



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 7D3W
BMRB ID : 36388
Title : Non-specific and specific interactions work cooperatively to promote cytidine deamination catalyzed by APOBEC3A
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Deposited on : 2020-09-21

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 : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
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) : 2.33

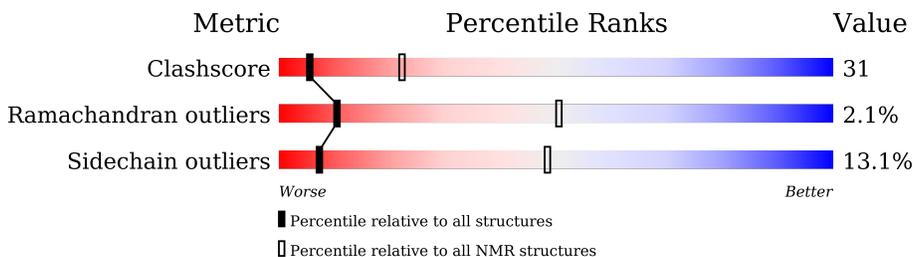
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 77%.

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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	199	
2	B	10	

2 Ensemble composition and analysis i

This entry contains 20 models. Model 17 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:12-A:59, A:70-A:101, A:106-A:197 (172)	0.82	17

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

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

The models can be grouped into 2 clusters and 1 single-model cluster was found.

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

3 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3490 atoms, of which 1664 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called DNA dC->dU-editing enzyme APOBEC-3A.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	199	3172	1029	1546	295	293	9	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	63	ASN	LEU	engineered mutation	UNP P31941
A	64	SER	CYS	engineered mutation	UNP P31941
A	72	GLN	GLU	engineered mutation	UNP P31941
A	171	GLN	CYS	engineered mutation	UNP P31941

- Molecule 2 is a DNA chain called DNA (5'-D(*AP*TP*TP*TP*TP*CP*AP*AP*TP*T)-3').

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	P	
2	B	10	317	99	118	30	61	9	0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	
			Total	Zn
3	A	1	1	1



- Molecule 2: DNA (5'-D(*AP*TP*TP*TP*TP*CP*AP*AP*TP*T)-3')

Chain B:
80% 20%

A horizontal bar chart for Chain B showing 80% in yellow and 20% in orange.



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
X-PLOR NIH	structure calculation	
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	2276
Number of shifts mapped to atoms	2276
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	77%

6 Model quality i

6.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	1.00±0.00	0±0/1460 (0.0± 0.0%)	0.91±0.00	0±0/1982 (0.0± 0.0%)
2	B	1.28±0.02	2±1/221 (0.9± 0.3%)	1.70±0.01	10±1/339 (2.8± 0.4%)
All	All	1.04	41/33620 (0.1%)	1.06	192/46420 (0.4%)

All unique bond 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(Å)	Ideal(Å)	Models	
								Worst	Total
2	B	208	DT	C5-C7	5.99	1.53	1.50	5	19
2	B	201	DT	C5-C7	5.51	1.53	1.50	14	13
2	B	204	DT	C5-C7	5.17	1.53	1.50	5	4
2	B	209	DT	C5-C7	5.11	1.53	1.50	11	5

5 of 12 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
2	B	202	DT	C6-C5-C7	-6.18	119.19	122.90	7	20
2	B	201	DT	C6-C5-C7	-6.11	119.23	122.90	13	19
2	B	208	DT	C6-C5-C7	-6.09	119.25	122.90	5	20
2	B	209	DT	C6-C5-C7	-6.06	119.26	122.90	13	20
2	B	203	DT	C6-C5-C7	-5.87	119.38	122.90	7	20

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	1419	1357	1349	88±9
2	B	199	118	118	12±2
All	All	32380	29500	29340	1908

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 31.

5 of 709 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:155:TYR:O	1:A:158:PHE:CD1	1.23	1.90	20	1
1:A:158:PHE:CD1	1:A:159:LYS:N	1.02	2.25	20	1
1:A:179:LEU:H	1:A:179:LEU:HD22	0.94	1.21	2	15
1:A:162:TRP:HE1	1:A:168:HIS:CD2	0.92	1.82	12	5
1:A:40:LEU:HD13	1:A:40:LEU:O	0.91	1.64	3	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	172/199 (86%)	157±1 (91±1%)	11±1 (6±1%)	4±1 (2±1%)	10	50
All	All	3440/3980 (86%)	3146 (91%)	221 (6%)	73 (2%)	10	50

5 of 11 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	148	ALA	20
1	A	134	PRO	19

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Mol	Chain	Res	Type	Models (Total)
1	A	133	ASP	9
1	A	50	GLN	8
1	A	101	CYS	4

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	151/171 (88%)	131±2 (87±1%)	20±2 (13±1%)	7 48
All	All	3020/3420 (88%)	2625 (87%)	395 (13%)	7 48

5 of 69 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	88	GLN	20
1	A	174	GLN	20
1	A	189	ARG	20
1	A	190	LEU	20
1	A	195	GLN	20

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 monosaccharides in this entry.

6.6 Ligand geometry [i](#)

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

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation [i](#)

The completeness of assignment taking into account all chemical shift lists is 77% for the well-defined parts and 76% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *A3A_shifts-nospecific_20200915.txt*

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	2276
Number of shifts mapped to atoms	2276
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	11

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
$^{13}\text{C}_\alpha$	192	0.06 \pm 0.16	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	176	0.64 \pm 0.15	Should be checked
$^{13}\text{C}'$	173	-0.02 \pm 0.11	None needed (< 0.5 ppm)
^{15}N	181	-0.34 \pm 0.31	None needed (< 0.5 ppm)

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 77%, i.e. 2019 atoms were assigned a chemical shift out of a possible 2620. 0 out of 26 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	823/855 (96%)	337/346 (97%)	325/344 (94%)	161/165 (98%)
Sidechain	995/1295 (77%)	710/838 (85%)	279/396 (70%)	6/61 (10%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	118/282 (42%)	102/138 (74%)	14/123 (11%)	2/21 (10%)
Sugar	70/120 (58%)	70/70 (100%)	0/50 (0%)	0/0 (—%)
Base	13/68 (19%)	13/38 (34%)	0/20 (0%)	0/10 (0%)
Overall	2019/2620 (77%)	1232/1430 (86%)	618/933 (66%)	169/257 (66%)

7.1.4 Statistically unusual chemical shifts [i](#)

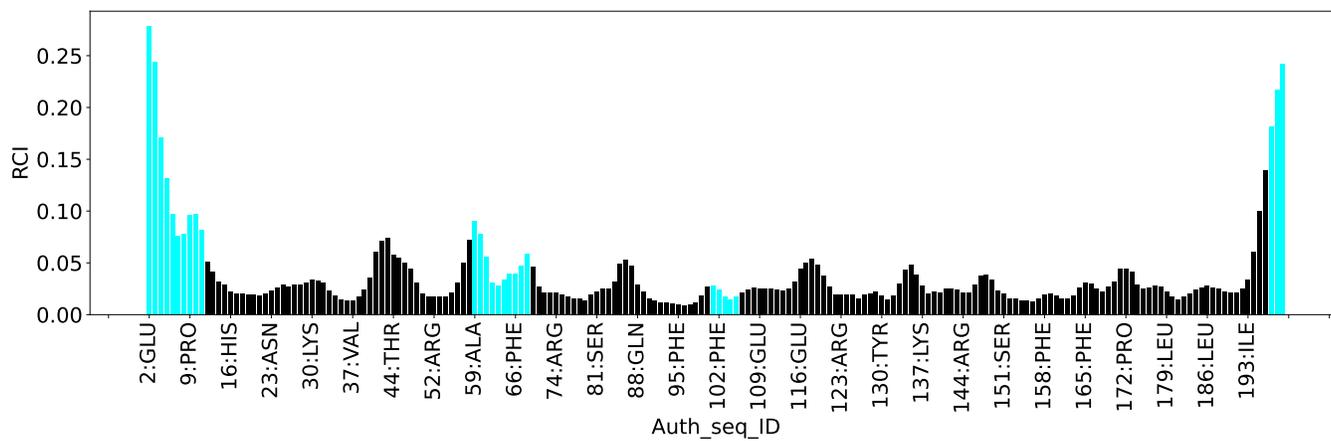
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	44	THR	HG1	5.07	0.08 – 2.19	18.6
1	A	70	HIS	CE1	118.42	126.08 – 149.12	-8.3
1	A	94	TRP	HE1	5.58	6.88 – 13.28	-7.0
1	A	66	PHE	CD2	124.86	125.53 – 137.61	-5.6
1	A	72	GLN	CB	38.88	20.34 – 37.98	5.5
1	A	131	ASP	CB	32.21	32.98 – 48.76	-5.5
1	A	66	PHE	CD1	124.86	125.33 – 137.83	-5.4
1	A	170	GLY	H	11.62	5.23 – 11.42	5.3
1	A	179	LEU	HG	-0.22	-0.13 – 3.16	-5.2
1	A	97	SER	HB3	2.44	2.49 – 5.20	-5.2
1	A	172	PRO	CG	32.94	21.69 – 32.72	5.2

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	3547
Intra-residue ($ i-j =0$)	1772
Sequential ($ i-j =1$)	701
Medium range ($ i-j >1$ and $ i-j <5$)	369
Long range ($ i-j \geq 5$)	655
Inter-chain	50
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	17.0
Number of long range restraints per residue ¹	3.1

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)	61.0	0.2
0.2-0.5 (Medium)	13.4	0.5
>0.5 (Large)	11.6	2.76

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](#)

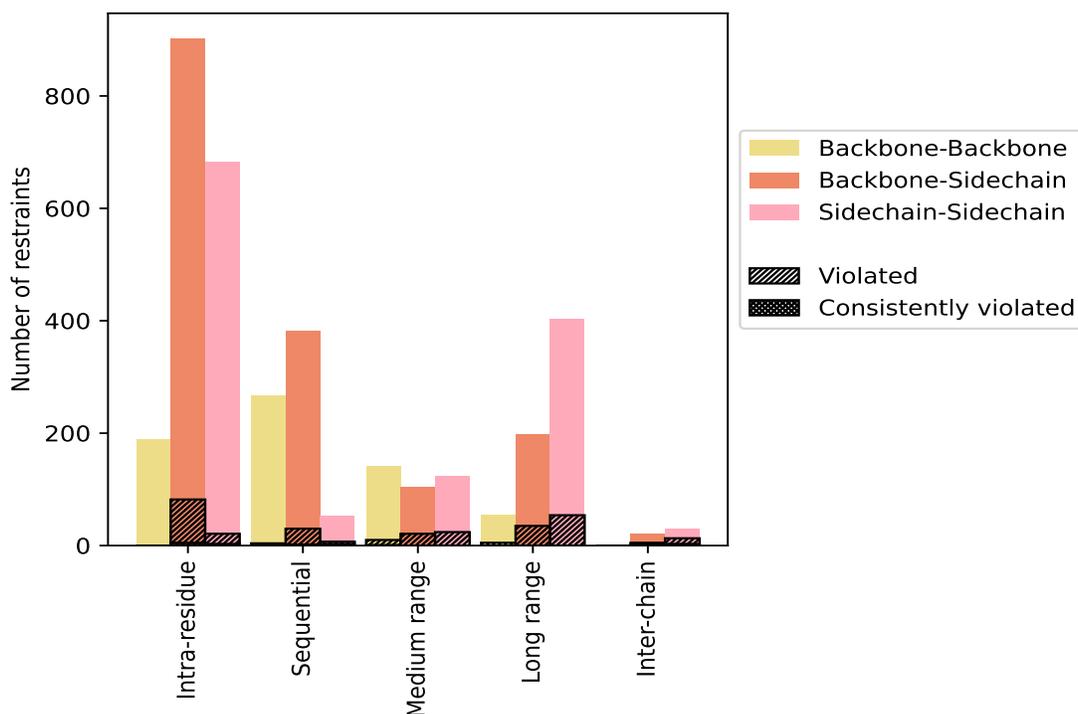
9.1 Summary of distance violations [i](#)

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)	1772	50.0	103	5.8	2.9	8	0.5	0.2
Backbone-Backbone	188	5.3	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	902	25.4	82	9.1	2.3	5	0.6	0.1
Sidechain-Sidechain	682	19.2	21	3.1	0.6	3	0.4	0.1
Sequential (i-j =1)	701	19.8	41	5.8	1.2	6	0.9	0.2
Backbone-Backbone	266	7.5	4	1.5	0.1	1	0.4	0.0
Backbone-Sidechain	382	10.8	30	7.9	0.8	2	0.5	0.1
Sidechain-Sidechain	53	1.5	7	13.2	0.2	3	5.7	0.1
Medium range (i-j >1 & i-j <5)	369	10.4	55	14.9	1.6	1	0.3	0.0
Backbone-Backbone	141	4.0	10	7.1	0.3	1	0.7	0.0
Backbone-Sidechain	104	2.9	21	20.2	0.6	0	0.0	0.0
Sidechain-Sidechain	124	3.5	24	19.4	0.7	0	0.0	0.0
Long range (i-j ≥5)	655	18.5	94	14.4	2.7	0	0.0	0.0
Backbone-Backbone	55	1.6	5	9.1	0.1	0	0.0	0.0
Backbone-Sidechain	198	5.6	35	17.7	1.0	0	0.0	0.0
Sidechain-Sidechain	402	11.3	54	13.4	1.5	0	0.0	0.0
Inter-chain	50	1.4	18	36.0	0.5	5	10.0	0.1
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	20	0.6	5	25.0	0.1	2	10.0	0.1
Sidechain-Sidechain	30	0.8	13	43.3	0.4	3	10.0	0.1
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	3547	100.0	311	8.8	8.8	20	0.6	0.6
Backbone-Backbone	650	18.3	19	2.9	0.5	2	0.3	0.1
Backbone-Sidechain	1606	45.3	173	10.8	4.9	9	0.6	0.3
Sidechain-Sidechain	1291	36.4	119	9.2	3.4	9	0.7	0.3

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	39	12	16	12	11	90	0.29	2.46	0.38	0.15
2	40	13	14	27	10	104	0.32	2.65	0.45	0.16
3	31	14	13	17	10	85	0.31	2.37	0.41	0.15
4	31	13	14	14	12	84	0.29	2.65	0.41	0.15
5	30	12	12	17	10	81	0.33	2.61	0.45	0.15
6	38	12	17	15	11	93	0.31	2.37	0.41	0.16
7	34	10	13	19	12	88	0.3	2.49	0.41	0.15
8	32	9	17	13	10	81	0.31	2.72	0.42	0.15
9	31	11	12	12	10	76	0.31	2.52	0.43	0.14
10	31	12	13	17	9	82	0.27	2.36	0.37	0.16
11	30	14	11	13	11	79	0.3	2.51	0.41	0.14

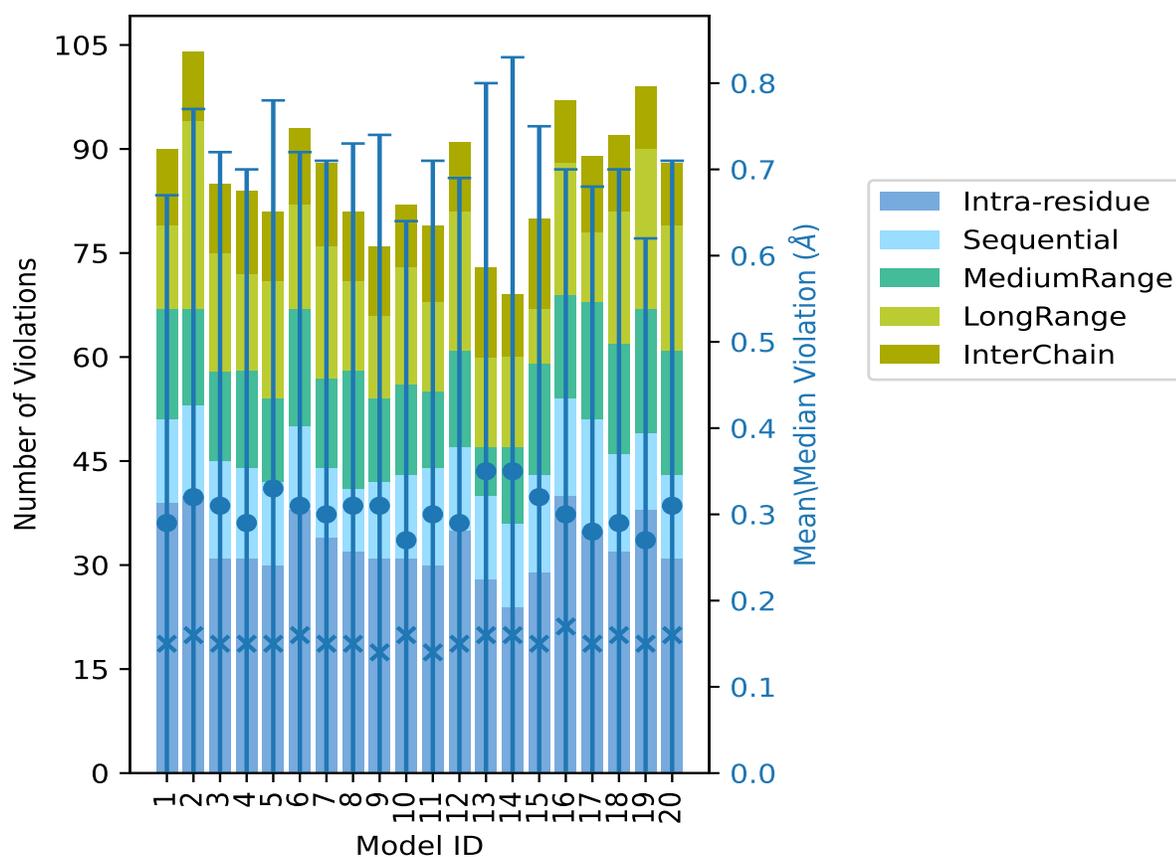
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Model ID	Number of violations					Total	Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵					
12	35	12	14	20	10	91	0.29	2.51	0.4	0.15
13	28	12	7	13	13	73	0.35	2.49	0.45	0.16
14	24	12	11	13	9	69	0.35	2.76	0.48	0.16
15	29	14	16	8	13	80	0.32	2.5	0.43	0.15
16	40	14	15	19	9	97	0.3	2.4	0.4	0.17
17	35	16	17	10	11	89	0.28	2.57	0.4	0.15
18	32	14	16	19	11	92	0.29	2.55	0.41	0.16
19	38	11	18	23	9	99	0.27	2.28	0.35	0.15
20	31	12	18	18	9	88	0.31	2.19	0.4	0.16

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

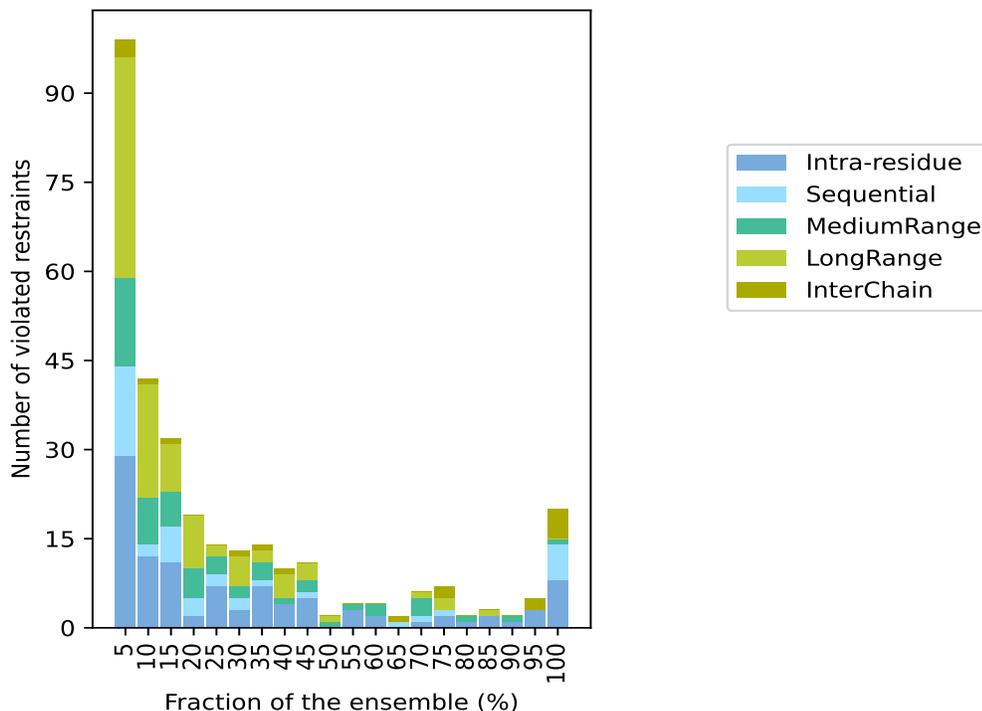
9.3 Distance violation statistics for the ensemble

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, 3236(IR:1669, SQ:660, MR:314, LR:561, IC:32) 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	%
29	15	15	37	3	99	1	5.0
12	2	8	19	1	42	2	10.0
11	6	6	8	1	32	3	15.0
2	3	5	9	0	19	4	20.0
7	2	3	2	0	14	5	25.0
3	2	2	5	1	13	6	30.0
7	1	3	2	1	14	7	35.0
4	0	1	4	1	10	8	40.0
5	1	2	3	0	11	9	45.0
0	0	1	1	0	2	10	50.0
3	0	1	0	0	4	11	55.0
2	0	2	0	0	4	12	60.0
0	1	0	0	1	2	13	65.0
1	1	3	1	0	6	14	70.0
2	1	0	2	2	7	15	75.0
1	0	1	0	0	2	16	80.0
2	0	0	1	0	3	17	85.0
1	0	1	0	0	2	18	90.0
3	0	0	0	2	5	19	95.0
8	6	1	0	5	20	20	100.0

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

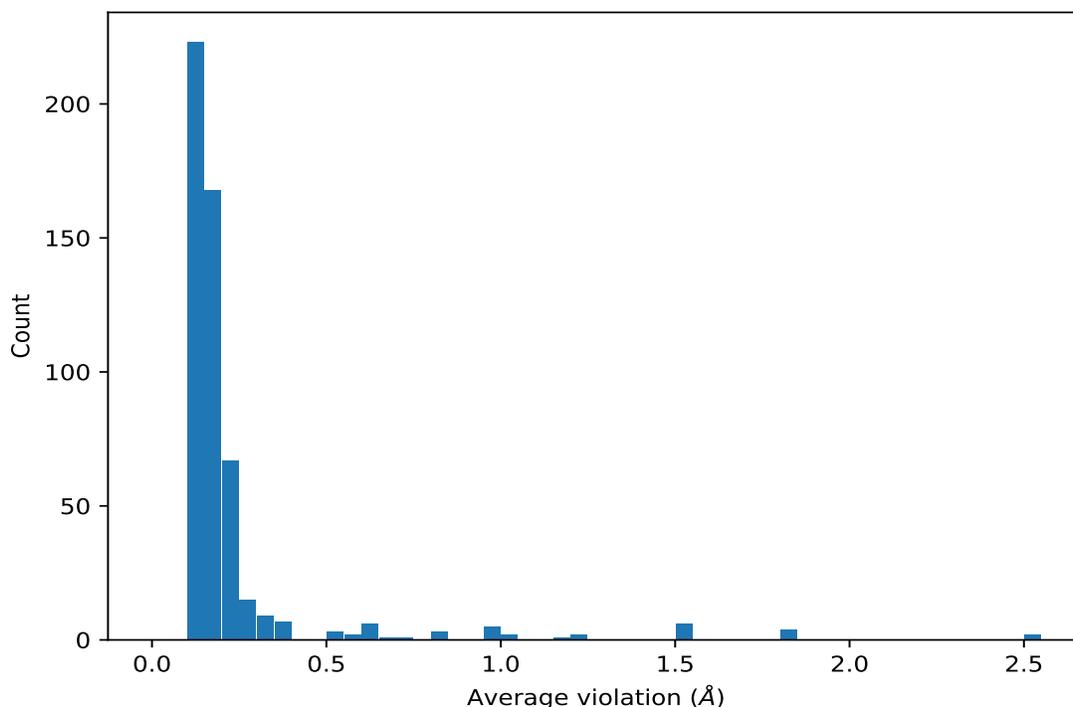
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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)
(1,3324)	2:B:201:DT:H5'	1:A:181:GLU:HB3	20	2.5	0.14	2.5
(1,3324)	2:B:201:DT:H5''	1:A:181:GLU:HB3	20	2.5	0.14	2.5
(1,3336)	2:B:204:DT:H5'	1:A:25:GLY:HA2	20	1.8	0.21	1.82
(1,3336)	2:B:204:DT:H5''	1:A:25:GLY:HA2	20	1.8	0.21	1.82
(1,3336)	2:B:204:DT:H5'	1:A:25:GLY:HA3	20	1.8	0.21	1.82
(1,3336)	2:B:204:DT:H5''	1:A:25:GLY:HA3	20	1.8	0.21	1.82
(1,3330)	2:B:202:DT:H5'	1:A:185:ALA:HB1	20	1.54	0.06	1.54
(1,3330)	2:B:202:DT:H5''	1:A:185:ALA:HB1	20	1.54	0.06	1.54
(1,3330)	2:B:202:DT:H5'	1:A:185:ALA:HB2	20	1.54	0.06	1.54
(1,3330)	2:B:202:DT:H5''	1:A:185:ALA:HB2	20	1.54	0.06	1.54
(1,3330)	2:B:202:DT:H5'	1:A:185:ALA:HB3	20	1.54	0.06	1.54
(1,3330)	2:B:202:DT:H5''	1:A:185:ALA:HB3	20	1.54	0.06	1.54
(1,3509)	2:B:207:DA:H8	2:B:208:DT:H5'	20	1.24	0.01	1.24
(1,3509)	2:B:207:DA:H8	2:B:208:DT:H5''	20	1.24	0.01	1.24
(1,3325)	2:B:201:DT:H5'	1:A:181:GLU:HB2	20	0.98	0.13	0.99
(1,3325)	2:B:201:DT:H5''	1:A:181:GLU:HB2	20	0.98	0.13	0.99

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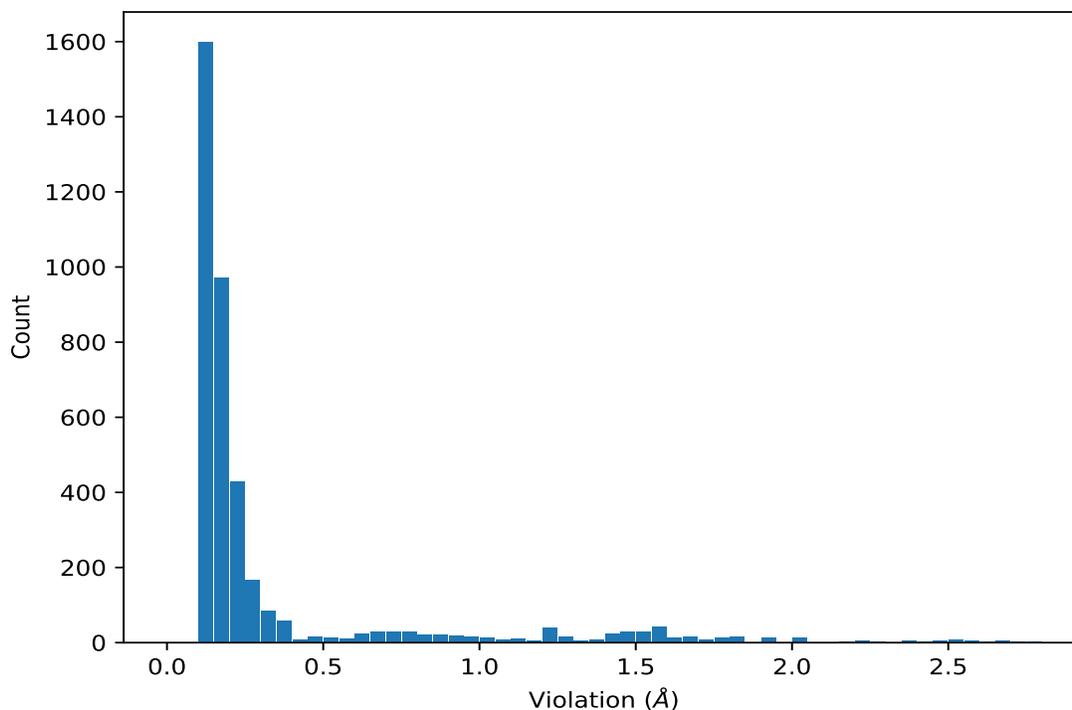
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,3377)	2:B:200:DA:H8	2:B:201:DT:H5'	20	0.96	0.25	0.85
(1,3377)	2:B:200:DA:H8	2:B:201:DT:H5''	20	0.96	0.25	0.85
(1,3328)	2:B:202:DT:H5'	1:A:25:GLY:HA2	20	0.63	0.14	0.65
(1,3328)	2:B:202:DT:H5'	1:A:25:GLY:HA3	20	0.63	0.14	0.65
(1,3328)	2:B:202:DT:H5''	1:A:25:GLY:HA2	20	0.63	0.14	0.65
(1,3328)	2:B:202:DT:H5''	1:A:25:GLY:HA3	20	0.63	0.14	0.65
(1,3531)	2:B:208:DT:H6	2:B:209:DT:H5'	20	0.25	0.03	0.25
(1,3531)	2:B:208:DT:H6	2:B:209:DT:H5''	20	0.25	0.03	0.25
(1,3257)	1:A:195:GLN:HB3	1:A:195:GLN:H	20	0.22	0.02	0.22
(1,1938)	1:A:113:PHE:HE1	1:A:113:PHE:H	20	0.2	0.01	0.2

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)
(1,3324)	2:B:201:DT:H5'	1:A:181:GLU:HB3	14	2.76
(1,3324)	2:B:201:DT:H5''	1:A:181:GLU:HB3	14	2.76
(1,3324)	2:B:201:DT:H5'	1:A:181:GLU:HB3	8	2.72
(1,3324)	2:B:201:DT:H5''	1:A:181:GLU:HB3	8	2.72
(1,3324)	2:B:201:DT:H5'	1:A:181:GLU:HB3	2	2.65
(1,3324)	2:B:201:DT:H5''	1:A:181:GLU:HB3	2	2.65
(1,3324)	2:B:201:DT:H5'	1:A:181:GLU:HB3	4	2.65
(1,3324)	2:B:201:DT:H5''	1:A:181:GLU:HB3	4	2.65
(1,3324)	2:B:201:DT:H5'	1:A:181:GLU:HB3	5	2.61
(1,3324)	2:B:201:DT:H5''	1:A:181:GLU:HB3	5	2.61
(1,3324)	2:B:201:DT:H5'	1:A:181:GLU:HB3	17	2.57
(1,3324)	2:B:201:DT:H5''	1:A:181:GLU:HB3	17	2.57
(1,3324)	2:B:201:DT:H5'	1:A:181:GLU:HB3	18	2.55
(1,3324)	2:B:201:DT:H5''	1:A:181:GLU:HB3	18	2.55
(1,3324)	2:B:201:DT:H5'	1:A:181:GLU:HB3	9	2.52
(1,3324)	2:B:201:DT:H5''	1:A:181:GLU:HB3	9	2.52
(1,3324)	2:B:201:DT:H5'	1:A:181:GLU:HB3	11	2.51
(1,3324)	2:B:201:DT:H5''	1:A:181:GLU:HB3	11	2.51
(1,3324)	2:B:201:DT:H5'	1:A:181:GLU:HB3	12	2.51

10 Dihedral-angle violation analysis

No dihedral-angle restraints found