



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 7DAC
Title : Human RIPK3 amyloid fibril revealed by solid-state NMR
Authors : Wu, X.L.; Zhang, J.; Dong, X.Q.; Liu, J.; Li, B.; Hu, H.; Wang, J.; Wang, H.Y.; Lu, J.X.
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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:

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	:	2.18
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.18

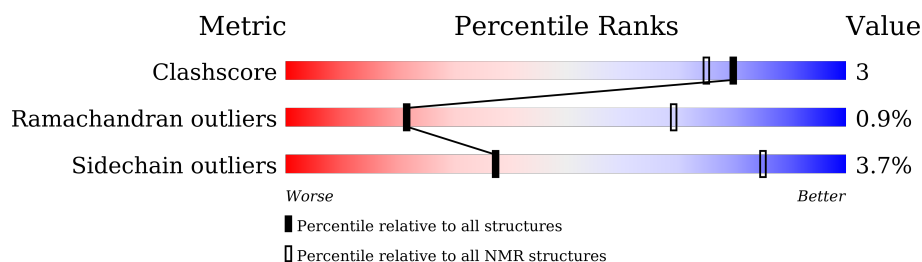
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLID-STATE NMR

The overall completeness of chemical shifts assignment is 8%.

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	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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	108	<div> <div style="width: 26%; background-color: green;"></div> <div style="width: 1%; background-color: yellow;"></div> <div style="width: 1%; background-color: orange;"></div> <div style="width: 1%; background-color: red;"></div> <div style="width: 73%; background-color: grey;"></div> </div> <div>26% . 73%</div>
1	B	108	<div> <div style="width: 26%; background-color: green;"></div> <div style="width: 1%; background-color: yellow;"></div> <div style="width: 1%; background-color: orange;"></div> <div style="width: 1%; background-color: red;"></div> <div style="width: 73%; background-color: grey;"></div> </div> <div>26% . 73%</div>
1	C	108	<div> <div style="width: 27%; background-color: green;"></div> <div style="width: 73%; background-color: grey;"></div> </div> <div>27% 73%</div>
1	D	108	<div> <div style="width: 25%; background-color: green;"></div> <div style="width: 1%; background-color: yellow;"></div> <div style="width: 1%; background-color: orange;"></div> <div style="width: 1%; background-color: red;"></div> <div style="width: 73%; background-color: grey;"></div> </div> <div>25% . 73%</div>
1	E	108	<div> <div style="width: 27%; background-color: green;"></div> <div style="width: 73%; background-color: grey;"></div> </div> <div>27% 73%</div>

2 Ensemble composition and analysis

This entry contains 12 models. Model 1 is the overall representative, medoid model (most similar to other models).

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

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:1-A:29, B:1-B:29, C:1-C:29, D:1-D:29, E:1-E:29 (145)	0.60	1

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 2 clusters and 1 single-model cluster was found.

Cluster number	Models
1	1, 2, 3, 4, 5, 6, 8, 9
2	7, 11, 12
Single-model clusters	10

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2210 atoms, of which 1095 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Receptor-interacting serine/threonine-protein kinase 3.

Mol	Chain	Residues	Atoms						Trace
1	A	29	Total	C	H	N	O	S	0
			442	138	219	39	44	2	
1	B	29	Total	C	H	N	O	S	0
			442	138	219	39	44	2	
1	C	29	Total	C	H	N	O	S	0
			442	138	219	39	44	2	
1	D	29	Total	C	H	N	O	S	0
			442	138	219	39	44	2	
1	E	29	Total	C	H	N	O	S	0
			442	138	219	39	44	2	

There are 35 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-35	MET	-	initiating methionine	UNP Q9Y572
A	-34	HIS	-	expression tag	UNP Q9Y572
A	-33	HIS	-	expression tag	UNP Q9Y572
A	-32	HIS	-	expression tag	UNP Q9Y572
A	-31	HIS	-	expression tag	UNP Q9Y572
A	-30	HIS	-	expression tag	UNP Q9Y572
A	-29	HIS	-	expression tag	UNP Q9Y572
B	-35	MET	-	initiating methionine	UNP Q9Y572
B	-34	HIS	-	expression tag	UNP Q9Y572
B	-33	HIS	-	expression tag	UNP Q9Y572
B	-32	HIS	-	expression tag	UNP Q9Y572
B	-31	HIS	-	expression tag	UNP Q9Y572
B	-30	HIS	-	expression tag	UNP Q9Y572
B	-29	HIS	-	expression tag	UNP Q9Y572
C	-35	MET	-	initiating methionine	UNP Q9Y572
C	-34	HIS	-	expression tag	UNP Q9Y572
C	-33	HIS	-	expression tag	UNP Q9Y572
C	-32	HIS	-	expression tag	UNP Q9Y572
C	-31	HIS	-	expression tag	UNP Q9Y572
C	-30	HIS	-	expression tag	UNP Q9Y572
C	-29	HIS	-	expression tag	UNP Q9Y572
D	-35	MET	-	initiating methionine	UNP Q9Y572
D	-34	HIS	-	expression tag	UNP Q9Y572

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-33	HIS	-	expression tag	UNP Q9Y572
D	-32	HIS	-	expression tag	UNP Q9Y572
D	-31	HIS	-	expression tag	UNP Q9Y572
D	-30	HIS	-	expression tag	UNP Q9Y572
D	-29	HIS	-	expression tag	UNP Q9Y572
E	-35	MET	-	initiating methionine	UNP Q9Y572
E	-34	HIS	-	expression tag	UNP Q9Y572
E	-33	HIS	-	expression tag	UNP Q9Y572
E	-32	HIS	-	expression tag	UNP Q9Y572
E	-31	HIS	-	expression tag	UNP Q9Y572
E	-30	HIS	-	expression tag	UNP Q9Y572
E	-29	HIS	-	expression tag	UNP Q9Y572

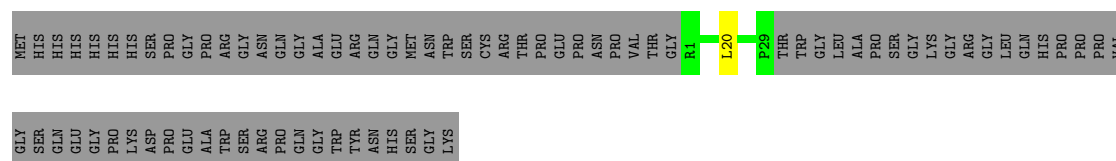
4 Residue-property plots [i](#)

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.

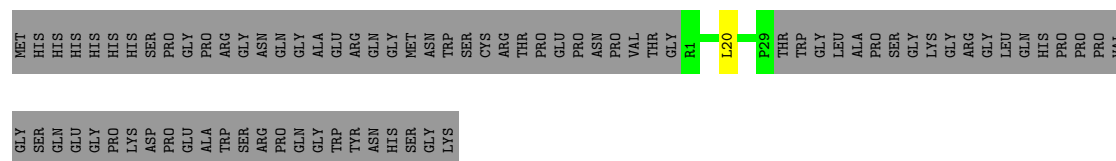
- Molecule 1: Receptor-interacting serine/threonine-protein kinase 3

Chain A:  26% 73%



- Molecule 1: Receptor-interacting serine/threonine-protein kinase 3

Chain B:  26% 73%



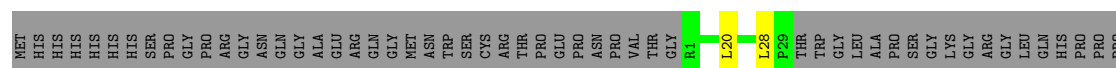
- Molecule 1: Receptor-interacting serine/threonine-protein kinase 3

Chain C:  27% 73%



- Molecule 1: Receptor-interacting serine/threonine-protein kinase 3

Chain D:  25% 73%



VAL
GLY
SER
GLN
GLY
GLY
PRO
LYS
ASP
PRO
GLY
GLY
ALA
TRP
SER
ARG
PRO
GLN
GLY
GLY
TRP
TYR
ASN
HIS
SER
SER
GLY
LYS

- Molecule 1: Receptor-interacting serine/threonine-protein kinase 3

Chain E:  27% 73%

MET
HIS
HIS
HIS
HIS
HIS
HIS
SER
PRO
GLY
PRO
GLY
TRP
SER
ARG
GLY
ASN
GLN
GLY
ALA
GLY
GLY
TRP
TYR
ASN
HIS
SER
SER
GLY
LYS

GLN
GLY
GLY
PRO
PRO
GLY
ASP
PRO
GLY
ALA
SER
SER
TRP
PRO
GLY
TRP
TYR
ASN
HIS
SER
SER
GLY
LYS

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

The representative model is number 1. Colouring as in section 4.1 above.

- Molecule 1: Receptor-interacting serine/threonine-protein kinase 3

Chain A:  26% 73%

MET
HIS
HIS
HIS
HIS
HIS
HIS
SER
PRO
GLY
PRO
GLY
TRP
SER
ARG
GLY
ASN
GLN
GLY
ALA
GLY
GLY
TRP
TYR
ASN
HIS
SER
SER
GLY
LYS

GLY
SER
GLN
GLY
GLY
PRO
PRO
GLY
ASP
PRO
GLY
ALA
ALA
TRP
SER
ARG
PRO
GLN
GLY
GLY
TRP
TYR
ASN
HIS
SER
SER
GLY
LYS

- Molecule 1: Receptor-interacting serine/threonine-protein kinase 3

Chain B:  26% 73%

MET
HIS
HIS
HIS
HIS
HIS
HIS
SER
PRO
GLY
PRO
GLY
TRP
SER
ARG
GLY
ASN
GLN
GLY
ALA
GLY
GLY
TRP
TYR
ASN
HIS
SER
SER
GLY
LYS

GLY
SER
GLN
GLY
GLY
PRO
PRO
GLY
ASP
PRO
GLY
ALA
ALA
TRP
SER
ARG
PRO
GLN
GLY
GLY
TRP
TYR
ASN
HIS
SER
SER
GLY
LYS

- Molecule 1: Receptor-interacting serine/threonine-protein kinase 3

Chain C:  26% 73%

MET
HIS
HIS
HIS
HIS
HIS
HIS
SER
PRO
GLY
PRO
GLY
TRP
SER
ARG
GLY
ASN
GLN
GLY
ALA
GLY
GLY
TRP
TYR
ASN
HIS
SER
SER
GLY
LYS

GLY
SER
GLN
GLY
GLY
PRO
PRO
GLY
ASP
PRO
GLY
ALA
ALA
TRP
SER
ARG
PRO
GLN
GLY
GLY
TRP
TYR
ASN
HIS
SER
SER
GLY
LYS

- Molecule 1: Receptor-interacting serine/threonine-protein kinase 3

Chain D:

27%

73%

MET	HIS	HIS	HIS	HIS	HIS	SER	PRO	GLY	PRO	ARG	GLY	ASN	GLN	GLY	ALA	GLU	ARG	GLN	GLY	MET	ASN	TRP	SER	CYS	ARG	THR	PRO	GLU	PRO	ASN	PRO	VAL	THR	GLY	R1	P29	THR	TRP	GLY	LEU	ALA	PRO	SER	GLY	LYS	GLY	ARG	GLY	LEU	GLN	HIS	PRO	PRO	VAL	GLY	SER		
GLN	GLU	GLY	PRO	LYS	ASP	PRO	GLU	ALA	TRP	SER	ARG	PRO	GLN	GLY	TRP	TYR	ASN	HIS	SER	GLY	LYS																																					

● Molecule 1: Receptor-interacting serine/threonine-protein kinase 3

Chain E:

27%

73%

MET	HIS	HIS	HIS	HIS	HIS	HIS	SER	PRO	GLY	PRO	ARG	GLY	ASN	GLN	GLY	ALA	GLU	ARG	GLN	GLY	MET	ASN	TRP	SER	CYS	ARG	THR	PRO	GLU	PRO	ASN	PRO	VAL	THR	GLY	R1	P29	THR	TRP	GLY	LEU	ALA	PRO	SER	SER	GLY	LYS	GLY	ARG	GLY	GLY	LEU	GLN	HIS	PRO	PRO	PRO	VAL	GLY	SER
GLN	GLU	GLY	PRO	LYS	ASP	PRO	GLU	ALA	TRP	SER	ARG	PRO	GLN	GLY	TRP	TYR	ASN	HIS	SER	GLY	LYS																																							

5 Refinement protocol and experimental data overview

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

Of the 96 calculated structures, 12 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	
X-PLOR NIH	structure calculation	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	139
Number of shifts mapped to atoms	139
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	8%

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

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	B	223	219	221	2±2
1	C	223	219	221	2±3
1	D	223	219	221	2±2
1	E	223	219	221	1±1
1	A	223	219	221	1±1
All	All	13380	13140	13260	72

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 3.

5 of 65 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:27:ALA:HB1	1:D:28:LEU:HD13	0.88	1.46	4	1
1:B:27:ALA:HB1	1:C:28:LEU:HD13	0.88	1.44	4	1
1:D:3:LEU:HD23	1:D:4:VAL:H	0.77	1.38	8	1
1:A:12:VAL:HG21	1:B:6:ILE:HD12	0.64	1.68	7	1
1:D:3:LEU:HD22	1:E:4:VAL:HG22	0.64	1.70	8	1

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	27/108 (25%)	25±1 (93±5%)	2±1 (6±4%)	0±0 (1±1%)	29	74
1	B	27/108 (25%)	24±1 (90±5%)	2±1 (9±4%)	0±0 (1±2%)	21	69
1	C	27/108 (25%)	25±1 (93±4%)	2±1 (6±5%)	0±1 (1±2%)	21	69
1	D	27/108 (25%)	25±1 (92±3%)	2±1 (6±3%)	0±1 (2±3%)	14	59
1	E	27/108 (25%)	25±1 (93±3%)	2±1 (7±2%)	0±0 (0±1%)	44	80
All	All	1620/6480 (25%)	1494 (92%)	112 (7%)	14 (1%)	21	69

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	D	3	LEU	2
1	A	18	ASN	1
1	B	2	PRO	1
1	D	2	PRO	1
1	B	18	ASN	1

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	26/89 (29%)	25±1 (97±3%)	1±1 (3±3%)	42	88
1	B	26/89 (29%)	25±1 (95±4%)	1±1 (5±4%)	27	77
1	C	26/89 (29%)	25±1 (96±5%)	1±1 (4±5%)	33	82
1	D	26/89 (29%)	25±1 (96±4%)	1±1 (4±4%)	31	80
1	E	26/89 (29%)	26±1 (98±2%)	0±1 (2±2%)	64	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1560/5340 (29%)	1502 (96%)	58 (4%)	37 85

5 of 31 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	20	LEU	6
1	B	20	LEU	4
1	D	20	LEU	4
1	C	1	ARG	4
1	D	13	GLN	3

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](#)

The completeness of assignment taking into account all chemical shift lists is 8% for the well-defined parts and 8% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *human_ripk3_cs-nmrstar.txt*

7.1.1 Bookkeeping [i](#)

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	139
Number of shifts mapped to atoms	139
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	27	-0.05 ± 0.37	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	24	—	None (insufficient data)
$^{13}\text{C}'$	24	—	None (insufficient data)
^{15}N	25	-0.35 ± 1.25	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 8%, i.e. 135 atoms were assigned a chemical shift out of a possible 1715. 1 out of 30 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	75/705 (11%)	0/280 (0%)	51/290 (18%)	24/135 (18%)
Sidechain	60/930 (6%)	0/540 (0%)	57/340 (17%)	3/50 (6%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	0/80 (0%)	0/40 (0%)	0/40 (0%)	0/0 (—%)
Overall	135/1715 (8%)	0/860 (0%)	108/670 (16%)	27/185 (15%)

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots [i](#)

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A:

