



wwPDB NMR Structure Validation Summary Report ⓘ

May 29, 2020 – 03:24 am BST

PDB ID : 2MC0
Title : Structural Basis of a Thiopeptide Antibiotic Multidrug Resistance System from Streptomyces lividans:Nosiheptide in Complex with TipAS
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Deposited on : 2013-08-12

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 ⓘ 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
Mogul : 1.8.5 (274361), CSD as541be (2020)
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 : 2.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

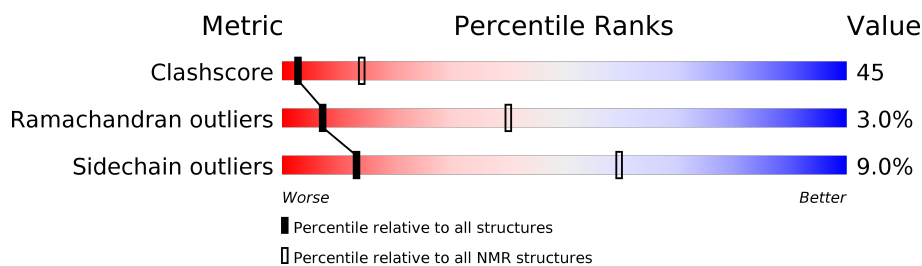
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 88%.

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	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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	144	<div> <div style="width: 33%; background-color: green;"></div> <div style="width: 59%; background-color: yellow;"></div> <div style="width: 8%; background-color: orange;"></div> <div style="width: 2%; background-color: red;"></div> <div style="width: 2%; background-color: cyan;"></div> <div style="width: 3%; background-color: grey;"></div> </div>
2	B	13	<div> <div style="width: 8%; background-color: green;"></div> <div style="width: 15%; background-color: yellow;"></div> <div style="width: 8%; background-color: orange;"></div> <div style="width: 69%; background-color: cyan;"></div> </div>

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
2	B	BB9	509	-	10
2	B	DBU	504	-	2
2	B	MH6	510	-	10

2 Ensemble composition and analysis ⓘ

This entry contains 10 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:112-A:209, A:214-A:253, B:501-B:501, B:503-B:503, B:508-B:508, B:512-B:512 (142)	0.31	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 3 clusters and 1 single-model cluster was found.

Cluster number	Models
1	3, 6, 8, 9
2	1, 2, 5
3	4, 10
Single-model clusters	7

3 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2330 atoms, of which 1094 are hydrogens and 0 are deuteriums.

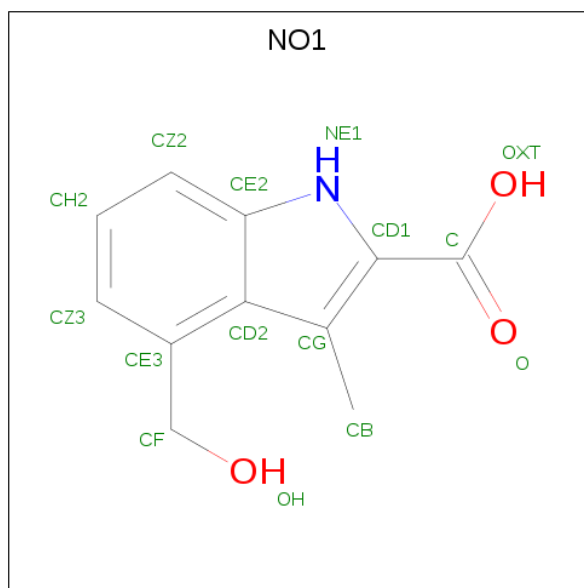
- Molecule 1 is a protein called HTH-type transcriptional activator TipA.

Mol	Chain	Residues	Atoms						Trace
1	A	143	Total	C	H	N	O	S	0
			2207	706	1053	204	237	7	

- Molecule 2 is a protein called nosiheptide.

Mol	Chain	Residues	Atoms						Trace
2	B	13	Total	C	H	N	O	S	1
			101	40	32	12	11	6	

- Molecule 3 is 4-(hydroxymethyl)-3-methyl-1H-indole-2-carboxylic acid (three-letter code: NO1) (formula: $C_{11}H_{11}NO_3$).



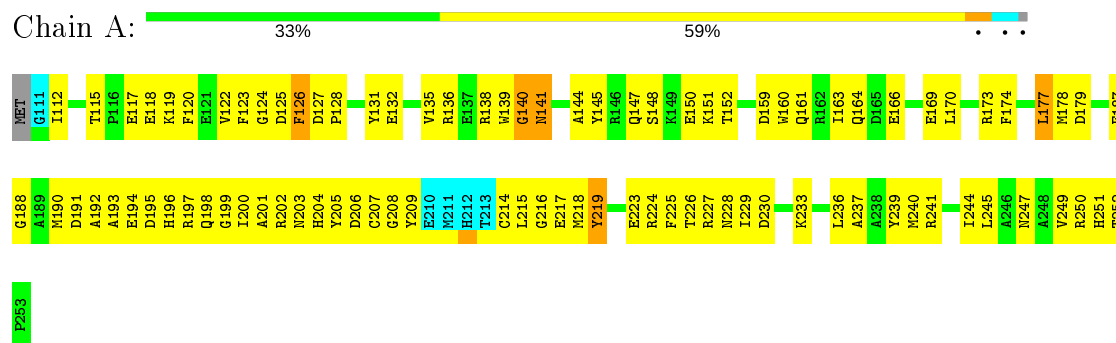
Mol	Chain	Residues	Atoms				
3	B	1	Total	C	H	N	O
			22	11	9	1	1

4 Residue-property plots

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: HTH-type transcriptional activator TipA



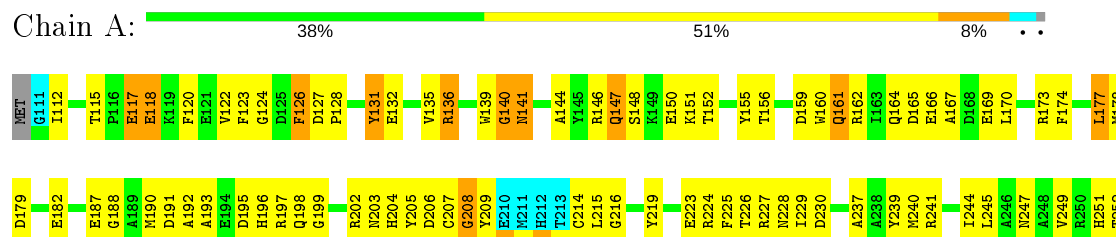
- Molecule 2: nosiheptide



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

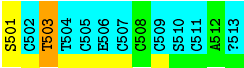
The representative model is number 4. Colouring as in section 4.1 above.

- Molecule 1: HTH-type transcriptional activator TipA



P253

● Molecule 2: nosiheptide



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 10 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
Xplor-NIH	structure solution	2.30
Xplor-NIH	refinement	2.30

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 6 of this report.

Chemical shift file(s)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	1736
Number of shifts mapped to atoms	1736
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	88%

No validations of the models with respect to experimental NMR restraints is performed at this time.

COVALENT-GEOMETRY INFOmissingINFO

5.1 Too-close contacts

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	1116	1021	1020	99±8
2	B	20	15	16	1±1
3	B	13	9	7	2±2
All	All	11490	10450	10430	988

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 45.

5 of 518 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:174:PHE:CE1	1:A:192:ALA:HB1	0.97	1.94	7	10
1:A:159:ASP:O	1:A:163:ILE:HD13	0.90	1.66	2	3
1:A:245:LEU:O	1:A:249:VAL:HG23	0.87	1.70	7	4
1:A:230:ASP:OD1	1:A:237:ALA:HB2	0.82	1.73	3	3
1:A:118:GLU:OE1	1:A:118:GLU:N	0.82	2.13	1	1

5.2 Torsion angles [i](#)

5.2.1 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	137/144 (95%)	129±3 (94±2%)	6±2 (4±1%)	3±1 (2±1%)	10	50
2	B	3/13 (23%)	1±1 (27±25%)	1±1 (30±23%)	1±0 (43±15%)	0	0
All	All	1400/1570 (89%)	1293 (92%)	65 (5%)	42 (3%)	7	40

5 of 7 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	140	GLY	10
2	B	503	THR	10
1	A	141	ASN	10
1	A	125	ASP	4
1	A	208	GLY	3

5.2.2 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	113/118 (96%)	103±3 (91±3%)	10±3 (9±3%)	13	59
2	B	2/3 (67%)	2±0 (95±15%)	0±0 (5±15%)	28	77
All	All	1150/1210 (95%)	1046 (91%)	104 (9%)	13	60

5 of 45 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	126	PHE	9
1	A	177	LEU	9
1	A	219	TYR	7
1	A	147	GLN	6
1	A	250	ARG	4

5.2.3 RNA [i](#)

There are no RNA molecules in this entry.

MODRES-GEOMETRY INFOmissingINFO

5.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

LIGAND-GEOMETRY INFOmissingINFO

5.4 Other polymers [i](#)

There are no such molecules in this entry.

5.5 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 88% for the well-defined parts and 88% for the entire structure.

6.1 Chemical shift list 1

File name: input_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

6.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1736
Number of shifts mapped to atoms	1736
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	6

6.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	143	-0.66 ± 0.18	Should be applied
$^{13}\text{C}_\beta$	132	0.31 ± 0.13	None needed (< 0.5 ppm)
$^{13}\text{C}'$	132	-0.57 ± 0.11	Should be applied
^{15}N	138	0.43 ± 0.38	None needed (< 0.5 ppm)

6.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 88%, i.e. 1529 atoms were assigned a chemical shift out of a possible 1734. 5 out of 11 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	675/700 (96%)	275/279 (99%)	267/284 (94%)	133/137 (97%)
Sidechain	720/887 (81%)	465/520 (89%)	243/316 (77%)	12/51 (24%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	134/147 (91%)	69/77 (90%)	63/64 (98%)	2/6 (33%)
Overall	1529/1734 (88%)	809/876 (92%)	573/664 (86%)	147/194 (76%)

6.1.4 Statistically unusual chemical shifts ⓘ

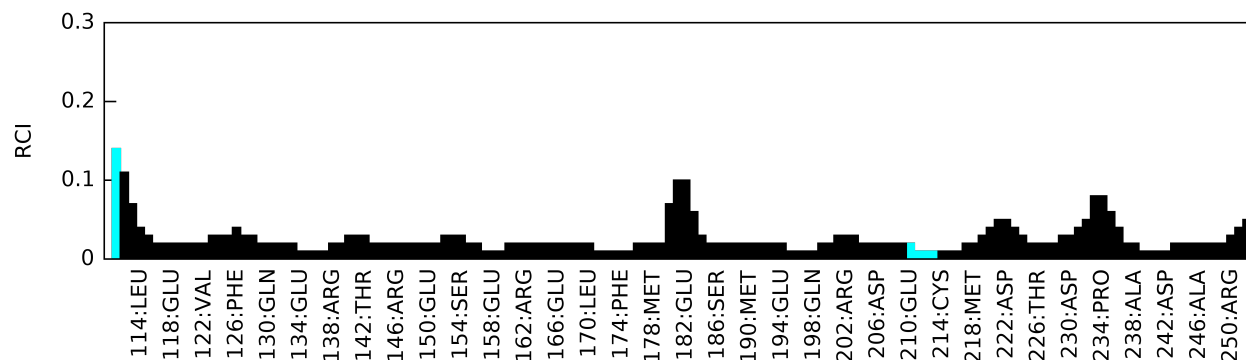
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
2	B	512	ALA	HB1	6.39	2.61 – 0.11	20.1
2	B	512	ALA	HB2	5.87	2.61 – 0.11	18.0
2	B	501	SER	HB2	7.03	5.18 – 2.58	12.1
2	B	501	SER	HB3	7.03	5.25 – 2.45	11.3
1	A	138	ARG	HG3	-0.26	3.00 – 0.10	-6.2
1	A	138	ARG	HG2	-0.04	2.92 – 0.22	-5.9

6.1.5 Random Coil Index (RCI) plots ⓘ

The images below report *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A:



Random coil index (RCI) for chain B:

