



# Full wwPDB NMR Structure Validation Report ⓘ

May 29, 2020 – 07:21 am BST

PDB ID : 5JXV  
Title : Solid-state MAS NMR structure of immunoglobulin beta 1 binding domain of protein G (GB1)  
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Deposited on : 2016-05-13

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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:

Cyrange : Kirchner and Güntert (2011)  
NmrClust : Kelley et al. (1996)  
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 : 2.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

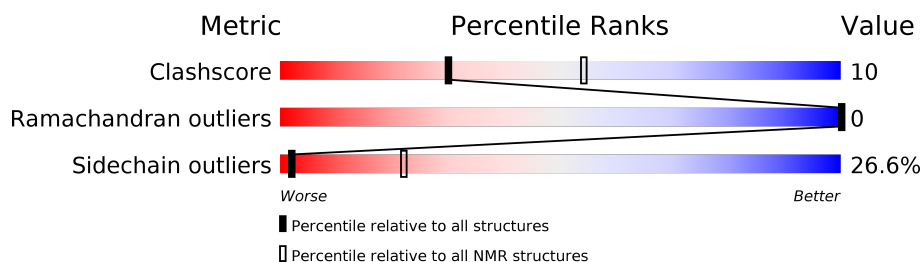
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLID-STATE 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	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	56	

## 2 Ensemble composition and analysis

This entry contains 20 models. Model 1 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:2-A:56 (55)	0.39	1

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 3 clusters and 3 single-model clusters were found.

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

### 3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 855 atoms, of which 418 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Immunoglobulin G-binding protein G.

Mol	Chain	Residues	Atoms							Trace
1	A	56	Total	C	H	N	O	S		0
			855	274	418	68	94	1		

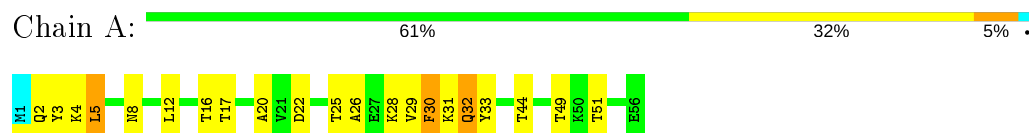
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	ASP	initiating methionine	UNP A0A0F5P4G8
A	2	GLN	THR	engineered mutation	UNP A0A0F5P4G8



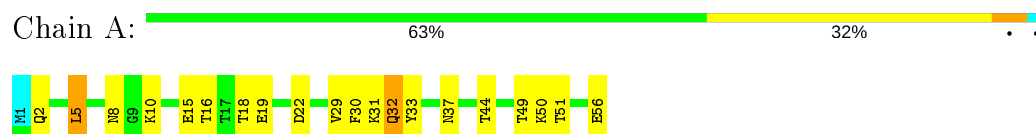
### 4.2.3 Score per residue for model 3

- Molecule 1: Immunoglobulin G-binding protein G



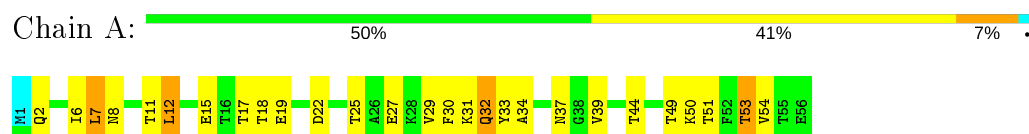
### 4.2.4 Score per residue for model 4

- Molecule 1: Immunoglobulin G-binding protein G



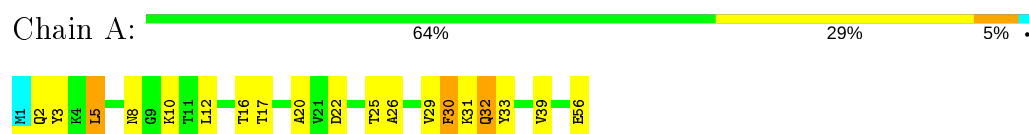
### 4.2.5 Score per residue for model 5

- Molecule 1: Immunoglobulin G-binding protein G



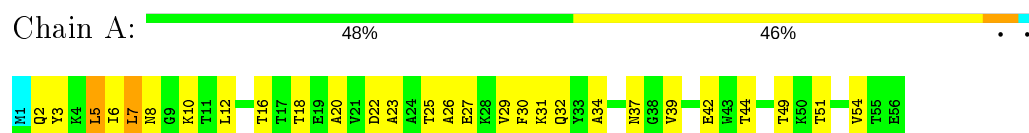
### 4.2.6 Score per residue for model 6

- Molecule 1: Immunoglobulin G-binding protein G



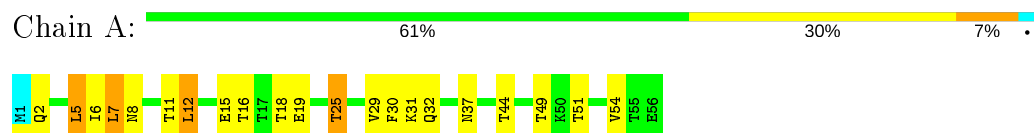
### 4.2.7 Score per residue for model 7

- Molecule 1: Immunoglobulin G-binding protein G



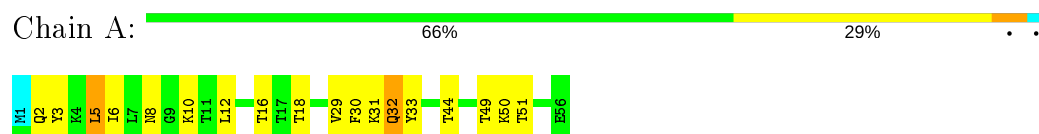
### 4.2.8 Score per residue for model 8

- Molecule 1: Immunoglobulin G-binding protein G



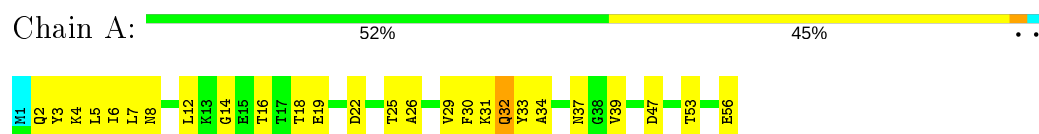
### 4.2.9 Score per residue for model 9

- Molecule 1: Immunoglobulin G-binding protein G



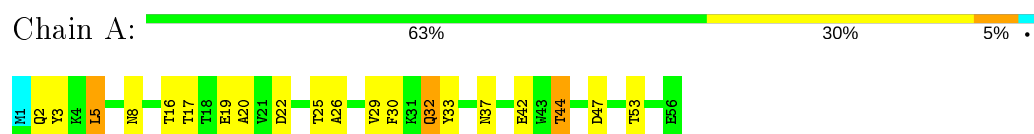
### 4.2.10 Score per residue for model 10

- Molecule 1: Immunoglobulin G-binding protein G



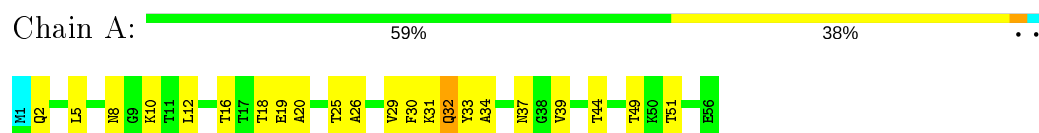
### 4.2.11 Score per residue for model 11

- Molecule 1: Immunoglobulin G-binding protein G



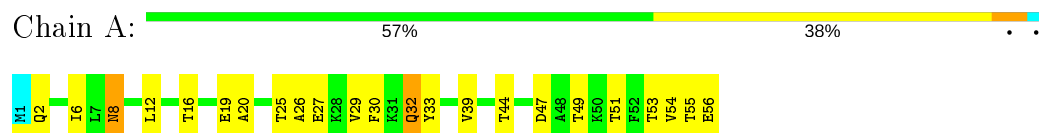
### 4.2.12 Score per residue for model 12

- Molecule 1: Immunoglobulin G-binding protein G



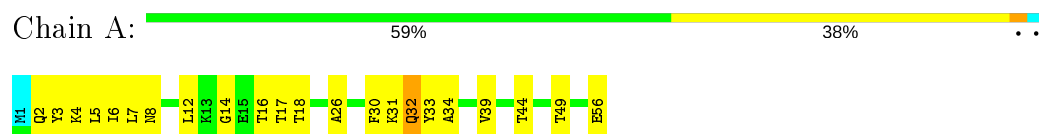
### 4.2.13 Score per residue for model 13

- Molecule 1: Immunoglobulin G-binding protein G



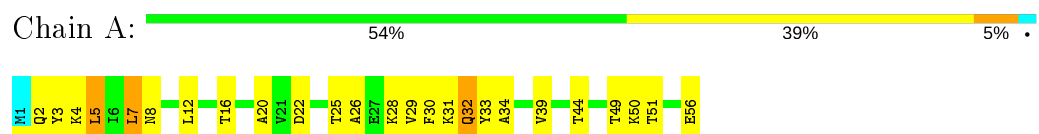
### 4.2.14 Score per residue for model 14

- Molecule 1: Immunoglobulin G-binding protein G



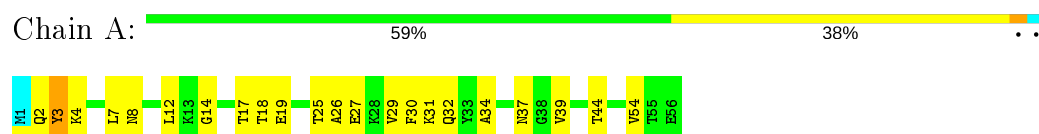
### 4.2.15 Score per residue for model 15

- Molecule 1: Immunoglobulin G-binding protein G



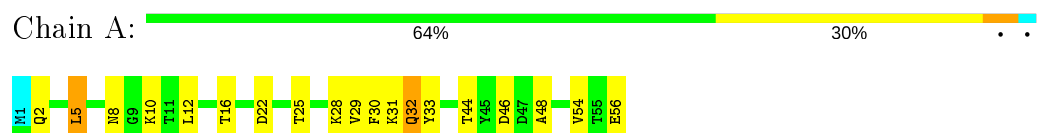
### 4.2.16 Score per residue for model 16

- Molecule 1: Immunoglobulin G-binding protein G



### 4.2.17 Score per residue for model 17

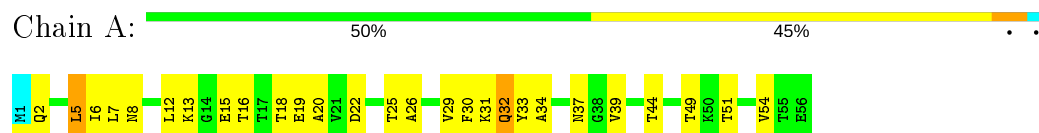
- Molecule 1: Immunoglobulin G-binding protein G





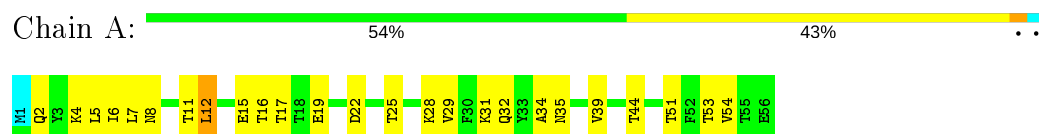
#### 4.2.18 Score per residue for model 18

- Molecule 1: Immunoglobulin G-binding protein G



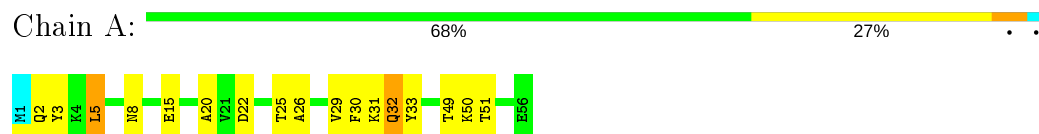
#### 4.2.19 Score per residue for model 19

- Molecule 1: Immunoglobulin G-binding protein G



#### 4.2.20 Score per residue for model 20

- Molecule 1: Immunoglobulin G-binding protein G



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics*.

Of the 80 calculated structures, 20 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
CANDID	structure calculation	2.6.0
TALOS	structure calculation	

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)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	649
Number of shifts mapped to atoms	649
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%

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

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	429	409	409	8±3
All	All	8580	8180	8180	167

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:20:ALA:HB3	1:A:26:ALA:HB2	0.87	1.46	18	11
1:A:25:THR:O	1:A:29:VAL:HG23	0.70	1.85	15	16
1:A:3:TYR:CE2	1:A:18:THR:HG22	0.69	2.23	16	1
1:A:26:ALA:HB1	1:A:30:PHE:CZ	0.67	2.25	16	1
1:A:7:LEU:HD23	1:A:54:VAL:CG1	0.66	2.21	7	4
1:A:5:LEU:HD13	1:A:30:PHE:CG	0.66	2.26	17	3
1:A:3:TYR:CE1	1:A:26:ALA:HB1	0.65	2.26	10	4
1:A:7:LEU:HD23	1:A:54:VAL:HG11	0.64	1.67	5	3
1:A:5:LEU:HD12	1:A:30:PHE:CD2	0.64	2.28	4	1
1:A:39:VAL:CG1	1:A:54:VAL:HG21	0.63	2.24	13	1
1:A:18:THR:HG22	1:A:30:PHE:CZ	0.61	2.30	1	3
1:A:11:THR:HG23	1:A:12:LEU:HG	0.59	1.74	5	3
1:A:3:TYR:CZ	1:A:26:ALA:HB1	0.59	2.32	14	2
1:A:7:LEU:HD12	1:A:14:GLY:C	0.59	2.18	14	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:3:TYR:CE2	1:A:26:ALA:HB1	0.59	2.33	15	3
1:A:18:THR:HG21	1:A:29:VAL:CG1	0.59	2.28	16	2
1:A:18:THR:HG22	1:A:30:PHE:CE2	0.58	2.33	7	4
1:A:3:TYR:CD1	1:A:26:ALA:HB1	0.58	2.34	11	1
1:A:5:LEU:HD13	1:A:6:ILE:N	0.57	2.15	14	5
1:A:34:ALA:HB1	1:A:39:VAL:HG11	0.57	1.75	14	5
1:A:5:LEU:HD12	1:A:7:LEU:CD1	0.56	2.31	15	1
1:A:6:ILE:HB	1:A:53:THR:HG23	0.56	1.76	10	3
1:A:5:LEU:HD23	1:A:30:PHE:CZ	0.55	2.36	14	2
1:A:8:ASN:HB3	1:A:55:THR:HG22	0.55	1.79	13	1
1:A:5:LEU:HD23	1:A:30:PHE:CG	0.54	2.38	2	1
1:A:20:ALA:CB	1:A:26:ALA:HB2	0.54	2.30	18	3
1:A:5:LEU:HD23	1:A:30:PHE:CE2	0.54	2.37	14	2
1:A:7:LEU:HD13	1:A:54:VAL:CG1	0.54	2.33	18	1
1:A:3:TYR:CE1	1:A:18:THR:HG23	0.53	2.39	9	2
1:A:49:THR:OG1	1:A:51:THR:HG22	0.52	2.05	15	13
1:A:5:LEU:HD23	1:A:30:PHE:CD2	0.52	2.39	2	1
1:A:30:PHE:C	1:A:30:PHE:CD1	0.52	2.83	18	1
1:A:4:LYS:CB	1:A:17:THR:HG22	0.52	2.35	3	1
1:A:29:VAL:HG12	1:A:33:TYR:CD2	0.51	2.41	4	2
1:A:34:ALA:O	1:A:39:VAL:HG12	0.50	2.07	16	9
1:A:30:PHE:CD1	1:A:30:PHE:C	0.50	2.84	12	1
1:A:30:PHE:C	1:A:30:PHE:CD2	0.50	2.84	20	3
1:A:39:VAL:HG13	1:A:56:GLU:OE2	0.49	2.07	6	1
1:A:4:LYS:HG3	1:A:17:THR:HG22	0.48	1.85	14	1
1:A:4:LYS:HA	1:A:17:THR:HG22	0.48	1.85	16	1
1:A:39:VAL:CG2	1:A:54:VAL:HG21	0.48	2.39	16	1
1:A:5:LEU:HD12	1:A:7:LEU:HD11	0.47	1.86	15	1
1:A:18:THR:CB	1:A:29:VAL:HG11	0.47	2.39	18	1
1:A:4:LYS:CG	1:A:17:THR:HG22	0.47	2.40	1	1
1:A:3:TYR:CD2	1:A:26:ALA:HB1	0.47	2.45	15	1
1:A:18:THR:HG22	1:A:30:PHE:CE1	0.47	2.43	8	2
1:A:39:VAL:HG23	1:A:56:GLU:CD	0.46	2.31	14	2
1:A:3:TYR:OH	1:A:23:ALA:HB1	0.45	2.11	7	1
1:A:18:THR:HG21	1:A:29:VAL:HG11	0.45	1.89	16	2
1:A:32:GLN:HE21	1:A:33:TYR:N	0.44	2.09	14	14
1:A:3:TYR:CE2	1:A:5:LEU:HD23	0.44	2.48	11	1
1:A:5:LEU:HD22	1:A:30:PHE:CZ	0.44	2.47	6	1
1:A:44:THR:HB	1:A:53:THR:HG22	0.43	1.90	1	2
1:A:6:ILE:HB	1:A:53:THR:HG22	0.43	1.90	13	1
1:A:5:LEU:HD21	1:A:30:PHE:HB2	0.43	1.90	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:5:LEU:HD12	1:A:7:LEU:CD2	0.43	2.43	18	1
1:A:7:LEU:HD13	1:A:54:VAL:HG13	0.42	1.90	18	1
1:A:46:ASP:OD2	1:A:48:ALA:HB3	0.42	2.15	17	1
1:A:5:LEU:HD22	1:A:30:PHE:CE2	0.41	2.50	3	1
1:A:18:THR:OG1	1:A:29:VAL:HG11	0.41	2.15	12	1
1:A:39:VAL:HG22	1:A:54:VAL:HG21	0.41	1.91	16	1
1:A:3:TYR:HE2	1:A:5:LEU:HD23	0.41	1.74	11	1
1:A:7:LEU:HD12	1:A:14:GLY:CA	0.40	2.46	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	54/56 (96%)	53±0 (98±0%)	1±0 (2±0%)	0±0 (0±0%)	100	100
All	All	1080/1120 (96%)	1060 (98%)	20 (2%)	0 (0%)	100	100

There are no Ramachandran outliers.

### 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	45/46 (98%)	33±2 (73±5%)	12±2 (27±5%)	2	22
All	All	900/920 (98%)	661 (73%)	239 (27%)	2	22

All 31 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	GLN	20
1	A	2	GLN	20
1	A	8	ASN	20
1	A	31	LYS	18
1	A	16	THR	17
1	A	44	THR	17
1	A	12	LEU	16
1	A	5	LEU	15
1	A	22	ASP	13
1	A	37	ASN	11
1	A	19	GLU	10
1	A	10	LYS	8
1	A	15	GLU	7
1	A	50	LYS	6
1	A	4	LYS	4
1	A	17	THR	4
1	A	27	GLU	4
1	A	7	LEU	4
1	A	28	LYS	4
1	A	56	GLU	4
1	A	42	GLU	3
1	A	47	ASP	3
1	A	30	PHE	3
1	A	49	THR	1
1	A	35	ASN	1
1	A	25	THR	1
1	A	13	LYS	1
1	A	54	VAL	1
1	A	53	THR	1
1	A	51	THR	1
1	A	3	TYR	1

### 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

The completeness of assignment taking into account all chemical shift lists is 86% for the well-defined parts and 87% for the entire structure.

### 7.1 Chemical shift list 1

File name: input\_cs.cif

Chemical shift list name: *D\_1000221368\_cs-upload\_P1.str.V3*

#### 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	649
Number of shifts mapped to atoms	649
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	4

#### 7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	56	$-0.22 \pm 0.19$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	51	$-0.01 \pm 0.22$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}'$	56	$0.08 \pm 0.17$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	56	$-0.19 \pm 0.56$	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 86%, i.e. 547 atoms were assigned a chemical shift out of a possible 633. 0 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	275/275 (100%)	110/110 (100%)	110/110 (100%)	55/55 (100%)
Sidechain	260/304 (86%)	158/172 (92%)	94/121 (78%)	8/11 (73%)

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	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Aromatic	12/54 (22%)	6/28 (21%)	5/25 (20%)	1/1 (100%)
Overall	547/633 (86%)	274/310 (88%)	209/256 (82%)	64/67 (96%)

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 87%, i.e. 559 atoms were assigned a chemical shift out of a possible 646. 0 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Backbone	279/280 (100%)	111/112 (99%)	112/112 (100%)	56/56 (100%)
Sidechain	268/312 (86%)	163/177 (92%)	97/124 (78%)	8/11 (73%)
Aromatic	12/54 (22%)	6/28 (21%)	5/25 (20%)	1/1 (100%)
Overall	559/646 (87%)	280/317 (88%)	214/261 (82%)	65/68 (96%)

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

#### 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	54	VAL	HB	-0.34	3.59 – 0.39	-7.3
1	A	5	LEU	HB3	-0.94	3.34 – -0.26	-6.9
1	A	31	LYS	HE3	1.64	3.86 – 1.96	-6.7
1	A	31	LYS	HE2	1.81	3.87 – 1.97	-5.9

#### 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:

