

Full wwPDB NMR Structure Validation Report (i)

Nov 5, 2023 – 04:30 AM EST

PDB ID : 1J4K Title : SOLUTION STRUCTURE OF THE FHA2 DOMAIN OF RAD53 COM-PLEXED WITH A PHOSPHOTYROSYL PEPTIDE DERIVED FROM RAD9 Authors : Byeon, I.-J.L.; Yongkiettrakul, S.; Tsai, M.-D. Deposited on : 2001-10-03

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 (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

SOFTWARE-VERSIONS INFOmissingINFO

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	Whole archive	NMR archive	
	$(\# { m Entries})$	$(\# { m Entries})$	
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	158	37%	47%	15% •	
2	Р	7	71%		29%	



2 Ensemble composition and analysis (i)

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



3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 2676 atoms, of which 1332 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called PROTEIN KINASE SPK1.

Mol	Chain	Residues	Atoms					Trace	
1	٨	150	Total	С	Η	Ν	0	\mathbf{S}	0
	A	199	2551	806	1277	222	239	7	U

• Molecule 2 is a protein called DNA REPAIR PROTEIN RAD9.

Mol	Chain	Residues	Atoms				Trace		
0	D	7	Total	С	Н	Ν	0	Р	0
	Г	1	125	43	55	7	19	1	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Р	829	PTR	TYR	modified residue	UNP P14737



4 Residue-property plots (i)

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: PROTEIN KINASE SPK1



5 Refinement protocol and experimental data overview (i)

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

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
X-PLOR	structure solution	3.851
X-PLOR	refinement	3.851

No chemical shift data was provided.



6 Model quality (i)

6.1 Standard geometry (i)

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

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	1274	1277	1273	102
All	All	1344	1332	1324	102

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 38.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:594:ILE:HD11	1:A:625:ILE:HD12	0.82	1.50
1:A:648:TRP:CH2	1:A:671:LEU:HD22	0.77	2.14
1:A:648:TRP:CZ3	1:A:671:LEU:HD22	0.75	2.15
1:A:594:ILE:CD1	1:A:625:ILE:HD12	0.73	2.13
1:A:587:ILE:HD13	1:A:688:PHE:CE1	0.70	2.21
1:A:578:LEU:HD11	1:A:694:VAL:CG1	0.70	2.17
1:A:580:LEU:HD11	1:A:625:ILE:HD11	0.70	1.63
1:A:603:ILE:HG23	1:A:611:CYS:SG	0.68	2.29
1:A:644:LEU:HD13	1:A:703:PHE:HA	0.65	1.68
1:A:592:LEU:HD13	1:A:611:CYS:SG	0.64	2.32
1:A:615:ASP:CB	1:A:618:LEU:HD13	0.64	2.22
1:A:621:VAL:HG11	1:A:727:VAL:CG2	0.63	2.24
1:A:592:LEU:HD22	1:A:611:CYS:SG	0.61	2.36



Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:615:ASP:HB2	1:A:618:LEU:HD13	0.60	1.73
1:A:641:ALA:O	1:A:644:LEU:HD12	0.59	1.97
1:A:672:LEU:HD13	1:A:694:VAL:HG21	0.59	1.73
1:A:621:VAL:HG11	1:A:727:VAL:HG23	0.58	1.75
1:A:578:LEU:HD11	1:A:694:VAL:HG13	0.58	1.74
1:A:594:ILE:HG23	1:A:601:PHE:CD2	0.58	2.34
1:A:602:PHE:CG	1:A:730:LEU:HD12	0.57	2.34
1:A:618:LEU:HD12	1:A:681:ILE:CD1	0.57	2.28
1:A:577:PHE:CE1	1:A:647:ILE:HG21	0.57	2.34
1:A:578:LEU:HD13	1:A:647:ILE:CD1	0.57	2.30
1:A:696:ILE:HD13	1:A:705:GLU:O	0.56	2.00
1:A:618:LEU:HD12	1:A:681:ILE:HD12	0.56	1.76
1:A:578:LEU:HD13	1:A:647:ILE:HD13	0.56	1.78
1:A:580:LEU:CD2	1:A:694:VAL:HG23	0.55	2.31
1:A:622:HIS:CD2	1:A:680:ILE:HG23	0.55	2.37
1:A:582:PRO:HD2	1:A:590:GLU:O	0.55	2.02
1:A:655:ASN:O	1:A:656:VAL:O	0.55	2.24
1:A:704:ASN:ND2	1:A:706:GLY:H	0.54	2.00
1:A:588:ILE:HD13	1:A:613:ILE:HG23	0.54	1.79
1:A:586:SER:OG	1:A:690:ILE:HD13	0.53	2.03
1:A:578:LEU:CD1	1:A:694:VAL:HG13	0.52	2.34
1:A:622:HIS:CD2	1:A:680:ILE:CG2	0.52	2.92
1:A:673:GLN:HB3	1:A:706:GLY:O	0.52	2.03
1:A:580:LEU:O	1:A:592:LEU:N	0.52	2.41
1:A:583:LEU:HD22	1:A:693:LYS:HB2	0.52	1.81
1:A:622:HIS:O	1:A:653:GLY:N	0.52	2.43
1:A:580:LEU:HD21	1:A:694:VAL:HG23	0.51	1.81
1:A:674:ASP:HB2	1:A:696:ILE:HD12	0.51	1.83
1:A:580:LEU:HD11	1:A:625:ILE:CD1	0.51	2.35
1:A:649:TYR:CD2	1:A:678:ILE:HD13	0.51	2.41
1:A:645:ASP:O	1:A:702:LEU:HD13	0.50	2.05
1:A:648:TRP:CH2	1:A:671:LEU:CD2	0.49	2.94
1:A:663:ARG:O	1:A:716:VAL:HG21	0.49	2.07
1:A:704:ASN:O	1:A:705:GLU:CB	0.49	2.59
1:A:578:LEU:CG	1:A:694:VAL:HG13	0.49	2.37
1:A:601:PHE:CZ	1:A:610:ASN:HB3	0.49	2.43
1:A:578:LEU:HD22	1:A:647:ILE:CD1	0.48	2.38
1:A:655:ASN:O	1:A:656:VAL:HG13	0.47	2.10
1:A:659:LEU:C	1:A:659:LEU:HD12	0.47	2.30
1:A:618:LEU:CD1	1:A:681:ILE:HD12	0.47	2.40
1:A:730:LEU:C	1:A:730:LEU:HD23	0.46	2.31
1:A:577:PHE:CD2	1:A:698:ASP:O	0.46	2.68

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:645:ASP:O	1:A:702:LEU:HD22	0.45	2.11
1:A:630:HIS:CD2	1:A:641:ALA:CB	0.45	2.99
1:A:577:PHE:CE1	1:A:647:ILE:CG2	0.45	2.99
1:A:723:GLU:HA	1:A:726:LEU:HD12	0.45	1.87
1:A:587:ILE:CD1	1:A:688:PHE:CE1	0.45	2.98
1:A:647:ILE:HD12	1:A:672:LEU:HB2	0.44	1.89
1:A:630:HIS:N	1:A:644:LEU:O	0.44	2.50
1:A:575:GLY:HA2	1:A:596:GLN:OE1	0.44	2.11
1:A:632:VAL:HG21	1:A:640:PRO:CG	0.44	2.43
1:A:594:ILE:HG23	1:A:601:PHE:CG	0.44	2.47
1:A:659:LEU:HD13	1:A:678:ILE:HG12	0.44	1.88
1:A:673:GLN:NE2	1:A:708:GLY:HA3	0.44	2.27
1:A:704:ASN:O	1:A:705:GLU:HB3	0.44	2.12
1:A:578:LEU:HD12	1:A:696:ILE:CG1	0.44	2.43
1:A:587:ILE:HG12	1:A:690:ILE:HD11	0.44	1.89
1:A:592:LEU:HD21	1:A:613:ILE:HD11	0.44	1.89
1:A:704:ASN:ND2	1:A:707:LEU:HB2	0.44	2.27
1:A:578:LEU:HD22	1:A:647:ILE:HD13	0.43	1.88
1:A:652:THR:O	1:A:666:GLN:NE2	0.43	2.51
1:A:626:PHE:CZ	1:A:628:LYS:CG	0.43	3.02
1:A:582:PRO:CD	1:A:590:GLU:O	0.43	2.66
1:A:580:LEU:CD2	1:A:694:VAL:CG2	0.43	2.96
1:A:603:ILE:HD12	1:A:624:PHE:HA	0.43	1.89
1:A:624:PHE:O	1:A:650:CYS:N	0.43	2.50
1:A:592:LEU:HD11	1:A:692:PHE:CE2	0.43	2.48
1:A:603:ILE:HG13	1:A:611:CYS:HB3	0.42	1.90
1:A:632:VAL:HG21	1:A:640:PRO:HG3	0.42	1.90
1:A:699:THR:O	1:A:699:THR:OG1	0.42	2.38
1:A:655:ASN:C	1:A:656:VAL:CG1	0.42	2.88
1:A:594:ILE:CD1	1:A:625:ILE:CD1	0.42	2.94
1:A:578:LEU:CD1	1:A:696:ILE:HG12	0.42	2.45
1:A:626:PHE:CE1	1:A:627:LYS:O	0.41	2.73
1:A:659:LEU:HD23	1:A:670:PHE:HB3	0.41	1.92
1:A:674:ASP:N	1:A:706:GLY:O	0.41	2.51
1:A:649:TYR:CB	1:A:672:LEU:HD21	0.41	2.46
1:A:673:GLN:CA	1:A:706:GLY:O	0.41	2.69
1:A:577:PHE:HB2	1:A:596:GLN:HB3	0.41	1.90
1:A:646:ASP:OD2	1:A:703:PHE:CE1	0.41	2.74
1:A:674:ASP:CB	1:A:696:ILE:HD12	0.41	2.45
1:A:626:PHE:CZ	1:A:628:LYS:HG3	0.41	2.51
1:A:629:ARG:CD	1:A:644:LEU:O	0.41	2.69
1:A:615:ASP:OD2	1:A:688:PHE:CE1	0.40	2.75

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<i>J</i> 1	1 0		
Atom-1	Atom-2	$\operatorname{Clash}(\operatorname{\AA})$	Distance(Å)
1:A:704:ASN:ND2	1:A:707:LEU:N	0.40	2.69
1:A:582:PRO:HG3	1:A:692:PHE:CE1	0.40	2.51
1:A:587:ILE:CD1	1:A:688:PHE:CZ	0.40	3.05
1:A:651:HIS:CE1	1:A:657:SER:N	0.40	2.89
1:A:600:PRO:HG2	1:A:602:PHE:CZ	0.40	2.52

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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	А	156/158~(99%)	131 (84%)	17 (11%)	8~(5%)	4 24
2	Р	4/7~(57%)	3~(75%)	1 (25%)	0 (0%)	100 100
All	All	160/165~(97%)	134 (84%)	18 (11%)	8~(5%)	4 25

All 8 Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	А	582	PRO
1	А	643	GLY
1	А	656	VAL
1	А	660	ASN
1	А	705	GLU
1	А	706	GLY
1	А	708	GLY
1	А	714	ARG

6.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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 side chain conformation was analysed and the total number of residues.



Mol	Chain	Analysed	d Rotameric Outliers		Percentiles		
1	А	142/142~(100%)	104 (73%)	38 (27%)	2 21		
2	Р	6/6~(100%)	5 (83%)	1 (17%)	5 41		
All	All	148/148 (100%)	109 (74%)	39 (26%)	2 22		

All 39 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
1	А	583	LEU
1	А	589	GLN
1	А	591	SER
1	А	592	LEU
1	А	593	GLU
1	А	595	GLN
1	А	596	GLN
1	А	606	SER
1	А	607	GLU
1	А	612	LYS
1	А	615	ASP
1	А	618	LEU
1	А	628	LYS
1	А	637	TYR
1	А	638	GLU
1	А	642	GLN
1	А	645	ASP
1	А	646	ASP
1	А	656	VAL
1	А	659	LEU
1	А	670	PHE
1	А	671	LEU
1	А	672	LEU
1	А	676	ASP
1	А	681	ILE
1	А	683	ASP
1	А	687	LYS
1	А	688	PHE
1	А	695	GLU
1	А	697	ASN
1	А	698	ASP
1	А	699	THR
1	А	702	LEU
1	А	704	ASN
1	А	707	LEU



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Mol	Chain	Res	Type
1	А	709	MET
1	А	718	LYS
1	А	722	GLU
2	Р	826	GLU

6.3.3 RNA (i)

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with |Z| > 2 is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mal	Tuno	Chain Reg Link Bond		Ros Link		nd lengt	\mathbf{hs}
	туре	Unam	nes		Counts	RMSZ	#Z>2
2	PTR	Р	829	2	$15,\!16,\!17$	0.74	0 (0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with |Z| > 2 is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Dog	Link	Bo	ond ang	es
WIOI		Chain	nes		Counts	RMSZ	$\#Z{>}2$
2	PTR	Р	829	2	19,22,24	0.84	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.



Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PTR	Р	829	2	-	0,10,11,13	0,1,1,1

There are no bond-length outliers.

All angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	Р	829	PTR	O3P-P-OH	2.37	112.64	105.24

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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

