



# wwPDB NMR Structure Validation Summary Report ⓘ

Feb 20, 2018 – 06:00 pm GMT

PDB ID : 1F3Y  
Title : SOLUTION STRUCTURE OF THE NUDIX ENZYME DIADENOSINE  
TETRAPHOSPHATE HYDROLASE FROM LUPINUS ANGUSTIFOLIUS  
L.  
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<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

Cyrange : Kirchner and Güntert (2011)  
NmrClust : Kelley et al. (1996)  
MolProbity : 4.02b-467  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
ShiftChecker : trunk30686  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30686

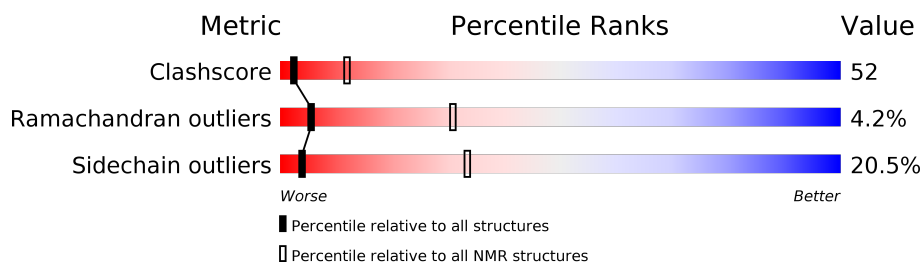
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 83%.

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)	NMR archive (#Entries)
Clashscore	136279	12091
Ramachandran outliers	132675	10835
Sidechain outliers	132484	10811

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  $\geq 3$ , 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  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	165	

## 2 Ensemble composition and analysis

This entry contains 25 models. Model 20 is the overall representative, medoid model (most similar to other models). The authors have identified model 3 as representative, based on the following criterion: *lowest energy*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:6-A:7, A:15-A:80, A:104-A:121, A:130-A:165 (122)	0.23	20

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 5 clusters and 1 single-model cluster was found.

Cluster number	Models
1	1, 3, 4, 5, 6, 8, 11, 14, 16, 20, 21, 22, 24, 25
2	10, 17, 18, 23
3	2, 9
4	13, 19
5	7, 12
Single-model clusters	15

### 3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2617 atoms, of which 1286 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE.

Mol	Chain	Residues	Atoms						Trace
1	A	165	Total	C	H	N	O	S	0
			2617	855	1286	220	252	4	

There are 4 discrepancies between the modelled and reference sequences:

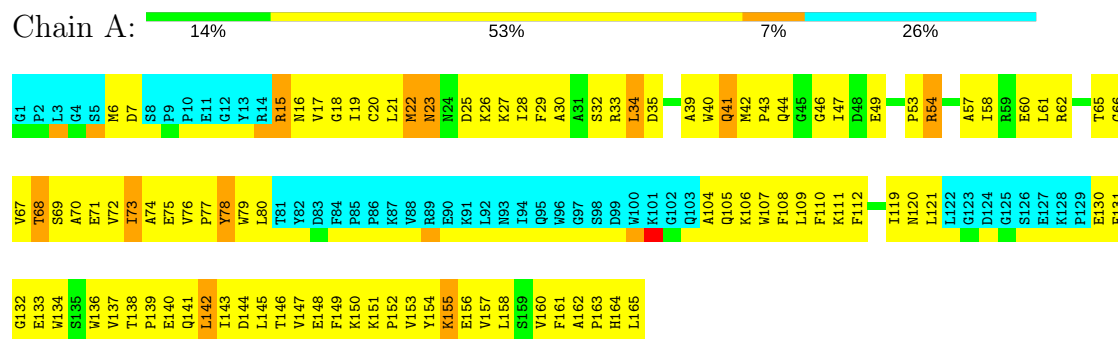
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	TYR	ENGINEERED	UNP O04841
A	2	PRO	CYS	ENGINEERED	UNP O04841
A	3	LEU	HIS	ENGINEERED	UNP O04841
A	4	GLY	SER	ENGINEERED	UNP O04841

## 4 Residue-property plots [i](#)

### 4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA 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.

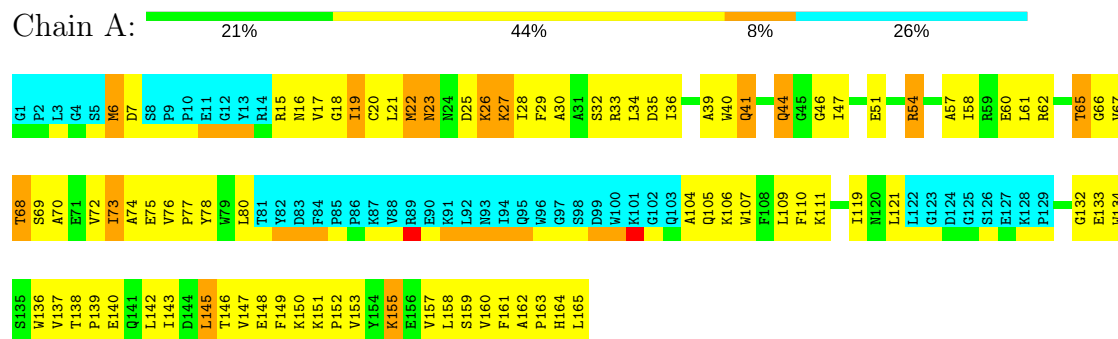
- Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE



### 4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 20. Colouring as in section 4.1 above.

- Molecule 1: DIADENOSINE 5',5'''-P1,P4-TETRAPHOSPHATE HYDROLASE



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics, simulated annealing*.

Of the 100 calculated structures, 25 were deposited, based on the following criterion: *structures with favorable non-bond energy, structures with the least restraint violations, target function*.

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

Software name	Classification	Version
DYANA	refinement	1.5,1.4
CNS	refinement	0.9

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	BMRB entry 4448
Number of chemical shift lists	1
Total number of shifts	1788
Number of shifts mapped to atoms	1788
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	83%

No validations of the models with respect to experimental NMR restraints is performed at this time.

## 6 Model quality [i](#)

### 6.1 Standard geometry [i](#)

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	A	993	964	963	102±14
All	All	24825	24100	24075	2545

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 52.

5 of 586 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:19:ILE:HG21	1:A:61:LEU:HD22	0.97	1.35	22	12
1:A:19:ILE:HG23	1:A:57:ALA:HB1	0.93	1.40	10	7
1:A:19:ILE:HG21	1:A:61:LEU:HD13	0.90	1.41	23	5
1:A:19:ILE:HG22	1:A:110:PHE:CE1	0.89	2.02	19	6
1:A:143:ILE:HG21	1:A:155:LYS:HD3	0.89	1.44	1	5

### 6.3 Torsion angles [i](#)

#### 6.3.1 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 PDB entries followed by that with respect to all NMR entries. 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	121/165 (73%)	99±2 (82±2%)	17±2 (14±2%)	5±2 (4±1%)	5	31
All	All	3025/4125 (73%)	2485 (82%)	413 (14%)	127 (4%)	5	31

5 of 13 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	69	SER	25
1	A	6	MET	16
1	A	49	GLU	14
1	A	77	PRO	12
1	A	15	ARG	11

### 6.3.2 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 PDB entries followed by that with respect to all NMR entries. 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	106/142 (75%)	84±4 (79±3%)	22±4 (21±3%)	4	33
All	All	2650/3550 (75%)	2106 (79%)	544 (21%)	4	33

5 of 59 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	54	ARG	25
1	A	144	ASP	24
1	A	34	LEU	23
1	A	155	LYS	23
1	A	68	THR	22

### 6.3.3 RNA ⓘ

There are no RNA molecules in this entry.



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

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

## 6.5 Carbohydrates [i](#)

There are no carbohydrates 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

The completeness of assignment taking into account all chemical shift lists is 83% for the well-defined parts and 78% for the entire structure.

### 7.1 Chemical shift list 1

File name: BMRB entry 4448

Chemical shift list name: *assigned\_chem\_shift\_list\_1*

#### 7.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1788
Number of shifts mapped to atoms	1788
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	8

#### 7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	158	$0.11 \pm 0.09$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	141	$0.50 \pm 0.13$	Should be applied
$^{13}\text{C}'$	157	$0.11 \pm 0.09$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	147	$-0.77 \pm 0.32$	Should be applied

#### 7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 83%, i.e. 1273 atoms were assigned a chemical shift out of a possible 1543. 18 out of 19 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	596/596 (100%)	237/237 (100%)	244/244 (100%)	115/115 (100%)
Sidechain	639/800 (80%)	395/468 (84%)	237/299 (79%)	7/33 (21%)

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	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Aromatic	38/147 (26%)	33/77 (43%)	0/63 (0%)	5/7 (71%)
Overall	1273/1543 (83%)	665/782 (85%)	481/606 (79%)	127/155 (82%)

#### 7.1.4 Statistically unusual chemical shifts [i](#)

The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	155	LYS	CD	67.00	34.86 – 23.06	32.2
1	A	80	LEU	CD2	6.00	32.60 – 15.60	-10.6
1	A	18	GLY	HA3	0.39	5.80 – 2.00	-9.2
1	A	106	LYS	HB3	-0.43	3.10 – 0.40	-8.1
1	A	109	LEU	HB2	-0.98	3.32 – -0.08	-7.6
1	A	109	LEU	HB3	-0.98	3.34 – -0.26	-7.0
1	A	32	SER	HB3	1.91	5.25 – 2.45	-6.9
1	A	23	ASN	HB3	0.91	4.41 – 1.11	-5.6

#### 7.1.5 Random Coil Index (RCI) plots [i](#)

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A:

