



wwPDB NMR Structure Validation Summary Report ⓘ

Mar 6, 2026 – 05:04 AM UTC

PDB ID : 2C06 / pdb_00002c06
BMRB ID : 6925
Title : NMR-based model of the complex of the toxin Kid and a 5-nucleotide substrate RNA fragment (AUACA)
Authors : Kamphuis, M.B.; Bonvin, A.M.J.J.; Monti, M.C.; Lemonnier, M.; Munoz-Gomez, A.; Van Den Heuvel, R.H.H.; Diaz-Orejas, R.; Boelens, R.
Deposited on : 2005-08-25

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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

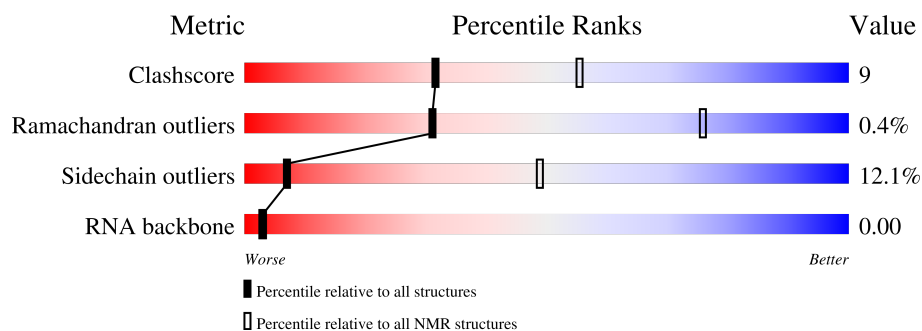
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 25%.

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
RNA backbone	8273	777

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	110	75% 17% 8%
1	B	110	75% 17% • 6%
2	C	5	20% 20% 60%

2 Ensemble composition and analysis

This entry contains 10 models. Model 7 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:1-A:46, A:56-A:110, B:1-B:47, B:55-B:110 (204)	1.14	7

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

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

The models can be grouped into 2 clusters. No single-model clusters were found.

Cluster number	Models
1	1, 3, 6, 7, 8, 9
2	2, 4, 5, 10

3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 2227 atoms, of which 459 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called KID TOXIN PROTEIN.

Mol	Chain	Residues	Atoms						Trace
1	A	110	Total	C	H	N	O	S	0
			1035	519	203	157	152	4	
1	B	110	Total	C	H	N	O	S	0
			1034	519	201	157	153	4	

- Molecule 2 is a RNA chain called 5'-R(*AP*UP*AP*CP*AP)-3'.

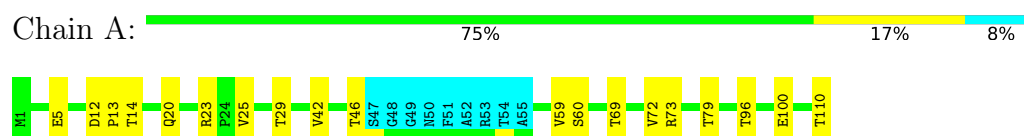
Mol	Chain	Residues	Atoms						Trace
2	C	5	Total	C	H	N	O	P	0
			158	48	55	20	31	4	

4 Residue-property plots [i](#)

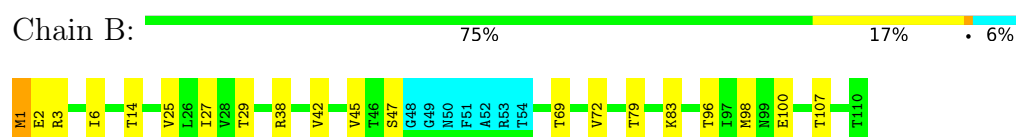
4.1 Average score per residue in the NMR ensemble

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.

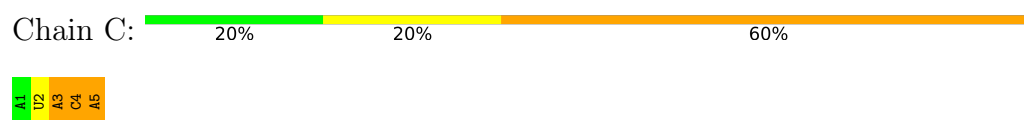
• Molecule 1: KID TOXIN PROTEIN



• Molecule 1: KID TOXIN PROTEIN



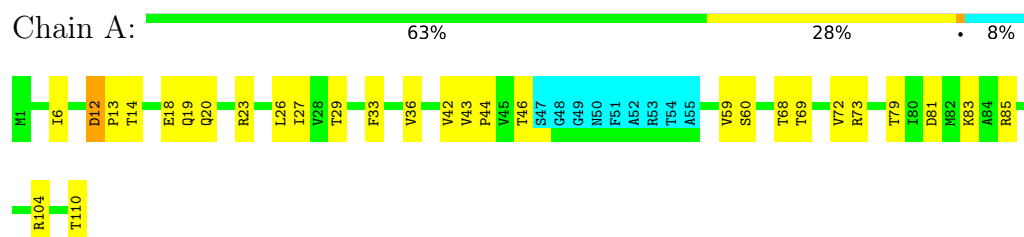
• Molecule 2: 5'-R(*AP*UP*AP*CP*AP)-3'



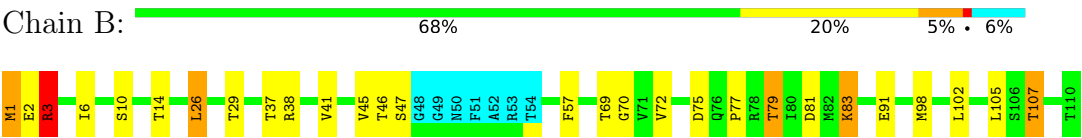
4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 7. Colouring as in section 4.1 above.

• Molecule 1: KID TOXIN PROTEIN



● Molecule 1: KID TOXIN PROTEIN



● Molecule 2: 5'-R(*AP*UP*AP*CP*AP)-3'



5 Refinement protocol and experimental data overview

The models were refined using the following method: *HADDOCK*.

Of the 200 calculated structures, 10 were deposited, based on the following criterion: *LOWEST 10 ENERGY STRUCTURES IN LOWEST ENERGY CLUSTER*.

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

Software name	Classification	Version
CNS	refinement	
NMRView	structure solution	
CNS	structure solution	
HADDOCK	structure solution	

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	794
Number of shifts mapped to atoms	512
Number of unparsed shifts	0
Number of shifts with mapping errors	282
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	25%

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	771	185	813	14±4
1	B	783	186	821	13±3
2	C	103	55	56	7±3
All	All	16570	4260	16899	292

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 9.

5 of 170 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:C:4:C:H2'	2:C:4:C:O2	0.92	1.64	7	2
2:C:4:C:HO2'	2:C:5:A:H2	0.88	1.12	4	1
1:A:78:ARG:HG3	1:B:78:ARG:HG3	0.81	1.53	8	1
1:B:1:MET:HE3	1:B:27:ILE:HB	0.80	1.49	6	6
1:A:21:GLY:HA2	2:C:5:A:C5	0.73	2.18	8	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	99/110 (90%)	91±2 (92±2%)	8±2 (8±2%)	0±0 (0±0%)	100	100
1	B	101/110 (92%)	92±2 (91±2%)	8±2 (8±2%)	1±0 (1±0%)	18	68
All	All	2000/2200 (91%)	1824 (91%)	168 (8%)	8 (0%)	31	76

All 3 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	B	3	ARG	6
1	B	13	PRO	1
1	B	74	CYS	1

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	86/91 (95%)	76±2 (88±3%)	10±2 (12±3%)	7	50
1	B	87/91 (96%)	76±2 (87±2%)	11±2 (13±2%)	7	48
All	All	1730/1820 (95%)	1521 (88%)	209 (12%)	7	49

5 of 66 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	96	THR	10
1	A	29	THR	9
1	A	110	THR	9
1	B	1	MET	9
1	B	29	THR	9

6.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
2	C	4/5 (80%)	3±0 (75±0%)	1±1 (15±17%)	0.01±0.00
All	All	40/50 (80%)	30 (75%)	6 (15%)	0.01

The overall RNA backbone suiteness is 0.00.

All unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
2	C	3	A	10
2	C	4	C	10
2	C	5	A	10

All unique RNA pucker outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
2	C	2	U	3
2	C	4	C	2
2	C	3	A	1

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 25% for the well-defined parts and 26% 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	794
Number of shifts mapped to atoms	512
Number of unparsed shifts	0
Number of shifts with mapping errors	282
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

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

- No matching atom found in the structure. First 5 (of 282) occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	1	MET	HA	4.007	0.005	1
1	A	1	MET	HB2	1.964	0.005	2
1	A	1	MET	HB3	1.568	0.005	2
1	A	2	GLU	HA	4.579	0.005	1
1	A	2	GLU	HB2	2.139	0.005	2
1	A	2	GLU	HB3	1.777	0.005	2
1	A	3	ARG	HA	3.801	0.005	1
1	A	3	ARG	HB2	1.724	0.005	2
1	A	3	ARG	HB3	1.667	0.005	2
1	A	4	GLY	HA2	4.654	0.005	2
1	A	4	GLY	HA3	3.921	0.005	2
1	A	5	GLU	HA	4.772	0.005	1
1	A	5	GLU	HB2	2.138	0.005	2
1	A	6	ILE	HA	5.557	0.005	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	6	ILE	HB	1.67	0.005	1
1	A	7	TRP	HA	5.214	0.005	1
1	A	7	TRP	HB2	3.027	0.005	2
1	A	7	TRP	HB3	2.634	0.005	2
1	A	8	LEU	HA	4.725	0.005	1
1	A	8	LEU	HB2	1.757	0.005	2
1	A	8	LEU	HB3	1.363	0.005	2
1	A	9	VAL	HA	4.657	0.005	1
1	A	9	VAL	HB	2.014	0.005	1
1	A	10	SER	HA	4.665	0.005	1
1	A	10	SER	HB2	3.981	0.005	2
1	A	10	SER	HB3	3.827	0.005	2
1	A	11	LEU	HA	4.176	0.005	1
1	A	11	LEU	HB2	1.841	0.005	2
1	A	11	LEU	HB3	1.46	0.005	2
1	A	12	ASP	HA	4.536	0.005	1
1	A	12	ASP	HB2	2.666	0.005	2
1	A	12	ASP	HB3	2.177	0.005	2
1	A	13	PRO	HA	4.813	0.005	1
1	A	13	PRO	HB2	2.628	0.005	2
1	A	13	PRO	HB3	2.003	0.005	2
1	A	14	THR	HA	4.445	0.005	1
1	A	14	THR	HB	4.464	0.005	1
1	A	15	ALA	HA	4.729	0.005	1
1	A	15	ALA	HB1	1.245	0.005	1
1	A	15	ALA	HB2	1.245	0.005	1
1	A	15	ALA	HB3	1.245	0.005	1
1	A	16	GLY	HA2	3.777	0.005	2
1	A	16	GLY	HA3	3.503	0.005	2
1	A	17	HIS	HA	4.654	0.005	1
1	A	17	HIS	HB2	3.582	0.005	2
1	A	17	HIS	HB3	2.895	0.005	2
1	A	18	GLU	HA	3.827	0.005	1
1	A	18	GLU	HB2	2.208	0.005	2
1	A	18	GLU	HB3	1.984	0.005	2
1	A	19	GLN	HA	3.864	0.005	1
1	A	19	GLN	HB2	1.937	0.005	2
1	A	19	GLN	HB3	1.81	0.005	2
1	A	20	GLN	HA	4.766	0.005	1
1	A	20	GLN	HB2	2.296	0.005	2
1	A	20	GLN	HB3	2.145	0.005	2

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	21	GLY	HA2	4.274	0.005	2
1	A	21	GLY	HA3	4.028	0.005	2
1	A	22	THR	HA	4.976	0.005	1
1	A	22	THR	HB	4.047	0.005	1
1	A	23	ARG	HA	4.995	0.005	1
1	A	23	ARG	HB2	2.034	0.005	2
1	A	23	ARG	HB3	1.744	0.005	2
1	A	24	PRO	HA	5.219	0.005	1
1	A	24	PRO	HB2	2.094	0.005	2
1	A	24	PRO	HB3	1.539	0.005	2
1	A	25	VAL	HA	5.017	0.005	1
1	A	25	VAL	HB	1.816	0.005	1
1	A	26	LEU	HA	5.272	0.005	1
1	A	26	LEU	HB2	1.915	0.005	2
1	A	26	LEU	HB3	0.913	0.005	2
1	A	27	ILE	HA	4.012	0.005	1
1	A	27	ILE	HB	2.399	0.005	1
1	A	28	VAL	HA	4.286	0.005	1
1	A	28	VAL	HB	1.936	0.005	1
1	A	29	THR	HA	4.579	0.005	1
1	A	29	THR	HB	4.096	0.005	1
1	A	30	PRO	HA	4.715	0.005	1
1	A	30	PRO	HB2	2.355	0.005	1
1	A	30	PRO	HB3	2.355	0.005	1
1	A	31	ALA	HA	4.323	0.005	1
1	A	31	ALA	HB1	1.548	0.005	1
1	A	31	ALA	HB2	1.548	0.005	1
1	A	31	ALA	HB3	1.548	0.005	1
1	A	32	ALA	HA	4.067	0.005	1
1	A	32	ALA	HB1	1.901	0.005	1
1	A	32	ALA	HB2	1.901	0.005	1
1	A	32	ALA	HB3	1.901	0.005	1
1	A	33	PHE	HA	4.361	0.005	1
1	A	33	PHE	HB2	3.225	0.005	1
1	A	33	PHE	HB3	3.225	0.005	1
1	A	34	ASN	HA	4.037	0.005	1
1	A	34	ASN	HB2	2.872	0.005	2
1	A	34	ASN	HB3	2.577	0.005	2
1	A	35	ARG	HA	4.067	0.005	1
1	A	35	ARG	HB2	1.901	0.005	2
1	A	35	ARG	HB3	1.508	0.005	2

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	36	VAL	HA	3.874	0.005	1
1	A	36	VAL	HB	2.066	0.005	1
1	A	37	THR	HA	3.893	0.005	1
1	A	37	THR	HB	4.085	0.005	1
1	A	38	ARG	HA	3.838	0.005	1
1	A	38	ARG	HB2	1.453	0.005	1
1	A	38	ARG	HB3	1.453	0.005	1
1	A	39	LEU	HA	5.225	0.005	1
1	A	39	LEU	HB2	1.26	0.005	2
1	A	39	LEU	HB3	1.212	0.005	2
1	A	40	PRO	HA	4.476	0.005	1
1	A	40	PRO	HB2	1.67	0.005	2
1	A	40	PRO	HB3	1.526	0.005	2
1	A	41	VAL	HA	4.396	0.005	1
1	A	41	VAL	HB	1.724	0.005	1
1	A	42	VAL	HA	5.759	0.005	1
1	A	42	VAL	HB	1.898	0.005	1
1	A	43	VAL	HA	5.014	0.005	1
1	A	43	VAL	HB	2.16	0.005	1
1	A	44	PRO	HA	4.825	0.005	1
1	A	44	PRO	HB2	1.925	0.005	2
1	A	44	PRO	HB3	1.653	0.005	2
1	A	45	VAL	HA	4.996	0.005	1
1	A	45	VAL	HB	1.918	0.005	1
1	A	46	THR	HA	4.728	0.005	1
1	A	46	THR	HB	4.408	0.005	1
1	A	47	SER	HA	4.593	0.005	1
1	A	47	SER	HB2	3.957	0.005	1
1	A	47	SER	HB3	3.957	0.005	1
1	A	48	GLY	HA2	3.993	0.005	1
1	A	48	GLY	HA3	3.993	0.005	1
1	A	49	GLY	HA2	3.88	0.005	1
1	A	49	GLY	HA3	3.88	0.005	1
1	A	50	ASN	HA	4.571	0.005	1
1	A	50	ASN	HB2	2.725	0.005	2
1	A	50	ASN	HB3	2.645	0.005	2
1	A	51	PHE	HA	4.567	0.005	1
1	A	51	PHE	HB2	3.082	0.005	2
1	A	51	PHE	HB3	3.0	0.005	2
1	A	52	ALA	HA	4.106	0.005	1
1	A	52	ALA	HB1	1.358	0.005	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	52	ALA	HB2	1.358	0.005	1
1	A	52	ALA	HB3	1.358	0.005	1
1	A	53	ARG	HA	4.215	0.005	1
1	A	53	ARG	HB2	1.86	0.005	2
1	A	53	ARG	HB3	1.795	0.005	2
1	A	54	THR	HA	4.355	0.005	1
1	A	54	THR	HB	4.358	0.005	1
1	A	55	ALA	HA	4.148	0.005	1
1	A	55	ALA	HB1	1.356	0.005	1
1	A	55	ALA	HB2	1.356	0.005	1
1	A	55	ALA	HB3	1.356	0.005	1
1	A	56	GLY	HA2	3.751	0.005	1
1	A	56	GLY	HA3	3.751	0.005	1
1	A	57	PHE	HA	4.498	0.005	1
1	A	57	PHE	HB2	3.494	0.005	2
1	A	57	PHE	HB3	2.754	0.005	2
1	A	58	ALA	HA	5.331	0.005	1
1	A	58	ALA	HB1	1.231	0.005	1
1	A	58	ALA	HB2	1.231	0.005	1
1	A	58	ALA	HB3	1.231	0.005	1
1	A	59	VAL	HA	4.283	0.005	1
1	A	59	VAL	HB	1.688	0.005	1
1	A	60	SER	HA	4.451	0.005	1
1	A	60	SER	HB2	3.889	0.005	2
1	A	60	SER	HB3	3.834	0.005	2
1	A	61	LEU	HA	4.478	0.005	1
1	A	61	LEU	HB2	1.582	0.005	2
1	A	62	ASP	HA	4.451	0.005	1
1	A	62	ASP	HB2	2.598	0.005	2
1	A	62	ASP	HB3	2.528	0.005	2
1	A	63	GLY	HA2	4.06	0.005	2
1	A	63	GLY	HA3	3.907	0.005	2
1	A	64	VAL	HA	4.266	0.005	1
1	A	64	VAL	HB	2.346	0.005	1
1	A	65	GLY	HA2	4.101	0.005	2
1	A	65	GLY	HA3	3.82	0.005	2
1	A	66	ILE	HA	4.681	0.005	1
1	A	66	ILE	HB	2.388	0.005	1
1	A	67	ARG	HA	4.091	0.005	1
1	A	67	ARG	HB2	1.826	0.005	2
1	A	68	THR	HA	3.86	0.005	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	68	THR	HB	3.744	0.005	1
1	A	69	THR	HA	4.466	0.005	1
1	A	69	THR	HB	4.343	0.005	1
1	A	70	GLY	HA2	4.666	0.005	2
1	A	70	GLY	HA3	3.698	0.005	2
1	A	71	VAL	HA	4.899	0.005	1
1	A	71	VAL	HB	1.689	0.005	1
1	A	72	VAL	HA	4.072	0.005	1
1	A	72	VAL	HB	2.021	0.005	1
1	A	73	ARG	HA	4.63	0.005	1
1	A	74	CYS	HA	3.998	0.005	1
1	A	74	CYS	HB2	3.395	0.005	2
1	A	74	CYS	HB3	2.876	0.005	2
1	A	75	ASP	HA	4.122	0.005	1
1	A	75	ASP	HB2	2.709	0.005	2
1	A	75	ASP	HB3	2.172	0.005	2
1	A	76	GLN	HA	5.388	0.005	1
1	A	76	GLN	HB2	2.326	0.005	2
1	A	76	GLN	HB3	1.49	0.005	2
1	A	77	PRO	HA	5.285	0.005	1
1	A	77	PRO	HB2	1.621	0.005	2
1	A	77	PRO	HB3	1.325	0.005	2
1	A	78	ARG	HA	4.689	0.005	1
1	A	78	ARG	HB2	1.928	0.005	2
1	A	78	ARG	HB3	1.773	0.005	2
1	A	79	THR	HA	4.99	0.005	1
1	A	79	THR	HB	3.654	0.005	1
1	A	80	ILE	HA	4.949	0.005	1
1	A	80	ILE	HB	1.454	0.005	1
1	A	81	ASP	HA	4.774	0.005	1
1	A	81	ASP	HB2	2.288	0.005	2
1	A	81	ASP	HB3	3.06	0.005	2
1	A	83	LYS	HA	4.308	0.005	1
1	A	83	LYS	HB2	1.915	0.005	1
1	A	83	LYS	HB3	1.915	0.005	1
1	A	84	ALA	HA	4.088	0.005	1
1	A	84	ALA	HB1	1.314	0.005	1
1	A	84	ALA	HB2	1.314	0.005	1
1	A	84	ALA	HB3	1.314	0.005	1
1	A	85	ARG	HA	4.244	0.005	1
1	A	85	ARG	HB2	2.165	0.005	2

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	85	ARG	HB3	1.285	0.005	2
1	A	86	GLY	HA2	4.029	0.005	1
1	A	86	GLY	HA3	4.029	0.005	1
1	A	87	GLY	HA2	4.701	0.005	2
1	A	87	GLY	HA3	3.696	0.005	2
1	A	88	LYS	HA	4.635	0.005	1
1	A	88	LYS	HB2	1.699	0.005	2
1	A	88	LYS	HB3	1.63	0.005	2
1	A	89	ARG	HA	4.602	0.005	1
1	A	89	ARG	HB2	2.406	0.005	2
1	A	90	LEU	HA	4.532	0.005	1
1	A	90	LEU	HB2	1.509	0.005	2
1	A	90	LEU	HB3	1.353	0.005	2
1	A	91	GLU	HA	4.653	0.005	1
1	A	91	GLU	HB2	2.44	0.005	2
1	A	91	GLU	HB3	2.094	0.005	2
1	A	92	ARG	HA	5.281	0.005	1
1	A	92	ARG	HB2	1.808	0.005	2
1	A	92	ARG	HB3	1.663	0.005	2
1	A	93	VAL	HA	4.656	0.005	1
1	A	93	VAL	HB	2.091	0.005	1
1	A	94	PRO	HA	4.635	0.005	1
1	A	94	PRO	HB2	2.598	0.005	2
1	A	94	PRO	HB3	1.993	0.005	2
1	A	95	GLU	HA	3.932	0.005	1
1	A	95	GLU	HB2	2.092	0.005	2
1	A	95	GLU	HB3	2.048	0.005	2
1	A	96	THR	HA	4.038	0.005	1
1	A	96	THR	HB	4.179	0.005	1
1	A	97	ILE	HA	3.976	0.005	1
1	A	97	ILE	HB	2.127	0.005	1
1	A	98	MET	HA	4.453	0.005	1
1	A	98	MET	HB2	2.264	0.005	2
1	A	98	MET	HB3	1.72	0.005	2
1	A	99	ASN	HA	4.464	0.005	1
1	A	99	ASN	HB2	2.878	0.005	2
1	A	99	ASN	HB3	2.823	0.005	2
1	A	100	GLU	HA	4.166	0.005	1
1	A	100	GLU	HB2	2.302	0.005	2
1	A	100	GLU	HB3	2.145	0.005	2
1	A	101	VAL	HA	3.897	0.005	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	101	VAL	HB	2.428	0.005	1
1	A	102	LEU	HA	4.049	0.005	1
1	A	102	LEU	HB2	1.91	0.005	2
1	A	102	LEU	HB3	1.593	0.005	2
1	A	103	GLY	HA2	4.013	0.005	2
1	A	103	GLY	HA3	3.86	0.005	2
1	A	104	ARG	HA	4.192	0.005	1
1	A	104	ARG	HB2	2.261	0.005	2
1	A	104	ARG	HB3	1.816	0.005	2
1	A	105	LEU	HA	4.036	0.005	1
1	A	105	LEU	HB2	2.014	0.005	2
1	A	105	LEU	HB3	1.383	0.005	2
1	A	106	SER	HA	4.023	0.005	1
1	A	107	THR	HA	4.395	0.005	1
1	A	107	THR	HB	4.179	0.005	1
1	A	108	ILE	HA	4.141	0.005	1
1	A	108	ILE	HB	1.585	0.005	1
1	A	109	LEU	HA	4.239	0.005	1
1	A	109	LEU	HB2	1.596	0.005	2
1	A	109	LEU	HB3	1.512	0.005	2
1	A	110	THR	HA	4.244	0.005	1
1	A	110	THR	HB	4.241	0.005	1

7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	110	-0.01 ± 0.16	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	98	0.37 ± 0.12	None needed (< 0.5 ppm)
$^{13}\text{C}'$	100	-0.21 ± 0.15	None needed (< 0.5 ppm)
^{15}N	102	0.79 ± 0.36	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 25%, i.e. 726 atoms were assigned a chemical shift out of a possible 2920. 0 out of 46 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	489/1012 (48%)	203/414 (49%)	193/408 (47%)	93/190 (49%)
Sidechain	237/1735 (14%)	146/1137 (13%)	91/518 (18%)	0/80 (0%)
Aromatic	0/80 (0%)	0/40 (0%)	0/34 (0%)	0/6 (0%)
Sugar	0/55 (0%)	0/30 (0%)	0/25 (0%)	0/0 (—%)
Base	0/38 (0%)	0/23 (0%)	0/10 (0%)	0/5 (0%)
Overall	726/2920 (25%)	349/1644 (21%)	284/995 (29%)	93/281 (33%)

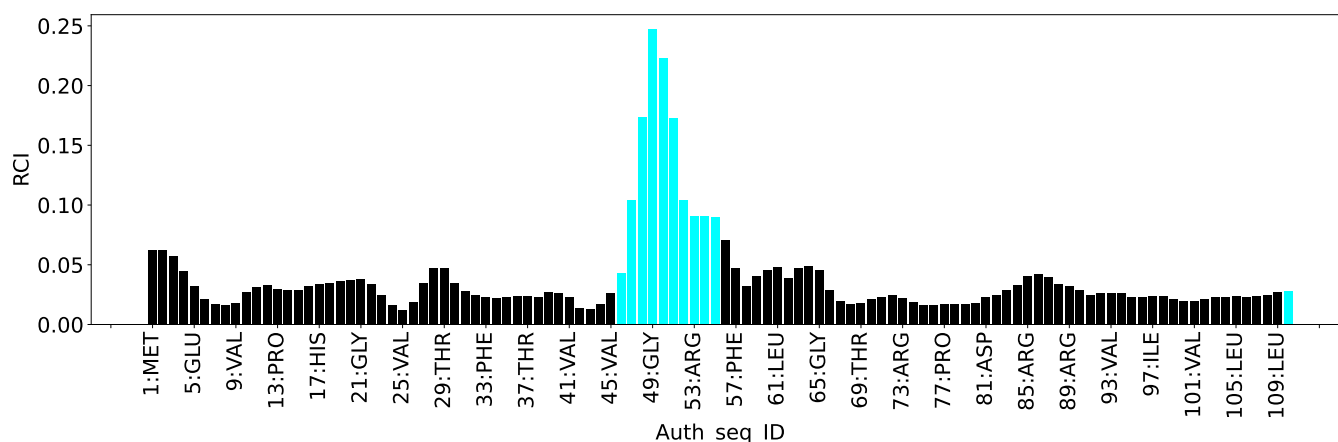
7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots [i](#)

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:



8 NMR restraints analysis

8.1 Conformationally restricting restraints

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

Description	Value
Total distance restraints	23
Intra-residue ($ i-j =0$)	0
Sequential ($ i-j =1$)	0
Medium range ($ i-j >1$ and $ i-j <5$)	0
Long range ($ i-j \geq 5$)	0
Inter-chain	15
Hydrogen bond restraints	8
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	0.1
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)	3.8	0.2
0.2-0.5 (Medium)	6.1	0.5
>0.5 (Large)	6.0	5.46

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

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

9 Distance violation analysis ⓘ

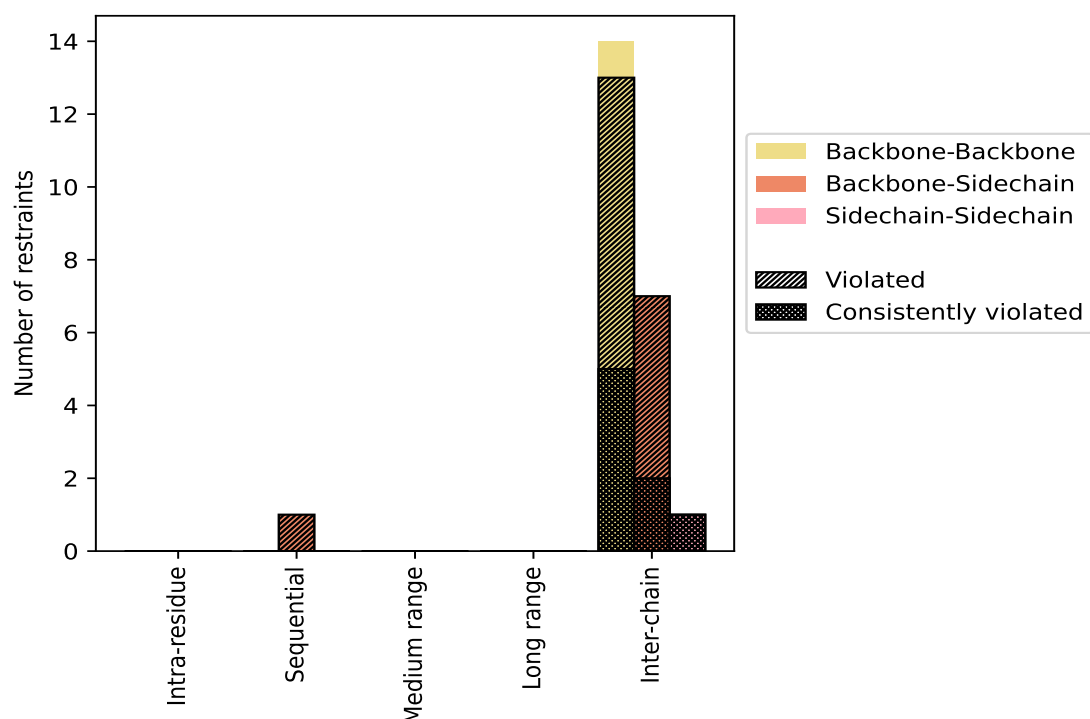
9.1 Summary of distance violations ⓘ

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$)	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sequential ($ i-j =1$)	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Medium range ($ i-j >1$ & $ i-j <5$)	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Long range ($ i-j \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	15	65.2	14	93.3	60.9	6	40.0	26.1
Backbone-Backbone	14	60.9	13	92.9	56.5	5	35.7	21.7
Backbone-Sidechain	1	4.3	1	100.0	4.3	1	100.0	4.3
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Hydrogen bond	8	34.8	8	100.0	34.8	2	25.0	8.7
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	23	100.0	22	95.7	95.7	8	34.8	34.8
Backbone-Backbone	14	60.9	13	92.9	56.5	5	35.7	21.7
Backbone-Sidechain	8	34.8	8	100.0	34.8	2	25.0	8.7
Sidechain-Sidechain	1	4.3	1	100.0	4.3	1	100.0	4.3

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 disulfid bonds are counted in their appropriate category on the x-axis

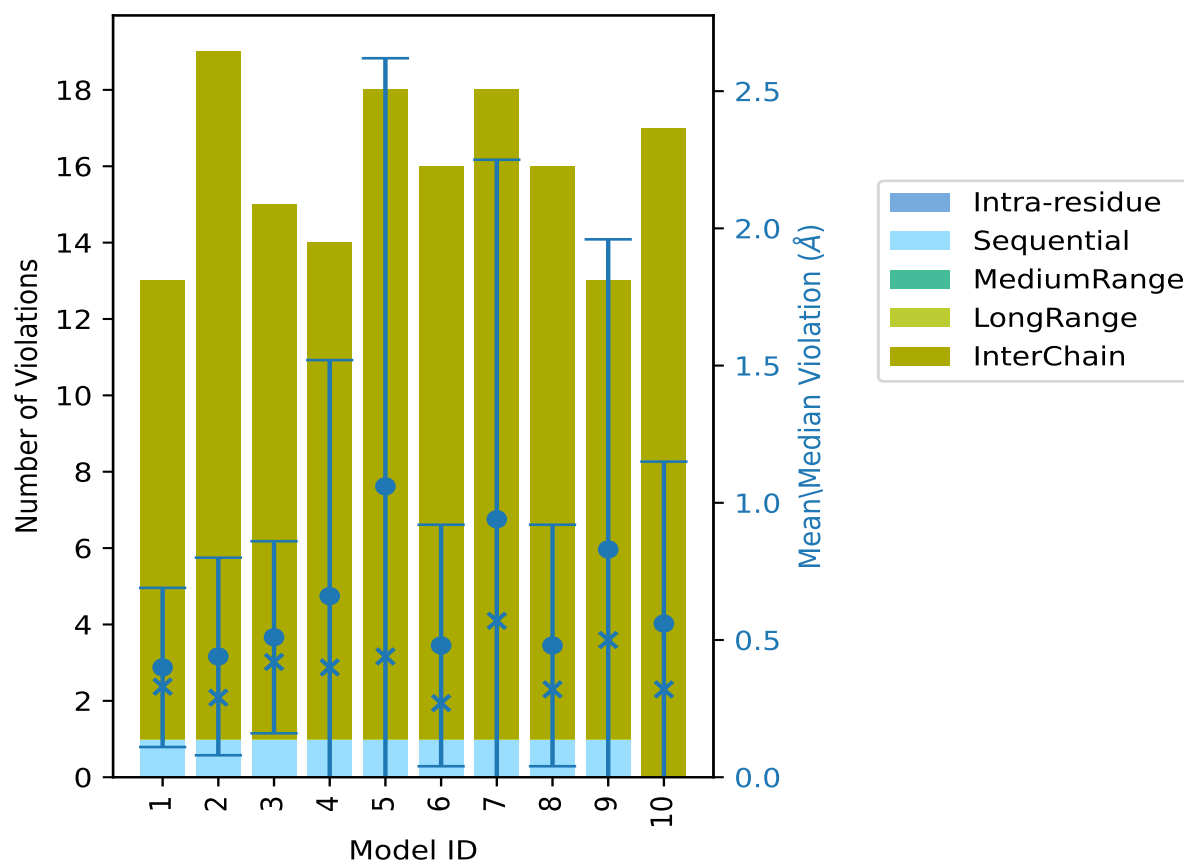
9.2 Distance violation statistics for each model [i](#)

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	1	0	0	12	13	0.4	1.21	0.29	0.33
2	0	1	0	0	18	19	0.44	1.74	0.36	0.29
3	0	1	0	0	14	15	0.51	1.41	0.35	0.42
4	0	1	0	0	13	14	0.66	3.61	0.86	0.4
5	0	1	0	0	17	18	1.06	5.46	1.56	0.44
6	0	1	0	0	15	16	0.48	1.88	0.44	0.27
7	0	1	0	0	17	18	0.94	4.59	1.31	0.57
8	0	1	0	0	15	16	0.48	1.83	0.44	0.32
9	0	1	0	0	12	13	0.83	4.61	1.13	0.5
10	0	0	0	0	17	17	0.56	2.69	0.59	0.32

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

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



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

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

Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 1(IR:0, SQ:0, MR:0, LR:0, IC:1) 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	0	0	0	1	1	1	10.0
0	0	0	0	2	2	2	20.0
0	0	0	0	0	0	3	30.0

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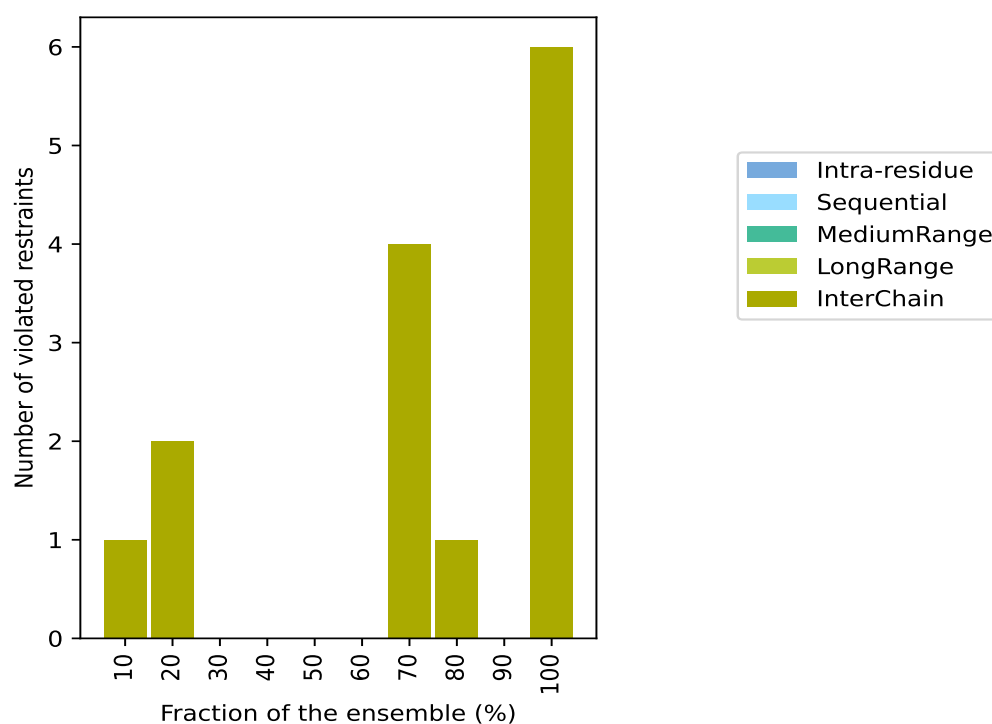
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Number of violated restraints						Fraction of the ensemble	
IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total	Count ⁶	%
0	0	0	0	0	0	4	40.0
0	0	0	0	0	0	5	50.0
0	0	0	0	0	0	6	60.0
0	0	0	0	4	4	7	70.0
0	0	0	0	1	1	8	80.0
0	0	0	0	0	0	9	90.0
0	0	0	0	6	6	10	100.0

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

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

9.3.1 Bar graph : Distance violation statistics for the ensemble ⓘ

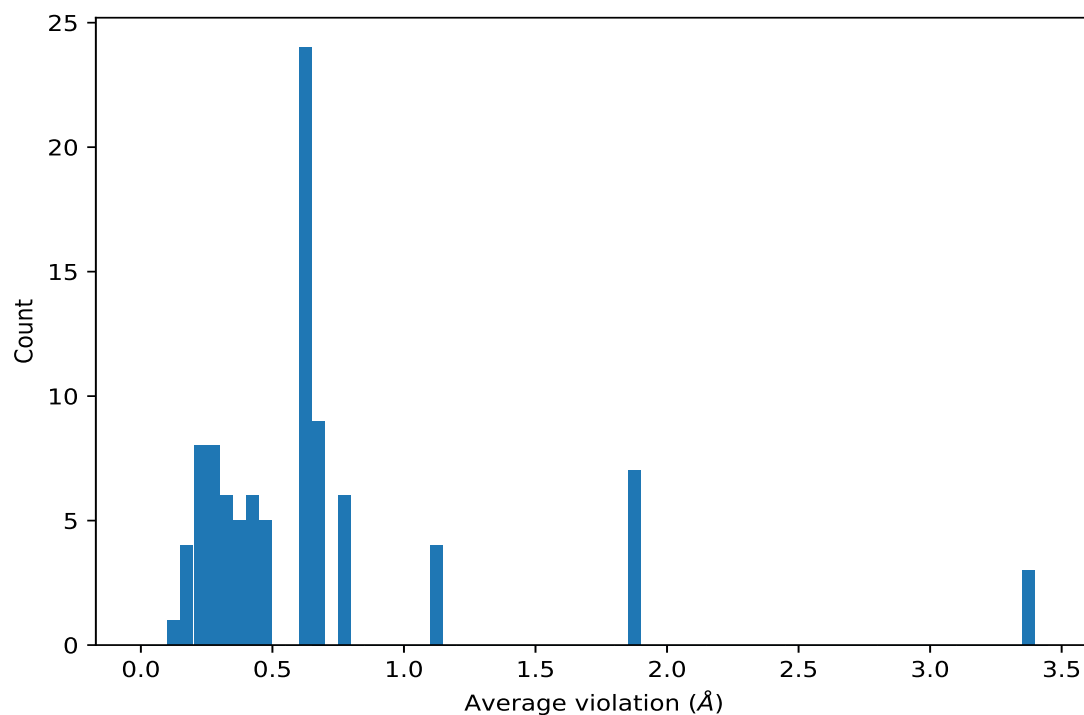


9.4 Most violated distance restraints in the ensemble ⓘ

9.4.1 Histogram : Distribution of mean distance violations ⓘ

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

in the ensemble



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

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

Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,2)	1:14:A:THR:HG1	2:5:C:A:HO2'	10	1.9	1.32	1.66
(1,2)	1:14:A:THR:HG1	2:5:C:A:O3'	10	1.9	1.32	1.66
(1,2)	1:14:A:THR:H	2:5:C:A:HO2'	10	1.9	1.32	1.66
(1,2)	1:14:A:THR:HG1	2:5:C:A:H2	10	1.9	1.32	1.66
(1,2)	1:14:A:THR:HG1	2:5:C:A:H61	10	1.9	1.32	1.66
(1,2)	1:14:A:THR:HG1	2:5:C:A:H5''	10	1.9	1.32	1.66
(1,2)	1:14:A:THR:HG1	2:5:C:A:H3'	10	1.9	1.32	1.66
(1,15)	2:2:C:U:H3	1:55:A:ALA:O	10	1.14	1.85	0.22
(1,15)	2:2:C:U:H3	1:75:A:ASP:OD2	10	1.14	1.85	0.22
(1,15)	2:2:C:U:H3	1:58:A:ALA:N	10	1.14	1.85	0.22
(1,15)	2:2:C:U:H3	1:53:A:ARG:NH2	10	1.14	1.85	0.22
(1,9)	1:70:A:GLY:CA	2:4:C:C:H41	10	0.67	0.42	0.6
(1,9)	1:70:A:GLY:CA	2:4:C:C:H42	10	0.67	0.42	0.6
(1,9)	1:70:A:GLY:N	2:4:C:C:H42	10	0.67	0.42	0.6
(1,18)	2:3:C:A:H2	1:46:A:THR:CB	10	0.66	0.14	0.66

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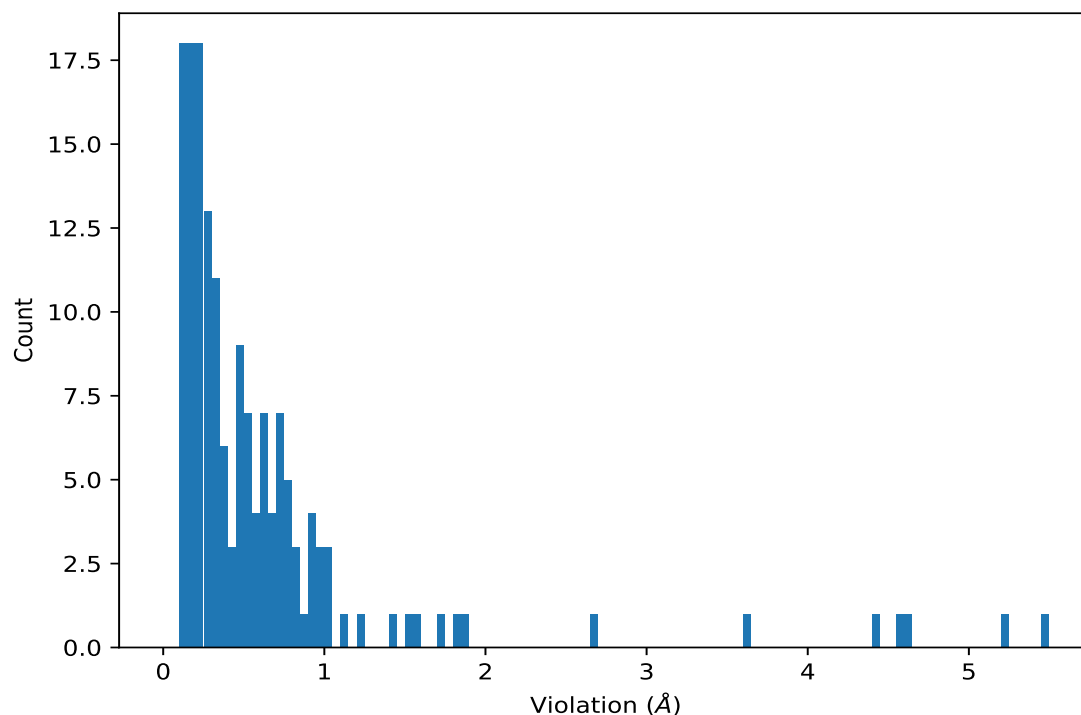
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,18)	2:3:C:A:H2	1:71:A:VAL:CG1	10	0.66	0.14	0.66
(1,18)	2:3:C:A:H2	1:47:A:SER:C	10	0.66	0.14	0.66
(1,18)	2:3:C:A:H2	1:47:A:SER:CB	10	0.66	0.14	0.66
(1,18)	2:3:C:A:H2	1:46:A:THR:CG2	10	0.66	0.14	0.66
(1,18)	2:3:C:A:H2	1:47:A:SER:CA	10	0.66	0.14	0.66
(1,5)	1:20:A:GLN:H	2:4:C:C:OP2	10	0.64	0.27	0.69
(1,5)	1:20:A:GLN:HE21	2:5:C:A:O3'	10	0.64	0.27	0.69
(1,5)	1:20:A:GLN:CB	2:5:C:A:HO2'	10	0.64	0.27	0.69
(1,5)	1:20:A:GLN:HE22	2:5:C:A:H3'	10	0.64	0.27	0.69
(1,5)	1:20:A:GLN:CB	2:5:C:A:H3'	10	0.64	0.27	0.69
(1,5)	1:20:A:GLN:O	2:5:C:A:H2'	10	0.64	0.27	0.69
(1,5)	1:20:A:GLN:O	2:4:C:C:OP2	10	0.64	0.27	0.69
(1,5)	1:20:A:GLN:O	2:5:C:A:H5''	10	0.64	0.27	0.69
(1,5)	1:20:A:GLN:HE21	2:5:C:A:H3'	10	0.64	0.27	0.69
(1,1)	1:10:A:SER:HG	2:5:C:A:H61	10	0.62	0.24	0.57
(1,1)	1:10:A:SER:OG	2:5:C:A:HO2'	10	0.62	0.24	0.57
(1,1)	1:10:A:SER:HG	2:5:C:A:H2	10	0.62	0.24	0.57
(1,1)	1:10:A:SER:HG	2:5:C:A:O2'	10	0.62	0.24	0.57
(1,1)	1:10:A:SER:HG	2:5:C:A:H62	10	0.62	0.24	0.57
(1,1)	1:10:A:SER:HG	2:5:C:A:HO2'	10	0.62	0.24	0.57
(1,1)	1:10:A:SER:HG	2:5:C:A:H8	10	0.62	0.24	0.57
(1,1)	1:10:A:SER:HG	2:5:C:A:H2'	10	0.62	0.24	0.57
(1,10)	1:71:A:VAL:H	2:4:C:C:H41	10	0.62	0.19	0.59
(1,10)	1:71:A:VAL:CG1	2:3:C:A:H2	10	0.62	0.19	0.59
(1,10)	1:71:A:VAL:H	2:4:C:C:H42	10	0.62	0.19	0.59
(1,10)	1:71:A:VAL:CG1	2:3:C:A:H62	10	0.62	0.19	0.59
(1,10)	1:71:A:VAL:CG2	2:3:C:A:H61	10	0.62	0.19	0.59
(1,10)	1:71:A:VAL:CG2	2:3:C:A:H2	10	0.62	0.19	0.59
(1,10)	1:71:A:VAL:CB	2:3:C:A:H2	10	0.62	0.19	0.59
(1,22)	2:3:C:A:O5'	1:73:A:ARG:HH22	10	0.22	0.05	0.22
(1,22)	2:3:C:A:O5'	1:73:A:ARG:HH21	10	0.22	0.05	0.22
(1,22)	2:3:C:A:O5'	1:73:A:ARG:HH12	10	0.22	0.05	0.22
(1,22)	2:3:C:A:O5'	1:73:A:ARG:HE	10	0.22	0.05	0.22
(1,16)	2:3:C:A:H61	1:48:A:GLY:O	9	0.34	0.29	0.18
(1,16)	2:3:C:A:H61	1:55:A:ALA:O	9	0.34	0.29	0.18
(1,16)	2:3:C:A:H61	1:49:A:GLY:N	9	0.34	0.29	0.18
(1,16)	2:3:C:A:H61	1:73:A:ARG:NE	9	0.34	0.29	0.18
(1,16)	2:3:C:A:H61	1:47:A:SER:O	9	0.34	0.29	0.18
(1,16)	2:3:C:A:H61	1:51:A:PHE:O	9	0.34	0.29	0.18
(2,1)	2:2:C:U:HO2'	2:3:C:A:OP2	9	0.15	0.04	0.14

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

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,14)	2:2:C:U:O4	1:57:A:PHE:H	5	5.46
(1,15)	2:2:C:U:H3	1:75:A:ASP:OD2	5	5.24
(1,2)	1:14:A:THR:HG1	2:5:C:A:H5''	9	4.61
(1,14)	2:2:C:U:O4	1:73:A:ARG:HH21	7	4.59
(1,15)	2:2:C:U:H3	1:75:A:ASP:OD2	7	4.42
(1,2)	1:14:A:THR:H	2:5:C:A:HO2'	4	3.61
(1,2)	1:14:A:THR:HG1	2:5:C:A:H3'	10	2.69
(1,2)	1:14:A:THR:HG1	2:5:C:A:H2	6	1.88
(1,9)	1:70:A:GLY:N	2:4:C:C:H42	8	1.83
(1,2)	1:14:A:THR:HG1	2:5:C:A:O3'	2	1.74

10 Dihedral-angle violation analysis ⓘ

No dihedral-angle restraints found