



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 2N1D
Title : Solution structure of the MRG15-MRGBP complex
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This is a wwPDB NMR Structure Validation Summary Report for a publicly released PDB entry.

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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
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

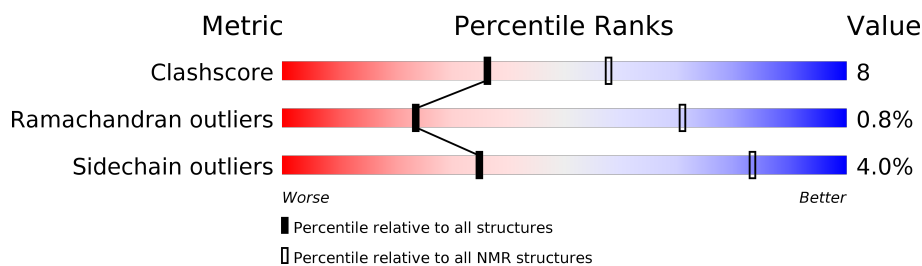
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 87%.

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	54	 59% 20% 20%
2	B	172	 78% 16% 6%

2 Ensemble composition and analysis ⓘ

This entry contains 20 models. Model 8 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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:75-A:117, B:156-B:203, B:211-B:323 (204)	0.56	8

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. No single-model clusters were found.

Cluster number	Models
1	1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 14, 15, 16, 17, 18, 19, 20
2	12, 13

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3684 atoms, of which 1839 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called MRG/MORF4L-binding protein.

Mol	Chain	Residues	Atoms						Trace
1	A	54	Total	C	H	N	O	S	0
			874	279	432	76	85	2	

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	66	SER	-	EXPRESSION TAG	UNP Q9NV56
A	67	ASN	-	EXPRESSION TAG	UNP Q9NV56
A	68	ALA	-	EXPRESSION TAG	UNP Q9NV56

- Molecule 2 is a protein called Mortality factor 4-like protein 1.

Mol	Chain	Residues	Atoms						Trace
2	B	172	Total	C	H	N	O	S	0
			2810	912	1407	229	259	3	

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	152	SER	-	EXPRESSION TAG	UNP Q9UBU8
B	153	ASN	-	EXPRESSION TAG	UNP Q9UBU8
B	154	ALA	-	EXPRESSION TAG	UNP Q9UBU8

Q256	V257	L264	D280	E281	K282	L286	Y311	R321	A322	V323
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5 Refinement protocol and experimental data overview

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

Of the 80 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy, restraint violations, and RMS deviations from the ideal covalent geometry*.

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

Software name	Classification	Version
ARIA	structure solution	1.2
CNS	refinement	1.1

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)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	2618
Number of shifts mapped to atoms	2618
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	87%

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	365	353	351	9±2
2	B	1320	1331	1327	22±4
All	All	33700	33680	33560	567

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 8.

5 of 265 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:B:293:ASP:HA	2:B:296:LYS:HE2	1.02	1.30	2	1
1:A:77:ILE:HD13	2:B:220:GLY:HA2	0.83	1.50	17	11
2:B:229:LEU:HA	2:B:233:LEU:HB2	0.83	1.50	8	9
2:B:185:PRO:HA	2:B:257:VAL:HA	0.83	1.49	17	7
2:B:194:LEU:HB3	2:B:218:VAL:HG13	0.82	1.50	15	17

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	43/54 (80%)	37±2 (87±4%)	4±2 (9±5%)	2±1 (4±2%)	5	33
2	B	160/172 (93%)	153±2 (95±1%)	7±2 (4±1%)	0±0 (0±0%)	100	100
All	All	4060/4520 (90%)	3803 (94%)	223 (5%)	34 (1%)	24	71

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	97	PRO	12
1	A	106	VAL	9
1	A	76	VAL	5
1	A	98	PHE	3
1	A	100	ASN	2

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	42/50 (84%)	41±1 (97±3%)	1±1 (3±3%)	39	86
2	B	141/150 (94%)	135±2 (96±1%)	6±2 (4±1%)	34	82
All	All	3660/4000 (92%)	3514 (96%)	146 (4%)	35	83

5 of 53 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	184	LEU	19
2	B	183	TYR	14
2	B	224	TYR	13
1	A	90	LEU	9
2	B	241	GLN	8

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

The completeness of assignment taking into account all chemical shift lists is 87% for the well-defined parts and 86% for the entire structure.

7.1 Chemical shift list 1

File name: input_cs.cif

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	2618
Number of shifts mapped to atoms	2618
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

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	225	-0.50 ± 0.08	Should be applied
$^{13}\text{C}_\beta$	216	0.17 ± 0.04	None needed (< 0.5 ppm)
$^{13}\text{C}'$	215	-0.12 ± 0.08	None needed (< 0.5 ppm)
^{15}N	197	0.55 ± 0.11	Should be applied

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 87%, i.e. 2290 atoms were assigned a chemical shift out of a possible 2644. 0 out of 42 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	967/992 (97%)	387/394 (98%)	399/408 (98%)	181/190 (95%)
Sidechain	1189/1384 (86%)	743/813 (91%)	433/520 (83%)	13/51 (25%)

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	Total	^1H	^{13}C	^{15}N
Aromatic	134/268 (50%)	119/138 (86%)	12/115 (10%)	3/15 (20%)
Overall	2290/2644 (87%)	1249/1345 (93%)	844/1043 (81%)	197/256 (77%)

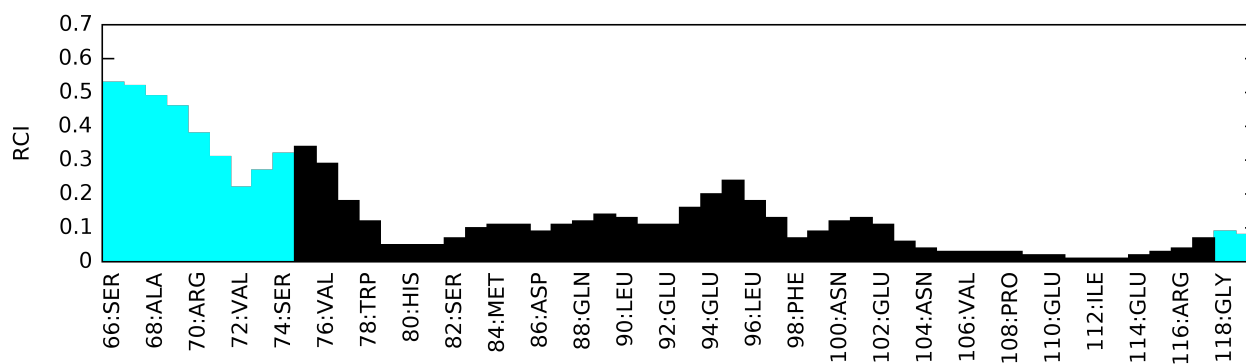
7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots [i](#)

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:

