wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	2JR0
Title	:	Solution structure of NusB from Aquifex Aeolicus
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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
http://wwpdb.org/validation/2016/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:

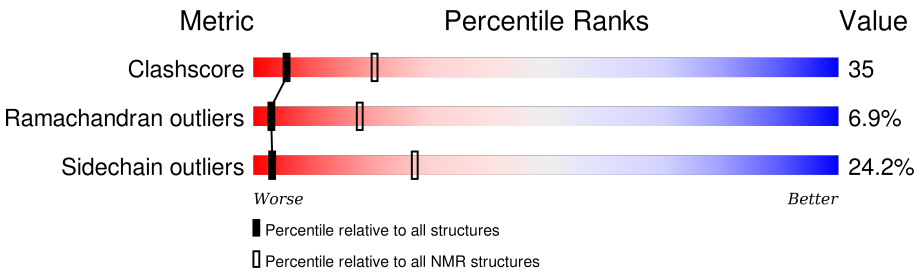
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027457

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 is 90%.

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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	148	36% 41% 13% 10%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 17 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:3-A:135 (133)	0.40	17

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, 6, 8, 10, 11, 17, 18, 19, 20
2	2, 4, 5, 9, 12, 13, 14, 15, 16
3	3, 7

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 2458 atoms, of which 1248 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called N utilization substance protein B homolog.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	148	2458	778	1248	208	223	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 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: N utilization substance protein B homolog

Chain A: 36% 41% 13% 10%

M1 R2 Y3 R4 F12 L13 V14 L15 Y16 R17 W18 D19 L20 R21 G22 E23 N24 F29 K30 V33 E34 E35 K36 N37 I38 K39 N40 K41 D42 A43 Y44 K48 K49 L50 V51 D52 T53 A54 V55 R56 H57 I58 E59 E60 I61 D62 S63 I64 I65 E66 K67 H68 L69 K70 G71 W72

S73 I74 D75 R76 L77 G78 Y79 V80 E81 R82 N83 A84 L85 R86 L87 G88 V89 A90 E91 L92 I93 F94 L95 K96 S97 R102 V103 F104 I105 D106 I107 V108 D109 L110 V111 A115 D116 A119 V123 V126 L127 S128 A129 I130 Y131 K132 I135 T136 S137 S138 K139 E140 E141 K142

P143 S144 L145 K146 S147 E148

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

The representative model is number 17. Colouring as in section 4.1 above.

- Molecule 1: N utilization substance protein B homolog

Chain A: 39% 34% 16% • 10%

M1 R2 Y3 R4 A11 F12 L13 V14 L15 Y16 R17 W18 D19 L20 R21 G22 E23 N24 F29 K30 V33 E34 N37 I38 K39 N40 K41 K48 K49 L50 V51 D52 T53 A54 V55 R56 H57 I58 E59 E60 I61 D62 I65 E66 K67 H68 L69 K70 G71 W72 S73 I74 D75 R76

L77 G78 Y79 V80 E81 R82 N83 A84 L85 R86 L87 G88 V89 A90 E91 L92 I93 F94 L95 P100 V103 F104 I105 D106 I107 V108 D109 L110 V111 K118 A119 G120 K121 V126 L127 S128 A129 I130 Y131 K132 I135 T136 S137 S138 K139 E140 E141 K142 P143 S144 L145 K146 S147 E148

5 Refinement protocol and experimental data overview (i)

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

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

The authors did not provide any information on software used for structure solution, optimization or refinement.

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	BMRB entry 15312
Number of chemical shift lists	1
Total number of shifts	1829
Number of shifts mapped to atoms	1829
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	90%

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

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	1090	1122	1122	78±8
All	All	21800	22440	22440	1555

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 35.

5 of 460 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:110:LEU:HD13	1:A:110:LEU:H	1.01	1.14	11	1
1:A:132:LYS:O	1:A:135:ILE:HD12	0.89	1.66	12	5
1:A:58:ILE:HG23	1:A:59:GLU:H	0.89	1.24	19	4
1:A:119:ALA:O	1:A:123:VAL:HG23	0.88	1.68	12	14
1:A:135:ILE:O	1:A:135:ILE:HD12	0.86	1.71	9	7

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	133/148 (90%)	115±1 (86±1%)	9±1 (7±1%)	9±2 (7±1%)	3 18
All	All	2660/2960 (90%)	2300 (86%)	176 (7%)	184 (7%)	3 18

5 of 20 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	92	LEU	20
1	A	58	ILE	19
1	A	76	ARG	18
1	A	40	ASN	16
1	A	69	LEU	13

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	113/128 (88%)	86±4 (76±3%)	27±4 (24±3%)	3 27
All	All	2260/2560 (88%)	1713 (76%)	547 (24%)	3 27

5 of 77 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	65	ILE	20
1	A	105	ILE	20
1	A	110	LEU	20
1	A	135	ILE	20
1	A	50	LEU	20

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 carbohydrates 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)

The completeness of assignment taking into account all chemical shift lists is 90% for the well-defined parts and 85% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 15312

Chemical shift list name: *assigned_ chem_ shift_ list_ 1*

7.1.1 Bookkeeping (i)

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	1829
Number of shifts mapped to atoms	1829
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	142	-0.80 ± 0.16	Should be applied
$^{13}C_{\beta}$	134	0.00 ± 0.05	None needed (< 0.5 ppm)
$^{13}C'$	132	-0.32 ± 0.13	None needed (< 0.5 ppm)
^{15}N	138	0.70 ± 0.30	Should be applied

7.1.3 Completeness of resonance assignments (i)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 90%, i.e. 1567 atoms were assigned a chemical shift out of a possible 1739. 23 out of 25 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	649/661 (98%)	260/264 (98%)	260/266 (98%)	129/131 (98%)
Sidechain	793/931 (85%)	491/542 (91%)	297/341 (87%)	5/48 (10%)

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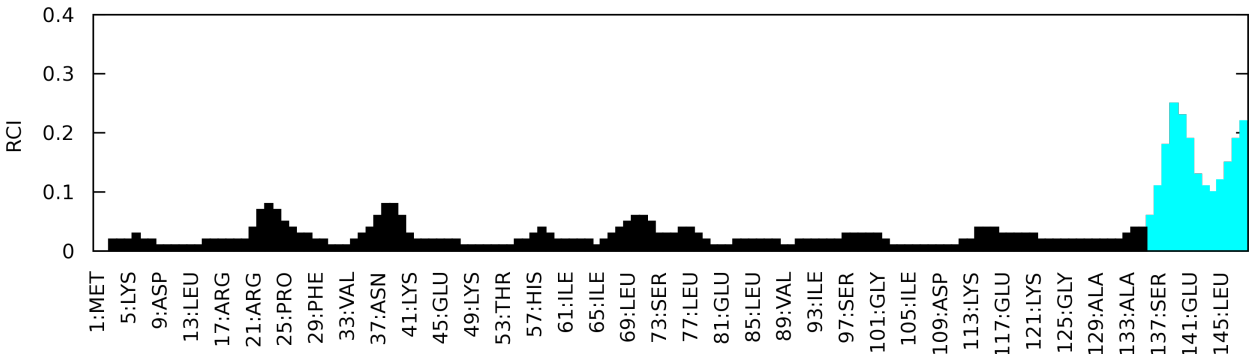
	Total	^{1}H	^{13}C	^{15}N
Aromatic	125/147 (85%)	65/77 (84%)	60/66 (91%)	0/4 (0%)
Overall	1567/1739 (90%)	816/883 (92%)	617/673 (92%)	134/183 (73%)

7.1.4 Statistically unusual chemical shifts (i)

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
1	A	12	PHE	CZ	120.36	137.04 – 121.44	-5.7

7.1.5 Random Coil Index (RCI) plots (i)

The image below reports *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: