



Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 11:08 pm GMT

PDB ID : 2KLU
Title : NMR structure of the transmembrane and cytoplasmic domains of human CD4
Authors : Wittlich, M.; Willbold, D.
Deposited on : 2009-07-08

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

<http://wwpdb.org/validation/2016/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:

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : trunk28760
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

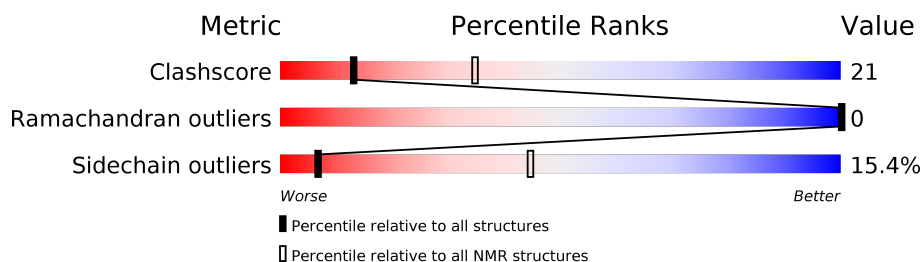
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 100%.

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	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

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	70	

2 Ensemble composition and analysis

This entry contains 20 models. Model 10 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:375-A:392 (18)	0.11	10

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 4 clusters and 5 single-model clusters were found.

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

3 Entry composition

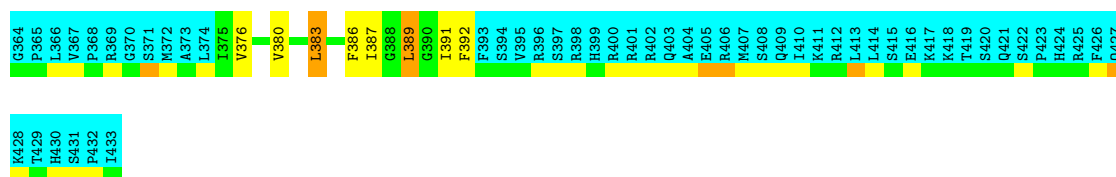
There is only 1 type of molecule in this entry. The entry contains 1153 atoms, of which 601 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called T-cell surface glycoprotein CD4.

Mol	Chain	Residues	Atoms						Trace
1	A	70	Total	C	H	N	O	S	0
			1153	351	601	111	88	2	

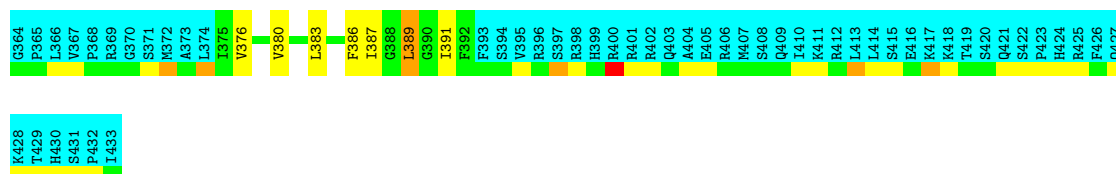
There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	364	GLY	-	EXPRESSION TAG	UNP P01730
A	365	PRO	-	EXPRESSION TAG	UNP P01730
A	366	LEU	-	EXPRESSION TAG	UNP P01730
A	367	VAL	-	EXPRESSION TAG	UNP P01730
A	368	PRO	-	EXPRESSION TAG	UNP P01730
A	369	ARG	-	EXPRESSION TAG	UNP P01730
A	370	GLY	-	EXPRESSION TAG	UNP P01730
A	371	SER	-	EXPRESSION TAG	UNP P01730
A	394	SER	CYS	ENGINEERED	UNP P01730
A	397	SER	CYS	ENGINEERED	UNP P01730
A	420	SER	CYS	ENGINEERED	UNP P01730
A	422	SER	CYS	ENGINEERED	UNP P01730
A	430	HIS	CYS	ENGINEERED	UNP P01730



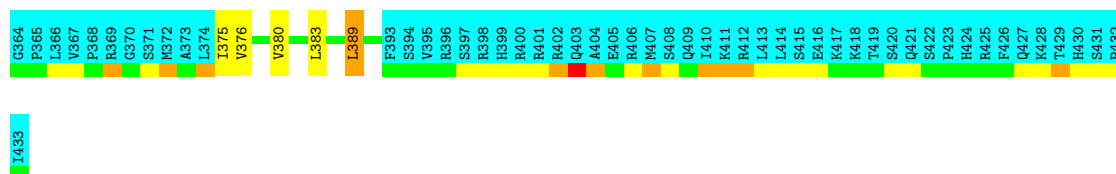
4.2.3 Score per residue for model 3

- Molecule 1: T-cell surface glycoprotein CD4



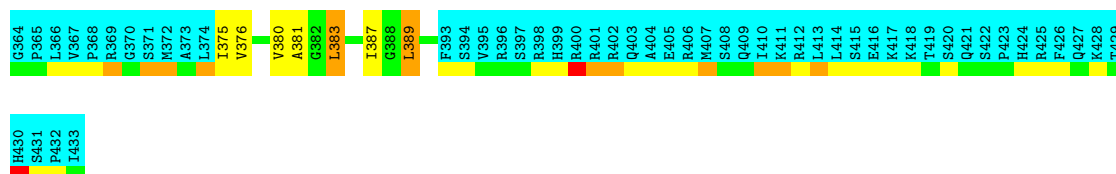
4.2.4 Score per residue for model 4

- Molecule 1: T-cell surface glycoprotein CD4



4.2.5 Score per residue for model 5

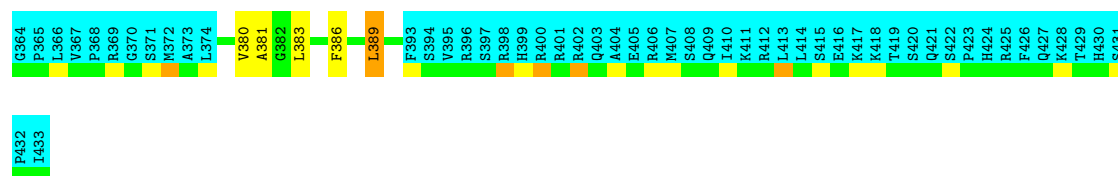
- Molecule 1: T-cell surface glycoprotein CD4



4.2.6 Score per residue for model 6

- Molecule 1: T-cell surface glycoprotein CD4

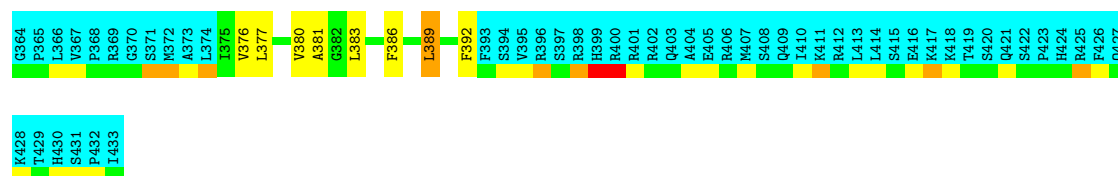
Chain A:  19% 6% 74%



4.2.7 Score per residue for model 7

- Molecule 1: T-cell surface glycoprotein CD4

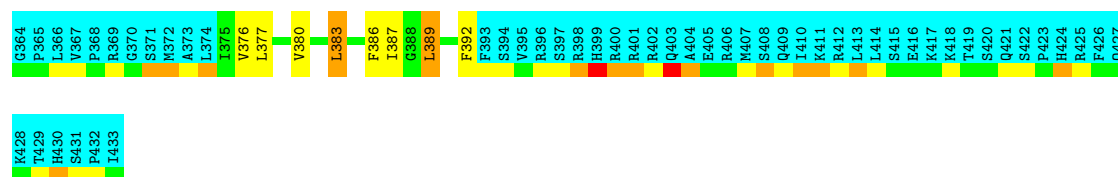
Chain A:  14% 10% 74%



4.2.8 Score per residue for model 8

- Molecule 1: T-cell surface glycoprotein CD4

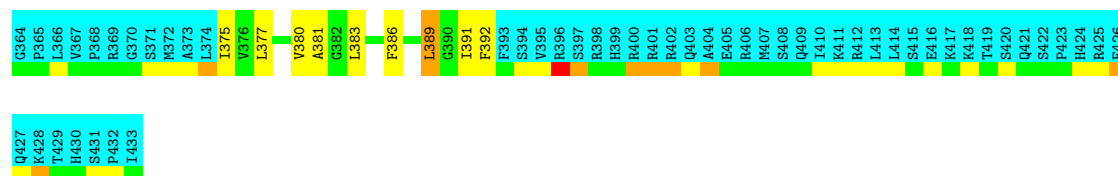
Chain A:  14% 9% 74%



4.2.9 Score per residue for model 9

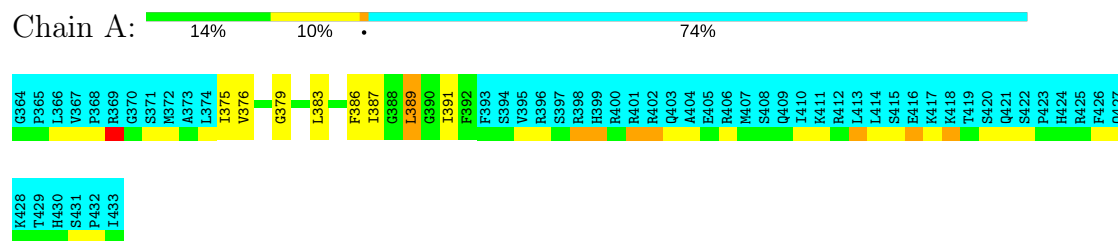
- Molecule 1: T-cell surface glycoprotein CD4

Chain A:  13% 11% 74%



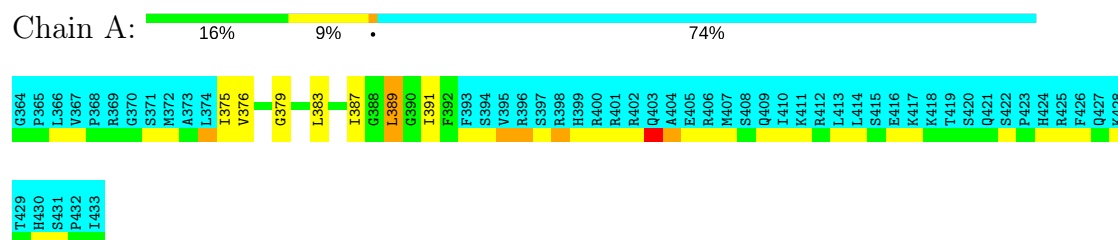
4.2.10 Score per residue for model 10 (medoid)

- Molecule 1: T-cell surface glycoprotein CD4



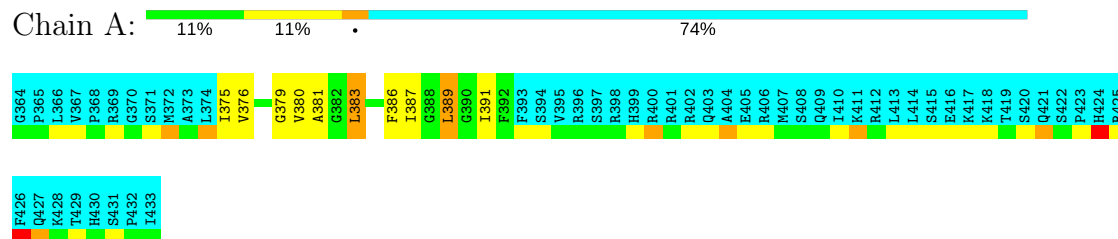
4.2.11 Score per residue for model 11

- Molecule 1: T-cell surface glycoprotein CD4



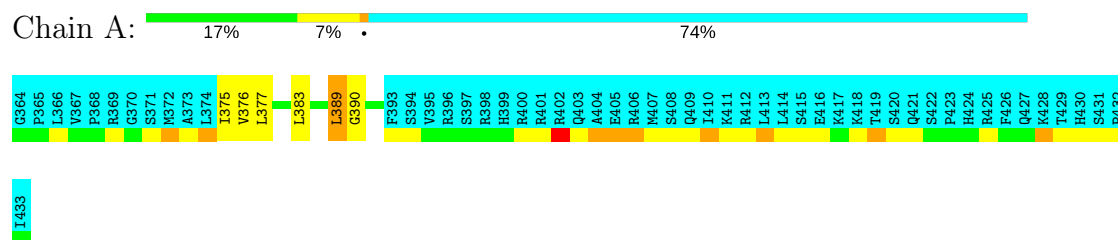
4.2.12 Score per residue for model 12

- Molecule 1: T-cell surface glycoprotein CD4



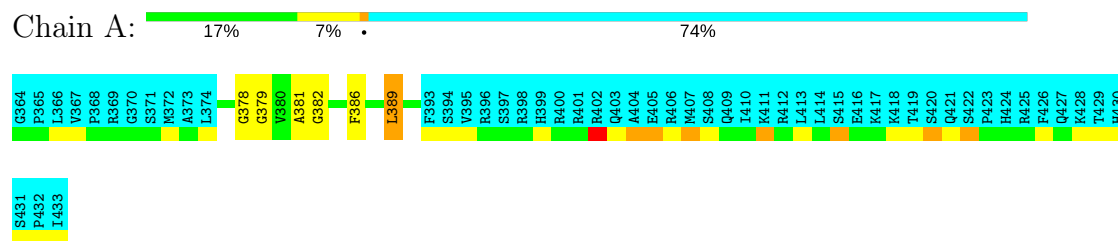
4.2.13 Score per residue for model 13

- Molecule 1: T-cell surface glycoprotein CD4



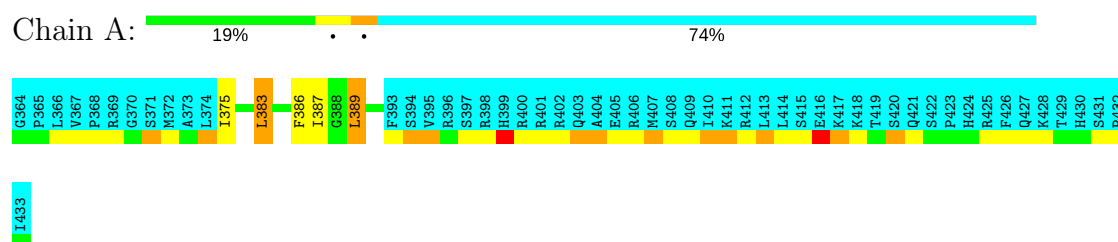
4.2.14 Score per residue for model 14

- Molecule 1: T-cell surface glycoprotein CD4



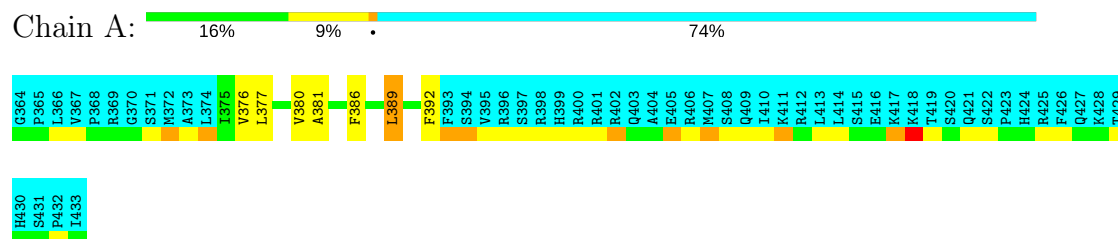
4.2.15 Score per residue for model 15

- Molecule 1: T-cell surface glycoprotein CD4



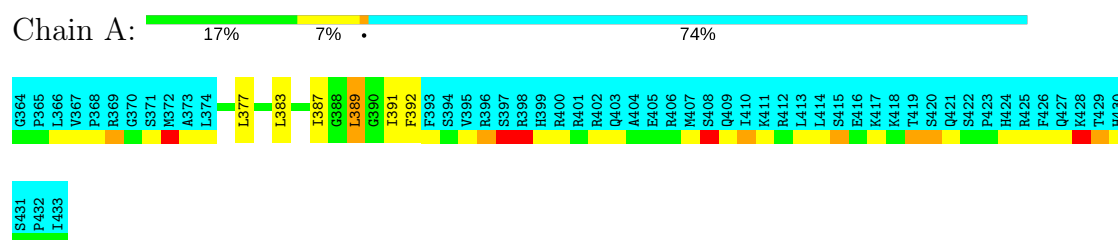
4.2.16 Score per residue for model 16

- Molecule 1: T-cell surface glycoprotein CD4



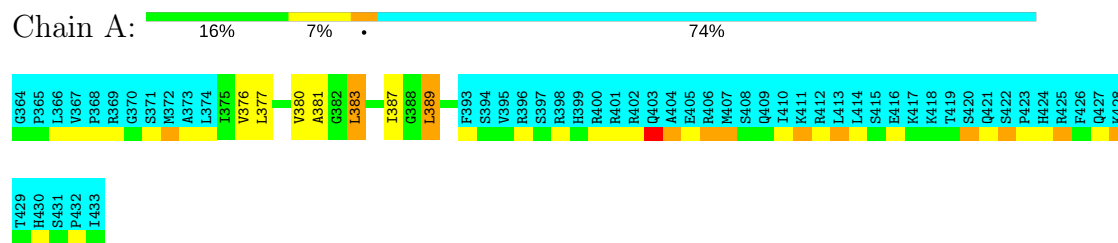
4.2.17 Score per residue for model 17

- Molecule 1: T-cell surface glycoprotein CD4



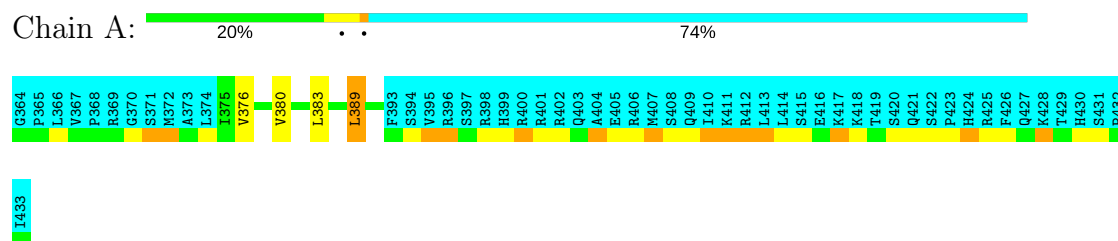
4.2.18 Score per residue for model 18

- Molecule 1: T-cell surface glycoprotein CD4



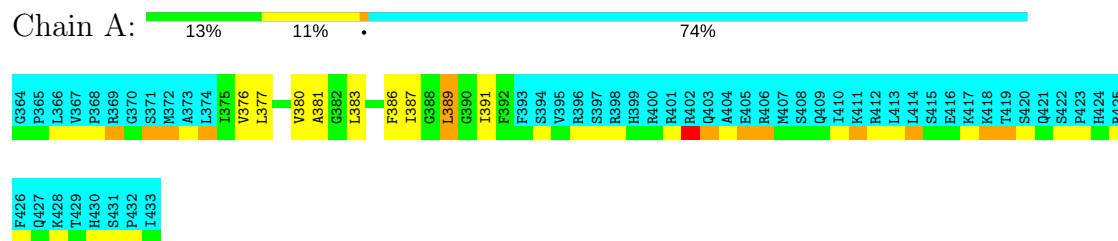
4.2.19 Score per residue for model 19

- Molecule 1: T-cell surface glycoprotein CD4



4.2.20 Score per residue for model 20

- Molecule 1: T-cell surface glycoprotein CD4



5 Refinement protocol and experimental data overview

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

Of the 100 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	2.1

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 16853
Number of chemical shift lists	1
Total number of shifts	926
Number of shifts mapped to atoms	926
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	100%

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	125	144	144	6±1
All	All	2500	2880	2880	111

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 21.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:389:LEU:HD12	1:A:389:LEU:C	0.71	2.06	6	9
1:A:389:LEU:C	1:A:389:LEU:HD12	0.70	2.07	7	10
1:A:383:LEU:O	1:A:387:ILE:HD12	0.66	1.91	17	5
1:A:376:VAL:O	1:A:380:VAL:HG23	0.65	1.91	18	7
1:A:389:LEU:HD12	1:A:389:LEU:O	0.61	1.95	16	3
1:A:383:LEU:C	1:A:387:ILE:HD12	0.61	2.16	1	2
1:A:387:ILE:O	1:A:391:ILE:HD12	0.57	1.98	20	7
1:A:389:LEU:O	1:A:389:LEU:HD12	0.56	2.00	11	8
1:A:383:LEU:CD1	1:A:387:ILE:HD11	0.55	2.32	2	4
1:A:383:LEU:CD1	1:A:387:ILE:CD1	0.52	2.88	18	4
1:A:383:LEU:HD13	1:A:387:ILE:CD1	0.52	2.35	5	4
1:A:389:LEU:C	1:A:389:LEU:CD1	0.49	2.80	7	5
1:A:386:PHE:HA	1:A:389:LEU:HD23	0.49	1.84	20	13
1:A:389:LEU:O	1:A:392:PHE:N	0.48	2.47	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:389:LEU:CD1	1:A:389:LEU:C	0.47	2.80	3	8
1:A:383:LEU:HD13	1:A:387:ILE:HD12	0.47	1.87	5	2
1:A:376:VAL:O	1:A:380:VAL:N	0.45	2.50	8	2
1:A:380:VAL:O	1:A:383:LEU:N	0.45	2.49	6	1
1:A:378:GLY:O	1:A:381:ALA:HB3	0.45	2.12	14	1
1:A:389:LEU:HD12	1:A:390:GLY:N	0.43	2.28	13	1
1:A:379:GLY:O	1:A:382:GLY:N	0.43	2.49	14	1
1:A:386:PHE:O	1:A:390:GLY:N	0.43	2.50	1	1
1:A:380:VAL:O	1:A:381:ALA:C	0.41	2.58	6	8
1:A:376:VAL:O	1:A:379:GLY:N	0.41	2.53	12	3
1:A:383:LEU:HD23	1:A:383:LEU:HA	0.40	1.78	19	1

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

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	18/70 (26%)	15±1 (85±8%)	3±1 (15±8%)	0±0 (0±0%)	100	100
All	All	360/1400 (26%)	307 (85%)	53 (15%)	0 (0%)	100	100

There are no Ramachandran outliers.

6.3.2 Protein sidechains ⓘ

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	12/60 (20%)	10±1 (85±5%)	2±1 (15±5%)	7	44
All	All	240/1200 (20%)	203 (85%)	37 (15%)	7	44

All 4 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	389	LEU	20
1	A	383	LEU	14
1	A	392	PHE	2
1	A	385	LEU	1

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 carbohydrates 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 100% for the well-defined parts and 88% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 16853

Chemical shift list name: *assigned_chem_shift_list_1*

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	926
Number of shifts mapped to atoms	926
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
$^{13}\text{C}_\alpha$	70	0.29 ± 0.17	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	63	0.63 ± 0.07	Should be applied
$^{13}\text{C}'$	70	0.33 ± 0.15	None needed (< 0.5 ppm)
^{15}N	64	-0.64 ± 0.27	Should be applied

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 100%, i.e. 200 atoms were assigned a chemical shift out of a possible 200. 7 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	90/90 (100%)	36/36 (100%)	36/36 (100%)	18/18 (100%)
Sidechain	92/92 (100%)	51/51 (100%)	41/41 (100%)	0/0 (—%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	18/18 (100%)	10/10 (100%)	8/8 (100%)	0/0 (—%)
Overall	200/200 (100%)	97/97 (100%)	85/85 (100%)	18/18 (100%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 88%, i.e. 820 atoms were assigned a chemical shift out of a possible 931. 13 out of 13 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	338/342 (99%)	134/136 (99%)	140/140 (100%)	64/66 (97%)
Sidechain	434/529 (82%)	269/316 (85%)	161/178 (90%)	4/35 (11%)
Aromatic	48/60 (80%)	26/32 (81%)	22/22 (100%)	0/6 (0%)
Overall	820/931 (88%)	429/484 (89%)	323/340 (95%)	68/107 (64%)

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:

