



Full wwPDB NMR Structure Validation Report ⓘ

Nov 23, 2017 – 05:10 AM EST

PDB ID : 1PAA
Title : STRUCTURE OF A HISTIDINE-X4-HISTIDINE ZINC FINGER DOMAIN:
INSIGHTS INTO ADR1-UAS1 PROTEIN-DNA RECOGNITION
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Deposited on : unknown

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

<http://wwpdb.org/validation/2016/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 : 20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20030345
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030345

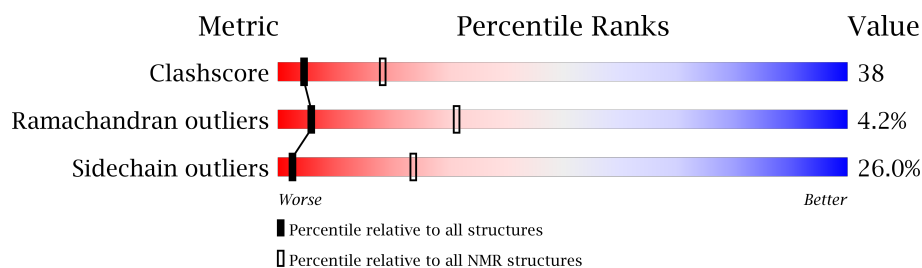
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment 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.



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

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	30	

2 Ensemble composition and analysis

This entry contains 10 models. Model 5 is the overall representative, medoid model (most similar to other models).

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:132-A:155 (24)	0.08	5

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. No single-model clusters were found.

Cluster number	Models
1	1, 2, 3, 5, 6, 7, 8, 10
2	4, 9

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 447 atoms, of which 207 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called YEAST TRANSCRIPTION FACTOR ADR1.

Mol	Chain	Residues	Atoms						Trace
1	A	30	Total	C	H	N	O	S	0
			446	148	207	51	38	2	

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	131	ALA	PRO	CONFLICT	UNP P07248
A	133	ALA	PRO	CONFLICT	UNP P07248
A	140	ALA	CYS	CONFLICT	UNP P07248

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

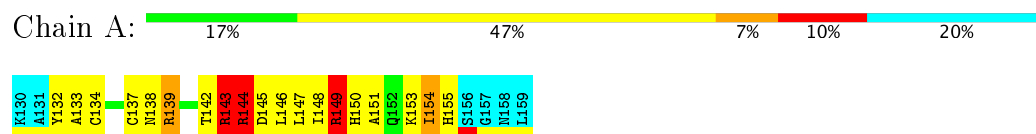
Mol	Chain	Residues	Atoms	
2	A	1	Total	Zn
			1	1

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: YEAST TRANSCRIPTION FACTOR ADR1

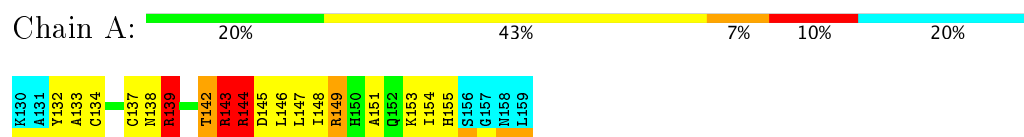


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

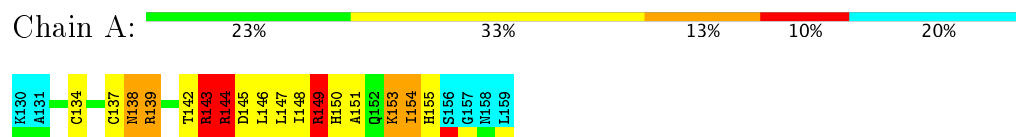
4.2.1 Score per residue for model 1

- Molecule 1: YEAST TRANSCRIPTION FACTOR ADR1



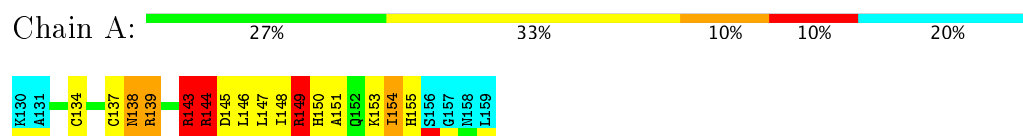
4.2.2 Score per residue for model 2

- Molecule 1: YEAST TRANSCRIPTION FACTOR ADR1



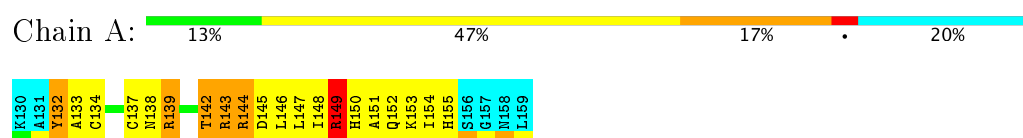
4.2.3 Score per residue for model 3

- Molecule 1: YEAST TRANSCRIPTION FACTOR ADR1



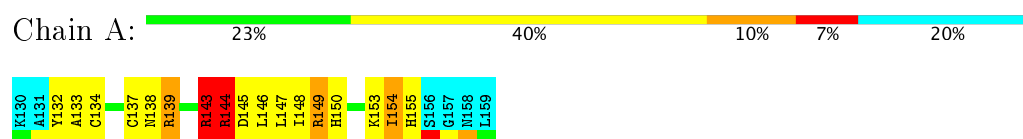
4.2.4 Score per residue for model 4

- Molecule 1: YEAST TRANSCRIPTION FACTOR ADR1



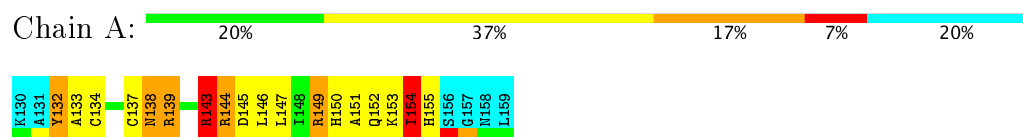
4.2.5 Score per residue for model 5 (medoid)

- Molecule 1: YEAST TRANSCRIPTION FACTOR ADR1



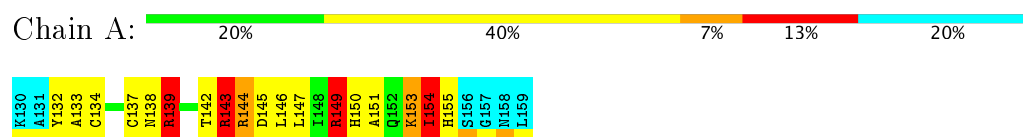
4.2.6 Score per residue for model 6

- Molecule 1: YEAST TRANSCRIPTION FACTOR ADR1



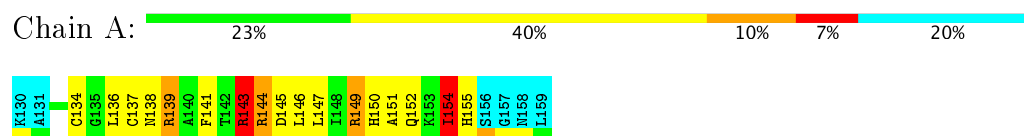
4.2.7 Score per residue for model 7

- Molecule 1: YEAST TRANSCRIPTION FACTOR ADR1



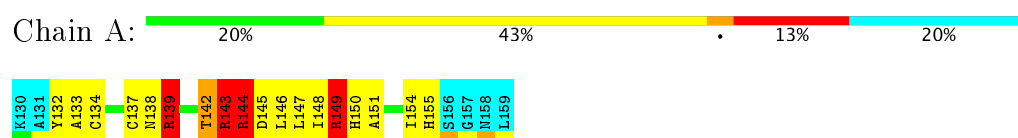
4.2.8 Score per residue for model 8

- Molecule 1: YEAST TRANSCRIPTION FACTOR ADR1



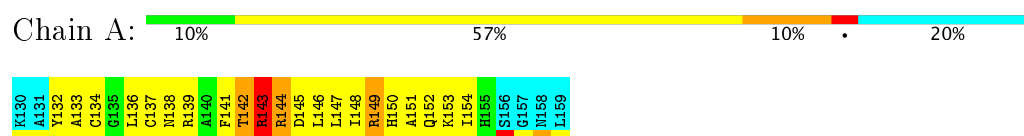
4.2.9 Score per residue for model 9

- Molecule 1: YEAST TRANSCRIPTION FACTOR ADR1



4.2.10 Score per residue for model 10

- Molecule 1: YEAST TRANSCRIPTION FACTOR ADR1



5 Refinement protocol and experimental data overview ⓘ

Of the ? calculated structures, 10 were deposited, based on the following criterion: ?.

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

Software name	Classification	Version
DIANA	refinement	
REPENT	refinement	

No chemical shift data was provided. 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](#)

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

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

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	A	0.0±0.0	3.7±0.5
All	All	0	37

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

All 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	A	144	ARG	Sidechain	10
1	A	149	ARG	Sidechain	10
1	A	143	ARG	Sidechain	9
1	A	139	ARG	Sidechain	8

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	199	169	203	15±3
All	All	2000	1690	2030	153

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 38.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:143:ARG:HD2	1:A:146:LEU:HD22	0.79	1.53	1	1
1:A:143:ARG:HD3	1:A:146:LEU:HD22	0.79	1.54	4	8
1:A:145:ASP:OD1	1:A:146:LEU:HD13	0.77	1.79	3	9
1:A:143:ARG:CD	1:A:146:LEU:HD22	0.71	2.15	9	9
1:A:147:LEU:HD12	1:A:147:LEU:O	0.69	1.88	9	1
1:A:147:LEU:O	1:A:147:LEU:HD12	0.66	1.91	4	1
1:A:142:THR:HG22	1:A:143:ARG:HG3	0.64	1.68	10	3
1:A:137:CYS:SG	1:A:150:HIS:CE1	0.62	2.92	10	6
1:A:137:CYS:O	1:A:138:ASN:CB	0.62	2.48	2	10
1:A:145:ASP:OD2	1:A:146:LEU:HD12	0.59	1.97	2	1
1:A:137:CYS:SG	1:A:139:ARG:HB2	0.55	2.41	4	10
1:A:145:ASP:OD2	1:A:146:LEU:CD1	0.55	2.55	2	2
1:A:143:ARG:NH2	1:A:145:ASP:CG	0.54	2.61	6	1
1:A:134:CYS:N	1:A:139:ARG:O	0.54	2.39	5	10
1:A:144:ARG:HE	1:A:148:ILE:HD11	0.53	1.64	3	1
1:A:144:ARG:O	1:A:147:LEU:N	0.53	2.42	6	8
1:A:144:ARG:HH21	1:A:148:ILE:HD11	0.52	1.65	9	1
1:A:148:ILE:O	1:A:151:ALA:N	0.52	2.41	4	6
1:A:149:ARG:O	1:A:153:LYS:N	0.51	2.43	6	5
1:A:142:THR:HB	1:A:143:ARG:CZ	0.51	2.35	1	1
1:A:137:CYS:O	1:A:138:ASN:OD1	0.50	2.30	6	2
1:A:144:ARG:O	1:A:144:ARG:CD	0.50	2.59	9	1
1:A:137:CYS:O	1:A:138:ASN:HB3	0.49	2.07	6	1
1:A:134:CYS:O	1:A:138:ASN:N	0.49	2.45	3	10
1:A:138:ASN:C	1:A:138:ASN:ND2	0.49	2.66	6	1
1:A:154:ILE:HG22	1:A:155:HIS:N	0.49	2.23	8	3
1:A:134:CYS:O	1:A:138:ASN:CA	0.48	2.62	6	9
1:A:145:ASP:OD1	1:A:146:LEU:N	0.48	2.47	6	1
1:A:150:HIS:O	1:A:154:ILE:N	0.47	2.47	6	5
1:A:137:CYS:O	1:A:138:ASN:CG	0.46	2.54	10	3
1:A:145:ASP:CG	1:A:146:LEU:HD13	0.46	2.31	9	5
1:A:145:ASP:CG	1:A:146:LEU:N	0.46	2.69	6	1
1:A:138:ASN:ND2	1:A:138:ASN:O	0.45	2.49	6	1
1:A:143:ARG:NH1	1:A:145:ASP:OD2	0.45	2.49	6	1
1:A:137:CYS:O	1:A:138:ASN:HB2	0.44	2.12	10	2
1:A:137:CYS:O	1:A:138:ASN:ND2	0.44	2.50	10	1
1:A:144:ARG:NE	1:A:148:ILE:CG1	0.43	2.81	5	1
1:A:143:ARG:HB2	1:A:145:ASP:OD1	0.43	2.13	6	1
1:A:143:ARG:HD3	1:A:146:LEU:CD2	0.43	2.41	8	2
1:A:134:CYS:SG	1:A:136:LEU:HD12	0.41	2.55	10	1
1:A:148:ILE:O	1:A:149:ARG:C	0.41	2.59	4	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:141:PHE:CD1	1:A:146:LEU:HB3	0.41	2.51	8	1
1:A:144:ARG:CZ	1:A:148:ILE:HG12	0.41	2.46	10	1
1:A:141:PHE:CD2	1:A:146:LEU:HB3	0.40	2.52	10	1
1:A:137:CYS:C	1:A:138:ASN:CG	0.40	2.79	9	1

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	24/30 (80%)	15±1 (64±3%)	8±1 (32±4%)	1±1 (4±3%)	6	31
All	All	240/300 (80%)	154 (64%)	76 (32%)	10 (4%)	6	31

All 2 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	132	TYR	7
1	A	154	ILE	3

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	20/24 (83%)	15±1 (74±6%)	5±1 (26±6%)	2	24
All	All	200/240 (83%)	148 (74%)	52 (26%)	2	24

All 10 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	154	ILE	10
1	A	143	ARG	10
1	A	149	ARG	8
1	A	144	ARG	6
1	A	142	THR	6
1	A	139	ARG	4
1	A	153	LYS	3
1	A	138	ASN	3
1	A	152	GLN	1
1	A	136	LEU	1

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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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

No chemical shift data were provided