



wwPDB NMR Structure Validation Summary Report ⓘ

Mar 5, 2026 – 09:37 PM UTC

PDB ID : 2MVB / pdb_00002mvb
BMRB ID : 25259
Title : NMR structure of the protein NP_344732.1 from Streptococcus pneumoniae TIGR4
Authors : Dutta, S.K.; Serrano, P.; Geralt, M.; Wuthrich, K.; Joint Center for Structural Genomics (JCSG)
Deposited on : 2014-10-01

This is a wwPDB NMR Structure Validation Summary 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

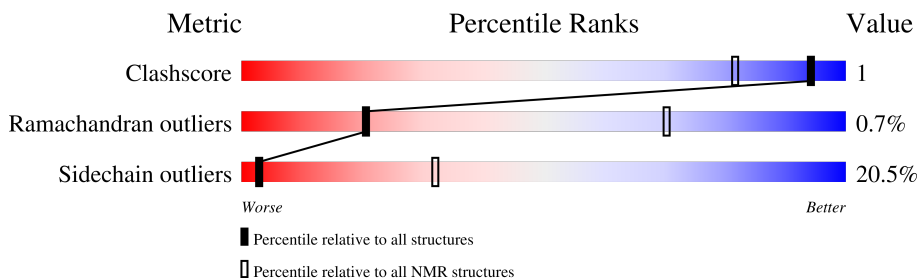
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 88%.

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	165	 73% 10% 18%

2 Ensemble composition and analysis

This entry contains 20 models. Model 12 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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:26-A:35, (136)	A:40-A:165 0.91	12

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 2396 atoms, of which 1104 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Uncharacterized protein.

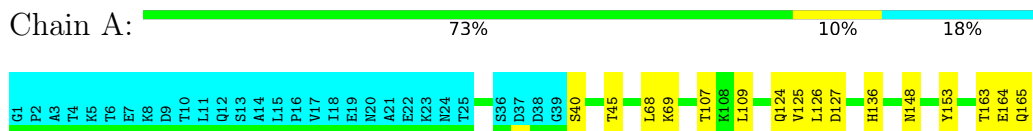
Mol	Chain	Residues	Atoms					Trace
			Total	C	H	N	O	
1	A	165	2396	809	1104	216	267	0

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.

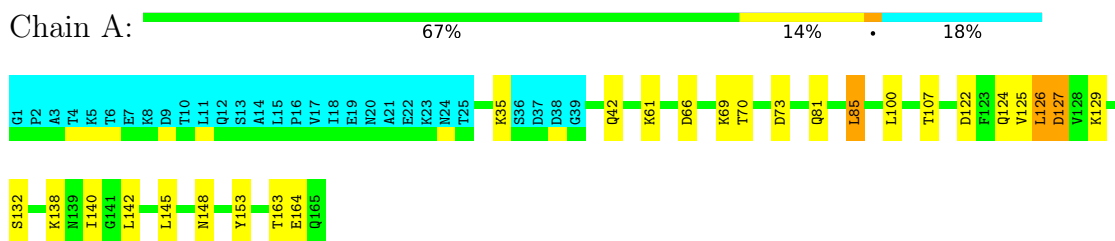
- Molecule 1: Uncharacterized protein



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

The representative model is number 12. Colouring as in section 4.1 above.

- Molecule 1: Uncharacterized protein



5 Refinement protocol and experimental data overview

The models were refined using the following method: *molecular dynamics*.

Of the 80 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	structure solution	3.0
OPAL	refinement	
CNS	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	1898
Number of shifts mapped to atoms	1690
Number of unparsed shifts	0
Number of shifts with mapping errors	208
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	88%

6 Model quality i

6.1 Standard geometry i

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.60±0.01	0±0/1092 (0.0± 0.0%)	1.34±0.03	2±2/1470 (0.2± 0.1%)
All	All	0.60	0/21840 (0.0%)	1.34	50/29400 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	0.3±0.5
All	All	0	7

There are no bond-length outliers.

5 of 27 unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	160	ASN	CA-CB-CG	7.53	120.13	112.60	1	5
1	A	148	ASN	CA-CB-CG	7.09	119.69	112.60	15	4
1	A	127	ASP	CA-CB-CG	6.83	119.43	112.60	4	2
1	A	136	HIS	CB-CG-CD2	-6.47	122.79	131.20	10	5
1	A	113	THR	CB-CA-C	6.27	118.75	109.29	16	1

There are no chirality outliers.

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

Mol	Chain	Res	Type	Group	Models (Total)
1	A	48	TYR	Sidechain	3
1	A	164	GLU	Peptide	1
1	A	68	LEU	Peptide	1

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Mol	Chain	Res	Type	Group	Models (Total)
1	A	62	ARG	Sidechain	1
1	A	71	TYR	Sidechain	1

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	1081	936	1125	3±2
All	All	21620	18720	22500	55

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 1.

5 of 35 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:31:LEU:HD21	1:A:154:ILE:HG23	0.65	1.67	1	4
1:A:121:PHE:CE1	1:A:137:LEU:HD21	0.58	2.33	9	2
1:A:102:GLY:CA	1:A:125:VAL:HG13	0.57	2.29	4	5
1:A:45:THR:HB	1:A:57:ALA:HB3	0.56	1.77	11	1
1:A:126:LEU:HD11	1:A:131:ALA:CB	0.55	2.32	1	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	135/165 (82%)	120±3 (89±2%)	14±3 (10±2%)	1±1 (1±1%)	20	70
All	All	2700/3300 (82%)	2398 (89%)	283 (10%)	19 (1%)	20	70

5 of 7 unique Ramachandran outliers are listed below. They are sorted by the frequency of

occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	65	SER	5
1	A	135	GLU	4
1	A	64	VAL	3
1	A	50	ASP	3
1	A	92	LYS	2

6.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	123/147 (84%)	98±4 (79±4%)	25±4 (21±4%)	3 32
All	All	2460/2940 (84%)	1955 (79%)	505 (21%)	3 32

5 of 94 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	124	GLN	18
1	A	163	THR	16
1	A	107	THR	16
1	A	69	LYS	15
1	A	125	VAL	15

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 i

The completeness of assignment taking into account all chemical shift lists is 88% for the well-defined parts and 84% 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 i

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	1898
Number of shifts mapped to atoms	1690
Number of unparsed shifts	0
Number of shifts with mapping errors	208
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. First 5 (of 208) occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	2	PRO	HB2	1.993	0.006	1
1	A	2	PRO	HD2	3.698	0.006	1
1	A	2	PRO	HG2	2.092	0.006	1
1	A	13	SER	HB2	3.914	0.006	1
1	A	15	LEU	HB2	1.622	0.006	1
1	A	16	PRO	HB2	2.325	0.006	1
1	A	16	PRO	HD2	3.705	0.006	2
1	A	16	PRO	HG2	2.084	0.006	1
1	A	18	ILE	HG12	1.522	0.006	2
1	A	19	GLU	HB2	1.984	0.006	2
1	A	19	GLU	HG2	2.317	0.006	1
1	A	20	ASN	HB2	2.839	0.006	2
1	A	22	GLU	HB2	2.045	0.006	2
1	A	22	GLU	HG2	2.32	0.006	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	23	LYS	HB2	1.899	0.006	2
1	A	24	ASN	HB2	2.812	0.006	2
1	A	29	LYS	HB2	1.824	0.006	1
1	A	29	LYS	HD2	1.853	0.006	1
1	A	29	LYS	HE2	3.071	0.006	1
1	A	29	LYS	HG2	1.594	0.006	2
1	A	31	LEU	HB2	1.244	0.006	2
1	A	33	LEU	HB2	2.125	0.006	2
1	A	34	PRO	HB2	2.43	0.006	2
1	A	34	PRO	HD2	3.474	0.006	2
1	A	34	PRO	HG2	2.249	0.006	2
1	A	35	LYS	HB2	1.833	0.006	1
1	A	35	LYS	HD2	1.747	0.006	1
1	A	35	LYS	HE2	3.049	0.006	1
1	A	35	LYS	HG2	1.501	0.006	2
1	A	36	SER	HB2	4.122	0.006	1
1	A	37	ASP	HB2	2.79	0.006	1
1	A	38	ASP	HB2	3.152	0.006	2
1	A	40	SER	HB2	4.071	0.006	2
1	A	41	GLN	HB2	1.873	0.006	2
1	A	41	GLN	HG2	2.287	0.006	2
1	A	42	GLN	HB2	2.118	0.006	2
1	A	42	GLN	HG2	2.117	0.006	2
1	A	44	GLN	HB2	2.109	0.006	1
1	A	44	GLN	HG2	2.449	0.006	2
1	A	46	ILE	HG12	1.871	0.006	2
1	A	48	TYR	HB2	2.863	0.006	2
1	A	49	LYS	HB2	1.77	0.006	2
1	A	49	LYS	HD2	1.678	0.006	1
1	A	49	LYS	HE2	2.988	0.006	1
1	A	49	LYS	HG2	1.388	0.006	2
1	A	50	ASP	HB2	3.196	0.006	2
1	A	51	LYS	HB2	2.167	0.006	2
1	A	51	LYS	HD2	1.951	0.006	2
1	A	51	LYS	HE2	3.049	0.006	1
1	A	51	LYS	HG2	1.412	0.006	2
1	A	53	PHE	HB2	2.77	0.006	2
1	A	54	LEU	HB2	1.61	0.006	2
1	A	55	SER	HB2	4.095	0.006	2
1	A	56	LEU	HB2	1.756	0.006	2
1	A	58	ILE	HG12	1.09	0.006	2

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	59	GLN	HB2	2.21	0.006	2
1	A	59	GLN	HG2	2.221	0.006	2
1	A	60	GLN	HB2	2.317	0.006	2
1	A	60	GLN	HG2	2.146	0.006	2
1	A	61	LYS	HB2	1.975	0.006	2
1	A	61	LYS	HD2	1.705	0.006	1
1	A	61	LYS	HE2	3.013	0.006	1
1	A	61	LYS	HG2	1.547	0.006	2
1	A	62	ARG	HB2	1.869	0.006	2
1	A	62	ARG	HD2	3.196	0.006	1
1	A	62	ARG	HG2	1.6	0.006	2
1	A	63	PRO	HB2	2.498	0.006	2
1	A	63	PRO	HD2	3.601	0.006	2
1	A	63	PRO	HG2	2.119	0.006	2
1	A	65	SER	HB2	4.16	0.006	2
1	A	66	ASP	HB2	2.783	0.006	2
1	A	67	GLU	HB2	2.131	0.006	2
1	A	67	GLU	HG2	2.392	0.006	1
1	A	68	LEU	HB2	1.776	0.006	2
1	A	69	LYS	HB2	2.129	0.006	2
1	A	69	LYS	HD2	1.745	0.006	1
1	A	69	LYS	HE2	3.049	0.006	1
1	A	69	LYS	HG2	1.502	0.006	2
1	A	71	TYR	HB2	3.49	0.006	2
1	A	72	ILE	HG12	2.243	0.006	2
1	A	73	ASP	HB2	2.946	0.006	2
1	A	74	GLN	HB2	1.769	0.006	2
1	A	74	GLN	HG2	2.4	0.006	2
1	A	75	HIS	HB2	3.207	0.006	2
1	A	78	GLU	HB2	2.13	0.006	2
1	A	78	GLU	HG2	2.429	0.006	1
1	A	79	GLU	HB2	2.124	0.006	2
1	A	79	GLU	HG2	2.493	0.006	2
1	A	81	GLN	HB2	2.406	0.006	1
1	A	81	GLN	HG2	2.649	0.006	2
1	A	82	LYS	HB2	2.045	0.006	2
1	A	82	LYS	HD2	1.749	0.006	1
1	A	82	LYS	HE2	3.049	0.006	1
1	A	82	LYS	HG2	1.691	0.006	2
1	A	84	LEU	HB2	1.978	0.006	2
1	A	85	LEU	HB2	1.73	0.006	2

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	86	GLU	HB2	2.073	0.006	2
1	A	86	GLU	HG2	2.518	0.006	2
1	A	88	GLU	HB2	2.083	0.006	2
1	A	88	GLU	HG2	2.629	0.006	2
1	A	89	GLU	HB2	2.213	0.006	1
1	A	89	GLU	HG2	2.524	0.006	2
1	A	90	LYS	HB2	2.101	0.006	2
1	A	90	LYS	HD2	1.746	0.006	1
1	A	90	LYS	HE2	3.049	0.006	1
1	A	90	LYS	HG2	1.529	0.006	2
1	A	91	ASP	HB2	2.645	0.006	2
1	A	92	LYS	HB2	1.988	0.006	1
1	A	92	LYS	HD2	1.749	0.006	1
1	A	92	LYS	HE2	3.061	0.006	1
1	A	92	LYS	HG2	1.673	0.006	1
1	A	93	SER	HB2	4.081	0.006	1
1	A	94	ILE	HG12	1.463	0.006	2
1	A	95	ILE	HG12	1.733	0.006	2
1	A	96	GLU	HB2	2.105	0.006	1
1	A	96	GLU	HG2	2.44	0.006	1
1	A	98	ARG	HB2	2.107	0.006	2
1	A	98	ARG	HD2	3.197	0.006	2
1	A	98	ARG	HG2	2.102	0.006	2
1	A	99	LYS	HB2	2.067	0.006	2
1	A	99	LYS	HD2	1.632	0.006	1
1	A	99	LYS	HE2	2.927	0.006	1
1	A	99	LYS	HG2	1.502	0.006	2
1	A	100	LEU	HB2	1.613	0.006	2
1	A	103	PHE	HB2	3.172	0.006	2
1	A	104	LYS	HB2	1.453	0.006	2
1	A	104	LYS	HD2	1.563	0.006	1
1	A	104	LYS	HE2	2.879	0.006	1
1	A	104	LYS	HG2	1.202	0.006	2
1	A	105	LEU	HB2	1.405	0.006	2
1	A	106	GLU	HB2	2.007	0.006	2
1	A	106	GLU	HG2	2.18	0.006	2
1	A	108	LYS	HB2	1.794	0.006	2
1	A	108	LYS	HD2	1.632	0.006	1
1	A	108	LYS	HE2	2.927	0.006	1
1	A	108	LYS	HG2	1.283	0.006	1
1	A	109	LEU	HB2	1.911	0.006	2

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	110	LEU	HB2	1.612	0.006	2
1	A	111	SER	HB2	4.149	0.006	2
1	A	114	GLU	HB2	1.892	0.006	1
1	A	114	GLU	HG2	2.034	0.006	2
1	A	115	LEU	HB2	1.721	0.006	2
1	A	116	GLN	HB2	2.146	0.006	2
1	A	116	GLN	HG2	1.96	0.006	1
1	A	120	SER	HB2	3.557	0.006	1
1	A	121	PHE	HB2	2.401	0.006	2
1	A	122	ASP	HB2	2.992	0.006	2
1	A	123	PHE	HB2	3.594	0.006	2
1	A	124	GLN	HB2	2.51	0.006	2
1	A	124	GLN	HG2	2.381	0.006	2
1	A	126	LEU	HB2	1.716	0.006	2
1	A	127	ASP	HB2	3.061	0.006	2
1	A	129	LYS	HB2	1.924	0.006	2
1	A	129	LYS	HD2	1.749	0.006	1
1	A	129	LYS	HE2	3.049	0.006	1
1	A	129	LYS	HG2	1.552	0.006	2
1	A	130	LYS	HB2	1.802	0.006	2
1	A	130	LYS	HD2	1.748	0.006	1
1	A	130	LYS	HE2	3.049	0.006	1
1	A	130	LYS	HG2	1.529	0.006	2
1	A	132	SER	HB2	3.991	0.006	2
1	A	133	GLN	HB2	2.371	0.006	2
1	A	133	GLN	HG2	2.452	0.006	2
1	A	134	LEU	HB2	1.901	0.006	2
1	A	135	GLU	HB2	2.208	0.006	2
1	A	135	GLU	HG2	2.398	0.006	1
1	A	136	HIS	HB2	3.119	0.006	2
1	A	137	LEU	HB2	2.034	0.006	2
1	A	138	LYS	HB2	1.85	0.006	2
1	A	138	LYS	HD2	1.715	0.006	1
1	A	138	LYS	HE2	3.024	0.006	1
1	A	138	LYS	HG2	1.496	0.006	1
1	A	139	ASN	HB2	2.907	0.006	2
1	A	140	ILE	HG12	1.385	0.006	2
1	A	142	LEU	HB2	1.271	0.006	2
1	A	143	GLU	HB2	1.943	0.006	1
1	A	143	GLU	HG2	2.258	0.006	2
1	A	144	ASN	HB2	2.802	0.006	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	145	LEU	HB2	1.388	0.006	2
1	A	146	LEU	HB2	1.508	0.006	1
1	A	147	LYS	HB2	1.9	0.006	2
1	A	147	LYS	HD2	1.745	0.006	1
1	A	147	LYS	HE2	3.048	0.006	1
1	A	147	LYS	HG2	1.651	0.006	2
1	A	148	ASN	HB2	2.938	0.006	2
1	A	149	GLU	HB2	1.999	0.006	2
1	A	149	GLU	HG2	2.48	0.006	2
1	A	150	PRO	HB2	0.475	0.006	2
1	A	150	PRO	HD2	3.288	0.006	2
1	A	150	PRO	HG2	1.272	0.006	2
1	A	151	SER	HB2	3.909	0.006	2
1	A	152	LYS	HB2	1.983	0.006	2
1	A	152	LYS	HD2	1.751	0.006	1
1	A	152	LYS	HE2	3.048	0.006	1
1	A	152	LYS	HG2	1.524	0.006	1
1	A	153	TYR	HB2	3.278	0.006	2
1	A	154	ILE	HG12	1.984	0.006	2
1	A	155	SER	HB2	4.071	0.006	2
1	A	156	ASP	HB2	2.598	0.006	2
1	A	157	ARG	HB2	1.916	0.006	2
1	A	157	ARG	HD2	3.013	0.006	1
1	A	157	ARG	HG2	1.122	0.006	2
1	A	158	LEU	HB2	1.982	0.006	2
1	A	160	ASN	HB2	3.1	0.006	2
1	A	164	GLU	HB2	2.032	0.006	2
1	A	164	GLU	HG2	2.329	0.006	2
1	A	165	GLN	HB2	2.064	0.006	2
1	A	165	GLN	HG2	2.293	0.006	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
$^{13}\text{C}_\alpha$	165	2.16 ± 0.03	Should be checked
$^{13}\text{C}_\beta$	159	2.42 ± 0.04	Should be checked
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	159	-3.30 ± 0.29	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 88%, i.e. 1671 atoms were assigned a chemical shift out of a possible 1900. 0 out of 26 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	542/678 (80%)	273/273 (100%)	136/272 (50%)	133/133 (100%)
Sidechain	1059/1141 (93%)	720/737 (98%)	325/363 (90%)	14/41 (34%)
Aromatic	70/81 (86%)	35/40 (88%)	35/39 (90%)	0/2 (0%)
Overall	1671/1900 (88%)	1028/1050 (98%)	496/674 (74%)	147/176 (84%)

7.1.4 Statistically unusual chemical shifts [i](#)

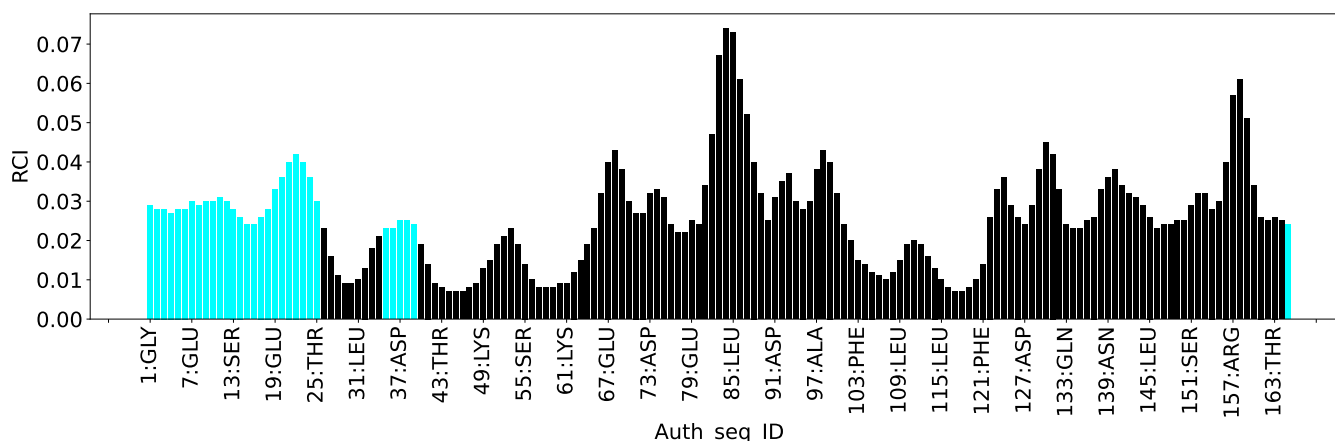
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	150	PRO	HG3	0.24	0.33 – 3.48	-5.3

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	2583
Intra-residue ($ i-j =0$)	699
Sequential ($ i-j =1$)	720
Medium range ($ i-j >1$ and $ i-j <5$)	467
Long range ($ i-j \geq 5$)	697
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	12
Number of restraints per residue	15.7
Number of long range restraints per residue ¹	4.2

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)	53.0	0.2
0.2-0.5 (Medium)	64.2	0.5
>0.5 (Large)	122.3	3.35

8.2.2 Average number of dihedral-angle violations per model

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

9 Distance violation analysis [i](#)

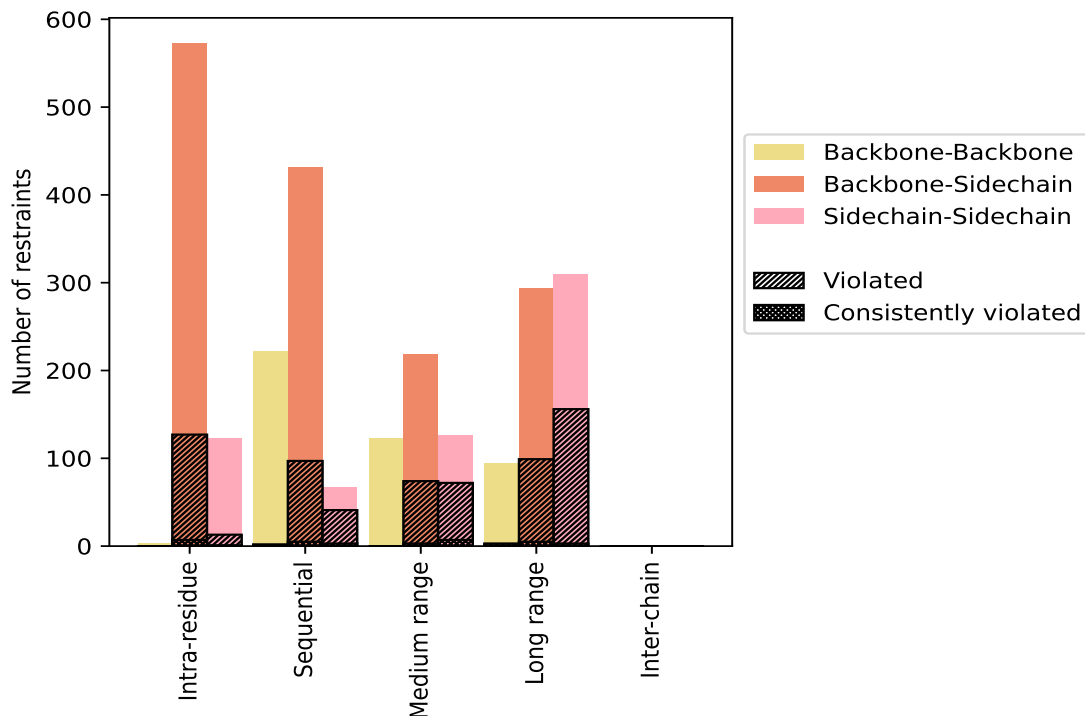
9.1 Summary of distance violations [i](#)

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

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue ($i-j =0$)	699	27.1	140	20.0	5.4	8	1.1	0.3
Backbone-Backbone	3	0.1	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	573	22.2	127	22.2	4.9	7	1.2	0.3
Sidechain-Sidechain	123	4.8	13	10.6	0.5	1	0.8	0.0
Sequential ($i-j =1$)	720	27.9	140	19.4	5.4	8	1.1	0.3
Backbone-Backbone	222	8.6	2	0.9	0.1	0	0.0	0.0
Backbone-Sidechain	431	16.7	97	22.5	3.8	5	1.2	0.2
Sidechain-Sidechain	67	2.6	41	61.2	1.6	3	4.5	0.1
Medium range ($i-j >1$ & $i-j <5$)	467	18.1	146	31.3	5.7	10	2.1	0.4
Backbone-Backbone	123	4.8	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	218	8.4	74	33.9	2.9	3	1.4	0.1
Sidechain-Sidechain	126	4.9	72	57.1	2.8	7	5.6	0.3
Long range ($i-j \geq 5$)	697	27.0	258	37.0	10.0	9	1.3	0.3
Backbone-Backbone	94	3.6	3	3.2	0.1	1	1.1	0.0
Backbone-Sidechain	294	11.4	99	33.7	3.8	5	1.7	0.2
Sidechain-Sidechain	309	12.0	156	50.5	6.0	3	1.0	0.1
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	0	0.0	0	0.0	0.0	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	2583	100.0	684	26.5	26.5	35	1.4	1.4
Backbone-Backbone	442	17.1	5	1.1	0.2	1	0.2	0.0
Backbone-Sidechain	1516	58.7	397	26.2	15.4	20	1.3	0.8
Sidechain-Sidechain	625	24.2	282	45.1	10.9	14	2.2	0.5

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	43	39	50	80	0	212	0.65	2.41	0.52	0.48
2	47	55	51	105	0	258	0.67	3.27	0.53	0.53
3	51	56	45	84	0	236	0.68	2.17	0.52	0.5
4	50	51	43	100	0	244	0.73	3.12	0.58	0.59
5	55	52	50	101	0	258	0.67	2.38	0.52	0.52
6	57	53	63	118	0	291	0.73	2.48	0.55	0.61
7	49	54	59	86	0	248	0.67	2.29	0.52	0.5
8	51	43	56	91	0	241	0.64	3.13	0.55	0.48
9	53	48	49	99	0	249	0.68	3.0	0.54	0.49
10	53	49	54	104	0	260	0.65	2.88	0.54	0.5

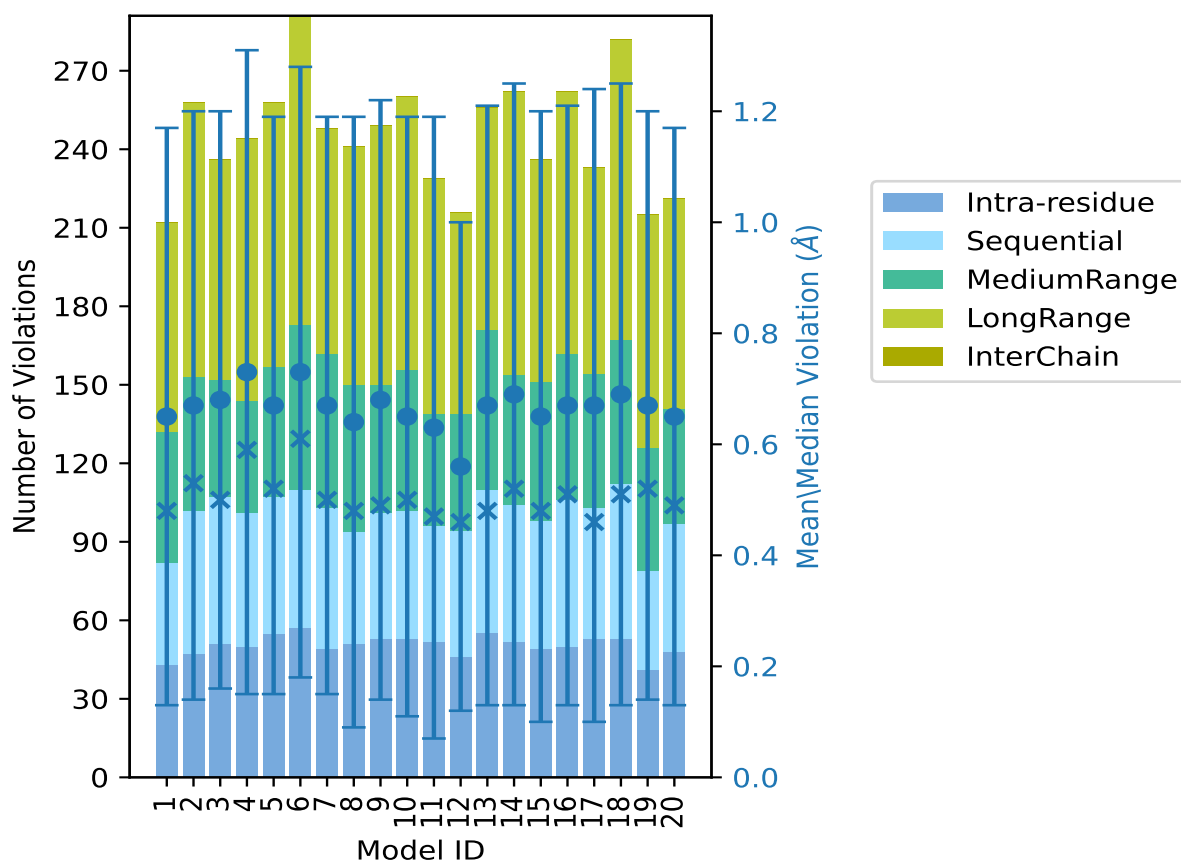
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Model ID	Number of violations					Total	Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵					
11	52	44	43	90	0	229	0.63	3.35	0.56	0.47
12	46	48	45	77	0	216	0.56	2.01	0.44	0.46
13	55	55	61	85	0	256	0.67	2.92	0.54	0.48
14	52	52	50	108	0	262	0.69	3.28	0.56	0.52
15	49	49	53	85	0	236	0.65	2.64	0.55	0.48
16	50	56	56	100	0	262	0.67	2.24	0.54	0.51
17	53	50	51	79	0	233	0.67	3.02	0.57	0.46
18	53	59	55	115	0	282	0.69	2.95	0.56	0.51
19	41	38	47	89	0	215	0.67	3.13	0.53	0.52
20	48	49	44	80	0	221	0.65	2.38	0.52	0.49

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

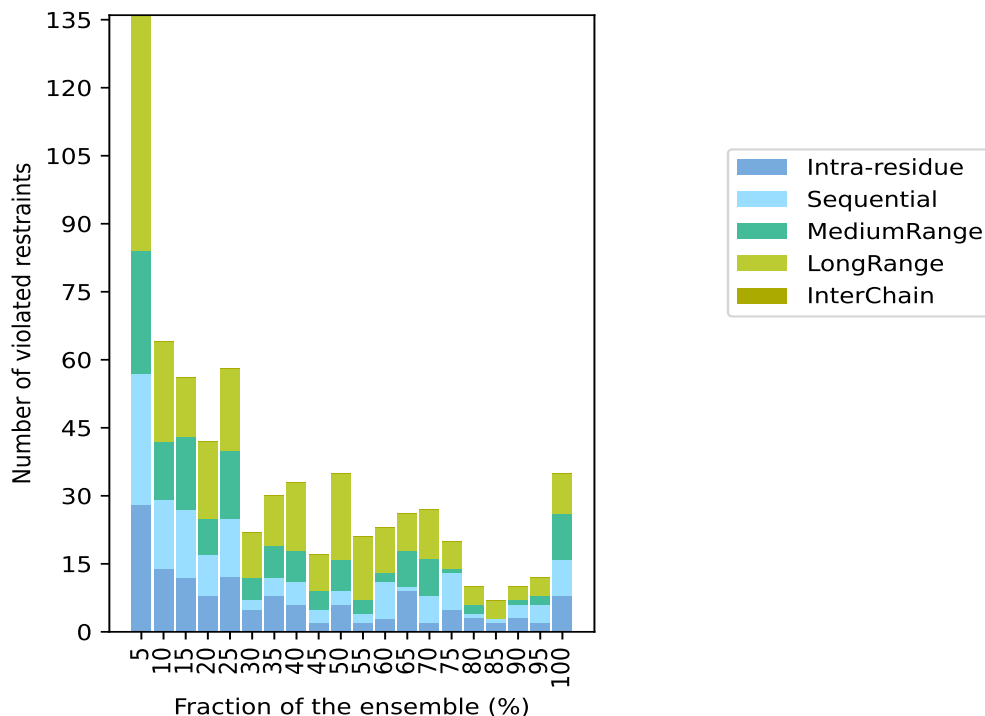
9.3 Distance violation statistics for the ensemble

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, 1899(IR:559, SQ:580, MR:321, LR:439, 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	%
28	29	27	52	0	136	1	5.0
14	15	13	22	0	64	2	10.0
12	15	16	13	0	56	3	15.0
8	9	8	17	0	42	4	20.0
12	13	15	18	0	58	5	25.0
5	2	5	10	0	22	6	30.0
8	4	7	11	0	30	7	35.0
6	5	7	15	0	33	8	40.0
2	3	4	8	0	17	9	45.0
6	3	7	19	0	35	10	50.0
2	2	3	14	0	21	11	55.0
3	8	2	10	0	23	12	60.0
9	1	8	8	0	26	13	65.0
2	6	8	11	0	27	14	70.0
5	8	1	6	0	20	15	75.0
3	1	2	4	0	10	16	80.0
2	1	0	4	0	7	17	85.0
3	3	1	3	0	10	18	90.0
2	4	2	4	0	12	19	95.0
8	8	10	9	0	35	20	100.0

¹Intra-residue restraints, ²Sequential restraints, ³Medium range restraints, ⁴Long range restraints, ⁵Inter-chain restraints, ⁶ Number of models with violations

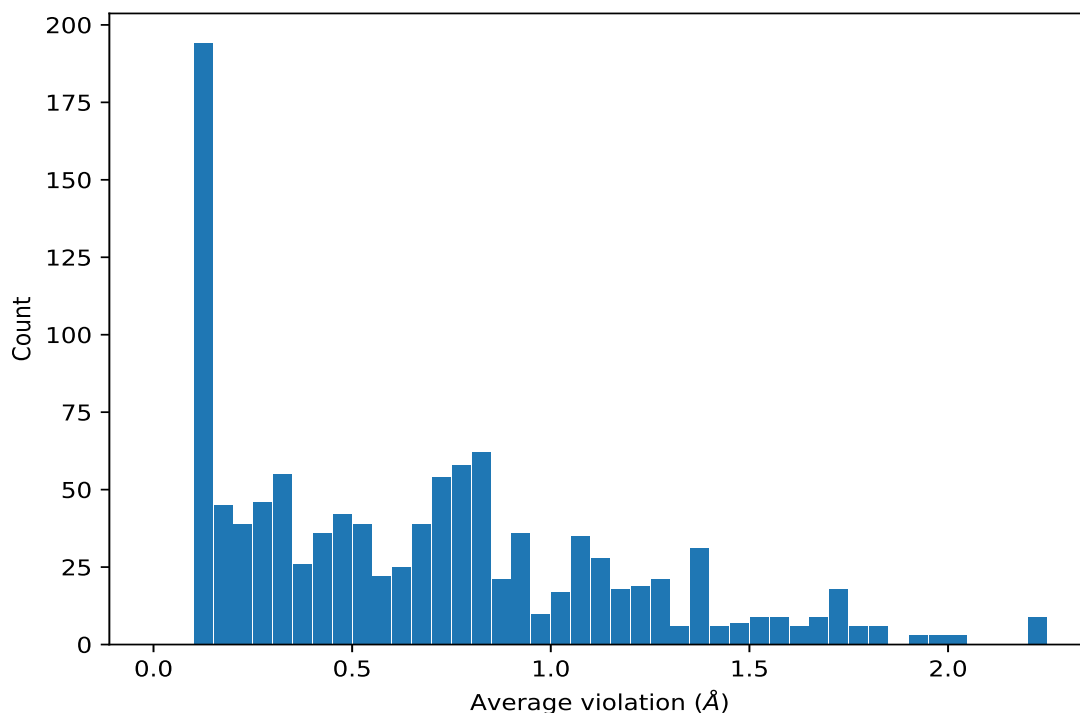
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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 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)
(1,129)	1:110:A:LEU:HD21	1:115:A:LEU:H	20	1.65	0.21	1.67
(1,129)	1:110:A:LEU:HD22	1:115:A:LEU:H	20	1.65	0.21	1.67
(1,129)	1:110:A:LEU:HD23	1:115:A:LEU:H	20	1.65	0.21	1.67
(1,1900)	1:108:A:LYS:HE3	1:110:A:LEU:HD11	20	1.65	0.53	1.72
(1,1900)	1:108:A:LYS:HE3	1:110:A:LEU:HD12	20	1.65	0.53	1.72
(1,1900)	1:108:A:LYS:HE3	1:110:A:LEU:HD13	20	1.65	0.53	1.72
(1,851)	1:102:A:GLY:HA2	1:126:A:LEU:HA	20	1.49	0.19	1.46
(1,1749)	1:102:A:GLY:HA2	1:126:A:LEU:HD21	20	1.4	0.49	1.46
(1,1749)	1:102:A:GLY:HA2	1:126:A:LEU:HD22	20	1.4	0.49	1.46
(1,1749)	1:102:A:GLY:HA2	1:126:A:LEU:HD23	20	1.4	0.49	1.46
(1,1459)	1:108:A:LYS:HD3	1:110:A:LEU:HD11	20	1.28	0.6	1.15
(1,1459)	1:108:A:LYS:HD3	1:110:A:LEU:HD12	20	1.28	0.6	1.15
(1,1459)	1:108:A:LYS:HD3	1:110:A:LEU:HD13	20	1.28	0.6	1.15
(1,1899)	1:110:A:LEU:HA	1:110:A:LEU:HD11	20	1.22	0.03	1.23
(1,1899)	1:110:A:LEU:HA	1:110:A:LEU:HD12	20	1.22	0.03	1.23
(1,1899)	1:110:A:LEU:HA	1:110:A:LEU:HD13	20	1.22	0.03	1.23

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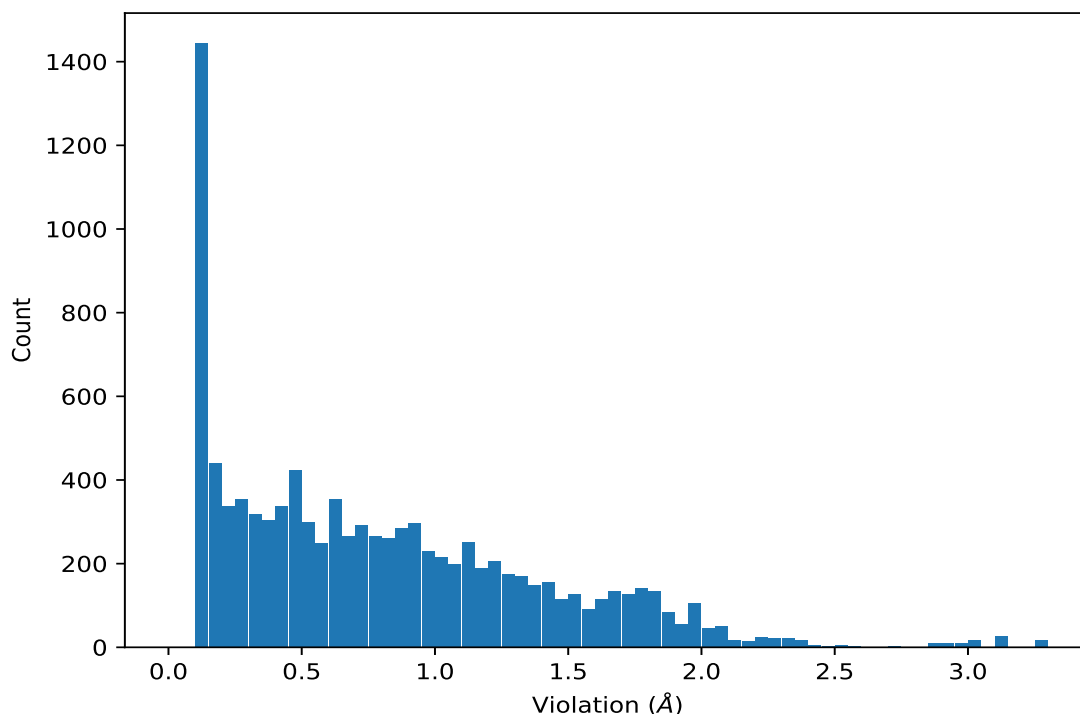
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,2446)	1:20:A:ASN:HA	1:20:A:ASN:HD22	20	1.15	0.11	1.14
(1,2484)	1:71:A:TYR:HD1	1:75:A:HIS:HB3	20	0.99	0.23	1.01
(1,2484)	1:71:A:TYR:HD2	1:75:A:HIS:HB3	20	0.99	0.23	1.01
(1,1405)	1:33:A:LEU:HG	1:34:A:PRO:HD3	20	0.98	0.14	0.98
(1,2410)	1:115:A:LEU:HB3	1:116:A:GLN:HA	20	0.98	0.13	1.0

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)
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD21	14	3.28
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD22	14	3.28
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD23	14	3.28
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD21	14	3.28
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD22	14	3.28
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD23	14	3.28
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD21	14	3.28
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD22	14	3.28
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD23	14	3.28
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD21	2	3.27
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD22	2	3.27
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD23	2	3.27
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD21	2	3.27
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD22	2	3.27
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD23	2	3.27
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD21	2	3.27
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD22	2	3.27
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD23	2	3.27
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD21	8	3.13
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD22	8	3.13
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD23	8	3.13
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD21	8	3.13
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD22	8	3.13
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD23	8	3.13
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD21	8	3.13
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD22	8	3.13
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD23	8	3.13
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD21	19	3.13
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD22	19	3.13
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD23	19	3.13
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD21	19	3.13
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD22	19	3.13
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD23	19	3.13
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD21	19	3.13
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD22	19	3.13
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD23	19	3.13
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD21	4	3.12
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD22	4	3.12
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD23	4	3.12
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD21	4	3.12
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD22	4	3.12
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD23	4	3.12
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD21	4	3.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD22	4	3.12
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD23	4	3.12
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD21	17	3.02
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD22	17	3.02
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD23	17	3.02
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD21	17	3.02
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD22	17	3.02
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD23	17	3.02
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD21	17	3.02
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD22	17	3.02
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD23	17	3.02
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD21	9	3.0
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD22	9	3.0
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD23	9	3.0
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD21	9	3.0
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD22	9	3.0
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD23	9	3.0
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD21	9	3.0
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD22	9	3.0
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD23	9	3.0
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD21	18	2.95
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD22	18	2.95
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD23	18	2.95
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD21	18	2.95
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD22	18	2.95
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD23	18	2.95
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD21	18	2.95
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD22	18	2.95
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD23	18	2.95
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD21	13	2.92
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD22	13	2.92
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD23	13	2.92
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD21	13	2.92
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD22	13	2.92
(1,1717)	1:145:A:LEU:HD12	1:146:A:LEU:HD23	13	2.92
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD21	13	2.92
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD22	13	2.92
(1,1717)	1:145:A:LEU:HD13	1:146:A:LEU:HD23	13	2.92
(1,1717)	1:145:A:LEU:HD11	1:146:A:LEU:HD21	10	2.88

10 Dihedral-angle violation analysis

No dihedral-angle restraints found