



Full wwPDB NMR Structure Validation Report ⓘ

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PDB ID : 1J4O
Title : REFINED NMR STRUCTURE OF THE FHA1 DOMAIN OF YEAST RAD53
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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

<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	:	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

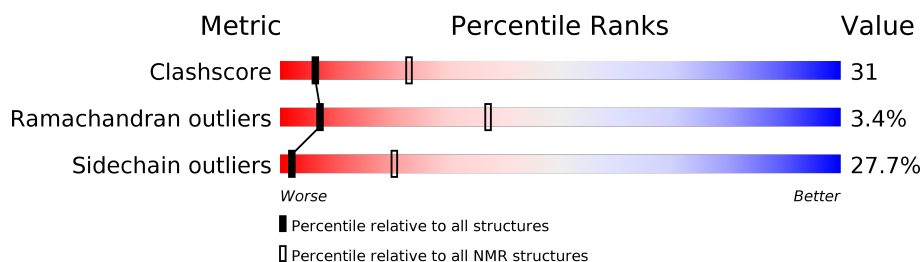
1 Overall quality at a glance

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 ≥ 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	151	

2 Ensemble composition and analysis ⓘ

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 2424 atoms, of which 1224 are hydrogens and 0 are deuteriums.

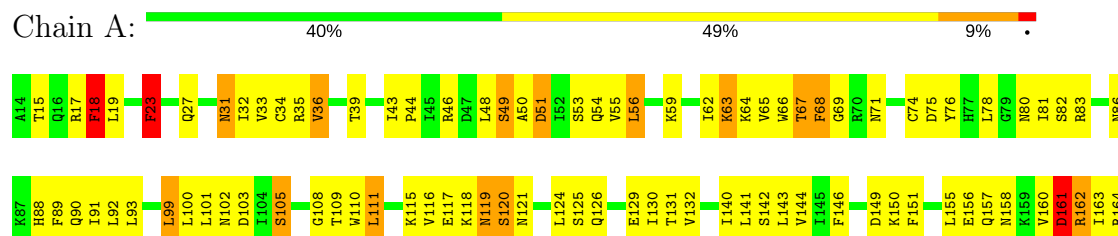
- Molecule 1 is a protein called PROTEIN KINASE SPK1.

Mol	Chain	Residues	Atoms						Trace
1	A	151	Total	C	H	N	O	S	0
			2424	751	1224	215	230	4	

4 Residue-property plots [i](#)

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 KINASE SPK1



5 Refinement protocol and experimental data overview

The models were refined using the following method: *THE STRUCTURES ARE BASED ON A TOTAL OF 2377 RESTRAINTS. AMONG THEM, 2107 ARE NOE-DERIVED DISTANCE CONSTRAINTS, 192 TALOS-DERIVED DIHEDRAL ANGLE RESTRAINTS, AND 78 RESTRAINTS FROM HYDROGEN BONDS..*

Of the ? calculated structures, 1 were deposited, based on the following criterion: ?.

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

Software name	Classification	Version
XWINNMR	structure solution	2.6
CNS	structure solution	1.0
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 [i](#)

6.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.35	0/1214 (0.0%)	4.07	14/1633 (0.9%)
All	All	0.35	0/1214 (0.0%)	4.07	14/1633 (0.9%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0	2
All	All	0	2

There are no bond-length outliers.

All angle outliers are listed below. They are sorted according to the Z-score.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	23	PHE	CZ-CE2-CD2	-65.24	41.81	120.10
1	A	18	PHE	CG-CD1-CE1	-60.33	54.44	120.80
1	A	18	PHE	CZ-CE2-CD2	-58.29	50.16	120.10
1	A	23	PHE	CG-CD1-CE1	-50.63	65.11	120.80
1	A	23	PHE	CG-CD2-CE2	-46.73	69.40	120.80
1	A	23	PHE	CD1-CE1-CZ	-43.40	68.02	120.10
1	A	18	PHE	CG-CD2-CE2	-42.56	73.98	120.80
1	A	18	PHE	CD1-CE1-CZ	-40.19	71.87	120.10
1	A	23	PHE	CD1-CG-CD2	-38.10	68.77	118.30
1	A	18	PHE	CD1-CG-CD2	-38.06	68.83	118.30
1	A	23	PHE	CB-CG-CD2	28.91	141.03	120.80
1	A	18	PHE	CE1-CZ-CE2	-27.97	69.66	120.00
1	A	23	PHE	CE1-CZ-CE2	-25.83	73.51	120.00
1	A	18	PHE	CB-CG-CD1	16.85	132.59	120.80

There are no chirality outliers.

All planar outliers are listed below.

Mol	Chain	Res	Type	Group
1	A	18	PHE	Sidechain
1	A	23	PHE	Sidechain

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	1200	1224	1221	75
All	All	1200	1224	1221	75

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.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:101:LEU:HD21	1:A:124:LEU:HD13	1.03	1.29
1:A:48:LEU:HD22	1:A:66:TRP:CD1	0.76	2.14
1:A:110:TRP:CE2	1:A:115:LYS:HB2	0.76	2.16
1:A:103:ASP:OD2	1:A:116:VAL:HG23	0.73	1.84
1:A:33:VAL:HG13	1:A:93:LEU:HD13	0.70	1.63
1:A:101:LEU:HD21	1:A:124:LEU:CD1	0.67	2.16
1:A:51:ASP:O	1:A:55:VAL:HG23	0.64	1.91
1:A:99:LEU:O	1:A:100:LEU:HD12	0.61	1.95
1:A:103:ASP:CG	1:A:118:LYS:HA	0.59	2.18
1:A:131:THR:HG22	1:A:140:ILE:CG2	0.59	2.28
1:A:32:ILE:HA	1:A:49:SER:HB3	0.57	1.76
1:A:33:VAL:HG23	1:A:50:ALA:N	0.57	2.13
1:A:68:PHE:CZ	1:A:91:ILE:HD12	0.55	2.36
1:A:163:ILE:O	1:A:163:ILE:HD12	0.55	2.02
1:A:62:ILE:HD11	1:A:65:VAL:HG22	0.54	1.77
1:A:69:GLY:HA3	1:A:86:ASN:O	0.54	2.03
1:A:67:THR:HG23	1:A:90:GLN:HG3	0.54	1.80
1:A:68:PHE:CG	1:A:89:PHE:CE2	0.53	2.97
1:A:43:ILE:CD1	1:A:78:LEU:HD22	0.53	2.34
1:A:100:LEU:HD23	1:A:121:ASN:HB3	0.52	1.81
1:A:68:PHE:N	1:A:68:PHE:CD1	0.51	2.78

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:34:CYS:SG	1:A:48:LEU:HD12	0.51	2.46
1:A:56:LEU:HD22	1:A:160:VAL:HG12	0.50	1.83
1:A:88:HIS:CE1	1:A:105:SER:HB3	0.49	2.42
1:A:68:PHE:CD2	1:A:76:TYR:CB	0.48	2.96
1:A:93:LEU:HD12	1:A:99:LEU:HG	0.48	1.85
1:A:43:ILE:HD13	1:A:78:LEU:HD22	0.47	1.84
1:A:88:HIS:CD2	1:A:105:SER:OG	0.47	2.68
1:A:88:HIS:CD2	1:A:132:VAL:CG1	0.47	2.98
1:A:129:GLU:HG3	1:A:144:VAL:HG22	0.47	1.84
1:A:160:VAL:O	1:A:160:VAL:HG23	0.47	2.10
1:A:65:VAL:HG13	1:A:91:ILE:O	0.47	2.09
1:A:43:ILE:HD13	1:A:78:LEU:CD2	0.46	2.39
1:A:131:THR:CG2	1:A:140:ILE:CG2	0.46	2.93
1:A:160:VAL:O	1:A:161:ASP:C	0.46	2.54
1:A:43:ILE:CG2	1:A:44:PRO:HD2	0.45	2.42
1:A:55:VAL:HG13	1:A:63:LYS:HG2	0.45	1.89
1:A:31:ASN:O	1:A:49:SER:HB3	0.45	2.12
1:A:36:VAL:HG22	1:A:48:LEU:HD11	0.45	1.87
1:A:62:ILE:HD11	1:A:65:VAL:CG2	0.44	2.42
1:A:151:PHE:CE1	1:A:155:LEU:CD2	0.44	3.00
1:A:33:VAL:HG23	1:A:50:ALA:H	0.44	1.72
1:A:51:ASP:CB	1:A:54:GLN:HG3	0.43	2.43
1:A:48:LEU:HB3	1:A:66:TRP:CE2	0.43	2.48
1:A:103:ASP:O	1:A:119:ASN:N	0.43	2.49
1:A:65:VAL:HG12	1:A:90:GLN:HG2	0.43	1.90
1:A:68:PHE:CD2	1:A:76:TYR:HB2	0.43	2.49
1:A:36:VAL:CG2	1:A:76:TYR:CE1	0.43	3.02
1:A:36:VAL:HG21	1:A:76:TYR:CE1	0.43	2.49
1:A:67:THR:O	1:A:75:ASP:N	0.43	2.52
1:A:110:TRP:NE1	1:A:115:LYS:HB2	0.42	2.27
1:A:65:VAL:CG1	1:A:91:ILE:O	0.42	2.67
1:A:81:ILE:HD11	1:A:141:LEU:CD1	0.42	2.45
1:A:66:TRP:O	1:A:90:GLN:HA	0.42	2.13
1:A:68:PHE:O	1:A:88:HIS:N	0.42	2.53
1:A:55:VAL:HG22	1:A:63:LYS:HG2	0.42	1.92
1:A:142:SER:C	1:A:143:LEU:HD22	0.41	2.35
1:A:105:SER:HB2	1:A:108:GLY:H	0.41	1.75
1:A:111:LEU:HD12	1:A:111:LEU:C	0.41	2.35
1:A:117:GLU:O	1:A:120:SER:HB2	0.41	2.15
1:A:142:SER:O	1:A:143:LEU:HD22	0.41	2.15
1:A:43:ILE:HG21	1:A:76:TYR:CE2	0.41	2.50
1:A:88:HIS:CE1	1:A:132:VAL:HB	0.41	2.50

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:110:TRP:O	1:A:131:THR:N	0.41	2.53
1:A:66:TRP:O	1:A:90:GLN:CG	0.41	2.68
1:A:109:THR:HG22	1:A:130:ILE:CG2	0.41	2.46
1:A:66:TRP:O	1:A:90:GLN:HG2	0.41	2.15
1:A:81:ILE:CD1	1:A:141:LEU:CD1	0.41	2.99
1:A:110:TRP:O	1:A:130:ILE:HG23	0.41	2.15
1:A:151:PHE:CE1	1:A:155:LEU:HD23	0.40	2.51
1:A:88:HIS:O	1:A:105:SER:N	0.40	2.53
1:A:90:GLN:O	1:A:102:ASN:N	0.40	2.50
1:A:88:HIS:CG	1:A:105:SER:HB3	0.40	2.51
1:A:49:SER:O	1:A:64:LYS:CE	0.40	2.69
1:A:33:VAL:HG11	1:A:66:TRP:CH2	0.40	2.52

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	149/151 (99%)	127 (85%)	17 (11%)	5 (3%)	7	37
All	All	149/151 (99%)	127 (85%)	17 (11%)	5 (3%)	7	37

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

Mol	Chain	Res	Type
1	A	162	ARG
1	A	31	ASN
1	A	119	ASN
1	A	161	ASP
1	A	80	ASN

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	137/137 (100%)	99 (72%)	38 (28%)	2	20
All	All	137/137 (100%)	99 (72%)	38 (28%)	2	20

All 38 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	17	ARG
1	A	156	GLU
1	A	82	SER
1	A	161	ASP
1	A	164	ARG
1	A	125	SER
1	A	63	LYS
1	A	74	CYS
1	A	27	GLN
1	A	120	SER
1	A	23	PHE
1	A	15	THR
1	A	67	THR
1	A	53	SER
1	A	36	VAL
1	A	150	LYS
1	A	157	GLN
1	A	126	GLN
1	A	92	LEU
1	A	39	THR
1	A	105	SER
1	A	35	ARG
1	A	149	ASP
1	A	51	ASP
1	A	158	ASN
1	A	162	ARG
1	A	46	ARG
1	A	83	ARG
1	A	111	LEU
1	A	146	PHE
1	A	19	LEU
1	A	68	PHE
1	A	56	LEU
1	A	18	PHE

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Mol	Chain	Res	Type
1	A	59	LYS
1	A	49	SER
1	A	99	LEU
1	A	71	ASN

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