



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 2LVH / pdb_00002lvh
BMRB ID : 18570
Title : Solution structure of the zinc finger AFV1p06 protein from the hyperthermophilic archaeal virus AFV1
Authors : Guilliere, F.; Sezonov, G.; Prangishvili, D.; Delepierre, M.; Guijarro, J.
Deposited on : 2012-07-05

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<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

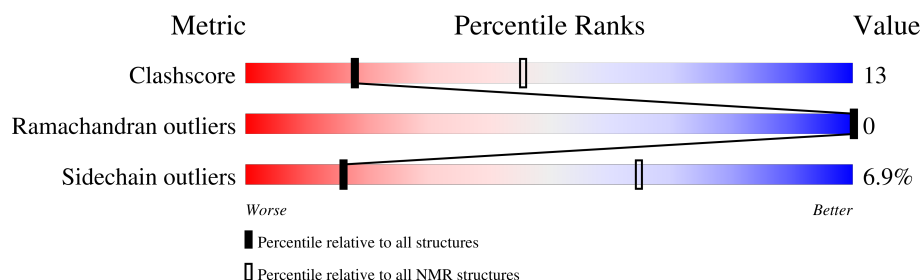
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 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	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	59	

2 Ensemble composition and analysis

This entry contains 10 models. Model 9 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:10-A:46 (37)	0.38	9

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 2 clusters and 2 single-model clusters were found.

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

3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 764 atoms, of which 384 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Putative zinc finger protein ORF59a.

Mol	Chain	Residues	Atoms						Trace
1	A	45	Total	C	H	N	O	S	0
			763	243	384	67	66	3	

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

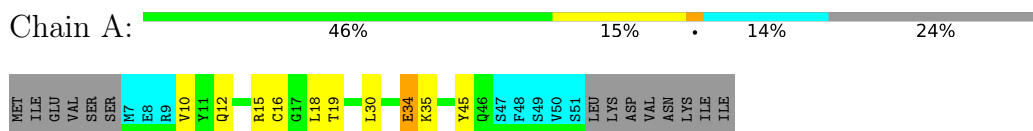
Mol	Chain	Residues	Atoms	
2	A	1	Total	Zn
			1	1

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.

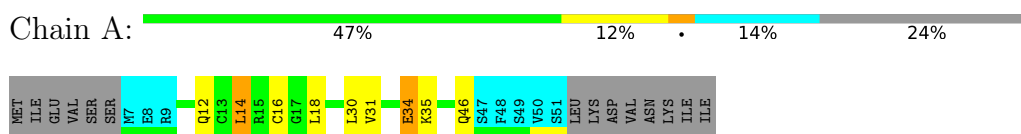
- Molecule 1: Putative zinc finger protein ORF59a



4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 9. Colouring as in section 4.1 above.

- Molecule 1: Putative zinc finger protein ORF59a



5 Refinement protocol and experimental data overview

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

Of the 150 calculated structures, 10 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 solution	2.2
CNS	structure solution	1.2
CNS	refinement	1.2

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	738
Number of shifts mapped to atoms	568
Number of unparsed shifts	0
Number of shifts with mapping errors	170
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	86%

6 Model quality

6.1 Standard geometry

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

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	316	324	324	8±2
All	All	3170	3240	3240	85

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.

5 of 37 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:10:VAL:HB	1:A:19:THR:HG22	0.70	1.62	2	2
1:A:12:GLN:HG2	1:A:19:THR:HG22	0.67	1.65	10	1
1:A:16:CYS:HB2	1:A:18:LEU:HG	0.65	1.67	1	10
1:A:42:ASP:HA	1:A:45:TYR:CE2	0.65	2.26	4	4
1:A:12:GLN:HG3	1:A:19:THR:HG23	0.58	1.74	2	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	37/59 (63%)	36±1 (97±1%)	1±1 (3±1%)	0±0 (0±0%)	100	100
All	All	370/590 (63%)	359 (97%)	11 (3%)	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	36/58 (62%)	34±1 (93±3%)	2±1 (7±3%)	16	65
All	All	360/580 (62%)	335 (93%)	25 (7%)	16	65

5 of 8 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	34	GLU	10
1	A	19	THR	5
1	A	10	VAL	3
1	A	14	LEU	2
1	A	35	LYS	2

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 oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

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

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 85% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

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	738
Number of shifts mapped to atoms	568
Number of unparsed shifts	0
Number of shifts with mapping errors	170
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. First 5 (of 170) occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	1	MET	HA	4.524	0.02	1
1	A	1	MET	HE1	1.997	0.02	1
1	A	1	MET	HE2	1.997	0.02	1
1	A	1	MET	HE3	1.997	0.02	1
1	A	1	MET	HG2	2.525	0.02	2
1	A	1	MET	HG3	2.525	0.02	2
1	A	1	MET	C	175.7	0.35	1
1	A	1	MET	CA	54.22	0.35	1
1	A	1	MET	CB	33.24	0.35	1
1	A	1	MET	CE	17.118	0.35	1
1	A	1	MET	CG	31.833	0.35	1
1	A	2	ILE	H	8.256	0.02	1
1	A	2	ILE	HA	4.12	0.02	1
1	A	2	ILE	HB	1.807	0.02	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	2	ILE	HD11	0.837	0.02	1
1	A	2	ILE	HD12	0.837	0.02	1
1	A	2	ILE	HD13	0.837	0.02	1
1	A	2	ILE	HG12	1.159	0.02	2
1	A	2	ILE	HG13	1.45	0.02	2
1	A	2	ILE	HG21	0.905	0.02	1
1	A	2	ILE	HG22	0.905	0.02	1
1	A	2	ILE	HG23	0.905	0.02	1
1	A	2	ILE	C	175.8	0.35	1
1	A	2	ILE	CA	61.14	0.35	1
1	A	2	ILE	CB	38.92	0.35	1
1	A	2	ILE	CD1	12.864	0.35	1
1	A	2	ILE	CG1	27.268	0.35	1
1	A	2	ILE	CG2	17.485	0.35	1
1	A	2	ILE	N	122.759	0.15	1
1	A	3	GLU	H	8.539	0.02	1
1	A	3	GLU	HA	4.34	0.02	1
1	A	3	GLU	HB2	1.921	0.02	2
1	A	3	GLU	HB3	2.015	0.02	2
1	A	3	GLU	HG2	2.214	0.02	2
1	A	3	GLU	HG3	2.214	0.02	2
1	A	3	GLU	C	176.3	0.35	1
1	A	3	GLU	CA	56.34	0.35	1
1	A	3	GLU	CB	30.49	0.35	1
1	A	3	GLU	CG	36.301	0.35	1
1	A	3	GLU	N	125.788	0.15	1
1	A	4	VAL	H	8.278	0.02	1
1	A	4	VAL	HA	4.123	0.02	1
1	A	4	VAL	HB	2.16	0.02	1
1	A	4	VAL	HG11	0.92	0.02	2
1	A	4	VAL	HG12	0.92	0.02	2
1	A	4	VAL	HG13	0.92	0.02	2
1	A	4	VAL	HG21	0.92	0.02	2
1	A	4	VAL	HG22	0.92	0.02	2
1	A	4	VAL	HG23	0.92	0.02	2
1	A	4	VAL	C	175.7	0.35	1
1	A	4	VAL	CA	62.414	0.35	1
1	A	4	VAL	CB	32.37	0.35	1
1	A	4	VAL	CG1	21.01	0.35	2
1	A	4	VAL	CG2	21.01	0.35	2
1	A	4	VAL	N	122.096	0.15	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	5	SER	H	7.514	0.02	1
1	A	5	SER	N	110.841	0.15	1
1	A	52	LEU	H	8.423	0.02	1
1	A	52	LEU	HA	4.226	0.02	1
1	A	52	LEU	HB2	1.572	0.02	2
1	A	52	LEU	HB3	1.572	0.02	2
1	A	52	LEU	HD11	0.802	0.02	2
1	A	52	LEU	HD12	0.802	0.02	2
1	A	52	LEU	HD13	0.802	0.02	2
1	A	52	LEU	HD21	0.802	0.02	2
1	A	52	LEU	HD22	0.802	0.02	2
1	A	52	LEU	HD23	0.802	0.02	2
1	A	52	LEU	HG	1.723	0.02	1
1	A	52	LEU	C	177.6	0.35	1
1	A	52	LEU	CA	56.07	0.35	1
1	A	52	LEU	CB	42.17	0.35	1
1	A	52	LEU	CD1	23.6	0.35	2
1	A	52	LEU	CD2	23.6	0.35	2
1	A	52	LEU	CG	27.003	0.35	1
1	A	52	LEU	N	125.326	0.15	1
1	A	53	LYS	H	8.126	0.02	1
1	A	53	LYS	HA	4.194	0.02	1
1	A	53	LYS	HB2	1.728	0.02	2
1	A	53	LYS	HB3	1.728	0.02	2
1	A	53	LYS	HD2	1.625	0.02	2
1	A	53	LYS	HD3	1.625	0.02	2
1	A	53	LYS	HG2	1.344	0.02	2
1	A	53	LYS	HG3	1.344	0.02	2
1	A	53	LYS	C	176.4	0.35	1
1	A	53	LYS	CA	56.94	0.35	1
1	A	53	LYS	CB	32.91	0.35	1
1	A	53	LYS	CG	24.473	0.35	1
1	A	53	LYS	N	119.682	0.15	1
1	A	54	ASP	H	8.057	0.02	1
1	A	54	ASP	HA	4.616	0.02	1
1	A	54	ASP	HB2	2.578	0.02	2
1	A	54	ASP	HB3	2.711	0.02	2
1	A	54	ASP	C	176.7	0.35	1
1	A	54	ASP	CA	54.62	0.35	1
1	A	54	ASP	CB	41.4	0.35	1
1	A	54	ASP	N	120.232	0.15	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	55	VAL	H	7.869	0.02	1
1	A	55	VAL	HA	3.95	0.02	1
1	A	55	VAL	HB	2.102	0.02	1
1	A	55	VAL	HG11	0.89	0.02	2
1	A	55	VAL	HG12	0.89	0.02	2
1	A	55	VAL	HG13	0.89	0.02	2
1	A	55	VAL	HG21	0.87	0.02	2
1	A	55	VAL	HG22	0.87	0.02	2
1	A	55	VAL	HG23	0.87	0.02	2
1	A	55	VAL	C	176.4	0.35	1
1	A	55	VAL	CA	63.24	0.35	1
1	A	55	VAL	CB	32.29	0.35	1
1	A	55	VAL	CG1	20.84	0.35	2
1	A	55	VAL	CG2	20.84	0.35	2
1	A	55	VAL	N	119.586	0.15	1
1	A	56	ASN	H	8.308	0.02	1
1	A	56	ASN	HA	4.652	0.02	1
1	A	56	ASN	HB2	2.7	0.02	2
1	A	56	ASN	HB3	2.781	0.02	2
1	A	56	ASN	HD21	6.876	0.02	2
1	A	56	ASN	HD22	7.6	0.02	2
1	A	56	ASN	C	174.9	0.35	1
1	A	56	ASN	CA	53.66	0.35	1
1	A	56	ASN	CB	38.82	0.35	1
1	A	56	ASN	N	119.722	0.15	1
1	A	56	ASN	ND2	112.966	0.15	1
1	A	57	LYS	H	7.912	0.02	1
1	A	57	LYS	HA	4.28	0.02	1
1	A	57	LYS	HB2	1.72	0.02	2
1	A	57	LYS	HB3	1.807	0.02	2
1	A	57	LYS	HG2	1.349	0.02	2
1	A	57	LYS	HG3	1.349	0.02	2
1	A	57	LYS	C	175.9	0.35	1
1	A	57	LYS	CA	56.31	0.35	1
1	A	57	LYS	CB	33.17	0.35	1
1	A	57	LYS	CD	29.085	0.35	1
1	A	57	LYS	CE	42.161	0.35	1
1	A	57	LYS	CG	24.725	0.35	1
1	A	57	LYS	N	120.734	0.15	1
1	A	58	ILE	H	8.031	0.02	1
1	A	58	ILE	HA	4.12	0.02	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	58	ILE	HB	1.831	0.02	1
1	A	58	ILE	HD11	0.789	0.02	1
1	A	58	ILE	HD12	0.789	0.02	1
1	A	58	ILE	HD13	0.789	0.02	1
1	A	58	ILE	HG12	1.119	0.02	2
1	A	58	ILE	HG13	1.434	0.02	2
1	A	58	ILE	HG21	0.842	0.02	1
1	A	58	ILE	HG22	0.842	0.02	1
1	A	58	ILE	HG23	0.842	0.02	1
1	A	58	ILE	C	175.1	0.35	1
1	A	58	ILE	CA	61.35	0.35	1
1	A	58	ILE	CB	38.51	0.35	1
1	A	58	ILE	CD1	12.843	0.35	1
1	A	58	ILE	CG1	27.183	0.35	1
1	A	58	ILE	CG2	17.53	0.35	1
1	A	58	ILE	N	122.483	0.15	1
1	A	59	ILE	H	7.686	0.02	1
1	A	59	ILE	HA	4.02	0.02	1
1	A	59	ILE	HB	1.759	0.02	1
1	A	59	ILE	HD11	0.79	0.02	1
1	A	59	ILE	HD12	0.79	0.02	1
1	A	59	ILE	HD13	0.79	0.02	1
1	A	59	ILE	HG12	1.087	0.02	2
1	A	59	ILE	HG13	1.371	0.02	2
1	A	59	ILE	HG21	0.829	0.02	1
1	A	59	ILE	HG22	0.829	0.02	1
1	A	59	ILE	HG23	0.829	0.02	1
1	A	59	ILE	CA	62.86	0.35	1
1	A	59	ILE	CB	39.62	0.35	1
1	A	59	ILE	CD1	13.195	0.35	1
1	A	59	ILE	CG1	27.14	0.35	1
1	A	59	ILE	CG2	17.7	0.35	1
1	A	59	ILE	N	129.371	0.15	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
$^{13}\text{C}_\alpha$	57	-0.44 ± 0.16	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	56	-0.02 ± 0.23	None needed (< 0.5 ppm)

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Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}'$	54	-0.02 ± 0.15	None needed (< 0.5 ppm)
^{15}N	54	2.09 ± 0.86	Should be applied

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 86%, i.e. 481 atoms were assigned a chemical shift out of a possible 560. 0 out of 8 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	180/184 (98%)	73/74 (99%)	72/74 (97%)	35/36 (97%)
Sidechain	257/323 (80%)	169/209 (81%)	84/97 (87%)	4/17 (24%)
Aromatic	44/53 (83%)	22/25 (88%)	22/27 (81%)	0/1 (0%)
Overall	481/560 (86%)	264/308 (86%)	178/198 (90%)	39/54 (72%)

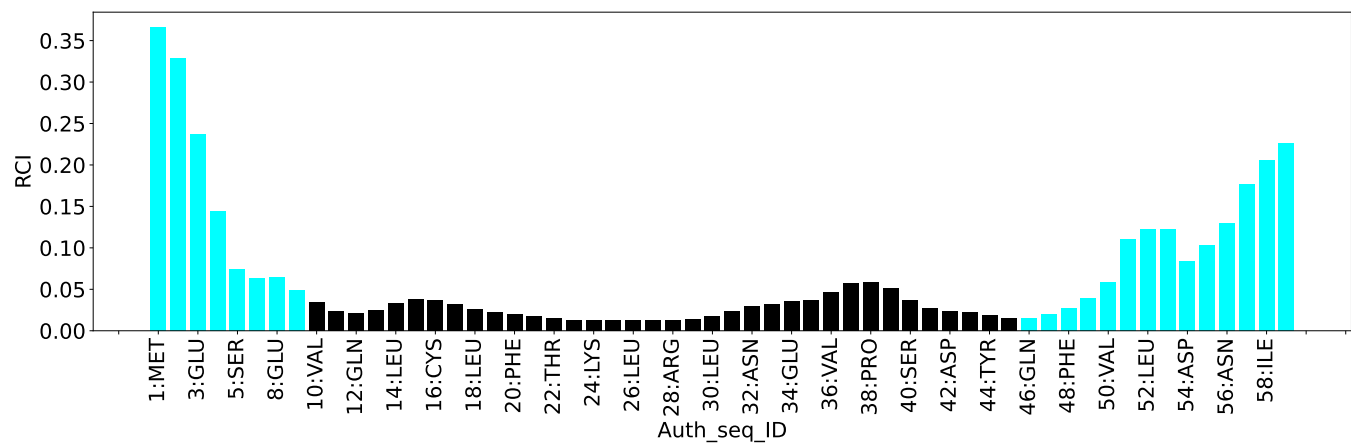
7.1.4 Statistically unusual chemical shifts [i](#)

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

8.1 Conformationally restricting restraints

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	978
Intra-residue ($ i-j =0$)	387
Sequential ($ i-j =1$)	193
Medium range ($ i-j >1$ and $ i-j <5$)	171
Long range ($ i-j \geq 5$)	208
Inter-chain	0
Hydrogen bond restraints	19
Disulfide bond restraints	0
Total dihedral-angle restraints	77
Number of unmapped restraints	0
Number of restraints per residue	17.6
Number of long range restraints per residue ¹	3.6

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

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

Distance violations less than 0.1 Å are not included in the calculation.

Bins (Å)	Average number of violations per model	Max (Å)
0.1-0.2 (Small)	13.2	0.2
0.2-0.5 (Medium)	27.9	0.5
>0.5 (Large)	40.7	3.04

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

Dihedral-angle violations less than 1° are not included in the calculation.

Bins (°)	Average number of violations per model	Max (°)
1.0-10.0 (Small)	4.7	5.37
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis ⓘ

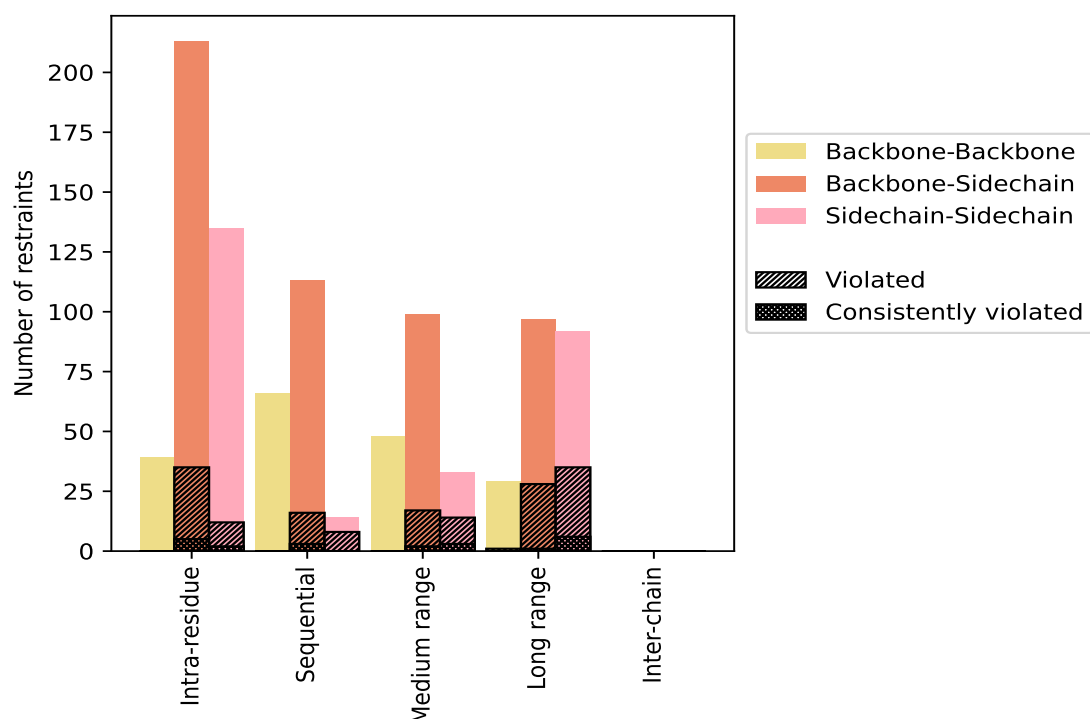
9.1 Summary of distance violations ⓘ

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.

Restraints type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue ($i-j =0$)	387	39.6	47	12.1	4.8	7	1.8	0.7
Backbone-Backbone	39	4.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	213	21.8	35	16.4	3.6	5	2.3	0.5
Sidechain-Sidechain	135	13.8	12	8.9	1.2	2	1.5	0.2
Sequential ($i-j =1$)	193	19.7	24	12.4	2.5	3	1.6	0.3
Backbone-Backbone	66	6.7	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	113	11.6	16	14.2	1.6	3	2.7	0.3
Sidechain-Sidechain	14	1.4	8	57.1	0.8	0	0.0	0.0
Medium range ($i-j >1$ & $i-j <5$)	171	17.5	31	18.1	3.2	5	2.9	0.5
Backbone-Backbone	48	4.9	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	90	9.2	17	18.9	1.7	2	2.2	0.2
Sidechain-Sidechain	33	3.4	14	42.4	1.4	3	9.1	0.3
Long range ($i-j \geq 5$)	208	21.3	62	29.8	6.3	7	3.4	0.7
Backbone-Backbone	29	3.0	1	3.4	0.1	0	0.0	0.0
Backbone-Sidechain	87	8.9	26	29.9	2.7	1	1.1	0.1
Sidechain-Sidechain	92	9.4	35	38.0	3.6	6	6.5	0.6
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	19	1.9	2	10.5	0.2	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	978	100.0	166	17.0	17.0	22	2.2	2.2
Backbone-Backbone	182	18.6	1	0.5	0.1	0	0.0	0.0
Backbone-Sidechain	522	53.4	96	18.4	9.8	11	2.1	1.1
Sidechain-Sidechain	274	28.0	69	25.2	7.1	11	4.0	1.1

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

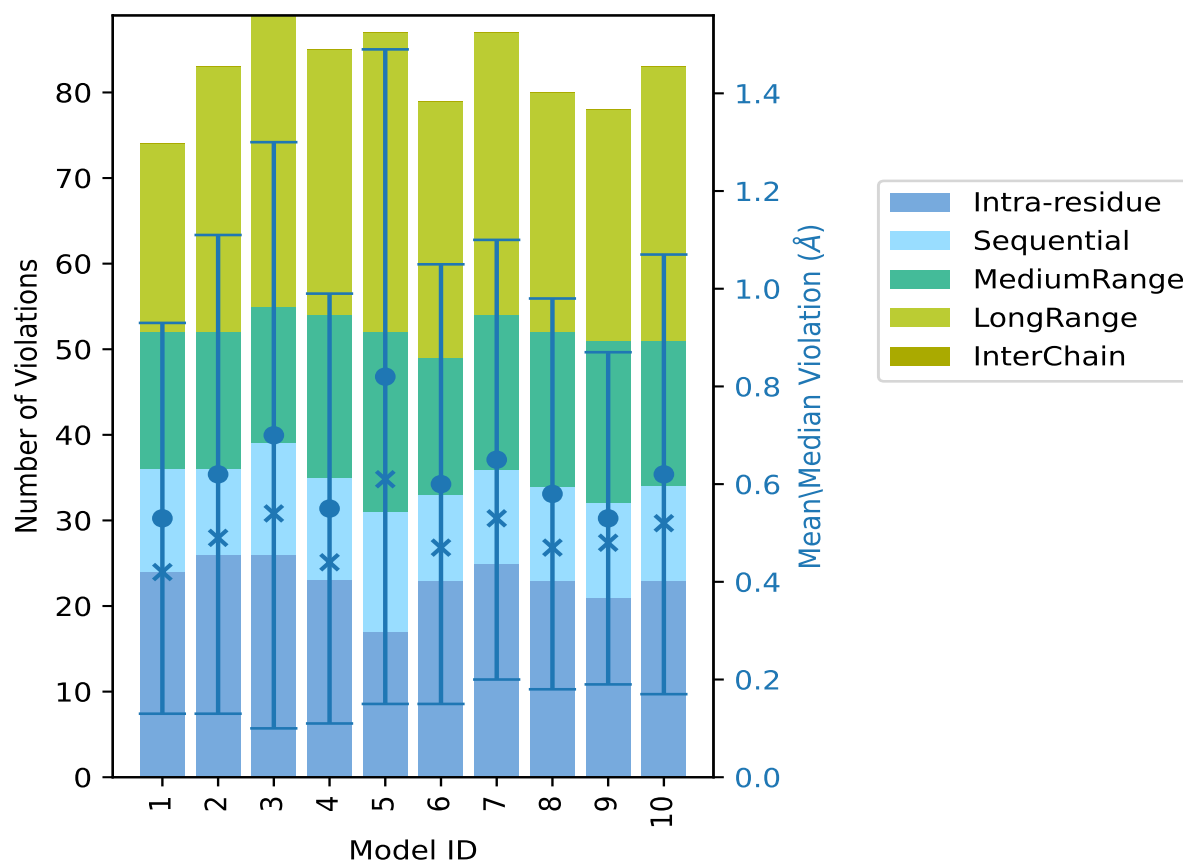
9.2 Distance violation statistics for each model [i](#)

The following table provides the distance violation statistics for each model in the ensemble. Violations less than 0.1 Å are not included in the statistics.

Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
1	24	12	16	22	0	74	0.53	1.72	0.4	0.42
2	26	10	16	31	0	83	0.62	2.83	0.49	0.49
3	26	13	16	34	0	89	0.7	2.99	0.6	0.54
4	23	12	19	31	0	85	0.55	2.19	0.44	0.44
5	17	14	21	35	0	87	0.82	3.04	0.67	0.61
6	23	10	16	30	0	79	0.6	2.04	0.45	0.47
7	25	11	18	33	0	87	0.65	1.94	0.45	0.53
8	23	11	18	28	0	80	0.58	1.63	0.4	0.47
9	21	11	19	27	0	78	0.53	1.63	0.34	0.48
10	23	11	17	32	0	83	0.62	2.1	0.45	0.52

¹Intra-residue restraints, ²Sequential restraints, ³Medium range restraints, ⁴Long range restraints, ⁵Inter-chain restraints, ⁶Standard deviation

9.2.1 Bar graph : Distance Violation statistics for each model [i](#)



The mean(dot),median(x) and the standard deviation are shown in blue with respect to the y axis on the right

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

Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 795(IR:340, SQ:169, MR:140, LR:146, IC:0) restraints are not violated in the ensemble.

Number of violated restraints						Fraction of the ensemble	
IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total	Count ⁶	%
12	6	6	20	0	44	1	10.0
5	2	4	7	0	18	2	20.0
4	2	0	2	0	8	3	30.0

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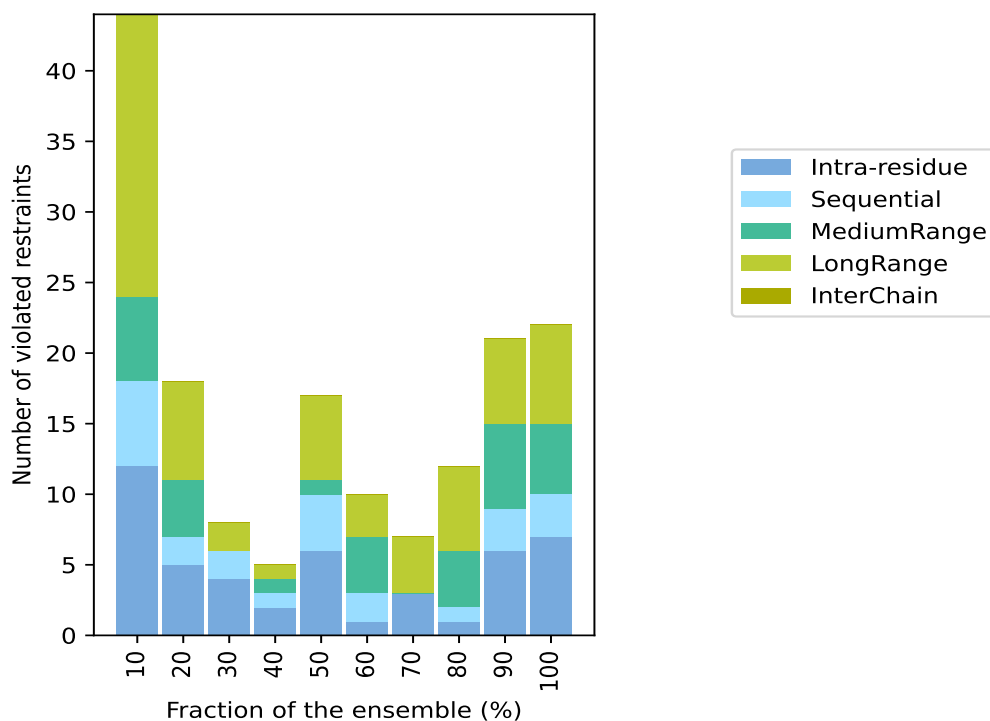
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Number of violated restraints						Fraction of the ensemble	
IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total	Count ⁶	%
2	1	1	1	0	5	4	40.0
6	4	1	6	0	17	5	50.0
1	2	4	3	0	10	6	60.0
3	0	0	4	0	7	7	70.0
1	1	4	6	0	12	8	80.0
6	3	6	6	0	21	9	90.0
7	3	5	7	0	22	10	100.0

¹Intra-residue restraints, ²Sequential restraints, ³Medium range restraints, ⁴Long range restraints,

⁵Inter-chain restraints, ⁶ Number of models with violations

9.3.1 Bar graph : Distance violation statistics for the ensemble ⓘ

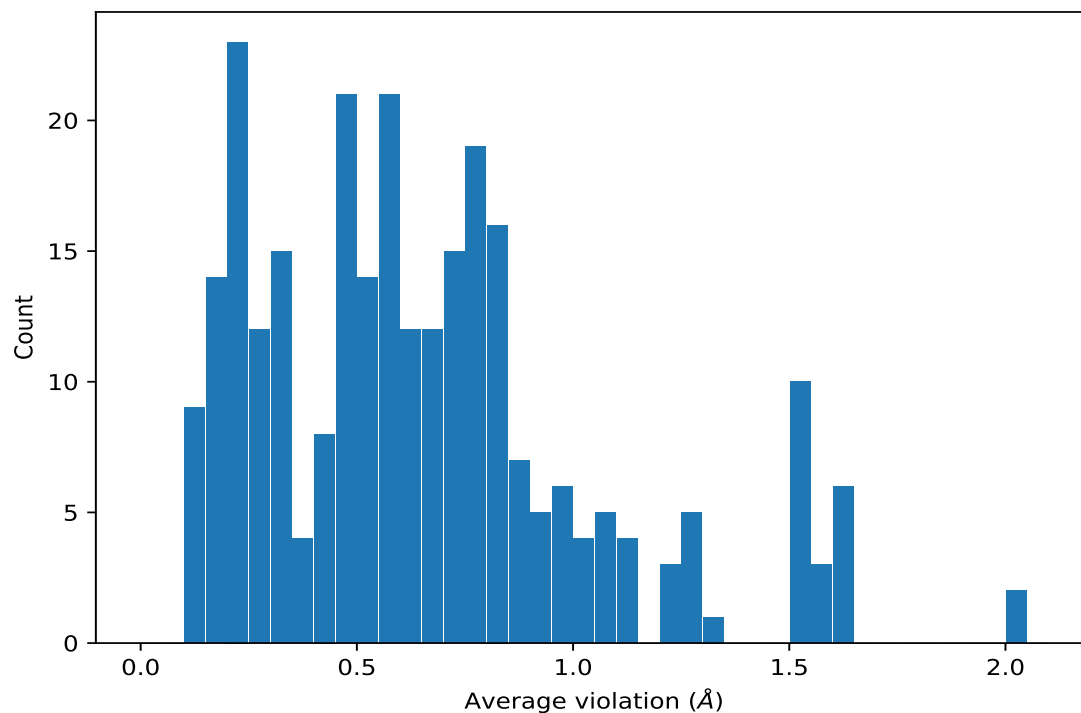


9.4 Most violated distance restraints in the ensemble ⓘ

9.4.1 Histogram : Distribution of mean distance violations ⓘ

The following histogram shows the distribution of the average value of the violation. The average is calculated for each restraint that is violated in more than one model over all the violated models

in the ensemble



9.4.2 Table: Most violated distance restraints [i](#)

The following table provides the mean and the standard deviation of the violations for the 10 worst performing restraints, sorted by number of violated models and the mean violation value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint. Rows with same key represent combinatorial or ambiguous restraints and are counted as a single restraint.

Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,253)	1:41:A:ILE:HG23	1:45:A:TYR:HB2	10	1.65	0.54	1.76
(1,253)	1:41:A:ILE:HG22	1:45:A:TYR:HB2	10	1.65	0.54	1.76
(1,253)	1:41:A:ILE:HG21	1:45:A:TYR:HB2	10	1.65	0.54	1.76
(1,89)	1:18:A:LEU:HA	1:18:A:LEU:HD13	10	1.6	0.04	1.61
(1,89)	1:18:A:LEU:HA	1:18:A:LEU:HD12	10	1.6	0.04	1.61
(1,89)	1:18:A:LEU:HA	1:18:A:LEU:HD11	10	1.6	0.04	1.61
(1,250)	1:10:A:VAL:HG13	1:50:A:VAL:HG12	10	1.54	0.77	1.68
(1,250)	1:10:A:VAL:HG12	1:50:A:VAL:HG13	10	1.54	0.77	1.68
(1,250)	1:10:A:VAL:HG12	1:50:A:VAL:HG11	10	1.54	0.77	1.68
(1,250)	1:10:A:VAL:HG12	1:50:A:VAL:HG12	10	1.54	0.77	1.68
(1,250)	1:10:A:VAL:HG11	1:50:A:VAL:HG13	10	1.54	0.77	1.68
(1,250)	1:10:A:VAL:HG11	1:50:A:VAL:HG12	10	1.54	0.77	1.68
(1,250)	1:10:A:VAL:HG13	1:50:A:VAL:HG11	10	1.54	0.77	1.68
(1,778)	1:19:A:THR:H	1:18:A:LEU:HD13	10	1.51	0.12	1.52
(1,778)	1:19:A:THR:H	1:18:A:LEU:HD12	10	1.51	0.12	1.52

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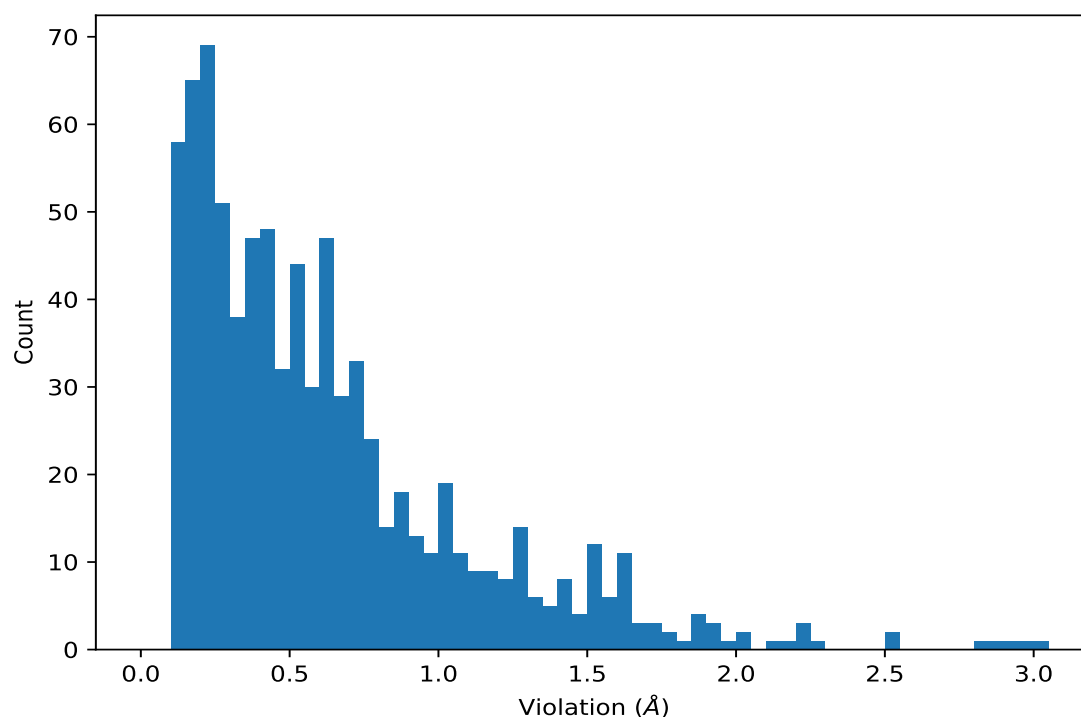
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,778)	1:19:A:THR:H	1:18:A:LEU:HD11	10	1.51	0.12	1.52
(1,110)	1:20:A:PHE:HB3	1:26:A:LEU:HB3	10	1.3	0.18	1.32
(1,254)	1:41:A:ILE:HG21	1:26:A:LEU:HD21	10	1.11	0.54	1.04
(1,254)	1:41:A:ILE:HG23	1:26:A:LEU:HD23	10	1.11	0.54	1.04
(1,254)	1:41:A:ILE:HG21	1:26:A:LEU:HD22	10	1.11	0.54	1.04
(1,254)	1:41:A:ILE:HG21	1:26:A:LEU:HD23	10	1.11	0.54	1.04
(1,297)	1:30:A:LEU:HG	1:44:A:TYR:HB3	10	1.06	0.17	1.06
(1,163)	1:38:A:PRO:HB2	1:41:A:ILE:HD11	10	0.94	0.39	1.17
(1,163)	1:38:A:PRO:HB2	1:41:A:ILE:HD13	10	0.94	0.39	1.17
(1,163)	1:38:A:PRO:HB2	1:41:A:ILE:HD12	10	0.94	0.39	1.17
(1,263)	1:41:A:ILE:HD12	1:27:A:ILE:HG13	10	0.74	0.24	0.74
(1,263)	1:41:A:ILE:HD13	1:27:A:ILE:HG13	10	0.74	0.24	0.74
(1,263)	1:41:A:ILE:HD11	1:27:A:ILE:HG13	10	0.74	0.24	0.74
(1,900)	1:26:A:LEU:H	1:30:A:LEU:HG	10	0.69	0.19	0.72

¹Number of violated models, ²Standard deviation

9.5 All violated distance restraints [i](#)

9.5.1 Histogram : Distribution of distance violations [i](#)

The following histogram shows the distribution of the absolute value of the violation for all violated restraints in the ensemble.



9.5.2 Table : All distance violations

The following table provides the 10 worst performing restraints, sorted by the violation value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint. Rows with same key represent combinatorial or ambiguous restraints and are counted as a single restraint.

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,857)	1:26:A:LEU:HD21	1:41:A:ILE:HD12	5	3.04
(1,332)	1:38:A:PRO:HB2	1:31:A:VAL:HG22	3	2.99
(1,105)	1:38:A:PRO:HD2	1:31:A:VAL:HG22	3	2.93
(1,250)	1:10:A:VAL:HG12	1:50:A:VAL:HG12	5	2.88
(1,235)	1:10:A:VAL:HG23	1:21:A:ARG:HG2	2	2.83
(1,254)	1:41:A:ILE:HG21	1:26:A:LEU:HD23	5	2.54
(1,250)	1:10:A:VAL:HG12	1:50:A:VAL:HG11	3	2.51
(1,266)	1:26:A:LEU:HD21	1:41:A:ILE:HD12	5	2.26
(1,220)	1:26:A:LEU:HD22	1:23:A:LYS:HD3	5	2.24
(1,253)	1:41:A:ILE:HG21	1:45:A:TYR:HB2	5	2.22

10 Dihedral-angle violation analysis [i](#)

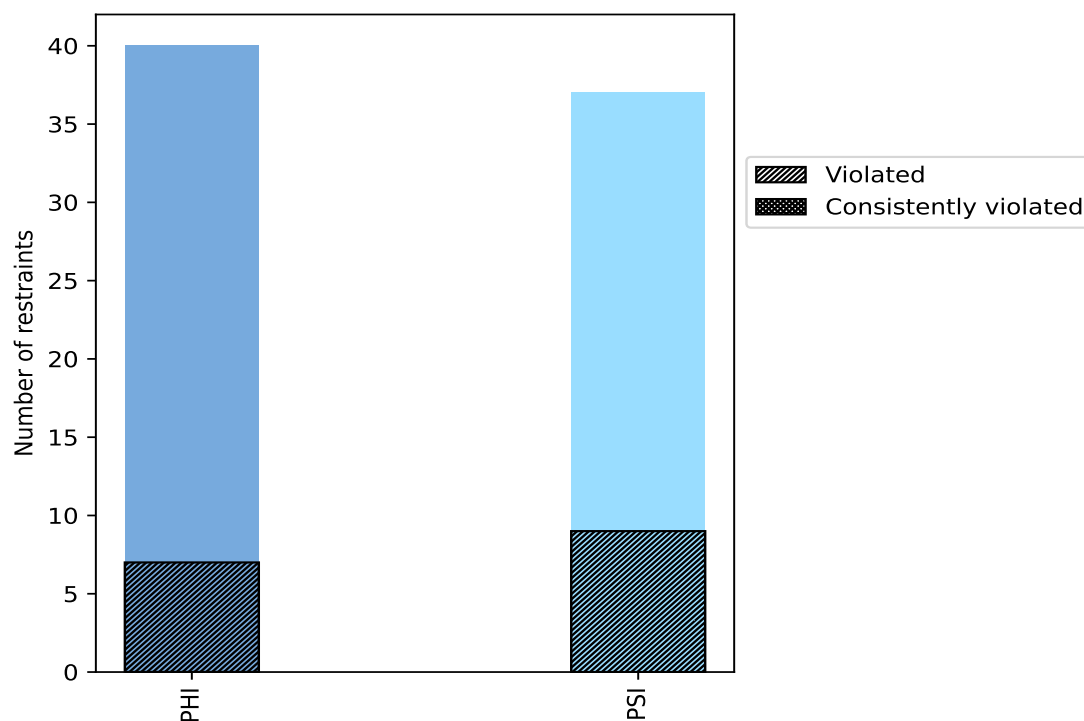
10.1 Summary of dihedral-angle violations [i](#)

The following table provides the summary of dihedral-angle violations in different dihedral-angle types. Violations less than 1° are not included in the calculation.

Angle type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
PHI	40	51.9	7	17.5	9.1	0	0.0	0.0
PSI	37	48.1	9	24.3	11.7	0	0.0	0.0
Total	77	100.0	16	20.8	20.8	0	0.0	0.0

¹ percentage calculated with respect to total number of dihedral-angle restraints, ² percentage calculated with respect to number of restraints in a particular dihedral-angle type, ³ violated in at least one model, ⁴ violated in all the models

10.1.1 Bar chart : Distribution of dihedral-angles and violations [i](#)



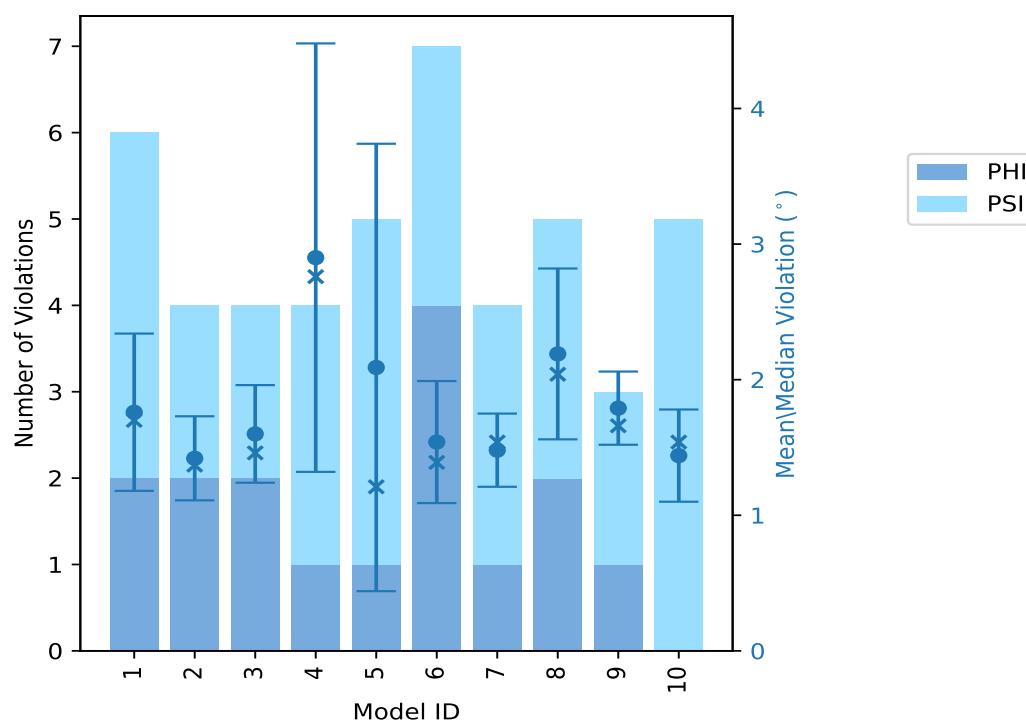
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

10.2 Dihedral-angle violation statistics for each model [i](#)

The following table provides the dihedral-angle violation statistics for each model in the ensemble. Violations less than 1° are not included in the statistics.

Model ID	Number of violations			Mean (°)	Max (°)	SD (°)	Median (°)
	PHI	PSI	Total				
1	2	4	6	1.76	2.83	0.58	1.7
2	2	2	4	1.42	1.88	0.31	1.37
3	2	2	4	1.6	2.19	0.36	1.46
4	1	3	4	2.9	4.97	1.58	2.76
5	1	4	5	2.09	5.37	1.65	1.21
6	4	3	7	1.54	2.45	0.45	1.39
7	1	3	4	1.48	1.78	0.27	1.54
8	2	3	5	2.19	3.27	0.63	2.04
9	1	2	3	1.79	2.16	0.27	1.66
10	0	5	5	1.44	1.91	0.34	1.54

10.2.1 Bar graph : Dihedral violation statistics for each model [i](#)



The mean(dot),median(x) and the standard deviation are shown in blue with respect to the y axis on the right

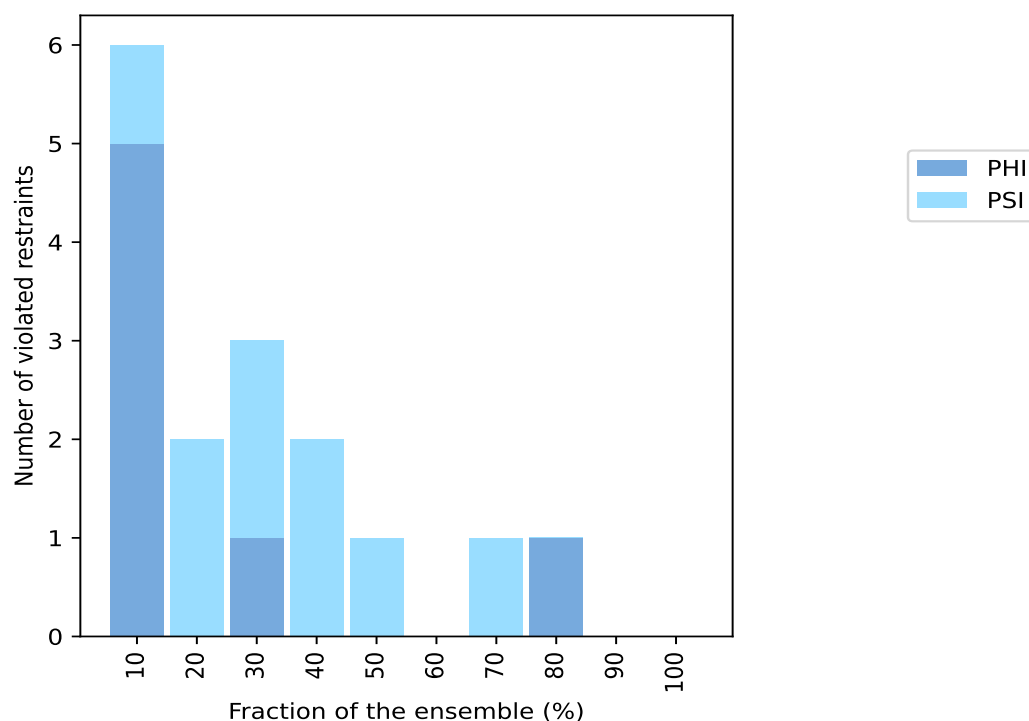
10.3 Dihedral-angle violation statistics for the ensemble [i](#)

Violation analysis may find that some restraints are violated in very few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of ensemble.

Number of violated restraints			Fraction of the ensemble	
PHI	PSI	Total	Count ¹	%
5	1	6	1	10.0
0	2	2	2	20.0
1	2	3	3	30.0
0	2	2	4	40.0
0	1	1	5	50.0
0	0	0	6	60.0
0	1	1	7	70.0
1	0	1	8	80.0
0	0	0	9	90.0
0	0	0	10	100.0

¹ Number of models with violations

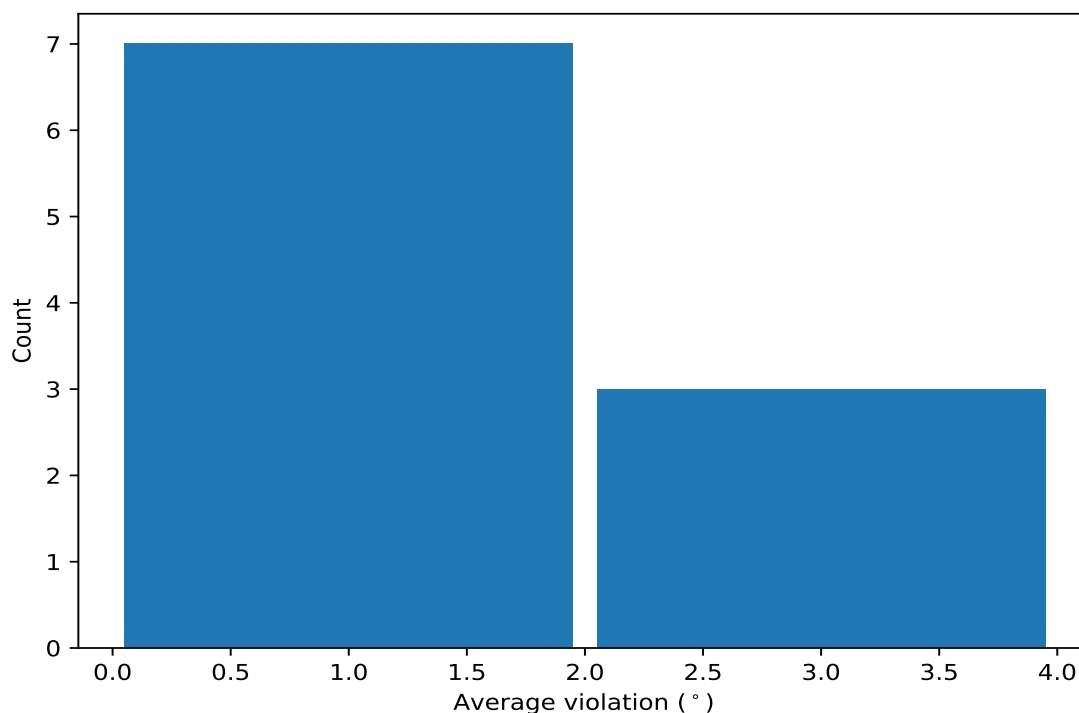
10.3.1 Bar graph : Dihedral-angle Violation statistics for the ensemble [i](#)



10.4 Most violated dihedral-angle restraints in the ensemble [i](#)

10.4.1 Histogram : Distribution of mean dihedral-angle violations [i](#)

The following histogram shows the distribution of the average value of the violation. The average is calculated for each restraint that is violated in more than one model over all the violated models in the ensemble



10.4.2 Table: Most violated dihedral-angle restraints [i](#)

The following table provides the mean and the standard deviation of the violations for the 10 worst performing restraints, sorted by number of violated models and the mean violation value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint.

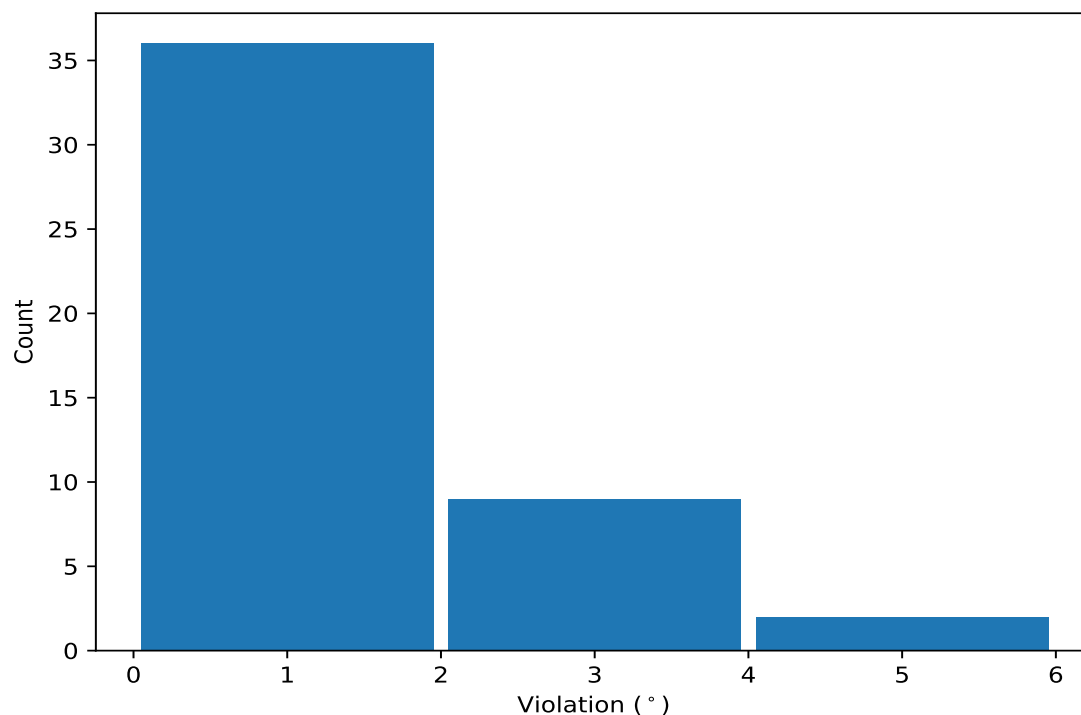
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,40)	1:50:A:VAL:C	1:51:A:SER:N	1:51:A:SER:CA	1:51:A:SER:C	8	1.86	0.63	1.65
(1,56)	1:26:A:LEU:N	1:26:A:LEU:CA	1:26:A:LEU:C	1:27:A:ILE:N	7	2.27	1.27	1.79
(1,59)	1:29:A:HIS:N	1:29:A:HIS:CA	1:29:A:HIS:C	1:30:A:LEU:N	5	1.51	0.21	1.55
(1,76)	1:49:A:SER:N	1:49:A:SER:CA	1:49:A:SER:C	1:50:A:VAL:N	4	1.31	0.19	1.34
(1,70)	1:43:A:TYR:N	1:43:A:TYR:CA	1:43:A:TYR:C	1:44:A:TYR:N	4	1.29	0.24	1.18
(1,36)	1:46:A:GLN:C	1:47:A:SER:N	1:47:A:SER:CA	1:47:A:SER:C	3	2.43	1.05	2.04
(1,75)	1:48:A:PHE:N	1:48:A:PHE:CA	1:48:A:PHE:C	1:49:A:SER:N	3	1.67	0.57	1.54
(1,47)	1:14:A:LEU:N	1:14:A:LEU:CA	1:14:A:LEU:C	1:15:A:ARG:N	3	1.65	0.83	1.06
(1,74)	1:47:A:SER:N	1:47:A:SER:CA	1:47:A:SER:C	1:48:A:PHE:N	2	3.48	1.48	3.48
(1,69)	1:42:A:ASP:N	1:42:A:ASP:CA	1:42:A:ASP:C	1:43:A:TYR:N	2	1.62	0.29	1.62

¹ Number of violated models, ²Standard deviation, All angle values are in degree (°)

10.5 All violated dihedral-angle restraints [i](#)

10.5.1 Histogram : Distribution of violations [i](#)

The following histogram shows the distribution of the absolute value of the violation for all violated restraints in the ensemble.



10.5.2 Table: All violated dihedral-angle restraints [i](#)

The following table provides the list of violations for the 10 worst performing restraints, sorted by the violation value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint.

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,56)	1:26:A:LEU:N	1:26:A:LEU:CA	1:26:A:LEU:C	1:27:A:ILE:N	5	5.37
(1,74)	1:47:A:SER:N	1:47:A:SER:CA	1:47:A:SER:C	1:48:A:PHE:N	4	4.97
(1,36)	1:46:A:GLN:C	1:47:A:SER:N	1:47:A:SER:CA	1:47:A:SER:C	4	3.87
(1,40)	1:50:A:VAL:C	1:51:A:SER:N	1:51:A:SER:CA	1:51:A:SER:C	8	3.27
(1,47)	1:14:A:LEU:N	1:14:A:LEU:CA	1:14:A:LEU:C	1:15:A:ARG:N	1	2.83
(1,29)	1:38:A:PRO:C	1:39:A:LEU:N	1:39:A:LEU:CA	1:39:A:LEU:C	6	2.45
(1,75)	1:48:A:PHE:N	1:48:A:PHE:CA	1:48:A:PHE:C	1:49:A:SER:N	8	2.43
(1,40)	1:50:A:VAL:C	1:51:A:SER:N	1:51:A:SER:CA	1:51:A:SER:C	3	2.19
(1,40)	1:50:A:VAL:C	1:51:A:SER:N	1:51:A:SER:CA	1:51:A:SER:C	9	2.16
(1,36)	1:46:A:GLN:C	1:47:A:SER:N	1:47:A:SER:CA	1:47:A:SER:C	8	2.04