



Full wwPDB NMR Structure Validation Report ⓘ

Mar 7, 2026 – 12:50 AM UTC

PDB ID : 5ZOR / pdb_00005zor
BMRB ID : 36179
Title : Solution structure of centrin4 from Trypanosoma brucei
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Deposited on : 2018-04-15

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with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

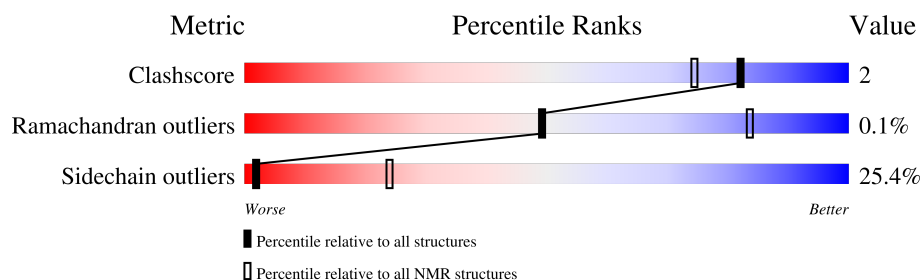
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 75%.

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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 ≥ 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	149	

2 Ensemble composition and analysis

This entry contains 20 models. Model 16 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:1-A:149 (149)	1.02	16

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 6 clusters and 3 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 2275 atoms, of which 1121 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Centrin, putative.

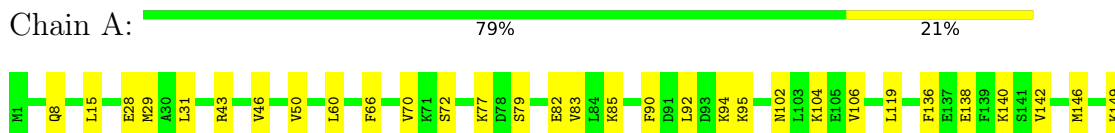
Mol	Chain	Residues	Atoms						Trace
1	A	149	Total	C	H	N	O	S	0
			2275	715	1121	192	237	10	

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: Centrin, putative

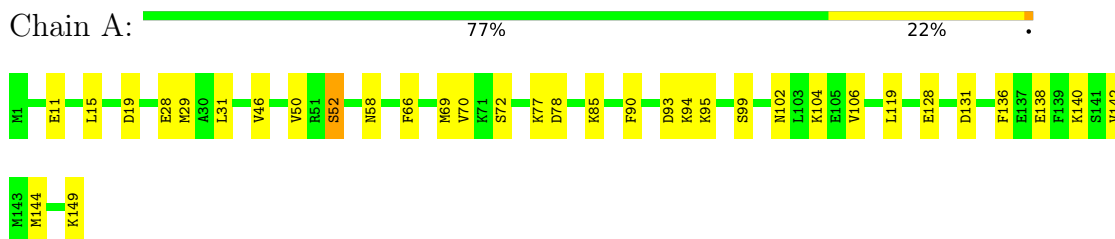


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

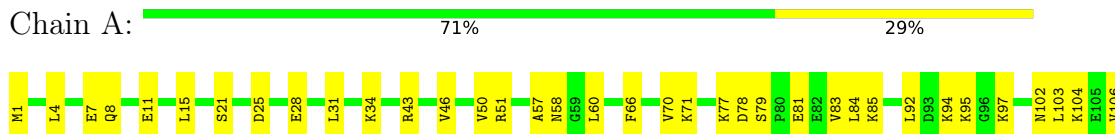
4.2.1 Score per residue for model 1

- Molecule 1: Centrin, putative



4.2.2 Score per residue for model 2

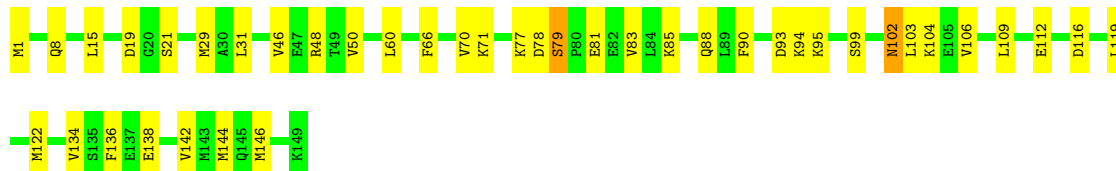
- Molecule 1: Centrin, putative





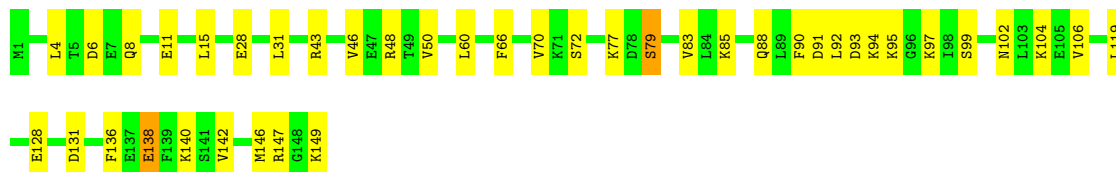
4.2.3 Score per residue for model 3

- Molecule 1: Centrin, putative



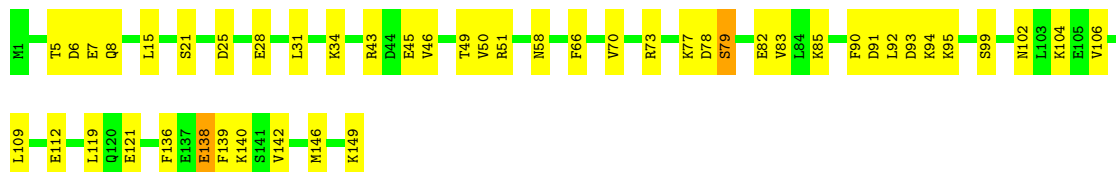
4.2.4 Score per residue for model 4

- Molecule 1: Centrin, putative



4.2.5 Score per residue for model 5

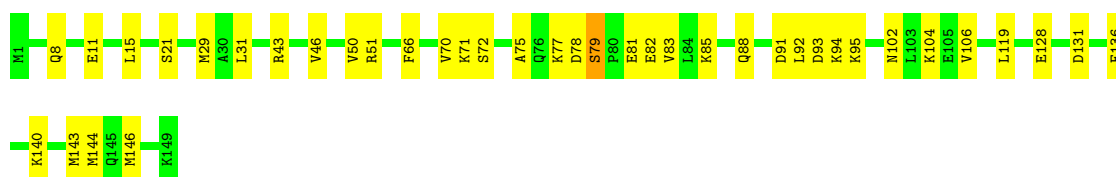
- Molecule 1: Centrin, putative



4.2.6 Score per residue for model 6

- Molecule 1: Centrin, putative

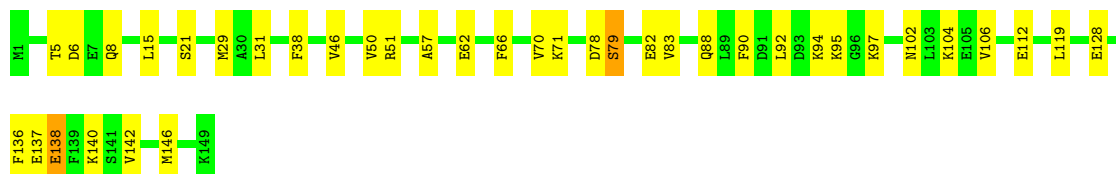




4.2.7 Score per residue for model 7

- Molecule 1: Centrin, putative

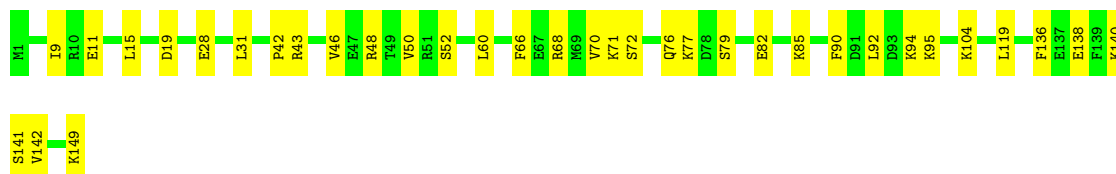
Chain A: 74% 24%



4.2.8 Score per residue for model 8

- Molecule 1: Centrin, putative

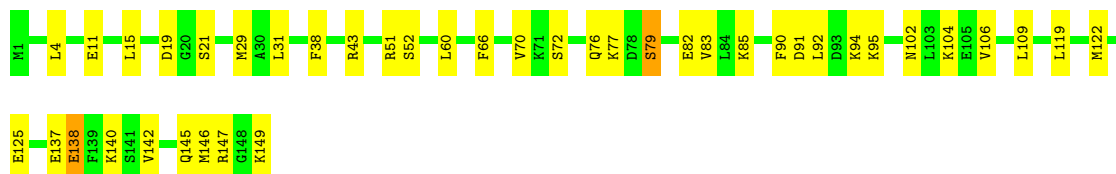
Chain A: 77% 23%



4.2.9 Score per residue for model 9

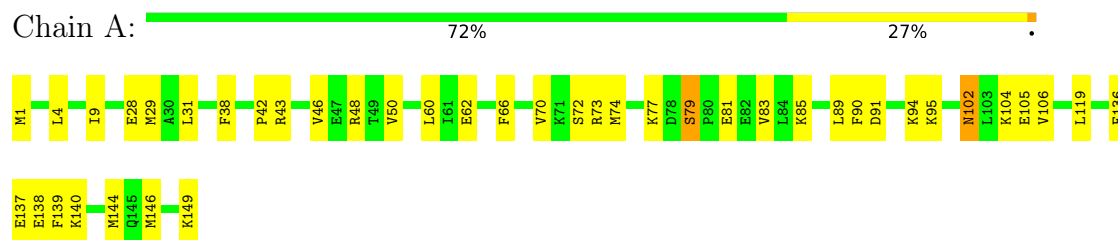
- Molecule 1: Centrin, putative

Chain A: 72% 26%



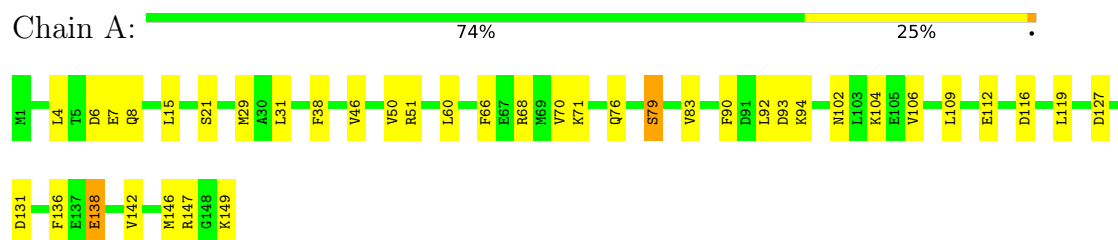
4.2.10 Score per residue for model 10

- Molecule 1: Centrin, putative



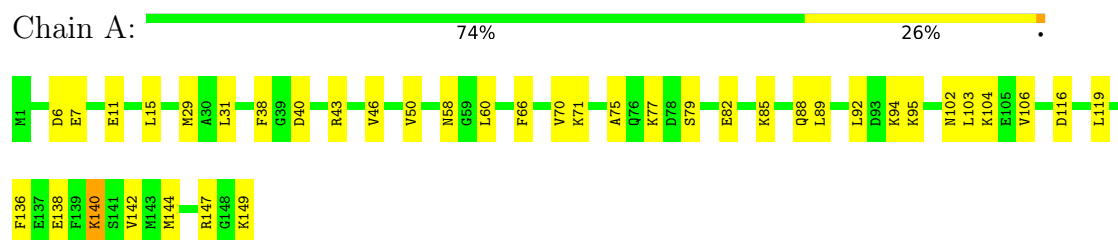
4.2.11 Score per residue for model 11

- Molecule 1: Centrin, putative



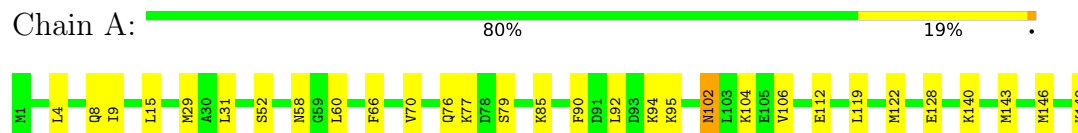
4.2.12 Score per residue for model 12

- Molecule 1: Centrin, putative



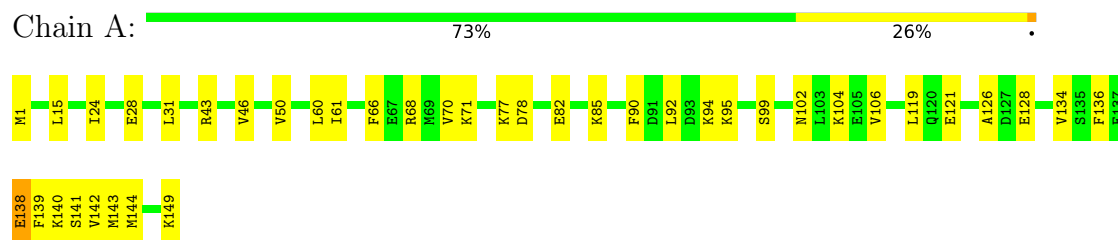
4.2.13 Score per residue for model 13

- Molecule 1: Centrin, putative



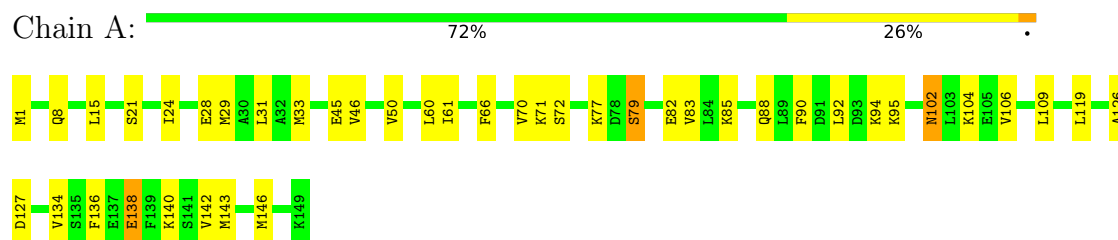
4.2.14 Score per residue for model 14

- Molecule 1: Centrin, putative



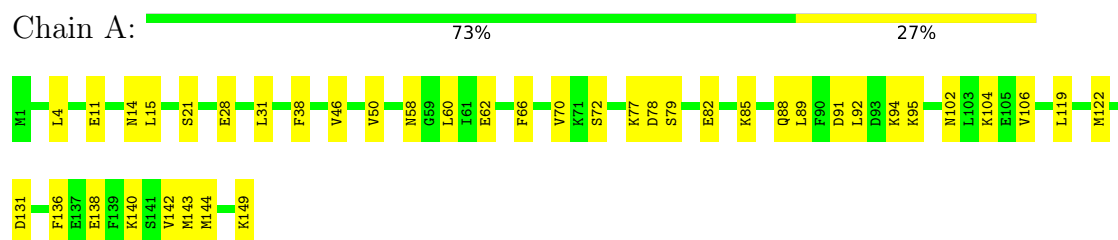
4.2.15 Score per residue for model 15

- Molecule 1: Centrin, putative



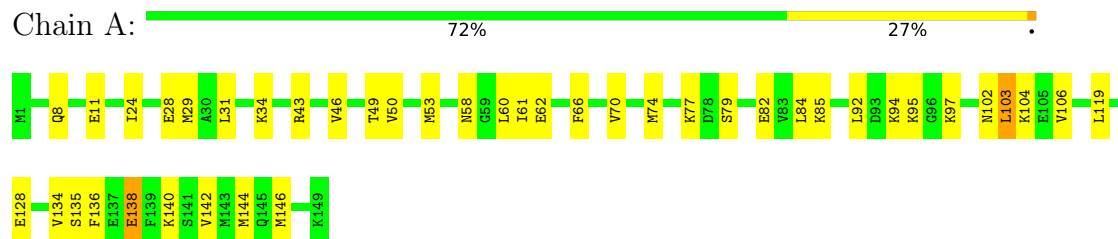
4.2.16 Score per residue for model 16 (medoid)

- Molecule 1: Centrin, putative



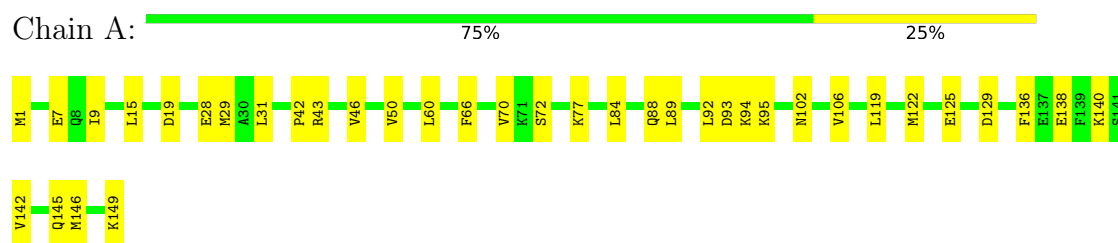
4.2.17 Score per residue for model 17

- Molecule 1: Centrin, putative



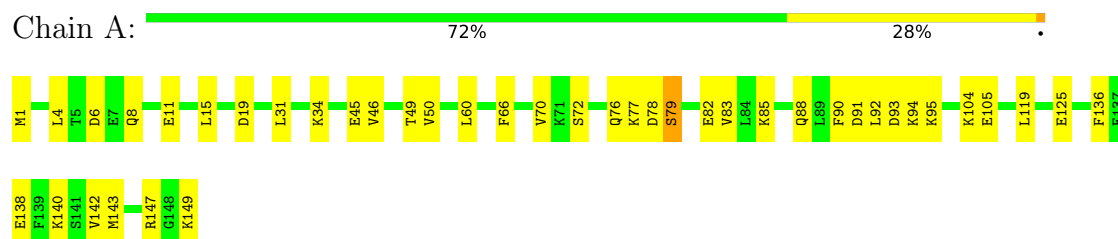
4.2.18 Score per residue for model 18

- Molecule 1: Centrin, putative



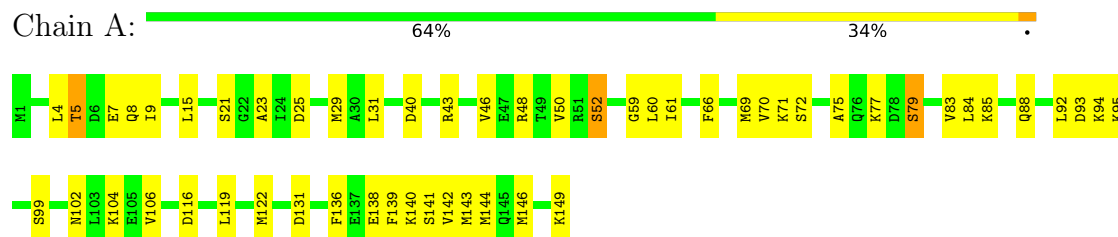
4.2.19 Score per residue for model 19

- Molecule 1: Centrin, putative



4.2.20 Score per residue for model 20

- Molecule 1: Centrin, putative



5 Refinement protocol and experimental data overview

The models were refined using the following method: *distance geometry*.

Of the 500 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	refinement	
CYANA	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)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1473
Number of shifts mapped to atoms	1473
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	75%

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	1154	1121	1123	6±2
All	All	23080	22420	22460	114

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 3.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:52:SER:C	1:A:69:MET:HE3	0.61	2.20	20	2
1:A:42:PRO:O	1:A:46:VAL:HG23	0.61	1.95	10	3
1:A:66:PHE:O	1:A:70:VAL:HG23	0.60	1.95	13	20
1:A:102:ASN:O	1:A:106:VAL:HG23	0.59	1.97	3	18
1:A:138:GLU:O	1:A:142:VAL:HG23	0.58	1.98	1	16
1:A:46:VAL:O	1:A:50:VAL:HG23	0.57	2.00	7	18
1:A:79:SER:O	1:A:83:VAL:HG23	0.57	2.00	3	12
1:A:103:LEU:HD22	1:A:134:VAL:HG11	0.55	1.77	17	3
1:A:9:ILE:HG22	1:A:70:VAL:HG11	0.51	1.83	10	3
1:A:59:GLY:C	1:A:60:LEU:HD12	0.48	2.32	20	1
1:A:126:ALA:CB	1:A:134:VAL:HG13	0.47	2.40	14	2
1:A:23:ALA:HB1	1:A:61:ILE:H	0.47	1.69	20	1
1:A:140:LYS:NZ	1:A:144:MET:HE2	0.46	2.25	12	1
1:A:29:MET:HG2	1:A:33:MET:HE2	0.45	1.88	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:9:ILE:HG22	1:A:70:VAL:CG1	0.45	2.42	8	2
1:A:24:ILE:O	1:A:61:ILE:HD12	0.44	2.13	15	3
1:A:9:ILE:HG21	1:A:70:VAL:HG11	0.43	1.89	20	1
1:A:45:GLU:O	1:A:49:THR:HG23	0.41	2.15	19	2
1:A:71:LYS:O	1:A:75:ALA:HB2	0.41	2.15	6	3
1:A:49:THR:HG22	1:A:53:MET:HE2	0.41	1.90	17	1
1:A:4:LEU:HD12	1:A:5:THR:N	0.40	2.31	20	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	147/149 (99%)	144±0 (98±0%)	3±0 (2±0%)	0±0 (0±0%)	49	83
All	All	2940/2980 (99%)	2882 (98%)	56 (2%)	2 (0%)	49	83

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	57	ALA	2

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	121/121 (100%)	90±3 (75±3%)	31±3 (25±3%)	2	24
All	All	2420/2420 (100%)	1806 (75%)	614 (25%)	2	24

All 77 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	31	LEU	20
1	A	94	LYS	20
1	A	119	LEU	20
1	A	95	LYS	19
1	A	104	LYS	19
1	A	15	LEU	18
1	A	77	LYS	18
1	A	140	LYS	18
1	A	85	LYS	17
1	A	136	PHE	17
1	A	92	LEU	17
1	A	79	SER	16
1	A	149	LYS	15
1	A	60	LEU	15
1	A	90	PHE	13
1	A	146	MET	13
1	A	29	MET	12
1	A	8	GLN	12
1	A	43	ARG	12
1	A	28	GLU	11
1	A	72	SER	11
1	A	82	GLU	11
1	A	11	GLU	10
1	A	21	SER	10
1	A	88	GLN	10
1	A	78	ASP	9
1	A	93	ASP	9
1	A	138	GLU	9
1	A	144	MET	8
1	A	4	LEU	8
1	A	58	ASN	7
1	A	128	GLU	7
1	A	1	MET	7
1	A	71	LYS	7
1	A	122	MET	7
1	A	91	ASP	7
1	A	143	MET	7
1	A	19	ASP	6
1	A	99	SER	6
1	A	131	ASP	6
1	A	7	GLU	6
1	A	51	ARG	6
1	A	112	GLU	6

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Mol	Chain	Res	Type	Models (Total)
1	A	6	ASP	6
1	A	38	PHE	6
1	A	52	SER	5
1	A	116	ASP	5
1	A	48	ARG	5
1	A	109	LEU	5
1	A	147	ARG	5
1	A	76	GLN	5
1	A	34	LYS	4
1	A	81	GLU	4
1	A	84	LEU	4
1	A	97	LYS	4
1	A	102	ASN	4
1	A	139	PHE	4
1	A	62	GLU	4
1	A	89	LEU	4
1	A	25	ASP	3
1	A	5	THR	3
1	A	137	GLU	3
1	A	68	ARG	3
1	A	141	SER	3
1	A	125	GLU	3
1	A	73	ARG	2
1	A	121	GLU	2
1	A	145	GLN	2
1	A	74	MET	2
1	A	105	GLU	2
1	A	127	ASP	2
1	A	40	ASP	2
1	A	103	LEU	2
1	A	45	GLU	1
1	A	14	ASN	1
1	A	135	SER	1
1	A	129	ASP	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 oligosaccharides 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 75% for the well-defined parts and 75% for the entire structure.

7.1 Chemical shift list 1

File name: `working_cs.cif`

Chemical shift list name: `shifts.txt`

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	1473
Number of shifts mapped to atoms	1473
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

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	149	-0.17 ± 0.08	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	136	0.17 ± 0.05	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	145	0.33 ± 0.15	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 75%, i.e. 1473 atoms were assigned a chemical shift out of a possible 1971. 0 out of 21 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	601/752 (80%)	307/308 (100%)	149/298 (50%)	145/146 (99%)
Sidechain	872/1120 (78%)	653/720 (91%)	219/357 (61%)	0/43 (0%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	0/99 (0%)	0/49 (0%)	0/50 (0%)	0/0 (—%)
Overall	1473/1971 (75%)	960/1077 (89%)	368/705 (52%)	145/189 (77%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 75%, i.e. 1473 atoms were assigned a chemical shift out of a possible 1971. 0 out of 21 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	601/752 (80%)	307/308 (100%)	149/298 (50%)	145/146 (99%)
Sidechain	872/1120 (78%)	653/720 (91%)	219/357 (61%)	0/43 (0%)
Aromatic	0/99 (0%)	0/49 (0%)	0/50 (0%)	0/0 (—%)
Overall	1473/1971 (75%)	960/1077 (89%)	368/705 (52%)	145/189 (77%)

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. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:

