



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:49 PM GMT

PDB ID : 4WC2
Title : Crystal structure of tRNA nucleotidyltransferase complexed with a primer tRNA and an incoming ATP analog
Authors : Yamashita, S.; Tomita, K.
Deposited on : 2014-09-04
Resolution : 2.80 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

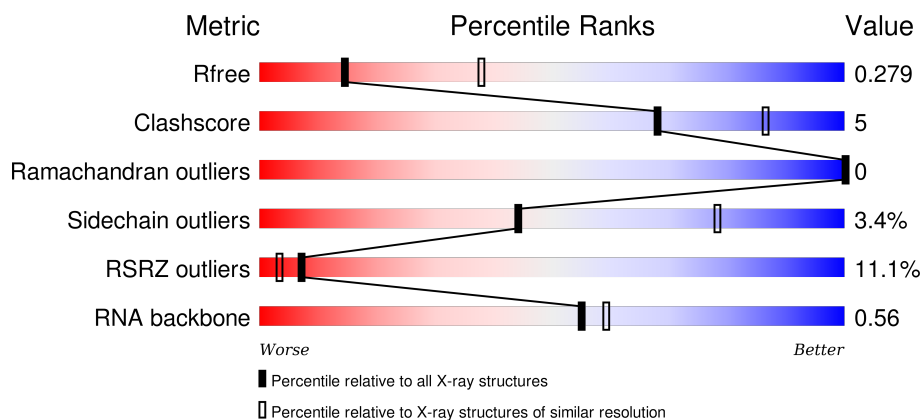
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)
RNA backbone	2183	1091 (3.20-2.40)

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. 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	A	396	<div> <div>5%</div> <div>81%</div> <div>11%</div> <div>7%</div> </div>
2	B	75	<div> <div>37%</div> <div>55%</div> <div>28%</div> <div>17%</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4679 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 protein called Poly A polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	367	Total	C	N	O	S	0	0	0
			3046	1978	527	534	7			

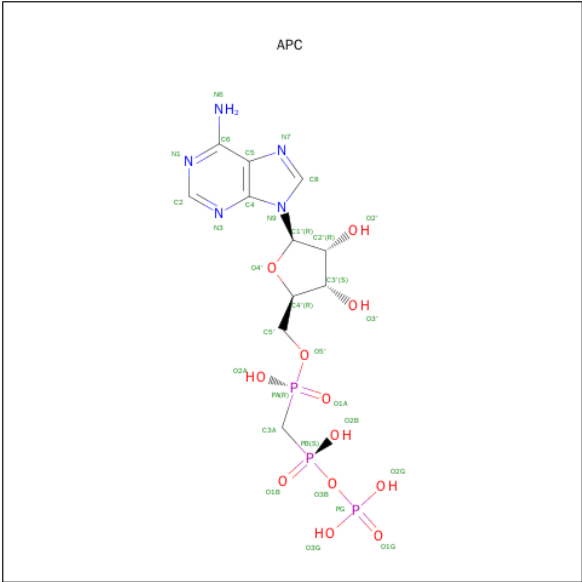
There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP O66728
A	384	LYS	-	expression tag	UNP O66728
A	385	LEU	-	expression tag	UNP O66728
A	386	ALA	-	expression tag	UNP O66728
A	387	ALA	-	expression tag	UNP O66728
A	388	ALA	-	expression tag	UNP O66728
A	389	LEU	-	expression tag	UNP O66728
A	390	GLU	-	expression tag	UNP O66728
A	391	HIS	-	expression tag	UNP O66728
A	392	HIS	-	expression tag	UNP O66728
A	393	HIS	-	expression tag	UNP O66728
A	394	HIS	-	expression tag	UNP O66728
A	395	HIS	-	expression tag	UNP O66728
A	396	HIS	-	expression tag	UNP O66728

- Molecule 2 is a RNA chain called RNA 75-mer.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	75	Total	C	N	O	P	0	0	0
			1601	713	286	527	75			

- Molecule 3 is DIPHOSPHOMETHYLPHOSPHONIC ACID ADENOSYL ESTER (three-letter code: APC) (formula: C₁₁H₁₈N₅O₁₂P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			31	11	5	12	3		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	58.92Å 109.48Å 125.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.80 – 2.80 39.19 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.1 (19.80-2.80) 99.0 (39.19-2.80)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	9.53 (at 2.81Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.215 , 0.267 0.221 , 0.279	Depositor DCC
R_{free} test set	1024 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	72.5	Xtriage
Anisotropy	0.308	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 97.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	1 of 20534 reflections (0.005%)	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4679	wwPDB-VP
Average B, all atoms (Å ²)	169.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.25% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: APC, MG

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	A	0.21	0/3097	0.38	0/4150
2	B	0.29	1/1788 (0.1%)	0.70	0/2784
All	All	0.24	1/4885 (0.0%)	0.53	0/6934

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	G	OP3-P	-10.63	1.48	1.61

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	A	3046	0	3205	24	0
2	B	1601	0	811	16	0
3	A	31	0	12	1	0
4	A	1	0	0	0	0
All	All	4679	0	4028	39	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 5.

All (39) 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:B:9:A:N3	2:B:45:U:H2'	1.97	0.80
2:B:27:C:H42	2:B:43:G:H1	1.30	0.77
2:B:74:C:H5'	2:B:75:C:H5'	1.85	0.57
1:A:372:ILE:HA	1:A:375:LEU:HD12	1.86	0.56
2:B:42:A:H5'	2:B:43:G:OP2	2.05	0.56
2:B:18:G:O2'	2:B:57:G:N2	2.38	0.56
1:A:21:ARG:NH1	1:A:109:ASN:OD1	2.40	0.55
2:B:27:C:N3	2:B:43:G:N2	2.46	0.55
1:A:149:ASP:OD2	1:A:191:ARG:NH2	2.39	0.55
1:A:34:PHE:HE1	1:A:73:LEU:HD22	1.73	0.54
1:A:293:MET:HA	1:A:297:LEU:HB2	1.89	0.54
2:B:9:A:O2'	2:B:10:G:N7	2.40	0.53
1:A:8:GLU:OE1	1:A:50:ARG:NH2	2.41	0.53
1:A:184:LEU:HD23	1:A:220:GLU:HB2	1.90	0.53
1:A:304:LEU:O	1:A:337:LYS:NZ	2.43	0.52
1:A:354:LYS:O	1:A:358:LEU:HG	2.08	0.51
2:B:9:A:H1'	2:B:45:U:O2'	2.11	0.50
1:A:358:LEU:HD13	1:A:375:LEU:HD13	1.94	0.50
2:B:30:G:H2'	2:B:31:A:H8	1.79	0.47
2:B:33:U:H2'	2:B:35:A:OP2	2.15	0.47
1:A:349:LYS:HB2	1:A:349:LYS:NZ	2.29	0.47
2:B:44:G:H2'	2:B:46:G:OP1	2.15	0.46
1:A:314:TYR:OH	1:A:376:LYS:NZ	2.48	0.46
1:A:25:LEU:HD21	1:A:133:LEU:HD11	1.98	0.45
2:B:19:G:H4'	2:B:20:U:C5'	2.47	0.45
1:A:275:HIS:NE2	1:A:279:GLU:OE2	2.51	0.44
2:B:68:U:H2'	2:B:69:G:C8	2.53	0.43
1:A:249:PHE:HE2	1:A:342:LEU:HD22	1.83	0.43
1:A:104:ARG:HA	3:A:401:APC:H2	2.01	0.43
1:A:100:ASP:O	1:A:103:ARG:HG2	2.19	0.43
1:A:355:ILE:HA	1:A:358:LEU:HD12	2.02	0.42
2:B:72:C:O2'	2:B:73:A:O4'	2.37	0.42
1:A:314:TYR:HB2	1:A:345:LEU:HD21	2.02	0.42
2:B:27:C:H2'	2:B:28:U:C6	2.54	0.41
1:A:366:LYS:HZ3	2:B:19:G:H8	1.67	0.41
1:A:150:PRO:HB2	1:A:187:ALA:HB2	2.02	0.41
1:A:249:PHE:HA	1:A:249:PHE:HD1	1.66	0.41
1:A:17:GLY:HA2	1:A:109:ASN:O	2.21	0.41
1:A:187:ALA:HB3	1:A:192:LEU:HD11	2.03	0.40

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	
1	A	361/396 (91%)	346 (96%)	15 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	
1	A	326/349 (93%)	315 (97%)	11 (3%)	44	78

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	VAL
1	A	82	THR
1	A	134	LYS
1	A	230	LYS
1	A	239	ARG
1	A	249	PHE
1	A	269	ASP
1	A	294	LYS
1	A	343	GLU
1	A	344	LYS
1	A	349	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	74/75 (98%)	23 (31%)	2 (2%)

All (23) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	10	G
2	B	13	C
2	B	17	U
2	B	18	G
2	B	19	G
2	B	20	U
2	B	21	A
2	B	22	G
2	B	25	C
2	B	27	C
2	B	42	A
2	B	43	G
2	B	44	G
2	B	45	U
2	B	46	G
2	B	47	U
2	B	48	C
2	B	49	G
2	B	61	C
2	B	71	C
2	B	72	C
2	B	73	A
2	B	75	C

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	19	G
2	B	45	U

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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	$\# Z > 2$
3	APC	A	401	4	25,33,33	3.53	11 (44%)	30,52,52	2.92	8 (26%)

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
3	APC	A	401	4	-	0/15/38/38	0/3/3/3

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	401	APC	C2'-C3'	-11.84	1.21	1.53
3	A	401	APC	O4'-C4'	-6.23	1.30	1.45
3	A	401	APC	C5-C4	-2.21	1.35	1.40
3	A	401	APC	C2-N1	2.15	1.38	1.33
3	A	401	APC	PA-O5'	2.61	1.60	1.57
3	A	401	APC	C6-N6	2.97	1.44	1.34
3	A	401	APC	O3'-C3'	3.90	1.52	1.43
3	A	401	APC	C2-N3	4.04	1.39	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	401	APC	C3'-C4'	4.13	1.64	1.53
3	A	401	APC	O4'-C1'	4.58	1.47	1.41
3	A	401	APC	O2'-C2'	4.64	1.54	1.43

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	401	APC	N3-C2-N1	-11.33	120.22	128.89
3	A	401	APC	C1'-N9-C4	-8.26	114.49	126.94
3	A	401	APC	N6-C6-N1	-3.34	112.03	119.20
3	A	401	APC	C4'-O4'-C1'	-3.08	106.34	109.72
3	A	401	APC	PG-O3B-PB	-2.71	123.57	132.67
3	A	401	APC	C2'-C1'-N9	-2.23	110.89	114.29
3	A	401	APC	O5'-PA-C3A	2.24	110.69	104.42
3	A	401	APC	C2'-C3'-C4'	2.25	107.23	102.61

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
3	A	401	APC	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 ⓘ

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, 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	A	367/396 (92%)	0.19	21 (5%)	27 17	45, 90, 233, 329	0
2	B	75/75 (100%)	2.01	28 (37%)	0 0	187, 269, 377, 407	0
All	All	442/471 (93%)	0.50	49 (11%)	7 3	45, 105, 303, 407	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	44	G	8.0
2	B	30	G	7.3
2	B	46	G	7.2
1	A	357	GLU	7.0
1	A	367	GLU	6.7
1	A	350	LEU	6.5
1	A	365	GLY	6.4
1	A	358	LEU	5.8
1	A	353	GLU	5.7
2	B	29	G	5.5
2	B	47	U	5.5
1	A	351	PRO	5.5
1	A	354	LYS	5.3
2	B	60	U	4.8
2	B	19	G	4.3
1	A	349	LYS	4.2
2	B	20	U	4.1
1	A	381	ASN	4.0
2	B	9	A	3.8
2	B	32	C	3.8
1	A	374	GLU	3.7
2	B	24	G	3.7
1	A	368	LEU	3.7
2	B	45	U	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	348	VAL	3.4
1	A	378	GLU	3.3
2	B	33	U	3.2
2	B	34	G	3.2
2	B	75	C	3.0
2	B	5	A	2.9
2	B	10	G	2.8
1	A	311	TYR	2.8
2	B	40	C	2.8
1	A	356	GLU	2.8
2	B	23	A	2.8
1	A	246	ALA	2.7
2	B	72	C	2.6
2	B	70	G	2.5
1	A	352	LYS	2.5
2	B	4	C	2.5
2	B	31	A	2.4
1	A	278	GLU	2.4
2	B	13	C	2.4
2	B	27	C	2.3
1	A	355	ILE	2.3
2	B	41	C	2.3
1	A	61	PHE	2.2
2	B	64	C	2.2
2	B	62	C	2.1

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 carbohydrates 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. 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, 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	LLDF	B-factors(\AA^2)	Q<0.9
3	APC	A	401	31/31	0.90	0.29	1.14	58,96,173,201	0
4	MG	A	402	1/1	0.97	0.23	-	98,98,98,98	0

6.5 Other polymers [i](#)

There are no such residues in this entry.