



# wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 2IFE  
Title : TRANSLATION INITIATION FACTOR IF3 FROM ESCHERICHIA COLI  
RIBOSOME BINDING DOMAIN (RESIDUES 84-180)  
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Deposited on : 1998-12-16

This is a wwPDB NMR Structure Validation Summary Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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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

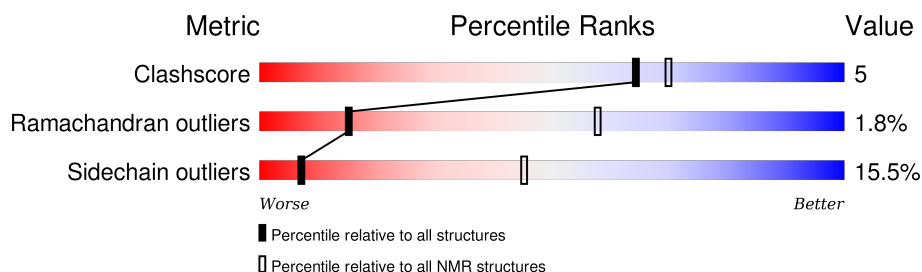
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 79%.

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  $\geq 3$ , 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	100	<div> <div style="width: 42%; background-color: green;"></div> <div style="width: 16%; background-color: yellow;"></div> <div style="width: 2%; background-color: orange;"></div> <div style="width: 2%; background-color: red;"></div> <div style="width: 27%; background-color: cyan;"></div> <div style="width: 9%; background-color: grey;"></div> </div> <div> 42%16%. .27%9% </div>

## 2 Ensemble composition and analysis

This entry contains 24 models. Model 19 is the overall representative, medoid model (most similar to other models). The authors have identified model 2 as representative.

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:92-A:99, A:106-A:130, A:140-A:161, A:169-A:177 (64)	0.23	19

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 and 1 single-model cluster was found.

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

### 3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1527 atoms, of which 784 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called PROTEIN (TRANSLATION INITIATION FACTOR IF3).

Mol	Chain	Residues	Atoms						Trace
1	A	91	Total	C	H	N	O	S	0
			1527	470	784	135	134	4	

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	81	MET	SER	SEE REMARK 999	UNP P0A707
A	82	GLU	LYS	SEE REMARK 999	UNP P0A707
A	83	PHE	GLU	SEE REMARK 999	UNP P0A707



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *DISTANCE GEOMETRY AND RESTRAINED SIMULATED ANNEALING*.

Of the 200 calculated structures, 24 were deposited, based on the following criterion: *LOWEST TARGET FUNCTION*.

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

Software name	Classification	Version
X-PLOR	refinement	3.1
DIANA	structure solution	
X-PLOR	structure solution	3.1

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 4394
Number of chemical shift lists	1
Total number of shifts	985
Number of shifts mapped to atoms	985
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	79%

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

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	1.19±0.01	0±0/536 (0.0±0.0%)	1.77±0.09	13±3/718 (1.8±0.4%)
All	All	1.19	0/12864 (0.0%)	1.77	310/17232 (1.8%)

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	3.7±0.9
All	All	0	88

There are no bond-length outliers.

5 of 39 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	107	TYR	CB-CG-CD2	-16.36	111.19	121.00	21	17
1	A	98	PHE	CB-CG-CD2	-14.22	110.84	120.80	13	4
1	A	98	PHE	CB-CG-CD1	14.16	130.71	120.80	13	4
1	A	117	PHE	CB-CG-CD2	-12.79	111.84	120.80	21	13
1	A	117	PHE	CB-CG-CD1	11.42	128.79	120.80	10	13

There are no chirality outliers.

5 of 6 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	107	TYR	Sidechain	24
1	A	156	ALA	Peptide	21
1	A	161	PHE	Sidechain,Peptide	18

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Mol	Chain	Res	Type	Group	Models (Total)
1	A	142	MET	Peptide	17
1	A	160	SER	Peptide	2

## 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	530	569	569	6±2
All	All	12720	13656	13656	138

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 5.

5 of 46 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:156:ALA:HB1	1:A:174:LEU:HD11	0.93	1.38	3	6
1:A:128:LEU:HD21	1:A:141:GLY:HA2	0.72	1.62	14	5
1:A:128:LEU:HD13	1:A:130:PHE:CZ	0.66	2.26	11	2
1:A:128:LEU:HD11	1:A:141:GLY:HA2	0.64	1.69	6	8
1:A:156:ALA:CB	1:A:174:LEU:HD11	0.63	2.24	8	7

## 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	64/100 (64%)	57±1 (89±2%)	6±1 (9±2%)	1±0 (2±1%)	15	58
All	All	1536/2400 (64%)	1370 (89%)	139 (9%)	27 (2%)	15	58

All 4 unique Ramachandran outliers are listed below. They are sorted by the frequency of occur-



rence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	153	GLN	24
1	A	144	VAL	1
1	A	169	GLN	1
1	A	106	ASP	1

### 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	59/90 (66%)	50±2 (84±4%)	9±2 (16±4%)	7	45
All	All	1416/2160 (66%)	1196 (84%)	220 (16%)	7	45

5 of 23 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	108	GLN	24
1	A	152	LEU	24
1	A	107	TYR	22
1	A	118	LEU	21
1	A	128	LEU	19

### 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 79% for the well-defined parts and 70% for the entire structure.

### 7.1 Chemical shift list 1

File name: BMRB entry 4394

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	985
Number of shifts mapped to atoms	985
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	3

#### 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
$^{13}\text{C}_\alpha$	83	$-0.15 \pm 0.20$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	70	$0.39 \pm 0.34$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}'$	0	—	—
$^{15}\text{N}$	86	$2.77 \pm 0.21$	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 79%, i.e. 685 atoms were assigned a chemical shift out of a possible 871. 10 out of 15 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	254/318 (80%)	127/127 (100%)	64/128 (50%)	63/63 (100%)
Sidechain	410/509 (81%)	263/297 (89%)	141/185 (76%)	6/27 (22%)

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	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Aromatic	21/44 (48%)	21/24 (88%)	0/20 (0%)	0/0 (—%)
Overall	685/871 (79%)	411/448 (92%)	205/333 (62%)	69/90 (77%)

#### 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	149	LYS	CE	36.30	46.00 – 37.80	-6.8
1	A	154	GLU	CG	29.40	42.24 – 29.94	-5.4
1	A	155	LEU	CG	32.80	32.55 – 21.05	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:

