



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 1DGQ
Title : NMR SOLUTION STRUCTURE OF THE INSERTED DOMAIN OF HUMAN LEUKOCYTE FUNCTION ASSOCIATED ANTIGEN-1
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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

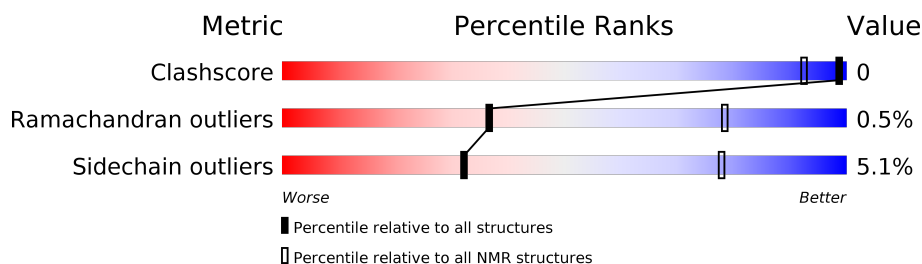
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 86%.

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	188	 84% 5% 12%

2 Ensemble composition and analysis

This entry contains 22 models. Model 13 is the overall representative, medoid model (most similar to other models).

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:130-A:161, A:166-A:299 (166)	0.19	13

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 2 single-model clusters were found.

Cluster number	Models
1	1, 3, 10, 11, 12, 19, 20, 21
2	7, 13, 14, 17, 18
3	2, 6, 9, 22
4	5, 8, 15
Single-model clusters	4; 16

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3029 atoms, of which 1519 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called LEUKOCYTE FUNCTION ASSOCIATED ANTIGEN-1.

Mol	Chain	Residues	Atoms						Trace
1	A	188	Total	C	H	N	O	S	0
			3029	978	1519	239	288	5	

There are 4 discrepancies between the modelled and reference sequences:

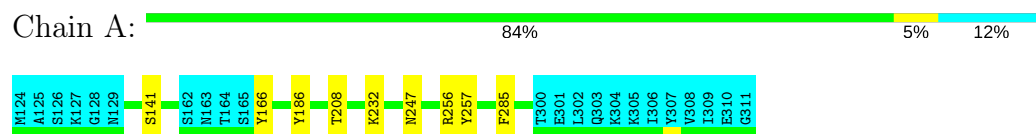
Chain	Residue	Modelled	Actual	Comment	Reference
A	124	MET	GLU	CONFLICT	UNP P20701
A	125	ALA	CYS	CONFLICT	UNP P20701
A	126	SER	ILE	CONFLICT	UNP P20701
A	189	TRP	ARG	CONFLICT	UNP P20701

4 Residue-property plots [i](#)

4.1 Average score per residue in the NMR ensemble

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.

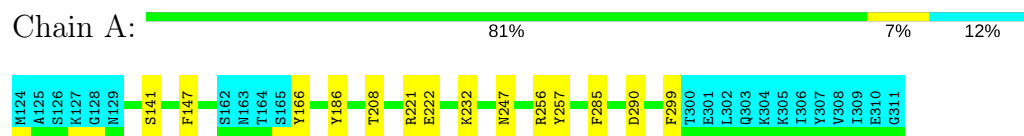
- Molecule 1: LEUKOCYTE FUNCTION ASSOCIATED ANTIGEN-1



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

The representative model is number 13. Colouring as in section 4.1 above.

- Molecule 1: LEUKOCYTE FUNCTION ASSOCIATED ANTIGEN-1



5 Refinement protocol and experimental data overview

The models were refined using the following method: *TORSION ANGLE DYNAMICS SIMULATED ANNEALING*.

Of the 100 calculated structures, 22 were deposited, based on the following criterion: *STRUCTURES WITH ACCEPTABLE COVALENT GEOMETRY, STRUCTURES WITH FAVORABLE NON- BOND ENERGY, STRUCTURES WITH THE LEAST RESTRAINT VIOLATIONS, STRUCTURES WITH THE LOWEST ENERGY*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
DYANA	structure solution	1.5
AMBER	structure solution	5.1
AMBER	refinement	5.1

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 4553
Number of chemical shift lists	1
Total number of shifts	2273
Number of shifts mapped to atoms	2273
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	86%

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.

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	4.8±1.1
All	All	0	105

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

5 of 14 unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	257	TYR	Sidechain	22
1	A	186	TYR	Sidechain	15
1	A	166	TYR	Sidechain	12
1	A	285	PHE	Sidechain	11
1	A	299	PHE	Sidechain	10

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	1343	1346	1346	0±0
All	All	29546	29612	29612	3

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 0.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:136:PHE:CE2	1:A:147:PHE:CE1	0.43	3.06	4	1
1:A:265:PHE:CZ	1:A:274:LEU:HD21	0.42	2.50	12	1
1:A:196:LEU:O	1:A:199:VAL:HG23	0.40	2.16	6	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	Percentiles	
1	A	166/188 (88%)	151±2 (91±1%)	15±2 (9±1%)	1±1 (0±0%)	37	78
All	All	3652/4136 (88%)	3311 (91%)	323 (9%)	18 (0%)	37	78

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	174	SER	10
1	A	290	ASP	5
1	A	265	PHE	3

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	147/166 (89%)	139±2 (95±1%)	8±2 (5±1%)	32	78
All	All	3234/3652 (89%)	3068 (95%)	166 (5%)	32	78

5 of 30 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	256	ARG	22
1	A	232	LYS	22
1	A	247	ASN	22
1	A	141	SER	17
1	A	208	THR	16

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

The completeness of assignment taking into account all chemical shift lists is 86% for the well-defined parts and 85% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 4553

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	2273
Number of shifts mapped to atoms	2273
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	10

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	186	-0.01 ± 0.10	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	177	0.31 ± 0.14	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	179	-0.60 ± 0.43	None needed (imprecise)

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 86%, i.e. 1789 atoms were assigned a chemical shift out of a possible 2090. 10 out of 26 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	654/822 (80%)	328/328 (100%)	166/332 (50%)	160/162 (99%)
Sidechain	943/1053 (90%)	584/613 (95%)	351/404 (87%)	8/36 (22%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	192/215 (89%)	108/117 (92%)	83/93 (89%)	1/5 (20%)
Overall	1789/2090 (86%)	1020/1058 (96%)	600/829 (72%)	169/203 (83%)

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	257	TYR	CZ	130.00	167.04 – 146.14	-12.7
1	A	186	TYR	CB	62.80	50.05 – 28.55	10.9
1	A	252	LYS	HB2	3.95	3.03 – 0.53	8.7
1	A	252	LYS	HB3	3.95	3.10 – 0.40	8.1
1	A	146	GLU	HB3	0.40	3.10 – 0.90	-7.3
1	A	248	ILE	CG1	15.70	36.54 – 18.94	-6.8
1	A	248	ILE	CG2	27.10	24.63 – 10.43	6.7
1	A	218	GLU	HB2	0.75	3.08 – 0.98	-6.1
1	A	141	SER	HG	10.92	10.51 – 0.11	5.4
1	A	158	MET	HG3	0.42	4.30 – 0.50	-5.2

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:

