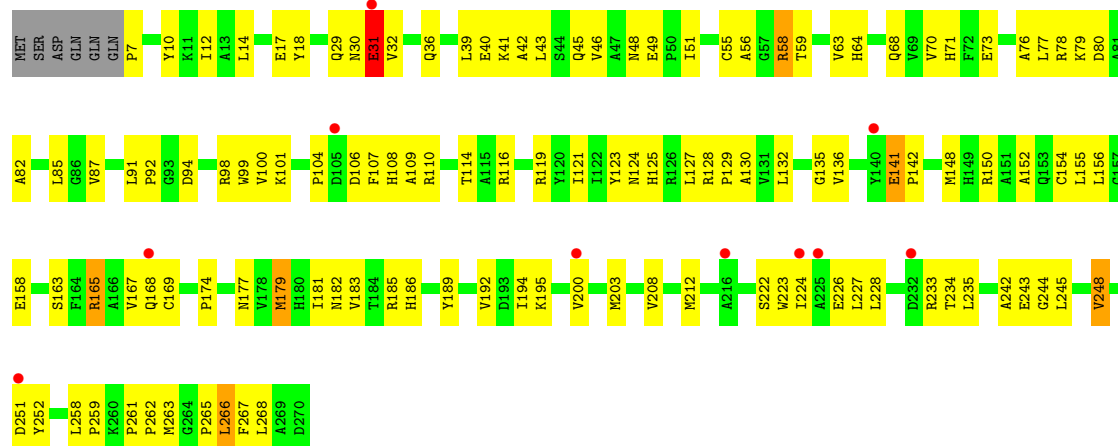
- Molecule 2 is a protein called tRNA pseudouridine synthase A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	264	Total	C	N	O	S	0	0	0
			2088	1327	379	374	8			
2	B	264	Total	C	N	O	S	0	0	0
			2083	1325	377	373	8			
2	C	264	Total	C	N	O	S	0	0	0
			2057	1306	373	370	8			
2	D	263	Total	C	N	O	S	18	0	0
			2090	1328	381	373	8			

- Molecule 3 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	F	5	Total	K	0	0
			5	5		
3	C	1	Total	K	0	0
			1	1		

- Molecule 2: tRNA pseudouridine synthase A



- Molecule 2: tRNA pseudouridine synthase A



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	96.28Å 128.59Å 159.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.50 20.00 – 3.50	Depositor EDS
% Data completeness (in resolution range)	94.1 (20.00-3.50) 93.5 (20.00-3.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.24	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 3.33Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.246 , 0.279 0.227 , 0.250	Depositor DCC
R_{free} test set	3032 reflections (10.00%)	wwPDB-VP
Wilson B-factor (Å ²)	53.2	Xtriage
Anisotropy	0.316	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 50.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	9765	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.22% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

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:
K

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	F	0.49	0/1604	0.88	4/2498 (0.2%)
2	A	0.65	0/2142	0.96	7/2915 (0.2%)
2	B	0.64	0/2139	0.96	8/2912 (0.3%)
2	C	0.59	0/2112	0.95	8/2881 (0.3%)
2	D	0.60	0/2145	0.93	5/2917 (0.2%)
All	All	0.60	0/10142	0.94	32/14123 (0.2%)

There are no bond length outliers.

The worst 5 of 32 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	B	248	VAL	N-CA-C	6.91	117.70	110.72
2	C	248	VAL	N-CA-C	6.70	117.49	110.72
2	A	248	VAL	N-CA-C	6.69	117.48	110.72
2	D	248	VAL	N-CA-C	6.61	117.40	110.72
2	B	18	TYR	N-CA-C	6.47	117.00	107.88

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	F	1441	0	722	44	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	2088	0	2039	98	0
2	B	2083	0	2039	89	0
2	C	2057	0	1982	91	0
2	D	2090	0	2059	104	0
3	C	1	0	0	0	0
3	F	5	0	0	0	0
All	All	9765	0	8841	402	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 22.

The worst 5 of 402 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)
2:A:130:ALA:HB3	2:B:17:GLU:HG2	1.46	0.95
2:A:17:GLU:HG2	2:B:130:ALA:HB3	1.51	0.92
2:C:130:ALA:HB1	2:D:94:ASP:O	1.70	0.88
1:F:58:A:H4'	1:F:59:G:OP1	1.70	0.88
2:A:41:LYS:CA	2:A:42:ALA:N	2.41	0.83

There are no symmetry-related clashes.

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	
2	A	260/270 (96%)	230 (88%)	28 (11%)	2 (1%)	16	49
2	B	262/270 (97%)	228 (87%)	31 (12%)	3 (1%)	11	43
2	C	262/270 (97%)	229 (87%)	29 (11%)	4 (2%)	8	37
2	D	261/270 (97%)	226 (87%)	31 (12%)	4 (2%)	8	37
All	All	1045/1080 (97%)	913 (87%)	119 (11%)	13 (1%)	10	41

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	243	GLU
2	B	243	GLU
2	C	243	GLU
2	D	243	GLU
2	C	168	GLN

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	214/223 (96%)	200 (94%)	14 (6%)	15	42
2	B	214/223 (96%)	200 (94%)	14 (6%)	15	42
2	C	207/223 (93%)	198 (96%)	9 (4%)	26	51
2	D	216/223 (97%)	200 (93%)	16 (7%)	13	37
All	All	851/892 (95%)	798 (94%)	53 (6%)	16	43

5 of 53 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	31	GLU
2	C	179	MET
2	D	171	SER
2	C	58	ARG
2	C	156	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	125	HIS
2	C	218	ASN
2	C	149	HIS
2	C	182	ASN
2	D	45	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	F	65/87 (74%)	14 (21%)	3 (4%)

5 of 14 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	F	7	A
1	F	9	G
1	F	10	G
1	F	14	A
1	F	17	C

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	F	18	G
1	F	58	A
1	F	60	U

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 6 are 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.

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, 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(Å ²)	Q<0.9
1	F	71/87 (81%)	2.20	35 (49%) 0 1	27, 80, 192, 226	5 (7%)
2	A	264/270 (97%)	-0.09	1 (0%) 88 72	8, 18, 43, 60	0
2	B	264/270 (97%)	-0.05	2 (0%) 82 60	8, 21, 42, 64	0
2	C	264/270 (97%)	0.27	10 (3%) 44 24	8, 34, 67, 81	0
2	D	263/270 (97%)	0.12	3 (1%) 78 54	10, 29, 52, 67	5 (1%)
All	All	1126/1167 (96%)	0.20	51 (4%) 38 20	8, 27, 66, 226	10 (0%)

The worst 5 of 51 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	70	G	8.2
1	F	19	G	5.9
1	F	50	C	4.7
1	F	45(D)	G	4.6
2	D	8	PRO	4.3

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 oligosaccharides 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, 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(Å ²)	Q<0.9
3	K	F	81	1/1	0.78	0.21	67,67,67,67	0
3	K	F	77	1/1	0.84	0.92	56,56,56,56	0
3	K	C	271	1/1	0.88	0.07	26,26,26,26	0
3	K	F	78	1/1	0.89	0.14	28,28,28,28	0
3	K	F	79	1/1	0.92	0.25	74,74,74,74	0
3	K	F	80	1/1	0.94	0.07	72,72,72,72	0

6.5 Other polymers ⓘ

There are no such residues in this entry.