



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 1I2V / pdb_00001i2v
Title : NMR SOLUTION STRUCTURES OF AN ANTIFUNGAL AND ANTIBACTERIAL MUTANT OF HELIOMICIN
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This is a wwPDB NMR Structure Validation Summary Report for a publicly released PDB entry.

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<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>.

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

MolProbity	:	4-5-2 with Phenix2.0
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

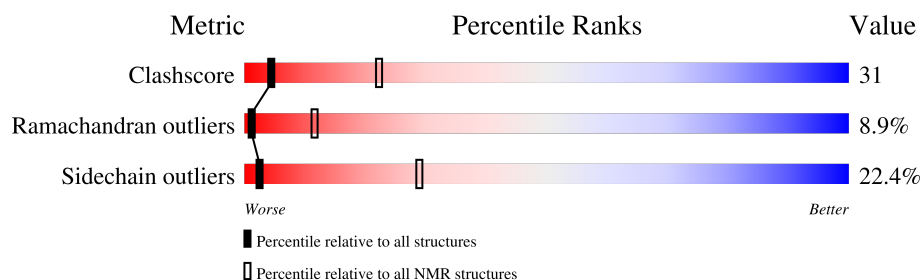
1 Overall quality at a glance

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
Ramachandran outliers	224038	12848
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 ≥ 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	44	18% 52% 18% • 9%

2 Ensemble composition and analysis

This entry contains 18 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) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:1-A:33, A:38-A:44 (40)	0.53	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 3 clusters. No single-model clusters were found.

Cluster number	Models
1	1, 3, 4, 6, 7, 9, 11, 14, 15, 16, 18
2	2, 8, 12, 17
3	5, 10, 13

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 623 atoms, of which 295 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called DEFENSIN HELIOMICIN.

Mol	Chain	Residues	Atoms							Trace
1	A	44	Total	C	H	N	O	S		0
			623	201	295	57	64	6		

There are 2 discrepancies between the modelled and reference sequences:

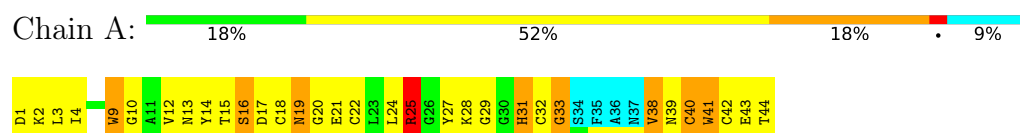
Chain	Residue	Modelled	Actual	Comment	Reference
A	23	LEU	LYS	engineered mutation	UNP P81544
A	24	LEU	ARG	engineered mutation	UNP P81544

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.

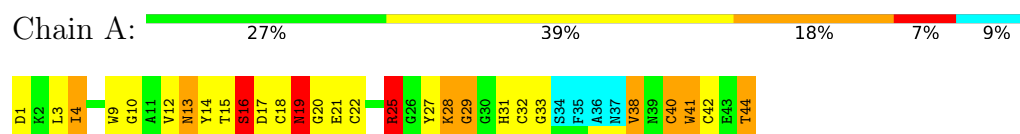
- Molecule 1: DEFENSIN HELIOMICIN



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: DEFENSIN HELIOMICIN



5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics (DYANA) and energy minimisation (XPLOR)*.

Of the 40 calculated structures, 18 were deposited, based on the following criterion: *structures with acceptable covalent geometry, structures with favorable non-bond energy, 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
DYANA	refinement	
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	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	1.66±0.03	3±1/304 (1.0± 0.3%)	1.67±0.05	7±1/409 (1.6± 0.3%)
All	All	1.66	52/5472 (1.0%)	1.67	120/7362 (1.6%)

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	1.0±0.0
All	All	0	18

5 of 7 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	31	HIS	CG-ND1	-7.06	1.30	1.38	17	18
1	A	38	VAL	CA-CB	6.59	1.63	1.54	2	5
1	A	31	HIS	CD2-NE2	-6.50	1.30	1.37	5	18
1	A	31	HIS	CB-CG	5.76	1.58	1.50	16	3
1	A	41	TRP	CG-CD2	-5.45	1.33	1.43	4	4

5 of 23 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	19	ASN	CA-CB-CG	-9.60	103.00	112.60	18	7
1	A	1	ASP	CA-CB-CG	-8.43	104.17	112.60	17	2
1	A	31	HIS	CA-CB-CG	-8.26	105.54	113.80	14	8
1	A	43	GLU	N-CA-CB	-7.21	100.60	111.64	17	1
1	A	41	TRP	NE1-CE2-CZ2	7.08	140.73	130.10	4	18

There are no chirality outliers.

All unique planar outliers are listed below.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	25	ARG	Sidechain	18

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	298	270	269	18±4
All	All	5364	4860	4842	320

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 31.

5 of 98 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:7:CYS:SG	1:A:40:CYS:SG	1.00	2.59	17	2
1:A:32:CYS:SG	1:A:40:CYS:SG	0.75	2.85	3	9
1:A:27:TYR:CD2	1:A:42:CYS:SG	0.74	2.80	13	13
1:A:4:ILE:HD11	1:A:22:CYS:SG	0.71	2.25	12	1
1:A:4:ILE:HD11	1:A:40:CYS:SG	0.69	2.27	11	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	38/44 (86%)	26±1 (68±4%)	9±1 (23±4%)	3±1 (9±2%)	1	11
All	All	684/792 (86%)	468 (68%)	155 (23%)	61 (9%)	1	11

All 5 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	10	GLY	14
1	A	33	GLY	14
1	A	38	VAL	12
1	A	29	GLY	11
1	A	16	SER	10

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	32/35 (91%)	25±2 (78±5%)	7±2 (22±5%)	2	29
All	All	576/630 (91%)	447 (78%)	129 (22%)	2	29

5 of 25 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	40	CYS	18
1	A	28	LYS	12
1	A	9	TRP	10
1	A	24	LEU	10
1	A	25	ARG	9

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 oligosaccharides in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided