



# Full wwPDB NMR Structure Validation Report ⓘ

Apr 27, 2016 – 01:20 AM BST

PDB ID : 2LJ8  
Title : Solution structure of ADF/Cofilin from trypanosoma brucei  
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Deposited on : 2011-09-08

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

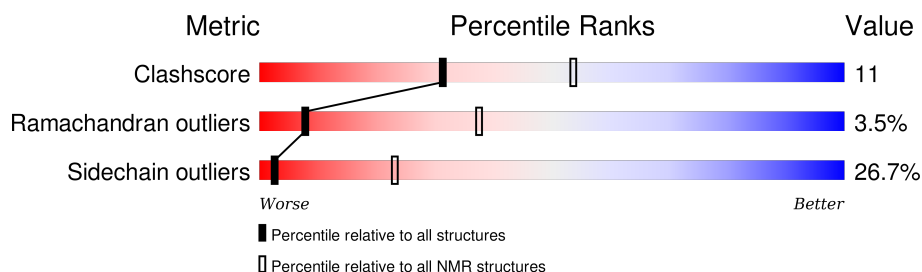
# 1 Overall quality at a glance

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	144	

## 2 Ensemble composition and analysis ⓘ

This entry contains 20 models. Model 7 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:14-A:77, A:85-A:144 (124)	0.48	7

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. No single-model clusters were found.

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

### 3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2107 atoms, of which 1047 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Cofilin/actin depolymerizing factor, putative.

Mol	Chain	Residues	Atoms						Trace
1	A	136	Total	C	H	N	O	S	0
			2107	662	1047	186	206	6	

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP Q580V7
A	2	GLY	-	EXPRESSION TAG	UNP Q580V7
A	3	HIS	-	EXPRESSION TAG	UNP Q580V7
A	4	HIS	-	EXPRESSION TAG	UNP Q580V7
A	5	HIS	-	EXPRESSION TAG	UNP Q580V7
A	6	HIS	-	EXPRESSION TAG	UNP Q580V7
A	7	HIS	-	EXPRESSION TAG	UNP Q580V7
A	8	HIS	-	EXPRESSION TAG	UNP Q580V7

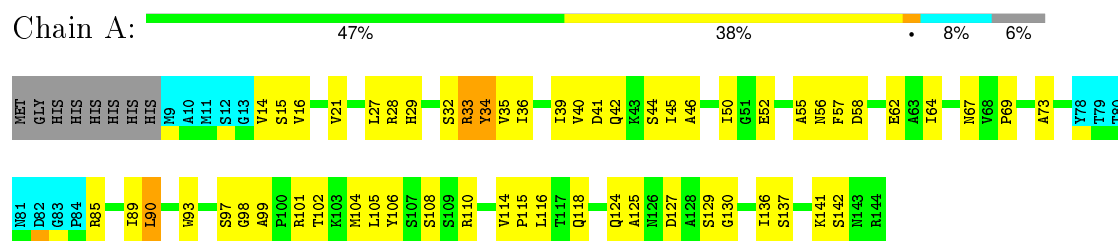






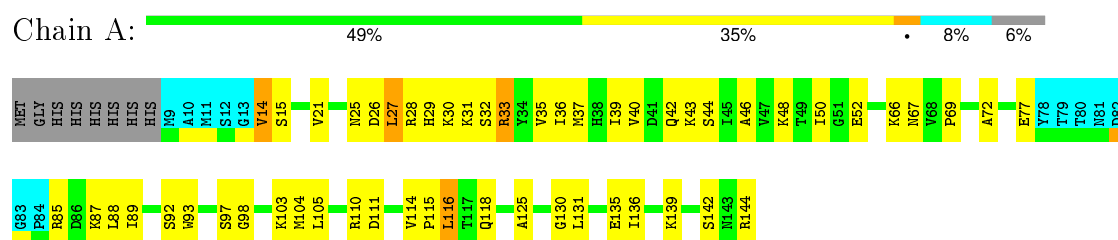
### 4.2.10 Score per residue for model 10

- Molecule 1: Cofilin/actin depolymerizing factor, putative



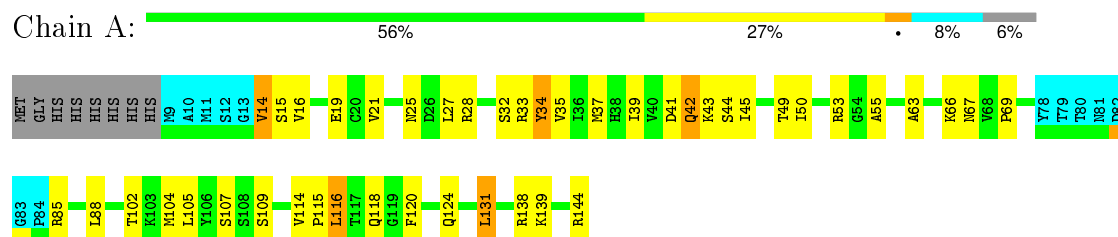
### 4.2.11 Score per residue for model 11

- Molecule 1: Cofilin/actin depolymerizing factor, putative



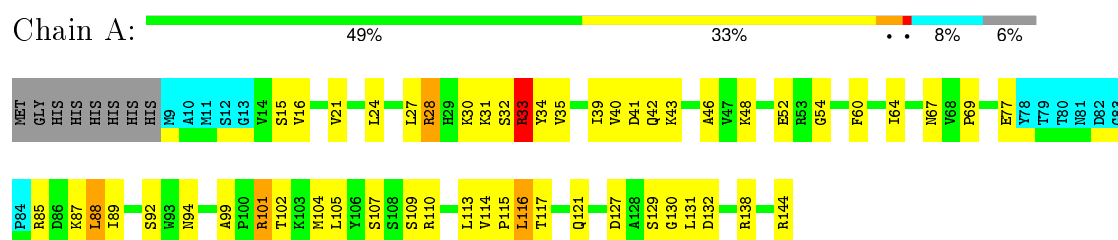
### 4.2.12 Score per residue for model 12

- Molecule 1: Cofilin/actin depolymerizing factor, putative



### 4.2.13 Score per residue for model 13

- Molecule 1: Cofilin/actin depolymerizing factor, putative

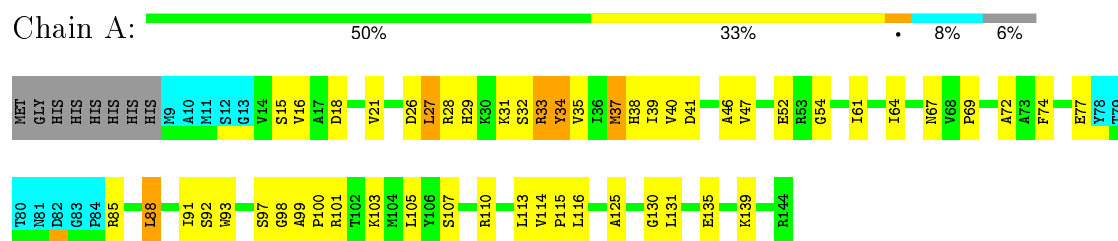






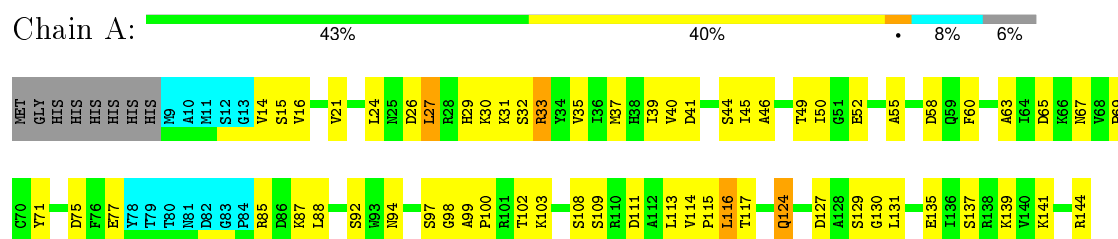
### 4.2.18 Score per residue for model 18

- Molecule 1: Cofilin/actin depolymerizing factor, putative



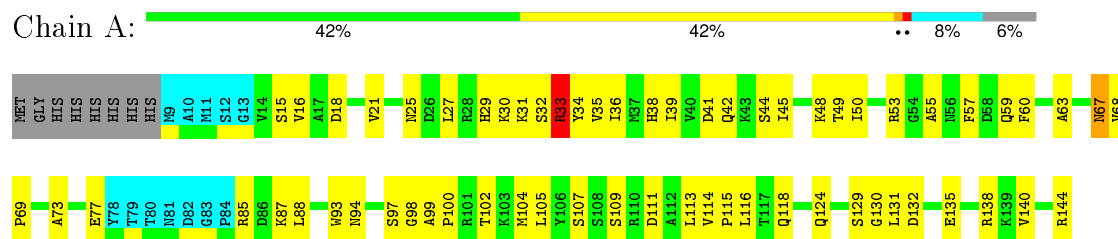
### 4.2.19 Score per residue for model 19

- Molecule 1: Cofilin/actin depolymerizing factor, putative



### 4.2.20 Score per residue for model 20

- Molecule 1: Cofilin/actin depolymerizing factor, putative



## 5 Refinement protocol and experimental data overview

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
CYANA	structure solution	
CYANA	refinement	

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)	2lj8_cs.str
Number of chemical shift lists	1
Total number of shifts	1469
Number of shifts mapped to atoms	1469
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 ⓘ

### 6.1 Standard geometry ⓘ

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 ⓘ

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	976	973	973	22±5
All	All	19520	19460	19460	448

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 11.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:21:VAL:HG13	1:A:116:LEU:HD11	0.94	1.34	6	4
1:A:21:VAL:HG22	1:A:116:LEU:HD11	0.92	1.38	10	13
1:A:16:VAL:HG21	1:A:116:LEU:HD22	0.86	1.48	20	2
1:A:27:LEU:HD13	1:A:35:VAL:HG13	0.82	1.50	14	6
1:A:27:LEU:HD23	1:A:88:LEU:HD11	0.81	1.52	17	1
1:A:27:LEU:HD22	1:A:35:VAL:HG22	0.81	1.51	4	3
1:A:27:LEU:HD23	1:A:88:LEU:HD21	0.81	1.49	2	2
1:A:36:ILE:HG21	1:A:64:ILE:HD11	0.80	1.54	10	4
1:A:36:ILE:HD13	1:A:64:ILE:HD11	0.75	1.58	3	2
1:A:27:LEU:HD13	1:A:35:VAL:HG12	0.70	1.63	6	3
1:A:16:VAL:HG12	1:A:45:ILE:HD12	0.69	1.63	4	1
1:A:27:LEU:HD22	1:A:35:VAL:HG12	0.68	1.65	1	3
1:A:40:VAL:HG21	1:A:46:ALA:HB3	0.64	1.68	14	16
1:A:35:VAL:HG12	1:A:50:ILE:HG23	0.64	1.66	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:34:TYR:CE1	1:A:55:ALA:HB3	0.64	2.27	12	3
1:A:93:TRP:CZ3	1:A:131:LEU:HD21	0.64	2.27	11	2
1:A:99:ALA:HB3	1:A:102:THR:HG23	0.64	1.70	1	4
1:A:14:VAL:HG21	1:A:109:SER:OG	0.64	1.93	16	1
1:A:122:GLY:O	1:A:123:ILE:HD13	0.63	1.93	2	2
1:A:14:VAL:HG21	1:A:109:SER:HB2	0.62	1.72	19	2
1:A:28:ARG:HA	1:A:88:LEU:HD12	0.62	1.69	13	4
1:A:73:ALA:HB2	1:A:90:LEU:HD12	0.62	1.72	10	2
1:A:36:ILE:HD11	1:A:60:PHE:CE2	0.62	2.30	20	2
1:A:35:VAL:HG12	1:A:50:ILE:CG2	0.61	2.24	10	1
1:A:36:ILE:HG21	1:A:64:ILE:CD1	0.60	2.26	1	3
1:A:28:ARG:HB3	1:A:88:LEU:HD12	0.60	1.71	3	2
1:A:45:ILE:HG21	1:A:71:TYR:OH	0.60	1.96	19	2
1:A:27:LEU:HD11	1:A:34:TYR:CA	0.60	2.26	18	3
1:A:39:ILE:HD12	1:A:69:PRO:HG2	0.60	1.72	3	14
1:A:16:VAL:HG21	1:A:116:LEU:CD2	0.60	2.25	20	2
1:A:34:TYR:OH	1:A:55:ALA:HB3	0.59	1.97	7	5
1:A:28:ARG:CB	1:A:88:LEU:HD12	0.59	2.26	3	1
1:A:123:ILE:HD13	1:A:139:LYS:HD2	0.59	1.74	7	1
1:A:55:ALA:HB3	1:A:60:PHE:CE2	0.59	2.33	19	1
1:A:16:VAL:HG11	1:A:116:LEU:HG	0.59	1.75	7	5
1:A:27:LEU:HD21	1:A:34:TYR:HA	0.58	1.74	1	3
1:A:27:LEU:HD11	1:A:34:TYR:HA	0.58	1.73	14	2
1:A:35:VAL:HG12	1:A:50:ILE:HG13	0.58	1.74	4	4
1:A:27:LEU:HD13	1:A:35:VAL:HG23	0.58	1.74	13	4
1:A:94:ASN:OD1	1:A:102:THR:HG21	0.57	1.99	6	1
1:A:24:LEU:HD13	1:A:117:THR:CG2	0.57	2.29	5	4
1:A:42:GLN:CB	1:A:105:LEU:HD11	0.57	2.28	9	3
1:A:130:GLY:O	1:A:131:LEU:HD23	0.57	1.99	19	9
1:A:93:TRP:CH2	1:A:131:LEU:HD11	0.57	2.34	11	2
1:A:73:ALA:HB1	1:A:88:LEU:CD2	0.57	2.29	15	2
1:A:16:VAL:HG11	1:A:116:LEU:CD2	0.57	2.29	13	6
1:A:27:LEU:HD11	1:A:33:ARG:C	0.56	2.20	4	4
1:A:39:ILE:HD12	1:A:69:PRO:CG	0.56	2.30	6	17
1:A:88:LEU:C	1:A:89:ILE:HD13	0.56	2.21	17	6
1:A:21:VAL:HG22	1:A:116:LEU:HD21	0.56	1.78	19	3
1:A:14:VAL:CG2	1:A:105:LEU:HD22	0.56	2.31	12	2
1:A:42:GLN:CG	1:A:105:LEU:HD21	0.55	2.31	10	1
1:A:42:GLN:CG	1:A:105:LEU:HD11	0.55	2.31	17	3
1:A:110:ARG:O	1:A:114:VAL:HG23	0.55	2.01	10	4
1:A:89:ILE:HG21	1:A:136:ILE:HD12	0.54	1.79	10	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:37:MET:CE	1:A:113:LEU:HD21	0.54	2.32	9	1
1:A:28:ARG:CA	1:A:88:LEU:HD12	0.54	2.33	4	3
1:A:74:PHE:CE2	1:A:91:ILE:HD13	0.54	2.37	18	1
1:A:14:VAL:HG21	1:A:109:SER:CB	0.54	2.33	19	2
1:A:40:VAL:CG2	1:A:46:ALA:HB3	0.54	2.33	14	15
1:A:27:LEU:CD2	1:A:88:LEU:HD11	0.54	2.29	17	1
1:A:99:ALA:HB3	1:A:102:THR:OG1	0.54	2.02	10	4
1:A:39:ILE:HD13	1:A:105:LEU:HD22	0.54	1.79	4	1
1:A:93:TRP:CZ2	1:A:131:LEU:HD11	0.54	2.38	20	1
1:A:14:VAL:HG11	1:A:109:SER:HB2	0.54	1.79	3	1
1:A:73:ALA:HB2	1:A:90:LEU:CD1	0.54	2.33	17	1
1:A:60:PHE:O	1:A:64:ILE:HG22	0.54	2.03	16	5
1:A:73:ALA:HB2	1:A:90:LEU:CD2	0.53	2.33	1	1
1:A:114:VAL:N	1:A:115:PRO:HD2	0.53	2.19	7	20
1:A:123:ILE:HD11	1:A:139:LYS:HG2	0.53	1.80	16	2
1:A:16:VAL:CG1	1:A:45:ILE:HD12	0.53	2.33	4	1
1:A:93:TRP:CE2	1:A:131:LEU:HD11	0.52	2.39	20	1
1:A:89:ILE:HG21	1:A:136:ILE:HG23	0.52	1.82	11	1
1:A:90:LEU:CD1	1:A:117:THR:HG21	0.52	2.34	3	1
1:A:28:ARG:CA	1:A:88:LEU:HD21	0.52	2.35	12	4
1:A:21:VAL:CG1	1:A:116:LEU:HD11	0.52	2.32	9	2
1:A:42:GLN:HG2	1:A:105:LEU:HD21	0.52	1.81	10	1
1:A:109:SER:O	1:A:113:LEU:HD12	0.51	2.04	8	2
1:A:27:LEU:HD11	1:A:33:ARG:O	0.51	2.04	17	2
1:A:99:ALA:HB3	1:A:102:THR:HG22	0.51	1.81	16	2
1:A:72:ALA:HB1	1:A:74:PHE:CE1	0.51	2.41	18	1
1:A:99:ALA:HB3	1:A:102:THR:CG2	0.51	2.35	1	3
1:A:93:TRP:CH2	1:A:131:LEU:HD21	0.51	2.41	11	1
1:A:93:TRP:CH2	1:A:131:LEU:HD23	0.50	2.41	18	2
1:A:41:ASP:O	1:A:42:GLN:C	0.50	2.49	16	3
1:A:101:ARG:O	1:A:105:LEU:HD13	0.50	2.06	18	5
1:A:21:VAL:CG2	1:A:116:LEU:HD11	0.50	2.25	10	4
1:A:28:ARG:HA	1:A:88:LEU:HD21	0.50	1.84	9	4
1:A:42:GLN:HB2	1:A:105:LEU:HD21	0.50	1.82	5	3
1:A:74:PHE:CZ	1:A:89:ILE:HD13	0.50	2.40	16	1
1:A:16:VAL:HA	1:A:45:ILE:HD12	0.50	1.83	20	8
1:A:35:VAL:HG22	1:A:50:ILE:HG13	0.50	1.83	9	3
1:A:21:VAL:HG13	1:A:116:LEU:CD1	0.50	2.33	9	4
1:A:69:PRO:N	1:A:102:THR:HG23	0.50	2.22	12	3
1:A:125:ALA:HB3	1:A:130:GLY:HA2	0.49	1.83	4	10
1:A:16:VAL:HG21	1:A:116:LEU:HG	0.49	1.82	14	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:90:LEU:HD13	1:A:117:THR:HG21	0.49	1.83	3	1
1:A:89:ILE:HD13	1:A:136:ILE:CG2	0.49	2.37	6	1
1:A:34:TYR:OH	1:A:72:ALA:HB1	0.49	2.08	3	1
1:A:14:VAL:HG21	1:A:105:LEU:HD22	0.49	1.83	12	1
1:A:113:LEU:HD23	1:A:116:LEU:HD23	0.48	1.85	20	2
1:A:87:LYS:HG2	1:A:140:VAL:HG23	0.48	1.85	14	2
1:A:37:MET:HG2	1:A:47:VAL:HG12	0.48	1.86	18	1
1:A:69:PRO:CD	1:A:102:THR:HG23	0.48	2.38	6	4
1:A:87:LYS:CG	1:A:140:VAL:HG23	0.47	2.39	14	2
1:A:24:LEU:HD12	1:A:25:ASN:N	0.47	2.24	1	1
1:A:16:VAL:HG11	1:A:116:LEU:HD23	0.47	1.87	19	1
1:A:14:VAL:HG12	1:A:45:ILE:HD11	0.47	1.85	5	1
1:A:122:GLY:C	1:A:123:ILE:HD13	0.47	2.30	2	2
1:A:49:THR:OG1	1:A:63:ALA:HB2	0.47	2.09	19	1
1:A:35:VAL:HG12	1:A:50:ILE:CG1	0.47	2.40	12	2
1:A:64:ILE:HD12	1:A:93:TRP:CZ3	0.47	2.45	4	1
1:A:27:LEU:HD21	1:A:73:ALA:O	0.47	2.10	2	3
1:A:27:LEU:CD2	1:A:88:LEU:HD21	0.47	2.31	2	1
1:A:27:LEU:HD23	1:A:88:LEU:CD2	0.46	2.40	6	2
1:A:89:ILE:HD11	1:A:140:VAL:CG2	0.46	2.40	17	1
1:A:73:ALA:HB1	1:A:88:LEU:HD21	0.46	1.86	8	2
1:A:60:PHE:CE2	1:A:131:LEU:HD22	0.46	2.46	4	1
1:A:28:ARG:HA	1:A:88:LEU:HD11	0.45	1.88	14	2
1:A:42:GLN:HB3	1:A:105:LEU:HD21	0.45	1.88	17	1
1:A:42:GLN:HB3	1:A:105:LEU:HD11	0.45	1.87	17	4
1:A:14:VAL:HG22	1:A:14:VAL:O	0.45	2.10	4	1
1:A:123:ILE:HD13	1:A:139:LYS:CD	0.45	2.42	7	1
1:A:27:LEU:HD22	1:A:35:VAL:HB	0.44	1.90	3	1
1:A:116:LEU:O	1:A:116:LEU:HD13	0.44	2.12	19	1
1:A:24:LEU:HD13	1:A:117:THR:HG22	0.44	1.89	19	1
1:A:16:VAL:HG11	1:A:116:LEU:CG	0.44	2.42	2	2
1:A:49:THR:HG21	1:A:63:ALA:HB1	0.44	1.90	12	1
1:A:124:GLN:NE2	1:A:124:GLN:H	0.44	2.10	19	1
1:A:27:LEU:HD22	1:A:35:VAL:HG23	0.44	1.89	9	1
1:A:42:GLN:N	1:A:42:GLN:HE21	0.43	2.12	16	1
1:A:74:PHE:CE1	1:A:91:ILE:HD11	0.43	2.48	17	1
1:A:60:PHE:HE2	1:A:131:LEU:HD22	0.43	1.73	4	1
1:A:42:GLN:HG2	1:A:105:LEU:HD11	0.43	1.89	6	1
1:A:21:VAL:CG2	1:A:116:LEU:HD21	0.43	2.42	7	2
1:A:114:VAL:N	1:A:115:PRO:CD	0.43	2.82	14	20
1:A:89:ILE:HD11	1:A:140:VAL:HG23	0.43	1.91	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:42:GLN:HE21	1:A:42:GLN:N	0.42	2.12	15	1
1:A:16:VAL:HG11	1:A:116:LEU:HD21	0.42	1.90	13	1
1:A:38:HIS:CE1	1:A:68:VAL:HG21	0.42	2.49	20	1
1:A:14:VAL:HG11	1:A:109:SER:OG	0.42	2.14	5	1
1:A:14:VAL:HG11	1:A:109:SER:CB	0.42	2.44	5	1
1:A:99:ALA:HB1	1:A:100:PRO:HD2	0.42	1.90	5	13
1:A:73:ALA:HB1	1:A:88:LEU:HD22	0.42	1.92	4	1
1:A:109:SER:OG	1:A:113:LEU:HD12	0.42	2.15	5	1
1:A:36:ILE:HD12	1:A:72:ALA:CB	0.41	2.45	11	1
1:A:34:TYR:CZ	1:A:55:ALA:HB3	0.41	2.50	12	1
1:A:55:ALA:HB3	1:A:60:PHE:CZ	0.41	2.50	19	1
1:A:21:VAL:HG22	1:A:116:LEU:CD1	0.41	2.46	18	1
1:A:49:THR:OG1	1:A:63:ALA:HB1	0.41	2.14	20	1
1:A:71:TYR:HB3	1:A:90:LEU:HD11	0.41	1.91	7	1
1:A:50:ILE:HD12	1:A:52:GLU:HG2	0.40	1.93	2	1
1:A:68:VAL:HG23	1:A:70:CYS:SG	0.40	2.57	2	1
1:A:50:ILE:HD11	1:A:52:GLU:OE2	0.40	2.15	11	1
1:A:21:VAL:HG22	1:A:116:LEU:HD13	0.40	1.94	20	1
1:A:16:VAL:CA	1:A:45:ILE:HD12	0.40	2.46	20	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	123/144 (85%)	108±2 (88±2%)	11±2 (9±2%)	4±1 (3±1%)	8	37
All	All	2460/2880 (85%)	2155 (88%)	219 (9%)	86 (3%)	8	37

All 12 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	67	ASN	19
1	A	33	ARG	18
1	A	98	GLY	13

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Mol	Chain	Res	Type	Models (Total)
1	A	52	GLU	13
1	A	14	VAL	7
1	A	54	GLY	4
1	A	53	ARG	3
1	A	43	LYS	3
1	A	131	LEU	3
1	A	66	LYS	1
1	A	55	ALA	1
1	A	32	SER	1

### 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	107/123 (87%)	78±4 (73±3%)	29±4 (27±3%)	2	23
All	All	2140/2460 (87%)	1569 (73%)	571 (27%)	2	23

All 80 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	32	SER	19
1	A	85	ARG	17
1	A	15	SER	17
1	A	87	LYS	16
1	A	116	LEU	16
1	A	129	SER	15
1	A	104	MET	15
1	A	44	SER	15
1	A	41	ASP	14
1	A	92	SER	13
1	A	31	LYS	13
1	A	37	MET	13
1	A	144	ARG	12
1	A	111	ASP	12
1	A	33	ARG	12
1	A	29	HIS	12

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Mol	Chain	Res	Type	Models (Total)
1	A	110	ARG	12
1	A	127	ASP	12
1	A	88	LEU	11
1	A	124	GLN	11
1	A	97	SER	11
1	A	66	LYS	10
1	A	138	ARG	10
1	A	113	LEU	10
1	A	107	SER	9
1	A	48	LYS	9
1	A	58	ASP	9
1	A	28	ARG	9
1	A	139	LYS	9
1	A	65	ASP	8
1	A	103	LYS	8
1	A	118	GLN	8
1	A	30	LYS	8
1	A	26	ASP	7
1	A	108	SER	7
1	A	94	ASN	7
1	A	67	ASN	7
1	A	77	GLU	7
1	A	132	ASP	7
1	A	135	GLU	7
1	A	27	LEU	6
1	A	25	ASN	6
1	A	93	TRP	5
1	A	52	GLU	5
1	A	34	TYR	5
1	A	56	ASN	5
1	A	90	LEU	5
1	A	109	SER	5
1	A	57	PHE	5
1	A	121	GLN	5
1	A	141	LYS	5
1	A	137	SER	5
1	A	62	GLU	4
1	A	18	ASP	4
1	A	42	GLN	4
1	A	61	ILE	4
1	A	133	PHE	3
1	A	43	LYS	3

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Mol	Chain	Res	Type	Models (Total)
1	A	96	ASP	3
1	A	120	PHE	3
1	A	53	ARG	3
1	A	19	GLU	3
1	A	75	ASP	3
1	A	86	ASP	2
1	A	20	CYS	2
1	A	134	GLU	2
1	A	131	LEU	2
1	A	101	ARG	2
1	A	59	GLN	2
1	A	142	SER	2
1	A	76	PHE	2
1	A	38	HIS	2
1	A	64	ILE	2
1	A	89	ILE	2
1	A	24	LEU	1
1	A	22	THR	1
1	A	71	TYR	1
1	A	106	TYR	1
1	A	105	LEU	1
1	A	74	PHE	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

The completeness of assignment taking into account all chemical shift lists is 79% for the well-defined parts and 79% for the entire structure.

### 7.1 Chemical shift list 1

File name: 2lj8\_cs.str

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	1469
Number of shifts mapped to atoms	1469
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

#### 7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	133	$0.19 \pm 0.12$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	127	$0.54 \pm 0.18$	Should be applied
$^{13}\text{C}'$	135	$0.12 \pm 0.17$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	130	$-0.19 \pm 0.32$	None needed ( $< 0.5$ ppm)

#### 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 79%, i.e. 1218 atoms were assigned a chemical shift out of a possible 1536. 11 out of 17 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	608/612 (99%)	243/244 (100%)	245/248 (99%)	120/120 (100%)
Sidechain	610/820 (74%)	371/480 (77%)	239/296 (81%)	0/44 (0%)

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	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Aromatic	0/104 (0%)	0/56 (0%)	0/45 (0%)	0/3 (0%)
Overall	1218/1536 (79%)	614/780 (79%)	484/589 (82%)	120/167 (72%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 79%, i.e. 1312 atoms were assigned a chemical shift out of a possible 1654. 11 out of 17 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	663/670 (99%)	265/267 (99%)	268/272 (99%)	130/131 (99%)
Sidechain	649/872 (74%)	395/511 (77%)	254/316 (80%)	0/45 (0%)
Aromatic	0/112 (0%)	0/60 (0%)	0/49 (0%)	0/3 (0%)
Overall	1312/1654 (79%)	660/838 (79%)	522/637 (82%)	130/179 (73%)

#### 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	51	GLY	HA3	1.38	5.80 – 2.00	-6.6

#### 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:

