

Full wwPDB NMR Structure Validation Report (i)

Dec 1, 2020 - 05:04 pm GMT

PDB ID : 7ATB

Title: Transmembrane helix of tumor necrosis factor alpha in trifluorethanol,

AGALLL mutant

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Deposited on : 2020-10-29

This is a Full wwPDB NMR Structure Validation 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

Cyrange : Kirchner and Güntert (2011)

NmrClust : Kelley et al. (1996)

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 : 2.14.6

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

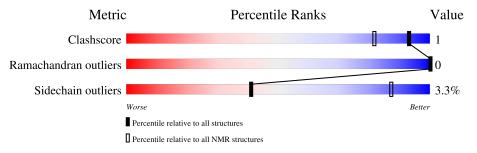
Validation Pipeline (wwPDB-VP) : 2.14.6

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $SOLUTION\ NMR$

The overall completeness of chemical shifts assignment is 60%.

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	NMR archive
Metric	$(\# \mathrm{Entries})$	$(\# \mathrm{Entries})$
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 <=5%

Mol	Chain	Length	Qua	lity of chain
1	A	33	45%	55%



2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 12 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	Well-defined core Residue range (total) Backbone RMSD (Å) Medoid model				
1 A:38-A:52 (15) 0.18 12					

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



3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 570 atoms, of which 299 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called Tumor necrosis factor.

Mol	Chain	Residues	Atoms					Trace	
1	Λ	2.2	Total	С	Н	N	О	S	0
1	A	33	570	185	299	45	39	2	U

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	42	LEU	ALA	engineered mutation	UNP P01375
A	43	LEU	GLY	engineered mutation	UNP P01375
A	44	LEU	ALA	engineered mutation	UNP P01375



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: Tumor necrosis factor

Chain A: 45% 55%

4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: Tumor necrosis factor

Chain A: 45% 55%

4.2.2 Score per residue for model 2

• Molecule 1: Tumor necrosis factor

Chain A: 42% . 55%



4.2.3 Score per residue for model 3

• Molecule 1: Tumor necrosis factor

Chain A: 45% 55%

R28 C30 C30 L31 F32 S34 S37 F53 F53 F53 F53 F53 R50 R60

4.2.4 Score per residue for model 4

• Molecule 1: Tumor necrosis factor

Chain A: 42% • 55%

4.2.5 Score per residue for model 5

• Molecule 1: Tumor necrosis factor

Chain A: 45% 55%

R28 R29 C30 C30 C33 F32 F33 F33 F33 F53 C54 C54 C65 R60

4.2.6 Score per residue for model 6

• Molecule 1: Tumor necrosis factor

Chain A: 42% . 55%



4.2.7 Score per residue for model 7

• Molecule 1: Tumor necrosis factor

Chain A: 42% . 55%





4.2.8 Score per residue for model 8

• Molecule 1: Tumor necrosis factor

Chain A: 39% 6% 55%

R28 R29 R230 I.33 I.33 R33 R33 R33 R43 I.43 I.43 I.56 G57 R60 R60

4.2.9 Score per residue for model 9

• Molecule 1: Tumor necrosis factor

Chain A: 45% 55%

4.2.10 Score per residue for model 10

• Molecule 1: Tumor necrosis factor

Chain A: 42% . 55%

4.2.11 Score per residue for model 11

• Molecule 1: Tumor necrosis factor

Chain A: 42% . 55%

4.2.12 Score per residue for model 12 (medoid)

• Molecule 1: Tumor necrosis factor

Chain A: 42% . 55%



4.2.13 Score per residue for model 13

• Molecule 1: Tumor necrosis factor

Chain A: 39% 6% 55%

R28 R29 R230 L331 L33 S34 L43 R55 R53 R56 R60 R60

4.2.14 Score per residue for model 14

• Molecule 1: Tumor necrosis factor

Chain A: 45% 55%

R28 R29 C30 C30 L31 L33 L33 F36 S37 F53 F53 F53 G54 G57 R60

4.2.15 Score per residue for model 15

• Molecule 1: Tumor necrosis factor

Chain A: 42% . 55%

R28 (30 (30 (30 (31 (131 (135 (135 (135 (143 (143 (156 (156 (157 (156 (156 (156 (156) (156

4.2.16 Score per residue for model 16

• Molecule 1: Tumor necrosis factor

Chain A: 45% 55%

R28 R29 C30 C30 C30 C33 R34 R35 R35 R53 R53 R53 R53 R60 R60

4.2.17 Score per residue for model 17

• Molecule 1: Tumor necrosis factor

Chain A: 39% 6% 55%

R28 R29 R29 I.33 I.33 S34 I.47 I.47 I.47 I.65 G54 G57 R60 R60



4.2.18 Score per residue for model 18

• Molecule 1: Tumor necrosis factor

Chain A: 42% . 55%

R28 R29 R29 R23 R33 R34 R35 R36 R36 R53 R69 R60

4.2.19 Score per residue for model 19

• Molecule 1: Tumor necrosis factor

Chain A: 42% • 55%

R R 28 R R 29 R R 29 R R 20 R 23 R 23 R 23 R 24 R 25 R 26 R 26

4.2.20 Score per residue for model 20

• Molecule 1: Tumor necrosis factor

Chain A: 42% • 55%



5 Refinement protocol and experimental data overview (i)



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

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
ARIA	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	298
Number of shifts mapped to atoms	298
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	60%

No validations of the models with respect to experimental NMR restraints is performed at this time.



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	123	142	141	0±0
All	All	2460	2840	2820	7

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 1.

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

Atom-1	Atom-2	Clash(Å)	$\mathbf{Distance}(\mathbf{\mathring{A}})$	Models	
Atom-1	A tom-2	Clash(A)	Distance(A)	Worst	Total
1:A:47:LEU:N	1:A:47:LEU:HD22	0.44	2.28	18	4
1:A:47:LEU:HD22	1:A:47:LEU:N	0.43	2.28	7	2
1:A:43:LEU:O	1:A:43:LEU:HD13	0.40	2.16	15	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	Perce	${f ntiles}$
1	A	15/33 (45%)	15±0 (99±2%)	0±0 (1±2%)	0±0 (0±0%)	100	100
All	All	300/660 (45%)	298 (99%)	2 (1%)	0 (0%)	100	100

There are no Ramachandran outliers.

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	15/31 (48%)	15±1 (97±4%)	1±1 (3±4%)	41 87
All	All	300/620 (48%)	290 (97%)	10 (3%)	41 87

All 2 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	42	LEU	7
1	A	43	LEU	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 60% for the well-defined parts and 55% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: TNFa_TM_AGALLL.str

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	298
Number of shifts mapped to atoms	298
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	${\bf Correction}\pm{\bf precision},ppm$	Suggested action
$^{13}\mathrm{C}_{\alpha}$	32	-0.09 ± 0.14	None needed ($< 0.5 \text{ ppm}$)
$^{13}C_{\beta}$	31	0.89 ± 0.08	Should be applied
¹³ C′	0		None (insufficient data)
^{15}N	0	_	None (insufficient data)

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 60%, i.e. 120 atoms were assigned a chemical shift out of a possible 199. 2 out of 8 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^{1}\mathbf{H}$	$^{13}\mathbf{C}$	$^{15}{ m N}$
Backbone	45/75~(60%)	30/30 (100%)	15/30~(50%)	0/15 (0%)
Sidechain	75/98 (77%)	42/55 (76%)	33/43 (77%)	0/0 (%)

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	Total	$^{1}\mathbf{H}$	$^{13}\mathbf{C}$	$^{15}{ m N}$
Aromatic	0/26~(0%)	$0/14 \; (0\%)$	0/10 (0%)	$0/2 \ (0\%)$
Overall	120/199~(60%)	72/99 (73%)	48/83 (58%)	0/17 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 55%, i.e. 248 atoms were assigned a chemical shift out of a possible 447. 3 out of 12 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^{1}\mathrm{H}$	$^{13}\mathbf{C}$	$^{15}{ m N}$
Backbone	94/163~(58%)	$62/65 \; (95\%)$	32/66 (48%)	0/32~(0%)
Sidechain	$154/231 \ (67\%)$	89/135~(66%)	65/86 (76%)	0/10 (0%)
Aromatic	$0/53 \; (0\%)$	0/29 (0%)	0/22~(0%)	$0/2 \ (0\%)$
Overall	248/447 (55%)	151/229~(66%)	97/174 (56%)	0/44~(0%)

7.1.4 Statistically unusual chemical shifts (i)

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots (1)

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:

