



# Full wwPDB NMR Structure Validation Report ⓘ

Dec 22, 2020 – 12:10 PM JST

PDB ID : 6LZP  
Title : The solution structure of N-terminal elongated hSNF5 RPT1 domain  
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Deposited on : 2020-02-19

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

<https://www.wwpdb.org/validation/2017/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:

MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
ShiftChecker : 2.16  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.16

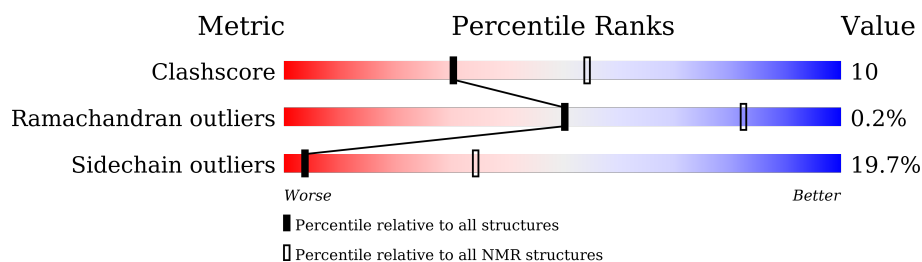
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 82%.

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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	89	

## 2 Ensemble composition and analysis

This entry contains 20 models. Model 3 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:184-A:246 (63)	0.36	3

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

NmrClust was unable to cluster the ensemble.

Error message: Inconsistent models

### 3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1377 atoms, of which 677 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	88	1377	440	677	113	142	5	0

There is a discrepancy between the modelled and reference sequences:

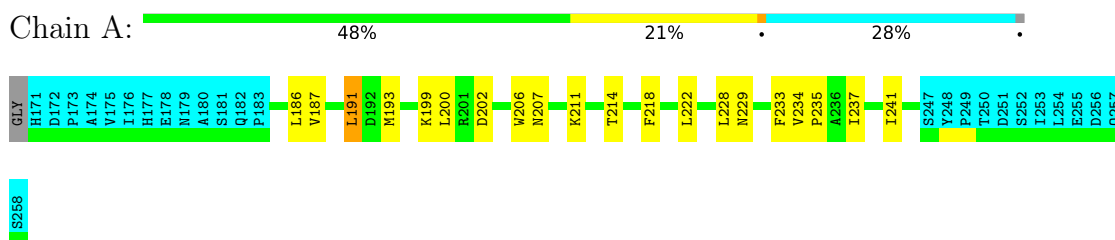
Chain	Residue	Modelled	Actual	Comment	Reference
A	170	GLY	-	expression tag	UNP A0A0G2JRV3

## 4 Residue-property plots

### 4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide 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: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family B member 1

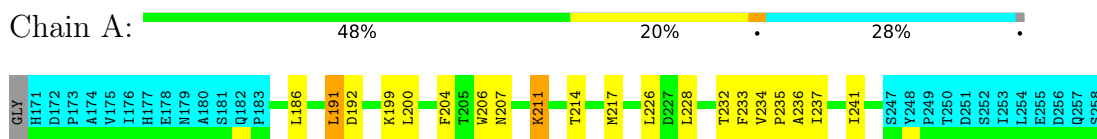


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

#### 4.2.1 Score per residue for model 1

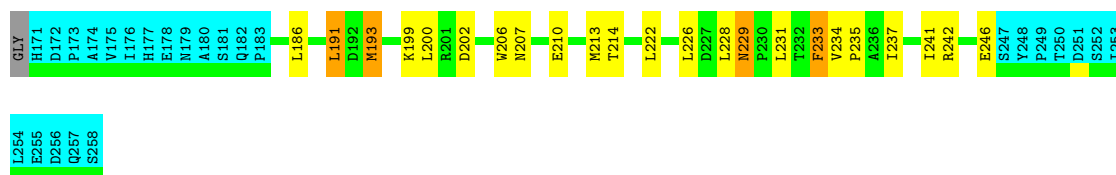
- Molecule 1: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family B member 1



#### 4.2.2 Score per residue for model 2

- Molecule 1: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family B member 1





#### 4.2.3 Score per residue for model 3 (medoid)

- Molecule 1: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family B member 1

Chain A: 49% 19% 28%



#### 4.2.4 Score per residue for model 4

- Molecule 1: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family B member 1

Chain A: 52% 17% 28%



#### 4.2.5 Score per residue for model 5

- Molecule 1: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family B member 1

Chain A: 51% 20% 28%



#### 4.2.6 Score per residue for model 6

- Molecule 1: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family B member 1

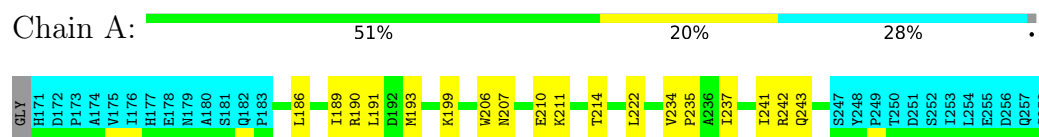
Chain A: 47% 20% 28%



Q257  
S256

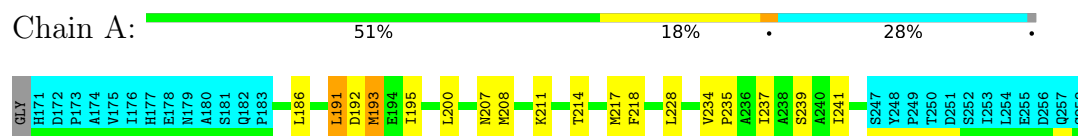
#### 4.2.7 Score per residue for model 7

- Molecule 1: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family B member 1



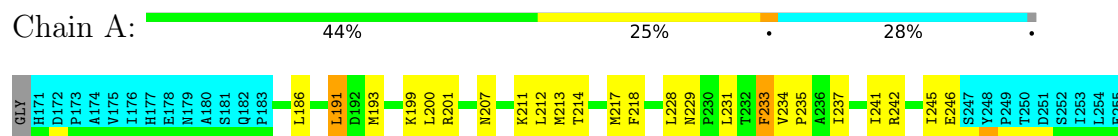
#### 4.2.8 Score per residue for model 8

- Molecule 1: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family B member 1



#### 4.2.9 Score per residue for model 9

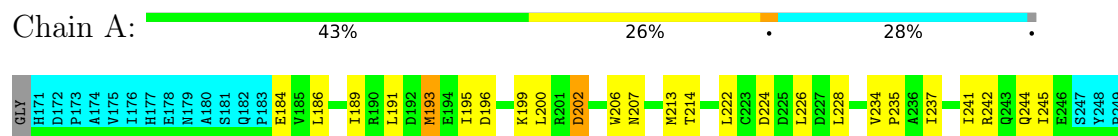
- Molecule 1: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family B member 1



Q257  
S256  
S258

#### 4.2.10 Score per residue for model 10

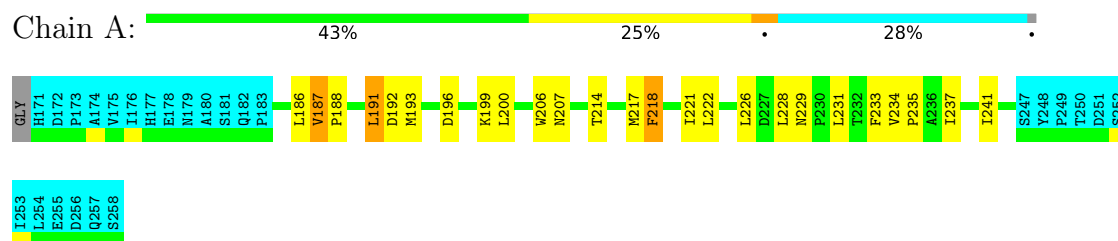
- Molecule 1: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family B member 1



T250  
D251  
S252  
L253  
L254  
L255  
D256  
Q257  
S258

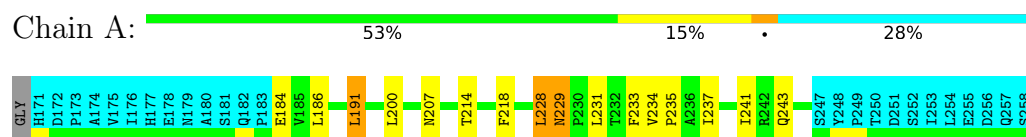
#### 4.2.11 Score per residue for model 11

- Molecule 1: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family B member 1



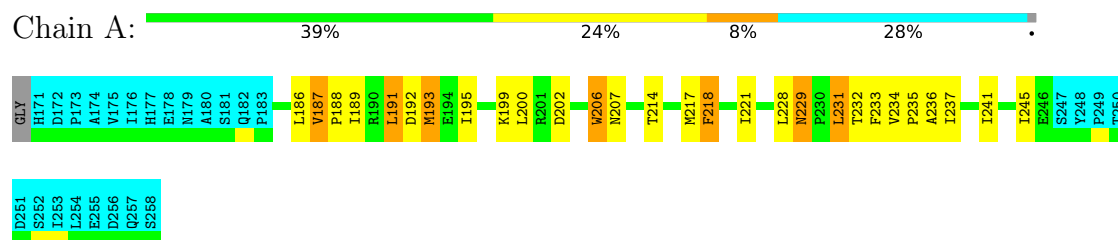
#### 4.2.12 Score per residue for model 12

- Molecule 1: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family B member 1



#### 4.2.13 Score per residue for model 13

- Molecule 1: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family B member 1

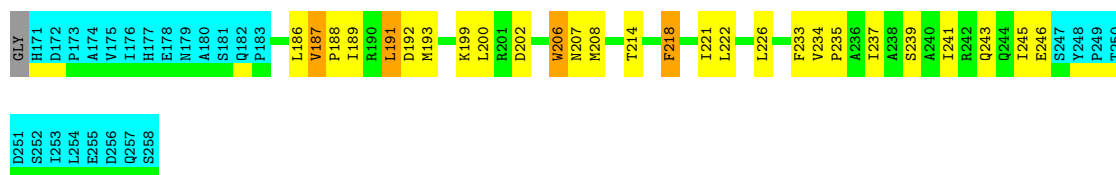


#### 4.2.14 Score per residue for model 14

- Molecule 1: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family B member 1



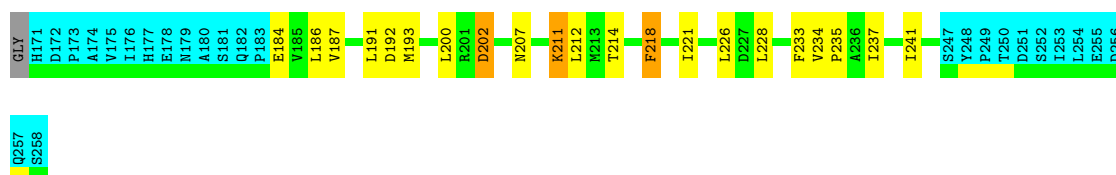




#### 4.2.15 Score per residue for model 15

- Molecule 1: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family B member 1

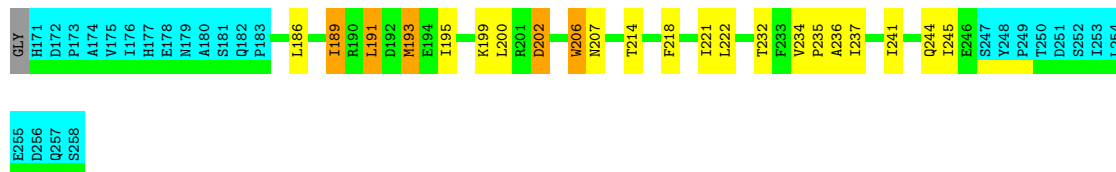
Chain A: 47% 20% 28%



#### 4.2.16 Score per residue for model 16

- Molecule 1: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family B member 1

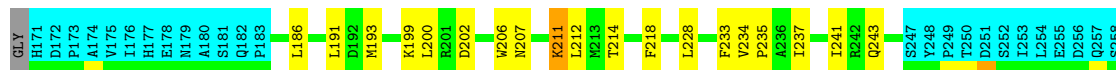
Chain A: 46% 19% 6% 28%



#### 4.2.17 Score per residue for model 17

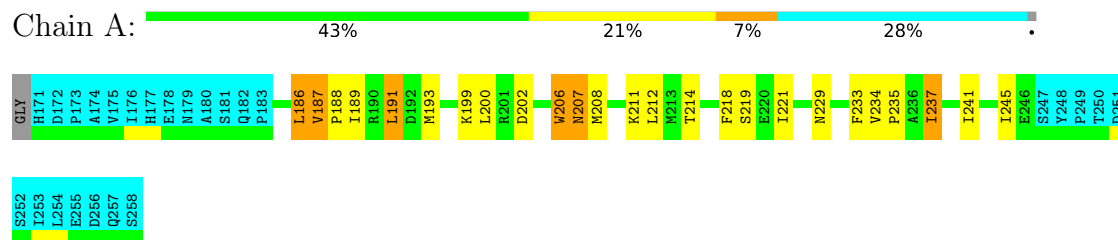
- Molecule 1: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family B member 1

Chain A: 49% 20% 28%



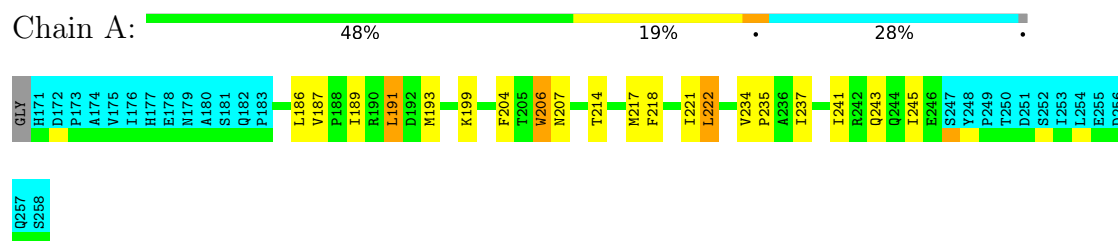
### 4.2.18 Score per residue for model 18

- Molecule 1: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family B member 1



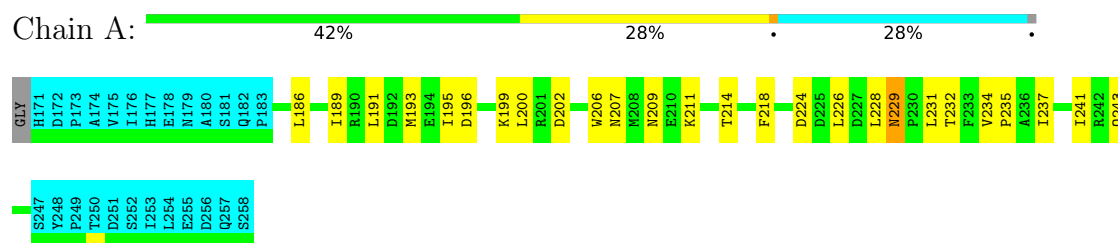
### 4.2.19 Score per residue for model 19

- Molecule 1: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family B member 1



### 4.2.20 Score per residue for model 20

- Molecule 1: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sub-family B member 1



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 1000 calculated structures, 20 were deposited, based on the following criterion: *20*.

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

Software name	Classification	Version
CYANA	structure calculation	
X-PLOR NIH	refinement	2.52

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)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	989
Number of shifts mapped to atoms	989
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	82%

## 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	507	508	508	10±4
All	All	10140	10160	10160	201

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 10.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:200:LEU:HD22	1:A:228:LEU:HD22	0.69	1.63	15	5
1:A:218:PHE:CD2	1:A:221:ILE:HD11	0.68	2.24	16	5
1:A:228:LEU:HD22	1:A:233:PHE:CE2	0.67	2.25	2	2
1:A:200:LEU:HD22	1:A:233:PHE:CE2	0.66	2.24	2	2
1:A:218:PHE:CD1	1:A:221:ILE:HD11	0.66	2.25	14	4
1:A:218:PHE:CE1	1:A:222:LEU:HD23	0.66	2.25	19	1
1:A:200:LEU:HD22	1:A:228:LEU:HD21	0.62	1.72	1	1
1:A:229:ASN:ND2	1:A:231:LEU:HD23	0.62	2.09	6	6
1:A:200:LEU:CD1	1:A:228:LEU:HD22	0.61	2.25	10	2
1:A:191:LEU:HD21	1:A:204:PHE:CE2	0.61	2.30	19	2
1:A:200:LEU:HD12	1:A:228:LEU:HD22	0.60	1.73	12	3
1:A:193:MET:HG2	1:A:200:LEU:HD23	0.60	1.72	9	4
1:A:226:LEU:HB2	1:A:228:LEU:HD23	0.59	1.73	4	3
1:A:206:TRP:CE2	1:A:245:ILE:HG22	0.59	2.33	19	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:186:LEU:HD22	1:A:207:ASN:OD1	0.59	1.98	4	2
1:A:193:MET:CG	1:A:200:LEU:HD23	0.59	2.28	16	4
1:A:191:LEU:HD23	1:A:202:ASP:OD2	0.58	1.99	16	3
1:A:191:LEU:HD12	1:A:202:ASP:OD2	0.58	1.99	10	1
1:A:237:ILE:O	1:A:241:ILE:HG23	0.57	1.99	11	18
1:A:195:ILE:HD13	1:A:232:THR:OG1	0.57	1.99	6	2
1:A:189:ILE:HD11	1:A:245:ILE:HG22	0.57	1.76	10	1
1:A:229:ASN:CG	1:A:231:LEU:HD23	0.56	2.20	2	3
1:A:211:LYS:C	1:A:212:LEU:HD12	0.56	2.21	9	1
1:A:195:ILE:HD13	1:A:232:THR:HB	0.55	1.77	13	1
1:A:222:LEU:HD22	1:A:233:PHE:CZ	0.55	2.37	6	1
1:A:228:LEU:HD13	1:A:233:PHE:CD2	0.54	2.37	9	2
1:A:241:ILE:O	1:A:245:ILE:HG23	0.54	2.03	10	1
1:A:200:LEU:HD22	1:A:228:LEU:CD2	0.54	2.33	15	2
1:A:191:LEU:HD11	1:A:241:ILE:HG22	0.54	1.78	14	6
1:A:200:LEU:HD13	1:A:226:LEU:HD13	0.53	1.78	1	1
1:A:211:LYS:O	1:A:212:LEU:HD22	0.53	2.04	17	1
1:A:233:PHE:CZ	1:A:237:ILE:HG21	0.52	2.39	4	4
1:A:228:LEU:HD13	1:A:233:PHE:CD1	0.52	2.39	17	1
1:A:229:ASN:HD21	1:A:231:LEU:HD12	0.51	1.66	9	2
1:A:191:LEU:HD22	1:A:237:ILE:HB	0.51	1.81	10	1
1:A:234:VAL:N	1:A:235:PRO:HD2	0.49	2.23	6	20
1:A:200:LEU:HD22	1:A:233:PHE:CE1	0.49	2.42	17	1
1:A:193:MET:SD	1:A:195:ILE:HD12	0.49	2.48	10	4
1:A:226:LEU:HD12	1:A:228:LEU:CD2	0.49	2.38	20	1
1:A:191:LEU:HD21	1:A:204:PHE:CD2	0.49	2.43	19	1
1:A:200:LEU:CD2	1:A:228:LEU:HD22	0.48	2.38	20	2
1:A:191:LEU:HB3	1:A:237:ILE:HG22	0.48	1.85	12	5
1:A:191:LEU:HD21	1:A:241:ILE:CG2	0.48	2.39	10	2
1:A:193:MET:SD	1:A:200:LEU:HD23	0.48	2.48	6	1
1:A:232:THR:O	1:A:236:ALA:HB2	0.48	2.08	1	3
1:A:228:LEU:HD22	1:A:233:PHE:CE1	0.48	2.43	17	1
1:A:226:LEU:HD12	1:A:228:LEU:HD23	0.47	1.86	2	3
1:A:200:LEU:HD21	1:A:233:PHE:CE1	0.46	2.46	11	5
1:A:191:LEU:CD1	1:A:241:ILE:HG22	0.46	2.40	19	4
1:A:228:LEU:HD13	1:A:233:PHE:HB2	0.46	1.88	1	2
1:A:187:VAL:HG12	1:A:188:PRO:HD2	0.46	1.87	14	4
1:A:191:LEU:HD21	1:A:241:ILE:HG22	0.46	1.87	17	1
1:A:200:LEU:HD13	1:A:226:LEU:HD22	0.46	1.87	15	1
1:A:218:PHE:CE1	1:A:221:ILE:HD11	0.46	2.44	15	1
1:A:228:LEU:HD22	1:A:233:PHE:CD2	0.46	2.45	9	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:222:LEU:O	1:A:226:LEU:HD12	0.46	2.10	14	2
1:A:218:PHE:CE1	1:A:222:LEU:HD22	0.45	2.47	16	1
1:A:191:LEU:HD22	1:A:191:LEU:N	0.45	2.27	11	7
1:A:191:LEU:HD23	1:A:202:ASP:CG	0.45	2.32	16	1
1:A:193:MET:HE1	1:A:237:ILE:HG23	0.44	1.89	14	1
1:A:233:PHE:CE1	1:A:237:ILE:HG21	0.44	2.48	15	2
1:A:211:LYS:C	1:A:212:LEU:HD22	0.43	2.33	18	1
1:A:222:LEU:HD21	1:A:226:LEU:HD11	0.43	1.90	11	1
1:A:206:TRP:CZ2	1:A:245:ILE:HG22	0.42	2.49	14	2
1:A:189:ILE:HD11	1:A:244:GLN:HB2	0.42	1.92	16	1
1:A:229:ASN:ND2	1:A:231:LEU:HD12	0.42	2.28	9	1
1:A:241:ILE:HD12	1:A:242:ARG:N	0.42	2.30	10	1
1:A:200:LEU:HD21	1:A:233:PHE:HE1	0.42	1.74	18	1
1:A:189:ILE:HG23	1:A:244:GLN:CD	0.42	2.34	10	1
1:A:200:LEU:HD11	1:A:226:LEU:CD1	0.42	2.45	4	1
1:A:228:LEU:HD12	1:A:228:LEU:O	0.42	2.15	1	1
1:A:218:PHE:HE1	1:A:222:LEU:HD22	0.41	1.76	16	1
1:A:200:LEU:HD13	1:A:226:LEU:CD1	0.41	2.46	1	1
1:A:231:LEU:C	1:A:231:LEU:HD12	0.40	2.36	12	2
1:A:234:VAL:CB	1:A:235:PRO:CD	0.40	3.00	13	3
1:A:189:ILE:HG21	1:A:241:ILE:HG22	0.40	1.93	10	1
1:A:234:VAL:N	1:A:235:PRO:CD	0.40	2.84	14	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	63/89 (71%)	59±1 (94±2%)	4±1 (6±2%)	0±0 (0±0%)	50	82
All	All	1260/1780 (71%)	1185 (94%)	73 (6%)	2 (0%)	50	82

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	211	LYS	2

### 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	58/81 (72%)	47±2 (80±4%)	11±2 (20±4%)	4 34
All	All	1160/1620 (72%)	931 (80%)	229 (20%)	4 34

All 37 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	207	ASN	20
1	A	214	THR	20
1	A	186	LEU	20
1	A	191	LEU	17
1	A	199	LYS	15
1	A	206	TRP	13
1	A	193	MET	12
1	A	218	PHE	9
1	A	202	ASP	9
1	A	243	GLN	7
1	A	217	MET	7
1	A	229	ASN	7
1	A	189	ILE	7
1	A	192	ASP	6
1	A	211	LYS	6
1	A	187	VAL	5
1	A	184	GLU	5
1	A	222	LEU	4
1	A	242	ARG	4
1	A	219	SER	4
1	A	196	ASP	4
1	A	246	GLU	4
1	A	213	MET	3
1	A	245	ILE	2
1	A	208	MET	2
1	A	224	ASP	2
1	A	210	GLU	2
1	A	233	PHE	2
1	A	239	SER	2

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Mol	Chain	Res	Type	Models (Total)
1	A	237	ILE	2
1	A	231	LEU	1
1	A	212	LEU	1
1	A	216	GLU	1
1	A	209	ASN	1
1	A	190	ARG	1
1	A	201	ARG	1
1	A	228	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 monosaccharides 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 82% for the well-defined parts and 80% for the entire structure.

### 7.1 Chemical shift list 1

File name: `working_cs.cif`

Chemical shift list name: `rpt1_all_manual.str`

#### 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	989
Number of shifts mapped to atoms	989
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
$^{13}\text{C}_\alpha$	87	$-0.18 \pm 0.14$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	84	$0.20 \pm 0.14$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
$^{15}\text{N}$	79	$-0.26 \pm 0.32$	None needed ( $< 0.5$ ppm)

#### 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 82%, i.e. 651 atoms were assigned a chemical shift out of a possible 796. 9 out of 11 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	244/307 (79%)	122/122 (100%)	63/126 (50%)	59/59 (100%)
Sidechain	394/450 (88%)	244/262 (93%)	144/171 (84%)	6/17 (35%)

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	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Aromatic	13/39 (33%)	12/21 (57%)	0/17 (0%)	1/1 (100%)
Overall	651/796 (82%)	378/405 (93%)	207/314 (66%)	66/77 (86%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 80%, i.e. 868 atoms were assigned a chemical shift out of a possible 1079. 11 out of 13 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	333/426 (78%)	167/169 (99%)	87/176 (49%)	79/81 (98%)
Sidechain	520/592 (88%)	325/346 (94%)	187/226 (83%)	8/20 (40%)
Aromatic	15/61 (25%)	14/33 (42%)	0/25 (0%)	1/3 (33%)
Overall	868/1079 (80%)	506/548 (92%)	274/427 (64%)	88/104 (85%)

#### 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:

