



# Full wwPDB NMR Structure Validation Report ⓘ

Apr 27, 2016 – 12:54 AM BST

PDB ID : 2LCV  
Title : Structure of the Cytidine Repressor DNA-Binding Domain; an alternate calculation  
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Deposited on : 2011-05-10

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

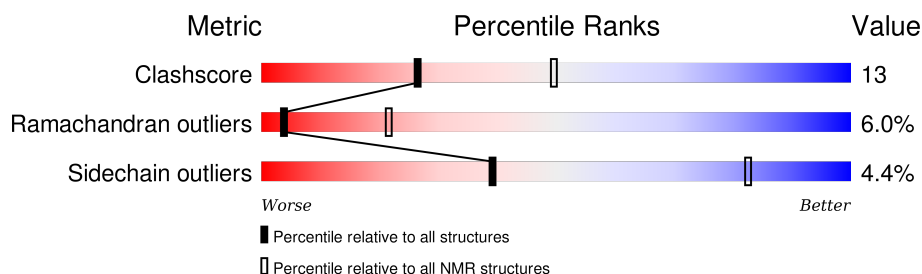
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 66%.

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	47	

## 2 Ensemble composition and analysis

This entry contains 11 models. Model 11 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *minimized average*.

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:10-A:53 (44)	0.38	11

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 2 single-model clusters were found.

Cluster number	Models
1	1, 2, 5, 11
2	3, 4, 9
3	6, 10
Single-model clusters	7; 8

### 3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 729 atoms, of which 378 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called HTH-type transcriptional repressor CytR.

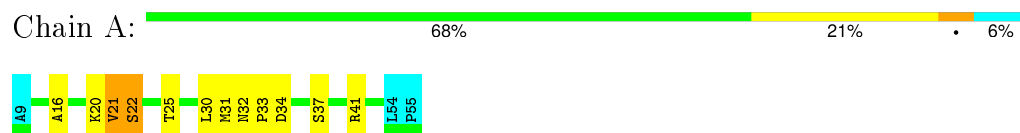
Mol	Chain	Residues	Atoms						Trace
1	A	47	Total	C	H	N	O	S	0
			729	216	378	67	66	2	

## 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: HTH-type transcriptional repressor CytR

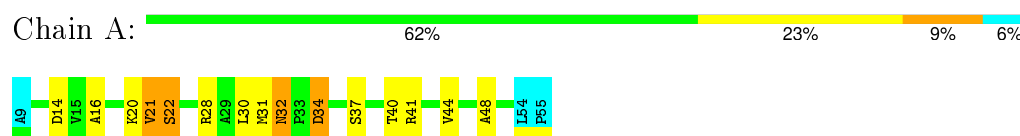


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section [4.1](#) above.

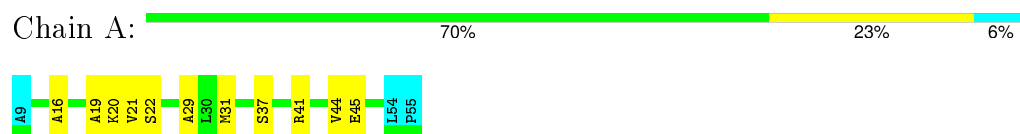
#### 4.2.1 Score per residue for model 1

- Molecule 1: HTH-type transcriptional repressor CytR



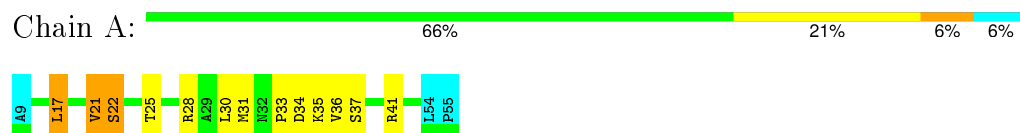
#### 4.2.2 Score per residue for model 2

- Molecule 1: HTH-type transcriptional repressor CytR



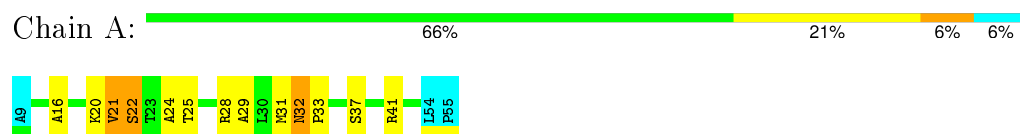
### 4.2.3 Score per residue for model 3

- Molecule 1: HTH-type transcriptional repressor CytR



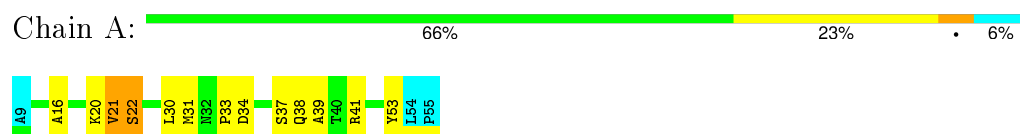
### 4.2.4 Score per residue for model 4

- Molecule 1: HTH-type transcriptional repressor CytR



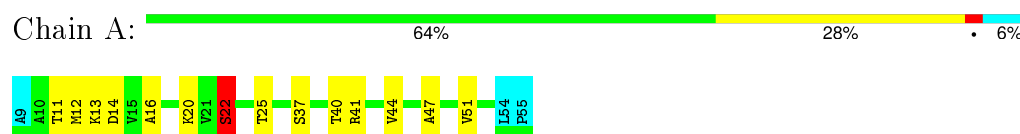
### 4.2.5 Score per residue for model 5

- Molecule 1: HTH-type transcriptional repressor CytR



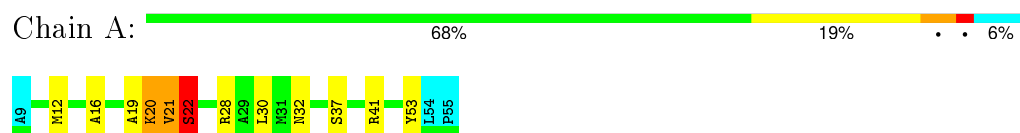
### 4.2.6 Score per residue for model 6

- Molecule 1: HTH-type transcriptional repressor CytR



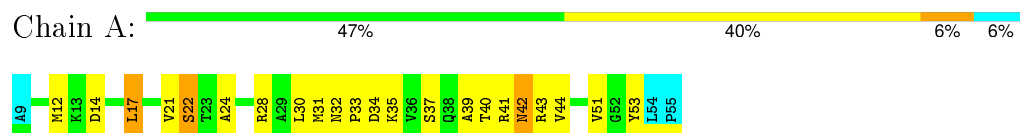
### 4.2.7 Score per residue for model 7

- Molecule 1: HTH-type transcriptional repressor CytR



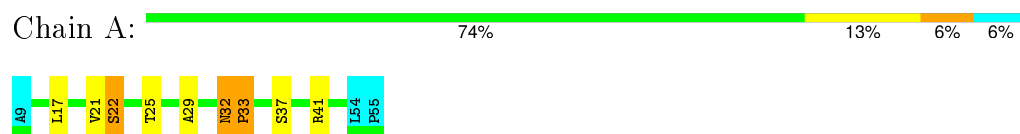
### 4.2.8 Score per residue for model 8

- Molecule 1: HTH-type transcriptional repressor CytR



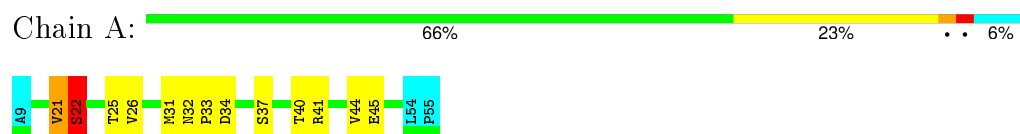
### 4.2.9 Score per residue for model 9

- Molecule 1: HTH-type transcriptional repressor CytR



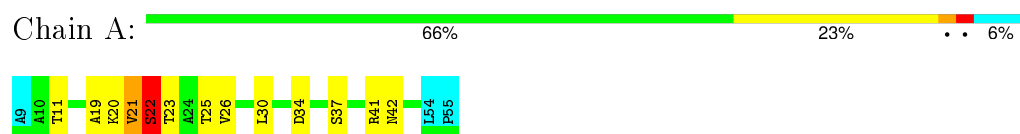
### 4.2.10 Score per residue for model 10

- Molecule 1: HTH-type transcriptional repressor CytR



### 4.2.11 Score per residue for model 11 (medoid)

- Molecule 1: HTH-type transcriptional repressor CytR



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *SIMULATED ANNEALING*.

Of the 100 calculated structures, 11 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
X-PLOR NIH	refinement	
VNMR	structure solution	
NMRPIPE	structure solution	
ANALYSIS - CCPN	structure solution	

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)	2lcv_cs.str
Number of chemical shift lists	1
Total number of shifts	595
Number of shifts mapped to atoms	446
Number of unparsed shifts	0
Number of shifts with mapping errors	149
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	66%

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	331	353	353	9±4
All	All	3641	3883	3883	99

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 13.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:25:THR:HG23	1:A:26:VAL:N	0.67	2.03	10	1
1:A:12:MET:SD	1:A:53:TYR:CD2	0.60	2.95	7	1
1:A:17:LEU:C	1:A:17:LEU:HD23	0.60	2.17	9	1
1:A:51:VAL:HG13	1:A:53:TYR:H	0.59	1.58	8	1
1:A:17:LEU:HD13	1:A:17:LEU:O	0.58	1.97	3	1
1:A:37:SER:O	1:A:41:ARG:N	0.57	2.38	2	11
1:A:25:THR:CG2	1:A:26:VAL:N	0.56	2.68	10	1
1:A:12:MET:SD	1:A:53:TYR:CE2	0.54	3.00	7	1
1:A:17:LEU:O	1:A:17:LEU:HD13	0.54	2.02	8	1
1:A:30:LEU:HD12	1:A:30:LEU:N	0.54	2.18	5	2
1:A:28:ARG:O	1:A:32:ASN:N	0.53	2.40	7	1
1:A:30:LEU:CD2	1:A:30:LEU:N	0.53	2.71	7	2
1:A:33:PRO:C	1:A:35:LYS:H	0.52	2.07	8	1
1:A:30:LEU:N	1:A:30:LEU:HD22	0.52	2.20	7	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:47:ALA:O	1:A:51:VAL:HG12	0.51	2.05	6	1
1:A:16:ALA:O	1:A:20:LYS:N	0.50	2.44	2	6
1:A:31:MET:N	1:A:31:MET:SD	0.50	2.84	5	1
1:A:11:THR:HG22	1:A:12:MET:N	0.49	2.22	6	1
1:A:12:MET:SD	1:A:53:TYR:O	0.49	2.70	8	1
1:A:25:THR:HG23	1:A:26:VAL:H	0.49	1.66	10	1
1:A:25:THR:O	1:A:29:ALA:N	0.49	2.45	9	2
1:A:28:ARG:O	1:A:31:MET:N	0.47	2.48	3	2
1:A:12:MET:CG	1:A:53:TYR:O	0.47	2.62	8	1
1:A:25:THR:HG22	1:A:28:ARG:HH21	0.47	1.69	3	1
1:A:42:ASN:ND2	1:A:43:ARG:N	0.47	2.63	8	1
1:A:44:VAL:HG13	1:A:45:GLU:N	0.47	2.25	2	1
1:A:44:VAL:HG23	1:A:45:GLU:N	0.46	2.26	10	1
1:A:30:LEU:CD1	1:A:30:LEU:N	0.46	2.78	5	1
1:A:25:THR:CG2	1:A:26:VAL:H	0.46	2.22	10	1
1:A:39:ALA:O	1:A:42:ASN:OD1	0.46	2.34	8	1
1:A:13:LYS:CG	1:A:14:ASP:N	0.46	2.79	6	1
1:A:19:ALA:O	1:A:20:LYS:C	0.45	2.54	2	2
1:A:21:VAL:O	1:A:22:SER:CB	0.45	2.64	10	6
1:A:32:ASN:HD22	1:A:32:ASN:C	0.45	2.14	1	1
1:A:25:THR:HG22	1:A:28:ARG:NH2	0.45	2.27	3	1
1:A:22:SER:O	1:A:25:THR:OG1	0.45	2.35	11	3
1:A:33:PRO:O	1:A:35:LYS:N	0.45	2.50	8	1
1:A:30:LEU:N	1:A:30:LEU:CD1	0.45	2.80	8	1
1:A:38:GLN:CG	1:A:39:ALA:N	0.44	2.80	5	1
1:A:24:ALA:HB1	1:A:28:ARG:NH1	0.44	2.26	4	1
1:A:32:ASN:O	1:A:33:PRO:O	0.44	2.35	9	1
1:A:33:PRO:O	1:A:34:ASP:OD1	0.44	2.36	10	2
1:A:40:THR:O	1:A:44:VAL:HG23	0.44	2.12	1	3
1:A:14:ASP:O	1:A:14:ASP:OD1	0.44	2.35	8	2
1:A:29:ALA:C	1:A:31:MET:N	0.44	2.71	2	1
1:A:34:ASP:C	1:A:36:VAL:H	0.44	2.16	3	1
1:A:31:MET:O	1:A:32:ASN:O	0.43	2.36	4	1
1:A:44:VAL:O	1:A:48:ALA:N	0.43	2.51	1	1
1:A:31:MET:O	1:A:32:ASN:C	0.43	2.57	4	1
1:A:28:ARG:C	1:A:30:LEU:N	0.43	2.72	3	1
1:A:24:ALA:HB1	1:A:28:ARG:HH12	0.43	1.73	8	1
1:A:31:MET:SD	1:A:31:MET:C	0.43	2.97	10	1
1:A:29:ALA:C	1:A:31:MET:H	0.42	2.18	2	1
1:A:21:VAL:HG12	1:A:22:SER:OG	0.42	2.14	7	1
1:A:11:THR:CG2	1:A:12:MET:N	0.42	2.83	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:33:PRO:C	1:A:35:LYS:N	0.42	2.73	8	1
1:A:34:ASP:O	1:A:34:ASP:OD1	0.42	2.37	1	1
1:A:12:MET:CE	1:A:53:TYR:CZ	0.42	3.03	7	1
1:A:42:ASN:C	1:A:42:ASN:ND2	0.41	2.74	8	1
1:A:21:VAL:C	1:A:22:SER:OG	0.41	2.58	7	1
1:A:31:MET:O	1:A:32:ASN:OD1	0.41	2.39	8	1
1:A:40:THR:O	1:A:44:VAL:HG22	0.41	2.16	10	1
1:A:28:ARG:O	1:A:30:LEU:N	0.41	2.54	3	1
1:A:19:ALA:O	1:A:21:VAL:N	0.41	2.53	7	1
1:A:17:LEU:O	1:A:17:LEU:HD23	0.40	2.17	9	1
1:A:31:MET:O	1:A:32:ASN:CG	0.40	2.60	8	1
1:A:22:SER:O	1:A:26:VAL:HG12	0.40	2.15	10	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	44/47 (94%)	39±2 (88±4%)	3±1 (6±3%)	3±1 (6±2%)	4	21
All	All	484/517 (94%)	426 (88%)	29 (6%)	29 (6%)	4	21

All 7 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	22	SER	11
1	A	21	VAL	10
1	A	33	PRO	3
1	A	34	ASP	2
1	A	32	ASN	1
1	A	20	LYS	1
1	A	35	LYS	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	35/37 (95%)	33±2 (96±5%)	2±2 (4±5%)	39	82
All	All	385/407 (95%)	368 (96%)	17 (4%)	39	82

All 9 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	22	SER	5
1	A	32	ASN	3
1	A	42	ASN	2
1	A	17	LEU	2
1	A	11	THR	1
1	A	30	LEU	1
1	A	23	THR	1
1	A	34	ASP	1
1	A	26	VAL	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 66% for the well-defined parts and 67% for the entire structure.

### 7.1 Chemical shift list 1

File name: 2lcv\_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	595
Number of shifts mapped to atoms	446
Number of unparsed shifts	0
Number of shifts with mapping errors	149
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- Residue not found in structure. All 149 occurrences are reported below.

Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	67	SER	N	122.1271	-1.0	1
A	62	VAL	HB	2.1196	-1.0	1
A	60	ARG	CB	30.8592	-1.0	1
A	62	VAL	HG13	0.932	-1.0	1
A	64	ARG	H	8.3473	-1.0	1
A	4	LYS	CB	33.3463	-1.0	1
A	56	GLN	H	8.5063	-1.0	1
A	65	ASN	H	8.4899	-1.0	1
A	7	GLU	HB2	2.0076	-1.0	1
A	8	THR	HG23	1.2598	-1.0	1
A	5	LYS	CA	56.4255	-1.0	1
A	6	GLN	H	8.4244	-1.0	1
A	58	MET	H	8.4291	-1.0	1
A	62	VAL	HG12	0.932	-1.0	1

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Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	61	ASN	H	8.5094	-1.0	1
A	60	ARG	H	8.1936	-1.0	1
A	3	ALA	CB	19.6097	-1.0	1
A	3	ALA	N	126.1333	-1.0	1
A	58	MET	HE3	0.9553	-1.0	1
A	4	LYS	H	8.2816	-1.0	1
A	8	THR	HA	4.4082	-1.0	1
A	7	GLU	HG3	2.327	-1.0	1
A	3	ALA	HB1	1.4162	-1.0	1
A	65	ASN	CB	39.0579	-1.0	1
A	65	ASN	N	120.1232	-1.0	1
A	58	MET	HA	4.5254	-1.0	1
A	62	VAL	CB	32.8521	-1.0	1
A	6	GLN	CB	29.7147	-1.0	1
A	7	GLU	HB3	2.1444	-1.0	1
A	58	MET	CB	33.2079	-1.0	1
A	59	GLY	CA	45.5484	-1.0	1
A	8	THR	HG22	1.2598	-1.0	1
A	67	SER	H	7.9331	-1.0	1
A	5	LYS	N	123.2627	-1.0	1
A	6	GLN	HG3	2.423	-1.0	1
A	5	LYS	CB	33.2387	-1.0	1
A	3	ALA	H	8.3759	-1.0	1
A	63	LYS	H	8.3311	-1.0	1
A	63	LYS	HG2	1.4693	-1.0	1
A	62	VAL	CA	62.3503	-1.0	1
A	65	ASN	CA	53.4787	-1.0	1
A	61	ASN	HB3	2.8851	-1.0	1
A	56	GLN	HG3	2.4437	-1.0	1
A	57	PRO	HB2	1.9608	-1.0	1
A	3	ALA	HA	4.378	-1.0	1
A	62	VAL	N	120.0893	-1.0	1
A	8	THR	N	114.864	-1.0	1
A	60	ARG	HB3	1.8819	-1.0	1
A	8	THR	CG2	21.7074	-1.0	1
A	60	ARG	HD2	3.2585	-1.0	1
A	7	GLU	HG2	2.327	-1.0	1
A	57	PRO	CD	50.5656	-1.0	1
A	3	ALA	HB2	1.4162	-1.0	1
A	58	MET	HB2	2.0995	-1.0	1
A	61	ASN	CB	38.973	-1.0	1

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Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	60	ARG	N	120.2487	-1.0	1
A	58	MET	N	120.2457	-1.0	1
A	58	MET	CA	55.7476	-1.0	1
A	4	LYS	N	121.32	-1.0	1
A	58	MET	HG2	2.6377	-1.0	1
A	67	SER	HA	4.3055	-1.0	1
A	5	LYS	H	8.3559	-1.0	1
A	60	ARG	HG3	1.6865	-1.0	1
A	57	PRO	CB	31.962	-1.0	1
A	58	MET	CG	32.0467	-1.0	1
A	57	PRO	HD2	3.6999	-1.0	1
A	57	PRO	HD3	3.7281	-1.0	1
A	59	GLY	HA3	4.0029	-1.0	1
A	61	ASN	N	119.5324	-1.0	1
A	6	GLN	HG2	2.423	-1.0	1
A	59	GLY	N	109.8508	-1.0	1
A	56	GLN	CA	53.6697	-1.0	1
A	63	LYS	HD2	1.7508	-1.0	1
A	63	LYS	HG3	1.5101	-1.0	1
A	66	GLU	CA	56.6788	-1.0	1
A	61	ASN	HB2	2.8013	-1.0	1
A	59	GLY	HA2	4.0029	-1.0	1
A	56	GLN	HG2	2.4437	-1.0	1
A	57	PRO	HG2	2.0595	-1.0	1
A	56	GLN	HE21	6.8594	-1.0	1
A	7	GLU	CG	36.3866	-1.0	1
A	62	VAL	CG2	21.5386	-1.0	1
A	64	ARG	HA	4.3759	-1.0	1
A	66	GLU	HA	4.4157	-1.0	1
A	61	ASN	HA	4.7591	-1.0	1
A	67	SER	HB3	3.8842	-1.0	1
A	63	LYS	N	125.1308	-1.0	1
A	3	ALA	HB3	1.4162	-1.0	1
A	62	VAL	HA	4.1399	-1.0	1
A	62	VAL	H	7.9053	-1.0	1
A	63	LYS	CA	56.3005	-1.0	1
A	66	GLU	H	8.3461	-1.0	1
A	4	LYS	CA	56.2606	-1.0	1
A	58	MET	HG3	2.6966	-1.0	1
A	56	GLN	CB	29.1753	-1.0	1
A	60	ARG	HG2	1.6575	-1.0	1

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Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	58	MET	HE1	0.9553	-1.0	1
A	57	PRO	CA	63.4954	-1.0	1
A	8	THR	CB	70.2225	-1.0	1
A	63	LYS	HD3	1.7508	-1.0	1
A	56	GLN	N	121.523	-1.0	1
A	59	GLY	H	8.3868	-1.0	1
A	57	PRO	HG3	2.0829	-1.0	1
A	3	ALA	CA	52.346	-1.0	1
A	66	GLU	N	121.679	-1.0	1
A	8	THR	HB	4.2943	-1.0	1
A	63	LYS	HB2	1.7884	-1.0	1
A	8	THR	H	8.09	-1.0	1
A	62	VAL	HG11	0.932	-1.0	1
A	6	GLN	HB2	2.0634	-1.0	1
A	60	ARG	HA	4.3597	-1.0	1
A	6	GLN	CG	33.7464	-1.0	1
A	6	GLN	CA	56.0064	-1.0	1
A	8	THR	CA	61.3682	-1.0	1
A	60	ARG	CA	56.3717	-1.0	1
A	63	LYS	CB	32.9944	-1.0	1
A	64	ARG	CA	56.1167	-1.0	1
A	8	THR	HG21	1.2598	-1.0	1
A	56	GLN	CG	33.2954	-1.0	1
A	62	VAL	CG1	21.5386	-1.0	1
A	63	LYS	HA	4.3714	-1.0	1
A	56	GLN	HA	4.6181	-1.0	1
A	60	ARG	HD3	3.2585	-1.0	1
A	7	GLU	HA	4.4033	-1.0	1
A	7	GLU	CA	56.8527	-1.0	1
A	58	MET	HB3	2.1668	-1.0	1
A	57	PRO	HB3	2.3392	-1.0	1
A	2	LYS	CB	33.2612	-1.0	1
A	67	SER	CB	65.0112	-1.0	1
A	6	GLN	HA	4.3464	-1.0	1
A	7	GLU	H	8.5469	-1.0	1
A	66	GLU	CB	30.5799	-1.0	1
A	6	GLN	HB3	2.1344	-1.0	1
A	61	ASN	CA	53.4535	-1.0	1
A	6	GLN	N	122.0811	-1.0	1
A	57	PRO	CG	28.0885	-1.0	1
A	64	ARG	N	122.7721	-1.0	1

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Chain	Res	Type	Atom	Shift Data		
				Value	Uncertainty	Ambiguity
A	56	GLN	HB2	1.9717	-1.0	1
A	64	ARG	CB	31.0832	-1.0	1
A	56	GLN	HB3	2.1396	-1.0	1
A	60	ARG	HB2	1.7982	-1.0	1
A	7	GLU	N	122.5524	-1.0	1
A	67	SER	HB2	3.8635	-1.0	1
A	7	GLU	CB	30.4222	-1.0	1
A	67	SER	CA	60.1037	-1.0	1
A	58	MET	HE2	0.9553	-1.0	1
A	2	LYS	CA	56.4808	-1.0	1
A	57	PRO	HA	4.468	-1.0	1
A	63	LYS	HB3	1.8695	-1.0	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
$^{13}\text{C}_\alpha$	66	$-0.56 \pm 0.20$	Should be applied
$^{13}\text{C}_\beta$	64	$0.08 \pm 0.17$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}'$	0	—	—
$^{15}\text{N}$	62	$0.77 \pm 0.48$	None needed (imprecise)

### 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 66%, i.e. 353 atoms were assigned a chemical shift out of a possible 532. 7 out of 8 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	173/218 (79%)	86/87 (99%)	44/88 (50%)	43/43 (100%)
Sidechain	178/306 (58%)	114/178 (64%)	64/108 (59%)	0/20 (0%)
Aromatic	2/8 (25%)	2/4 (50%)	0/4 (0%)	0/0 (—%)
Overall	353/532 (66%)	202/269 (75%)	108/200 (54%)	43/63 (68%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 67%, i.e. 381 atoms were assigned a chemical shift out of a possible 565. 8 out of 9 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	183/231 (79%)	91/92 (99%)	47/94 (50%)	45/45 (100%)
Sidechain	196/326 (60%)	124/190 (65%)	72/116 (62%)	0/20 (0%)
Aromatic	2/8 (25%)	2/4 (50%)	0/4 (0%)	0/0 (—%)
Overall	381/565 (67%)	217/286 (76%)	119/214 (56%)	45/65 (69%)

#### 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:

