



Full wwPDB NMR Structure Validation Report ⓘ

Mar 5, 2026 – 01:41 PM UTC

PDB ID : 7MC3 / pdb_00007mc3
BMRB ID : 50842
Title : Solution structure of Miz-1 zinc finger 12
Authors : Boisvert, O.; Lavigne, P.
Deposited on : 2021-04-01

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at 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.

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
BMRB Restraints Analysis : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

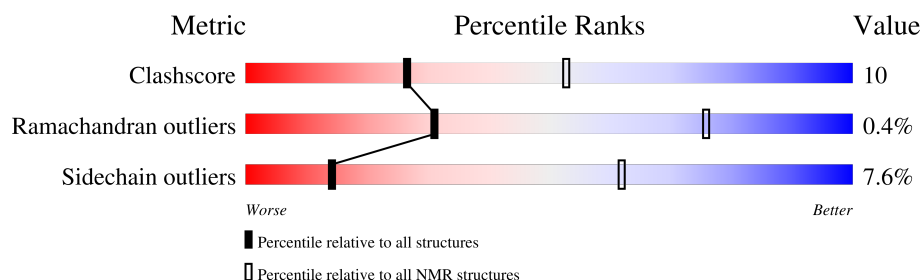
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 78%.

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	85	

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:60-A:85 (26)	0.32	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 4 clusters and 1 single-model cluster was found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 486 atoms, of which 239 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Isoform 2 of Zinc finger and BTB domain-containing protein 17.

Mol	Chain	Residues	Atoms						Trace
1	A	31	Total	C	H	N	O	S	0
			485	149	239	50	45	2	

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q13105
A	32	TYR	HIS	engineered mutation	UNP Q13105

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

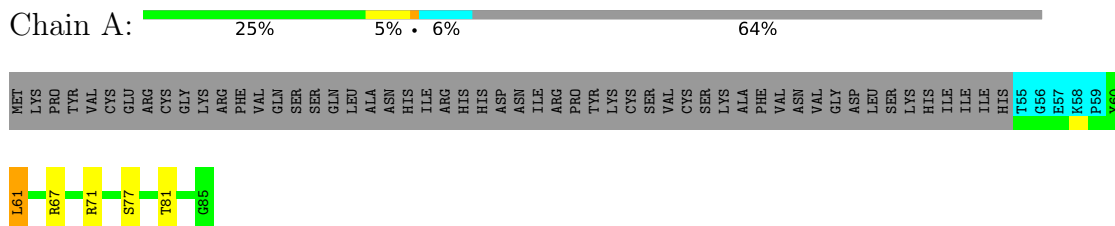
Mol	Chain	Residues	Atoms	
2	A	1	Total	Zn
			1	1

4 Residue-property plots [i](#)

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: Isoform 2 of Zinc finger and BTB domain-containing protein 17

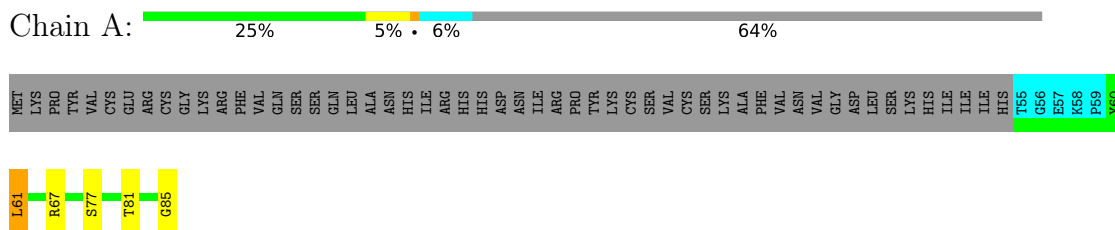


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1 (medoid)

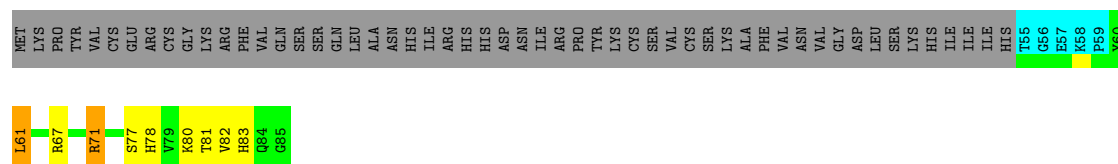
- Molecule 1: Isoform 2 of Zinc finger and BTB domain-containing protein 17



4.2.2 Score per residue for model 2

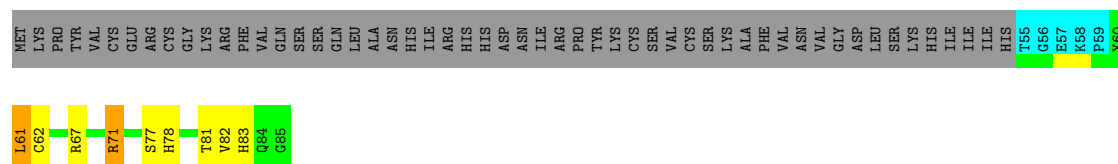
- Molecule 1: Isoform 2 of Zinc finger and BTB domain-containing protein 17





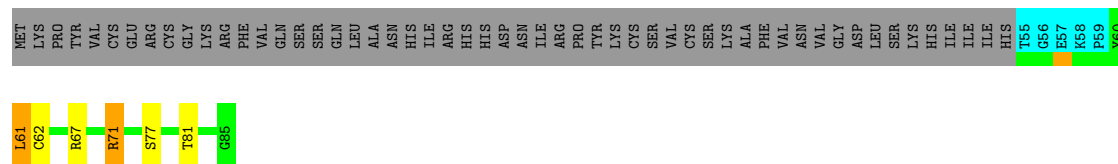
4.2.3 Score per residue for model 3

- Molecule 1: Isoform 2 of Zinc finger and BTB domain-containing protein 17



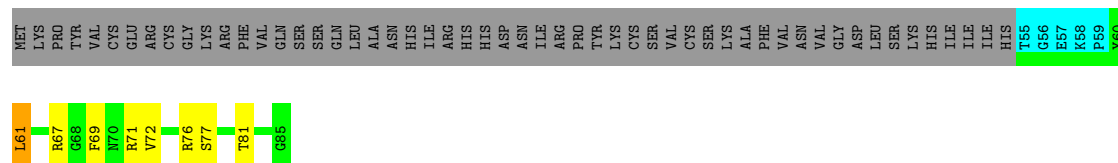
4.2.4 Score per residue for model 4

- Molecule 1: Isoform 2 of Zinc finger and BTB domain-containing protein 17



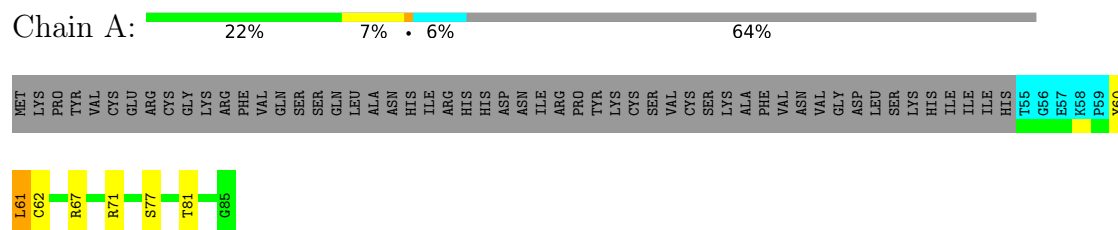
4.2.5 Score per residue for model 5

- Molecule 1: Isoform 2 of Zinc finger and BTB domain-containing protein 17



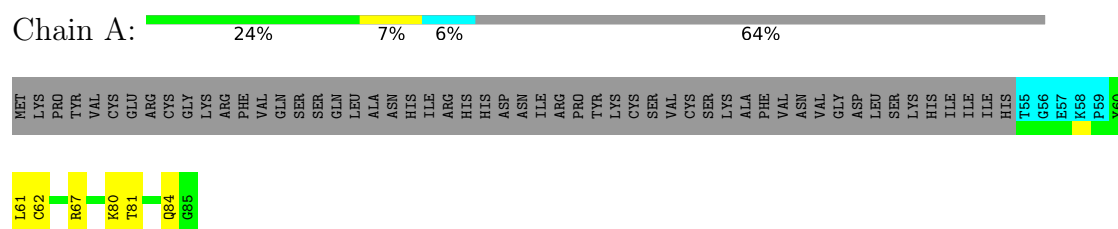
4.2.6 Score per residue for model 6

- Molecule 1: Isoform 2 of Zinc finger and BTB domain-containing protein 17



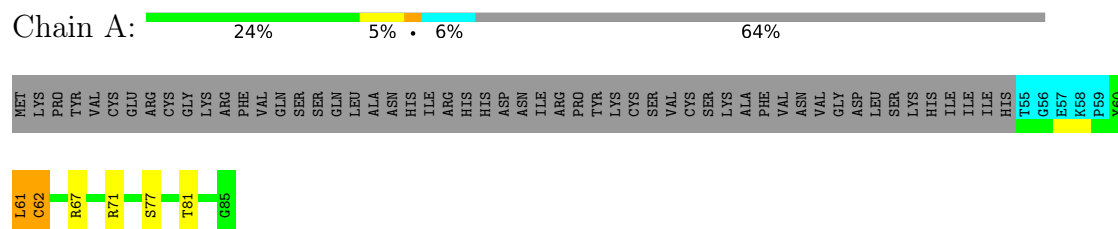
4.2.7 Score per residue for model 7

- Molecule 1: Isoform 2 of Zinc finger and BTB domain-containing protein 17



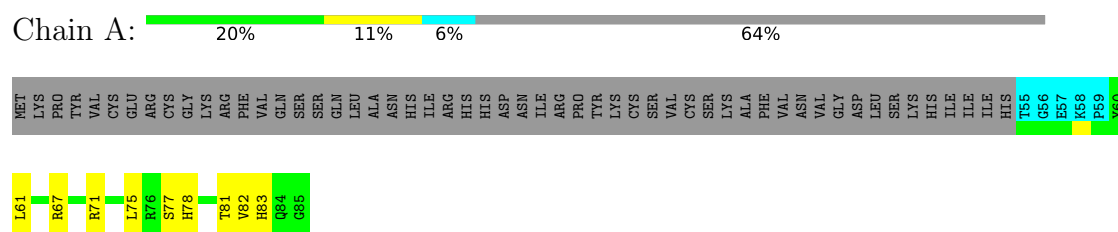
4.2.8 Score per residue for model 8

- Molecule 1: Isoform 2 of Zinc finger and BTB domain-containing protein 17



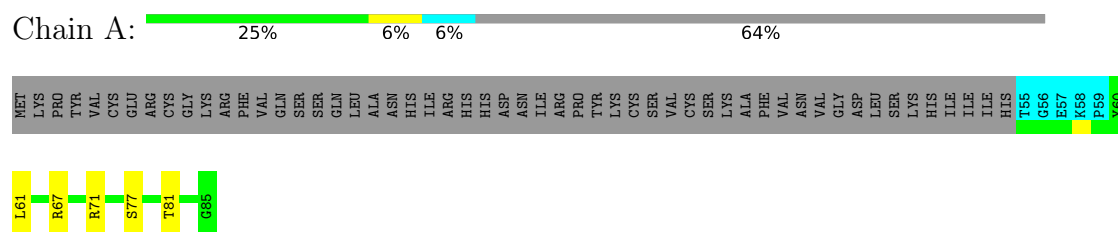
4.2.9 Score per residue for model 9

- Molecule 1: Isoform 2 of Zinc finger and BTB domain-containing protein 17



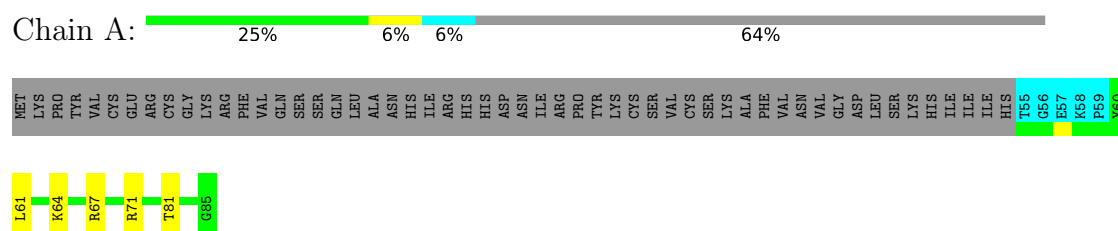
4.2.10 Score per residue for model 10

- Molecule 1: Isoform 2 of Zinc finger and BTB domain-containing protein 17



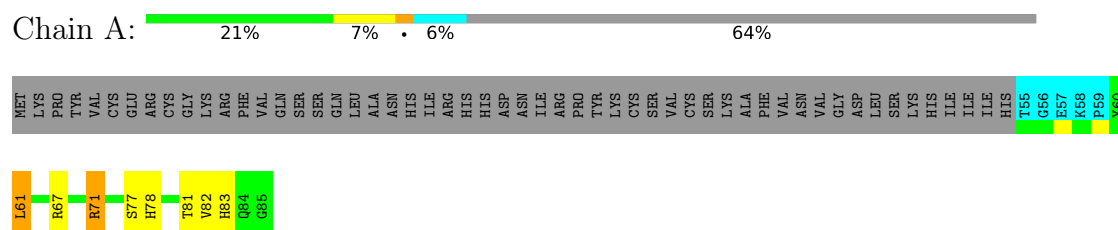
4.2.11 Score per residue for model 11

- Molecule 1: Isoform 2 of Zinc finger and BTB domain-containing protein 17



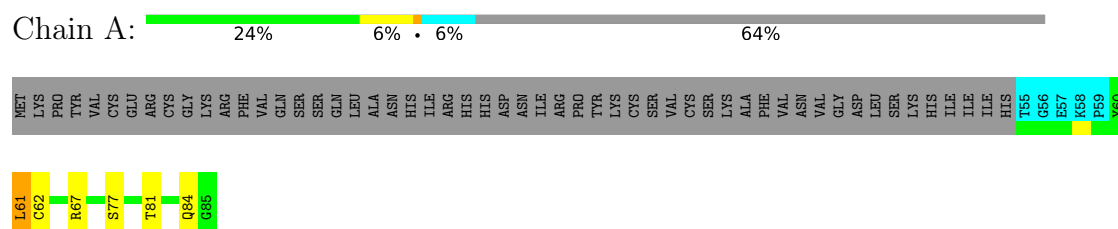
4.2.12 Score per residue for model 12

- Molecule 1: Isoform 2 of Zinc finger and BTB domain-containing protein 17



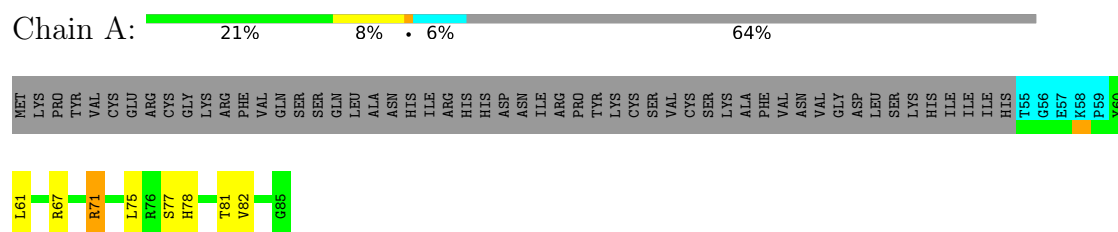
4.2.13 Score per residue for model 13

- Molecule 1: Isoform 2 of Zinc finger and BTB domain-containing protein 17



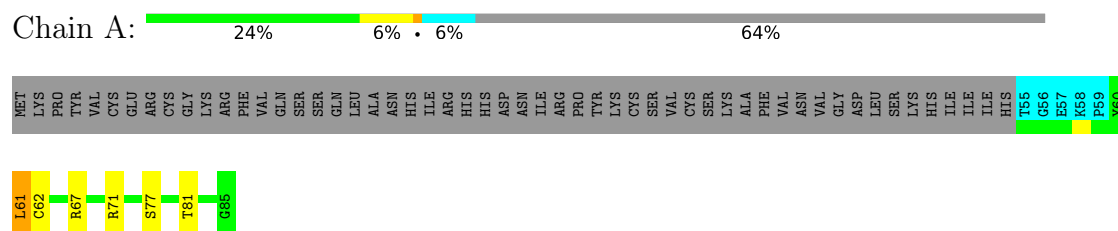
4.2.14 Score per residue for model 14

- Molecule 1: Isoform 2 of Zinc finger and BTB domain-containing protein 17



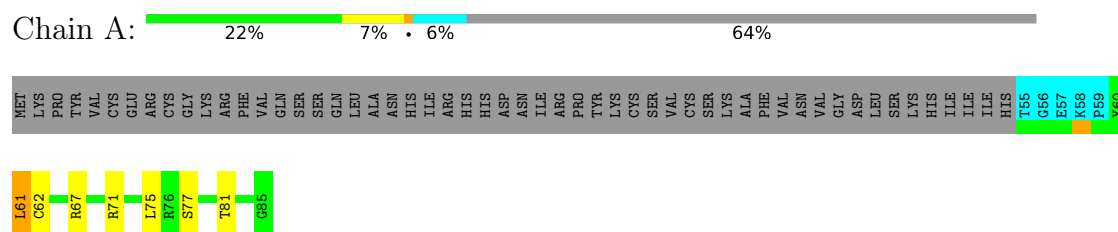
4.2.15 Score per residue for model 15

- Molecule 1: Isoform 2 of Zinc finger and BTB domain-containing protein 17



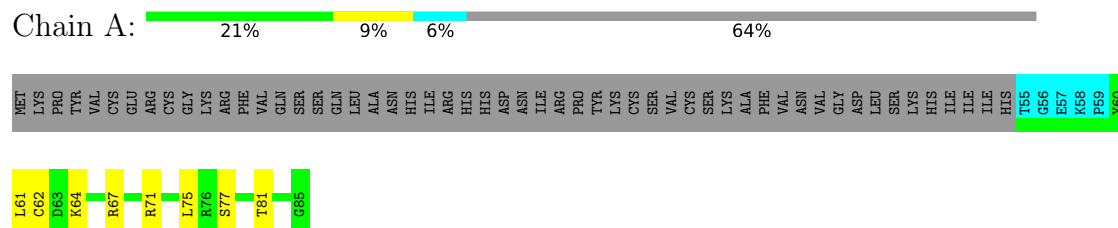
4.2.16 Score per residue for model 16

- Molecule 1: Isoform 2 of Zinc finger and BTB domain-containing protein 17



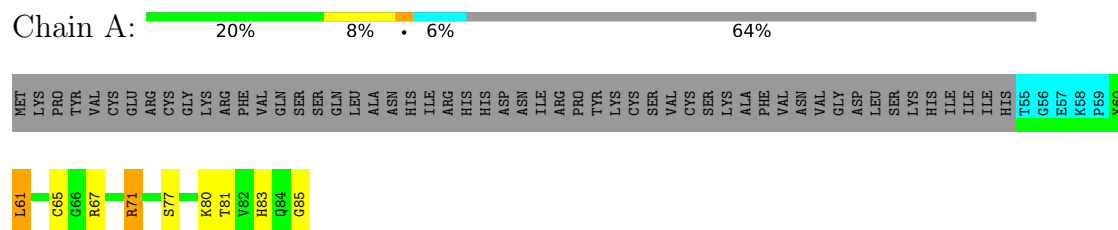
4.2.17 Score per residue for model 17

- Molecule 1: Isoform 2 of Zinc finger and BTB domain-containing protein 17



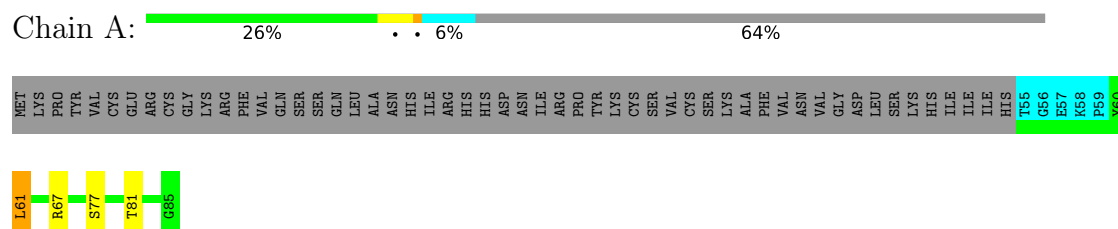
4.2.18 Score per residue for model 18

- Molecule 1: Isoform 2 of Zinc finger and BTB domain-containing protein 17



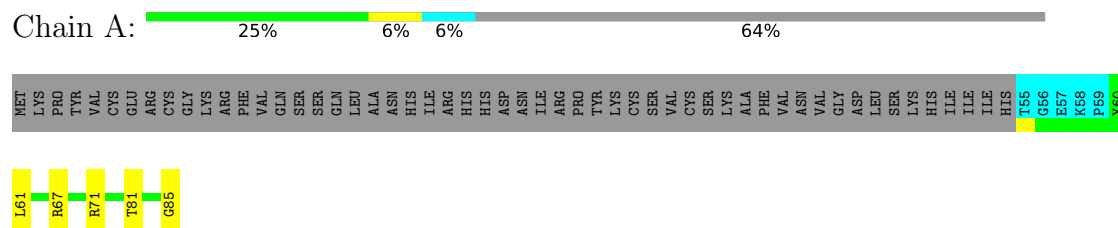
4.2.19 Score per residue for model 19

- Molecule 1: Isoform 2 of Zinc finger and BTB domain-containing protein 17



4.2.20 Score per residue for model 20

- Molecule 1: Isoform 2 of Zinc finger and BTB domain-containing protein 17



5 Refinement protocol and experimental data overview

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

Of the 300 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
ARIA	structure calculation	2.3.2
CNS	structure calculation	1.3

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	905
Number of shifts mapped to atoms	326
Number of unparsed shifts	0
Number of shifts with mapping errors	579
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	78%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section:
ZN

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	210	203	203	4±2
All	All	4220	4060	4060	83

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:61:LEU:HA	1:A:67:ARG:O	0.69	1.87	8	19
1:A:61:LEU:HB2	1:A:67:ARG:O	0.65	1.91	7	1
1:A:77:SER:O	1:A:81:THR:HG22	0.63	1.94	2	17
1:A:82:VAL:HG13	1:A:83:HIS:CD2	0.53	2.38	2	4
1:A:80:LYS:O	1:A:80:LYS:HD3	0.53	2.02	18	2
1:A:78:HIS:O	1:A:82:VAL:HG12	0.51	2.05	2	5
1:A:67:ARG:HG2	1:A:69:PHE:CE2	0.49	2.42	5	1
1:A:72:VAL:O	1:A:76:ARG:HD3	0.49	2.08	5	1
1:A:61:LEU:HD13	1:A:61:LEU:O	0.49	2.07	13	2
1:A:62:CYS:HB3	1:A:67:ARG:CB	0.48	2.37	7	1
1:A:62:CYS:HB3	1:A:67:ARG:HB3	0.48	1.86	4	8
1:A:81:THR:HG23	1:A:82:VAL:N	0.46	2.26	9	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:62:CYS:N	1:A:75:LEU:HD21	0.46	2.26	17	1
1:A:81:THR:HA	1:A:85:GLY:O	0.43	2.13	20	1
1:A:71:ARG:N	1:A:71:ARG:HD2	0.43	2.29	14	5
1:A:75:LEU:C	1:A:75:LEU:HD13	0.42	2.39	9	3
1:A:81:THR:HA	1:A:85:GLY:OXT	0.42	2.15	1	1
1:A:71:ARG:HD2	1:A:71:ARG:N	0.41	2.31	4	1
1:A:65:CYS:HB3	1:A:83:HIS:CE1	0.41	2.50	18	1
1:A:80:LYS:HD3	1:A:80:LYS:C	0.41	2.40	18	1
1:A:61:LEU:CA	1:A:67:ARG:O	0.40	2.69	5	1
1:A:64:LYS:HE2	1:A:64:LYS:HA	0.40	1.93	11	1
1:A:80:LYS:O	1:A:85:GLY:N	0.40	2.53	18	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	25/85 (29%)	22±2 (90±7%)	2±2 (10±7%)	0±0 (0±1%)	31	76
All	All	500/1700 (29%)	450 (90%)	48 (10%)	2 (0%)	31	76

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	62	CYS	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	23/77 (30%)	21±1 (92±2%)	2±1 (8±2%)	14	62

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	460/1540 (30%)	425 (92%)	35 (8%)	14 62

All 6 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	71	ARG	16
1	A	61	LEU	13
1	A	81	THR	2
1	A	84	GLN	2
1	A	80	LYS	1
1	A	64	LYS	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 ⓘ

There are no oligosaccharides in this entry.

6.6 Ligand geometry ⓘ

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

6.7 Other polymers ⓘ

There are no such molecules in this entry.

6.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 78% for the well-defined parts and 78% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list*

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	905
Number of shifts mapped to atoms	326
Number of unparsed shifts	0
Number of shifts with mapping errors	579
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.

- No matching atom found in the structure. All 579 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	1	MET	C	172.026	0.0	1
1	A	1	MET	CA	55.026	0.017	1
1	A	1	MET	CB	32.836	0.001	1
1	A	1	MET	CG	30.757	0.001	1
1	A	2	LYS	H	8.627	0.009	1
1	A	2	LYS	HA	4.689	0.011	1
1	A	2	LYS	HB2	2.128	.	1
1	A	2	LYS	HB3	2.128	.	1
1	A	2	LYS	HE2	3.196	.	1
1	A	2	LYS	HG2	1.534	0.013	1
1	A	2	LYS	HG3	1.534	0.013	1
1	A	2	LYS	CA	54.459	0.005	1
1	A	2	LYS	CB	32.875	0.016	1
1	A	2	LYS	N	125.107	0.038	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	3	PRO	C	176.039	.	1
1	A	3	PRO	CA	63.251	0.024	1
1	A	3	PRO	CB	32.277	0.024	1
1	A	3	PRO	CD	50.637	0.015	1
1	A	3	PRO	CG	26.806	.	1
1	A	4	TYR	H	8.066	0.007	1
1	A	4	TYR	HA	4.56	0.004	1
1	A	4	TYR	HB2	2.906	0.019	1
1	A	4	TYR	HB3	2.906	0.019	1
1	A	4	TYR	HD1	6.958	0.012	1
1	A	4	TYR	HD2	6.958	0.012	1
1	A	4	TYR	C	174.687	0.003	1
1	A	4	TYR	CA	57.938	0.039	1
1	A	4	TYR	CB	38.692	0.056	1
1	A	4	TYR	N	119.262	0.052	1
1	A	5	VAL	H	8.501	0.01	1
1	A	5	VAL	HA	4.739	0.015	1
1	A	5	VAL	HB	1.763	0.008	1
1	A	5	VAL	HG11	0.723	0.015	2
1	A	5	VAL	HG12	0.723	0.015	2
1	A	5	VAL	HG13	0.723	0.015	2
1	A	5	VAL	HG21	0.723	0.014	2
1	A	5	VAL	HG22	0.723	0.014	2
1	A	5	VAL	HG23	0.723	0.014	2
1	A	5	VAL	C	174.458	0.004	1
1	A	5	VAL	CA	60.38	0.036	1
1	A	5	VAL	CB	35.032	0.024	1
1	A	5	VAL	CG1	21.347	0.157	2
1	A	5	VAL	CG2	20.083	0.034	2
1	A	5	VAL	N	123.393	0.035	1
1	A	6	CYS	H	9.043	0.007	1
1	A	6	CYS	HA	4.52	0.005	1
1	A	6	CYS	HB2	2.772	0.009	2
1	A	6	CYS	HB3	3.312	0.013	2
1	A	6	CYS	C	177.241	.	1
1	A	6	CYS	CA	59.421	0.052	1
1	A	6	CYS	CB	29.665	0.052	1
1	A	6	CYS	N	128.483	0.046	1
1	A	7	GLU	H	9.471	0.01	1
1	A	7	GLU	HA	4.151	0.022	1
1	A	7	GLU	HB2	2.118	0.014	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	7	GLU	HB3	2.063	0.015	1
1	A	7	GLU	HG2	2.286	0.022	1
1	A	7	GLU	HG3	2.286	0.022	1
1	A	7	GLU	C	176.592	0.003	1
1	A	7	GLU	CA	58.387	0.184	1
1	A	7	GLU	CB	29.399	0.046	1
1	A	7	GLU	CG	35.956	0.054	1
1	A	7	GLU	N	132.248	0.08	1
1	A	8	ARG	H	8.773	0.005	1
1	A	8	ARG	HA	4.228	0.012	1
1	A	8	ARG	HB2	1.392	0.007	1
1	A	8	ARG	HB3	1.392	0.007	1
1	A	8	ARG	HD2	3.069	0.012	1
1	A	8	ARG	HD3	3.069	0.012	1
1	A	8	ARG	HG2	0.641	0.013	1
1	A	8	ARG	HG3	0.641	0.013	1
1	A	8	ARG	C	177.363	.	1
1	A	8	ARG	CA	57.841	0.055	1
1	A	8	ARG	CB	30.364	0.032	1
1	A	8	ARG	CD	42.896	0.01	1
1	A	8	ARG	CG	26.474	0.053	1
1	A	8	ARG	N	119.93	0.047	1
1	A	9	CYS	H	8.158	0.012	1
1	A	9	CYS	HA	5.136	0.005	1
1	A	9	CYS	HB2	2.828	0.011	2
1	A	9	CYS	HB3	3.389	0.011	2
1	A	9	CYS	C	176.222	0.003	1
1	A	9	CYS	CA	58.479	0.037	1
1	A	9	CYS	CB	32.585	0.059	1
1	A	9	CYS	N	115.311	0.052	1
1	A	10	GLY	H	8.33	0.01	1
1	A	10	GLY	HA2	3.657	0.012	2
1	A	10	GLY	HA3	4.151	0.01	2
1	A	10	GLY	C	173.685	0.005	1
1	A	10	GLY	CA	45.935	0.132	1
1	A	10	GLY	N	113.68	0.038	1
1	A	11	LYS	H	7.995	0.009	1
1	A	11	LYS	HA	3.881	0.007	1
1	A	11	LYS	HB2	1.396	0.012	1
1	A	11	LYS	HB3	1.396	0.012	1
1	A	11	LYS	HE2	2.862	0.032	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	11	LYS	HE3	2.868	0.029	1
1	A	11	LYS	HG2	1.116	0.013	1
1	A	11	LYS	HG3	1.116	0.013	1
1	A	11	LYS	C	173.943	0.002	1
1	A	11	LYS	CA	58.227	0.05	1
1	A	11	LYS	CB	33.664	0.059	1
1	A	11	LYS	CD	29.448	0.012	1
1	A	11	LYS	CG	26.222	0.009	1
1	A	11	LYS	N	123.441	0.065	1
1	A	12	ARG	H	7.681	0.004	1
1	A	12	ARG	HA	5.091	0.007	1
1	A	12	ARG	HB2	1.484	0.02	1
1	A	12	ARG	HB3	1.484	0.02	1
1	A	12	ARG	C	175.508	.	1
1	A	12	ARG	CA	54.544	0.053	1
1	A	12	ARG	CB	33.48	0.027	1
1	A	12	ARG	CD	43.476	0.007	1
1	A	12	ARG	CG	28.332	0.0	1
1	A	12	ARG	N	119.873	0.066	1
1	A	13	PHE	H	8.892	0.006	1
1	A	13	PHE	HA	4.758	0.009	1
1	A	13	PHE	HB2	2.517	0.016	2
1	A	13	PHE	HB3	3.425	0.008	2
1	A	13	PHE	HD1	7.019	0.018	1
1	A	13	PHE	HD2	7.019	0.018	1
1	A	13	PHE	HE1	7.027	.	1
1	A	13	PHE	HE2	7.027	.	1
1	A	13	PHE	C	175.232	0.0	1
1	A	13	PHE	CA	56.897	0.074	1
1	A	13	PHE	CB	43.469	0.026	1
1	A	13	PHE	N	117.956	0.107	1
1	A	14	VAL	H	8.681	0.006	1
1	A	14	VAL	HA	4.224	0.005	1
1	A	14	VAL	HB	2.26	0.014	1
1	A	14	VAL	HG11	1.064	0.008	2
1	A	14	VAL	HG12	1.064	0.008	2
1	A	14	VAL	HG13	1.064	0.008	2
1	A	14	VAL	HG21	1.059	0.012	2
1	A	14	VAL	HG22	1.059	0.012	2
1	A	14	VAL	HG23	1.059	0.012	2
1	A	14	VAL	C	175.977	0.002	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	14	VAL	CA	64.381	0.021	1
1	A	14	VAL	CB	32.75	0.044	1
1	A	14	VAL	CG1	21.597	0.058	2
1	A	14	VAL	CG2	21.596	0.053	2
1	A	14	VAL	N	118.985	0.051	1
1	A	15	GLN	H	7.654	0.008	1
1	A	15	GLN	HA	4.804	0.006	1
1	A	15	GLN	HB2	2.233	0.011	1
1	A	15	GLN	HB3	1.688	0.015	1
1	A	15	GLN	HG2	2.342	0.023	1
1	A	15	GLN	HG3	2.333	0.011	1
1	A	15	GLN	C	176.854	.	1
1	A	15	GLN	CA	53.789	0.036	1
1	A	15	GLN	CB	31.904	0.013	1
1	A	15	GLN	CG	33.746	0.037	1
1	A	15	GLN	N	114.899	0.019	1
1	A	16	SER	H	8.687	0.005	1
1	A	16	SER	HA	4.693	0.012	1
1	A	16	SER	HB2	2.922	0.01	1
1	A	16	SER	HB3	2.922	0.01	1
1	A	16	SER	C	177.79	.	1
1	A	16	SER	CA	61.242	0.024	1
1	A	16	SER	CB	61.403	0.232	1
1	A	16	SER	N	121.472	0.05	1
1	A	17	SER	H	8.476	0.004	1
1	A	17	SER	HA	4.697	0.021	1
1	A	17	SER	HB2	4.003	0.014	1
1	A	17	SER	HB3	4.005	0.014	1
1	A	17	SER	C	176.855	.	1
1	A	17	SER	CA	60.669	0.016	1
1	A	17	SER	CB	61.435	0.02	1
1	A	17	SER	N	117.209	0.066	1
1	A	18	GLN	H	6.717	0.012	1
1	A	18	GLN	HA	4.013	0.011	1
1	A	18	GLN	HB2	2.027	0.017	1
1	A	18	GLN	HB3	2.027	0.017	1
1	A	18	GLN	HG2	2.459	0.014	1
1	A	18	GLN	HG3	2.459	0.014	1
1	A	18	GLN	C	178.988	.	1
1	A	18	GLN	CA	57.597	0.03	1
1	A	18	GLN	CB	28.324	0.066	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	18	GLN	CG	33.967	0.061	1
1	A	18	GLN	N	121.116	0.151	1
1	A	19	LEU	H	6.747	0.006	1
1	A	19	LEU	HA	3.1	0.008	1
1	A	19	LEU	HB2	1.798	0.009	1
1	A	19	LEU	HB3	1.798	0.009	1
1	A	19	LEU	HD11	1.063	0.014	2
1	A	19	LEU	HD12	1.063	0.014	2
1	A	19	LEU	HD13	1.063	0.014	2
1	A	19	LEU	HD21	0.962	0.025	2
1	A	19	LEU	HD22	0.962	0.025	2
1	A	19	LEU	HD23	0.962	0.025	2
1	A	19	LEU	HG	1.538	0.01	1
1	A	19	LEU	C	177.227	.	1
1	A	19	LEU	CA	57.48	0.095	1
1	A	19	LEU	CB	40.226	0.07	1
1	A	19	LEU	CD1	23.562	1.415	2
1	A	19	LEU	CD2	23.503	1.369	2
1	A	19	LEU	CG	27.211	0.017	1
1	A	19	LEU	N	121.455	0.032	1
1	A	20	ALA	H	7.929	0.009	1
1	A	20	ALA	HA	3.944	0.005	1
1	A	20	ALA	HB1	1.306	0.009	1
1	A	20	ALA	HB2	1.306	0.009	1
1	A	20	ALA	HB3	1.306	0.009	1
1	A	20	ALA	C	180.324	.	1
1	A	20	ALA	CA	55.326	0.091	1
1	A	20	ALA	CB	17.587	0.06	1
1	A	20	ALA	N	120.602	0.053	1
1	A	21	ASN	H	7.552	0.014	1
1	A	21	ASN	HA	4.282	0.015	1
1	A	21	ASN	HB2	2.734	0.023	2
1	A	21	ASN	HB3	2.734	0.023	2
1	A	21	ASN	HD21	6.838	.	1
1	A	21	ASN	HD22	6.838	.	1
1	A	21	ASN	C	176.726	.	1
1	A	21	ASN	CA	56.123	0.199	1
1	A	21	ASN	CB	38.745	0.06	1
1	A	21	ASN	N	115.201	0.086	1
1	A	22	HIS	H	7.561	0.003	1
1	A	22	HIS	HA	4.197	0.009	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	22	HIS	HB2	3.211	0.018	1
1	A	22	HIS	HB3	2.833	0.003	1
1	A	22	HIS	CA	59.381	0.08	1
1	A	22	HIS	CB	28.437	0.062	1
1	A	22	HIS	N	119.947	0.032	1
1	A	23	ILE	H	7.871	.	1
1	A	23	ILE	HA	3.924	0.021	1
1	A	23	ILE	HB	1.769	0.007	1
1	A	23	ILE	HD11	0.951	0.011	1
1	A	23	ILE	HD12	0.951	0.011	1
1	A	23	ILE	HD13	0.951	0.011	1
1	A	23	ILE	HG12	1.772	0.003	1
1	A	23	ILE	HG13	1.772	0.003	1
1	A	23	ILE	HG21	1.375	0.019	1
1	A	23	ILE	HG22	1.375	0.019	1
1	A	23	ILE	HG23	1.375	0.019	1
1	A	23	ILE	C	178.347	.	1
1	A	23	ILE	CA	65.251	0.055	1
1	A	23	ILE	CB	37.903	0.042	1
1	A	23	ILE	CD1	13.69	0.161	1
1	A	23	ILE	CG1	29.27	0.06	1
1	A	23	ILE	CG2	17.496	.	1
1	A	24	ARG	H	7.4	0.012	1
1	A	24	ARG	HA	4.012	0.003	1
1	A	24	ARG	HB2	1.703	0.006	1
1	A	24	ARG	HB3	1.703	0.006	1
1	A	24	ARG	C	177.471	.	1
1	A	24	ARG	CA	58.426	0.105	1
1	A	24	ARG	CB	30.0	0.063	1
1	A	24	ARG	CD	43.457	.	1
1	A	24	ARG	CG	27.458	.	1
1	A	24	ARG	N	118.918	0.031	1
1	A	25	HIS	H	7.526	0.014	1
1	A	25	HIS	HA	4.532	0.012	1
1	A	25	HIS	HB2	3.223	0.017	1
1	A	25	HIS	HB3	2.908	0.012	1
1	A	25	HIS	HD2	6.917	0.0	1
1	A	25	HIS	CA	56.138	0.032	1
1	A	25	HIS	CB	28.16	0.137	1
1	A	25	HIS	N	114.897	0.056	1
1	A	26	HIS	C	175.52	0.001	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	26	HIS	CA	57.785	.	1
1	A	26	HIS	CB	28.992	.	1
1	A	27	ASP	H	8.1	0.008	1
1	A	27	ASP	HA	4.547	0.013	1
1	A	27	ASP	HB2	2.647	0.023	1
1	A	27	ASP	HB3	2.647	0.023	1
1	A	27	ASP	C	175.913	.	1
1	A	27	ASP	CA	54.68	0.104	1
1	A	27	ASP	CB	40.999	0.021	1
1	A	27	ASP	N	119.45	0.072	1
1	A	28	ASN	H	8.186	0.018	1
1	A	28	ASN	HA	4.591	0.027	1
1	A	28	ASN	HB2	2.705	0.016	2
1	A	28	ASN	HB3	2.705	0.016	2
1	A	28	ASN	HD21	7.491	0.013	1
1	A	28	ASN	HD22	6.8	0.011	1
1	A	28	ASN	C	174.911	0.001	1
1	A	28	ASN	CA	53.183	0.106	1
1	A	28	ASN	CB	38.78	0.044	1
1	A	28	ASN	N	118.563	0.025	1
1	A	28	ASN	ND2	112.34	0.04	1
1	A	29	ILE	H	7.85	0.017	1
1	A	29	ILE	HA	4.002	0.012	1
1	A	29	ILE	HB	1.798	0.014	1
1	A	29	ILE	HD11	0.747	0.008	1
1	A	29	ILE	HD12	0.747	0.008	1
1	A	29	ILE	HD13	0.747	0.008	1
1	A	29	ILE	HG12	1.103	0.007	1
1	A	29	ILE	HG13	1.103	0.007	1
1	A	29	ILE	HG21	0.806	0.015	1
1	A	29	ILE	HG22	0.806	0.015	1
1	A	29	ILE	HG23	0.806	0.015	1
1	A	29	ILE	C	175.626	.	1
1	A	29	ILE	CA	61.566	0.099	1
1	A	29	ILE	CB	38.06	0.112	1
1	A	29	ILE	CD1	12.69	0.106	1
1	A	29	ILE	CG1	27.031	0.162	1
1	A	29	ILE	CG2	17.479	0.148	1
1	A	29	ILE	N	120.52	0.017	1
1	A	30	ARG	H	8.135	0.004	1
1	A	30	ARG	HA	4.546	0.008	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	30	ARG	HB2	1.542	0.004	1
1	A	30	ARG	HB3	1.542	0.004	1
1	A	30	ARG	HD2	2.937	0.005	1
1	A	30	ARG	HD3	2.937	0.005	1
1	A	30	ARG	HG2	1.319	0.024	1
1	A	30	ARG	HG3	1.319	0.024	1
1	A	30	ARG	CA	53.187	0.032	1
1	A	30	ARG	CB	30.851	0.05	1
1	A	30	ARG	CG	27.403	0.067	1
1	A	30	ARG	N	124.146	0.049	1
1	A	31	PRO	C	176.458	.	1
1	A	31	PRO	CA	63.481	.	1
1	A	31	PRO	CB	32.34	.	1
1	A	32	TYR	H	7.726	0.018	1
1	A	32	TYR	HA	4.562	0.013	1
1	A	32	TYR	HB2	2.734	0.015	1
1	A	32	TYR	HB3	2.734	0.015	1
1	A	32	TYR	HD1	7.242	0.0	1
1	A	32	TYR	HD2	7.242	0.0	1
1	A	32	TYR	HE1	6.919	.	1
1	A	32	TYR	HE2	6.919	.	1
1	A	32	TYR	C	174.551	.	1
1	A	32	TYR	CA	57.529	0.055	1
1	A	32	TYR	CB	38.711	0.173	1
1	A	32	TYR	N	118.04	0.153	1
1	A	33	LYS	H	8.553	0.008	1
1	A	33	LYS	HA	4.97	0.011	1
1	A	33	LYS	HB2	1.563	0.006	1
1	A	33	LYS	HB3	1.563	0.006	1
1	A	33	LYS	HE2	2.858	0.013	1
1	A	33	LYS	HE3	2.858	0.013	1
1	A	33	LYS	HG2	1.177	0.012	1
1	A	33	LYS	HG3	1.176	0.012	1
1	A	33	LYS	C	175.505	.	1
1	A	33	LYS	CA	54.99	0.093	1
1	A	33	LYS	CB	35.175	0.049	1
1	A	33	LYS	CD	29.539	.	1
1	A	33	LYS	CE	41.922	.	1
1	A	33	LYS	CG	25.015	0.069	1
1	A	33	LYS	N	124.426	0.049	1
1	A	34	CYS	H	9.056	0.005	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	34	CYS	HA	4.419	0.007	1
1	A	34	CYS	HB2	2.794	0.012	2
1	A	34	CYS	HB3	3.304	0.02	2
1	A	34	CYS	C	177.141	.	1
1	A	34	CYS	CA	60.034	0.11	1
1	A	34	CYS	CB	29.739	0.006	1
1	A	34	CYS	N	126.654	0.082	1
1	A	35	SER	H	8.896	0.014	1
1	A	35	SER	HA	4.718	0.006	1
1	A	35	SER	HB2	4.223	0.023	1
1	A	35	SER	HB3	4.223	0.023	1
1	A	35	SER	C	174.355	.	1
1	A	35	SER	CA	60.724	0.123	1
1	A	35	SER	CB	63.216	0.044	1
1	A	35	SER	N	126.486	0.047	1
1	A	36	VAL	H	8.944	0.007	1
1	A	36	VAL	HA	3.806	0.008	1
1	A	36	VAL	HB	1.098	0.01	1
1	A	36	VAL	HG11	0.274	0.01	2
1	A	36	VAL	HG12	0.274	0.01	2
1	A	36	VAL	HG13	0.274	0.01	2
1	A	36	VAL	HG21	0.814	0.002	2
1	A	36	VAL	HG22	0.814	0.002	2
1	A	36	VAL	HG23	0.814	0.002	2
1	A	36	VAL	C	176.913	0.003	1
1	A	36	VAL	CA	64.904	0.013	1
1	A	36	VAL	CB	32.886	0.041	1
1	A	36	VAL	CG1	20.778	0.353	2
1	A	36	VAL	CG2	20.816	0.334	2
1	A	36	VAL	N	124.529	0.053	1
1	A	37	CYS	H	8.194	0.008	1
1	A	37	CYS	HA	5.11	0.009	1
1	A	37	CYS	HB2	3.429	0.007	2
1	A	37	CYS	HB3	2.728	0.012	2
1	A	37	CYS	C	175.681	0.001	1
1	A	37	CYS	CA	58.329	0.053	1
1	A	37	CYS	CB	32.166	0.019	1
1	A	37	CYS	N	117.691	0.009	1
1	A	38	SER	H	7.856	0.008	1
1	A	38	SER	HA	4.149	0.013	1
1	A	38	SER	C	173.01	0.002	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	38	SER	CA	61.277	0.022	1
1	A	38	SER	CB	62.256	0.028	1
1	A	38	SER	N	114.203	0.022	1
1	A	39	LYS	H	8.027	0.006	1
1	A	39	LYS	HA	3.884	0.003	1
1	A	39	LYS	HB2	1.419	0.021	2
1	A	39	LYS	HB3	1.401	0.021	2
1	A	39	LYS	HG2	1.147	0.019	1
1	A	39	LYS	HG3	1.142	0.014	1
1	A	39	LYS	C	173.746	0.0	1
1	A	39	LYS	CA	58.467	0.057	1
1	A	39	LYS	CB	33.479	0.023	1
1	A	39	LYS	CD	29.411	0.005	1
1	A	39	LYS	CE	42.196	0.028	1
1	A	39	LYS	CG	25.956	0.0	1
1	A	39	LYS	N	123.915	0.033	1
1	A	40	ALA	H	7.723	0.008	1
1	A	40	ALA	HA	5.053	0.013	1
1	A	40	ALA	HB1	1.152	0.005	1
1	A	40	ALA	HB2	1.152	0.005	1
1	A	40	ALA	HB3	1.152	0.005	1
1	A	40	ALA	C	176.484	0.002	1
1	A	40	ALA	CA	50.365	0.038	1
1	A	40	ALA	CB	22.405	0.012	1
1	A	40	ALA	N	123.902	0.019	1
1	A	41	PHE	H	8.797	0.009	1
1	A	41	PHE	HA	4.674	0.011	1
1	A	41	PHE	HB2	2.624	0.013	2
1	A	41	PHE	HB3	3.407	0.023	2
1	A	41	PHE	HD1	7.229	0.016	1
1	A	41	PHE	HD2	7.229	0.016	1
1	A	41	PHE	C	175.336	.	1
1	A	41	PHE	CA	57.563	0.039	1
1	A	41	PHE	CB	43.626	0.058	1
1	A	41	PHE	N	118.02	0.018	1
1	A	42	VAL	H	9.203	0.003	1
1	A	42	VAL	HA	4.209	0.011	1
1	A	42	VAL	HB	2.213	0.008	1
1	A	42	VAL	HG11	1.069	0.014	1
1	A	42	VAL	HG12	1.069	0.014	1
1	A	42	VAL	HG13	1.069	0.014	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	42	VAL	HG21	1.069	0.014	1
1	A	42	VAL	HG22	1.069	0.014	1
1	A	42	VAL	HG23	1.069	0.014	1
1	A	42	VAL	C	175.311	0.0	1
1	A	42	VAL	CA	64.085	0.091	1
1	A	42	VAL	CB	32.776	0.067	1
1	A	42	VAL	CG1	21.514	0.15	1
1	A	42	VAL	CG2	21.501	0.145	1
1	A	42	VAL	N	118.084	0.053	1
1	A	43	ASN	H	7.535	0.007	1
1	A	43	ASN	HA	4.941	0.006	1
1	A	43	ASN	HB2	2.816	0.009	1
1	A	43	ASN	HB3	2.816	0.009	1
1	A	43	ASN	HD21	6.856	0.015	1
1	A	43	ASN	HD22	6.856	0.015	1
1	A	43	ASN	C	175.016	0.003	1
1	A	43	ASN	CA	51.672	0.109	1
1	A	43	ASN	CB	41.201	0.029	1
1	A	43	ASN	N	113.174	0.02	1
1	A	44	VAL	H	8.225	0.008	1
1	A	44	VAL	HA	3.096	0.011	1
1	A	44	VAL	HB	1.386	0.015	1
1	A	44	VAL	HG11	0.629	0.009	1
1	A	44	VAL	HG12	0.629	0.009	1
1	A	44	VAL	HG13	0.629	0.009	1
1	A	44	VAL	HG21	0.63	0.01	1
1	A	44	VAL	HG22	0.63	0.01	1
1	A	44	VAL	HG23	0.63	0.01	1
1	A	44	VAL	C	177.291	.	1
1	A	44	VAL	CA	64.842	0.076	1
1	A	44	VAL	CB	31.308	0.09	1
1	A	44	VAL	CG1	21.628	0.672	1
1	A	44	VAL	CG2	21.628	0.672	1
1	A	44	VAL	N	121.491	0.038	1
1	A	45	GLY	H	8.431	0.007	1
1	A	45	GLY	HA2	3.74	0.01	1
1	A	45	GLY	HA3	3.74	0.01	1
1	A	45	GLY	C	176.688	0.002	1
1	A	45	GLY	CA	46.666	0.064	1
1	A	45	GLY	N	111.792	0.027	1
1	A	46	ASP	H	7.91	0.01	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	46	ASP	HA	4.228	0.01	1
1	A	46	ASP	HB2	2.71	0.014	1
1	A	46	ASP	HB3	2.724	0.013	1
1	A	46	ASP	C	178.851	0.001	1
1	A	46	ASP	CA	56.555	0.036	1
1	A	46	ASP	CB	40.198	0.046	1
1	A	46	ASP	N	121.717	0.034	1
1	A	47	LEU	H	6.865	0.008	1
1	A	47	LEU	HA	3.123	0.015	1
1	A	47	LEU	HB2	1.893	0.023	2
1	A	47	LEU	HB3	1.893	0.023	2
1	A	47	LEU	HD11	0.938	0.015	1
1	A	47	LEU	HD12	0.938	0.015	1
1	A	47	LEU	HD13	0.938	0.015	1
1	A	47	LEU	HD21	0.946	0.013	1
1	A	47	LEU	HD22	0.946	0.013	1
1	A	47	LEU	HD23	0.946	0.013	1
1	A	47	LEU	HG	1.545	0.01	1
1	A	47	LEU	C	177.717	.	1
1	A	47	LEU	CA	57.841	0.031	1
1	A	47	LEU	CB	40.44	0.052	1
1	A	47	LEU	CD1	22.872	0.028	1
1	A	47	LEU	CD2	26.495	0.063	1
1	A	47	LEU	CG	27.088	0.178	1
1	A	47	LEU	N	121.668	0.027	1
1	A	48	SER	H	8.354	0.002	1
1	A	48	SER	HA	4.183	0.006	1
1	A	48	SER	HB2	3.963	0.011	1
1	A	48	SER	HB3	3.963	0.011	1
1	A	48	SER	C	176.127	.	1
1	A	48	SER	CA	61.96	0.044	1
1	A	48	SER	CB	62.619	0.102	1
1	A	48	SER	N	114.881	0.035	1
1	A	49	LYS	H	7.314	0.006	1
1	A	49	LYS	HA	3.998	0.006	1
1	A	49	LYS	HB2	1.693	0.01	1
1	A	49	LYS	HB3	1.693	0.01	1
1	A	49	LYS	C	177.569	0.001	1
1	A	49	LYS	CA	58.366	0.094	1
1	A	49	LYS	CB	32.779	0.046	1
1	A	49	LYS	CD	29.281	.	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	49	LYS	CE	42.118	0.02	1
1	A	49	LYS	CG	25.275	.	1
1	A	49	LYS	N	118.704	0.063	1
1	A	50	HIS	H	7.316	0.005	1
1	A	50	HIS	HA	4.196	0.01	1
1	A	50	HIS	HB2	2.849	0.024	1
1	A	50	HIS	HB3	2.862	0.021	1
1	A	50	HIS	C	176.848	.	1
1	A	50	HIS	CA	58.834	0.081	1
1	A	50	HIS	CB	29.074	0.004	1
1	A	50	HIS	N	117.984	0.031	1
1	A	51	ILE	H	8.078	0.006	1
1	A	51	ILE	HA	3.588	0.02	1
1	A	51	ILE	HB	1.968	0.006	1
1	A	51	ILE	HD11	0.943	0.002	1
1	A	51	ILE	HD12	0.943	0.002	1
1	A	51	ILE	HD13	0.943	0.002	1
1	A	51	ILE	HG12	1.236	0.008	1
1	A	51	ILE	HG13	1.236	0.008	1
1	A	51	ILE	HG21	1.18	0.009	1
1	A	51	ILE	HG22	1.18	0.009	1
1	A	51	ILE	HG23	1.18	0.009	1
1	A	51	ILE	C	176.897	.	1
1	A	51	ILE	CA	65.419	0.029	1
1	A	51	ILE	CB	38.464	0.117	1
1	A	51	ILE	CD1	14.551	0.07	1
1	A	51	ILE	CG1	28.241	.	1
1	A	51	ILE	CG2	18.312	0.124	1
1	A	51	ILE	N	113.406	0.053	1
1	A	52	ILE	H	6.659	0.006	1
1	A	52	ILE	HA	3.88	0.012	1
1	A	52	ILE	HB	1.856	0.005	1
1	A	52	ILE	HD11	0.745	0.006	1
1	A	52	ILE	HD12	0.745	0.006	1
1	A	52	ILE	HD13	0.745	0.006	1
1	A	52	ILE	HG12	1.291	0.008	1
1	A	52	ILE	HG13	1.291	0.008	1
1	A	52	ILE	HG21	0.831	0.004	1
1	A	52	ILE	HG22	0.831	0.004	1
1	A	52	ILE	HG23	0.831	0.004	1
1	A	52	ILE	C	178.1	0.002	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	52	ILE	CA	62.816	0.067	1
1	A	52	ILE	CB	37.864	0.024	1
1	A	52	ILE	CD1	13.326	0.026	1
1	A	52	ILE	CG1	27.641	0.018	1
1	A	52	ILE	CG2	17.978	0.066	1
1	A	52	ILE	N	117.506	0.073	1
1	A	53	ILE	H	7.722	0.003	1
1	A	53	ILE	HA	3.895	0.008	1
1	A	53	ILE	HB	1.836	0.006	1
1	A	53	ILE	HD11	0.629	0.001	1
1	A	53	ILE	HD12	0.629	0.001	1
1	A	53	ILE	HD13	0.629	0.001	1
1	A	53	ILE	HG12	0.826	.	1
1	A	53	ILE	HG13	1.668	0.022	1
1	A	53	ILE	HG21	0.499	0.001	1
1	A	53	ILE	HG22	0.499	0.001	1
1	A	53	ILE	HG23	0.499	0.001	1
1	A	53	ILE	C	177.209	.	1
1	A	53	ILE	CA	63.205	0.02	1
1	A	53	ILE	CB	37.542	0.027	1
1	A	53	ILE	CD1	14.401	0.036	1
1	A	53	ILE	CG1	26.494	0.032	1
1	A	53	ILE	CG2	16.425	0.019	1
1	A	53	ILE	N	118.835	0.023	1
1	A	54	HIS	H	7.325	0.005	1
1	A	54	HIS	HA	4.795	0.014	1
1	A	54	HIS	HB2	3.24	0.023	1
1	A	54	HIS	HB3	3.24	0.023	1
1	A	54	HIS	C	175.607	.	1
1	A	54	HIS	CA	55.061	0.113	1
1	A	54	HIS	CB	28.447	0.023	1
1	A	54	HIS	N	117.239	0.072	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
$^{13}\text{C}_\alpha$	85	-0.38 ± 0.34	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	79	0.28 ± 0.18	None needed (< 0.5 ppm)
$^{13}\text{C}'$	79	0.01 ± 0.20	None needed (< 0.5 ppm)

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Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
^{15}N	79	0.23 $\pm$ 0.90	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 78%, i.e. 283 atoms were assigned a chemical shift out of a possible 361. 0 out of 5 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	132/133 (99%)	55/55 (100%)	51/52 (98%)	26/26 (100%)
Sidechain	145/195 (74%)	95/124 (77%)	48/57 (84%)	2/14 (14%)
Aromatic	6/33 (18%)	6/17 (35%)	0/14 (0%)	0/2 (0%)
Overall	283/361 (78%)	156/196 (80%)	99/123 (80%)	28/42 (67%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 78%, i.e. 326 atoms were assigned a chemical shift out of a possible 420. 0 out of 5 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	153/157 (97%)	63/65 (97%)	60/62 (97%)	30/30 (100%)
Sidechain	167/230 (73%)	109/146 (75%)	56/69 (81%)	2/15 (13%)
Aromatic	6/33 (18%)	6/17 (35%)	0/14 (0%)	0/2 (0%)
Overall	326/420 (78%)	178/228 (78%)	116/145 (80%)	32/47 (68%)

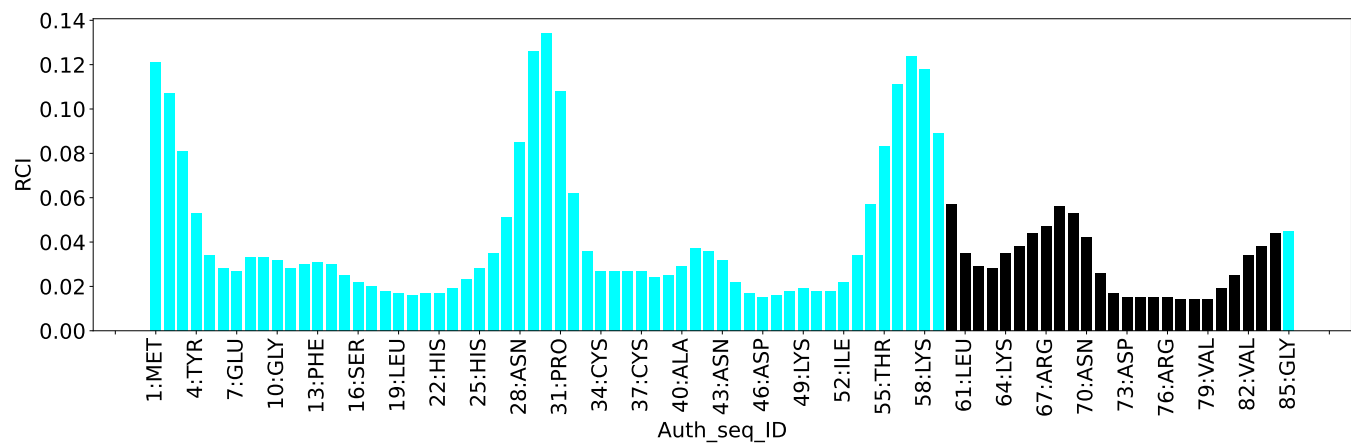
7.1.4 Statistically unusual chemical shifts [i](#)

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:



8 NMR restraints analysis [i](#)

8.1 Conformationally restricting restraints [i](#)

The following table provides the summary of experimentally observed NMR restraints in different categories. Restraints are classified into different categories based on the sequence separation of the atoms involved.

Description	Value
Total distance restraints	20
Intra-residue ($ i-j =0$)	0
Sequential ($ i-j =1$)	0
Medium range ($ i-j >1$ and $ i-j <5$)	0
Long range ($ i-j \geq 5$)	0
Inter-chain	0
Hydrogen bond restraints	20
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	0.2
Number of long range restraints per residue ¹	0.0

¹Long range hydrogen bonds and disulfide bonds are counted as long range restraints while calculating the number of long range restraints per residue

8.2 Residual restraint violations [i](#)

This section provides the overview of the restraint violations analysis. The violations are binned as small, medium and large violations based on its absolute value. Average number of violations per model is calculated by dividing the total number of violations in each bin by the size of the ensemble.

8.2.1 Average number of distance violations per model [i](#)

Distance violations less than 0.1 Å are not included in the calculation. There are no distance violations

8.2.2 Average number of dihedral-angle violations per model [i](#)

Dihedral-angle violations less than 1° are not included in the calculation. There are no dihedral-angle violations

9 Distance violation analysis [i](#)

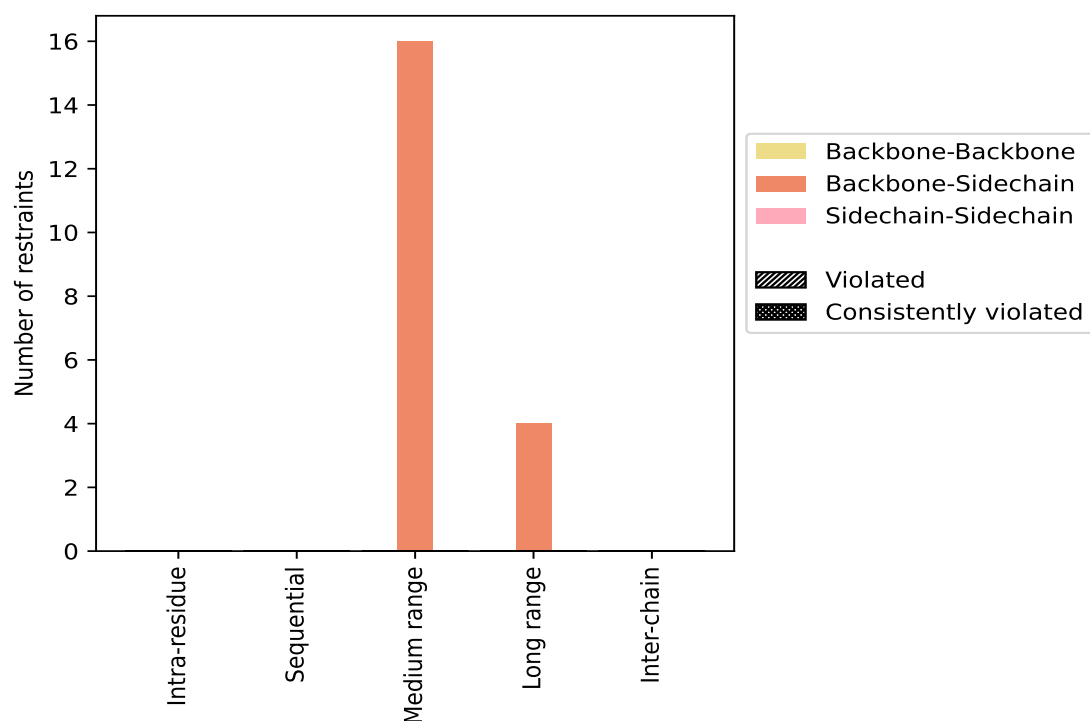
9.1 Summary of distance violations [i](#)

The following table shows the summary of distance violations in different restraint categories based on the sequence separation of the atoms involved. Each category is further sub-divided into three sub-categories based on the atoms involved. Violations less than 0.1 Å are not included in the statistics.

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue (i-j =0)	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sequential (i-j =1)	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Medium range (i-j >1 & i-j <5)	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Long range (i-j ≥5)	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Inter-chain	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Hydrogen bond	20	100.0	0	0.0	0.0	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	20	100.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	20	100.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0

¹ percentage calculated with respect to the total number of distance restraints, ² percentage calculated with respect to the number of restraints in a particular restraint category, ³ violated in at least one model, ⁴ violated in all the models

9.1.1 Bar chart : Distribution of distance restraints and violations [i](#)



Violated and consistently violated restraints are shown using different hatch patterns in their respective categories. The hydrogen bonds and disulfied bonds are counted in their appropriate category on the x-axis

9.2 Distance violation statistics for each model [i](#)

No violations found

9.3 Distance violation statistics for the ensemble [i](#)

No violations found

9.4 Most violated distance restraints in the ensemble [i](#)

No violations found

9.5 All violated distance restraints [i](#)

No violations found

10 Dihedral-angle violation analysis ⓘ

No dihedral-angle restraints found