



Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 06:25 pm GMT

PDB ID : 1IUF
Title : LOW RESOLUTION SOLUTION STRUCTURE OF THE TWO DNA-BINDING DOMAINS IN *Schizosaccharomyces pombe* ABP1 PROTEIN
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Deposited on : 2002-03-04

This is a Full wwPDB NMR Structure Validation 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
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

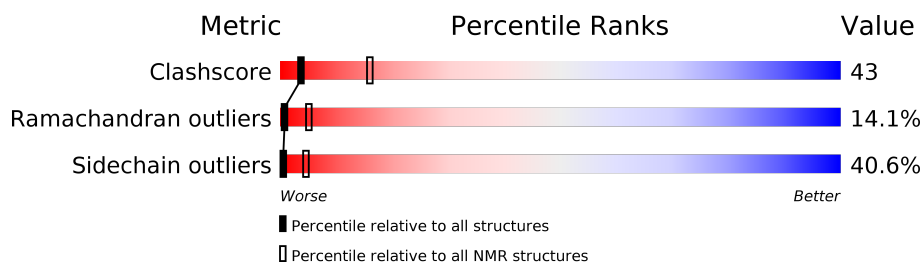
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment 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	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	144	<div> <div></div> <div>23%</div> <div>49%</div> <div>28%</div> <div>.</div> </div>

2 Ensemble composition and analysis ⓘ

This entry contains 1 models. Identification of well-defined residues and clustering analysis are not possible.

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2412 atoms, of which 1202 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called centromere abp1 protein.

Mol	Chain	Residues	Atoms						Trace
1	A	144	Total	C	H	N	O	S	0
			2412	775	1202	222	212	1	

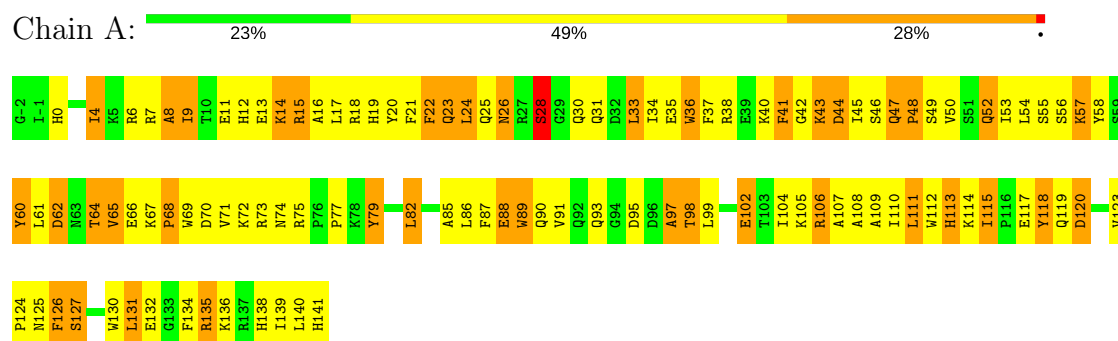
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	CLONING ARTIFACT	UNP P49777
A	-1	ILE	-	CLONING ARTIFACT	UNP P49777
A	0	HIS	-	CLONING ARTIFACT	UNP P49777

4 Residue-property plots

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: centromere abp1 protein



5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics followed with simulated annealing*.

Of the 10 calculated structures, 1 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	refinement	1.0

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

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	1210	1202	1196	103
All	All	1210	1202	1196	103

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 43.

All clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:104:ILE:HG12	1:A:131:LEU:HD13	0.73	1.56
1:A:47:GLN:N	1:A:48:PRO:HD3	0.73	1.98
1:A:67:LYS:N	1:A:68:PRO:HD3	0.72	2.00
1:A:17:LEU:HD13	1:A:36:TRP:CZ2	0.72	2.19
1:A:4:ILE:O	1:A:8:ALA:HB2	0.71	1.86
1:A:82:LEU:HD13	1:A:86:LEU:CD2	0.68	2.17
1:A:4:ILE:HD12	1:A:40:LYS:HD3	0.67	1.67
1:A:31:GLN:HA	1:A:34:ILE:HD12	0.66	1.66
1:A:115:ILE:HG23	1:A:115:ILE:O	0.62	1.94
1:A:87:PHE:HA	1:A:134:PHE:CZ	0.60	2.30
1:A:87:PHE:CE1	1:A:91:VAL:HG21	0.60	2.32
1:A:68:PRO:HB2	1:A:69:TRP:CE3	0.59	2.32
1:A:25:GLN:O	1:A:26:ASN:CB	0.58	2.52
1:A:21:PHE:HA	1:A:28:SER:OG	0.57	2.00
1:A:131:LEU:HG	1:A:134:PHE:CE2	0.57	2.34

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:134:PHE:CD1	1:A:135:ARG:N	0.57	2.73
1:A:86:LEU:O	1:A:89:TRP:CD1	0.56	2.58
1:A:47:GLN:N	1:A:48:PRO:CD	0.56	2.67
1:A:82:LEU:O	1:A:86:LEU:HD23	0.56	2.00
1:A:104:ILE:O	1:A:107:ALA:N	0.55	2.39
1:A:67:LYS:N	1:A:68:PRO:CD	0.55	2.68
1:A:53:ILE:HA	1:A:57:LYS:HB2	0.55	1.78
1:A:115:ILE:HD13	1:A:117:GLU:H	0.55	1.61
1:A:64:THR:HG21	1:A:68:PRO:HB3	0.54	1.80
1:A:127:SER:O	1:A:130:TRP:CZ2	0.54	2.61
1:A:66:GLU:C	1:A:68:PRO:HD3	0.53	2.23
1:A:139:ILE:O	1:A:139:ILE:HG22	0.53	2.03
1:A:86:LEU:CG	1:A:130:TRP:CZ3	0.53	2.92
1:A:17:LEU:CD1	1:A:36:TRP:CZ2	0.53	2.91
1:A:86:LEU:HG	1:A:130:TRP:CZ3	0.52	2.40
1:A:86:LEU:HD12	1:A:130:TRP:CZ3	0.52	2.39
1:A:58:TYR:O	1:A:62:ASP:HB2	0.51	2.05
1:A:82:LEU:HD13	1:A:86:LEU:HD21	0.51	1.81
1:A:14:LYS:HD3	1:A:15:ARG:N	0.51	2.21
1:A:86:LEU:HD12	1:A:130:TRP:CH2	0.51	2.41
1:A:115:ILE:O	1:A:115:ILE:CG2	0.50	2.58
1:A:36:TRP:C	1:A:36:TRP:CD1	0.50	2.84
1:A:104:ILE:O	1:A:106:ARG:N	0.49	2.46
1:A:111:LEU:HD21	1:A:118:TYR:CE2	0.49	2.41
1:A:127:SER:O	1:A:130:TRP:CE2	0.49	2.65
1:A:82:LEU:HD13	1:A:86:LEU:HD23	0.49	1.81
1:A:38:ARG:O	1:A:42:GLY:CA	0.49	2.60
1:A:106:ARG:O	1:A:110:ILE:HG22	0.48	2.08
1:A:45:ILE:CG2	1:A:50:VAL:HG13	0.48	2.38
1:A:45:ILE:HG23	1:A:48:PRO:HD2	0.48	1.83
1:A:9:ILE:HG21	1:A:57:LYS:HD2	0.48	1.85
1:A:25:GLN:O	1:A:26:ASN:HB3	0.48	2.09
1:A:111:LEU:O	1:A:115:ILE:HG22	0.47	2.09
1:A:115:ILE:HD12	1:A:118:TYR:HB3	0.47	1.86
1:A:87:PHE:HE2	1:A:139:ILE:HD11	0.47	1.69
1:A:14:LYS:HB3	1:A:61:LEU:CD1	0.47	2.39
1:A:130:TRP:HZ3	1:A:131:LEU:HD12	0.47	1.68
1:A:130:TRP:CE3	1:A:131:LEU:N	0.46	2.84
1:A:97:ALA:O	1:A:98:THR:HG23	0.46	2.11
1:A:64:THR:OG1	1:A:65:VAL:N	0.46	2.49
1:A:134:PHE:C	1:A:134:PHE:CD1	0.46	2.89
1:A:126:PHE:CD1	1:A:126:PHE:N	0.46	2.83

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:60:TYR:CD2	1:A:69:TRP:CH2	0.46	3.03
1:A:14:LYS:CD	1:A:15:ARG:N	0.46	2.79
1:A:16:ALA:HB3	1:A:36:TRP:CH2	0.45	2.46
1:A:86:LEU:CD1	1:A:130:TRP:CH2	0.45	2.99
1:A:19:HIS:O	1:A:23:GLN:CB	0.45	2.65
1:A:86:LEU:HA	1:A:89:TRP:HD1	0.45	1.71
1:A:107:ALA:O	1:A:111:LEU:N	0.45	2.50
1:A:47:GLN:O	1:A:47:GLN:CG	0.45	2.65
1:A:18:ARG:O	1:A:22:PHE:HB2	0.45	2.11
1:A:34:ILE:HA	1:A:37:PHE:HB2	0.45	1.87
1:A:79:TYR:CG	1:A:82:LEU:HB2	0.45	2.47
1:A:46:SER:N	1:A:48:PRO:HD3	0.45	2.27
1:A:108:ALA:HB1	1:A:126:PHE:CZ	0.45	2.47
1:A:46:SER:C	1:A:48:PRO:HD3	0.45	2.32
1:A:87:PHE:O	1:A:90:GLN:N	0.45	2.50
1:A:11:GLU:HB2	1:A:71:VAL:HG11	0.44	1.89
1:A:37:PHE:CD1	1:A:41:PHE:CZ	0.44	3.05
1:A:87:PHE:CZ	1:A:91:VAL:HG21	0.44	2.47
1:A:33:LEU:HD23	1:A:37:PHE:CE2	0.44	2.47
1:A:86:LEU:HD13	1:A:89:TRP:CD1	0.44	2.48
1:A:68:PRO:HG2	1:A:69:TRP:CE3	0.44	2.47
1:A:123:VAL:HG11	1:A:126:PHE:CE2	0.44	2.48
1:A:107:ALA:O	1:A:111:LEU:CB	0.43	2.67
1:A:86:LEU:CD1	1:A:130:TRP:CZ3	0.43	3.02
1:A:42:GLY:O	1:A:43:LYS:HB3	0.42	2.14
1:A:74:ASN:O	1:A:75:ARG:HG3	0.42	2.14
1:A:60:TYR:CD2	1:A:69:TRP:CZ2	0.42	3.08
1:A:109:ALA:O	1:A:113:HIS:HB2	0.42	2.15
1:A:17:LEU:HG	1:A:33:LEU:HD21	0.42	1.91
1:A:46:SER:O	1:A:47:GLN:HG2	0.42	2.14
1:A:11:GLU:CB	1:A:61:LEU:HD22	0.41	2.45
1:A:132:GLU:O	1:A:136:LYS:HB2	0.41	2.15
1:A:135:ARG:HA	1:A:139:ILE:HG12	0.41	1.91
1:A:33:LEU:HD23	1:A:37:PHE:HE2	0.41	1.73
1:A:24:LEU:CG	1:A:28:SER:HB3	0.41	2.45
1:A:85:ALA:O	1:A:88:GLU:CG	0.41	2.67
1:A:37:PHE:O	1:A:40:LYS:HG2	0.41	2.15
1:A:18:ARG:HG3	1:A:19:HIS:N	0.41	2.30
1:A:37:PHE:O	1:A:41:PHE:CD1	0.41	2.74
1:A:40:LYS:HG3	1:A:41:PHE:N	0.41	2.31
1:A:37:PHE:O	1:A:41:PHE:CE1	0.41	2.73
1:A:17:LEU:CD2	1:A:53:ILE:CG2	0.41	2.99

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:64:THR:CG2	1:A:68:PRO:HB3	0.41	2.45
1:A:58:TYR:CZ	1:A:62:ASP:OD2	0.40	2.74
1:A:14:LYS:HG3	1:A:58:TYR:HA	0.40	1.93
1:A:49:SER:O	1:A:52:GLN:N	0.40	2.54

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	142/144 (99%)	90 (63%)	32 (23%)	20 (14%)	1	5
All	All	142/144 (99%)	90 (63%)	32 (23%)	20 (14%)	1	5

All 20 Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	68	PRO
1	A	99	LEU
1	A	8	ALA
1	A	124	PRO
1	A	105	LYS
1	A	48	PRO
1	A	77	PRO
1	A	26	ASN
1	A	102	GLU
1	A	28	SER
1	A	43	LYS
1	A	9	ILE
1	A	120	ASP
1	A	4	ILE
1	A	44	ASP
1	A	97	ALA
1	A	56	SER
1	A	88	GLU
1	A	65	VAL

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Mol	Chain	Res	Type
1	A	138	HIS

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	128/128 (100%)	76 (59%)	52 (41%)	0	4
All	All	128/128 (100%)	76 (59%)	52 (41%)	0	4

All 52 residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	115	ILE
1	A	20	TYR
1	A	82	LEU
1	A	13	GLU
1	A	54	LEU
1	A	113	HIS
1	A	89	TRP
1	A	60	TYR
1	A	0	HIS
1	A	141	HIS
1	A	33	LEU
1	A	23	GLN
1	A	98	THR
1	A	64	THR
1	A	106	ARG
1	A	14	LYS
1	A	15	ARG
1	A	57	LYS
1	A	28	SER
1	A	30	GLN
1	A	127	SER
1	A	6	ARG
1	A	70	ASP
1	A	112	TRP

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Mol	Chain	Res	Type
1	A	12	HIS
1	A	140	LEU
1	A	102	GLU
1	A	52	GLN
1	A	135	ARG
1	A	114	LYS
1	A	95	ASP
1	A	55	SER
1	A	118	TYR
1	A	44	ASP
1	A	125	ASN
1	A	47	GLN
1	A	131	LEU
1	A	62	ASP
1	A	73	ARG
1	A	126	PHE
1	A	79	TYR
1	A	111	LEU
1	A	7	ARG
1	A	35	GLU
1	A	119	GLN
1	A	22	PHE
1	A	41	PHE
1	A	120	ASP
1	A	24	LEU
1	A	93	GLN
1	A	36	TRP
1	A	72	LYS

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided