

wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	2EPP
Title	:	Solution structure of the first C2H2 type zinc finger domain of Zinc finger
		protein 278
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Deposited on	:	2007-03-30

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 (i)) were used in the production of this report:

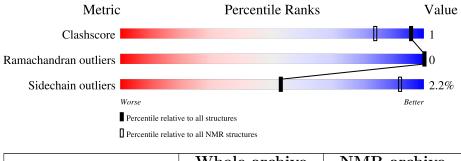
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.27
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

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	66	38%	62%		



2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 4 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:291-A:315 (25)	0.16	4		

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 1 single-model cluster was found.

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



3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 936 atoms, of which 464 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called POZ-, AT hook-, and zinc finger-containing protein 1.

Mol	Chain	Residues	Atoms					Trace	
1	Δ	66	Total	С	Η	Ν	0	S	0
	A	66	935	289	464	88	92	2	U

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	279	GLY	-	expression tag	UNP Q9HBE1
А	280	SER	-	expression tag	UNP Q9HBE1
А	281	SER	-	expression tag	UNP Q9HBE1
A	282	GLY	-	expression tag	UNP Q9HBE1
А	283	SER	-	expression tag	UNP Q9HBE1
А	284	SER	-	expression tag	UNP Q9HBE1
А	285	GLY	-	expression tag	UNP Q9HBE1
A	339	SER	-	expression tag	UNP Q9HBE1
А	340	GLY	-	expression tag	UNP Q9HBE1
А	341	PRO	-	expression tag	UNP Q9HBE1
А	342	SER	-	expression tag	UNP Q9HBE1
А	343	SER	-	expression tag	UNP Q9HBE1
А	344	GLY	-	expression tag	UNP Q9HBE1

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

Mol	Chain	Residues	Atoms	
0	۸	1	Total Zn	
	A	1	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, 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: POZ-, AT hook-, and zinc finger-containing protein 1

Chain A:	38%	62%	
G279 S280 S281 S281 S284 S284 S284 L286 L286 R287 R287 R287 C290	V316 T317 S318 L319 Q320 L321 G322 Y323 T324 D325	L1326 P327 P328 P328 P328 P329 L331 C333 C335 C335 C335 C335 C335 C335 C	

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

The representative model is number 4. Colouring as in section 4.1 above.

 \bullet Molecule 1: POZ-, AT hook-, and zinc finger-containing protein 1

Chain A:	36%	·	62%
6279 S280 S281 G281 G285 S283 S283 S283 S283 S283 S283 S283 S283	V316 T317 S318 L319 Q320 C322 C322 Y323 T324 T324	L326 P327 P327 P328 P329 L330 L333 L333 L336 L336 L336 L336 L336	G340 P341 S342 S343 G344



5 Refinement protocol and experimental data overview (i)

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

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the least restraint violations, structures with the lowest energy, target function.*

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

Software name	Classification	Version
CYANA	structure solution	2.1
CYANA	refinement	2.1

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: ZN

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	А	192	188	188	0±1
All	All	3860	3760	3760	7

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.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total
1:A:296:LEU:HD12	1:A:314:HIS:CD2	0.47	2.44	10	3
1:A:301:PHE:CD1	1:A:307:LEU:HD13	0.45	2.46	11	2
1:A:307:LEU:HD11	1:A:311:GLU:HG2	0.42	1.90	14	1
1:A:309:GLN:O	1:A:312:ALA:HB3	0.41	2.16	15	1

All 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



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percer	ntiles
1	А	25/66~(38%)	23 ± 1 (93 $\pm4\%$)	$2\pm1~(7\pm4\%)$	0±0 (0±0%)	100	100
All	All	500/1320~(38%)	466 (93%)	34 (7%)	0 (0%)	100	100

entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

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	А	20/51~(39%)	20 ± 1 (98 $\pm3\%$)	$0\pm1~(2\pm3\%)$	53 9)2
All	All	400/1020~(39%)	391~(98%)	9~(2%)	53 9)2

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	А	302	THR	4
1	А	308	ARG	2
1	А	309	GLN	2
1	А	303	ASP	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 monosaccharides 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 (i)

No chemical shift data were provided

