



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 2M8P / pdb_00002m8p
BMRB ID : 19264
Title : The structure of the W184AM185A mutant of the HIV-1 capsid protein
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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
BMRB Restraints Analysis : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

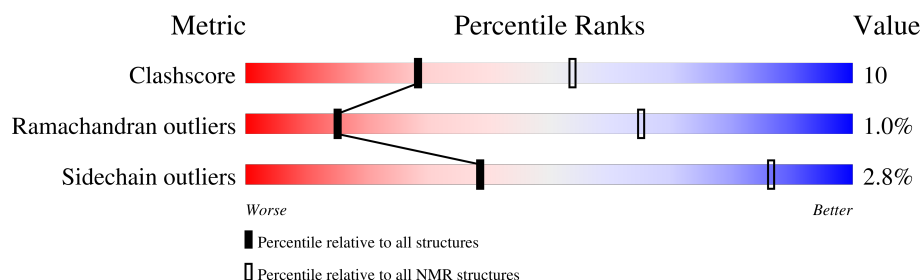
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR, SOLUTION SCATTERING

The overall completeness of chemical shifts assignment is 34%.

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	231	 81% 11% ...

2 Ensemble composition and analysis

This entry contains 100 models. Model 35 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:1-A:145 (145)	0.05	35
2	A:150-A:221 (72)	0.04	51

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 15 clusters and 4 single-model clusters were found.

Cluster number	Models
1	3, 5, 8, 10, 15, 20, 21, 28, 30, 35, 40, 45, 50, 51, 60, 63, 70, 73, 76, 85, 90, 93, 98, 100
2	1, 6, 11, 25, 26, 36, 46, 49, 55, 65, 66, 75, 80, 81, 95, 96
3	7, 12, 27, 37, 47, 67, 82, 97
4	19, 23, 34, 44, 53, 59, 78
5	24, 54, 64, 74, 79, 94
6	4, 9, 14, 29, 39, 99
7	17, 32, 42, 57, 87
8	16, 31, 41, 56
9	18, 43, 58, 88
10	13, 38, 48, 72
11	61, 71, 91
12	22, 52, 77
13	62, 92
14	2, 33
15	69, 84
Single-model clusters	68; 83; 86; 89

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3436 atoms, of which 1723 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Capsid protein p24.

Mol	Chain	Residues	Atoms						Trace
1	A	221	Total	C	H	N	O	S	0
			3436	1078	1723	300	323	12	

There are 2 discrepancies between the modelled and reference sequences:

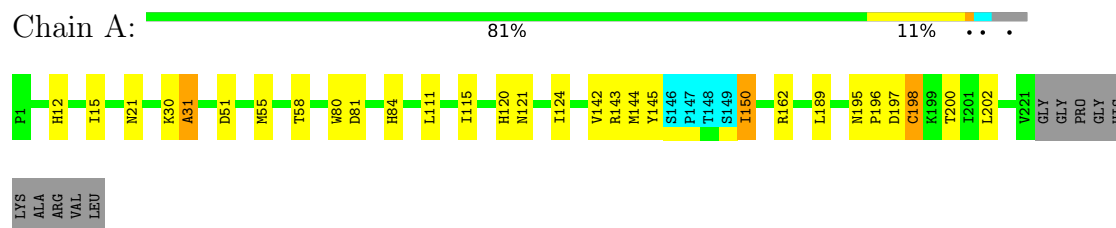
Chain	Residue	Modelled	Actual	Comment	Reference
A	184	ALA	TRP	engineered mutation	UNP P12497
A	185	ALA	MET	engineered mutation	UNP P12497

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.

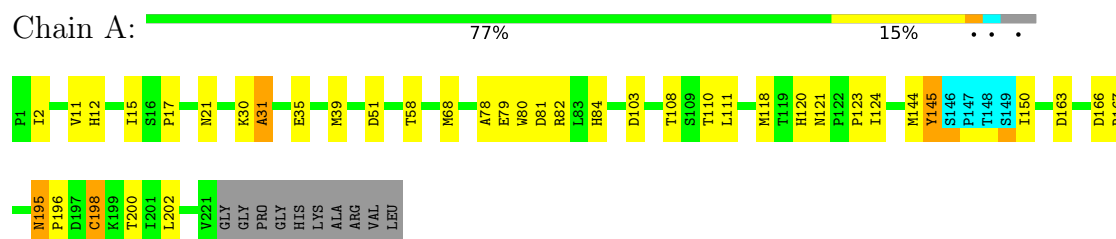
- Molecule 1: Capsid protein p24



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

The representative model is number 35. Colouring as in section 4.1 above.

- Molecule 1: Capsid protein p24



5 Refinement protocol and experimental data overview

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

Of the 480 calculated structures, 100 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
X-PLOR NIH	refinement	2.32

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	1060
Number of shifts mapped to atoms	1016
Number of unparsed shifts	0
Number of shifts with mapping errors	44
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	34%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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	0.53±0.01	0±0/1723 (0.0± 0.0%)	0.84±0.01	0±1/2341 (0.0± 0.0%)
All	All	0.53	8/172300 (0.0%)	0.84	44/234100 (0.0%)

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	150	ILE	C-N	-6.79	1.24	1.34	37	2
1	A	150	ILE	N-CA	6.10	1.53	1.46	37	5
1	A	145	TYR	CA-C	5.02	1.59	1.52	98	1

5 of 6 unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	150	ILE	CA-C-N	8.16	132.03	120.28	19	10
1	A	150	ILE	C-N-CA	8.16	132.03	120.28	19	10
1	A	122	PRO	N-CD-CG	-5.80	96.84	103.80	38	20
1	A	145	TYR	CA-CB-CG	-5.72	103.60	113.90	11	2
1	A	144	MET	CA-C-N	-5.20	113.52	120.54	25	1

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	1687	1699	1694	32±5
All	All	168700	169900	169400	3217

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 10.

5 of 291 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:150:ILE:HG22	1:A:171:THR:HG22	0.88	1.45	27	8
1:A:12:HIS:CD2	1:A:111:LEU:HD11	0.82	2.10	21	41
1:A:145:TYR:CG	1:A:145:TYR:O	0.81	2.33	7	2
1:A:144:MET:O	1:A:145:TYR:C	0.77	2.27	31	16
1:A:150:ILE:HD12	1:A:150:ILE:O	0.74	1.83	47	2

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	215/231 (93%)	211±1 (98±0%)	2±1 (1±0%)	2±1 (1±0%)	15	65
All	All	21500/23100 (93%)	21055 (98%)	235 (1%)	210 (1%)	15	65

All 3 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	31	ALA	100
1	A	150	ILE	73
1	A	145	TYR	37

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	182/192 (95%)	177±1 (97±1%)	5±1 (3±1%)	38	86
All	All	18200/19200 (95%)	17695 (97%)	505 (3%)	38	86

5 of 24 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	198	CYS	97
1	A	58	THR	60
1	A	189	LEU	60
1	A	195	ASN	54
1	A	162	ARG	28

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

The completeness of assignment taking into account all chemical shift lists is 34% for the well-defined parts and 34% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

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	1060
Number of shifts mapped to atoms	1016
Number of unparsed shifts	0
Number of shifts with mapping errors	44
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- No matching atom found in the structure. First 5 (of 44) occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	222	GLY	H	8.566	0.02	1
1	A	222	GLY	C	174.119	0.2	1
1	A	222	GLY	CA	44.634	0.2	1
1	A	222	GLY	N	115.64	0.2	1
1	A	223	GLY	H	7.917	0.02	1
1	A	223	GLY	C	172.071	0.2	1
1	A	223	GLY	CA	44.124	0.2	1
1	A	223	GLY	N	108.671	0.2	1
1	A	224	PRO	C	177.881	0.2	1
1	A	224	PRO	CA	63.264	0.2	1
1	A	224	PRO	CB	31.122	0.2	1
1	A	225	GLY	H	8.414	0.02	1
1	A	225	GLY	C	174.067	0.2	1
1	A	225	GLY	CA	44.876	0.2	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	225	GLY	N	109.295	0.2	1
1	A	226	HIS	H	8.048	0.02	1
1	A	226	HIS	CA	55.859	0.2	1
1	A	226	HIS	CB	28.879	0.2	1
1	A	226	HIS	N	119.97	0.2	1
1	A	227	LYS	H	8.106	0.02	1
1	A	227	LYS	C	175.898	0.2	1
1	A	227	LYS	CA	55.692	0.2	1
1	A	227	LYS	CB	31.835	0.2	1
1	A	227	LYS	N	123.511	0.2	1
1	A	228	ALA	H	8.139	0.02	1
1	A	228	ALA	C	177.383	0.2	1
1	A	228	ALA	CA	51.91	0.2	1
1	A	228	ALA	CB	18.4	0.2	1
1	A	228	ALA	N	125.583	0.2	1
1	A	229	ARG	H	8.16	0.02	1
1	A	229	ARG	C	175.894	0.2	1
1	A	229	ARG	CA	55.678	0.2	1
1	A	229	ARG	CB	29.898	0.2	1
1	A	229	ARG	N	121.105	0.2	1
1	A	230	VAL	H	8.088	0.02	1
1	A	230	VAL	C	175.019	0.2	1
1	A	230	VAL	CA	61.949	0.2	1
1	A	230	VAL	CB	31.655	0.2	1
1	A	230	VAL	N	123.049	0.2	1
1	A	231	LEU	H	7.757	0.02	1
1	A	231	LEU	C	182.069	0.2	1
1	A	231	LEU	CA	56.348	0.2	1
1	A	231	LEU	CB	42.393	0.2	1
1	A	231	LEU	N	131.889	0.2	1

7.1.2 Chemical shift referencing ⓘ

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	226	0.14 ± 0.11	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	205	1.33 ± 0.08	Should be checked
$^{13}\text{C}'$	217	-0.34 ± 0.13	None needed (< 0.5 ppm)
^{15}N	206	0.08 ± 0.28	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 34%, i.e. 999 atoms were assigned a chemical shift out of a possible 2957. 0 out of 31 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	805/1068 (75%)	194/433 (45%)	417/434 (96%)	194/201 (97%)
Sidechain	194/1725 (11%)	0/1126 (0%)	194/534 (36%)	0/65 (0%)
Aromatic	0/164 (0%)	0/80 (0%)	0/70 (0%)	0/14 (0%)
Overall	999/2957 (34%)	194/1639 (12%)	611/1038 (59%)	194/280 (69%)

7.1.4 Statistically unusual chemical shifts [i](#)

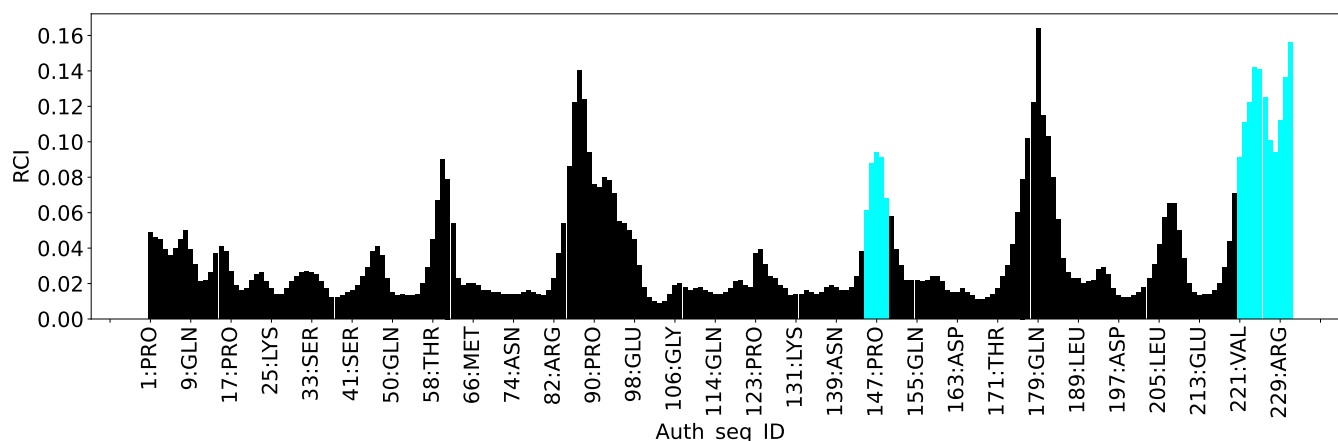
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	101	GLY	H	11.57	5.23 – 11.42	5.2

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. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:



8 NMR restraints analysis

No restraints data found

9 Distance violation analysis

No distance restraints data found

10 Dihedral-angle violation analysis

No dihedral-angle restraints found