wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	2UZ5
Title	:	Solution structure of the fkbp-domain of Legionella pneumophila Mip
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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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

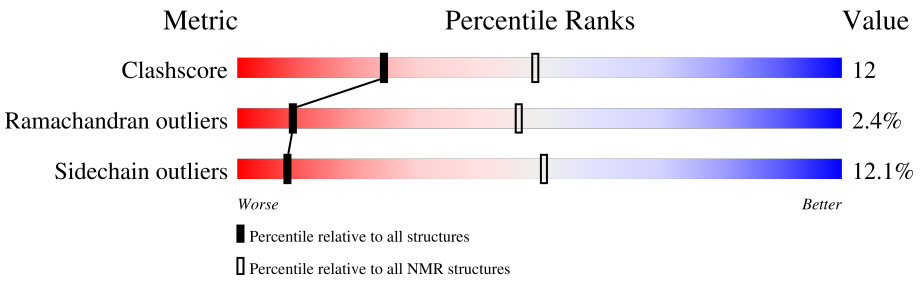
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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	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 <=5%

Mol	Chain	Length	Quality of chain
1	A	137	66% 23% • 8%

2 Ensemble composition and analysis (i)

This entry contains 10 models. Model 5 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative.

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:4-A:108, A:117-A:137 (126)	0.46	5

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 2 clusters and 2 single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 2094 atoms, of which 1059 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called MACROPHAGE INFECTIVITY POTENTIATOR.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	137	2094	663	1059	172	199	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: MACROPHAGE INFECTIVITY POTENTIATOR

Chain A: 66% 23% • 8%

F1 M2 K3 L16 N19 K20 N21 K22 V25 L32 Q33 Y34 S39 V43 K44 P45 G46 K47 S48 D49 R58 L59 I60 F65 D66 S67 T68 A75 Q78 V79 S80 G85 W86 W99 E100 I101 Y102 S105 G106 L107 A108 Y109 G110 P111 R112 S113 V114

G115 G116 P117 I118 L124 H129 L130 V133 K134 S137

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

The representative model is number 5. Colouring as in section 4.1 above.

• Molecule 1: MACROPHAGE INFECTIVITY POTENTIATOR

Chain A: 64% 21% 7% 8%

F1 M2 K3 L16 N19 K20 N21 K22 V25 S30 G31 L32 Q33 Y34 M38 S39 G40 N41 G42 V43 K44 P45 G46 K47 S48 D49 I60 F65 D66 S67 T68 A75 Q78 I83 W86 A89 W99 E100 I101 Y102 V103 P104 S105 G106 L107 A108 Y109

G110 P111 R112 S113 V114 G115 G116 P117 I118 T123 L124 H129 V133 K134 S137

5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *ARIA*.

Of the 40 calculated structures, 10 were deposited, based on the following criterion: *ENERGY*.

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

Software name	Classification	Version
ARIA/CNS	refinement	
NMRPipe	structure solution	
NMRView	structure solution	
ARIA	structure solution	
CNS	structure solution	
PyMOL	structure solution	
MANY OTHERS	structure solution	OTHERS

No chemical shift data was provided.

6 Model quality (i)

6.1 Standard geometry (i)

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	A	952	977	976	23±3
All	All	9520	9770	9760	230

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.

5 of 95 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:85:GLY:H	1:A:107:LEU:HD11	0.77	1.38	8	1
1:A:22:LYS:O	1:A:25:VAL:HG23	0.69	1.88	7	8
1:A:68:THR:HG21	1:A:75:ALA:HB2	0.68	1.65	8	6
1:A:51:VAL:HG12	1:A:133:VAL:HG22	0.64	1.68	10	3
1:A:133:VAL:HG22	1:A:134:LYS:HG2	0.64	1.69	9	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	125/137 (91%)	109±1 (87±1%)	13±1 (10±1%)	3±1 (2±1%)	9 46
All	All	1250/1370 (91%)	1089 (87%)	131 (10%)	30 (2%)	9 46

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	44	LYS	10
1	A	47	LYS	10
1	A	41	ASN	4
1	A	20	LYS	2
1	A	134	LYS	2

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	107/115 (93%)	94±2 (88±2%)	13±2 (12±2%)	8 51
All	All	1070/1150 (93%)	941 (88%)	129 (12%)	8 51

5 of 35 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	19	ASN	10
1	A	21	ASN	10
1	A	65	PHE	10
1	A	102	TYR	10
1	A	86	TRP	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 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