



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 2KTY / pdb_00002kty
BMRB ID : 16715
Title : Solution Structure of human Vaccinia Related Kinase-1
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This is a wwPDB NMR Structure Validation Summary 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

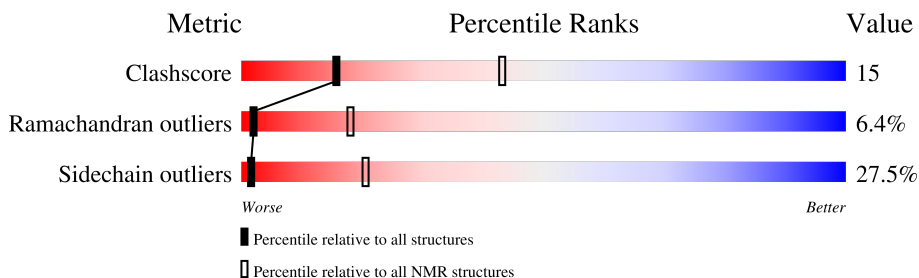
1 Overall quality at a glance

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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	368	

2 Ensemble composition and analysis i

This entry contains 20 models. Model 4 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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:25-A:56, A:66-A:335, A:339-A:345, A:350-A:356 (316)	1.45	4

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. No single-model clusters were found.

Cluster number	Models
1	2, 3, 4, 5, 6, 7, 10, 11, 12, 13, 14, 15, 17, 18, 19
2	1, 8, 9, 16, 20

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 5833 atoms, of which 2932 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Serine/threonine-protein kinase VRK1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	360	5833	1848	2932	508	531	14	0

There are 8 discrepancies between the modelled and reference sequences:

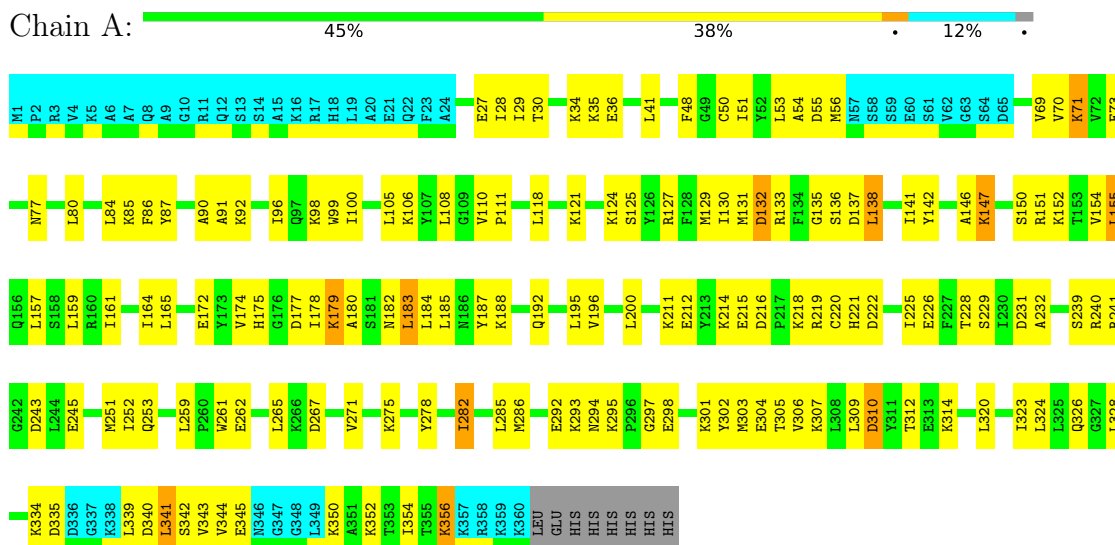
Chain	Residue	Modelled	Actual	Comment	Reference
A	361	LEU	-	expression tag	UNP Q99986
A	362	GLU	-	expression tag	UNP Q99986
A	363	HIS	-	expression tag	UNP Q99986
A	364	HIS	-	expression tag	UNP Q99986
A	365	HIS	-	expression tag	UNP Q99986
A	366	HIS	-	expression tag	UNP Q99986
A	367	HIS	-	expression tag	UNP Q99986
A	368	HIS	-	expression tag	UNP Q99986

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.

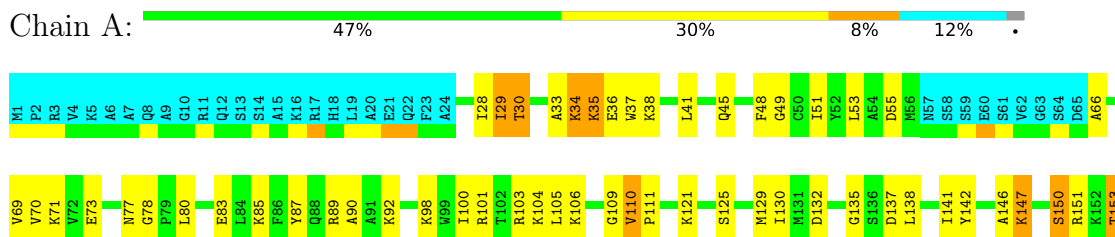
- Molecule 1: Serine/threonine-protein kinase VRK1



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

The representative model is number 4. Colouring as in section 4.1 above.

- Molecule 1: Serine/threonine-protein kinase VRK1



V154	K237	K329
L155	P238	K334
Q156	S239	D335
L157	R240	D336
R160	D243	G337
I161	M251	K338
I164	I252	L339
L165	L255	D340
E172	L259	L341
V173	F260	S342
V174	W261	V343
H175	E262	M346
G176	D267	G347
D177	L268	G348
I178	L269	L349
K179	V271	K350
A180	R272	A351
S181	D273	T352
N182	D274	T353
L183	K275	I354
L184	Y278	T355
L185	M281	K356
N186	L282	K357
Y187	L285	R358
K188	K293	K359
Q192	N294	K360
L195	K295	LEU
V196	P296	GLU
D197	G297	HIS
Y198	E298	HIS
G199	Y302	HIS
L200	M303	HIS
A201	F304	HIS
K211	T305	HIS
E212	L309	
Y213	T312	
K214	F313	
E215	K314	
K218	L320	
R219	R321	
D222	L324	
I225	L325	
E226	Q326	
F227	G327	
T228	L328	
S229		
I230		
D231		
A232		
V236		

5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics*.

Of the 200 calculated structures, 20 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
CYANA	refinement	

No chemical shift data was provided.

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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	A	2574	2599	2599	76±10
All	All	51480	51980	51980	1512

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 15.

5 of 763 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:185:LEU:HD11	1:A:341:LEU:HD22	0.95	1.36	6	2
1:A:252:ILE:HD12	1:A:286:MET:HE3	0.91	1.41	17	1
1:A:252:ILE:HD12	1:A:286:MET:HE2	0.87	1.46	16	1
1:A:138:LEU:HD22	1:A:183:LEU:HD22	0.85	1.46	5	4
1:A:184:LEU:HD23	1:A:196:VAL:HG22	0.84	1.49	16	5

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	316/368 (86%)	250±4 (79±1%)	46±4 (14±1%)	20±4 (6±1%)	2	18
All	All	6320/7360 (86%)	5002 (79%)	913 (14%)	405 (6%)	2	18

5 of 71 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	297	GLY	20
1	A	356	LYS	17
1	A	219	ARG	15
1	A	135	GLY	14
1	A	172	GLU	14

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	278/319 (87%)	202±7 (73±2%)	76±7 (27±2%)	1	20
All	All	5560/6380 (87%)	4033 (73%)	1527 (27%)	1	20

5 of 228 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	305	THR	20
1	A	70	VAL	19
1	A	130	ILE	19
1	A	147	LYS	19
1	A	155	LEU	19

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 oligosaccharides 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