



# Full wwPDB NMR Structure Validation Report ⓘ

Mar 8, 2026 – 09:01 AM UTC

PDB ID : 1EVC / pdb\_00001evc  
Title : NMR structure of CYANOBACTERIAL TOXIN, PHOSPHATASE-1/-2A INHIBITOR  
Authors : Bagu, J.R.; Sykes, B.D.  
Deposited on : 1996-02-14

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
wwPDB-RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
wwPDB-ShiftChecker : v1.2  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

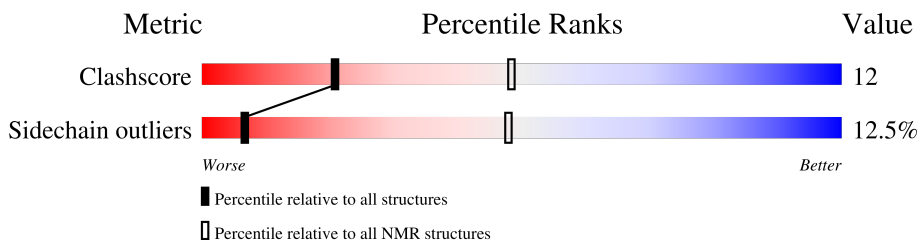
# 1 Overall quality at a glance

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	229148	14424
Sidechain outliers	223484	12823

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	5	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA and RNA chains that are outliers for geometric criteria:

Mol	Chain	Compound	Res	Total models with violations	
				Chirality	Geometry
1	A	ACB	1	-	5

## 2 Ensemble composition and analysis

This entry contains 48 models.

Cyrange was unable to find well-defined residues.

Error message: Less than two structures selected.

NmrClust was unable to cluster the ensemble.

Error message: Wrapper check: not enough residues in core to run NmrClust

### 3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 109 atoms, of which 55 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called MOTUPORIN.

Mol	Chain	Residues	Atoms					Trace
			Total	C	H	N	O	
1	A	5	109	40	55	5	9	0

## 4 Residue-property plots

### 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: MOTUPORIN

Chain A: 



### 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

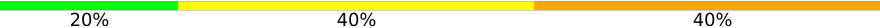
- Molecule 1: MOTUPORIN

Chain A: 



#### 4.2.2 Score per residue for model 2

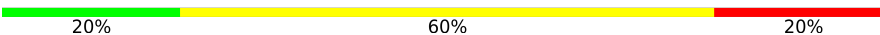
- Molecule 1: MOTUPORIN

Chain A: 



### 4.2.3 Score per residue for model 3

- Molecule 1: MOTUPORIN

Chain A:  20% 60% 20%



### 4.2.4 Score per residue for model 4

- Molecule 1: MOTUPORIN

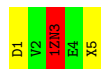
Chain A:  40% 40% 20%



### 4.2.5 Score per residue for model 5

- Molecule 1: MOTUPORIN

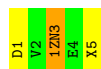
Chain A:  40% 40% 20%



### 4.2.6 Score per residue for model 6

- Molecule 1: MOTUPORIN

Chain A:  40% 40% 20%



### 4.2.7 Score per residue for model 7

- Molecule 1: MOTUPORIN

Chain A:  40% 40% 20%



#### 4.2.8 Score per residue for model 8

- Molecule 1: MOTUPORIN

Chain A:  20% 60% 20%



#### 4.2.9 Score per residue for model 9

- Molecule 1: MOTUPORIN

Chain A:  40% 60%



#### 4.2.10 Score per residue for model 10

- Molecule 1: MOTUPORIN

Chain A:  40% 40% 20%



#### 4.2.11 Score per residue for model 11

- Molecule 1: MOTUPORIN

Chain A:  40% 40% 20%



#### 4.2.12 Score per residue for model 12

- Molecule 1: MOTUPORIN

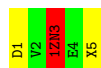
Chain A:  40% 40% 20%



#### 4.2.13 Score per residue for model 13

- Molecule 1: MOTUPORIN

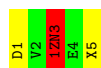
Chain A:  40% 40% 20%



#### 4.2.14 Score per residue for model 14

- Molecule 1: MOTUPORIN

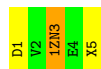
Chain A:  40% 40% 20%



#### 4.2.15 Score per residue for model 15

- Molecule 1: MOTUPORIN

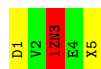
Chain A:  40% 40% 20%



#### 4.2.16 Score per residue for model 16

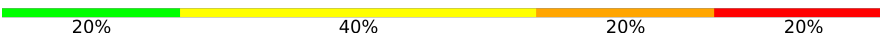
- Molecule 1: MOTUPORIN

Chain A:  40% 40% 20%



#### 4.2.17 Score per residue for model 17

- Molecule 1: MOTUPORIN

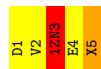
Chain A:  20% 40% 20% 20%



#### 4.2.18 Score per residue for model 18

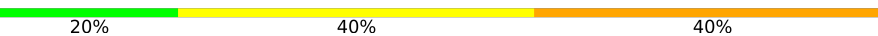
- Molecule 1: MOTUPORIN

Chain A:  60% 20% 20%



#### 4.2.19 Score per residue for model 19

- Molecule 1: MOTUPORIN

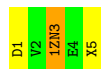
Chain A:  20% 40% 40%



#### 4.2.20 Score per residue for model 20

- Molecule 1: MOTUPORIN

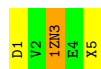
Chain A:  40% 40% 20%



#### 4.2.21 Score per residue for model 21

- Molecule 1: MOTUPORIN

Chain A:  40% 40% 20%



#### 4.2.22 Score per residue for model 22

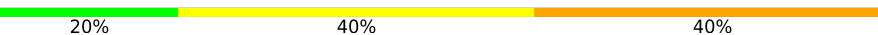
- Molecule 1: MOTUPORIN

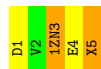
Chain A:  40% 40% 20%



#### 4.2.23 Score per residue for model 23

- Molecule 1: MOTUPORIN

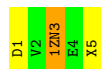
Chain A:  20% 40% 40%



#### 4.2.24 Score per residue for model 24

- Molecule 1: MOTUPORIN

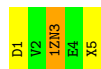
Chain A:  40% 40% 20%



#### 4.2.25 Score per residue for model 25

- Molecule 1: MOTUPORIN

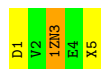
Chain A:  40% 40% 20%



#### 4.2.26 Score per residue for model 26

- Molecule 1: MOTUPORIN

Chain A:  40% 40% 20%



#### 4.2.27 Score per residue for model 27

- Molecule 1: MOTUPORIN

Chain A:  40% 40% 20%



#### 4.2.28 Score per residue for model 28

- Molecule 1: MOTUPORIN

Chain A:  40% 40% 20%



#### 4.2.29 Score per residue for model 29

- Molecule 1: MOTUPORIN

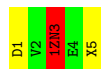
Chain A:  40% 40% 20%



#### 4.2.30 Score per residue for model 30

- Molecule 1: MOTUPORIN

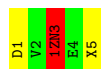
Chain A:  40% 40% 20%



#### 4.2.31 Score per residue for model 31

- Molecule 1: MOTUPORIN

Chain A:  40% 40% 20%



#### 4.2.32 Score per residue for model 32

- Molecule 1: MOTUPORIN

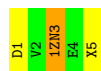
Chain A:  20% 60% 20%



#### 4.2.33 Score per residue for model 33

- Molecule 1: MOTUPORIN

Chain A:  40% 40% 20%



#### 4.2.34 Score per residue for model 34

- Molecule 1: MOTUPORIN

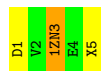
Chain A:  60% 40%



#### 4.2.35 Score per residue for model 35

- Molecule 1: MOTUPORIN

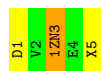
Chain A:  40% 40% 20%



#### 4.2.36 Score per residue for model 36

- Molecule 1: MOTUPORIN

Chain A:  40% 40% 20%



#### 4.2.37 Score per residue for model 37

- Molecule 1: MOTUPORIN

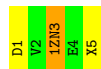
Chain A:  40% 60%



#### 4.2.38 Score per residue for model 38

- Molecule 1: MOTUPORIN

Chain A:  40% 40% 20%



#### 4.2.39 Score per residue for model 39

- Molecule 1: MOTUPORIN

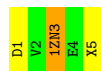
Chain A:  20% 60% 20%



#### 4.2.40 Score per residue for model 40

- Molecule 1: MOTUPORIN

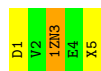
Chain A:  40% 40% 20%



#### 4.2.41 Score per residue for model 41

- Molecule 1: MOTUPORIN

Chain A:  40% 40% 20%



#### 4.2.42 Score per residue for model 42

- Molecule 1: MOTUPORIN

Chain A:  60% 40%



#### 4.2.43 Score per residue for model 43

- Molecule 1: MOTUPORIN

Chain A:  40% 40% 20%



#### 4.2.44 Score per residue for model 44

- Molecule 1: MOTUPORIN

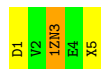
Chain A:  40% 40% 20%



#### 4.2.45 Score per residue for model 45

- Molecule 1: MOTUPORIN

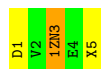
Chain A:  40% 40% 20%



#### 4.2.46 Score per residue for model 46

- Molecule 1: MOTUPORIN

Chain A:  40% 40% 20%



#### 4.2.47 Score per residue for model 47

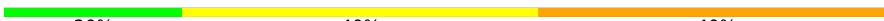
- Molecule 1: MOTUPORIN

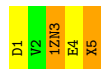
Chain A:  40% 40% 20%



#### 4.2.48 Score per residue for model 48

- Molecule 1: MOTUPORIN

Chain A:  20% 40% 40%



## 5 Refinement protocol and experimental data overview

Of the ? calculated structures, 48 were deposited, based on the following criterion: ?.

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

Software name	Classification	Version
DGII	refinement	

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: 1ZN, ACB, FGA, MDH

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	1.3±0.7
All	All	0	63

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

All unique planar outliers are listed below.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	3	1ZN	Peptide,Mainchain	41

### 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	54	55	45	1±2
All	All	2592	2640	2163	57

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 12.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:3:1ZN:H5	1:A:3:1ZN:H18	1.00	1.29	3	2
1:A:3:1ZN:H18	1:A:3:1ZN:C4	0.93	1.93	16	1
1:A:3:1ZN:C5	1:A:3:1ZN:H3	0.87	1.98	39	1
1:A:3:1ZN:H18	1:A:3:1ZN:C3	0.78	2.07	3	3
1:A:4:FGA:N	1:A:5:MDH:HM1	0.75	1.97	42	6
1:A:3:1ZN:H5	1:A:3:1ZN:C14	0.69	2.17	39	2
1:A:3:1ZN:C	1:A:4:FGA:HG3	0.67	2.19	34	6
1:A:3:1ZN:H14	1:A:3:1ZN:C9	0.65	2.22	7	1
1:A:3:1ZN:H14	1:A:3:1ZN:C4	0.65	2.22	7	1
1:A:3:1ZN:C4	1:A:3:1ZN:H15	0.63	2.23	31	1
1:A:3:1ZN:H4	1:A:3:1ZN:H19	0.63	1.70	39	2
1:A:3:1ZN:C9	1:A:3:1ZN:H2	0.62	2.24	30	2
1:A:3:1ZN:H15	1:A:3:1ZN:C9	0.58	2.27	31	1
1:A:3:1ZN:H3	1:A:3:1ZN:C4	0.57	2.29	39	2
1:A:3:1ZN:C14	1:A:3:1ZN:C2	0.56	2.83	39	3
1:A:3:1ZN:H2	1:A:3:1ZN:C4	0.56	2.31	30	2
1:A:3:1ZN:C4	1:A:3:1ZN:H2	0.55	2.31	13	2
1:A:3:1ZN:H4	1:A:3:1ZN:C14	0.52	2.34	16	1
1:A:3:1ZN:C14	1:A:3:1ZN:H4	0.52	2.34	39	2
1:A:3:1ZN:C14	1:A:3:1ZN:C3	0.51	2.86	39	1
1:A:3:1ZN:C4	1:A:3:1ZN:C11	0.49	2.90	7	2
1:A:3:1ZN:H18	1:A:3:1ZN:C2	0.48	2.37	3	2
1:A:3:1ZN:C4	1:A:3:1ZN:H14	0.47	2.39	34	1
1:A:3:1ZN:C4	1:A:3:1ZN:C1	0.46	2.93	39	3
1:A:3:1ZN:H14	1:A:3:1ZN:C5	0.45	2.41	34	1
1:A:3:1ZN:H18	1:A:3:1ZN:H4	0.43	1.89	16	1
1:A:3:1ZN:H2	1:A:3:1ZN:C5	0.43	2.44	23	1
1:A:2:VAL:O	1:A:2:VAL:HG13	0.42	2.15	18	1
1:A:4:FGA:HG3	1:A:5:MDH:HM1	0.40	1.72	17	2
1:A:4:FGA:CB	1:A:5:MDH:HM1	0.40	2.46	19	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	0	-	-	-	-

*Continued on next page...*

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	0	-	-	-	-

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	1/1 (100%)	1±0 (88±33%)	0±0 (12±33%)	<b>7</b> 48
All	All	48/48 (100%)	42 (88%)	6 (12%)	<b>7</b> 48

All 1 unique residues with a non-rotameric sidechain are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	2	VAL	6

### 6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
1	ACB	A	1	1	8,8,9	2.17±0.01	2±0 (25±0%)
1	FGA	A	4	1	5,7,9	1.14±0.02	0±0 (0±0%)

Mol	Type	Chain	Res	Link	Counts	Bond lengths	
						RMSZ	#Z>2
1	MDH	A	5	1	4,6,7	3.54±0.01	2±0 (50±0%)
1	1ZN	A	3	1	21,23,24	1.53±0.01	2±0 (9±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Counts	Bond angles	
						RMSZ	#Z>2
1	ACB	A	1	1	8,10,12	2.09±0.03	3±0 (37±0%)
1	FGA	A	4	1	2,7,11	1.31±0.05	0±0 (0±0%)
1	MDH	A	5	1	4,6,8	3.56±0.02	2±0 (50±0%)
1	1ZN	A	3	1	25,29,31	1.41±0.01	3±0 (12±0%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	FGA	A	4	1	-	0±0,5,6,9	-
1	MDH	A	5	1	-	0±0,2,6,8	-
1	1ZN	A	3	1	-	0±0,23,25,27	0±0,1,1,1
1	ACB	A	1	1	-	0±0,10,10,12	-

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	5	MDH	C-CA	6.73	1.54	1.43	20	48
1	A	3	1ZN	C15-C13	4.66	1.36	1.46	30	48
1	A	1	ACB	OD2-CG	4.38	1.24	1.42	4	48
1	A	1	ACB	CG-CB	3.28	1.56	1.52	4	48
1	A	3	1ZN	C3-C2	3.11	1.56	1.52	25	48
1	A	5	MDH	CM-N	2.23	1.49	1.45	47	48

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	5	MDH	CM-N-CA	5.11	116.23	123.98	8	48
1	A	5	MDH	O-C-CA	5.02	119.09	125.39	20	48
1	A	1	ACB	OD2-CG-CB	4.81	121.39	111.51	48	48
1	A	3	1ZN	C14-C13-C15	3.39	123.27	118.09	7	48
1	A	3	1ZN	C4-C3-C2	3.33	118.31	113.23	39	48
1	A	3	1ZN	C16-CA-N	3.24	117.30	109.92	28	48
1	A	1	ACB	C-CA-N	2.35	104.54	109.49	44	48
1	A	3	1ZN	C11-C10-C12	2.25	106.26	110.08	39	3
1	A	1	ACB	C4-CB-CG	2.12	107.06	109.76	25	48

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 6.5 Carbohydrates [i](#)

There are no oligosaccharides 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

No chemical shift data were provided