



# wwPDB NMR Structure Validation Summary Report ⓘ

Feb 19, 2018 – 09:28 pm GMT

PDB ID : 2A93  
Title : NMR SOLUTION STRUCTURE OF THE C-MYC-MAX HET-  
ERODIMERIC LEUCINE ZIPPER, 40 STRUCTURES  
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Deposited on : 1998-06-09

This is a wwPDB NMR Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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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
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	trunk30686
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk30686

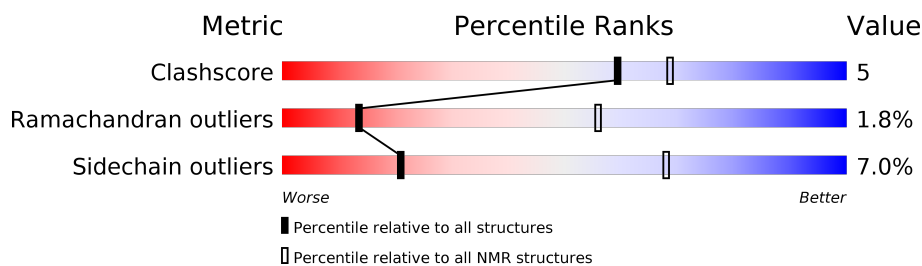
# 1 Overall quality at a glance

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	136279	12091
Ramachandran outliers	132675	10835
Sidechain outliers	132484	10811

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  $\geq 3$ , 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	34	
2	B	34	

## 2 Ensemble composition and analysis

This entry contains 40 models. Model 32 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:7-A:29, B:9-B:34 (49)	0.52	32

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 8 clusters and 2 single-model clusters were found.

Cluster number	Models
1	1, 2, 4, 11, 14, 21, 23, 29, 32, 38
2	6, 7, 12, 13, 20, 33, 36
3	8, 19, 26, 30, 31
4	10, 16, 24, 27, 28
5	5, 15, 17, 34
6	3, 22, 39
7	35, 40
8	9, 25
Single-model clusters	18; 37

### 3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 1078 atoms, of which 545 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called C-MYC-MAX HETERODIMERIC LEUCINE ZIPPER.

Mol	Chain	Residues	Atoms						Trace
1	A	34	Total	C	H	N	O	S	1
			550	164	281	52	52	1	

- Molecule 2 is a protein called C-MYC-MAX HETERODIMERIC LEUCINE ZIPPER.

Mol	Chain	Residues	Atoms						Trace
2	B	34	Total	C	H	N	O	S	1
			528	155	264	56	51	2	



## 5 Refinement protocol and experimental data overview ⓘ

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

Of the 40 calculated structures, 40 were deposited, based on the following criterion: *LEAST RESTRAINT VIOLATION ONLY*..

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

Software name	Classification	Version
X-PLOR	refinement	3.1
X-PLOR	structure solution	

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

## 6 Model quality

### 6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ACE, NH2

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

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	201	208	208	2±1
2	B	216	214	214	4±1
All	All	16680	16880	16880	174

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 5.

5 of 49 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:27:LEU:O	2:B:31:VAL:HG23	0.77	1.80	37	38
1:A:13:LEU:HD22	2:B:13:HIS:HB3	0.68	1.66	18	13
2:B:33:ALA:O	2:B:34:LEU:HD22	0.68	1.89	39	1
1:A:16:GLU:OE2	1:A:20:LEU:HD12	0.66	1.91	40	1
1:A:19:LEU:HD23	1:A:19:LEU:O	0.64	1.92	20	3

## 6.3 Torsion angles

### 6.3.1 Protein backbone

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	23/34 (68%)	23±0 (100±1%)	0±0 (0±1%)	0±0 (0±0%)	100	100
2	B	26/34 (76%)	24±1 (91±4%)	1±1 (6±4%)	1±1 (3±2%)	7	36
All	All	1960/2720 (72%)	1864 (95%)	60 (3%)	36 (2%)	13	56

All 2 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	B	17	ILE	32
2	B	34	LEU	4

### 6.3.2 Protein sidechains

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	22/29 (76%)	21±1 (94±5%)	1±1 (6±5%)	26	73
2	B	24/28 (86%)	22±1 (92±4%)	2±1 (8±4%)	17	64
All	All	1840/2280 (81%)	1711 (93%)	129 (7%)	21	68

5 of 30 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)
2	B	18	ASP	23
2	B	32	ARG	13
1	A	23	ARG	10
2	B	23	GLN	7
1	A	28	LYS	7



### 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

No chemical shift data were provided