

wwPDB NMR Structure Validation Summary Report (i)

Feb 16, 2022 – 11:08 AM EST

PDB ID	:	1LUU
Title	:	NMR SOLUTION STRUCTURE OF THE ANTICODON OF YEAST
		TRNA-PHE WITH 4 MODIFICATIONS (OMC32 OMG34 1MG37 5MC40)
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Deposited on	:	2002-05-23

This is a wwPDB NMR 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/NMRValidationReportHelp with specific help available everywhere you see the (i) symbol.

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

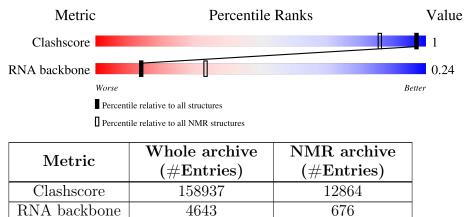
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.26
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)		
Validation Pipeline (wwPDB-VP)	:	2.26

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $SOLUTION\ NMR$

The overall completeness of chemical shifts assignment was not calculated.

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.



The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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%

Mol	Chain	Length	Quality of chain					
1	А	17	18%	47%	35%			



2 Ensemble composition and analysis (i)

This entry contains 11 models. This entry does not contain polypeptide chains, therefore identification of well-defined residues and clustering analysis are not possible. All residues are included in the validation scores.



3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 561 atoms, of which 195 are hydrogens and 0 are deuteriums.

• Molecule 1 is a RNA chain called 5'-R(*CP*CP*AP*GP*AP*(OMC)P*UP*(OMG)P*AP* AP*(1MG)P*AP*UP*(5MC)P*UP*GP*G)-3'.

Mol	Chain	Residues		Atoms					Trace
1	٨	17	Total	С	Η	Ν	0	Р	0
	1 A	17	561	167	195	68	115	16	0



4 Residue-property plots (i)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

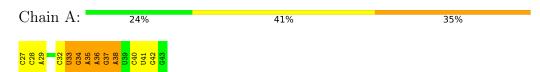
• Molecule 1: 5'-R(*CP*CP*AP*GP*AP*(OMC)P*UP*(OMG)P*AP*AP*(1MG)P*AP*UP*(5 MC)P*UP*GP*G)-3'

Chain A:	18%	47%	35%
C27 C28 A29 G30 G30 C32 C32 C33	634 635 637 637 637 637 637 633 041 041 041 643 643		

4.2 Residue scores for the representative (author defined) model from the NMR ensemble

The representative model is number 1. Colouring as in section 4.1 above.

• Molecule 1: 5'-R(*CP*CP*AP*GP*AP*(OMC)P*UP*(OMG)P*AP*AP*(1MG)P*AP*UP*(5 MC)P*UP*GP*G)-3'





5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *GLOBAL FOLD BY DISTANCE GE-OMETRY. REFINEMENT BY SIMULATED ANNEALING USING THE AMBER FORCE-FIELD.*

Of the 50 calculated structures, 11 were deposited, based on the following criterion: *structures with the least restraint violations, structures with the lowest energy.*

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
Discover	refinement	98

No chemical shift data was provided.



6 Model quality (i)

6.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 1MG, OMG, 5MC, OMC

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 (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	E	Bond lengths	Bond angles		
IVIOI	Chain	RMSZ	#Z > 5	RMSZ	#Z > 5	
1	А	$1.36 {\pm} 0.03$	$2{\pm}0/309~(~0.6{\pm}~0.0\%)$	1.82 ± 0.06	$6{\pm}2/480~(~1.3{\pm}~0.4\%)$	
All	All	1.36	22/3399~(~0.6%)	1.82	69/5280~(~1.3%)	

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	Planarity
1	А	$0.0{\pm}0.0$	$5.4{\pm}1.4$
All	All	0	59

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	n Res Type Atoms Z Observed(Å	$Observed(\lambda)$	$(\hat{\lambda})$ Ideal $(\hat{\lambda})$	Models				
	Ullalli	nes	\mathbf{z} Type Atoms \mathbf{z} Observed(A)	Observed(A)	Ideal(A)	Worst	Total		
1	А	38	A	C6-N1	6.13	1.39	1.35	8	11
1	А	38	А	N1-C2	6.09	1.39	1.34	8	11

5 of 13 unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Mol Chain I		Type	Atoms	$\mathbf{Z} = \mathbf{Observed}(^{o})$		$Ideal(^{o})$	Models	
WIOI	Unam	Res	tes Type Atoms Z Observed(Observed()	iucai()	Worst	Total	
1	А	38	A	N1-C2-N3	-11.32	123.64	129.30	6	11
1	А	36	А	O4'-C1'-N9	9.60	115.88	108.20	11	8
1	А	33	U	O4'-C1'-N1	8.98	115.38	108.20	6	8
1	А	35	А	O4'-C1'-N9	8.87	115.30	108.20	6	5
1	А	38	А	C2-N3-C4	8.51	114.85	110.60	1	11



There are no chirality outliers.

5 of 10 unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	А	27	С	Sidechain	11
1	А	42	G	Sidechain	11
1	А	28	С	Sidechain	9
1	А	30	G	Sidechain	8
1	А	29	А	Sidechain	6

6.2 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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	А	366	195	194	0 ± 0
All	All	4026	2145	2134	4

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 1.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$Clack(\lambda)$	Distance(Å)	Models	
	Atom-2	Clash(A)	Distance(A)	Worst	Total
1:A:34:OMG:HM22	1:A:35:A:H2'	0.56	1.76	10	4

6.3 Torsion angles (i)

6.3.1 Protein backbone (i)

There are no protein molecules in this entry.

6.3.2 Protein sidechains (i)

There are no protein molecules in this entry.

6.3.3 RNA (i)



Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
1	А	16/17~(94%)	$6\pm1 (38\pm4\%)$	$2\pm0~(14\pm3\%)$	$0.24{\pm}0.08$
All	All	176/187~(94%)	67 (38%)	25~(14%)	0.24

The overall RNA backbone suiteness is 0.24.

5 of 8 unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	А	33	U	11
1	А	34	OMG	11
1	А	35	А	11
1	А	37	1MG	11
1	А	38	А	11

A11	unique	RNA	pucker	outliers	are	listed	below:
1 111	unque	TUTIT	pucher	outiful	arc	mouca	DC10W.

Mol	Chain	Res	Type	Models (Total)
1	А	33	U	11
1	А	34	OMG	11
1	А	35	А	2
1	А	37	1MG	1

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

4 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds 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 is the number of standard deviations the observed value is removed from the expected value. A bond length with |Z| > 2 is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link Bond lengths				
MOI	туре	Unam	nes	LIIIK	Counts	RMSZ	#Z>2	
1	OMG	А	34	1	$18,\!26,\!27$	$1.36{\pm}0.03$	3 ± 0 (16 $\pm1\%$)	
1	5MC	А	40	1	15,22,23	$0.87 {\pm} 0.01$	0±0 (0±0%)	
1	OMC	А	32	1	15,22,23	$0.82 {\pm} 0.04$	$0\pm0~(0\pm0\%)$	
1	1MG	А	37	1	18,26,27	$1.00{\pm}0.11$	2 ± 1 (10±4%)	

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of 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 angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with |Z| > 2 is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Turne	Chain	Res	Link	Bond angles				
10101	Type	Unam	nes	LIIIK	Counts	RMSZ	#Z>2		
1	OMG	А	34	1	20,38,41	2.57 ± 0.04	$5\pm1(23\pm4\%)$		
1	5MC	А	40	1	19,32,35	$1.27 {\pm} 0.04$	$1\pm0 (5\pm0\%)$		
1	OMC	А	32	1	17,31,34	$1.51 {\pm} 0.16$	2±0 (13±2%)		
1	1MG	А	37	1	19,39,42	$1.67 {\pm} 0.34$	2±2 (10±8%)		

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	1MG	А	37	1	-	$0\pm 0,3,25,26$	$0\pm0,3,3,3$
1	5MC	А	40	1	-	$0\pm 0,5,25,26$	$0\pm0,2,2,2$
1	OMC	А	32	1	-	$0\pm 0,7,27,28$	$0\pm0,2,2,2$
1	OMG	А	34	1	-	$0\pm 0, 5, 27, 28$	$0\pm 0,3,3,3$

5 of 7 unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mal	Mol Chain F		Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
MOI	Ullalli	\mathbf{Res}	Type	Atoms		Observeu(A)	Iueai(A)	Worst	Total
1	А	34	OMG	C6-N1	4.11	1.40	1.33	5	11
1	А	37	1MG	O4'-C4'	2.32	1.39	1.45	1	1
1	А	37	1MG	O4'-C1'	2.32	1.37	1.41	1	1
1	А	37	1MG	C8-N7	2.31	1.30	1.34	11	11
1	А	34	OMG	C8-N7	2.29	1.30	1.34	6	11

5 of 20 unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain Res Type Atoms		7	Observed(°)	$Ideal(^{o})$	Models			
	Unain	nes	Type	Atoms		Observed(*)	Ideal(*)	Worst	Total
1	А	34	OMG	C5-C6-N1	8.12	112.32	123.43	4	11
1	А	37	1MG	C5-C6-N1	6.31	111.47	118.20	1	11
1	А	34	OMG	C2-N1-C6	5.34	124.41	115.93	7	11
1	А	32	OMC	O2'-C2'-C1'	4.95	118.91	109.09	5	7

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Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$\mathbf{Ideal}(^{o})$	Moo Worst	d els Total
1	А	40	5MC	C4-N3-C2	4.84	121.86	116.02	7	11

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6.5 Carbohydrates (i)

There are no monosaccharides in this entry.

6.6 Ligand geometry (i)

There are no ligands in this entry.

6.7 Other polymers (i)

There are no such molecules in this entry.

6.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



7 Chemical shift validation (i)

No chemical shift data were provided

