



Full wwPDB NMR Structure Validation Report ⓘ

Dec 25, 2024 – 05:07 AM EST

PDB ID : 5VWL
BMRB ID : 30297
Title : Solution NMR Structure of the Membrane Associated Segment of HIV-1 gp41
Cytoplasmic Tail
Authors : Saad, J.S.; Murphy, R.E.; Samal, A.; Vlach, J.
Deposited on : 2017-05-22

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 : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.40

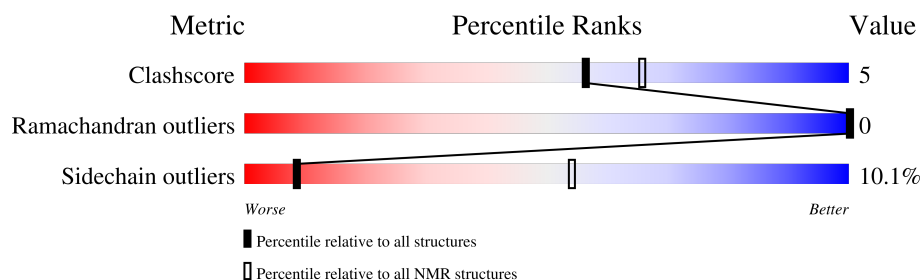
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 79%.

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	210492	14027
Ramachandran outliers	207382	12486
Sidechain outliers	206894	12463

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	105	<div> <div>53%</div> <div>9%</div> <div>38%</div> </div>

2 Ensemble composition and analysis

This entry contains 20 models. Model 10 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *target function*.

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:768-A:783 (16)	0.15	8
2	A:800-A:823 (24)	0.09	10
3	A:826-A:842 (17)	0.26	7
4	A:848-A:855 (8)	0.19	13

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 3 clusters and 1 single-model cluster was found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1792 atoms, of which 916 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Cytoplasmic tail of HIV-1 gp41 protein.

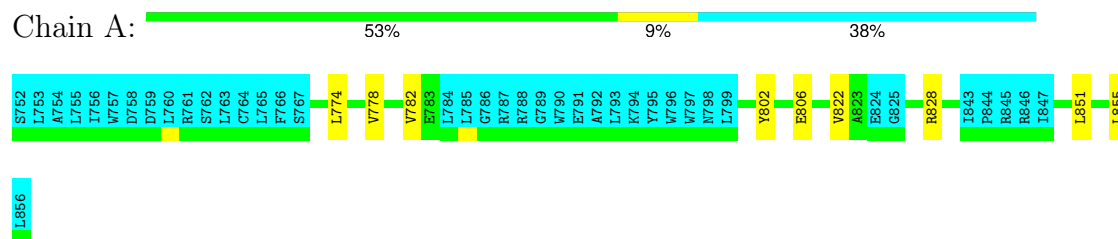
Mol	Chain	Residues	Atoms						Trace
1	A	105	Total	C	H	N	O	S	0
			1792	567	916	163	145	1	

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: Cytoplasmic tail of HIV-1 gp41 protein

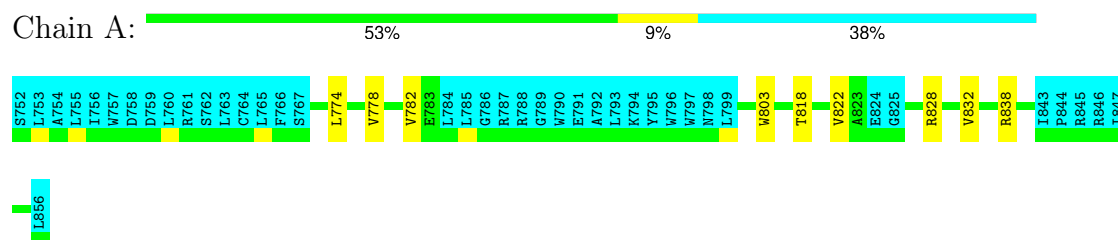


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

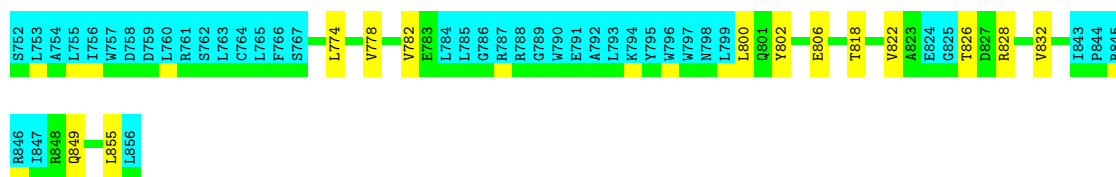
- Molecule 1: Cytoplasmic tail of HIV-1 gp41 protein



4.2.2 Score per residue for model 2

- Molecule 1: Cytoplasmic tail of HIV-1 gp41 protein

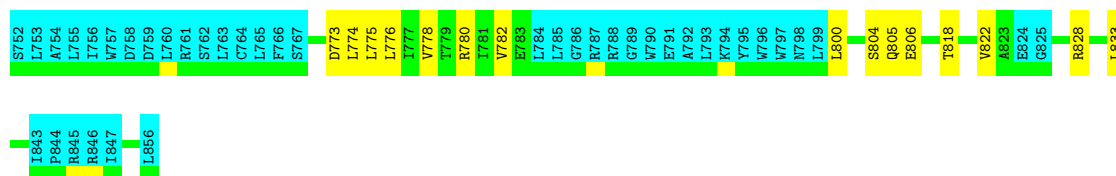




4.2.3 Score per residue for model 3

- Molecule 1: Cytoplasmic tail of HIV-1 gp41 protein

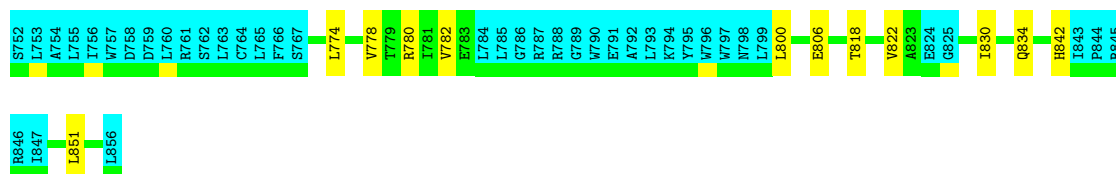
Chain A: 48% 14% 38%



4.2.4 Score per residue for model 4

- Molecule 1: Cytoplasmic tail of HIV-1 gp41 protein

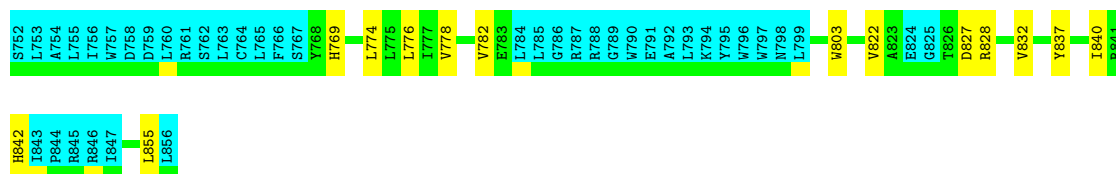
Chain A: 50% 11% 38%



4.2.5 Score per residue for model 5

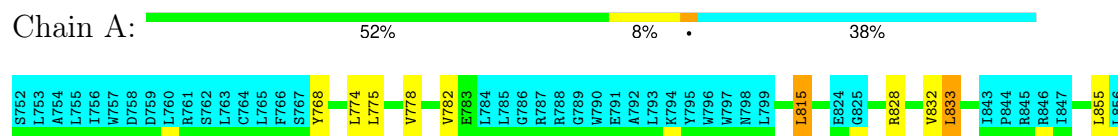
- Molecule 1: Cytoplasmic tail of HIV-1 gp41 protein

Chain A: 49% 13% 38%



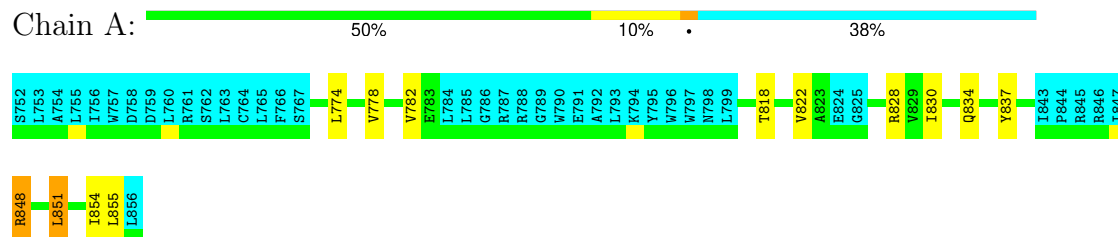
4.2.6 Score per residue for model 6

- Molecule 1: Cytoplasmic tail of HIV-1 gp41 protein



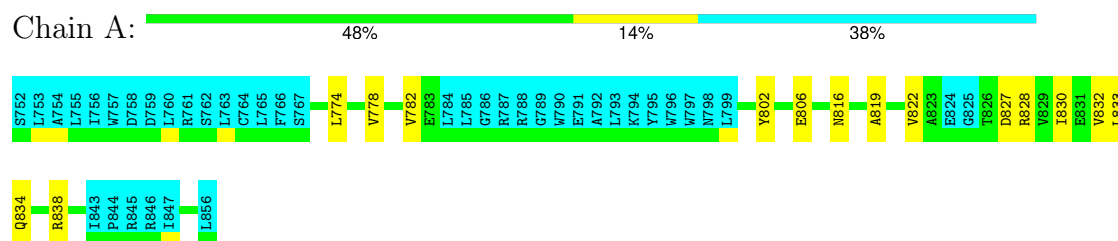
4.2.7 Score per residue for model 7

- Molecule 1: Cytoplasmic tail of HIV-1 gp41 protein



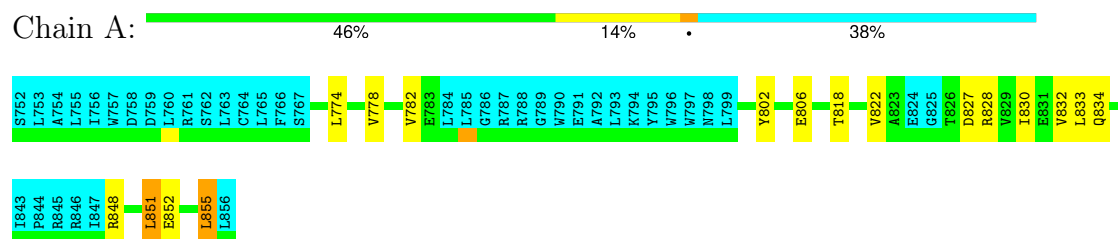
4.2.8 Score per residue for model 8

- Molecule 1: Cytoplasmic tail of HIV-1 gp41 protein



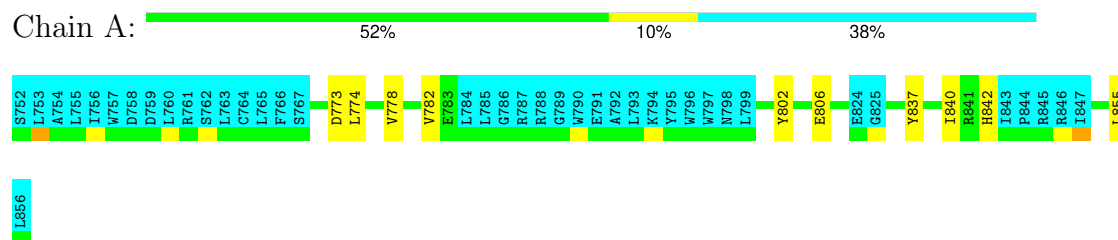
4.2.9 Score per residue for model 9

- Molecule 1: Cytoplasmic tail of HIV-1 gp41 protein



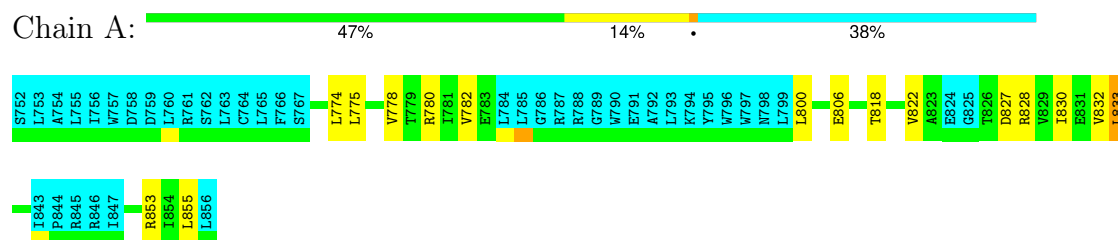
4.2.10 Score per residue for model 10 (medoid)

- Molecule 1: Cytoplasmic tail of HIV-1 gp41 protein



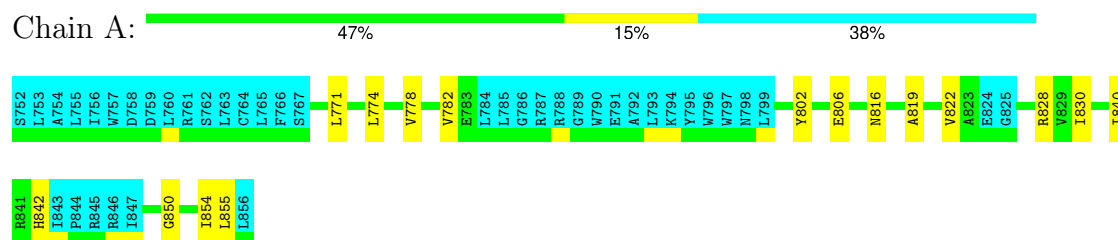
4.2.11 Score per residue for model 11

- Molecule 1: Cytoplasmic tail of HIV-1 gp41 protein



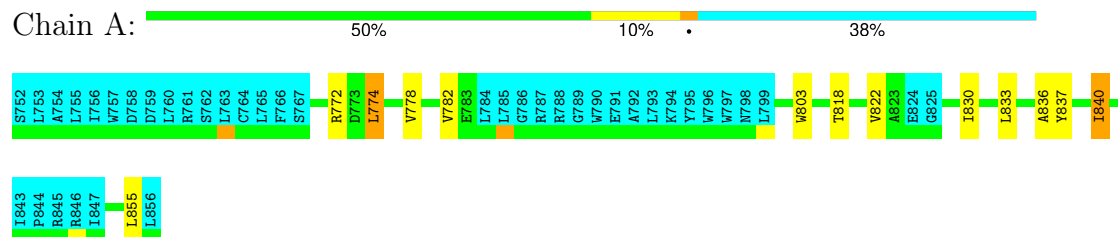
4.2.12 Score per residue for model 12

- Molecule 1: Cytoplasmic tail of HIV-1 gp41 protein



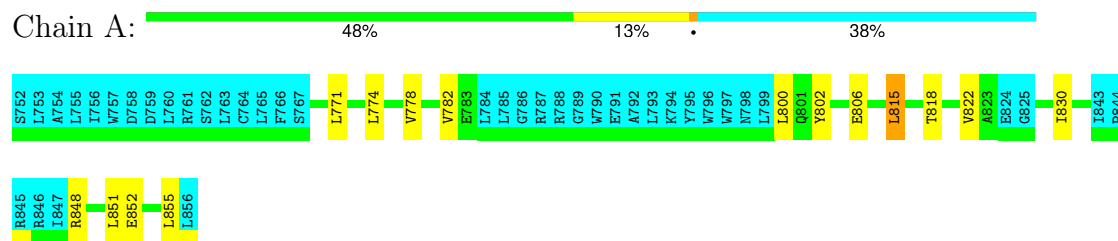
4.2.13 Score per residue for model 13

- Molecule 1: Cytoplasmic tail of HIV-1 gp41 protein



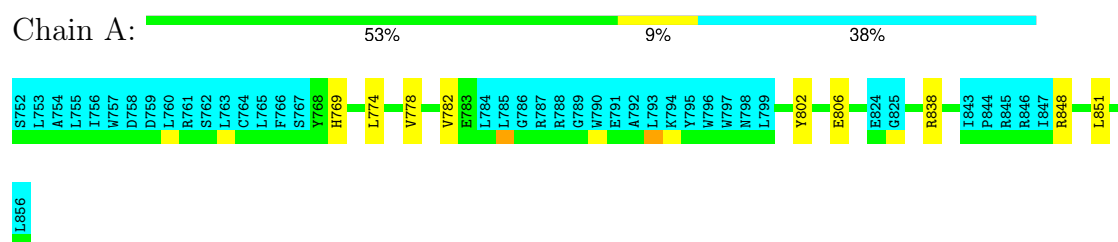
4.2.14 Score per residue for model 14

- Molecule 1: Cytoplasmic tail of HIV-1 gp41 protein



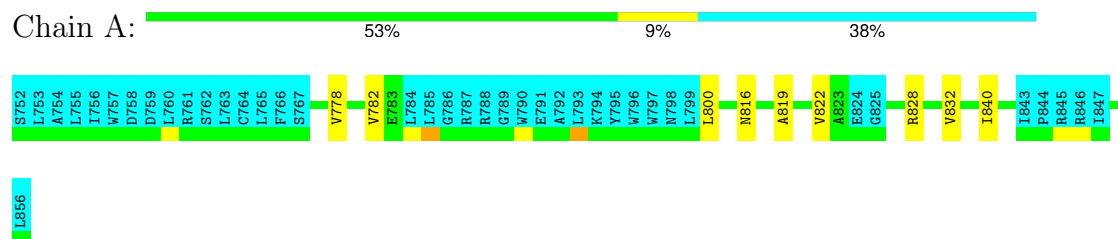
4.2.15 Score per residue for model 15

- Molecule 1: Cytoplasmic tail of HIV-1 gp41 protein



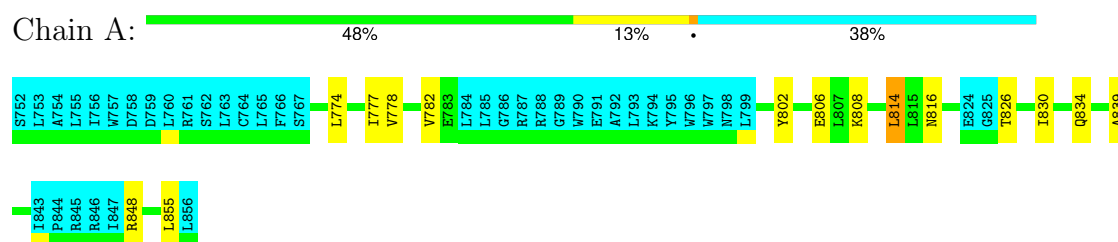
4.2.16 Score per residue for model 16

- Molecule 1: Cytoplasmic tail of HIV-1 gp41 protein



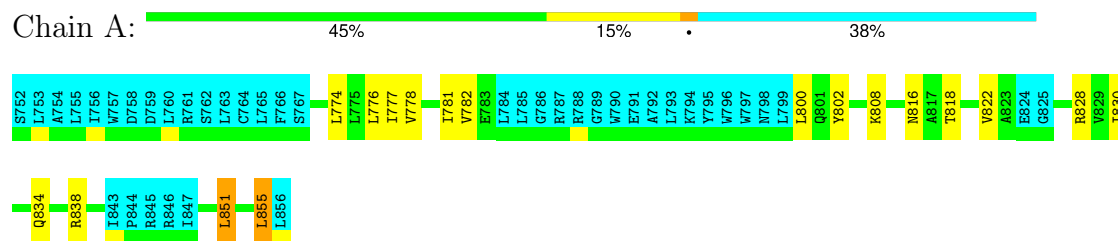
4.2.17 Score per residue for model 17

- Molecule 1: Cytoplasmic tail of HIV-1 gp41 protein



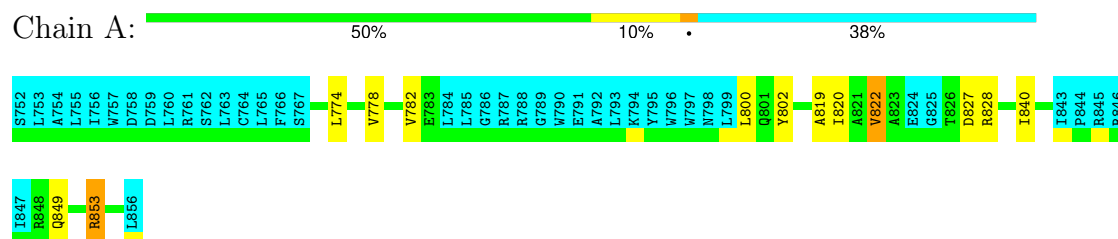
4.2.18 Score per residue for model 18

- Molecule 1: Cytoplasmic tail of HIV-1 gp41 protein



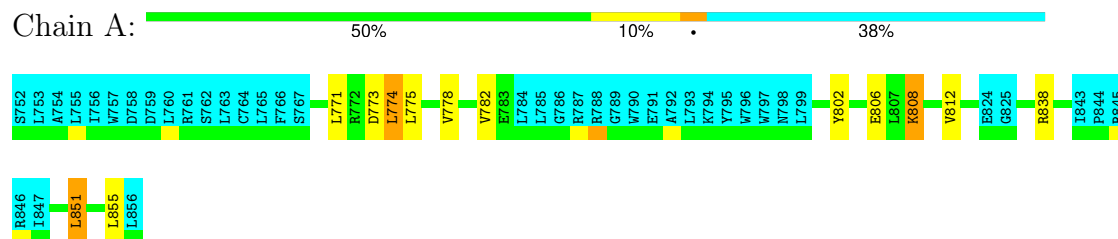
4.2.19 Score per residue for model 19

- Molecule 1: Cytoplasmic tail of HIV-1 gp41 protein



4.2.20 Score per residue for model 20

- Molecule 1: Cytoplasmic tail of HIV-1 gp41 protein



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
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	1261
Number of shifts mapped to atoms	1261
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	79%

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	534	565	565	5±1
All	All	10680	11300	11300	103

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 5.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:778:VAL:O	1:A:782:VAL:HG23	0.66	1.90	16	20
1:A:774:LEU:O	1:A:778:VAL:HG23	0.61	1.95	5	19
1:A:774:LEU:HD12	1:A:777:ILE:HD11	0.60	1.74	17	1
1:A:822:VAL:HG22	1:A:827:ASP:HB2	0.60	1.71	19	1
1:A:851:LEU:HD22	1:A:854:ILE:HD11	0.60	1.74	7	1
1:A:836:ALA:O	1:A:840:ILE:HG23	0.56	2.00	13	1
1:A:828:ARG:O	1:A:832:VAL:HG23	0.56	2.01	8	8
1:A:822:VAL:HG23	1:A:828:ARG:CB	0.56	2.31	16	1
1:A:822:VAL:HG23	1:A:828:ARG:HB2	0.55	1.77	16	1
1:A:777:ILE:HD11	1:A:781:ILE:HD11	0.55	1.79	18	1
1:A:851:LEU:HD23	1:A:851:LEU:O	0.55	2.02	15	1
1:A:822:VAL:HG22	1:A:828:ARG:CD	0.54	2.32	7	1
1:A:822:VAL:HG22	1:A:827:ASP:CB	0.53	2.34	19	2
1:A:855:LEU:HD12	1:A:855:LEU:O	0.52	2.05	11	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:851:LEU:HD12	1:A:852:GLU:N	0.52	2.19	14	1
1:A:837:TYR:HA	1:A:840:ILE:HD12	0.51	1.80	10	1
1:A:833:LEU:O	1:A:833:LEU:HD13	0.51	2.06	6	2
1:A:830:ILE:HG22	1:A:834:GLN:NE2	0.50	2.22	18	1
1:A:851:LEU:O	1:A:851:LEU:HD13	0.49	2.08	20	3
1:A:818:THR:O	1:A:822:VAL:HG23	0.49	2.08	3	10
1:A:830:ILE:HG22	1:A:834:GLN:OE1	0.49	2.08	7	5
1:A:851:LEU:HD13	1:A:855:LEU:HD23	0.48	1.85	9	1
1:A:848:ARG:HG2	1:A:851:LEU:HD11	0.47	1.87	14	1
1:A:822:VAL:HG13	1:A:828:ARG:HG2	0.46	1.87	3	1
1:A:850:GLY:O	1:A:854:ILE:HG23	0.46	2.10	12	1
1:A:814:LEU:O	1:A:814:LEU:HD13	0.44	2.13	17	1
1:A:808:LYS:O	1:A:812:VAL:HG23	0.44	2.13	20	1
1:A:819:ALA:HA	1:A:822:VAL:HG12	0.43	1.90	19	4
1:A:827:ASP:HA	1:A:830:ILE:HD12	0.43	1.91	11	1
1:A:800:LEU:HD13	1:A:800:LEU:C	0.43	2.35	14	3
1:A:822:VAL:HG12	1:A:828:ARG:HB2	0.42	1.91	18	1
1:A:815:LEU:C	1:A:815:LEU:HD12	0.42	2.35	6	2
1:A:776:LEU:HD23	1:A:777:ILE:N	0.42	2.30	18	1
1:A:822:VAL:HG13	1:A:828:ARG:HB2	0.41	1.93	7	1

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

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	65/105 (62%)	63±1 (97±1%)	2±1 (3±1%)	0±0 (0±0%)	100	100
All	All	1300/2100 (62%)	1257 (97%)	43 (3%)	0 (0%)	100	100

There are no Ramachandran outliers.

6.3.2 Protein sidechains ⓘ

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	56/91 (62%)	50±2 (90±4%)	6±2 (10±4%)	9	54
All	All	1120/1820 (62%)	1007 (90%)	113 (10%)	9	54

All 35 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	806	GLU	12
1	A	802	TYR	11
1	A	855	LEU	10
1	A	833	LEU	6
1	A	838	ARG	5
1	A	851	LEU	5
1	A	816	ASN	5
1	A	775	LEU	4
1	A	848	ARG	4
1	A	773	ASP	3
1	A	800	LEU	3
1	A	842	HIS	3
1	A	837	TYR	3
1	A	771	LEU	3
1	A	830	ILE	3
1	A	840	ILE	3
1	A	808	LYS	3
1	A	826	THR	2
1	A	776	LEU	2
1	A	780	ARG	2
1	A	769	HIS	2
1	A	815	LEU	2
1	A	827	ASP	2
1	A	853	ARG	2
1	A	828	ARG	2
1	A	774	LEU	2
1	A	849	GLN	1
1	A	804	SER	1
1	A	805	GLN	1
1	A	768	TYR	1
1	A	852	GLU	1
1	A	772	ARG	1
1	A	814	LEU	1

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Mol	Chain	Res	Type	Models (Total)
1	A	820	ILE	1
1	A	822	VAL	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates [i](#)

There are no 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 79% 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	1261
Number of shifts mapped to atoms	1261
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

The following errors were found when reading this chemical shift list.

- Chemical shift has been reported more than once. All 12 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	799	LEU	HD11	0.715	0.003	2
1	A	799	LEU	HD12	0.715	0.003	2
1	A	799	LEU	HD13	0.715	0.003	2
1	A	833	LEU	HD11	0.826	0.003	2
1	A	833	LEU	HD12	0.826	0.003	2
1	A	833	LEU	HD13	0.826	0.003	2
1	A	851	LEU	HD11	0.862	0.0	2
1	A	851	LEU	HD12	0.862	0.0	2
1	A	851	LEU	HD13	0.862	0.0	2
1	A	815	LEU	HD11	0.891	.	2
1	A	815	LEU	HD12	0.891	.	2
1	A	815	LEU	HD13	0.891	.	2

7.1.2 Chemical shift referencing ⓘ

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	101	-0.35 ± 0.11	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	97	0.02 ± 0.04	None needed (< 0.5 ppm)
$^{13}\text{C}'$	94	0.48 ± 0.12	None needed (< 0.5 ppm)
^{15}N	94	0.84 ± 0.11	Should be applied

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 79%, i.e. 783 atoms were assigned a chemical shift out of a possible 988. 0 out of 17 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	308/326 (94%)	123/131 (94%)	124/130 (95%)	61/65 (94%)
Sidechain	432/609 (71%)	285/399 (71%)	140/178 (79%)	7/32 (22%)
Aromatic	43/53 (81%)	22/26 (85%)	20/24 (83%)	1/3 (33%)
Overall	783/988 (79%)	430/556 (77%)	284/332 (86%)	69/100 (69%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 78%, i.e. 1249 atoms were assigned a chemical shift out of a possible 1604. 0 out of 27 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	485/527 (92%)	196/213 (92%)	195/210 (93%)	94/104 (90%)
Sidechain	662/957 (69%)	429/627 (68%)	225/281 (80%)	8/49 (16%)
Aromatic	102/120 (85%)	55/59 (93%)	42/54 (78%)	5/7 (71%)
Overall	1249/1604 (78%)	680/899 (76%)	462/545 (85%)	107/160 (67%)

7.1.4 Statistically unusual chemical shifts ⓘ

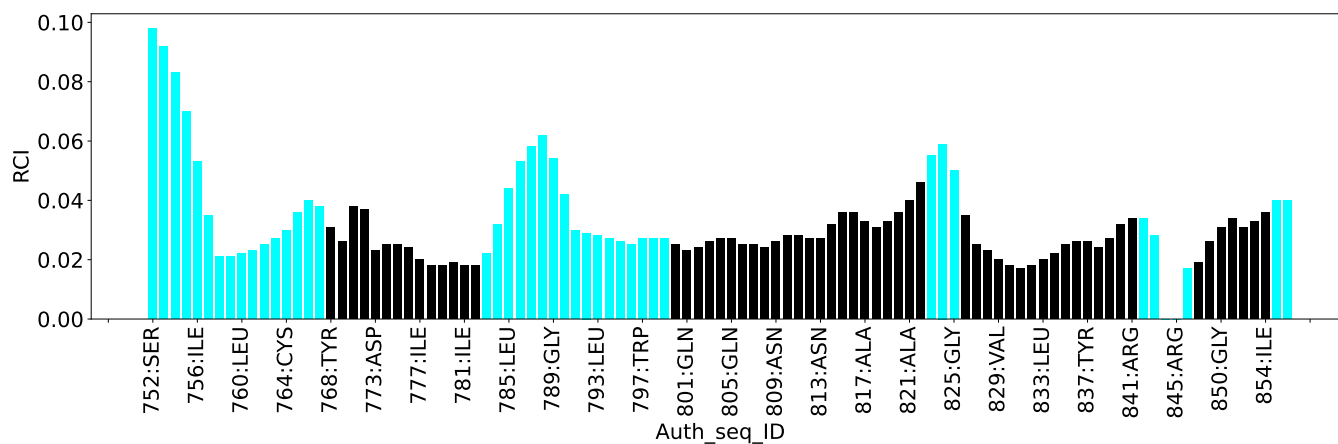
There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots ⓘ

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-

defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition. 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	724
Intra-residue ($ i-j =0$)	100
Sequential ($ i-j =1$)	144
Medium range ($ i-j >1$ and $ i-j <5$)	326
Long range ($ i-j \geq 5$)	0
Inter-chain	0
Hydrogen bond restraints	154
Disulfide bond restraints	0
Total dihedral-angle restraints	360
Number of unmapped restraints	0
Number of restraints per residue	10.3
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

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)	8.2	0.2
0.2-0.5 (Medium)	0.2	0.27
>0.5 (Large)	None	None

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)	0.6	2.6
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis ⓘ

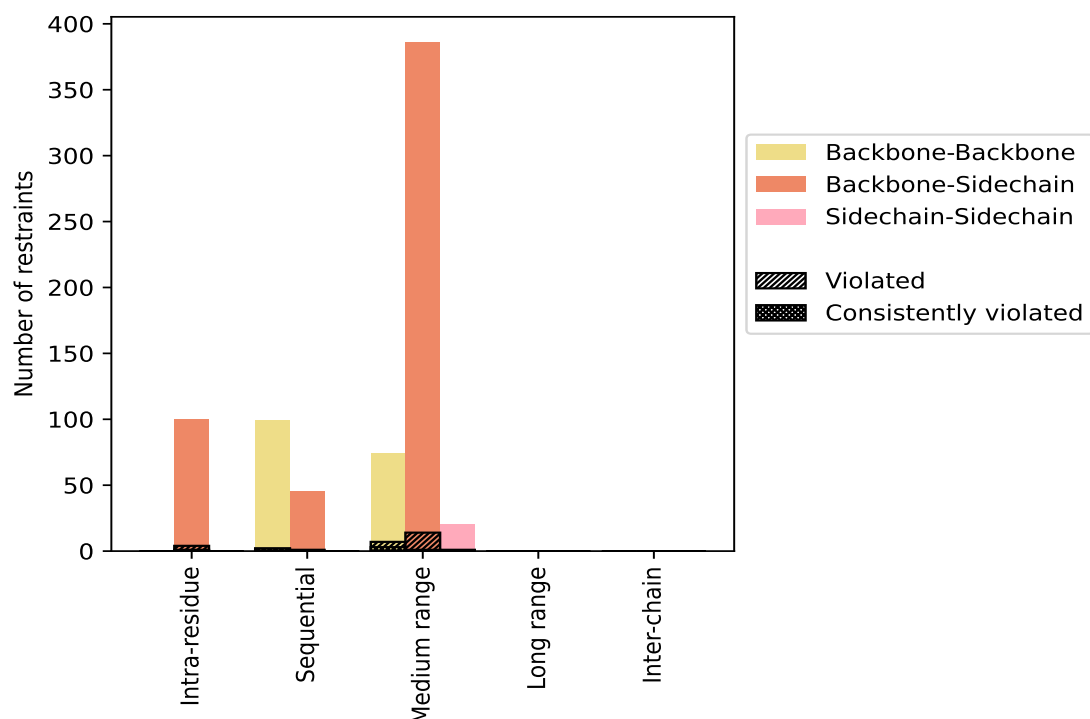
9.1 Summary of distance violations ⓘ

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.

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue ($i-j =0$)	100	13.8	4	4.0	0.6	1	1.0	0.1
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	100	13.8	4	4.0	0.6	1	1.0	0.1
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sequential ($i-j =1$)	144	19.9	3	2.1	0.4	2	1.4	0.3
Backbone-Backbone	99	13.7	2	2.0	0.3	2	2.0	0.3
Backbone-Sidechain	45	6.2	1	2.2	0.1	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Medium range ($i-j >1$ & $i-j <5$)	326	45.0	11	3.4	1.5	3	0.9	0.4
Backbone-Backbone	74	10.2	7	9.5	1.0	3	4.1	0.4
Backbone-Sidechain	232	32.0	3	1.3	0.4	0	0.0	0.0
Sidechain-Sidechain	20	2.8	1	5.0	0.1	0	0.0	0.0
Long range ($i-j \geq 5$)	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	154	21.3	11	7.1	1.5	1	0.6	0.1
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	724	100.0	29	4.0	4.0	7	1.0	1.0
Backbone-Backbone	173	23.9	9	5.2	1.2	5	2.9	0.7
Backbone-Sidechain	531	73.3	19	3.6	2.6	2	0.4	0.3
Sidechain-Sidechain	20	2.8	1	5.0	0.1	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](#)

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	1	2	4	0	0	7	0.14	0.19	0.03	0.14
2	1	2	5	0	0	8	0.16	0.27	0.05	0.15
3	2	2	4	0	0	8	0.14	0.19	0.03	0.15
4	2	2	4	0	0	8	0.14	0.19	0.03	0.14
5	1	2	6	0	0	9	0.14	0.19	0.03	0.15
6	1	2	7	0	0	10	0.15	0.21	0.03	0.15
7	2	2	5	0	0	9	0.14	0.19	0.03	0.14
8	1	2	4	0	0	7	0.14	0.19	0.03	0.14
9	3	2	6	0	0	11	0.14	0.22	0.04	0.14
10	3	2	5	0	0	10	0.14	0.19	0.03	0.14

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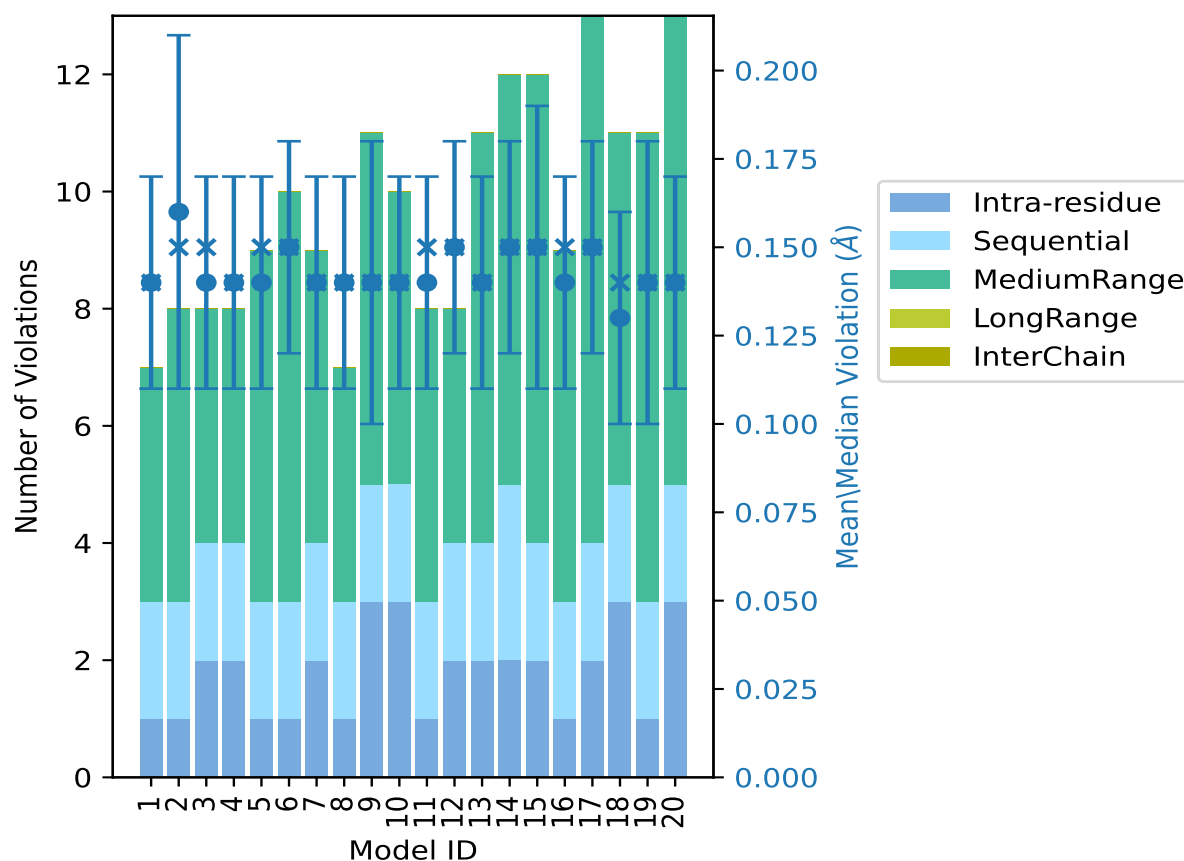
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	1	2	5	0	0	8	0.14	0.19	0.03	0.15
12	2	2	4	0	0	8	0.15	0.19	0.03	0.15
13	2	2	7	0	0	11	0.14	0.19	0.03	0.14
14	2	3	7	0	0	12	0.15	0.2	0.03	0.15
15	2	2	8	0	0	12	0.15	0.25	0.04	0.15
16	1	2	6	0	0	9	0.14	0.19	0.03	0.15
17	2	2	9	0	0	13	0.15	0.2	0.03	0.15
18	3	2	6	0	0	11	0.13	0.19	0.03	0.14
19	1	2	8	0	0	11	0.14	0.22	0.04	0.14
20	3	2	8	0	0	13	0.14	0.19	0.03	0.14

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 ⓘ



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

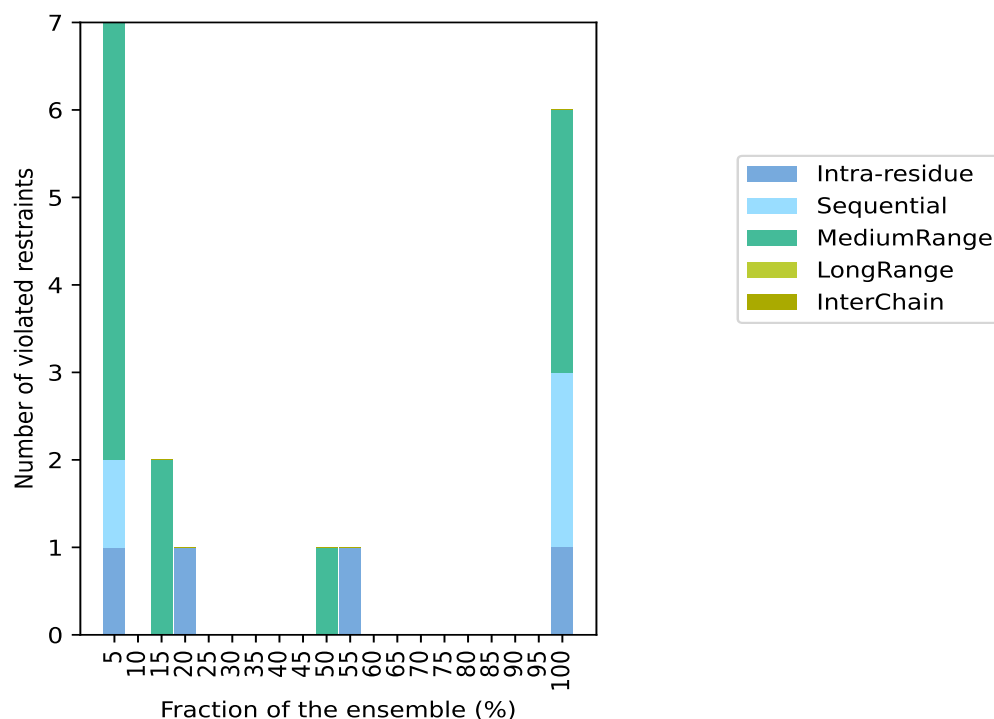
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 552(IR:96, SQ:141, MR:315, LR:0, IC:0) restraints are not 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	%
1	1	5	0	0	7	1	5.0
0	0	0	0	0	0	2	10.0
0	0	2	0	0	2	3	15.0
1	0	0	0	0	1	4	20.0
0	0	0	0	0	0	5	25.0
0	0	0	0	0	0	6	30.0
0	0	0	0	0	0	7	35.0
0	0	0	0	0	0	8	40.0
0	0	0	0	0	0	9	45.0
0	0	1	0	0	1	10	50.0
1	0	0	0	0	1	11	55.0
0	0	0	0	0	0	12	60.0
0	0	0	0	0	0	13	65.0
0	0	0	0	0	0	14	70.0
0	0	0	0	0	0	15	75.0
0	0	0	0	0	0	16	80.0
0	0	0	0	0	0	17	85.0
0	0	0	0	0	0	18	90.0
0	0	0	0	0	0	19	95.0
1	2	3	0	0	6	20	100.0

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

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

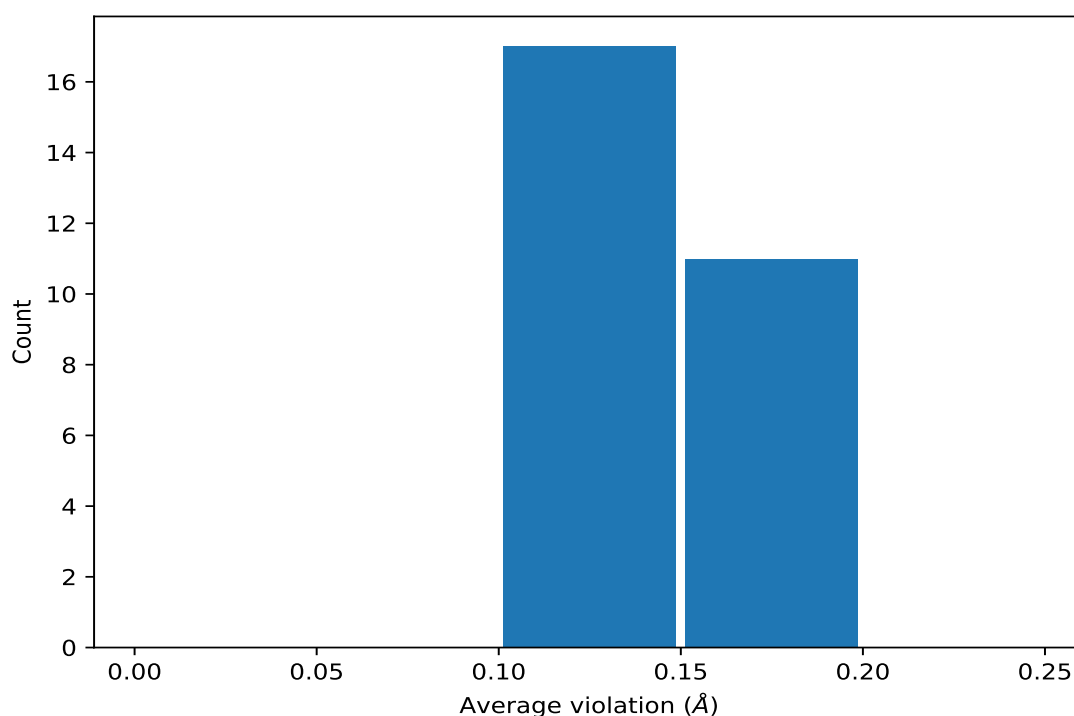
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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

9.4.1 Histogram : Distribution of mean distance 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



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

The following table provides the mean and the standard deviation of the violation for each restraint sorted by number of violated models and the mean 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)
(1,234)	1:812:A:VAL:HA	1:815:A:LEU:H	20	0.19	0.01	0.19
(1,277)	1:821:A:ALA:HA	1:822:A:VAL:H	20	0.17	0.01	0.17
(1,254)	1:816:A:ASN:HA	1:819:A:ALA:H	20	0.16	0.01	0.15
(1,221)	1:810:A:SER:HA	1:813:A:ASN:H	20	0.15	0.01	0.14
(1,62)	1:770:A:ARG:H	1:770:A:ARG:HG2	20	0.14	0.01	0.14
(1,297)	1:827:A:ASP:H	1:826:A:THR:HA	20	0.12	0.03	0.11
(2,115)	1:817:A:ALA:O	1:821:A:ALA:H	20	0.11	0.01	0.11
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD11	11	0.16	0.04	0.15
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD12	11	0.16	0.04	0.15
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD13	11	0.16	0.04	0.15
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD21	11	0.16	0.04	0.15
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD22	11	0.16	0.04	0.15
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD23	11	0.16	0.04	0.15
(1,226)	1:811:A:ALA:H	1:813:A:ASN:H	10	0.1	0.0	0.1
(1,154)	1:795:A:TYR:H	1:795:A:TYR:HE1	4	0.16	0.04	0.14
(1,154)	1:795:A:TYR:H	1:795:A:TYR:HE2	4	0.16	0.04	0.14

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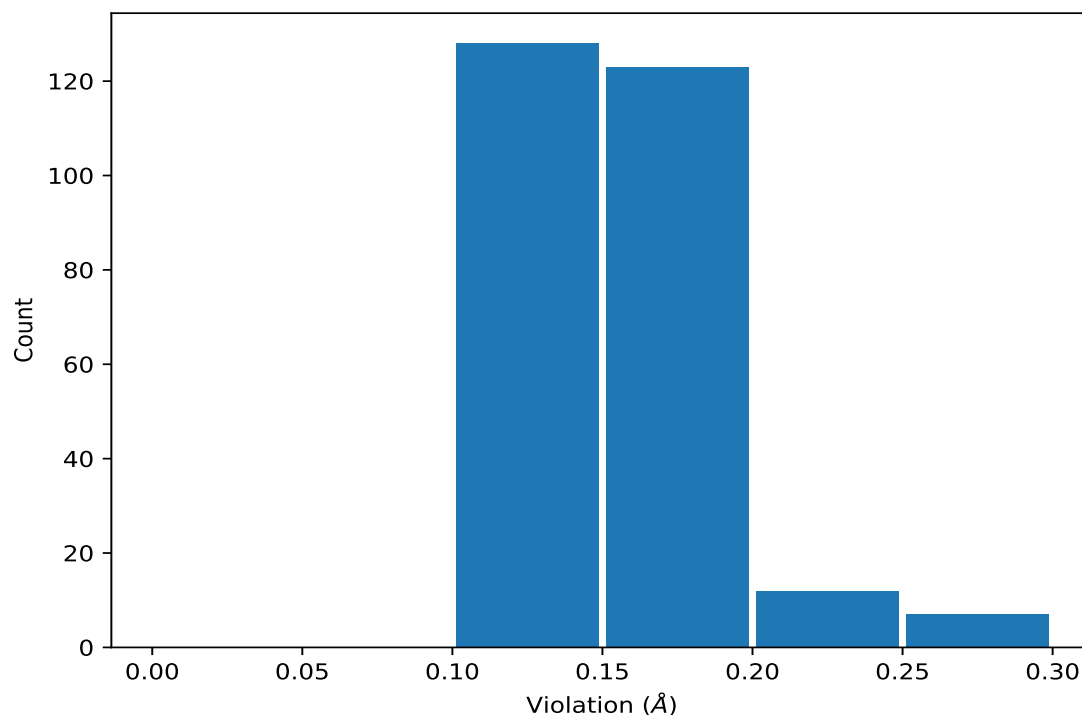
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(2,147)	1:839:A:ALA:O	1:843:A:ILE:H	3	0.15	0.02	0.15
(1,359)	1:837:A:TYR:HD1	1:840:A:ILE:HG21	3	0.15	0.0	0.15
(1,359)	1:837:A:TYR:HD1	1:840:A:ILE:HG22	3	0.15	0.0	0.15
(1,359)	1:837:A:TYR:HD1	1:840:A:ILE:HG23	3	0.15	0.0	0.15
(1,359)	1:837:A:TYR:HD2	1:840:A:ILE:HG21	3	0.15	0.0	0.15
(1,359)	1:837:A:TYR:HD2	1:840:A:ILE:HG22	3	0.15	0.0	0.15
(1,359)	1:837:A:TYR:HD2	1:840:A:ILE:HG23	3	0.15	0.0	0.15
(2,111)	1:815:A:LEU:O	1:819:A:ALA:H	3	0.14	0.03	0.15
(1,268)	1:819:A:ALA:HA	1:822:A:VAL:H	3	0.11	0.01	0.1
(2,145)	1:838:A:ARG:O	1:842:A:HIS:H	2	0.15	0.05	0.15
(2,67)	1:793:A:LEU:O	1:797:A:TRP:H	2	0.1	0.0	0.1
(2,107)	1:813:A:ASN:O	1:817:A:ALA:H	2	0.1	0.0	0.1

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 [i](#)

The following table lists the absolute value of the violation for each restraint in the ensemble sorted by its 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)
(1,297)	1:827:A:ASP:H	1:826:A:THR:HA	2	0.27
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD11	15	0.25
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD12	15	0.25
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD13	15	0.25
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD21	15	0.25
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD22	15	0.25
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD23	15	0.25
(1,234)	1:812:A:VAL:HA	1:815:A:LEU:H	19	0.22
(1,154)	1:795:A:TYR:H	1:795:A:TYR:HE1	9	0.22
(1,154)	1:795:A:TYR:H	1:795:A:TYR:HE2	9	0.22
(1,234)	1:812:A:VAL:HA	1:815:A:LEU:H	6	0.21
(2,145)	1:838:A:ARG:O	1:842:A:HIS:H	17	0.2
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD11	14	0.2
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD12	14	0.2
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD13	14	0.2
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD21	14	0.2
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD22	14	0.2
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD23	14	0.2
(1,234)	1:812:A:VAL:HA	1:815:A:LEU:H	14	0.2
(1,254)	1:816:A:ASN:HA	1:819:A:ALA:H	6	0.19
(1,254)	1:816:A:ASN:HA	1:819:A:ALA:H	14	0.19
(1,254)	1:816:A:ASN:HA	1:819:A:ALA:H	19	0.19
(1,234)	1:812:A:VAL:HA	1:815:A:LEU:H	1	0.19
(1,234)	1:812:A:VAL:HA	1:815:A:LEU:H	2	0.19
(1,234)	1:812:A:VAL:HA	1:815:A:LEU:H	3	0.19
(1,234)	1:812:A:VAL:HA	1:815:A:LEU:H	4	0.19
(1,234)	1:812:A:VAL:HA	1:815:A:LEU:H	5	0.19
(1,234)	1:812:A:VAL:HA	1:815:A:LEU:H	7	0.19
(1,234)	1:812:A:VAL:HA	1:815:A:LEU:H	8	0.19
(1,234)	1:812:A:VAL:HA	1:815:A:LEU:H	9	0.19
(1,234)	1:812:A:VAL:HA	1:815:A:LEU:H	10	0.19
(1,234)	1:812:A:VAL:HA	1:815:A:LEU:H	11	0.19
(1,234)	1:812:A:VAL:HA	1:815:A:LEU:H	12	0.19
(1,234)	1:812:A:VAL:HA	1:815:A:LEU:H	13	0.19
(1,234)	1:812:A:VAL:HA	1:815:A:LEU:H	15	0.19
(1,234)	1:812:A:VAL:HA	1:815:A:LEU:H	16	0.19
(1,234)	1:812:A:VAL:HA	1:815:A:LEU:H	17	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,234)	1:812:A:VAL:HA	1:815:A:LEU:H	18	0.19
(1,234)	1:812:A:VAL:HA	1:815:A:LEU:H	20	0.19
(1,221)	1:810:A:SER:HA	1:813:A:ASN:H	20	0.19
(1,142)	1:793:A:LEU:H	1:793:A:LEU:HG	12	0.19
(1,322)	1:831:A:GLU:HG2	1:832:A:VAL:H	14	0.18
(1,322)	1:831:A:GLU:HG3	1:832:A:VAL:H	14	0.18
(1,277)	1:821:A:ALA:HA	1:822:A:VAL:H	1	0.18
(1,277)	1:821:A:ALA:HA	1:822:A:VAL:H	4	0.18
(1,277)	1:821:A:ALA:HA	1:822:A:VAL:H	7	0.18
(1,277)	1:821:A:ALA:HA	1:822:A:VAL:H	11	0.18
(1,277)	1:821:A:ALA:HA	1:822:A:VAL:H	13	0.18
(2,147)	1:839:A:ALA:O	1:843:A:ILE:H	17	0.17
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD11	10	0.17
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD12	10	0.17
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD13	10	0.17
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD21	10	0.17
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD22	10	0.17
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD23	10	0.17
(1,277)	1:821:A:ALA:HA	1:822:A:VAL:H	2	0.17
(1,277)	1:821:A:ALA:HA	1:822:A:VAL:H	3	0.17
(1,277)	1:821:A:ALA:HA	1:822:A:VAL:H	5	0.17
(1,277)	1:821:A:ALA:HA	1:822:A:VAL:H	8	0.17
(1,277)	1:821:A:ALA:HA	1:822:A:VAL:H	9	0.17
(1,277)	1:821:A:ALA:HA	1:822:A:VAL:H	12	0.17
(1,277)	1:821:A:ALA:HA	1:822:A:VAL:H	14	0.17
(1,277)	1:821:A:ALA:HA	1:822:A:VAL:H	15	0.17
(1,277)	1:821:A:ALA:HA	1:822:A:VAL:H	16	0.17
(1,277)	1:821:A:ALA:HA	1:822:A:VAL:H	17	0.17
(1,277)	1:821:A:ALA:HA	1:822:A:VAL:H	18	0.17
(1,277)	1:821:A:ALA:HA	1:822:A:VAL:H	19	0.17
(1,277)	1:821:A:ALA:HA	1:822:A:VAL:H	20	0.17
(2,111)	1:815:A:LEU:O	1:819:A:ALA:H	6	0.16
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD11	20	0.16
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD12	20	0.16
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD13	20	0.16
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD21	20	0.16
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD22	20	0.16
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD23	20	0.16
(1,277)	1:821:A:ALA:HA	1:822:A:VAL:H	6	0.16
(1,277)	1:821:A:ALA:HA	1:822:A:VAL:H	10	0.16
(1,258)	1:817:A:ALA:HA	1:820:A:ILE:HG12	19	0.16
(1,254)	1:816:A:ASN:HA	1:819:A:ALA:H	3	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,254)	1:816:A:ASN:HA	1:819:A:ALA:H	9	0.16
(2,147)	1:839:A:ALA:O	1:843:A:ILE:H	5	0.15
(2,127)	1:829:A:VAL:O	1:833:A:LEU:H	15	0.15
(2,115)	1:817:A:ALA:O	1:821:A:ALA:H	6	0.15
(2,111)	1:815:A:LEU:O	1:819:A:ALA:H	14	0.15
(1,359)	1:837:A:TYR:HD1	1:840:A:ILE:HG21	9	0.15
(1,359)	1:837:A:TYR:HD1	1:840:A:ILE:HG22	9	0.15
(1,359)	1:837:A:TYR:HD1	1:840:A:ILE:HG23	9	0.15
(1,359)	1:837:A:TYR:HD2	1:840:A:ILE:HG21	9	0.15
(1,359)	1:837:A:TYR:HD2	1:840:A:ILE:HG22	9	0.15
(1,359)	1:837:A:TYR:HD2	1:840:A:ILE:HG23	9	0.15
(1,359)	1:837:A:TYR:HD1	1:840:A:ILE:HG21	13	0.15
(1,359)	1:837:A:TYR:HD1	1:840:A:ILE:HG22	13	0.15
(1,359)	1:837:A:TYR:HD1	1:840:A:ILE:HG23	13	0.15
(1,359)	1:837:A:TYR:HD2	1:840:A:ILE:HG21	13	0.15
(1,359)	1:837:A:TYR:HD2	1:840:A:ILE:HG22	13	0.15
(1,359)	1:837:A:TYR:HD2	1:840:A:ILE:HG23	13	0.15
(1,359)	1:837:A:TYR:HD1	1:840:A:ILE:HG21	17	0.15
(1,359)	1:837:A:TYR:HD1	1:840:A:ILE:HG22	17	0.15
(1,359)	1:837:A:TYR:HD1	1:840:A:ILE:HG23	17	0.15
(1,359)	1:837:A:TYR:HD2	1:840:A:ILE:HG21	17	0.15
(1,359)	1:837:A:TYR:HD2	1:840:A:ILE:HG22	17	0.15
(1,359)	1:837:A:TYR:HD2	1:840:A:ILE:HG23	17	0.15
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD11	13	0.15
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD12	13	0.15
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD13	13	0.15
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD21	13	0.15
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD22	13	0.15
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD23	13	0.15
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD11	18	0.15
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD12	18	0.15
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD13	18	0.15
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD21	18	0.15
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD22	18	0.15
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD23	18	0.15
(1,254)	1:816:A:ASN:HA	1:819:A:ALA:H	1	0.15
(1,254)	1:816:A:ASN:HA	1:819:A:ALA:H	2	0.15
(1,254)	1:816:A:ASN:HA	1:819:A:ALA:H	4	0.15
(1,254)	1:816:A:ASN:HA	1:819:A:ALA:H	5	0.15
(1,254)	1:816:A:ASN:HA	1:819:A:ALA:H	7	0.15
(1,254)	1:816:A:ASN:HA	1:819:A:ALA:H	8	0.15
(1,254)	1:816:A:ASN:HA	1:819:A:ALA:H	10	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,254)	1:816:A:ASN:HA	1:819:A:ALA:H	11	0.15
(1,254)	1:816:A:ASN:HA	1:819:A:ALA:H	12	0.15
(1,254)	1:816:A:ASN:HA	1:819:A:ALA:H	13	0.15
(1,254)	1:816:A:ASN:HA	1:819:A:ALA:H	15	0.15
(1,254)	1:816:A:ASN:HA	1:819:A:ALA:H	16	0.15
(1,254)	1:816:A:ASN:HA	1:819:A:ALA:H	17	0.15
(1,254)	1:816:A:ASN:HA	1:819:A:ALA:H	18	0.15
(1,254)	1:816:A:ASN:HA	1:819:A:ALA:H	20	0.15
(1,221)	1:810:A:SER:HA	1:813:A:ASN:H	5	0.15
(1,221)	1:810:A:SER:HA	1:813:A:ASN:H	6	0.15
(1,221)	1:810:A:SER:HA	1:813:A:ASN:H	12	0.15
(1,221)	1:810:A:SER:HA	1:813:A:ASN:H	14	0.15
(1,221)	1:810:A:SER:HA	1:813:A:ASN:H	16	0.15
(1,221)	1:810:A:SER:HA	1:813:A:ASN:H	19	0.15
(1,62)	1:770:A:ARG:H	1:770:A:ARG:HG2	3	0.15
(1,62)	1:770:A:ARG:H	1:770:A:ARG:HG2	5	0.15
(1,62)	1:770:A:ARG:H	1:770:A:ARG:HG2	11	0.15
(1,62)	1:770:A:ARG:H	1:770:A:ARG:HG2	12	0.15
(1,62)	1:770:A:ARG:H	1:770:A:ARG:HG2	15	0.15
(1,62)	1:770:A:ARG:H	1:770:A:ARG:HG2	16	0.15
(1,62)	1:770:A:ARG:H	1:770:A:ARG:HG2	17	0.15
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD11	4	0.14
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD12	4	0.14
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD13	4	0.14
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD21	4	0.14
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD22	4	0.14
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD23	4	0.14
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD11	17	0.14
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD12	17	0.14
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD13	17	0.14
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD21	17	0.14
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD22	17	0.14
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD23	17	0.14
(1,221)	1:810:A:SER:HA	1:813:A:ASN:H	1	0.14
(1,221)	1:810:A:SER:HA	1:813:A:ASN:H	2	0.14
(1,221)	1:810:A:SER:HA	1:813:A:ASN:H	3	0.14
(1,221)	1:810:A:SER:HA	1:813:A:ASN:H	4	0.14
(1,221)	1:810:A:SER:HA	1:813:A:ASN:H	7	0.14
(1,221)	1:810:A:SER:HA	1:813:A:ASN:H	8	0.14
(1,221)	1:810:A:SER:HA	1:813:A:ASN:H	9	0.14
(1,221)	1:810:A:SER:HA	1:813:A:ASN:H	10	0.14
(1,221)	1:810:A:SER:HA	1:813:A:ASN:H	11	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,221)	1:810:A:SER:HA	1:813:A:ASN:H	13	0.14
(1,221)	1:810:A:SER:HA	1:813:A:ASN:H	15	0.14
(1,221)	1:810:A:SER:HA	1:813:A:ASN:H	17	0.14
(1,221)	1:810:A:SER:HA	1:813:A:ASN:H	18	0.14
(1,154)	1:795:A:TYR:H	1:795:A:TYR:HE1	10	0.14
(1,154)	1:795:A:TYR:H	1:795:A:TYR:HE2	10	0.14
(1,154)	1:795:A:TYR:H	1:795:A:TYR:HE1	20	0.14
(1,154)	1:795:A:TYR:H	1:795:A:TYR:HE2	20	0.14
(1,62)	1:770:A:ARG:H	1:770:A:ARG:HG2	4	0.14
(1,62)	1:770:A:ARG:H	1:770:A:ARG:HG2	7	0.14
(1,62)	1:770:A:ARG:H	1:770:A:ARG:HG2	8	0.14
(1,62)	1:770:A:ARG:H	1:770:A:ARG:HG2	10	0.14
(1,62)	1:770:A:ARG:H	1:770:A:ARG:HG2	13	0.14
(1,62)	1:770:A:ARG:H	1:770:A:ARG:HG2	14	0.14
(1,62)	1:770:A:ARG:H	1:770:A:ARG:HG2	18	0.14
(1,62)	1:770:A:ARG:H	1:770:A:ARG:HG2	19	0.14
(1,62)	1:770:A:ARG:H	1:770:A:ARG:HG2	20	0.14
(2,147)	1:839:A:ALA:O	1:843:A:ILE:H	11	0.13
(2,146)	1:838:A:ARG:O	1:842:A:HIS:N	17	0.13
(2,125)	1:828:A:ARG:O	1:832:A:VAL:H	15	0.13
(2,115)	1:817:A:ALA:O	1:821:A:ALA:H	14	0.13
(1,154)	1:795:A:TYR:H	1:795:A:TYR:HE1	18	0.13
(1,154)	1:795:A:TYR:H	1:795:A:TYR:HE2	18	0.13
(1,62)	1:770:A:ARG:H	1:770:A:ARG:HG2	1	0.13
(1,62)	1:770:A:ARG:H	1:770:A:ARG:HG2	2	0.13
(1,62)	1:770:A:ARG:H	1:770:A:ARG:HG2	6	0.13
(1,62)	1:770:A:ARG:H	1:770:A:ARG:HG2	9	0.13
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD11	3	0.12
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD12	3	0.12
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD13	3	0.12
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD21	3	0.12
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD22	3	0.12
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD23	3	0.12
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD11	7	0.12
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD12	7	0.12
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD13	7	0.12
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD21	7	0.12
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD22	7	0.12
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD23	7	0.12
(1,268)	1:819:A:ALA:HA	1:822:A:VAL:H	14	0.12
(2,139)	1:835:A:ALA:O	1:839:A:ALA:H	13	0.11
(2,115)	1:817:A:ALA:O	1:821:A:ALA:H	3	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,115)	1:817:A:ALA:O	1:821:A:ALA:H	5	0.11
(2,115)	1:817:A:ALA:O	1:821:A:ALA:H	8	0.11
(2,115)	1:817:A:ALA:O	1:821:A:ALA:H	10	0.11
(2,115)	1:817:A:ALA:O	1:821:A:ALA:H	12	0.11
(2,115)	1:817:A:ALA:O	1:821:A:ALA:H	15	0.11
(2,115)	1:817:A:ALA:O	1:821:A:ALA:H	16	0.11
(2,115)	1:817:A:ALA:O	1:821:A:ALA:H	17	0.11
(2,115)	1:817:A:ALA:O	1:821:A:ALA:H	20	0.11
(2,3)	1:753:A:LEU:O	1:757:A:TRP:H	20	0.11
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD11	9	0.11
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD12	9	0.11
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD13	9	0.11
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD21	9	0.11
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD22	9	0.11
(1,333)	1:833:A:LEU:H	1:833:A:LEU:HD23	9	0.11
(1,297)	1:827:A:ASP:H	1:826:A:THR:HA	1	0.11
(1,297)	1:827:A:ASP:H	1:826:A:THR:HA	3	0.11
(1,297)	1:827:A:ASP:H	1:826:A:THR:HA	4	0.11
(1,297)	1:827:A:ASP:H	1:826:A:THR:HA	5	0.11
(1,297)	1:827:A:ASP:H	1:826:A:THR:HA	6	0.11
(1,297)	1:827:A:ASP:H	1:826:A:THR:HA	7	0.11
(1,297)	1:827:A:ASP:H	1:826:A:THR:HA	8	0.11
(1,297)	1:827:A:ASP:H	1:826:A:THR:HA	9	0.11
(1,297)	1:827:A:ASP:H	1:826:A:THR:HA	10	0.11
(1,297)	1:827:A:ASP:H	1:826:A:THR:HA	11	0.11
(1,297)	1:827:A:ASP:H	1:826:A:THR:HA	12	0.11
(1,297)	1:827:A:ASP:H	1:826:A:THR:HA	13	0.11
(1,297)	1:827:A:ASP:H	1:826:A:THR:HA	14	0.11
(1,297)	1:827:A:ASP:H	1:826:A:THR:HA	15	0.11
(1,297)	1:827:A:ASP:H	1:826:A:THR:HA	16	0.11
(1,297)	1:827:A:ASP:H	1:826:A:THR:HA	17	0.11
(1,297)	1:827:A:ASP:H	1:826:A:THR:HA	18	0.11
(1,297)	1:827:A:ASP:H	1:826:A:THR:HA	19	0.11
(1,297)	1:827:A:ASP:H	1:826:A:THR:HA	20	0.11
(1,226)	1:811:A:ALA:H	1:813:A:ASN:H	6	0.11
(1,226)	1:811:A:ALA:H	1:813:A:ASN:H	14	0.11
(1,226)	1:811:A:ALA:H	1:813:A:ASN:H	19	0.11
(1,211)	1:808:A:LYS:H	1:810:A:SER:H	20	0.11
(1,202)	1:805:A:GLN:HA	1:808:A:LYS:H	20	0.11
(2,145)	1:838:A:ARG:O	1:842:A:HIS:H	13	0.1
(2,115)	1:817:A:ALA:O	1:821:A:ALA:H	1	0.1
(2,115)	1:817:A:ALA:O	1:821:A:ALA:H	2	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,115)	1:817:A:ALA:O	1:821:A:ALA:H	4	0.1
(2,115)	1:817:A:ALA:O	1:821:A:ALA:H	7	0.1
(2,115)	1:817:A:ALA:O	1:821:A:ALA:H	9	0.1
(2,115)	1:817:A:ALA:O	1:821:A:ALA:H	11	0.1
(2,115)	1:817:A:ALA:O	1:821:A:ALA:H	13	0.1
(2,115)	1:817:A:ALA:O	1:821:A:ALA:H	18	0.1
(2,115)	1:817:A:ALA:O	1:821:A:ALA:H	19	0.1
(2,111)	1:815:A:LEU:O	1:819:A:ALA:H	19	0.1
(2,107)	1:813:A:ASN:O	1:817:A:ALA:H	19	0.1
(2,107)	1:813:A:ASN:O	1:817:A:ALA:H	20	0.1
(2,67)	1:793:A:LEU:O	1:797:A:TRP:H	15	0.1
(2,67)	1:793:A:LEU:O	1:797:A:TRP:H	16	0.1
(1,269)	1:819:A:ALA:HA	1:822:A:VAL:HB	6	0.1
(1,268)	1:819:A:ALA:HA	1:822:A:VAL:H	2	0.1
(1,268)	1:819:A:ALA:HA	1:822:A:VAL:H	18	0.1
(1,226)	1:811:A:ALA:H	1:813:A:ASN:H	5	0.1
(1,226)	1:811:A:ALA:H	1:813:A:ASN:H	7	0.1
(1,226)	1:811:A:ALA:H	1:813:A:ASN:H	9	0.1
(1,226)	1:811:A:ALA:H	1:813:A:ASN:H	10	0.1
(1,226)	1:811:A:ALA:H	1:813:A:ASN:H	15	0.1
(1,226)	1:811:A:ALA:H	1:813:A:ASN:H	17	0.1
(1,226)	1:811:A:ALA:H	1:813:A:ASN:H	18	0.1
(1,66)	1:775:A:LEU:HA	1:778:A:VAL:HB	16	0.1

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

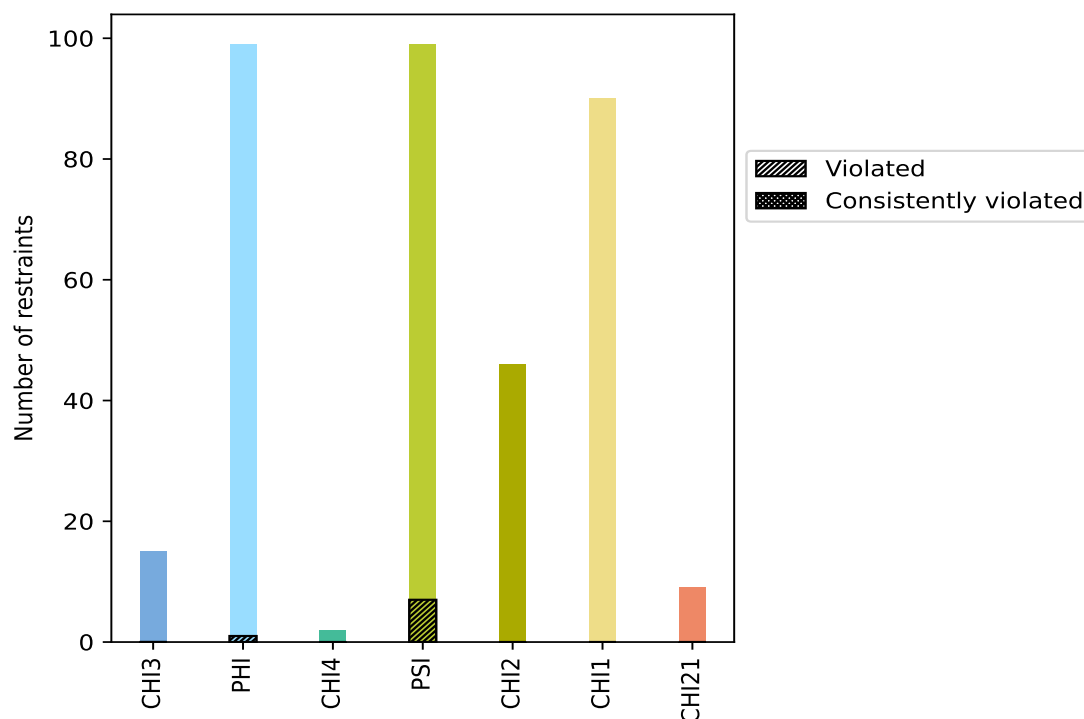
10.1 Summary of dihedral-angle violations [i](#)

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
CHI3	15	4.2	0	0.0	0.0	0	0.0	0.0
PHI	99	27.5	1	1.0	0.3	0	0.0	0.0
CHI4	2	0.6	0	0.0	0.0	0	0.0	0.0
PSI	99	27.5	7	7.1	1.9	0	0.0	0.0
CHI2	46	12.8	0	0.0	0.0	0	0.0	0.0
CHI1	90	25.0	0	0.0	0.0	0	0.0	0.0
CHI21	9	2.5	0	0.0	0.0	0	0.0	0.0
Total	360	100.0	8	2.2	2.2	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](#)



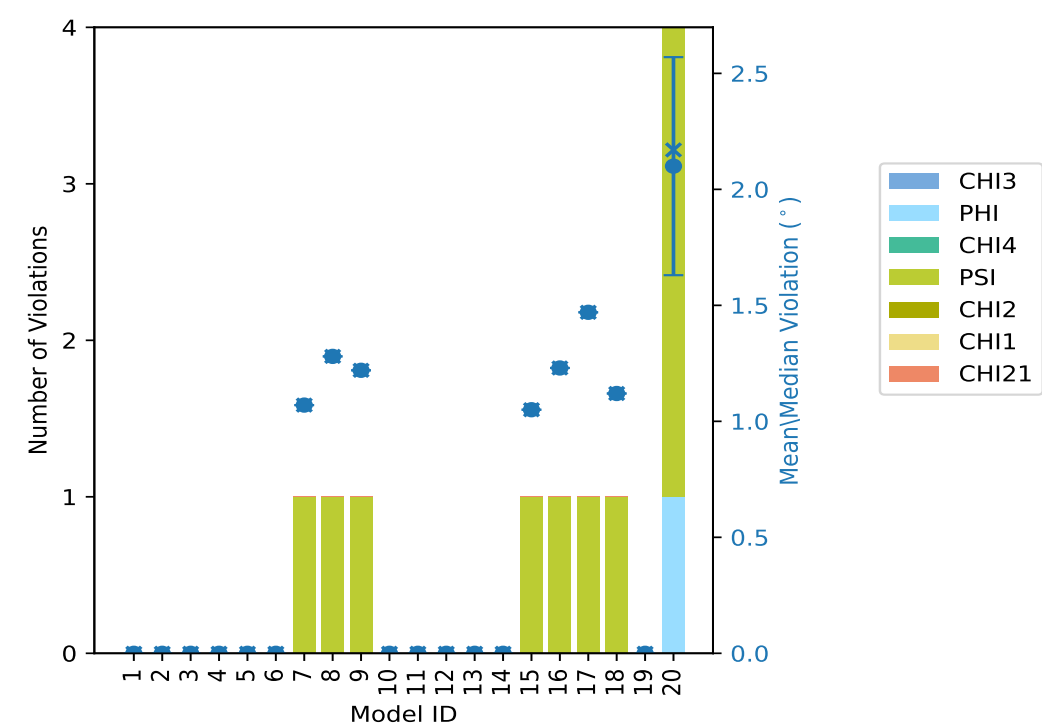
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

10.2 Dihedral-angle violation statistics for each model ⓘ

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 (°)
	CHI3	PHI	CHI4	PSI	CHI2	CHI1	CHI21	Total				
1	0	0	0	0	0	0	0	0	0.0	0.0	0.0	0.0
2	0	0	0	0	0	0	0	0	0.0	0.0	0.0	0.0
3	0	0	0	0	0	0	0	0	0.0	0.0	0.0	0.0
4	0	0	0	0	0	0	0	0	0.0	0.0	0.0	0.0
5	0	0	0	0	0	0	0	0	0.0	0.0	0.0	0.0
6	0	0	0	0	0	0	0	0	0.0	0.0	0.0	0.0
7	0	0	0	1	0	0	0	1	1.07	1.07	0.0	1.07
8	0	0	0	1	0	0	0	1	1.28	1.28	0.0	1.28
9	0	0	0	1	0	0	0	1	1.22	1.22	0.0	1.22
10	0	0	0	0	0	0	0	0	0.0	0.0	0.0	0.0
11	0	0	0	0	0	0	0	0	0.0	0.0	0.0	0.0
12	0	0	0	0	0	0	0	0	0.0	0.0	0.0	0.0
13	0	0	0	0	0	0	0	0	0.0	0.0	0.0	0.0
14	0	0	0	0	0	0	0	0	0.0	0.0	0.0	0.0
15	0	0	0	1	0	0	0	1	1.05	1.05	0.0	1.05
16	0	0	0	1	0	0	0	1	1.23	1.23	0.0	1.23
17	0	0	0	1	0	0	0	1	1.47	1.47	0.0	1.47
18	0	0	0	1	0	0	0	1	1.12	1.12	0.0	1.12
19	0	0	0	0	0	0	0	0	0.0	0.0	0.0	0.0
20	0	1	0	3	0	0	0	4	2.1	2.6	0.47	2.17

10.2.1 Bar graph : Dihedral violation statistics for each model ⓘ



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

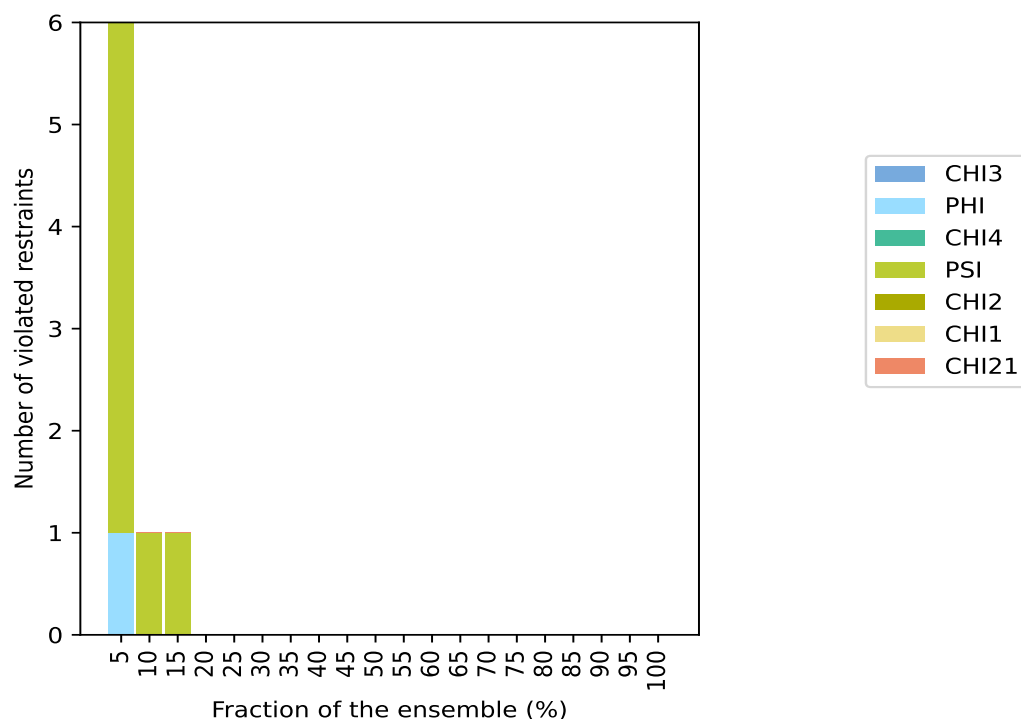
10.3 Dihedral-angle violation statistics for the ensemble [i](#)

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	
CHI3	PHI	CHI4	PSI	CHI2	CHI1	CHI21	Total	Count ¹	%
0	1	0	5	0	0	0	6	1	5.0
0	0	0	1	0	0	0	1	2	10.0
0	0	0	1	0	0	0	1	3	15.0
0	0	0	0	0	0	0	0	4	20.0
0	0	0	0	0	0	0	0	5	25.0
0	0	0	0	0	0	0	0	6	30.0
0	0	0	0	0	0	0	0	7	35.0
0	0	0	0	0	0	0	0	8	40.0
0	0	0	0	0	0	0	0	9	45.0
0	0	0	0	0	0	0	0	10	50.0
0	0	0	0	0	0	0	0	11	55.0
0	0	0	0	0	0	0	0	12	60.0
0	0	0	0	0	0	0	0	13	65.0
0	0	0	0	0	0	0	0	14	70.0
0	0	0	0	0	0	0	0	15	75.0
0	0	0	0	0	0	0	0	16	80.0
0	0	0	0	0	0	0	0	17	85.0
0	0	0	0	0	0	0	0	18	90.0
0	0	0	0	0	0	0	0	19	95.0
0	0	0	0	0	0	0	0	20	100.0

¹ Number of models with violations

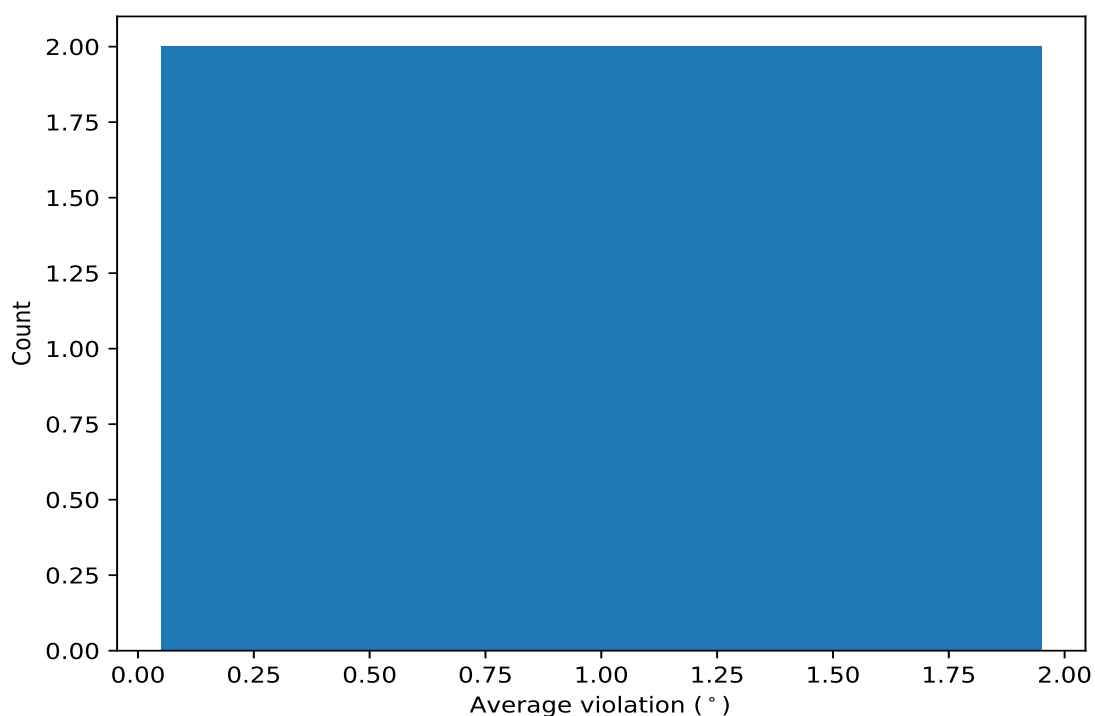
10.3.1 Bar graph : Dihedral-angle Violation statistics for the ensemble [i](#)



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 violation for each restraint sorted by number of violated models and the mean value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint.

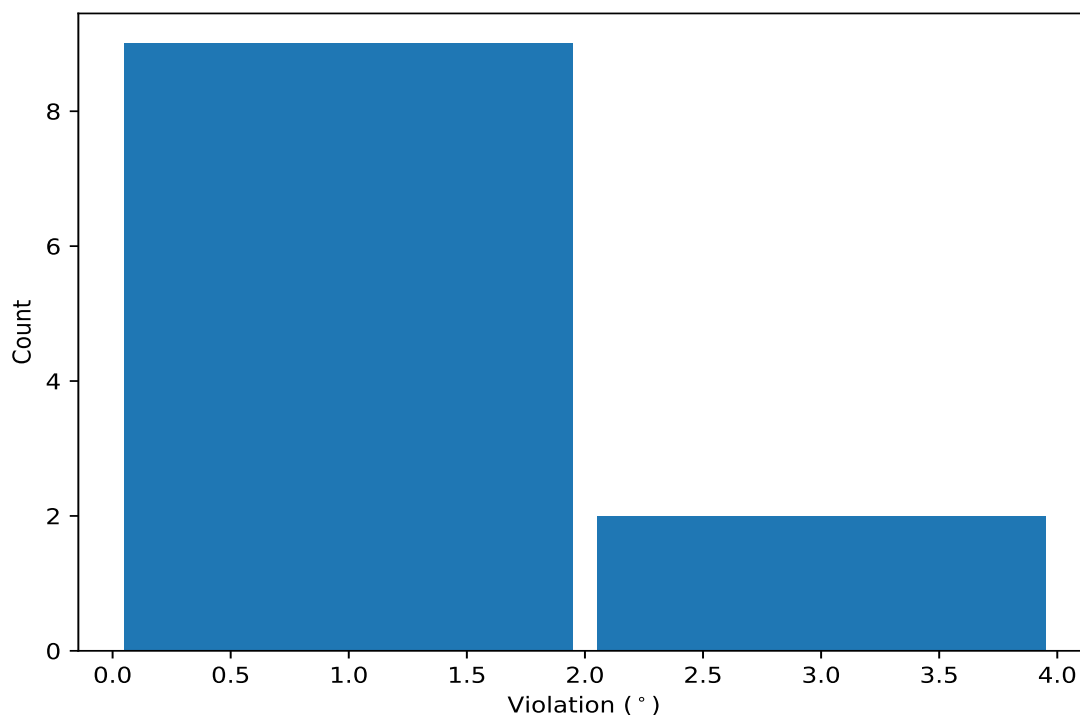
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,172)	1:839:A:ALA:N	1:839:A:ALA:CA	1:839:A:ALA:C	1:840:A:ILE:N	3	1.29	0.14	1.28
(1,6)	1:755:A:LEU:N	1:755:A:LEU:CA	1:755:A:LEU:C	1:756:A:ILE:N	2	1.54	0.31	1.54

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 lists the absolute value of the violation for each restraint in the ensemble sorted by its 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 (°)
(1,68)	1:786:A:GLY:N	1:786:A:GLY:CA	1:786:A:GLY:C	1:787:A:ARG:N	20	2.6
(1,64)	1:784:A:LEU:N	1:784:A:LEU:CA	1:784:A:LEU:C	1:785:A:LEU:N	20	2.5
(1,6)	1:755:A:LEU:N	1:755:A:LEU:CA	1:755:A:LEU:C	1:756:A:ILE:N	20	1.84
(1,172)	1:839:A:ALA:N	1:839:A:ALA:CA	1:839:A:ALA:C	1:840:A:ILE:N	17	1.47
(1,65)	1:784:A:LEU:C	1:785:A:LEU:N	1:785:A:LEU:CA	1:785:A:LEU:C	20	1.46
(1,172)	1:839:A:ALA:N	1:839:A:ALA:CA	1:839:A:ALA:C	1:840:A:ILE:N	8	1.28
(1,6)	1:755:A:LEU:N	1:755:A:LEU:CA	1:755:A:LEU:C	1:756:A:ILE:N	16	1.23
(1,178)	1:842:A:HIS:N	1:842:A:HIS:CA	1:842:A:HIS:C	1:843:A:ILE:N	9	1.22
(1,172)	1:839:A:ALA:N	1:839:A:ALA:CA	1:839:A:ALA:C	1:840:A:ILE:N	18	1.12
(1,104)	1:804:A:SER:N	1:804:A:SER:CA	1:804:A:SER:C	1:805:A:GLN:N	7	1.07
(1,188)	1:850:A:GLY:N	1:850:A:GLY:CA	1:850:A:GLY:C	1:851:A:LEU:N	15	1.05