



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 7I1B
Title : HIGH-RESOLUTION THREE-DIMENSIONAL STRUCTURE OF
INTERLEUKIN-1 BETA IN SOLUTION BY THREE-AND FOUR-
DIMENSIONAL NUCLEAR MAGNETIC RESONANCE SPECTROSCOPY
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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
<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
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

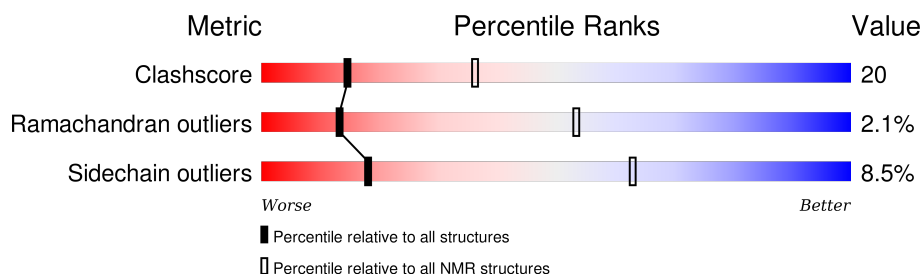
1 Overall quality at a glance

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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	153	 58% 37% . .

2 Ensemble composition and analysis

This entry contains 32 models. Model 20 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:3-A:151 (149)	0.29	20

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 8 clusters and 1 single-model cluster was found.

Cluster number	Models
1	1, 3, 7, 16, 18, 27, 28, 31
2	5, 9, 10, 19, 20, 25
3	11, 12, 22, 24, 30
4	15, 17, 29
5	2, 4, 8
6	6, 21
7	26, 32
8	13, 23
Single-model clusters	14

3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 2458 atoms, of which 1232 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called INTERLEUKIN-1 BETA.

Mol	Chain	Residues	Atoms						Trace
1	A	153	Total	C	H	N	O	S	0
			2437	773	1218	201	237	8	

- Molecule 2 is water.

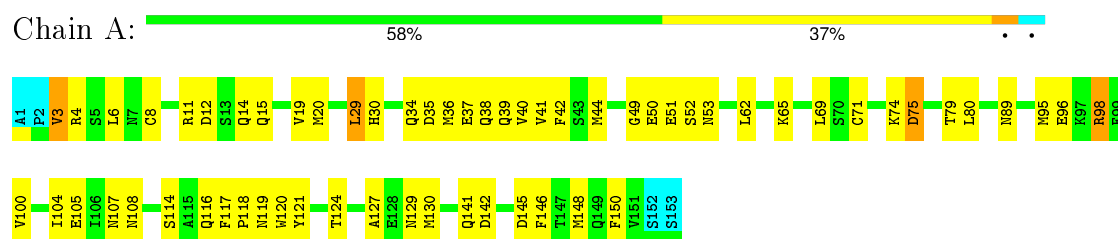
Mol	Chain	Residues	Atoms		
2	A	7	Total	H	O
			21	14	7

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.

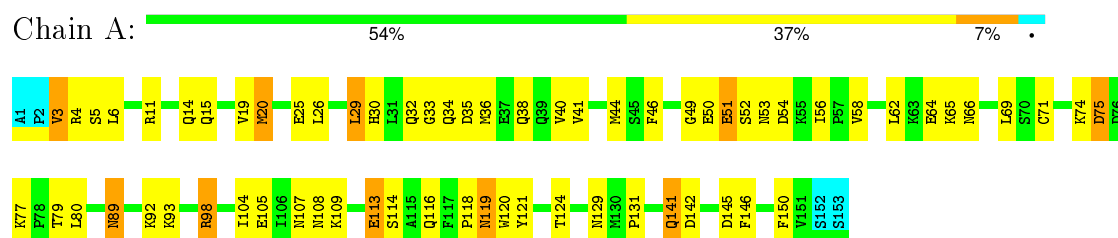
- Molecule 1: INTERLEUKIN-1 BETA



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

The representative model is number 20. Colouring as in section 4.1 above.

- Molecule 1: INTERLEUKIN-1 BETA



5 Refinement protocol and experimental data overview ⓘ

The models were refined using the following method: ?.

Of the ? calculated structures, 32 were deposited, based on the following criterion: ?.

The authors did not provide any information on software used for structure solution, optimization or refinement.

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality

6.1 Standard geometry

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	1.05±0.00	2±0/1217 (0.2±0.0%)	1.08±0.00	5±0/1638 (0.3±0.0%)
All	All	1.05	64/38944 (0.2%)	1.08	160/52416 (0.3%)

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	2.7±0.5
All	All	0	87

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	120	TRP	CG-CD2	-6.56	1.32	1.43	18	32
1	A	30	HIS	CG-ND1	-5.94	1.25	1.38	28	32

All 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	120	TRP	NE1-CE2-CZ2	8.40	139.64	130.40	18	32
1	A	120	TRP	NE1-CE2-CD2	-7.08	100.22	107.30	18	32
1	A	120	TRP	CG-CD1-NE1	-6.35	103.75	110.10	32	32
1	A	120	TRP	CD1-NE1-CE2	6.19	114.57	109.00	13	32
1	A	120	TRP	CD1-CG-CD2	5.80	110.94	106.30	5	32

There are no chirality outliers.

All 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	98	ARG	Sidechain	30
1	A	4	ARG	Sidechain	30
1	A	11	ARG	Sidechain	27

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	1194	1194	1194	48±6
2	A	7	14	0	0±1
All	All	38432	38656	38208	1534

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 20.

5 of 422 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:20:MET:SD	1:A:40:VAL:HG22	0.81	2.16	32	4
1:A:6:LEU:HD21	1:A:150:PHE:CE2	0.79	2.11	18	6
1:A:3:VAL:HG12	1:A:4:ARG:H	0.79	1.35	2	1
1:A:96:GLU:O	1:A:100:VAL:HG23	0.76	1.81	16	27
1:A:105:GLU:C	1:A:106:ILE:HD12	0.72	2.04	16	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	149/153 (97%)	126±2 (85±2%)	19±2 (13±2%)	3±1 (2±1%)	13	53

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	4768/4896 (97%)	4046 (85%)	620 (13%)	102 (2%)	13 53

5 of 13 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	75	ASP	32
1	A	50	GLU	29
1	A	127	ALA	17
1	A	15	GLN	5
1	A	52	SER	5

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	137/140 (98%)	125±3 (91±2%)	12±3 (9±2%)	18 63
All	All	4384/4480 (98%)	4011 (91%)	373 (9%)	18 63

5 of 58 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	3	VAL	26
1	A	124	THR	22
1	A	29	LEU	21
1	A	19	VAL	21
1	A	20	MET	16

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

No chemical shift data were provided