



# Full wwPDB NMR Structure Validation Report ⓘ

Feb 18, 2018 – 11:17 pm GMT

PDB ID : 1HFG  
Title : NMR solution structure of vMIP-II 1-71 from Kaposi's sarcoma-associated herpesvirus (minimized average structure).  
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Deposited on : 2000-12-01

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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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
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

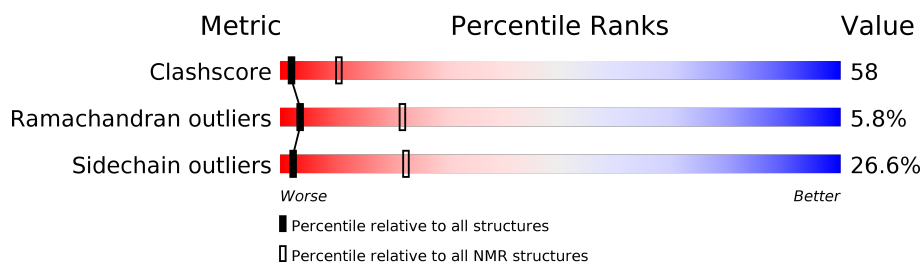
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 46%.

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  $\geq 3$ , 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	71	<div> <div style="width: 20%; background-color: green;"></div> <div style="width: 65%; background-color: yellow;"></div> <div style="width: 14%; background-color: orange;"></div> <div style="width: 1%; background-color: red;"></div> <div style="width: 1%; background-color: cyan;"></div> <div style="width: 1%; background-color: grey;"></div> </div> <div>20% 65% 14% .</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 [i](#)

There is only 1 type of molecule in this entry. The entry contains 1165 atoms, of which 595 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called VIRAL MACROPHAGE INFLAMMATORY PROTEIN-II.

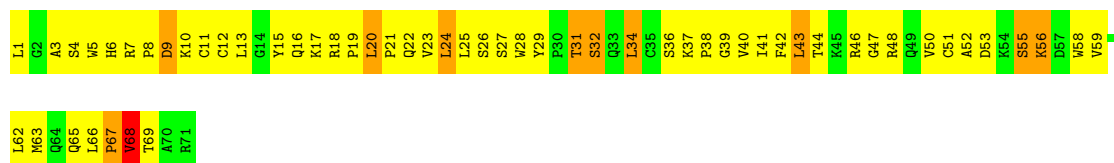
Mol	Chain	Residues	Atoms						Trace
1	A	71	Total	C	H	N	O	S	0
			1165	365	595	105	95	5	

## 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: VIRAL MACROPHAGE INFLAMMATORY PROTEIN-II

Chain A: 



## 5 Refinement protocol and experimental data overview

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

Of the 1 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	
X-PLOR	structure solution	

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)	BMRB entry 4914
Number of chemical shift lists	1
Total number of shifts	506
Number of shifts mapped to atoms	506
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	46%

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	570	595	595	67
All	All	570	595	595	67

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 58.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:16:GLN:HG2	1:A:20:LEU:HD21	0.85	1.47
1:A:24:LEU:HD22	1:A:24:LEU:O	0.80	1.76
1:A:20:LEU:HD11	1:A:50:VAL:HG11	0.77	1.56
1:A:21:PRO:HB2	1:A:23:VAL:HG12	0.75	1.56
1:A:25:LEU:HD23	1:A:62:LEU:HD22	0.74	1.57
1:A:16:GLN:OE1	1:A:50:VAL:HG13	0.72	1.84
1:A:43:LEU:CD1	1:A:69:THR:HG21	0.70	2.16
1:A:24:LEU:HD22	1:A:24:LEU:C	0.69	2.08
1:A:5:TRP:NE1	1:A:6:HIS:CD2	0.63	2.67
1:A:28:TRP:CZ3	1:A:63:MET:CE	0.62	2.81
1:A:52:ALA:HB1	1:A:59:VAL:CG2	0.60	2.26
1:A:25:LEU:HD12	1:A:44:THR:HA	0.58	1.74
1:A:31:THR:HG22	1:A:39:GLY:O	0.58	1.98
1:A:52:ALA:HB1	1:A:59:VAL:HG21	0.58	1.74
1:A:22:GLN:CG	1:A:66:LEU:HD21	0.58	2.28

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:25:LEU:CD1	1:A:44:THR:HG22	0.56	2.29
1:A:15:TYR:CZ	1:A:53:ASP:CG	0.55	2.80
1:A:25:LEU:CD2	1:A:62:LEU:HD22	0.55	2.31
1:A:16:GLN:O	1:A:17:LYS:CB	0.54	2.55
1:A:59:VAL:HA	1:A:62:LEU:HD12	0.53	1.79
1:A:21:PRO:O	1:A:24:LEU:CD1	0.53	2.57
1:A:28:TRP:CZ3	1:A:63:MET:HE1	0.53	2.38
1:A:13:LEU:O	1:A:37:LYS:CE	0.53	2.57
1:A:31:THR:OG1	1:A:32:SER:N	0.52	2.42
1:A:58:TRP:CE2	1:A:59:VAL:HG23	0.52	2.40
1:A:44:THR:OG1	1:A:47:GLY:CA	0.52	2.57
1:A:44:THR:OG1	1:A:48:ARG:N	0.51	2.43
1:A:29:TYR:CE2	1:A:41:ILE:HB	0.50	2.42
1:A:43:LEU:HD11	1:A:69:THR:HG21	0.50	1.82
1:A:3:ALA:HB1	1:A:6:HIS:CD2	0.50	2.42
1:A:8:PRO:O	1:A:10:LYS:N	0.50	2.43
1:A:28:TRP:CE3	1:A:63:MET:HE2	0.49	2.42
1:A:28:TRP:CZ3	1:A:63:MET:HE2	0.49	2.41
1:A:43:LEU:HD13	1:A:69:THR:HG21	0.49	1.82
1:A:29:TYR:CZ	1:A:41:ILE:HB	0.49	2.42
1:A:15:TYR:CZ	1:A:53:ASP:OD1	0.49	2.65
1:A:24:LEU:CD2	1:A:24:LEU:O	0.48	2.57
1:A:28:TRP:HB3	1:A:42:PHE:CD2	0.47	2.44
1:A:28:TRP:CE3	1:A:40:VAL:HG11	0.46	2.46
1:A:24:LEU:C	1:A:24:LEU:CD2	0.46	2.80
1:A:24:LEU:HD13	1:A:25:LEU:N	0.46	2.26
1:A:3:ALA:HB1	1:A:6:HIS:HD2	0.46	1.69
1:A:28:TRP:HE3	1:A:40:VAL:HG11	0.46	1.71
1:A:16:GLN:CG	1:A:20:LEU:HD21	0.45	2.31
1:A:55:SER:O	1:A:56:LYS:O	0.45	2.34
1:A:19:PRO:HA	1:A:58:TRP:CD2	0.45	2.46
1:A:34:LEU:HD13	1:A:34:LEU:N	0.45	2.27
1:A:19:PRO:HB3	1:A:58:TRP:CG	0.45	2.47
1:A:63:MET:O	1:A:66:LEU:O	0.44	2.36
1:A:46:ARG:O	1:A:46:ARG:CG	0.44	2.66
1:A:46:ARG:HG2	1:A:46:ARG:O	0.44	2.13
1:A:24:LEU:CD2	1:A:44:THR:HB	0.43	2.44
1:A:34:LEU:H	1:A:34:LEU:HD22	0.43	1.72
1:A:58:TRP:HE3	1:A:62:LEU:HD11	0.43	1.74
1:A:67:PRO:O	1:A:68:VAL:HB	0.43	2.12
1:A:15:TYR:CE2	1:A:53:ASP:OD2	0.43	2.71
1:A:15:TYR:O	1:A:16:GLN:C	0.43	2.57

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:43:LEU:CD1	1:A:69:THR:CG2	0.42	2.95
1:A:29:TYR:C	1:A:29:TYR:CD1	0.42	2.92
1:A:41:ILE:HG13	1:A:51:CYS:SG	0.42	2.55
1:A:29:TYR:HB3	1:A:69:THR:OG1	0.42	2.15
1:A:44:THR:OG1	1:A:47:GLY:N	0.41	2.53
1:A:31:THR:HG23	1:A:38:PRO:HB2	0.41	1.92
1:A:29:TYR:HD2	1:A:43:LEU:HD11	0.41	1.75
1:A:28:TRP:HB3	1:A:42:PHE:CE2	0.41	2.50
1:A:11:CYS:O	1:A:12:CYS:C	0.41	2.59
1:A:29:TYR:O	1:A:40:VAL:HG13	0.40	2.16

## 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	69/71 (97%)	52 (75%)	13 (19%)	4 (6%)	3	22
All	All	69/71 (97%)	52 (75%)	13 (19%)	4 (6%)	3	22

All 4 Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	56	LYS
1	A	9	ASP
1	A	68	VAL
1	A	67	PRO

### 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	64/64 (100%)	47 (73%)	17 (27%)	2	22
All	All	64/64 (100%)	47 (73%)	17 (27%)	2	22

All 17 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	32	SER
1	A	1	LEU
1	A	4	SER
1	A	27	SER
1	A	24	LEU
1	A	31	THR
1	A	55	SER
1	A	43	LEU
1	A	9	ASP
1	A	7	ARG
1	A	68	VAL
1	A	65	GLN
1	A	26	SER
1	A	34	LEU
1	A	36	SER
1	A	18	ARG
1	A	20	LEU

### 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 [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

The completeness of assignment taking into account all chemical shift lists is 46% for the well-defined parts and 46% for the entire structure.

### 7.1 Chemical shift list 1

File name: BMRB entry 4914

Chemical shift list name: *assigned\_chem\_shift\_list\_1*

#### 7.1.1 Bookkeeping

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	506
Number of shifts mapped to atoms	506
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	5

#### 7.1.2 Chemical shift referencing

No chemical shift referencing corrections were calculated (not enough data).

#### 7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 46%, i.e. 431 atoms were assigned a chemical shift out of a possible 928. 0 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	133/343 (39%)	133/136 (98%)	0/142 (0%)	0/65 (0%)
Sidechain	265/517 (51%)	265/310 (85%)	0/178 (0%)	0/29 (0%)
Aromatic	33/68 (49%)	33/35 (94%)	0/29 (0%)	0/4 (0%)
Overall	431/928 (46%)	431/481 (90%)	0/349 (0%)	0/98 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 46%, i.e. 431 atoms were assigned a chemical shift out of a possible 928. 0 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	133/343 (39%)	133/136 (98%)	0/142 (0%)	0/65 (0%)
Sidechain	265/517 (51%)	265/310 (85%)	0/178 (0%)	0/29 (0%)
Aromatic	33/68 (49%)	33/35 (94%)	0/29 (0%)	0/4 (0%)
Overall	431/928 (46%)	431/481 (90%)	0/349 (0%)	0/98 (0%)

### 7.1.4 Statistically unusual chemical shifts ⓘ

The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	19	PRO	HA	1.84	6.05 – 2.75	-7.8
1	A	59	VAL	HG11	-0.78	2.13 – -0.47	-6.2
1	A	59	VAL	HG12	-0.78	2.13 – -0.47	-6.2
1	A	59	VAL	HG13	-0.78	2.13 – -0.47	-6.2
1	A	63	MET	HG3	0.18	4.30 – 0.50	-5.8

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

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:

