

wwPDB NMR Structure Validation Summary Report (i)

Feb 20, 2022 – 01:44 AM EST

PDB ID	:	1U38
Title	:	Auto-inhibition Mechanism of X11s/Mints Family Scaffold Proteins Revealed
		by the Closed Conformation of the Tandem PDZ Domains
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Deposited on	:	2004-07-21

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

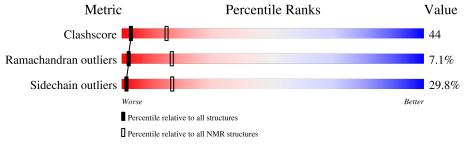
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.26
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.26

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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f NMR} \ { m archive} \ (\#{ m Entries})$
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	А	89	39%	45%	13% •	
2	В	4	25%	75%		



2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 16 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *minimized average structure*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues						
Well-defined core	Medoid model					
1	A:17-A:105, B:-3-B:0 (93)	0.25	16			

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



3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1453 atoms, of which 751 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called amyloid beta A4 precursor protein-binding, family A, member 1.

Mol	Chain	Residues		Atoms				Trace	
1	٨	20	Total	С	Η	Ν	0	S	0
	А	89	1382	425	715	115	123	4	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	17	GLU	-	cloning artifact	UNP Q02410
А	18	PHE	-	cloning artifact	UNP Q02410

• Molecule 2 is a protein called PVYI.

Mol	Chain	Residues	Atoms				Trace	
2	В	4	Total	С	Η	Ν	0	0
		1	71	25	36	4	6	0

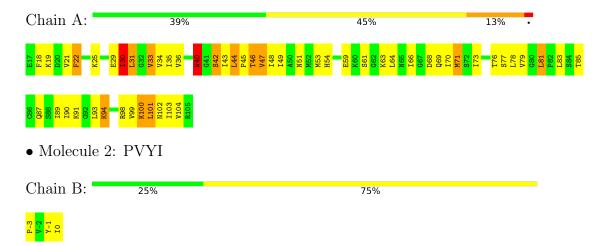


4 Residue-property plots (i)

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: amyloid beta A4 precursor protein-binding, family A, member 1



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

The representative model is number 16. Colouring as in section 4.1 above.

• Molecule 1: amyloid beta A4 precursor protein-binding, family A, member 1

Chain A:		44%	37%	16% •	
E17 F18 N19 D20 D20 P20 P21 F22 F22 F22 F22	E29 130 131 032 V33 V33 E37	040 143 143 144 145 146 146 148 148	MIG3 HI63 H164 H164 H164 H164 H164 H166 H166 H166	T76 S77 L78 L81 L81 L81 L83 C82 C83 S84 S84 S84 S84	189 190 L93
K94 N95 297 897 897 898 199 100 1101 N102	1103 V104 R105				
• Molecule 2	2: PVYI				
Chain B:	25%		75%		







5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: torsion angle dynamics.

Of the 200 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
CNS	structure solution	1.1
CNS	refinement	1.1

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	А	667	715	713	61 ± 5
2	В	35	36	38	11±1
All	All	14040	15020	15020	1265

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 44.

5 of 277 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Moo	lels
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total
1:A:33:VAL:HG22	2:B:0:ILE:HD11	1.08	1.22	13	20
1:A:49:ILE:HG22	1:A:66:ILE:HD13	1.07	1.27	15	19
1:A:90:ILE:HG21	2:B:0:ILE:HD13	1.06	1.26	16	20
1:A:76:THR:HG21	1:A:89:ILE:HD12	0.95	1.33	19	13
1:A:73:ILE:HD12	1:A:78:LEU:HD11	0.88	1.43	13	12

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



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	А	87/89~(98%)	$68 \pm 1 (78 \pm 2\%)$	$13\pm2~(15\pm2\%)$	$6\pm1~(7\pm1\%)$	2 17
2	В	2/4~(50%)	$1\pm1 (70\pm33\%)$	$0\pm1~(18\pm29\%)$	0 ± 0 (12 $\pm22\%$)	1 6
All	All	1780/1860~(96%)	1388 (78%)	265 (15%)	127 (7%)	2 16

entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

5 of 13 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	А	30	ILE	20
1	А	31	LEU	20
1	А	40	TRP	20
1	А	45	PRO	16
1	А	42	SER	15

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	А	76/76~(100%)	52 ± 2 (69 $\pm2\%$)	24 ± 2 (31 $\pm2\%$)	1 15
2	В	4/4~(100%)	4 ± 0 (94 $\pm11\%$)	$0\pm0~(6\pm11\%)$	21 70
All	All	1600/1600~(100%)	1124 (70%)	476 (30%)	1 17

5 of 51 unique residues with a non-rotameric side chain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	А	22	PHE	20
1	А	30	ILE	20
1	А	33	VAL	20
1	А	40	TRP	20
1	А	48	ILE	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 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

