



Full wwPDB NMR Structure Validation Report ⓘ

May 29, 2020 – 12:04 am BST

PDB ID : 2N0O
Title : NMR Solution Structure and Model Membrane Interaction Studies of the Peptide Hylin a1 from the Arboreal South American Frog *Hypsiboas albopunctatus*
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Deposited on : 2015-03-11

This is a Full wwPDB NMR Structure Validation 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 ⓘ symbol.

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 : 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 : 2.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

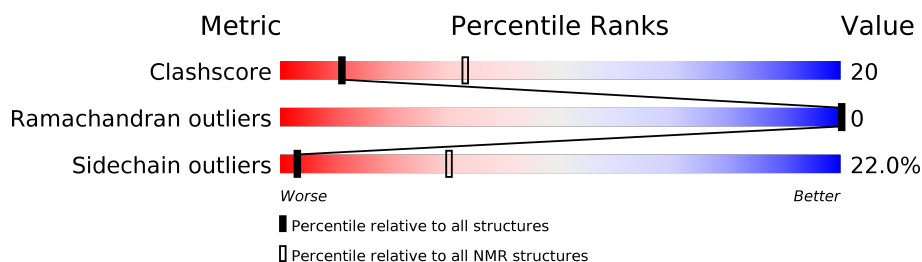
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 40%.

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	19	

2 Ensemble composition and analysis

This entry contains 10 models. Model 7 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 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:4-A:17 (14)	0.23	7

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 2 clusters and 1 single-model cluster was found.

Cluster number	Models
1	1, 2, 3, 7, 9, 10
2	4, 5, 6
Single-model clusters	8

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 293 atoms, of which 161 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Hylin-a1.

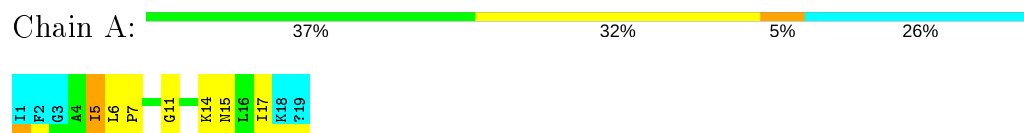
Mol	Chain	Residues	Atoms					Trace
1	A	19	Total	C	H	N	O	1
			293	91	161	22	19	

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	19	NH2	-	AMIDATION	UNP P85982

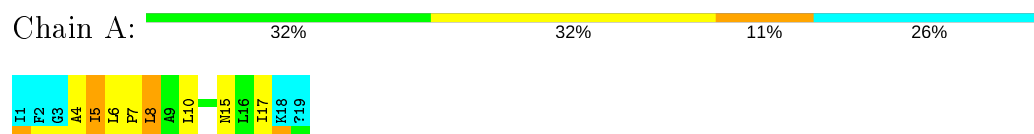
4.2.3 Score per residue for model 3

- Molecule 1: Hylin-a1



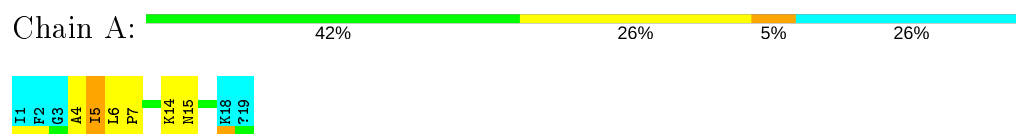
4.2.4 Score per residue for model 4

- Molecule 1: Hylin-a1



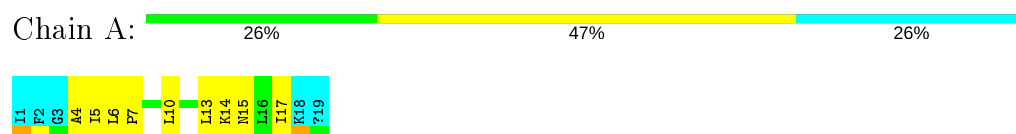
4.2.5 Score per residue for model 5

- Molecule 1: Hylin-a1



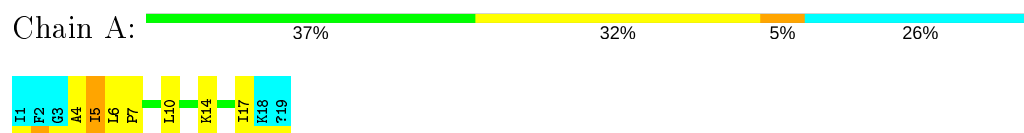
4.2.6 Score per residue for model 6

- Molecule 1: Hylin-a1



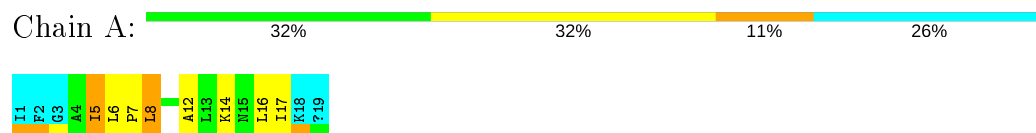
4.2.7 Score per residue for model 7 (medoid)

- Molecule 1: Hylin-a1



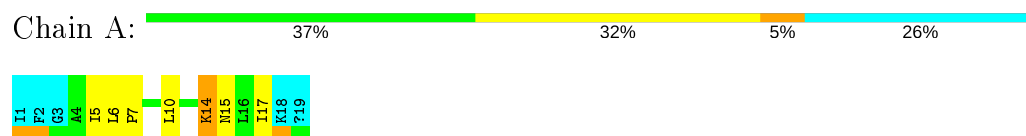
4.2.8 Score per residue for model 8

- Molecule 1: Hylin-a1



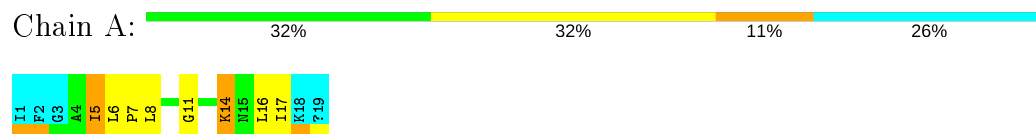
4.2.9 Score per residue for model 9

- Molecule 1: Hylin-a1



4.2.10 Score per residue for model 10

- Molecule 1: Hylin-a1



5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 200 calculated structures, 10 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
X-PLOR NIH	refinement	2.28
X-PLOR NIH	structure solution	2.28

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)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	125
Number of shifts mapped to atoms	125
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	40%

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

6 Model quality ⓘ

6.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: NH2

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 ⓘ

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	99	121	121	4±1
All	All	990	1210	1210	45

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 20.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:8:LEU:C	1:A:8:LEU:HD12	0.68	2.09	8	1
1:A:5:ILE:CG1	1:A:6:LEU:N	0.58	2.66	6	10
1:A:8:LEU:HD12	1:A:8:LEU:C	0.55	2.21	4	1
1:A:6:LEU:N	1:A:7:PRO:CD	0.54	2.70	5	10
1:A:6:LEU:N	1:A:7:PRO:HD2	0.54	2.18	6	5
1:A:14:LYS:N	1:A:14:LYS:HD3	0.53	2.19	10	2
1:A:13:LEU:O	1:A:17:ILE:HG22	0.51	2.04	6	1
1:A:8:LEU:O	1:A:12:ALA:HB2	0.49	2.06	8	1
1:A:8:LEU:C	1:A:8:LEU:CD1	0.48	2.79	8	1
1:A:14:LYS:N	1:A:14:LYS:CD	0.48	2.76	10	1
1:A:5:ILE:HG13	1:A:6:LEU:N	0.46	2.26	6	1
1:A:14:LYS:HA	1:A:17:ILE:HG22	0.45	1.87	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:11:GLY:O	1:A:14:LYS:N	0.44	2.50	10	3
1:A:8:LEU:CD1	1:A:8:LEU:C	0.42	2.86	4	1
1:A:8:LEU:O	1:A:8:LEU:HD12	0.41	2.15	4	1
1:A:5:ILE:HG12	1:A:6:LEU:N	0.41	2.31	5	2
1:A:14:LYS:N	1:A:14:LYS:HD2	0.41	2.31	2	1
1:A:6:LEU:HB2	1:A:7:PRO:HD3	0.40	1.92	9	2

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	14/19 (74%)	14±0 (99±3%)	0±0 (1±3%)	0±0 (0±0%)	100	100
All	All	140/190 (74%)	138 (99%)	2 (1%)	0 (0%)	100	100

There are no Ramachandran outliers.

6.3.2 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 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	10/13 (77%)	8±1 (78±7%)	2±1 (22±7%)	3	30
All	All	100/130 (77%)	78 (78%)	22 (22%)	3	30

All 4 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	14	LYS	7
1	A	5	ILE	6

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Mol	Chain	Res	Type	Models (Total)
1	A	10	LEU	6
1	A	8	LEU	3

6.3.3 RNA [i](#)

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 40% for the well-defined parts and 38% for the entire structure.

7.1 Chemical shift list 1

File name: input_cs.cif

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	125
Number of shifts mapped to atoms	125
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

7.1.2 Chemical shift referencing

No chemical shift referencing corrections were calculated (not enough data).

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 40%, i.e. 66 atoms were assigned a chemical shift out of a possible 166. 0 out of 5 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	27/68 (40%)	27/27 (100%)	0/28 (0%)	0/13 (0%)
Sidechain	39/98 (40%)	39/56 (70%)	0/40 (0%)	0/2 (0%)
Aromatic	0/0 (—%)	0/0 (—%)	0/0 (—%)	0/0 (—%)
Overall	66/166 (40%)	66/83 (80%)	0/68 (0%)	0/15 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 38%, i.e. 83 atoms were assigned a chemical shift out of a possible 220. 0 out of 5 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	35/88 (40%)	34/35 (97%)	1/36 (3%)	0/17 (0%)
Sidechain	47/123 (38%)	47/71 (66%)	0/49 (0%)	0/3 (0%)
Aromatic	1/9 (11%)	1/5 (20%)	0/4 (0%)	0/0 (—%)
Overall	83/220 (38%)	82/111 (74%)	1/89 (1%)	0/20 (0%)

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, <i>ppm</i>	Expected range, <i>ppm</i>	Z-score
1	A	18	LYS	HD2	168.00	2.76 – 0.46	723.4
1	A	2	PHE	CA	4.62	70.99 – 45.29	-20.8

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

No *random coil index* (RCI) plot could be generated from the current chemical shift list (assigned_chem_shift_list_1). RCI is only applicable to proteins.