



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 2NMB
Title : DNUMB PTB DOMAIN COMPLEXED WITH A PHOSPHOTYROSINE PEPTIDE, NMR, ENSEMBLE OF STRUCTURES.
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Deposited on : 1998-10-29

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 ⓘ 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	:	1.7.2 (RC1), CSD as538be (2017)
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	trunk28760
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

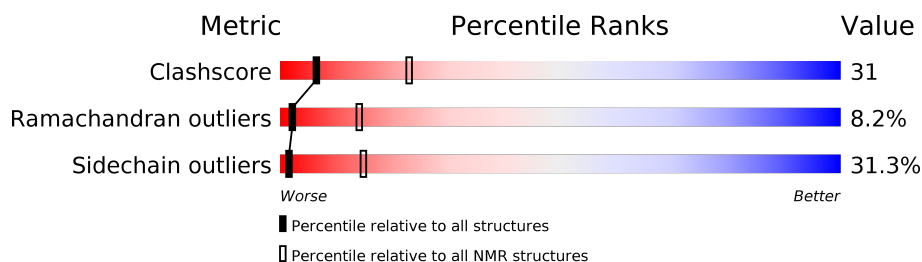
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 83%.

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	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

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	160	 29% 46% • 13% 8%
2	B	7	 71% 14% 14%

2 Ensemble composition and analysis

This entry contains 14 models. Model 1 is the overall representative, medoid model (most similar to other models). The authors have identified model 4 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:69-A:152, A:158-A:200, B:1-B:5, B:7-B:7 (133)	0.46	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 2 clusters and 4 single-model clusters were found.

Cluster number	Models
1	1, 2, 5, 6, 7, 9, 11, 12
2	4, 8
Single-model clusters	3; 10; 13; 14

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2422 atoms, of which 1202 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called PROTEIN (NUMB PROTEIN).

Mol	Chain	Residues	Atoms						Trace
1	A	147	Total	C	H	N	O	S	0
			2305	710	1146	227	211	11	

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	206	THR	-	SEE REMARK 999	UNP P16554
A	207	ARG	-	SEE REMARK 999	UNP P16554
A	208	ALA	-	SEE REMARK 999	UNP P16554
A	209	ALA	-	SEE REMARK 999	UNP P16554
A	210	ALA	-	SEE REMARK 999	UNP P16554

- Molecule 2 is a protein called PROTEIN (GPPY PEPTIDE).

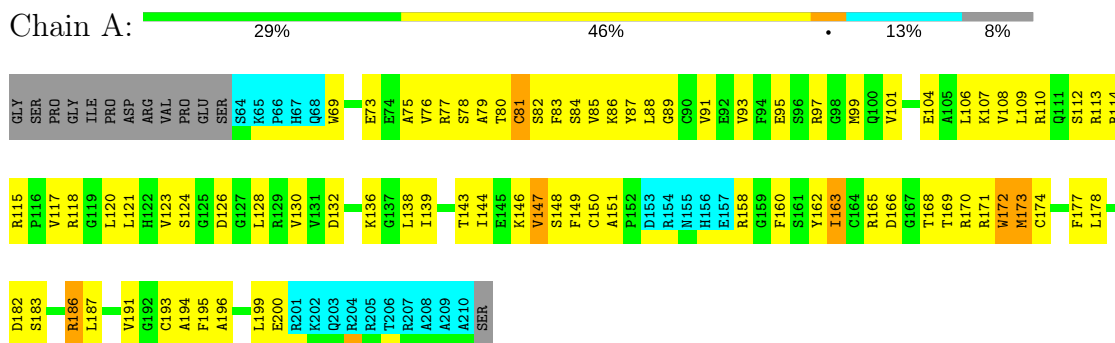
Mol	Chain	Residues	Atoms						Trace
2	B	7	Total	C	H	N	O	P	0
			117	40	56	7	13	1	

4 Residue-property plots

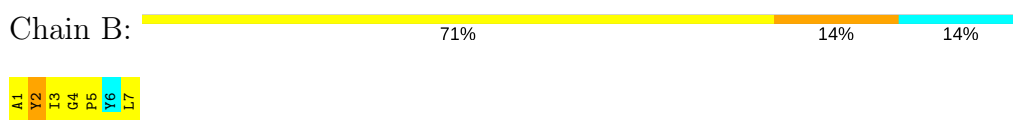
4.1 Average score per residue in the NMR ensemble

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: PROTEIN (NUMB PROTEIN)



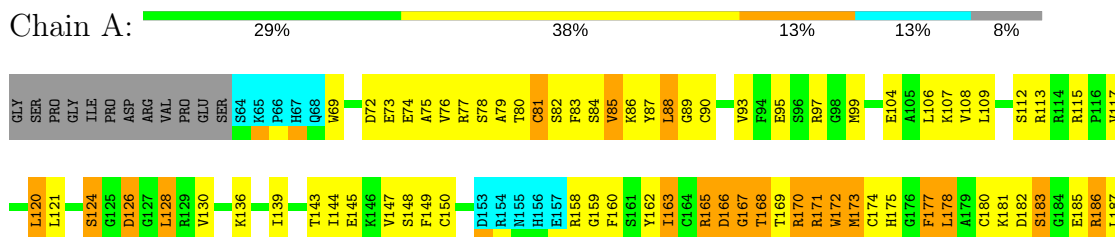
• Molecule 2: PROTEIN (GPPY PEPTIDE)



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

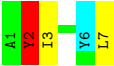
The representative model is number 1. Colouring as in section 4.1 above.

• Molecule 1: PROTEIN (NUMB PROTEIN)





● Molecule 2: PROTEIN (GPPY PEPTIDE)



5 Refinement protocol and experimental data overview

The models were refined using the following method: *SIMULATED ANNEALING WITH AMBIGUOUS RESTRAINTS*.

Of the 200 calculated structures, 14 were deposited, based on the following criterion: *NO NOE VIOLATION* > 0.3 Å.

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

Software name	Classification	Version
X-PLOR	refinement	3.851
ARIA/X-PLOR	structure solution	3.851

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 4263
Number of chemical shift lists	2
Total number of shifts	1891
Number of shifts mapped to atoms	1891
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	83%

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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PTR

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	988	976	976	61±9
2	B	45	48	48	4±2
All	All	14462	14336	14336	906

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:149:PHE:CE1	1:A:163:ILE:HD11	0.94	1.96	9	3
1:A:199:LEU:HD21	2:B:3:ILE:HG21	0.89	1.45	9	4
1:A:149:PHE:CZ	1:A:163:ILE:HD11	0.87	2.04	13	2
1:A:143:THR:O	1:A:147:VAL:HG23	0.84	1.71	13	2
1:A:147:VAL:HG12	1:A:163:ILE:O	0.84	1.72	14	5

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	127/160 (79%)	92±4 (72±3%)	26±4 (20±3%)	10±3 (8±2%)	2	16
2	B	4/7 (57%)	1±1 (25±13%)	2±1 (45±29%)	1±1 (30±22%)	0	1
All	All	1834/2338 (78%)	1298 (71%)	385 (21%)	151 (8%)	2	14

5 of 39 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	80	THR	14
1	A	170	ARG	11
1	A	166	ASP	11
1	A	183	SER	9
1	A	126	ASP	8

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	107/135 (79%)	74±5 (69±4%)	33±5 (31±4%)	1	15
2	B	4/4 (100%)	3±0 (64±12%)	1±0 (36±12%)	1	9
All	All	1554/1946 (80%)	1068 (69%)	486 (31%)	1	15

5 of 91 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	113	ARG	14
1	A	99	MET	14

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Mol	Chain	Res	Type	Models (Total)
2	B	2	TYR	14
1	A	107	LYS	12
1	A	136	LYS	11

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is 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
2	PTR	B	6	2	15,16,17	0.80±0.03	0±0 (0±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	Bond angles		
					Counts	RMSZ	#Z>2
2	PTR	B	6	2	19,22,24	0.57±0.03	0±0 (0±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
2	PTR	B	6	2	-	0±0,9,11,13	0±0,1,1,1

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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

The completeness of assignment taking into account all chemical shift lists is 83% for the well-defined parts and 83% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 4263

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 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	1820
Number of shifts mapped to atoms	1820
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	15

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	158	0.07 ± 0.10	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	146	0.24 ± 0.11	None needed (< 0.5 ppm)
$^{13}\text{C}'$	153	0.34 ± 0.15	None needed (< 0.5 ppm)
^{15}N	152	-0.09 ± 0.17	None needed (< 0.5 ppm)

7.1.3 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 80%, i.e. 1294 atoms were assigned a chemical shift out of a possible 1620. 24 out of 25 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	629/659 (95%)	252/263 (96%)	252/266 (95%)	125/130 (96%)
Sidechain	620/838 (74%)	375/492 (76%)	238/298 (80%)	7/48 (15%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	45/123 (37%)	43/66 (65%)	0/52 (0%)	2/5 (40%)
Overall	1294/1620 (80%)	670/821 (82%)	490/616 (80%)	134/183 (73%)

7.1.4 Statistically unusual chemical shifts [i](#)

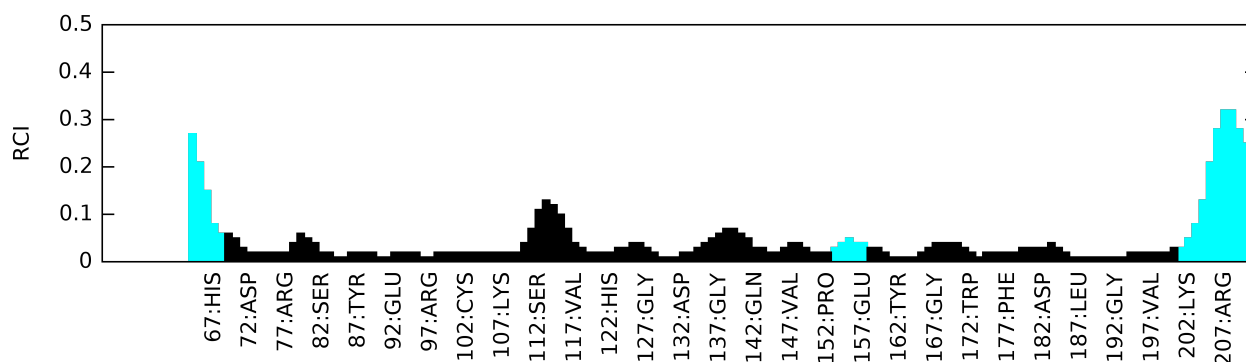
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	158	ARG	NE	113.10	92.63 – 76.73	17.9
1	A	201	ARG	NE	112.96	92.63 – 76.73	17.8
1	A	154	ARG	NE	112.69	92.63 – 76.73	17.6
1	A	114	ARG	NE	112.67	92.63 – 76.73	17.6
1	A	171	ARG	NE	112.67	92.63 – 76.73	17.6
1	A	207	ARG	NE	112.67	92.63 – 76.73	17.6
1	A	205	ARG	NE	112.67	92.63 – 76.73	17.6
1	A	129	ARG	NE	112.24	92.63 – 76.73	17.3
1	A	165	ARG	NE	112.02	92.63 – 76.73	17.2
1	A	170	ARG	NE	111.41	92.63 – 76.73	16.8
1	A	96	SER	HB2	1.48	5.18 – 2.58	-9.2
1	A	98	GLY	H	3.15	11.63 – 5.03	-7.8
1	A	152	PRO	HB3	3.98	3.81 – 0.21	5.5
1	A	152	PRO	HB2	3.98	3.82 – 0.32	5.5
1	A	192	GLY	HA3	1.91	5.80 – 2.00	-5.2

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:



7.2 Chemical shift list 2

File name: BMRB entry 4263

Chemical shift list name: *assigned_chem_shift_list_2*

7.2.1 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	71
Number of shifts mapped to atoms	71
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.2.2 Chemical shift referencing [i](#)

No chemical shift referencing corrections were calculated (not enough data).

7.2.3 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 3%, i.e. 56 atoms were assigned a chemical shift out of a possible 1620. 1 out of 25 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	18/659 (3%)	11/263 (4%)	3/266 (1%)	4/130 (3%)
Sidechain	30/838 (4%)	19/492 (4%)	11/298 (4%)	0/48 (0%)
Aromatic	8/123 (7%)	4/66 (6%)	4/52 (8%)	0/5 (0%)

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	Total	¹H	¹³C	¹⁵N
Overall	56/1620 (3%)	34/821 (4%)	18/616 (3%)	4/183 (2%)

7.2.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

7.2.5 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 B:

