



Full wwPDB NMR Structure Validation Report ⓘ

Mar 9, 2026 – 08:29 AM UTC

PDB ID : 2LMB / pdb_00002lmb
BMRB ID : 18110
Title : Solution Structure of C-terminal RAGE (ctRAGE)
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Deposited on : 2011-11-29

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

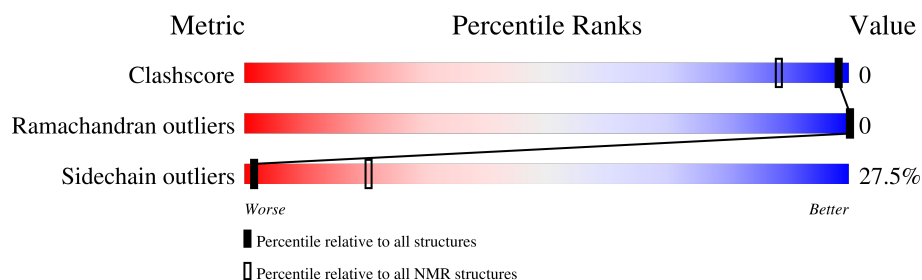
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 59%.

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	43	16% 5% 14% 65%

2 Ensemble composition and analysis

This entry contains 20 models. Model 6 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:3-A:11 (9)	0.10	6

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. No single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 245 atoms, of which 107 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Advanced glycosylation end product-specific receptor.

Mol	Chain	Residues	Atoms						Trace
1	A	15	Total	C	H	N	O	S	0
			245	82	107	34	21	1	

There is a discrepancy between the modelled and reference sequences:

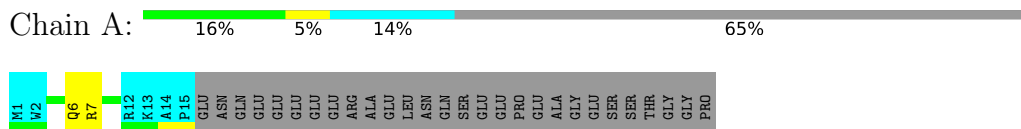
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q15109

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: Advanced glycosylation end product-specific receptor

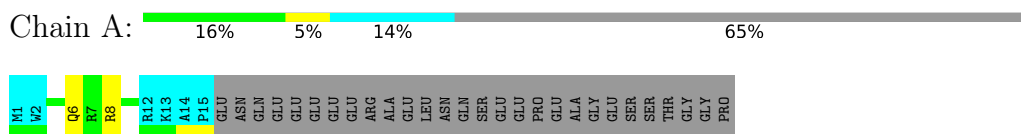


4.2 Scores per residue for each member of the ensemble

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

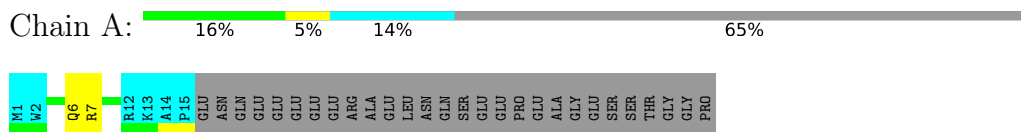
4.2.1 Score per residue for model 1

- Molecule 1: Advanced glycosylation end product-specific receptor



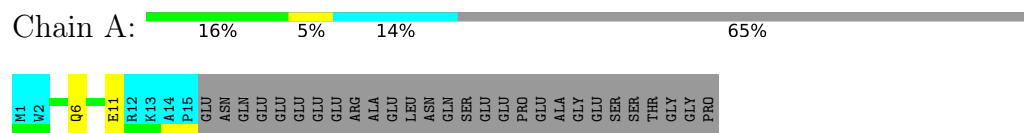
4.2.2 Score per residue for model 2

- Molecule 1: Advanced glycosylation end product-specific receptor



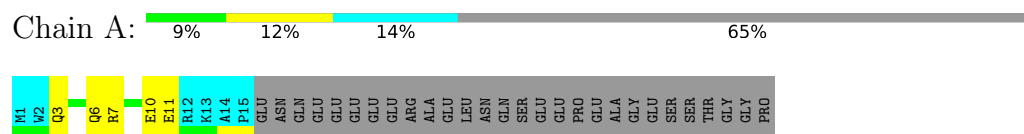
4.2.3 Score per residue for model 3

- Molecule 1: Advanced glycosylation end product-specific receptor



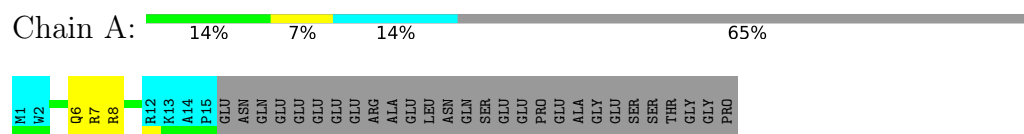
4.2.4 Score per residue for model 4

- Molecule 1: Advanced glycosylation end product-specific receptor



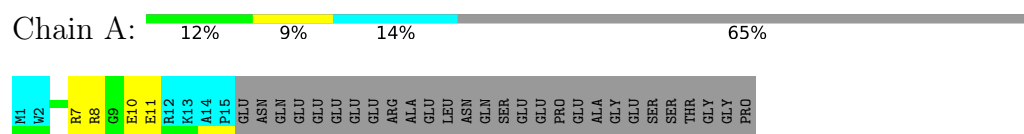
4.2.5 Score per residue for model 5

- Molecule 1: Advanced glycosylation end product-specific receptor



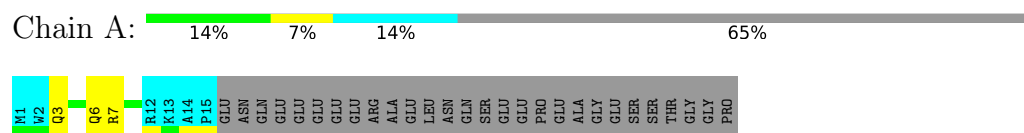
4.2.6 Score per residue for model 6 (medoid)

- Molecule 1: Advanced glycosylation end product-specific receptor



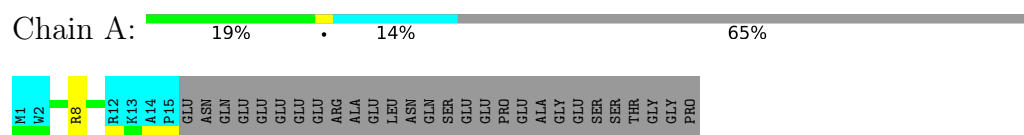
4.2.7 Score per residue for model 7

- Molecule 1: Advanced glycosylation end product-specific receptor



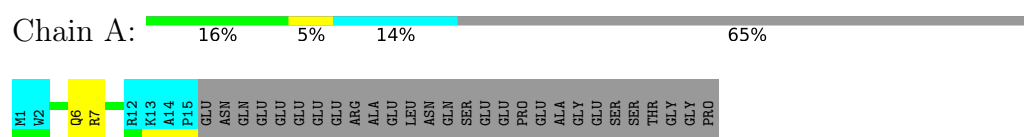
4.2.8 Score per residue for model 8

- Molecule 1: Advanced glycosylation end product-specific receptor



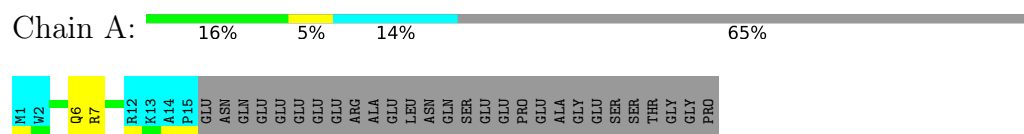
4.2.9 Score per residue for model 9

- Molecule 1: Advanced glycosylation end product-specific receptor



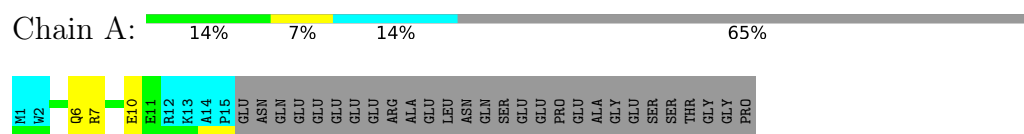
4.2.10 Score per residue for model 10

- Molecule 1: Advanced glycosylation end product-specific receptor



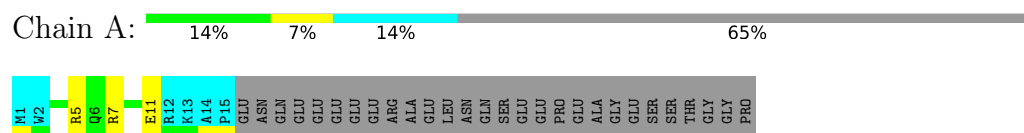
4.2.11 Score per residue for model 11

- Molecule 1: Advanced glycosylation end product-specific receptor



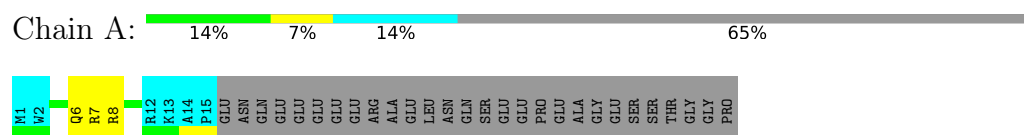
4.2.12 Score per residue for model 12

- Molecule 1: Advanced glycosylation end product-specific receptor



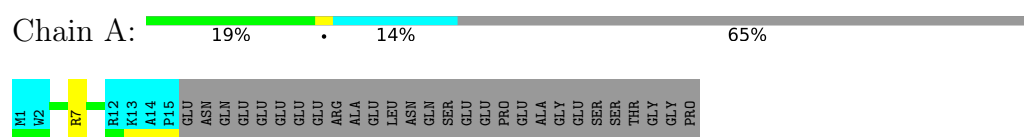
4.2.13 Score per residue for model 13

- Molecule 1: Advanced glycosylation end product-specific receptor



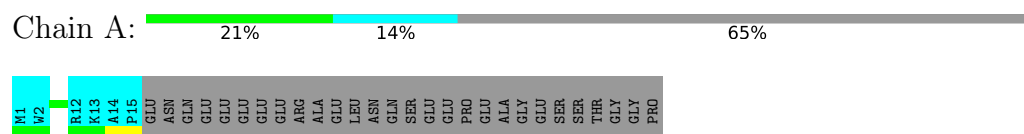
4.2.14 Score per residue for model 14

- Molecule 1: Advanced glycosylation end product-specific receptor



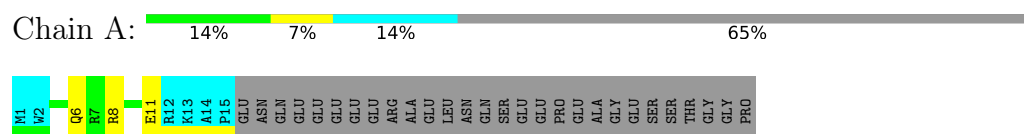
4.2.15 Score per residue for model 15

- Molecule 1: Advanced glycosylation end product-specific receptor



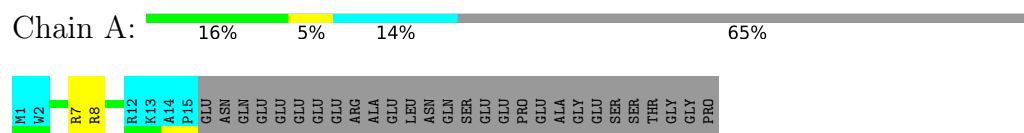
4.2.16 Score per residue for model 16

- Molecule 1: Advanced glycosylation end product-specific receptor



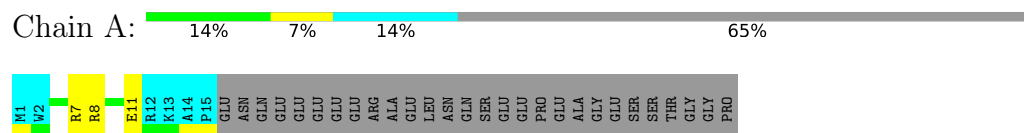
4.2.17 Score per residue for model 17

- Molecule 1: Advanced glycosylation end product-specific receptor



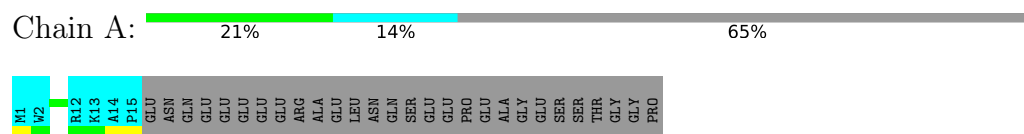
4.2.18 Score per residue for model 18

- Molecule 1: Advanced glycosylation end product-specific receptor



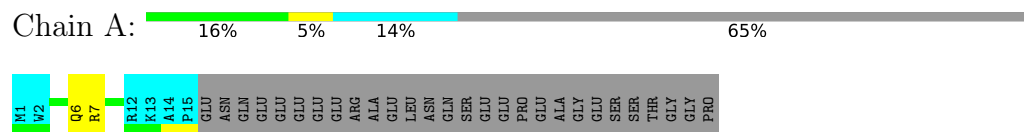
4.2.19 Score per residue for model 19

- Molecule 1: Advanced glycosylation end product-specific receptor



4.2.20 Score per residue for model 20

- Molecule 1: Advanced glycosylation end product-specific receptor



5 Refinement protocol and experimental data overview

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

Of the 1000 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
CYANA	refinement	

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	371
Number of shifts mapped to atoms	116
Number of unparsed shifts	0
Number of shifts with mapping errors	255
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	59%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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	84	63	83	0±0
All	All	1680	1260	1577	1

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 0.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:6:GLN:NE2	1:A:7:ARG:HE	0.47	2.08	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	9/43 (21%)	8±0 (89±0%)	1±0 (11±0%)	0±0 (0±0%)	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	180/860 (21%)	160 (89%)	20 (11%)	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	8/36 (22%)	6±1 (72±16%)	2±1 (28±16%)	1	20
All	All	160/720 (22%)	116 (72%)	44 (28%)	1	20

All 7 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	7	ARG	13
1	A	6	GLN	11
1	A	8	ARG	8
1	A	11	GLU	6
1	A	10	GLU	3
1	A	3	GLN	2
1	A	5	ARG	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

There are no ligands in this entry.

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 59% for the well-defined parts and 57% 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	371
Number of shifts mapped to atoms	116
Number of unparsed shifts	0
Number of shifts with mapping errors	255
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

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

- No matching atom found in the structure. All 255 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	1	MET	HB2	1.898	0.020	2
1	A	1	MET	HG2	2.16	0.020	1
1	A	2	TRP	HB2	3.087	0.020	1
1	A	3	GLN	HB2	1.794	0.020	2
1	A	3	GLN	HG2	2.052	0.020	1
1	A	4	ARG	HB2	1.565	0.020	2
1	A	4	ARG	HD2	3.037	0.020	1
1	A	5	ARG	HB2	1.644	0.020	1
1	A	5	ARG	HD2	2.996	0.020	1
1	A	5	ARG	HG2	1.462	0.020	1
1	A	6	GLN	HB2	1.891	0.020	2
1	A	6	GLN	HG2	2.17	0.020	1
1	A	7	ARG	HB2	1.658	0.020	1
1	A	7	ARG	HD2	3.037	0.020	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	7	ARG	HG2	1.481	0.020	1
1	A	8	ARG	HB2	1.723	0.020	1
1	A	8	ARG	HD2	3.037	0.020	1
1	A	8	ARG	HG2	1.509	0.020	1
1	A	10	GLU	HB2	1.962	0.020	2
1	A	11	GLU	HB2	1.921	0.020	2
1	A	11	GLU	HG2	2.174	0.020	1
1	A	12	ARG	HB2	1.723	0.020	2
1	A	12	ARG	HD2	3.027	0.020	1
1	A	12	ARG	HG2	1.462	0.020	1
1	A	13	LYS	HB2	1.704	0.020	1
1	A	13	LYS	HD2	1.54	0.020	1
1	A	13	LYS	HE2	2.855	0.020	1
1	A	13	LYS	HG2	1.281	0.020	1
1	A	16	GLU	H	8.585	0.020	1
1	A	16	GLU	HA	4.065	0.020	1
1	A	16	GLU	HB2	1.889	0.020	2
1	A	16	GLU	HB3	1.795	0.020	2
1	A	16	GLU	HG2	2.143	0.020	1
1	A	16	GLU	HG3	2.143	0.020	1
1	A	16	GLU	CA	54.124	0.3	1
1	A	16	GLU	CB	26.893	0.3	1
1	A	16	GLU	CG	33.089	0.3	1
1	A	16	GLU	N	119.943	0.3	1
1	A	17	ASN	H	8.21	0.020	1
1	A	17	ASN	HA	4.565	0.020	1
1	A	17	ASN	HB2	2.754	0.020	2
1	A	17	ASN	HB3	2.662	0.020	2
1	A	17	ASN	CA	50.33	0.3	1
1	A	17	ASN	CB	35.745	0.3	1
1	A	17	ASN	N	117.894	0.3	1
1	A	18	GLN	H	8.25	0.020	1
1	A	18	GLN	HA	4.077	0.020	1
1	A	18	GLN	HB2	1.96	0.020	2
1	A	18	GLN	HB3	1.81	0.020	2
1	A	18	GLN	HG2	2.173	0.020	1
1	A	18	GLN	HG3	2.173	0.020	1
1	A	18	GLN	CA	52.956	0.3	1
1	A	18	GLN	CB	26.515	0.3	1
1	A	18	GLN	N	120.795	0.3	1
1	A	19	GLU	H	8.347	0.020	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	19	GLU	HA	4.081	0.020	1
1	A	19	GLU	HB2	1.946	0.020	2
1	A	19	GLU	HB3	1.81	0.020	2
1	A	19	GLU	HG2	2.148	0.020	1
1	A	19	GLU	HG3	2.148	0.020	1
1	A	19	GLU	CA	53.929	0.3	1
1	A	19	GLU	CB	26.591	0.3	1
1	A	19	GLU	CG	32.845	0.3	1
1	A	19	GLU	N	121.241	0.3	1
1	A	20	GLU	H	8.259	0.020	1
1	A	20	GLU	HA	4.065	0.020	1
1	A	20	GLU	HB2	1.826	0.020	1
1	A	20	GLU	HB3	1.826	0.020	1
1	A	20	GLU	HG2	2.118	0.020	1
1	A	20	GLU	HG3	2.118	0.020	1
1	A	20	GLU	CA	53.864	0.3	1
1	A	20	GLU	CB	26.818	0.3	1
1	A	20	GLU	CG	33.089	0.3	1
1	A	20	GLU	N	121.391	0.3	1
1	A	21	GLU	H	8.236	0.020	1
1	A	21	GLU	HA	4.197	0.020	1
1	A	21	GLU	HB2	1.99	0.020	2
1	A	21	GLU	HB3	1.831	0.020	2
1	A	21	GLU	HG2	2.2	0.020	1
1	A	21	GLU	HG3	2.2	0.020	1
1	A	21	GLU	CA	53.605	0.3	1
1	A	21	GLU	CB	27.045	0.3	1
1	A	21	GLU	CG	32.926	0.3	1
1	A	21	GLU	N	120.699	0.3	1
1	A	22	GLU	H	8.27	0.020	1
1	A	22	GLU	HA	4.072	0.020	1
1	A	22	GLU	HB2	1.918	0.020	2
1	A	22	GLU	HB3	1.833	0.020	2
1	A	22	GLU	HG2	2.143	0.020	1
1	A	22	GLU	HG3	2.143	0.020	1
1	A	22	GLU	CA	53.378	0.3	1
1	A	22	GLU	CG	32.682	0.3	1
1	A	22	GLU	N	121.468	0.3	1
1	A	23	GLU	H	8.27	0.020	1
1	A	23	GLU	HA	4.067	0.020	1
1	A	23	GLU	HB2	1.834	0.020	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	23	GLU	HB3	1.834	0.020	1
1	A	23	GLU	HG2	2.144	0.020	1
1	A	23	GLU	HG3	2.144	0.020	1
1	A	23	GLU	CA	54.149	0.3	1
1	A	23	GLU	CB	27.072	0.3	1
1	A	23	GLU	CG	32.845	0.3	1
1	A	23	GLU	N	121.711	0.3	1
1	A	24	ARG	H	8.147	0.020	1
1	A	24	ARG	HA	4.124	0.020	1
1	A	24	ARG	HB2	1.704	0.020	2
1	A	24	ARG	HB3	1.621	0.020	2
1	A	24	ARG	HD2	3.027	0.020	1
1	A	24	ARG	HD3	3.027	0.020	1
1	A	24	ARG	HG2	1.462	0.020	1
1	A	24	ARG	HG3	1.462	0.020	1
1	A	24	ARG	CA	53.119	0.3	1
1	A	24	ARG	CB	27.423	0.3	1
1	A	24	ARG	CD	40.443	0.3	1
1	A	24	ARG	CG	24.226	0.3	1
1	A	24	ARG	N	121.861	0.3	1
1	A	25	ALA	H	8.163	0.020	1
1	A	25	ALA	HA	4.13	0.020	1
1	A	25	ALA	HB1	1.236	0.020	1
1	A	25	ALA	HB2	1.236	0.020	1
1	A	25	ALA	HB3	1.236	0.020	1
1	A	25	ALA	CA	49.876	0.3	1
1	A	25	ALA	CB	16.075	0.3	1
1	A	25	ALA	N	124.853	0.3	1
1	A	26	GLU	H	8.25	0.020	1
1	A	26	GLU	HA	4.08	0.020	1
1	A	26	GLU	HB2	1.886	0.020	2
1	A	26	GLU	HB3	1.78	0.020	2
1	A	26	GLU	HG2	2.135	0.020	1
1	A	26	GLU	HG3	2.135	0.020	1
1	A	26	GLU	CA	53.605	0.3	1
1	A	26	GLU	CB	26.667	0.3	1
1	A	26	GLU	CG	32.926	0.3	1
1	A	26	GLU	N	119.357	0.3	1
1	A	27	LEU	H	8.037	0.020	1
1	A	27	LEU	HA	4.171	0.020	1
1	A	27	LEU	HD11	0.736	0.020	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	27	LEU	HD12	0.736	0.020	1
1	A	27	LEU	HD13	0.736	0.020	1
1	A	27	LEU	HD21	0.736	0.020	1
1	A	27	LEU	HD22	0.736	0.020	1
1	A	27	LEU	HD23	0.736	0.020	1
1	A	27	LEU	HG	1.462	0.020	1
1	A	27	LEU	CA	52.243	0.3	1
1	A	27	LEU	CB	39.149	0.3	1
1	A	27	LEU	CD1	22.03	0.3	1
1	A	27	LEU	CD2	20.567	0.3	1
1	A	27	LEU	CG	24.063	0.3	1
1	A	27	LEU	N	122.281	0.3	1
1	A	28	ASN	H	8.305	0.020	1
1	A	28	ASN	HA	4.535	0.020	1
1	A	28	ASN	HB2	2.703	0.020	2
1	A	28	ASN	HB3	2.602	0.020	2
1	A	28	ASN	CA	50.265	0.3	1
1	A	28	ASN	CB	35.821	0.3	1
1	A	28	ASN	N	119.118	0.3	1
1	A	29	GLN	H	8.233	0.020	1
1	A	29	GLN	HA	4.141	0.020	1
1	A	29	GLN	HB2	1.977	0.020	2
1	A	29	GLN	HB3	1.841	0.020	2
1	A	29	GLN	HG2	2.165	0.020	1
1	A	29	GLN	HG3	2.165	0.020	1
1	A	29	GLN	CA	52.957	0.3	1
1	A	29	GLN	CB	26.061	0.3	1
1	A	29	GLN	N	120.191	0.3	1
1	A	30	SER	H	8.248	0.020	1
1	A	30	SER	HA	4.292	0.020	1
1	A	30	SER	HB2	3.73	0.020	1
1	A	30	SER	HB3	3.73	0.020	1
1	A	30	SER	CA	55.518	0.3	1
1	A	30	SER	CB	60.786	0.3	1
1	A	30	SER	N	116.695	0.3	1
1	A	31	GLU	H	8.297	0.020	1
1	A	31	GLU	HA	4.179	0.020	1
1	A	31	GLU	HB2	1.924	0.020	2
1	A	31	GLU	HB3	1.754	0.020	2
1	A	31	GLU	HG2	2.102	0.020	1
1	A	31	GLU	HG3	2.102	0.020	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	31	GLU	CA	52.994	0.3	1
1	A	31	GLU	CB	27.12	0.3	1
1	A	31	GLU	CG	33.495	0.3	1
1	A	31	GLU	N	122.324	0.3	1
1	A	32	GLU	H	8.44	0.020	1
1	A	32	GLU	HA	4.08	0.020	1
1	A	32	GLU	HB2	1.838	0.020	1
1	A	32	GLU	HB3	1.838	0.020	1
1	A	32	GLU	HG2	2.113	0.020	1
1	A	32	GLU	HG3	2.113	0.020	1
1	A	32	GLU	CA	53.832	0.3	1
1	A	32	GLU	CB	27.12	0.3	1
1	A	32	GLU	N	121.78	0.3	1
1	A	34	GLU	H	8.431	0.020	1
1	A	34	GLU	HA	4.08	0.020	1
1	A	34	GLU	HB2	1.893	0.020	2
1	A	34	GLU	HB3	1.785	0.020	2
1	A	34	GLU	HG2	2.166	0.020	1
1	A	34	GLU	HG3	2.166	0.020	1
1	A	34	GLU	CA	53.335	0.3	1
1	A	34	GLU	CB	26.893	0.3	1
1	A	34	GLU	CG	32.926	0.3	1
1	A	34	GLU	N	121.105	0.3	1
1	A	35	ALA	H	8.296	0.020	1
1	A	35	ALA	HA	4.171	0.020	1
1	A	35	ALA	HB1	1.245	0.020	1
1	A	35	ALA	HB2	1.245	0.020	1
1	A	35	ALA	HB3	1.245	0.020	1
1	A	35	ALA	CA	49.681	0.3	1
1	A	35	ALA	CB	16.151	0.3	1
1	A	35	ALA	N	125.374	0.3	1
1	A	36	GLY	H	8.247	0.020	1
1	A	36	GLY	HA2	3.8	0.020	1
1	A	36	GLY	HA3	3.8	0.020	1
1	A	36	GLY	CA	42.126	0.3	1
1	A	36	GLY	N	108.005	0.3	1
1	A	37	GLU	H	8.198	0.020	1
1	A	37	GLU	HA	4.171	0.020	1
1	A	37	GLU	HB2	1.946	0.020	2
1	A	37	GLU	HB3	1.795	0.020	2
1	A	37	GLU	HG2	2.112	0.020	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	37	GLU	HG3	2.112	0.020	1
1	A	37	GLU	CA	53.363	0.3	1
1	A	37	GLU	CB	27.196	0.3	1
1	A	37	GLU	CG	33.089	0.3	1
1	A	37	GLU	N	120.397	0.3	1
1	A	38	SER	H	8.362	0.020	1
1	A	38	SER	HA	4.353	0.020	1
1	A	38	SER	HB2	3.744	0.020	1
1	A	38	SER	HB3	3.744	0.020	1
1	A	38	SER	CA	55.356	0.3	1
1	A	38	SER	CB	60.635	0.3	1
1	A	38	SER	N	116.797	0.3	1
1	A	39	SER	H	8.378	0.020	1
1	A	39	SER	HA	4.429	0.020	1
1	A	39	SER	HB2	3.763	0.020	1
1	A	39	SER	HB3	3.763	0.020	1
1	A	39	SER	CA	55.421	0.3	1
1	A	39	SER	CB	60.56	0.3	1
1	A	39	SER	N	118.032	0.3	1
1	A	40	THR	H	8.141	0.020	1
1	A	40	THR	HA	4.292	0.020	1
1	A	40	THR	HB	4.164	0.020	1
1	A	40	THR	HG1	1.075	0.020	1
1	A	40	THR	CA	58.988	0.3	1
1	A	40	THR	CB	66.612	0.3	1
1	A	40	THR	N	114.868	0.3	1
1	A	41	GLY	H	8.266	0.020	1
1	A	41	GLY	HA2	3.869	0.020	1
1	A	41	GLY	HA3	3.869	0.020	1
1	A	41	GLY	CA	42.32	0.3	1
1	A	41	GLY	N	110.981	0.3	1
1	A	42	GLY	H	8.012	0.020	1
1	A	42	GLY	HA2	4.02	0.020	2
1	A	42	GLY	HA3	3.899	0.020	2
1	A	42	GLY	CA	41.25	0.3	1
1	A	42	GLY	N	109.356	0.3	1

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, <i>ppm</i>	Suggested action
$^{13}\text{C}_\alpha$	40	3.45 ± 0.57	Should be applied
$^{13}\text{C}_\beta$	35	2.83 ± 2.83	None needed (imprecise)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	40	-1.93 ± 0.58	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 59%, i.e. 90 atoms were assigned a chemical shift out of a possible 152. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	37/46 (80%)	19/19 (100%)	9/18 (50%)	9/9 (100%)
Sidechain	53/106 (50%)	34/64 (53%)	19/28 (68%)	0/14 (0%)
Overall	90/152 (59%)	53/83 (64%)	28/46 (61%)	9/23 (39%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 57%, i.e. 143 atoms were assigned a chemical shift out of a possible 249. 0 out of 0 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	56/74 (76%)	28/30 (93%)	14/30 (47%)	14/14 (100%)
Sidechain	87/163 (53%)	57/101 (56%)	30/44 (68%)	0/18 (0%)
Aromatic	0/12 (0%)	0/6 (0%)	0/5 (0%)	0/1 (0%)
Overall	143/249 (57%)	85/137 (62%)	44/79 (56%)	14/33 (42%)

7.1.4 Statistically unusual chemical shifts [i](#)

The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

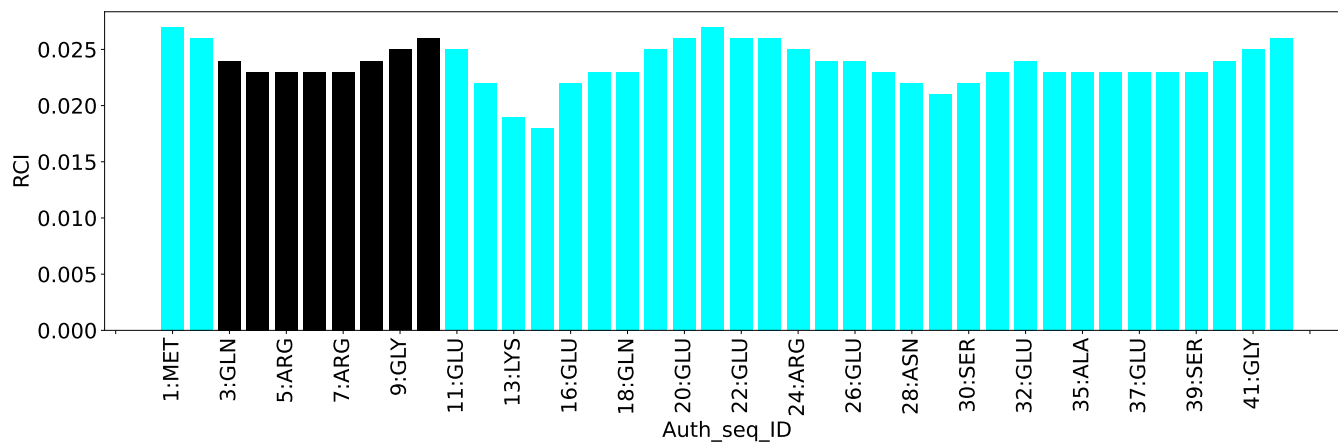
List Id	Chain	Res	Type	Atom	Shift, <i>ppm</i>	Expected range, <i>ppm</i>	Z-score
1	A	1	MET	CG	22.68	25.46 – 38.60	-7.1

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	283
Intra-residue ($ i-j =0$)	82
Sequential ($ i-j =1$)	140
Medium range ($ i-j >1$ and $ i-j <5$)	38
Long range ($ i-j \geq 5$)	19
Inter-chain	0
Hydrogen bond restraints	4
Disulfide bond restraints	0
Total dihedral-angle restraints	54
Number of unmapped restraints	127
Number of restraints per residue	7.8
Number of long range restraints per residue ¹	0.5

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)	2.1	0.2
0.2-0.5 (Medium)	0.1	0.36
>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)	1.3	3.0
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis ⓘ

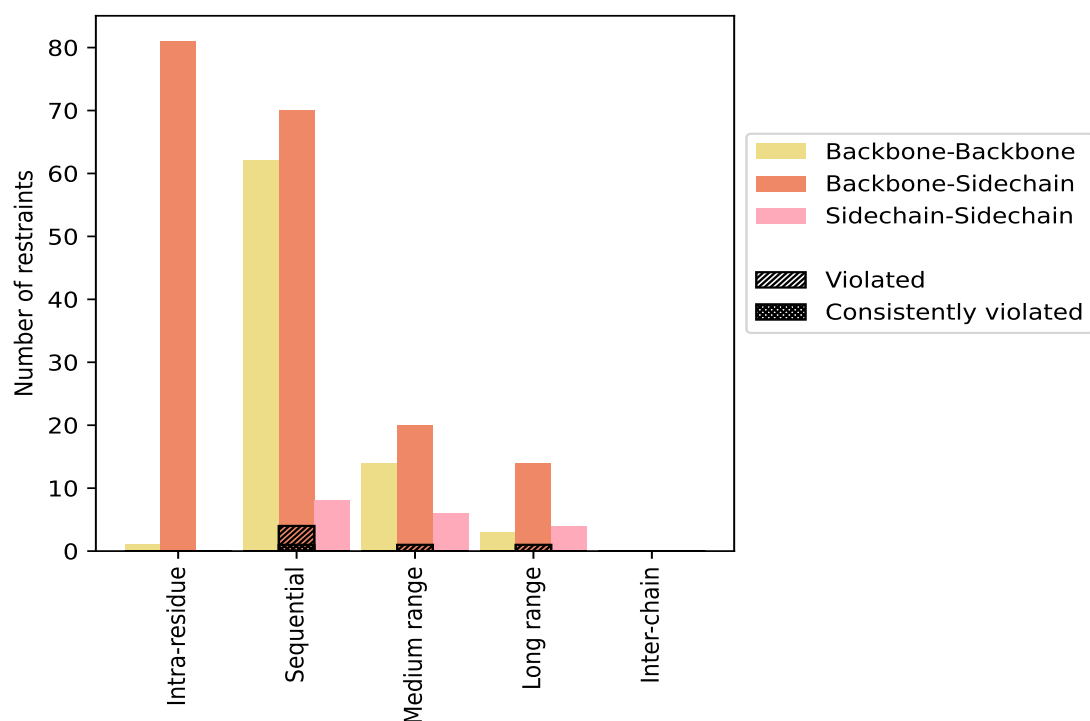
9.1 Summary of distance violations ⓘ

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$)	82	29.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	1	0.4	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	81	28.6	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sequential ($ i-j =1$)	140	49.5	4	2.9	1.4	1	0.7	0.4
Backbone-Backbone	62	21.9	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	70	24.7	4	5.7	1.4	1	1.4	0.4
Sidechain-Sidechain	8	2.8	0	0.0	0.0	0	0.0	0.0
Medium range ($ i-j >1$ & $ i-j <5$)	38	13.4	1	2.6	0.4	0	0.0	0.0
Backbone-Backbone	14	4.9	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	18	6.4	1	5.6	0.4	0	0.0	0.0
Sidechain-Sidechain	6	2.1	0	0.0	0.0	0	0.0	0.0
Long range ($ i-j \geq 5$)	19	6.7	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	3	1.1	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	12	4.2	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	4	1.4	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	4	1.4	1	25.0	0.4	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	283	100.0	6	2.1	2.1	1	0.4	0.4
Backbone-Backbone	80	28.3	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	185	65.4	6	3.2	2.1	1	0.5	0.4
Sidechain-Sidechain	18	6.4	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](#)

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	0	2	1	1	0	4	0.14	0.16	0.02	0.14
2	0	2	0	1	0	3	0.14	0.17	0.02	0.13
3	0	1	0	0	0	1	0.14	0.14	0.0	0.14
4	0	1	0	0	0	1	0.2	0.2	0.0	0.2
5	0	1	0	0	0	1	0.15	0.15	0.0	0.15
6	0	2	0	0	0	2	0.15	0.16	0.01	0.15
7	0	2	1	1	0	4	0.15	0.17	0.02	0.16
8	0	2	0	0	0	2	0.18	0.21	0.03	0.18
9	0	1	1	1	0	3	0.13	0.2	0.05	0.1
10	0	2	0	0	0	2	0.14	0.15	0.01	0.14

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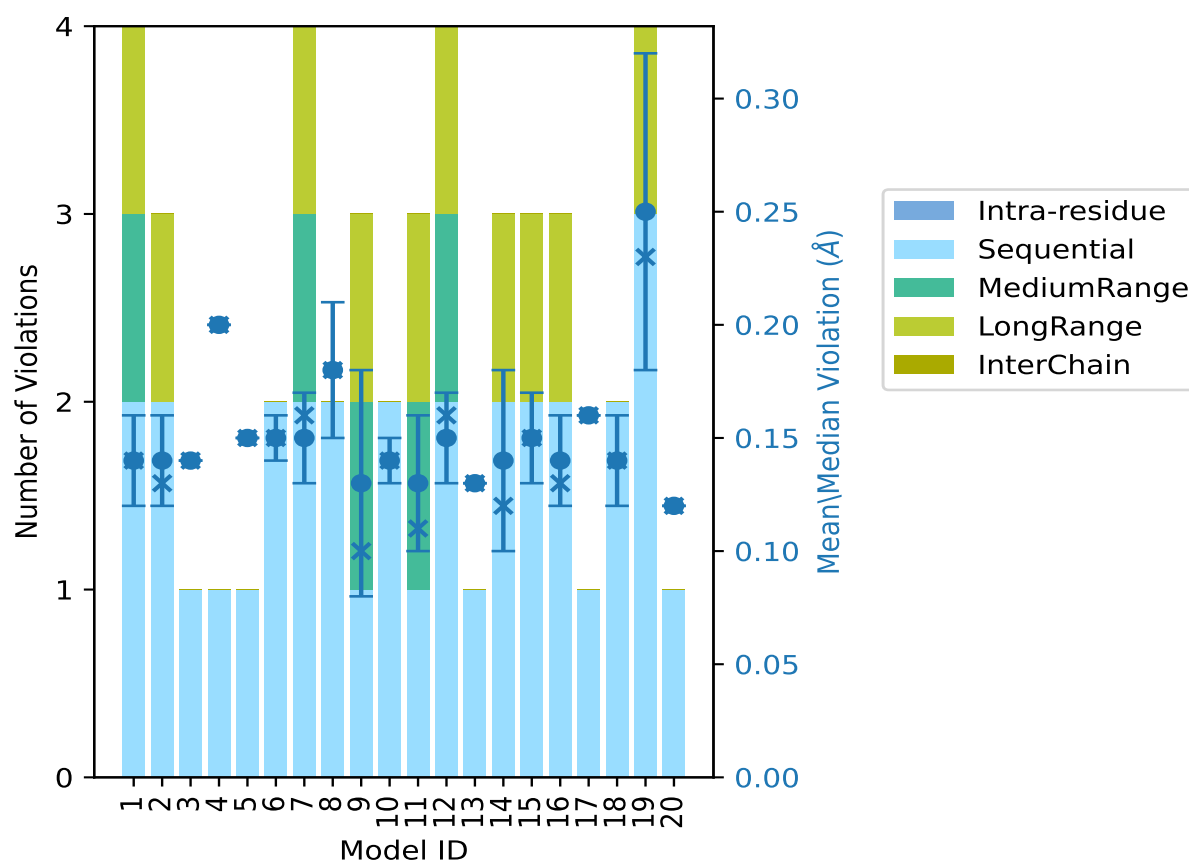
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	0	1	1	1	0	3	0.13	0.17	0.03	0.11
12	0	2	1	1	0	4	0.15	0.17	0.02	0.16
13	0	1	0	0	0	1	0.13	0.13	0.0	0.13
14	0	2	0	1	0	3	0.14	0.19	0.04	0.12
15	0	2	0	1	0	3	0.15	0.17	0.02	0.15
16	0	2	0	1	0	3	0.14	0.17	0.02	0.13
17	0	1	0	0	0	1	0.16	0.16	0.0	0.16
18	0	2	0	0	0	2	0.14	0.16	0.02	0.14
19	0	3	0	1	0	4	0.25	0.36	0.07	0.23
20	0	1	0	0	0	1	0.12	0.12	0.0	0.12

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

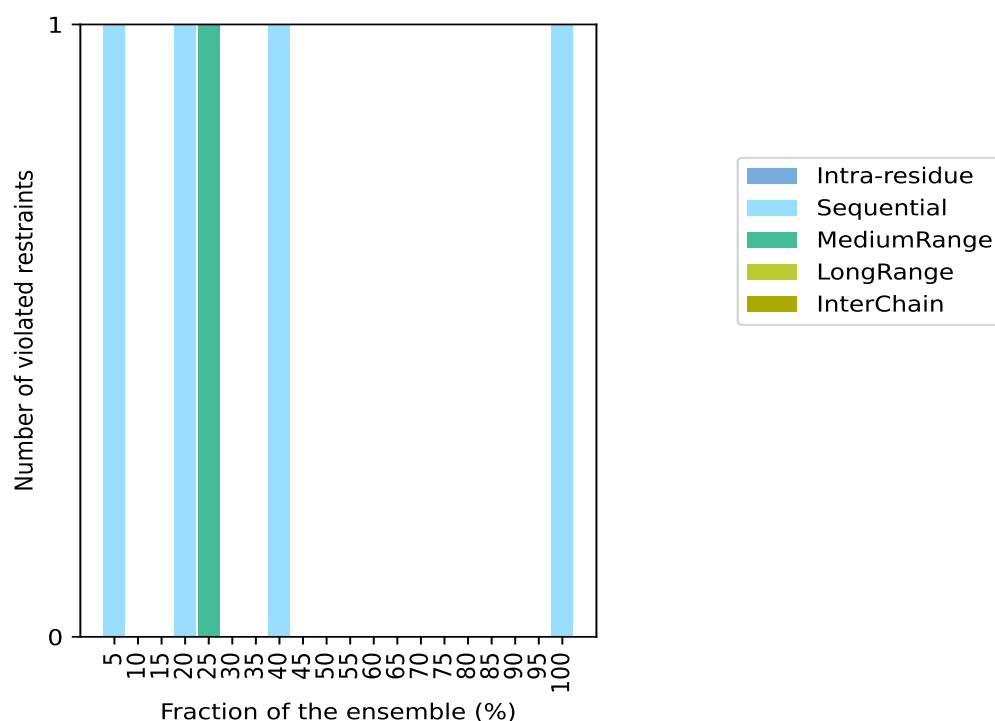
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 274(IR:82, SQ:136, MR:37, LR:19, IC:0) restraints are not 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	%
0	1	0	0	0	1	1	5.0
0	0	0	0	0	0	2	10.0
0	0	0	0	0	0	3	15.0
0	1	0	0	0	1	4	20.0
0	0	1	0	0	1	5	25.0
0	0	0	0	0	0	6	30.0
0	0	0	0	0	0	7	35.0
0	1	0	0	0	1	8	40.0
0	0	0	0	0	0	9	45.0
0	0	0	0	0	0	10	50.0
0	0	0	0	0	0	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
0	1	0	0	0	1	20	100.0

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

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

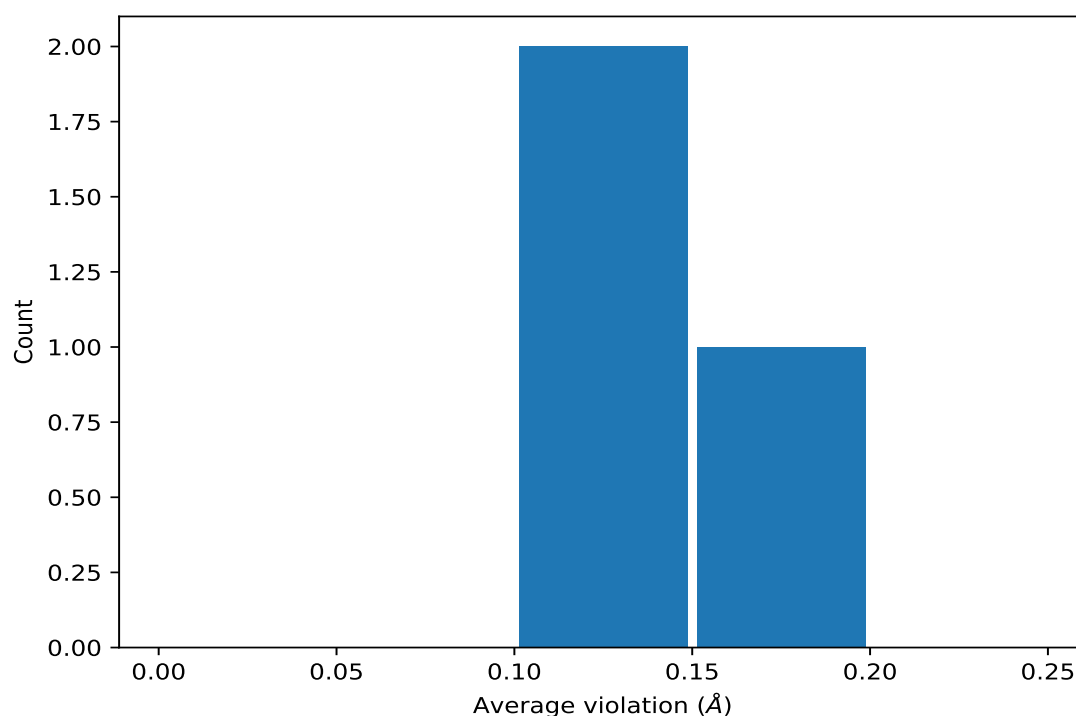
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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.

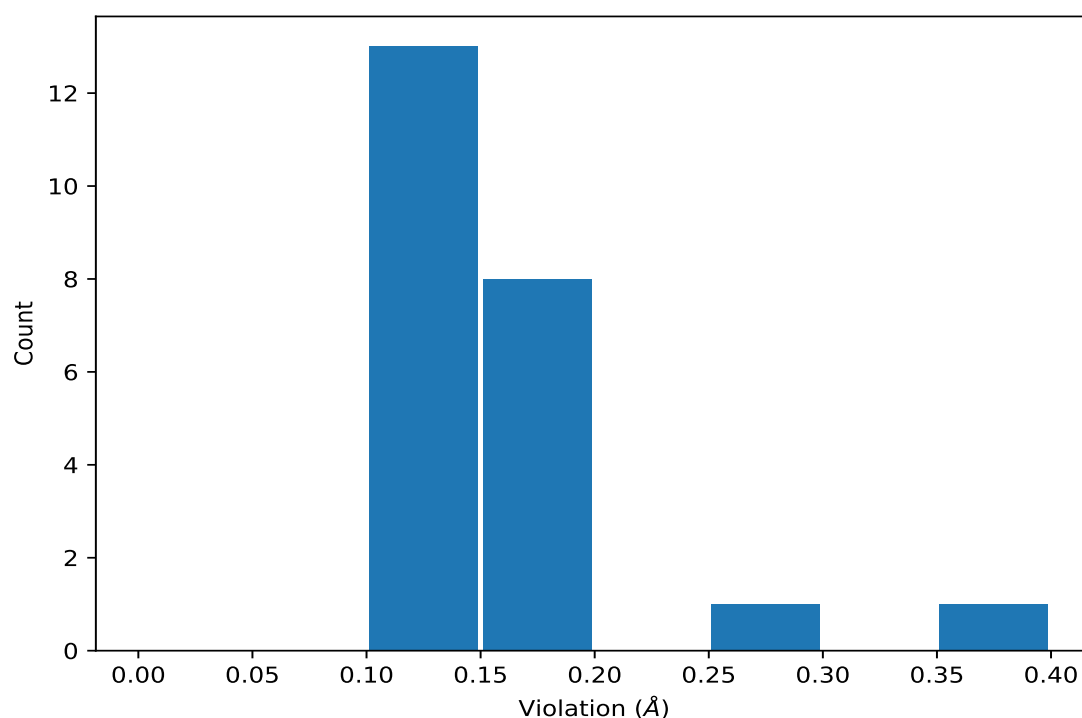
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(3,3)	1:5:A:ARG:H	1:11:A:GLU:O	10	0.13	0.03	0.13
(2,204)	1:5:A:ARG:HG3	1:6:A:GLN:H	8	0.19	0.07	0.17
(2,128)	1:4:A:ARG:HA	1:5:A:ARG:HB3	4	0.12	0.01	0.12

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)
(2,204)	1:5:A:ARG:HG3	1:6:A:GLN:H	19	0.36
(2,127)	1:4:A:ARG:HA	1:5:A:ARG:HG3	19	0.27
(3,3)	1:5:A:ARG:H	1:11:A:GLU:O	19	0.19
(2,204)	1:5:A:ARG:HG3	1:6:A:GLN:H	2	0.17
(2,204)	1:5:A:ARG:HG3	1:6:A:GLN:H	7	0.17
(2,204)	1:5:A:ARG:HG3	1:6:A:GLN:H	12	0.17
(2,204)	1:5:A:ARG:HG3	1:6:A:GLN:H	15	0.17
(2,204)	1:5:A:ARG:HG3	1:6:A:GLN:H	16	0.17
(3,3)	1:5:A:ARG:H	1:11:A:GLU:O	12	0.16
(2,204)	1:5:A:ARG:HG3	1:6:A:GLN:H	1	0.16
(3,3)	1:5:A:ARG:H	1:11:A:GLU:O	7	0.15
(2,204)	1:5:A:ARG:HG3	1:6:A:GLN:H	8	0.14
(2,128)	1:4:A:ARG:HA	1:5:A:ARG:HB3	6	0.14
(3,3)	1:5:A:ARG:H	1:11:A:GLU:O	1	0.13
(3,3)	1:5:A:ARG:H	1:11:A:GLU:O	2	0.13
(3,3)	1:5:A:ARG:H	1:11:A:GLU:O	15	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,3)	1:5:A:ARG:H	1:11:A:GLU:O	16	0.13
(2,128)	1:4:A:ARG:HA	1:5:A:ARG:HB3	10	0.13
(2,128)	1:4:A:ARG:HA	1:5:A:ARG:HB3	14	0.12
(3,3)	1:5:A:ARG:H	1:11:A:GLU:O	11	0.11
(3,3)	1:5:A:ARG:H	1:11:A:GLU:O	14	0.11
(2,128)	1:4:A:ARG:HA	1:5:A:ARG:HB3	18	0.11
(3,3)	1:5:A:ARG:H	1:11:A:GLU:O	9	0.1

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

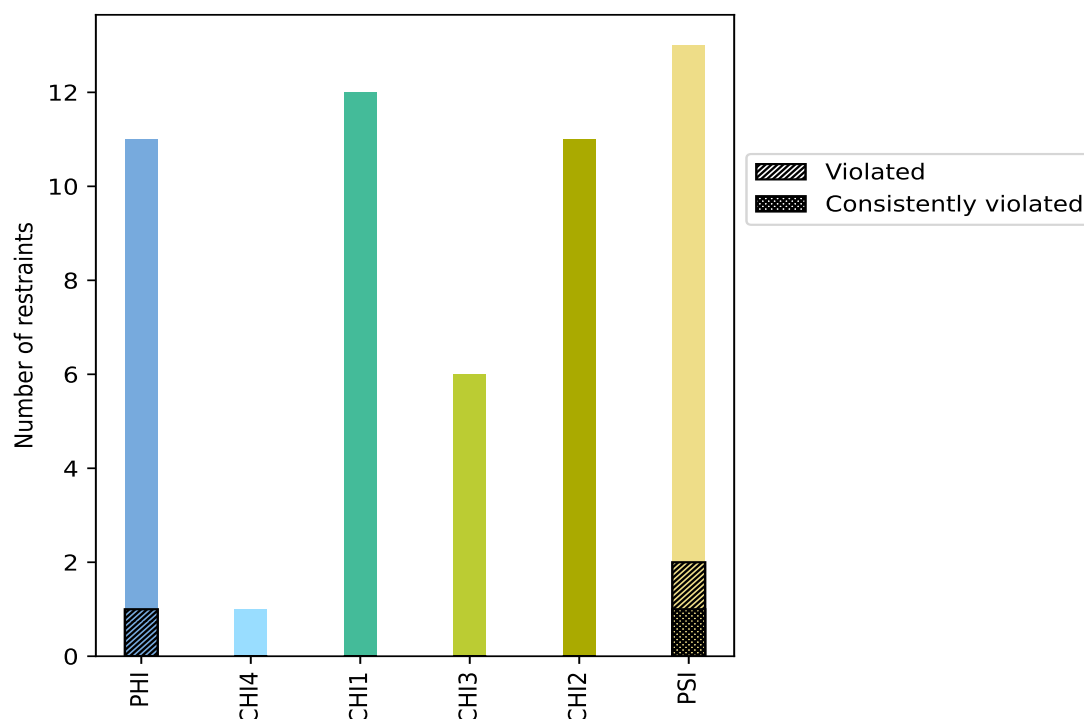
10.1 Summary of dihedral-angle violations [i](#)

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
PHI	11	20.4	1	9.1	1.9	0	0.0	0.0
CHI4	1	1.9	0	0.0	0.0	0	0.0	0.0
CHI1	12	22.2	0	0.0	0.0	0	0.0	0.0
CHI3	6	11.1	0	0.0	0.0	0	0.0	0.0
CHI2	11	20.4	0	0.0	0.0	0	0.0	0.0
PSI	13	24.1	2	15.4	3.7	1	7.7	1.9
Total	54	100.0	3	5.6	5.6	1	1.9	1.9

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

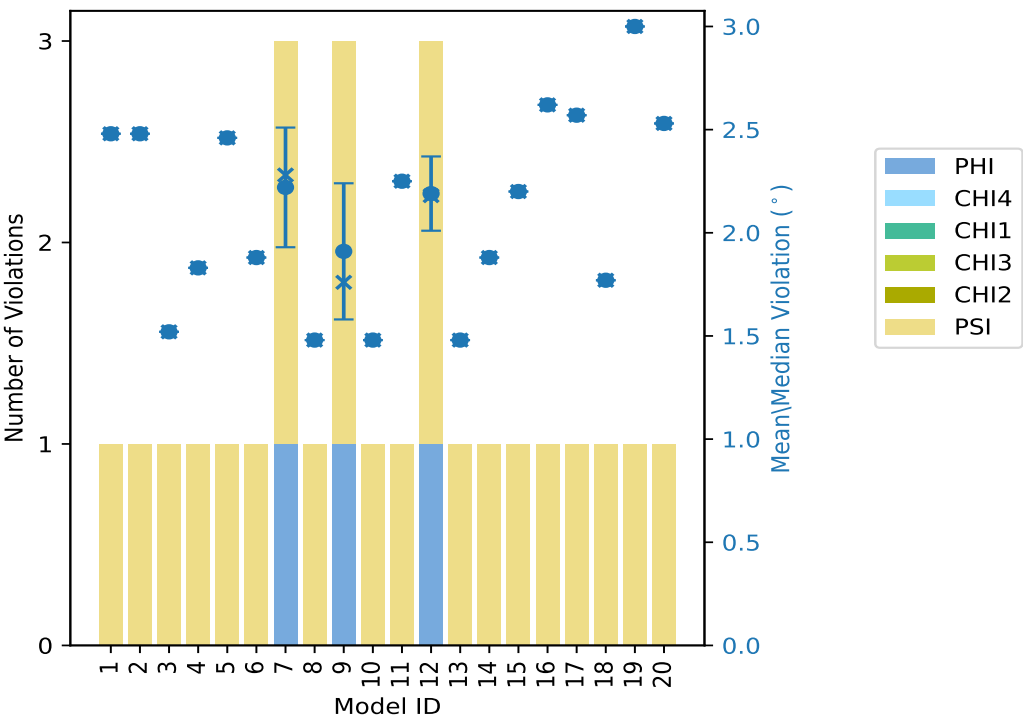
respective categories

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
	PHI	CHI4	CHI1	CHI3	CHI2	PSI	Total				
1	0	0	0	0	0	1	1	2.48	2.48	0.0	2.48
2	0	0	0	0	0	1	1	2.48	2.48	0.0	2.48
3	0	0	0	0	0	1	1	1.52	1.52	0.0	1.52
4	0	0	0	0	0	1	1	1.83	1.83	0.0	1.83
5	0	0	0	0	0	1	1	2.46	2.46	0.0	2.46
6	0	0	0	0	0	1	1	1.88	1.88	0.0	1.88
7	1	0	0	0	0	2	3	2.22	2.53	0.29	2.28
8	0	0	0	0	0	1	1	1.48	1.48	0.0	1.48
9	1	0	0	0	0	2	3	1.91	2.36	0.33	1.76
10	0	0	0	0	0	1	1	1.48	1.48	0.0	1.48
11	0	0	0	0	0	1	1	2.25	2.25	0.0	2.25
12	1	0	0	0	0	2	3	2.19	2.41	0.18	2.18
13	0	0	0	0	0	1	1	1.48	1.48	0.0	1.48
14	0	0	0	0	0	1	1	1.88	1.88	0.0	1.88
15	0	0	0	0	0	1	1	2.2	2.2	0.0	2.2
16	0	0	0	0	0	1	1	2.62	2.62	0.0	2.62
17	0	0	0	0	0	1	1	2.57	2.57	0.0	2.57
18	0	0	0	0	0	1	1	1.77	1.77	0.0	1.77
19	0	0	0	0	0	1	1	3.0	3.0	0.0	3.0
20	0	0	0	0	0	1	1	2.53	2.53	0.0	2.53

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	CHI4	CHI1	CHI3	CHI2	PSI	Total	Count ¹	%
0	0	0	0	0	0	0	1	5.0
0	0	0	0	0	0	0	2	10.0
1	0	0	0	0	1	2	3	15.0
0	0	0	0	0	0	0	4	20.0
0	0	0	0	0	0	0	5	25.0
0	0	0	0	0	0	0	6	30.0
0	0	0	0	0	0	0	7	35.0
0	0	0	0	0	0	0	8	40.0
0	0	0	0	0	0	0	9	45.0
0	0	0	0	0	0	0	10	50.0
0	0	0	0	0	0	0	11	55.0

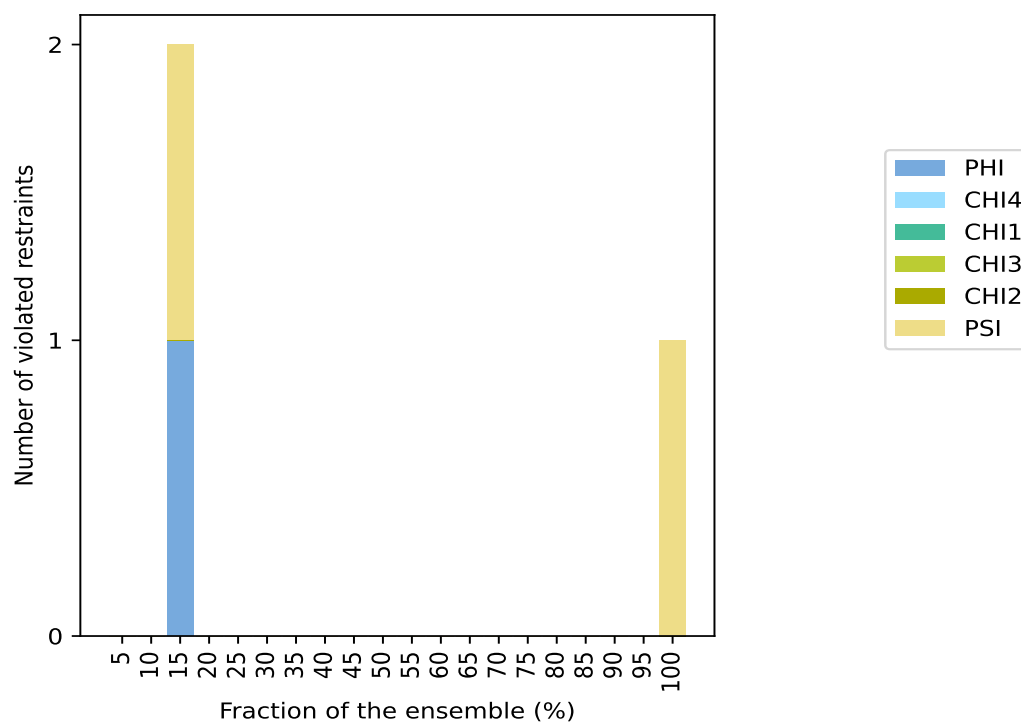
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PHI	Number of violated restraints						Fraction of the ensemble	
	CHI4	CHI1	CHI3	CHI2	PSI	Total	Count ¹	%
0	0	0	0	0	0	0	12	60.0
0	0	0	0	0	0	0	13	65.0
0	0	0	0	0	0	0	14	70.0
0	0	0	0	0	0	0	15	75.0
0	0	0	0	0	0	0	16	80.0
0	0	0	0	0	0	0	17	85.0
0	0	0	0	0	0	0	18	90.0
0	0	0	0	0	0	0	19	95.0
0	0	0	0	0	1	1	20	100.0

¹ Number of models with violations

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

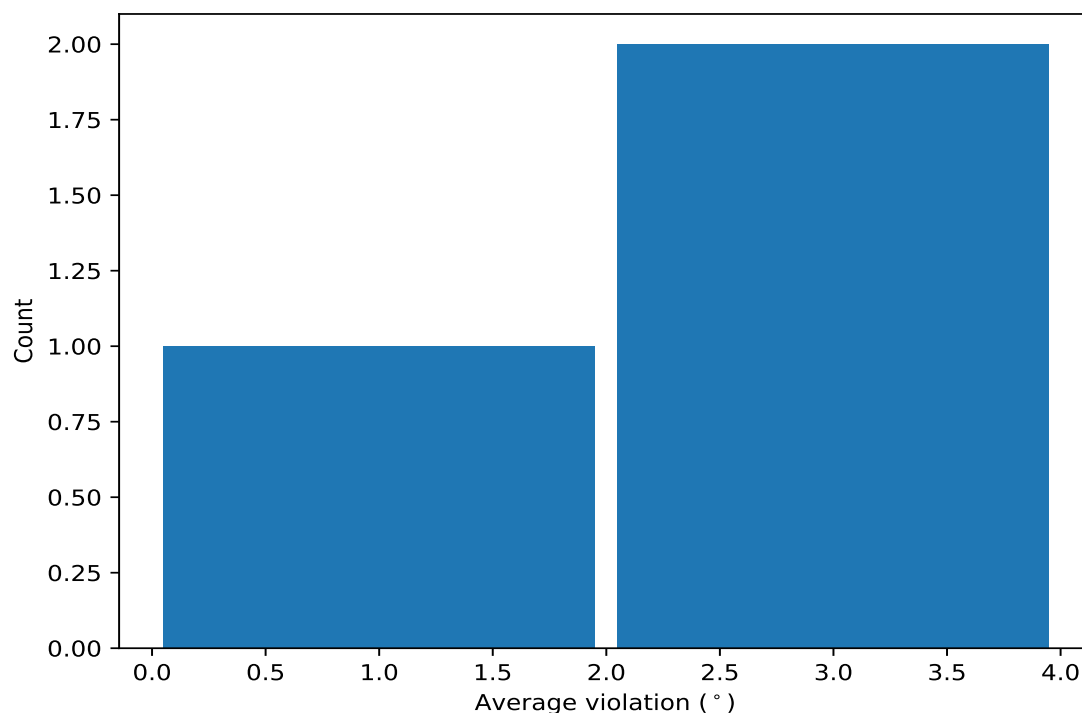


10.4 Most violated dihedral-angle restraints in the ensemble [i](#)

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.

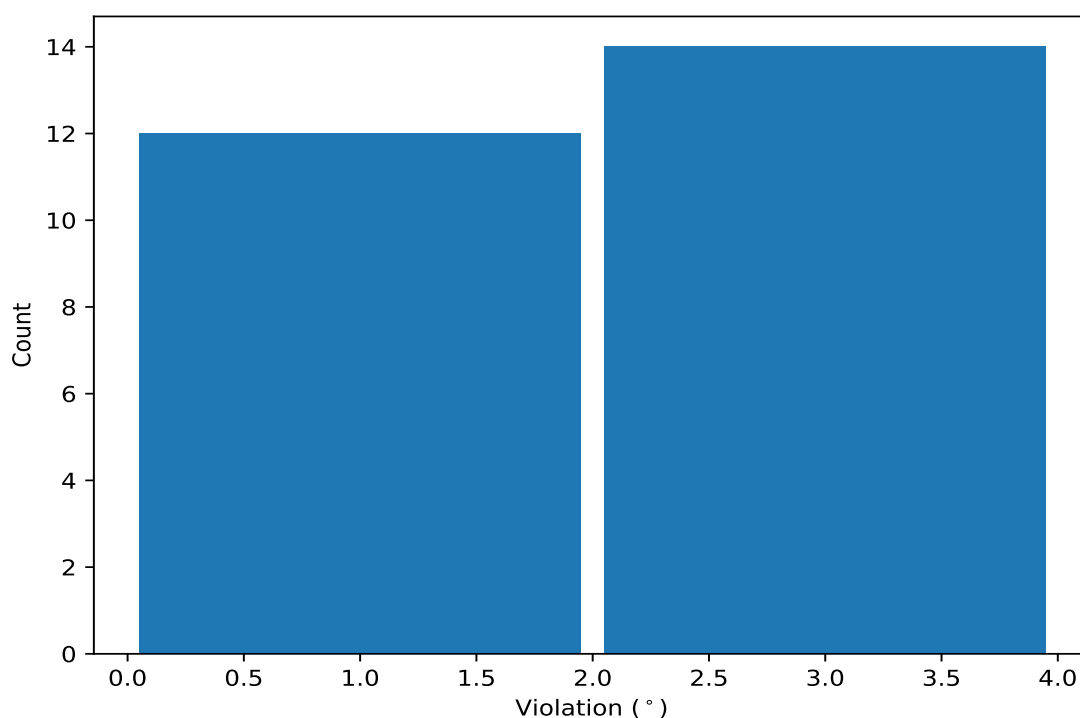
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,18)	1:11:A:GLU:N	1:11:A:GLU:CA	1:11:A:GLU:C	1:12:A:ARG:N	20	2.12	0.46	2.22
(1,20)	1:12:A:ARG:N	1:12:A:ARG:CA	1:12:A:ARG:C	1:13:A:LYS:N	3	2.27	0.07	2.28
(1,21)	1:12:A:ARG:C	1:13:A:LYS:N	1:13:A:LYS:CA	1:13:A:LYS:C	3	1.86	0.09	1.84

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 (°)
(1,18)	1:11:A:GLU:N	1:11:A:GLU:CA	1:11:A:GLU:C	1:12:A:ARG:N	19	3.0
(1,18)	1:11:A:GLU:N	1:11:A:GLU:CA	1:11:A:GLU:C	1:12:A:ARG:N	16	2.62
(1,18)	1:11:A:GLU:N	1:11:A:GLU:CA	1:11:A:GLU:C	1:12:A:ARG:N	17	2.57
(1,18)	1:11:A:GLU:N	1:11:A:GLU:CA	1:11:A:GLU:C	1:12:A:ARG:N	7	2.53
(1,18)	1:11:A:GLU:N	1:11:A:GLU:CA	1:11:A:GLU:C	1:12:A:ARG:N	20	2.53
(1,18)	1:11:A:GLU:N	1:11:A:GLU:CA	1:11:A:GLU:C	1:12:A:ARG:N	1	2.48
(1,18)	1:11:A:GLU:N	1:11:A:GLU:CA	1:11:A:GLU:C	1:12:A:ARG:N	2	2.48
(1,18)	1:11:A:GLU:N	1:11:A:GLU:CA	1:11:A:GLU:C	1:12:A:ARG:N	5	2.46
(1,18)	1:11:A:GLU:N	1:11:A:GLU:CA	1:11:A:GLU:C	1:12:A:ARG:N	12	2.41
(1,20)	1:12:A:ARG:N	1:12:A:ARG:CA	1:12:A:ARG:C	1:13:A:LYS:N	9	2.36
(1,20)	1:12:A:ARG:N	1:12:A:ARG:CA	1:12:A:ARG:C	1:13:A:LYS:N	7	2.28
(1,18)	1:11:A:GLU:N	1:11:A:GLU:CA	1:11:A:GLU:C	1:12:A:ARG:N	11	2.25
(1,18)	1:11:A:GLU:N	1:11:A:GLU:CA	1:11:A:GLU:C	1:12:A:ARG:N	15	2.2
(1,20)	1:12:A:ARG:N	1:12:A:ARG:CA	1:12:A:ARG:C	1:13:A:LYS:N	12	2.18
(1,21)	1:12:A:ARG:C	1:13:A:LYS:N	1:13:A:LYS:CA	1:13:A:LYS:C	12	1.97
(1,18)	1:11:A:GLU:N	1:11:A:GLU:CA	1:11:A:GLU:C	1:12:A:ARG:N	6	1.88
(1,18)	1:11:A:GLU:N	1:11:A:GLU:CA	1:11:A:GLU:C	1:12:A:ARG:N	14	1.88
(1,21)	1:12:A:ARG:C	1:13:A:LYS:N	1:13:A:LYS:CA	1:13:A:LYS:C	7	1.84
(1,18)	1:11:A:GLU:N	1:11:A:GLU:CA	1:11:A:GLU:C	1:12:A:ARG:N	4	1.83
(1,18)	1:11:A:GLU:N	1:11:A:GLU:CA	1:11:A:GLU:C	1:12:A:ARG:N	18	1.77
(1,21)	1:12:A:ARG:C	1:13:A:LYS:N	1:13:A:LYS:CA	1:13:A:LYS:C	9	1.76

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,18)	1:11:A:GLU:N	1:11:A:GLU:CA	1:11:A:GLU:C	1:12:A:ARG:N	9	1.6
(1,18)	1:11:A:GLU:N	1:11:A:GLU:CA	1:11:A:GLU:C	1:12:A:ARG:N	3	1.52
(1,18)	1:11:A:GLU:N	1:11:A:GLU:CA	1:11:A:GLU:C	1:12:A:ARG:N	8	1.48
(1,18)	1:11:A:GLU:N	1:11:A:GLU:CA	1:11:A:GLU:C	1:12:A:ARG:N	10	1.48
(1,18)	1:11:A:GLU:N	1:11:A:GLU:CA	1:11:A:GLU:C	1:12:A:ARG:N	13	1.48