

wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	1QRY
Title	:	Homeobox protein VND (ventral nervous system defective protein)
Authors	:	Xiang, B.
Deposited on	:	1999-06-16

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:

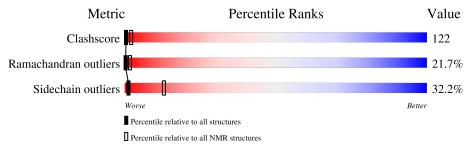
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.26
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
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.



Metric	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f NMR} \ { m archive} \ (\#{ m Entries})$
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 <=5%

Mol	Chain	Length		Quality of chain	
1	А	80	• 38%	20% •	39%



2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 1 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) p	protein residues	
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:19-A:67 (49)	0.37	1

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 4 clusters and 2 single-model clusters were found.

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



3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1387 atoms, of which 699 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called PROTEIN (HOMEOBOX VENTRAL NERVOUS SYSTEM DEFECTIVE PROTEIN).

Mol	Chain	Residues		Atoms										
1	Δ	80	Total	С	Н	Ν	0	S	0					
	A	80	1387	430	699	139	118	1	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.

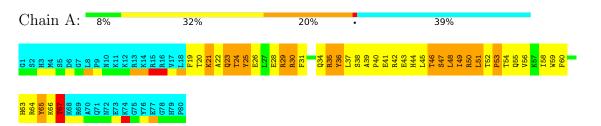
• Molecule 1: PROTEIN (HOMEOBOX VENTRAL NERVOUS SYSTEM DEFECTIVE PROTEIN)

Chain A	A: •				3	8%									Ĩ	20	%			·							3	9%							
61 82 85 85	67 118 128	N10 K11	R13	K14 R15	R16	L18	F19 T20	K21	A22	Q23 T24	Y25	E26	L27	E28 R29	R30	F31	R32	034 034	R35	Y36	L37 S38	A39	P40	E41	E43	H44	L45	140 S47	L48	149 PEA	L51		u56 V56		
Q61 N62 H63 R64 Y65 V66	T67 K68 R69	A70 Q71 M72	E73	C N	Y76	Б/ - G78	H79 PRO																												

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

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

• Molecule 1: PROTEIN (HOMEOBOX VENTRAL NERVOUS SYSTEM DEFECTIVE PROTEIN)





5 Refinement protocol and experimental data overview (i)

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

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *STRUC*-*TURES WITH ACCEPTABLE COVALENT GEOMETRY,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
X-PLOR	structure solution	
X-PLOR	refinement	

No chemical shift data was provided.



6 Model quality (i)

6.1 Standard geometry (i)

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	Sond lengths	I	Bond angles
	Unam	RMSZ	$\#Z{>}5$	RMSZ	#Z > 5
1	А	1.07 ± 0.01	$0{\pm}0/449~(~0.1{\pm}~0.1\%)$	$1.04{\pm}0.02$	$0{\pm}0/606~(~0.0{\pm}~0.1\%)$
All	All	1.07	8/8980~(~0.1%)	1.04	3/12120 ($0.0%$)

All unique bond outliers are listed below.

I	Mol	Chain	Res	Type	Atoms	Z	$Observed(\text{\AA})$	$\mathrm{Ideal}(\mathrm{\AA})$	Moo Worst	iels Total
	1	А	25	TYR	CB-CG	-5.21	1.43	1.51	14	8

All unique angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$\mathrm{Ideal}(^{o})$	Moo Worst	
1	А	39	ALA	C-N-CD	-5.49	108.51	120.60	19	3

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	А	437	440	440	107 ± 11
All	All	8740	8800	8800	2148

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 122.



Atom-1	Atom-2	$\mathrm{Clash}(\mathrm{\AA})$	Distance(Å)	Models	
Atom-1	Atom-2		Distance(A)	Worst	Total
1:A:45:LEU:HD21	1:A:49:ILE:HD12	1.00	1.31	14	14
1:A:52:THR:O	1:A:56:VAL:HG23	0.97	1.59	9	12
1:A:45:LEU:HD11	1:A:49:ILE:CD1	0.92	1.94	10	14
1:A:45:LEU:C	1:A:45:LEU:HD13	0.90	1.87	13	13
1:A:45:LEU:CD2	1:A:49:ILE:HD12	0.86	2.00	11	14

5 of 521 unique clashes are listed below, sorted by their clash magnitude.

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	А	49/80~(61%)	24 ± 2 (50 $\pm3\%$)	$14\pm2~(28\pm4\%)$	$11\pm2(22\pm4\%)$	0 2
All	All	980/1600~(61%)	490 (50%)	277 (28%)	213 (22%)	0 2

5 of 24 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	А	21	LYS	20
1	А	23	GLN	20
1	А	24	THR	19
1	А	46	THR	19
1	А	53	PRO	18

6.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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 side chain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	47/73~(64%)	$32\pm3~(68\pm6\%)$	$15\pm3 (32\pm6\%)$	1 13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	940/1460~(64%)	637~(68%)	303~(32%)	1 13

5 of 41 unique residues with a non-rotameric side chain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	А	25	TYR	20
1	А	35	ARG	20
1	А	49	ILE	20
1	А	30	ARG	19
1	А	36	TYR	18

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 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

