



# Full wwPDB NMR Structure Validation Report ⓘ

Apr 27, 2016 – 04:20 AM BST

PDB ID : 2PNB  
Title : STRUCTURE OF AN SH2 DOMAIN OF THE P85 ALPHA SUBUNIT OF PHOSPHATIDYLINOSITOL-3-OH KINASE  
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We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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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  
Mogul : unknown  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
ShiftChecker : rb-20027457  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20027457

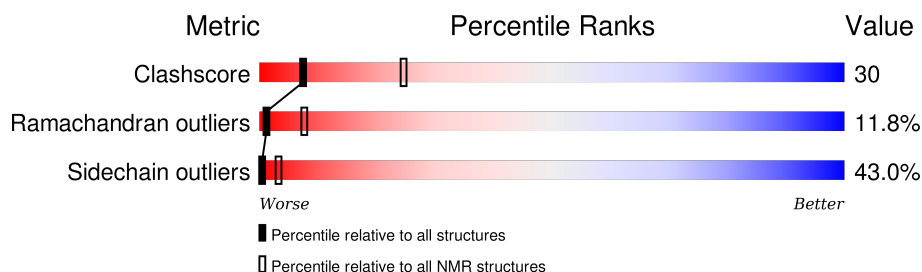
# 1 Overall quality at a glance

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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  $\geq 3$ , 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	104	<div> <div></div> <div>28%</div> <div>38%</div> <div>27%</div> <div>7%</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 1699 atoms, of which 840 are hydrogens and 0 are deuteriums.

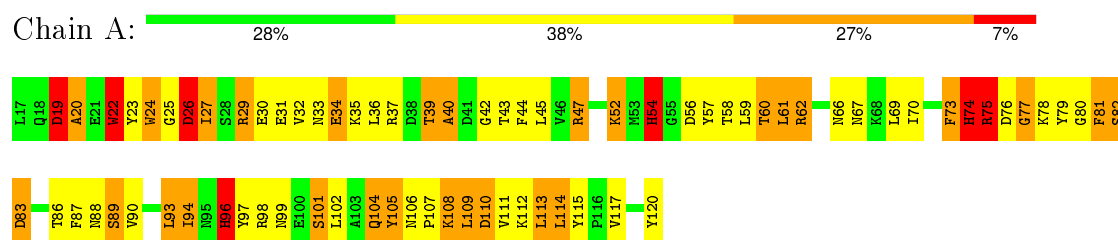
- Molecule 1 is a protein called PHOSPHATIDYLINOSITOL 3-KINASE P85-ALPHA SUB-UNIT N-TERMINAL SH2 DOMAIN.

Mol	Chain	Residues	Atoms						Trace
1	A	104	Total	C	H	N	O	S	0
			1699	547	840	148	163	1	

## 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: PHOSPHATIDYLINOSITOL 3-KINASE P85-ALPHA SUBUNIT N-TERMINAL SH2 DOMAIN



## 5 Refinement protocol and experimental data overview

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
X-PLOR	refinement	

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

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	1.13	5/879 (0.6%)	1.33	13/1186 (1.1%)
All	All	1.13	5/879 (0.6%)	1.33	13/1186 (1.1%)

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	5
All	All	0	5

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	24	TRP	CG-CD2	-7.61	1.30	1.43
1	A	22	TRP	CG-CD2	-6.88	1.31	1.43
1	A	74	HIS	CG-ND1	-6.17	1.25	1.38
1	A	54	HIS	CG-ND1	-6.10	1.25	1.38
1	A	96	HIS	CG-ND1	-6.07	1.25	1.38

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	24	TRP	NE1-CE2-CZ2	8.56	139.81	130.40
1	A	22	TRP	NE1-CE2-CZ2	8.53	139.79	130.40
1	A	29	ARG	CG-CD-NE	8.17	128.96	111.80
1	A	22	TRP	NE1-CE2-CD2	-7.29	100.01	107.30
1	A	24	TRP	NE1-CE2-CD2	-7.26	100.04	107.30
1	A	24	TRP	CG-CD1-NE1	-6.69	103.41	110.10
1	A	24	TRP	CG-CD2-CE3	-6.28	128.25	133.90
1	A	22	TRP	CG-CD1-NE1	-6.05	104.05	110.10
1	A	22	TRP	CD1-CG-CD2	5.82	110.95	106.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	24	TRP	CD1-NE1-CE2	5.69	114.12	109.00
1	A	22	TRP	CD1-NE1-CE2	5.67	114.10	109.00
1	A	24	TRP	CD1-CG-CD2	5.55	110.74	106.30
1	A	24	TRP	CE2-CD2-CG	5.47	111.68	107.30

There are no chirality outliers.

All planar outliers are listed below.

Mol	Chain	Res	Type	Group
1	A	29	ARG	Sidechain
1	A	75	ARG	Sidechain
1	A	62	ARG	Sidechain
1	A	47	ARG	Sidechain
1	A	98	ARG	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	859	840	837	51
All	All	859	840	837	51

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 30.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:60:THR:C	1:A:61:LEU:HD23	0.73	2.04
1:A:73:PHE:N	1:A:73:PHE:CD1	0.65	2.63
1:A:74:HIS:CG	1:A:75:ARG:N	0.64	2.65
1:A:61:LEU:N	1:A:61:LEU:HD23	0.64	2.06
1:A:20:ALA:HB1	1:A:22:TRP:CZ3	0.62	2.30
1:A:73:PHE:CD2	1:A:80:GLY:O	0.56	2.58
1:A:74:HIS:CD2	1:A:75:ARG:N	0.56	2.74
1:A:44:PHE:CE1	1:A:113:LEU:O	0.54	2.60
1:A:97:TYR:OH	1:A:104:GLN:NE2	0.53	2.42

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:56:ASP:O	1:A:57:TYR:CD1	0.53	2.62
1:A:82:SER:OG	1:A:83:ASP:N	0.53	2.42
1:A:113:LEU:CD2	1:A:113:LEU:H	0.52	2.18
1:A:33:ASN:O	1:A:35:LYS:N	0.52	2.42
1:A:56:ASP:OD2	1:A:79:TYR:CZ	0.51	2.63
1:A:74:HIS:CD2	1:A:75:ARG:H	0.51	2.24
1:A:107:PRO:O	1:A:109:LEU:N	0.51	2.43
1:A:24:TRP:CD1	1:A:24:TRP:N	0.51	2.77
1:A:107:PRO:C	1:A:109:LEU:H	0.50	2.09
1:A:23:TYR:OH	1:A:59:LEU:HD11	0.50	2.06
1:A:33:ASN:O	1:A:36:LEU:N	0.49	2.45
1:A:36:LEU:O	1:A:62:ARG:NE	0.49	2.46
1:A:115:TYR:CD1	1:A:115:TYR:N	0.49	2.81
1:A:56:ASP:OD2	1:A:79:TYR:CE1	0.49	2.65
1:A:87:PHE:O	1:A:88:ASN:ND2	0.49	2.46
1:A:81:PHE:CE2	1:A:105:TYR:OH	0.48	2.63
1:A:67:ASN:N	1:A:67:ASN:OD1	0.48	2.42
1:A:61:LEU:N	1:A:61:LEU:CD2	0.47	2.70
1:A:114:LEU:C	1:A:115:TYR:CG	0.47	2.88
1:A:60:THR:OG1	1:A:69:LEU:HD12	0.47	2.10
1:A:87:PHE:O	1:A:89:SER:OG	0.46	2.33
1:A:25:GLY:O	1:A:26:ASP:OD2	0.45	2.35
1:A:114:LEU:C	1:A:115:TYR:CD1	0.44	2.90
1:A:61:LEU:HD21	1:A:70:ILE:HD12	0.43	1.89
1:A:19:ASP:O	1:A:20:ALA:O	0.43	2.36
1:A:33:ASN:C	1:A:35:LYS:N	0.43	2.72
1:A:74:HIS:NE2	1:A:77:GLY:N	0.42	2.66
1:A:107:PRO:C	1:A:109:LEU:N	0.42	2.72
1:A:26:ASP:O	1:A:26:ASP:CG	0.42	2.58
1:A:52:LYS:C	1:A:54:HIS:N	0.42	2.73
1:A:113:LEU:CD2	1:A:113:LEU:N	0.42	2.81
1:A:87:PHE:N	1:A:87:PHE:CD1	0.41	2.85
1:A:93:LEU:O	1:A:94:ILE:C	0.41	2.58
1:A:39:THR:O	1:A:40:ALA:O	0.41	2.37
1:A:33:ASN:O	1:A:34:GLU:C	0.41	2.59
1:A:108:LYS:CB	1:A:108:LYS:NZ	0.41	2.83
1:A:93:LEU:O	1:A:96:HIS:N	0.41	2.53
1:A:110:ASP:OD1	1:A:110:ASP:N	0.41	2.53
1:A:97:TYR:CD1	1:A:102:LEU:HD23	0.40	2.52
1:A:30:GLU:O	1:A:34:GLU:CG	0.40	2.69
1:A:87:PHE:O	1:A:88:ASN:CG	0.40	2.60
1:A:31:GLU:O	1:A:32:VAL:C	0.40	2.60

## 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	102/104 (98%)	56 (55%)	34 (33%)	12 (12%)	1	8
All	All	102/104 (98%)	56 (55%)	34 (33%)	12 (12%)	1	8

All 12 Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	105	TYR
1	A	108	LYS
1	A	34	GLU
1	A	40	ALA
1	A	27	ILE
1	A	101	SER
1	A	42	GLY
1	A	52	LYS
1	A	19	ASP
1	A	26	ASP
1	A	77	GLY
1	A	20	ALA

### 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	A	93/93 (100%)	53 (57%)	40 (43%)	0	3
All	All	93/93 (100%)	53 (57%)	40 (43%)	0	3

All 40 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	78	LYS
1	A	90	VAL
1	A	61	LEU
1	A	99	ASN
1	A	43	THR
1	A	47	ARG
1	A	81	PHE
1	A	58	THR
1	A	109	LEU
1	A	26	ASP
1	A	114	LEU
1	A	96	HIS
1	A	120	TYR
1	A	76	ASP
1	A	45	LEU
1	A	83	ASP
1	A	75	ARG
1	A	37	ARG
1	A	101	SER
1	A	66	ASN
1	A	89	SER
1	A	113	LEU
1	A	112	LYS
1	A	86	THR
1	A	73	PHE
1	A	82	SER
1	A	110	ASP
1	A	106	ASN
1	A	27	ILE
1	A	117	VAL
1	A	22	TRP
1	A	19	ASP
1	A	104	GLN
1	A	60	THR
1	A	74	HIS
1	A	94	ILE
1	A	111	VAL
1	A	39	THR
1	A	54	HIS
1	A	93	LEU

### 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