



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 7OLG / pdb_00007olg
BMRB ID : 34629
Title : EB1 bound to MACF peptide
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Deposited on : 2021-05-20

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

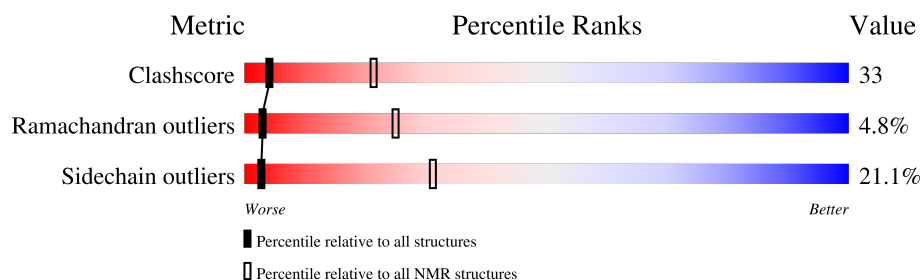
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 40%.

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	70	37% 39% 20% .
1	B	70	39% 37% 20% .
2	C	11	18% 27% 9% 45%
2	D	11	18% 27% 9% 45%

2 Ensemble composition and analysis

This entry contains 20 models. Model 6 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:192-A:258, B:192-B:258, C:5477-C:5482, D:5477- D:5482 (146)	0.67	6

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

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

The models can be grouped into 5 clusters and 6 single-model clusters were found.

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

3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 2624 atoms, of which 1314 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Microtubule-associated protein RP/EB family member 1.

Mol	Chain	Residues	Atoms						Trace
1	A	70	Total	C	H	N	O	S	0
			1116	355	551	90	118	2	
1	B	70	Total	C	H	N	O	S	0
			1116	355	551	90	118	2	

- Molecule 2 is a protein called 11MACF.

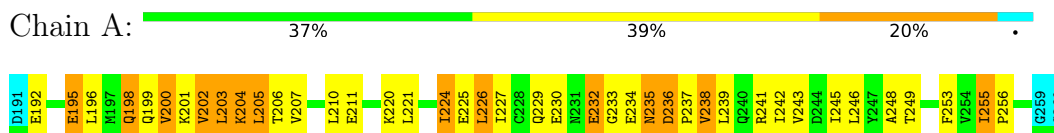
Mol	Chain	Residues	Atoms					Trace
2	C	11	Total	C	H	N	O	0
			196	57	106	18	15	
2	D	11	Total	C	H	N	O	0
			196	57	106	18	15	

4 Residue-property plots

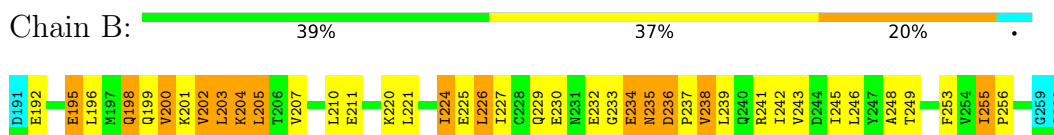
4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

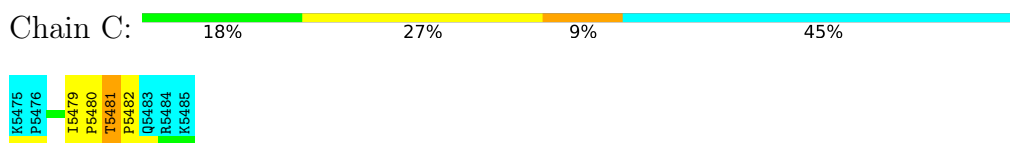
- Molecule 1: Microtubule-associated protein RP/EB family member 1



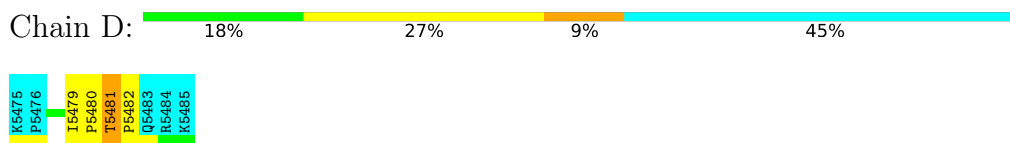
- Molecule 1: Microtubule-associated protein RP/EB family member 1



- Molecule 2: 11MACF



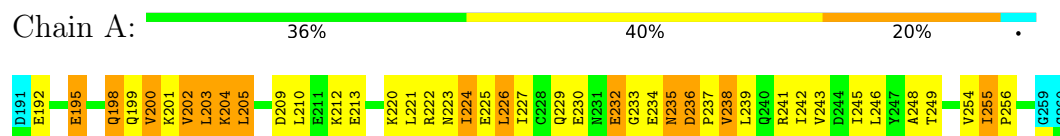
- Molecule 2: 11MACF



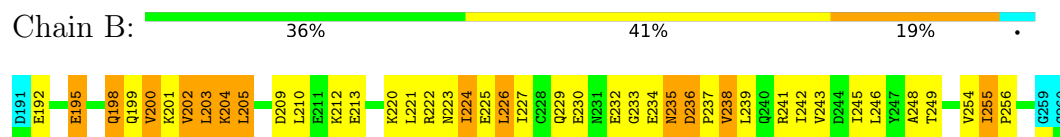
4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 6. Colouring as in section 4.1 above.

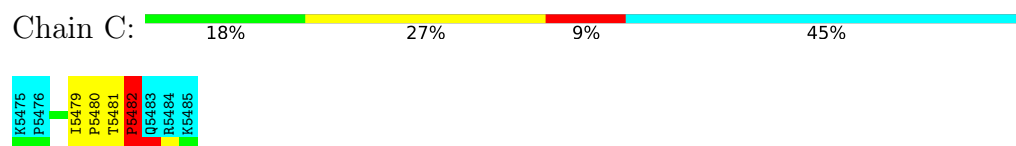
- Molecule 1: Microtubule-associated protein RP/EB family member 1



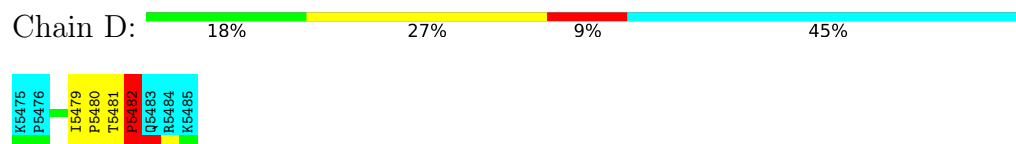
- Molecule 1: Microtubule-associated protein RP/EB family member 1



- Molecule 2: 11MACF



- Molecule 2: 11MACF



5 Refinement protocol and experimental data overview

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

Of the 160 calculated structures, 20 were deposited, based on the following criterion: *all calculated structures submitted*.

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

Software name	Classification	Version
CNS	refinement	
ARIA	structure calculation	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	849
Number of shifts mapped to atoms	849
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	40%

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	0.61±0.03	0±0/555 (0.0± 0.0%)	0.90±0.02	0±0/750 (0.0± 0.0%)
1	B	0.57±0.02	0±0/555 (0.0± 0.0%)	0.89±0.02	0±0/750 (0.0± 0.0%)
2	C	1.17±0.09	0±0/46 (0.3± 0.8%)	1.36±0.13	0±0/64 (0.1± 0.3%)
2	D	1.17±0.09	0±0/46 (0.3± 0.8%)	1.36±0.13	0±0/64 (0.1± 0.3%)
All	All	0.66	6/24040 (0.0%)	0.94	3/32560 (0.0%)

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	0.8±0.4
2	C	0.0±0.0	0.3±0.5
2	D	0.0±0.0	0.3±0.5
All	All	0	30

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	C	5482	PRO	N-CA	-6.12	1.39	1.47	6	2
2	D	5482	PRO	N-CA	-6.10	1.39	1.47	6	2
2	C	5481	THR	CA-C	-5.11	1.46	1.52	15	1
2	D	5481	THR	CA-C	-5.05	1.46	1.52	15	1

All 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	B	234	GLU	N-CA-C	-5.21	105.38	112.26	18	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	C	5479	ILE	N-CA-CB	5.01	115.15	109.99	16	1
2	D	5479	ILE	N-CA-CB	5.00	115.14	109.99	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	232	GLU	Peptide	16
2	C	5481	THR	Peptide	7
2	D	5481	THR	Peptide	7

6.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	548	539	539	42±5
1	B	548	539	539	42±6
2	C	44	50	50	4±1
2	D	44	50	50	4±2
All	All	23680	23560	23560	1547

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 33.

5 of 310 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:200:VAL:O	1:A:204:LYS:HG2	0.83	1.73	13	3
1:B:200:VAL:O	1:B:204:LYS:HG2	0.82	1.74	13	3
1:A:239:LEU:HD21	1:B:238:VAL:HG11	0.78	1.54	1	18
1:A:206:THR:O	1:A:210:LEU:HG	0.78	1.78	15	6
1:B:206:THR:O	1:B:210:LEU:HG	0.78	1.78	8	6

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	67/70 (96%)	62±1 (92±2%)	2±2 (3±2%)	3±0 (4±0%)	3	28
1	B	67/70 (96%)	62±1 (93±2%)	2±2 (3±2%)	3±0 (4±1%)	3	28
2	C	6/11 (55%)	4±1 (67±13%)	1±1 (23±11%)	1±1 (10±10%)	1	9
2	D	6/11 (55%)	4±1 (67±13%)	1±1 (23±11%)	1±1 (10±10%)	1	9
All	All	2920/3240 (90%)	2644 (91%)	137 (5%)	139 (5%)	3	25

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	235	ASN	20
1	B	235	ASN	20
1	A	233	GLY	19
1	B	233	GLY	19
1	A	248	ALA	18

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	61/62 (98%)	47±2 (77±3%)	14±2 (23±3%)	2	29
1	B	61/62 (98%)	47±2 (78±4%)	14±2 (22±4%)	2	29
2	C	6/11 (55%)	6±1 (92±10%)	0±1 (8±10%)	14	62
2	D	6/11 (55%)	6±1 (92±10%)	0±1 (8±10%)	14	62
All	All	2680/2920 (92%)	2114 (79%)	566 (21%)	3	31

5 of 61 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	200	VAL	20
1	A	203	LEU	20
1	A	205	LEU	20
1	A	224	ILE	20
1	A	226	LEU	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 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 40% for the well-defined parts and 37% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list*

7.1.1 Bookkeeping [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	849
Number of shifts mapped to atoms	849
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

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
$^{13}\text{C}_\alpha$	66	-0.40 ± 0.13	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	61	0.16 ± 0.11	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	65	-0.28 ± 0.15	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 40%, i.e. 815 atoms were assigned a chemical shift out of a possible 2056. 0 out of 28 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	265/720 (37%)	139/290 (48%)	63/292 (22%)	63/138 (46%)
Sidechain	504/1240 (41%)	348/798 (44%)	149/400 (37%)	7/42 (17%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	46/96 (48%)	23/46 (50%)	23/50 (46%)	0/0 (—%)
Overall	815/2056 (40%)	510/1134 (45%)	235/742 (32%)	70/180 (39%)

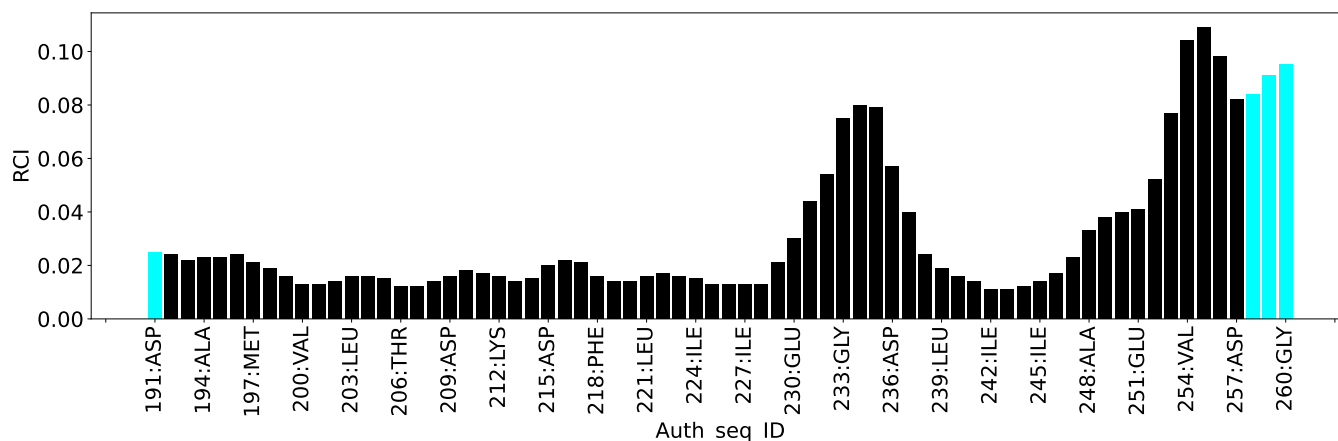
7.1.4 Statistically unusual chemical shifts ⓘ

There are no statistically unusual chemical shifts.

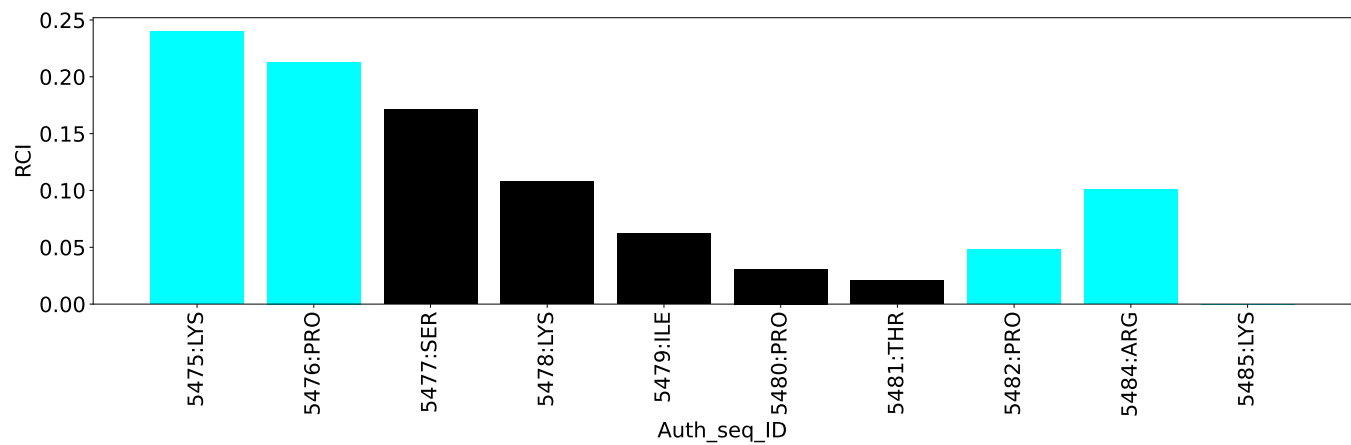
7.1.5 Random Coil Index (RCI) plots ⓘ

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

Random coil index (RCI) for chain A:



Random coil index (RCI) for chain C:



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	3863
Intra-residue ($ i-j =0$)	1066
Sequential ($ i-j =1$)	780
Medium range ($ i-j >1$ and $ i-j <5$)	1001
Long range ($ i-j \geq 5$)	121
Inter-chain	895
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	23.8
Number of long range restraints per residue ¹	0.7

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)	125.1	0.2
0.2-0.5 (Medium)	269.8	0.5
>0.5 (Large)	340.9	5.18

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 ⓘ

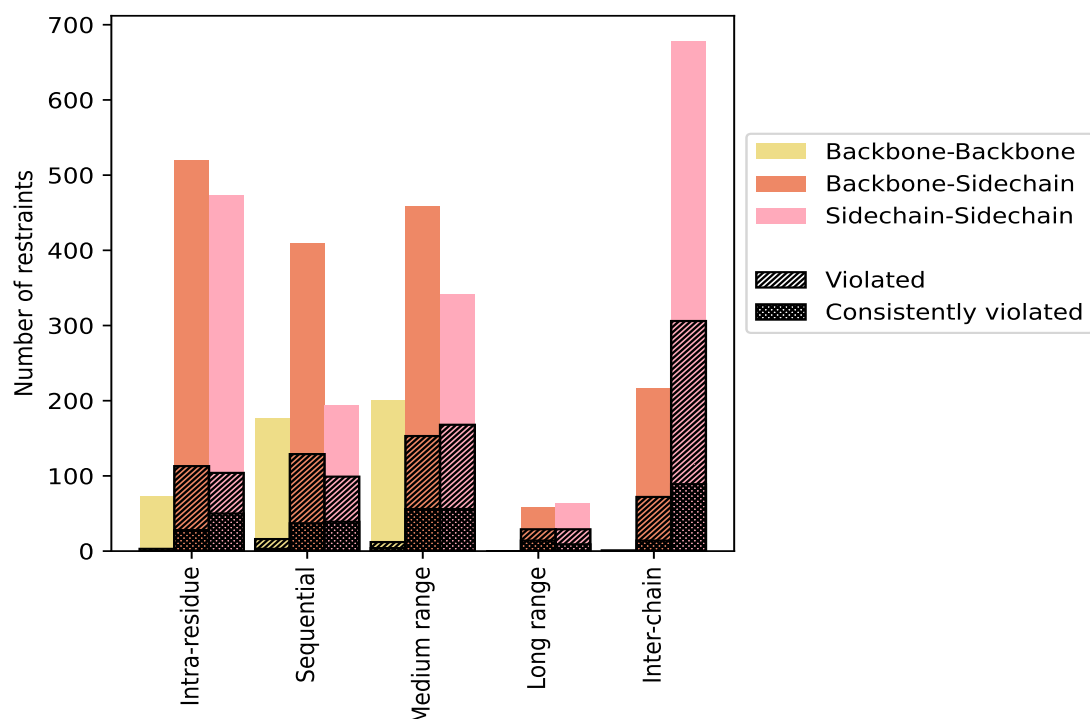
9.1 Summary of distance violations ⓘ

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.

Restraints type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue (i-j =0)	1066	27.6	220	20.6	5.7	78	7.3	2.0
Backbone-Backbone	73	1.9	3	4.1	0.1	0	0.0	0.0
Backbone-Sidechain	520	13.5	113	21.7	2.9	28	5.4	0.7
Sidechain-Sidechain	473	12.2	104	22.0	2.7	50	10.6	1.3
Sequential (i-j =1)	780	20.2	244	31.3	6.3	79	10.1	2.0
Backbone-Backbone	177	4.6	16	9.0	0.4	3	1.7	0.1
Backbone-Sidechain	409	10.6	129	31.5	3.3	37	9.0	1.0
Sidechain-Sidechain	194	5.0	99	51.0	2.6	39	20.1	1.0
Medium range (i-j >1 & i-j <5)	1001	25.9	333	33.3	8.6	116	11.6	3.0
Backbone-Backbone	201	5.2	12	6.0	0.3	4	2.0	0.1
Backbone-Sidechain	459	11.9	153	33.3	4.0	56	12.2	1.4
Sidechain-Sidechain	341	8.8	168	49.3	4.3	56	16.4	1.4
Long range (i-j ≥5)	121	3.1	58	47.9	1.5	23	19.0	0.6
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	58	1.5	29	50.0	0.8	14	24.1	0.4
Sidechain-Sidechain	63	1.6	29	46.0	0.8	9	14.3	0.2
Inter-chain	895	23.2	379	42.3	9.8	103	11.5	2.7
Backbone-Backbone	1	0.0	1	100.0	0.0	0	0.0	0.0
Backbone-Sidechain	216	5.6	72	33.3	1.9	14	6.5	0.4
Sidechain-Sidechain	678	17.6	306	45.1	7.9	89	13.1	2.3
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	3863	100.0	1234	31.9	31.9	399	10.3	10.3
Backbone-Backbone	452	11.7	32	7.1	0.8	7	1.5	0.2
Backbone-Sidechain	1662	43.0	496	29.8	12.8	149	9.0	3.9
Sidechain-Sidechain	1749	45.3	706	40.4	18.3	243	13.9	6.3

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

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

The following table provides the distance violation statistics for each model in the ensemble. Violations less than 0.1 Å are not included in the statistics.

Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
1	148	157	208	27	224	764	0.6	4.35	0.5	0.44
2	141	144	197	25	226	733	0.62	4.44	0.49	0.47
3	135	146	206	28	235	750	0.62	4.46	0.51	0.45
4	138	148	211	26	239	762	0.63	4.55	0.51	0.47
5	130	153	200	28	236	747	0.63	4.38	0.5	0.49
6	141	153	194	29	234	751	0.61	4.59	0.49	0.45
7	136	164	212	27	228	767	0.61	4.41	0.51	0.44
8	147	142	202	28	229	748	0.61	4.45	0.49	0.46
9	131	148	197	25	226	727	0.62	4.53	0.5	0.47
10	131	156	203	27	222	739	0.63	4.38	0.51	0.47

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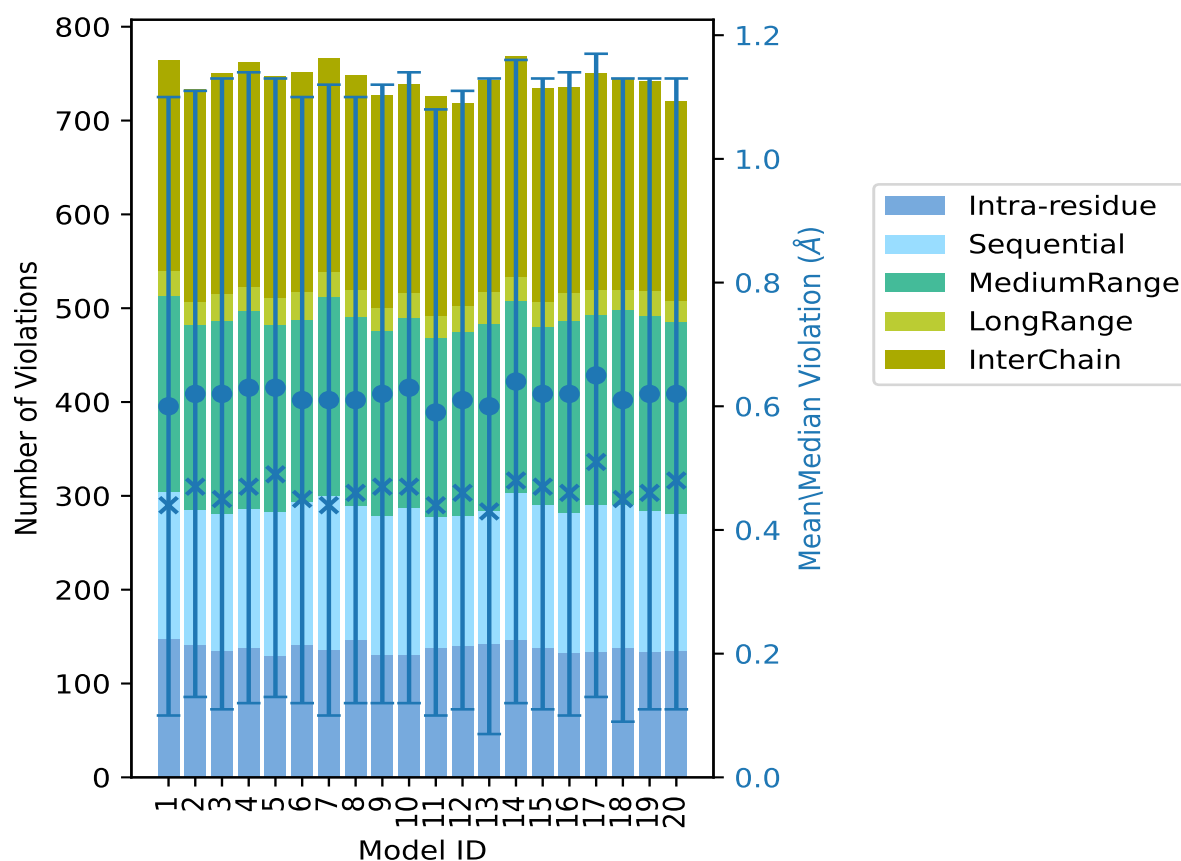
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	138	140	191	23	234	726	0.59	4.72	0.49	0.44
12	140	139	196	28	216	719	0.61	4.57	0.5	0.46
13	142	142	199	35	225	743	0.6	5.18	0.53	0.43
14	147	156	205	26	235	769	0.64	4.46	0.52	0.48
15	138	153	189	27	228	735	0.62	4.67	0.51	0.47
16	133	149	205	29	219	735	0.62	4.88	0.52	0.46
17	134	157	202	27	231	751	0.65	4.54	0.52	0.51
18	138	153	207	22	224	744	0.61	4.53	0.52	0.45
19	134	150	208	27	223	742	0.62	4.65	0.51	0.46
20	135	146	204	23	213	721	0.62	4.58	0.51	0.48

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

⁵Inter-chain restraints, ⁶Standard deviation

9.2.1 Bar graph : Distance Violation statistics for each model ⓘ



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

9.3 Distance violation statistics for the ensemble ⓘ

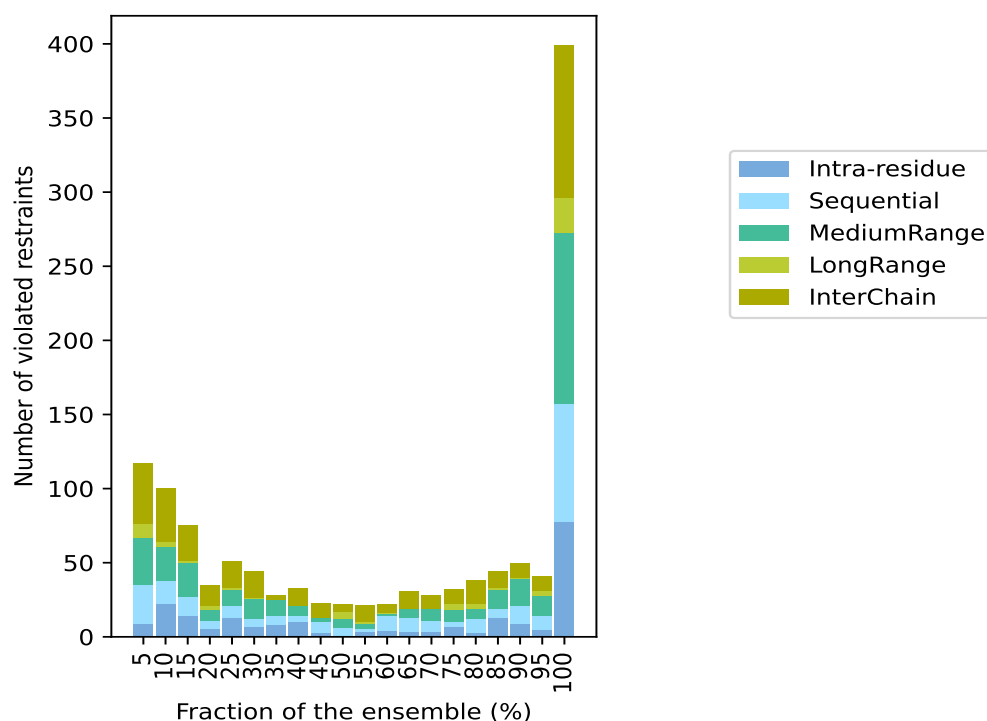
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 2629(IR:846, SQ:536, MR:668, LR:63, IC:516) restraints are 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	%
9	26	32	9	41	117	1	5.0
22	16	23	3	36	100	2	10.0
14	13	23	1	24	75	3	15.0
5	6	7	3	14	35	4	20.0
13	8	11	1	18	51	5	25.0
7	5	14	0	18	44	6	30.0
8	6	11	0	3	28	7	35.0
10	4	7	0	12	33	8	40.0
3	7	3	0	10	23	9	45.0
1	5	6	5	5	22	10	50.0
3	2	4	1	11	21	11	55.0
4	10	2	0	6	22	12	60.0
3	10	6	0	12	31	13	65.0
3	8	8	0	9	28	14	70.0
7	3	8	4	10	32	15	75.0
3	9	7	3	16	38	16	80.0
13	6	13	1	11	44	17	85.0
9	12	18	1	10	50	18	90.0
5	9	14	3	10	41	19	95.0
78	79	116	23	103	399	20	100.0

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

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

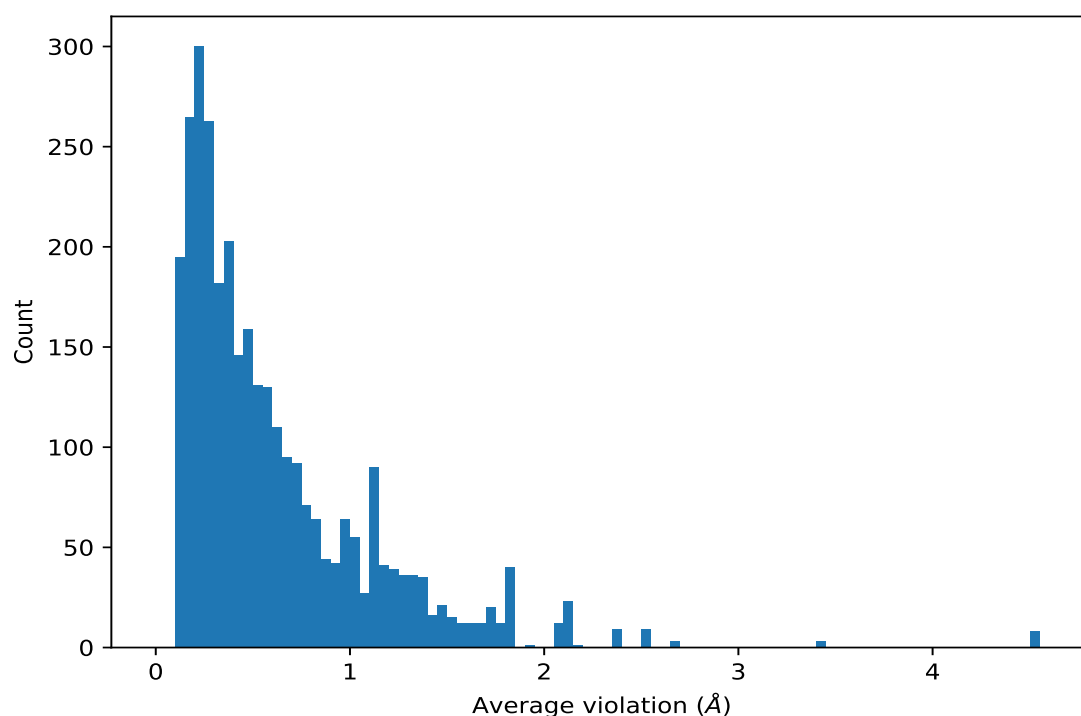
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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)
(2,100)	1:206:A:THR:HG23	1:202:A:VAL:HG13	20	4.54	0.13	4.54
(2,100)	1:206:A:THR:HG22	1:202:A:VAL:HG12	20	4.54	0.13	4.54
(2,100)	1:206:A:THR:HG21	1:202:A:VAL:HG11	20	4.54	0.13	4.54
(2,100)	1:206:A:THR:HG21	1:202:A:VAL:HG13	20	4.54	0.13	4.54
(2,100)	1:206:A:THR:HG23	1:202:A:VAL:HG11	20	4.54	0.13	4.54
(2,100)	1:206:A:THR:HG21	1:202:A:VAL:HG12	20	4.54	0.13	4.54
(2,100)	1:206:A:THR:HG22	1:202:A:VAL:HG13	20	4.54	0.13	4.54
(2,100)	1:206:A:THR:HG22	1:202:A:VAL:HG11	20	4.54	0.13	4.54
(1,1011)	1:249:A:THR:HG21	2:5478:C:LYS:HD3	20	3.44	0.42	3.38
(1,1011)	1:249:A:THR:HG22	2:5478:C:LYS:HD3	20	3.44	0.42	3.38
(1,1011)	1:249:A:THR:HG23	2:5478:C:LYS:HD3	20	3.44	0.42	3.38
(2,1314)	1:204:A:LYS:HD3	1:203:A:LEU:HD23	20	2.67	0.47	2.5
(2,1314)	1:204:A:LYS:HD3	1:203:A:LEU:HD22	20	2.67	0.47	2.5
(2,1314)	1:204:A:LYS:HD3	1:203:A:LEU:HD21	20	2.67	0.47	2.5
(1,470)	1:239:A:LEU:HD13	1:243:A:VAL:HG22	20	2.5	0.07	2.48
(1,470)	1:239:A:LEU:HD12	1:243:A:VAL:HG23	20	2.5	0.07	2.48

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,470)	1:239:A:LEU:HD11	1:243:A:VAL:HG21	20	2.5	0.07	2.48
(1,470)	1:239:A:LEU:HD13	1:243:A:VAL:HG23	20	2.5	0.07	2.48
(1,470)	1:239:A:LEU:HD12	1:243:A:VAL:HG21	20	2.5	0.07	2.48
(1,470)	1:239:A:LEU:HD11	1:243:A:VAL:HG23	20	2.5	0.07	2.48
(1,470)	1:239:A:LEU:HD12	1:243:A:VAL:HG22	20	2.5	0.07	2.48
(1,470)	1:239:A:LEU:HD11	1:243:A:VAL:HG22	20	2.5	0.07	2.48
(1,470)	1:239:A:LEU:HD13	1:243:A:VAL:HG21	20	2.5	0.07	2.48
(2,216)	1:227:A:ILE:HD12	1:242:B:ILE:HD11	20	2.37	0.17	2.38
(2,216)	1:227:A:ILE:HD13	1:242:B:ILE:HD11	20	2.37	0.17	2.38
(2,216)	1:227:A:ILE:HD12	1:242:B:ILE:HD12	20	2.37	0.17	2.38
(2,216)	1:227:A:ILE:HD13	1:242:B:ILE:HD12	20	2.37	0.17	2.38
(2,216)	1:227:A:ILE:HD11	1:242:B:ILE:HD11	20	2.37	0.17	2.38
(2,216)	1:227:A:ILE:HD12	1:242:B:ILE:HD13	20	2.37	0.17	2.38
(2,216)	1:227:A:ILE:HD11	1:242:B:ILE:HD13	20	2.37	0.17	2.38
(2,216)	1:227:A:ILE:HD11	1:242:B:ILE:HD12	20	2.37	0.17	2.38
(2,216)	1:227:A:ILE:HD13	1:242:B:ILE:HD13	20	2.37	0.17	2.38
(1,235)	1:254:A:VAL:HG22	1:255:A:ILE:HG13	20	2.13	0.42	2.26
(1,235)	1:254:A:VAL:HG21	1:249:A:THR:HG22	20	2.13	0.42	2.26
(1,235)	1:254:A:VAL:HG23	1:249:A:THR:HG21	20	2.13	0.42	2.26
(1,235)	1:254:A:VAL:HG23	1:255:A:ILE:HG13	20	2.13	0.42	2.26
(1,235)	1:254:A:VAL:HG21	1:249:A:THR:HG21	20	2.13	0.42	2.26
(1,235)	1:254:A:VAL:HG21	1:255:A:ILE:HG13	20	2.13	0.42	2.26
(1,235)	1:254:A:VAL:HG23	1:249:A:THR:HG23	20	2.13	0.42	2.26
(1,235)	1:254:A:VAL:HG21	1:249:A:THR:HG23	20	2.13	0.42	2.26
(1,235)	1:254:A:VAL:HG22	1:249:A:THR:HG22	20	2.13	0.42	2.26
(1,235)	1:254:A:VAL:HG23	1:249:A:THR:HG22	20	2.13	0.42	2.26
(1,235)	1:254:A:VAL:HG22	1:249:A:THR:HG23	20	2.13	0.42	2.26
(1,235)	1:254:A:VAL:HG22	1:249:A:THR:HG21	20	2.13	0.42	2.26
(2,1261)	1:207:A:VAL:HG11	1:204:A:LYS:HG2	20	2.12	0.23	2.2
(2,1261)	1:207:A:VAL:HG12	1:204:A:LYS:HG2	20	2.12	0.23	2.2
(2,1261)	1:207:A:VAL:HG13	1:204:A:LYS:HG2	20	2.12	0.23	2.2
(1,59)	1:200:A:VAL:HG12	1:202:A:VAL:HG11	20	2.1	0.15	2.1
(1,59)	1:200:A:VAL:HG13	1:202:A:VAL:HG13	20	2.1	0.15	2.1
(1,59)	1:200:A:VAL:HG11	1:202:A:VAL:HG12	20	2.1	0.15	2.1
(1,59)	1:200:A:VAL:HG11	1:202:A:VAL:HG11	20	2.1	0.15	2.1
(1,59)	1:200:A:VAL:HG13	1:202:A:VAL:HG11	20	2.1	0.15	2.1
(1,59)	1:200:A:VAL:HG11	1:202:A:VAL:HG13	20	2.1	0.15	2.1
(1,59)	1:200:A:VAL:HG12	1:202:A:VAL:HG12	20	2.1	0.15	2.1
(1,59)	1:200:A:VAL:HG12	1:202:A:VAL:HG13	20	2.1	0.15	2.1
(2,2345)	1:196:A:LEU:HD23	1:196:B:LEU:HB2	20	2.09	0.16	2.16
(2,2345)	1:196:A:LEU:HD21	1:196:B:LEU:HB2	20	2.09	0.16	2.16
(2,2345)	1:196:A:LEU:HD22	1:196:B:LEU:HB2	20	2.09	0.16	2.16

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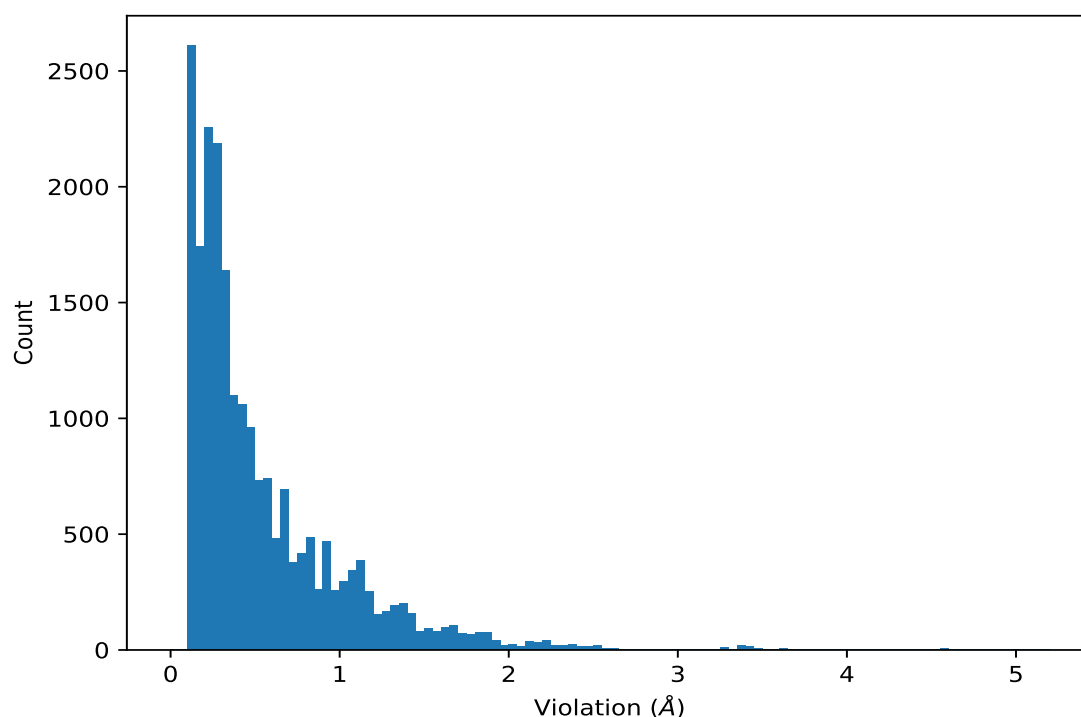
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(2,2546)	1:239:A:LEU:HD11	1:242:B:ILE:HD11	20	2.08	0.24	2.12

¹Number of violated models, ²Standard deviation

9.5 All violated distance restraints [i](#)

9.5.1 Histogram : Distribution of distance violations [i](#)

The following histogram shows the distribution of the absolute value of the violation for all violated restraints in the ensemble.



9.5.2 Table : All distance violations [i](#)

The following table 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)
(1,1011)	1:249:A:THR:HG21	2:5478:C:LYS:HD3	13	5.18
(1,1011)	1:249:A:THR:HG22	2:5478:C:LYS:HD3	13	5.18
(1,1011)	1:249:A:THR:HG23	2:5478:C:LYS:HD3	13	5.18
(2,100)	1:206:A:THR:HG22	1:202:A:VAL:HG13	16	4.88

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,100)	1:206:A:THR:HG22	1:202:A:VAL:HG13	11	4.72
(2,100)	1:206:A:THR:HG21	1:202:A:VAL:HG12	15	4.67
(2,100)	1:206:A:THR:HG21	1:202:A:VAL:HG12	19	4.65
(2,100)	1:206:A:THR:HG21	1:202:A:VAL:HG11	13	4.6
(2,100)	1:206:A:THR:HG21	1:202:A:VAL:HG13	6	4.59
(2,100)	1:206:A:THR:HG21	1:202:A:VAL:HG12	20	4.58
(2,100)	1:206:A:THR:HG22	1:202:A:VAL:HG12	12	4.57
(2,100)	1:206:A:THR:HG21	1:202:A:VAL:HG11	4	4.55

10 Dihedral-angle violation analysis ⓘ

No dihedral-angle restraints found