



wwPDB NMR Structure Validation Summary Report ⓘ

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BMRB ID : 16935
Title : Solution structure of the PECAM-1 cytoplasmic tail with DPC
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Deposited on : 2010-05-14

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We welcome your comments at validation@mail.wwpdb.org

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<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

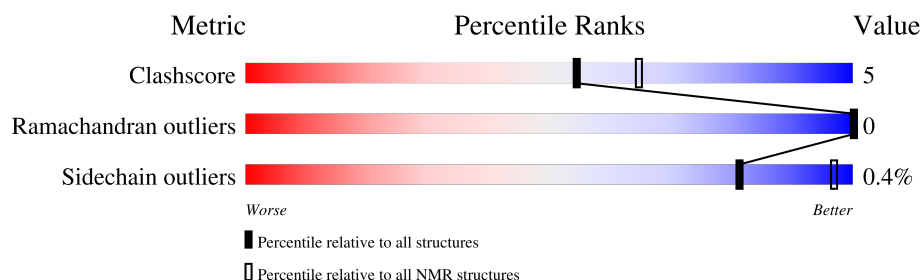
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 86%.

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	55	

2 Ensemble composition and analysis

This entry contains 20 models. Model 14 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:682-A:697 (16)	0.43	14

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 and 5 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 534 atoms, of which 264 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Platelet endothelial cell adhesion molecule.

Mol	Chain	Residues	Atoms					Trace
1	A	35	Total	C	H	N	O	0
			534	163	264	47	60	

There are 2 discrepancies between the modelled and reference sequences:

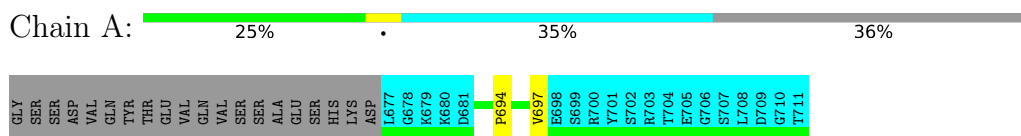
Chain	Residue	Modelled	Actual	Comment	Reference
A	657	GLY	-	expression tag	UNP P16284
A	658	SER	-	expression tag	UNP P16284

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.

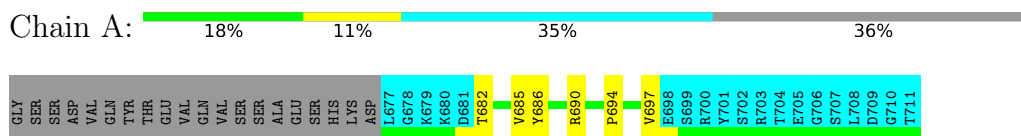
- Molecule 1: Platelet endothelial cell adhesion molecule



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

The representative model is number 14. Colouring as in section 4.1 above.

- Molecule 1: Platelet endothelial cell adhesion molecule



5 Refinement protocol and experimental data overview

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

Of the 100 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
Xplor-NIH	refinement	2.9.3

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	479
Number of shifts mapped to atoms	332
Number of unparsed shifts	0
Number of shifts with mapping errors	147
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	86%

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	0.96±0.05	0±0/125 (0.0± 0.2%)	0.92±0.04	0±0/172 (0.0± 0.0%)
All	All	0.96	1/2500 (0.0%)	0.92	0/3440 (0.0%)

All unique bond outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	693	VAL	CA-CB	5.17	1.57	1.54	16	1

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	123	123	123	1±1
All	All	2460	2460	2460	25

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 5.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:686:TYR:O	1:A:690:ARG:HG2	0.54	2.02	19	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:694:PRO:HA	1:A:697:VAL:HG12	0.49	1.82	17	11
1:A:689:VAL:O	1:A:693:VAL:HG23	0.48	2.07	15	5
1:A:685:VAL:O	1:A:689:VAL:HG23	0.40	2.16	7	2
1:A:693:VAL:HB	1:A:694:PRO:HD3	0.40	1.93	17	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	16/55 (29%)	16±0 (99±2%)	0±0 (1±2%)	0±0 (0±0%)	100	100
All	All	320/1100 (29%)	318 (99%)	2 (1%)	0 (0%)	100	100

There are no Ramachandran outliers.

6.3.2 Protein sidechains [i](#)

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	14/48 (29%)	14±0 (100±2%)	0±0 (0±2%)	81	97
All	All	280/960 (29%)	279 (100%)	1 (0%)	81	97

All 1 unique residues with a non-rotameric sidechain are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	691	LYS	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [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 86% for the well-defined parts and 73% 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	479
Number of shifts mapped to atoms	332
Number of unparsed shifts	0
Number of shifts with mapping errors	147
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 147) occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	659	SER	CA	58.731	0.1	1
1	A	660	ASP	HA	4.698	0.02	1
1	A	660	ASP	HB2	2.786	0.02	2
1	A	660	ASP	C	176.193	0.1	1
1	A	660	ASP	CA	54.821	0.1	1
1	A	660	ASP	CB	41.576	0.1	1
1	A	661	VAL	H	8.023	0.02	1
1	A	661	VAL	HA	4.101	0.02	1
1	A	661	VAL	HB	2.059	0.02	1
1	A	661	VAL	HG11	0.94	0.02	2
1	A	661	VAL	HG12	0.94	0.02	2
1	A	661	VAL	HG13	0.94	0.02	2
1	A	661	VAL	HG21	0.975	0.02	2
1	A	661	VAL	HG22	0.975	0.02	2

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	661	VAL	HG23	0.975	0.02	2
1	A	661	VAL	C	176.193	0.1	1
1	A	661	VAL	CA	62.562	0.1	1
1	A	661	VAL	CB	32.988	0.1	1
1	A	661	VAL	CG2	21.078	0.1	1
1	A	661	VAL	N	119.984	0.1	1
1	A	662	GLN	H	8.475	0.02	1
1	A	662	GLN	HA	4.413	0.02	1
1	A	662	GLN	HB2	2.102	0.02	2
1	A	662	GLN	HB3	2.042	0.02	2
1	A	662	GLN	HG3	2.379	0.02	2
1	A	662	GLN	C	176.021	0.1	1
1	A	662	GLN	CA	55.858	0.1	1
1	A	662	GLN	CB	29.702	0.1	1
1	A	662	GLN	CG	34.027	0.1	1
1	A	662	GLN	N	124.579	0.1	1
1	A	663	TYR	H	8.32	0.02	1
1	A	663	TYR	HA	4.69	0.02	1
1	A	663	TYR	HB2	3.139	0.02	2
1	A	663	TYR	HB3	3.0	0.02	2
1	A	663	TYR	HD1	7.154	0.02	1
1	A	663	TYR	HD2	7.154	0.02	1
1	A	663	TYR	C	175.794	0.1	1
1	A	663	TYR	CA	58.174	0.1	1
1	A	663	TYR	CB	39.169	0.1	1
1	A	663	TYR	CD1	133.083	0.1	1
1	A	663	TYR	N	121.961	0.1	1
1	A	664	THR	H	8.012	0.02	1
1	A	664	THR	HA	4.326	0.02	1
1	A	664	THR	HB	4.194	0.02	1
1	A	664	THR	HG21	1.199	0.02	1
1	A	664	THR	HG22	1.199	0.02	1
1	A	664	THR	HG23	1.199	0.02	1
1	A	664	THR	C	174.116	0.1	1
1	A	664	THR	CA	61.993	0.1	1
1	A	664	THR	CB	70.385	0.1	1
1	A	664	THR	CG2	21.841	0.1	1
1	A	664	THR	N	115.81	0.1	1
1	A	665	GLU	H	8.391	0.02	1
1	A	665	GLU	HA	4.323	0.02	1
1	A	665	GLU	HB2	2.112	0.02	2

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	665	GLU	HB3	1.984	0.02	2
1	A	665	GLU	HG3	2.299	0.02	2
1	A	665	GLU	C	176.588	0.1	1
1	A	665	GLU	CA	56.711	0.1	1
1	A	665	GLU	CB	30.543	0.1	1
1	A	665	GLU	CG	36.628	0.1	1
1	A	665	GLU	N	123.393	0.1	1
1	A	666	VAL	H	8.171	0.02	1
1	A	666	VAL	HA	4.126	0.02	1
1	A	666	VAL	HB	2.078	0.02	1
1	A	666	VAL	HG11	0.865	0.02	2
1	A	666	VAL	HG12	0.865	0.02	2
1	A	666	VAL	HG13	0.865	0.02	2
1	A	666	VAL	HG21	0.983	0.02	2
1	A	666	VAL	HG22	0.983	0.02	2
1	A	666	VAL	HG23	0.983	0.02	2
1	A	666	VAL	C	176.008	0.1	1
1	A	666	VAL	CA	62.44	0.1	1
1	A	666	VAL	CB	32.978	0.1	1
1	A	666	VAL	CG1	21.269	0.1	1
1	A	666	VAL	CG2	20.749	0.1	1
1	A	666	VAL	N	121.607	0.1	1
1	A	667	GLN	H	8.398	0.02	1
1	A	667	GLN	HA	4.36	0.02	1
1	A	667	GLN	HB3	2.06	0.02	2
1	A	667	GLN	HG3	2.291	0.02	2
1	A	667	GLN	C	175.811	0.1	1
1	A	667	GLN	CA	55.711	0.1	1
1	A	667	GLN	CB	29.749	0.1	1
1	A	667	GLN	CG	33.969	0.1	1
1	A	667	GLN	N	123.663	0.1	1
1	A	668	VAL	H	8.31	0.02	1
1	A	668	VAL	HA	4.195	0.02	1
1	A	668	VAL	HB	2.167	0.02	1
1	A	668	VAL	HG21	0.99	0.02	2
1	A	668	VAL	HG22	0.99	0.02	2
1	A	668	VAL	HG23	0.99	0.02	2
1	A	668	VAL	C	176.193	0.1	1
1	A	668	VAL	CA	62.496	0.1	1
1	A	668	VAL	CB	32.808	0.1	1
1	A	668	VAL	CG1	20.999	0.1	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	668	VAL	N	121.854	0.1	1
1	A	669	SER	H	8.477	0.02	1
1	A	669	SER	HA	4.534	0.02	1
1	A	669	SER	HB3	3.95	0.02	2
1	A	669	SER	C	174.964	0.1	1
1	A	669	SER	CA	58.516	0.1	1
1	A	669	SER	CB	63.187	0.1	1
1	A	669	SER	N	119.384	0.1	1
1	A	670	SER	H	8.538	0.02	1
1	A	670	SER	HA	4.499	0.02	1
1	A	670	SER	HB3	3.986	0.02	2
1	A	670	SER	C	175.0	0.1	1
1	A	670	SER	CA	58.683	0.1	1
1	A	670	SER	CB	64.05	0.1	1
1	A	670	SER	N	118.23	0.1	1
1	A	671	ALA	H	8.399	0.02	1
1	A	671	ALA	HA	4.377	0.02	1
1	A	671	ALA	HB1	1.454	0.02	1
1	A	671	ALA	HB2	1.454	0.02	1
1	A	671	ALA	HB3	1.454	0.02	1
1	A	671	ALA	C	178.243	0.1	1
1	A	671	ALA	CA	53.742	0.1	1
1	A	671	ALA	CB	19.578	0.1	1
1	A	671	ALA	N	125.784	0.1	1
1	A	672	GLU	H	8.328	0.02	1
1	A	672	GLU	HA	4.336	0.02	1
1	A	672	GLU	HB2	2.102	0.02	2
1	A	672	GLU	HB3	1.982	0.02	2
1	A	672	GLU	C	177.028	0.1	1
1	A	672	GLU	CA	56.947	0.1	1
1	A	672	GLU	CB	30.362	0.1	1
1	A	672	GLU	CG	36.636	0.1	1
1	A	672	GLU	N	119.272	0.1	1
1	A	673	SER	H	8.242	0.02	1
1	A	673	SER	CA	58.863	0.1	1
1	A	673	SER	CB	64.05	0.1	1
1	A	673	SER	N	115.947	0.1	1
1	A	675	LYS	HA	4.301	0.02	1
1	A	675	LYS	HB3	1.832	0.02	2
1	A	675	LYS	C	176.196	0.1	1
1	A	675	LYS	CA	56.684	0.1	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	675	LYS	CB	33.339	0.1	1
1	A	675	LYS	CG	24.94	0.1	1
1	A	676	ASP	H	8.441	0.02	1
1	A	676	ASP	HA	4.663	0.02	1
1	A	676	ASP	HB2	2.811	0.02	2
1	A	676	ASP	HB3	2.668	0.02	2
1	A	676	ASP	C	176.601	0.1	1
1	A	676	ASP	CA	54.701	0.1	1
1	A	676	ASP	CB	41.387	0.1	1
1	A	676	ASP	N	121.27	0.1	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
$^{13}\text{C}_\alpha$	52	-0.85 ± 0.24	Should be checked
$^{13}\text{C}_\beta$	48	0.00 ± 0.09	None needed (< 0.5 ppm)
$^{13}\text{C}'$	43	-0.56 ± 0.17	Should be applied
^{15}N	46	-0.19 ± 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 86%, i.e. 182 atoms were assigned a chemical shift out of a possible 211. 0 out of 4 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	74/78 (95%)	30/31 (97%)	30/32 (94%)	14/15 (93%)
Sidechain	102/124 (82%)	67/81 (83%)	34/39 (87%)	1/4 (25%)
Aromatic	6/9 (67%)	4/4 (100%)	2/5 (40%)	0/0 (—%)
Overall	182/211 (86%)	101/116 (87%)	66/76 (87%)	15/19 (79%)

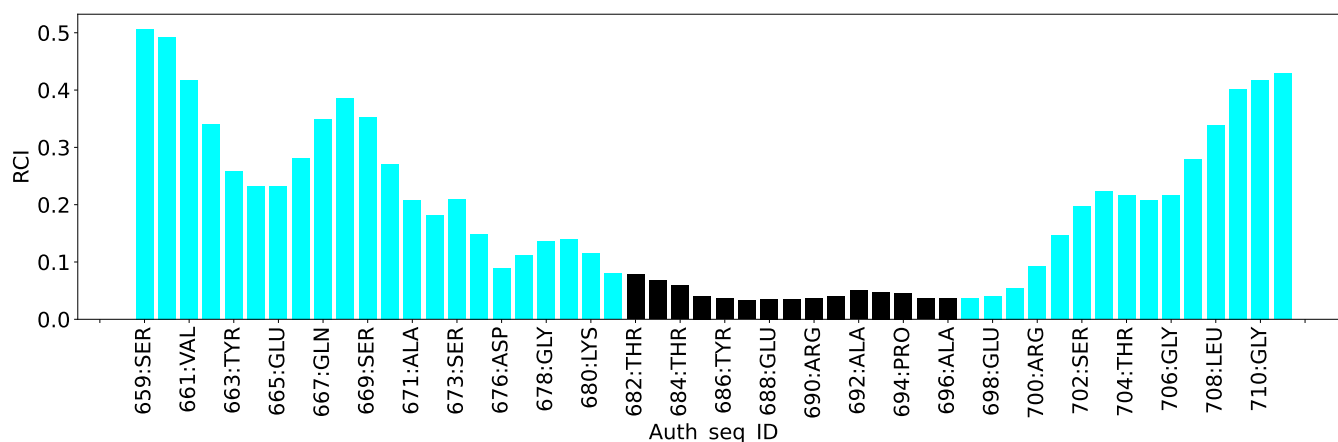
7.1.4 Statistically unusual chemical shifts [i](#)

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	148
Intra-residue ($ i-j =0$)	71
Sequential ($ i-j =1$)	37
Medium range ($ i-j >1$ and $ i-j <5$)	40
Long range ($ i-j \geq 5$)	0
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	33
Number of unmapped restraints	0
Number of restraints per residue	3.3
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)	3.4	0.19
0.2-0.5 (Medium)	1.0	0.49
>0.5 (Large)	0.2	0.72

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

Dihedral-angle violations less than 1° are not included in the calculation.

Bins (°)	Average number of violations per model	Max (°)
1.0-10.0 (Small)	1.9	2.54
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis ⓘ

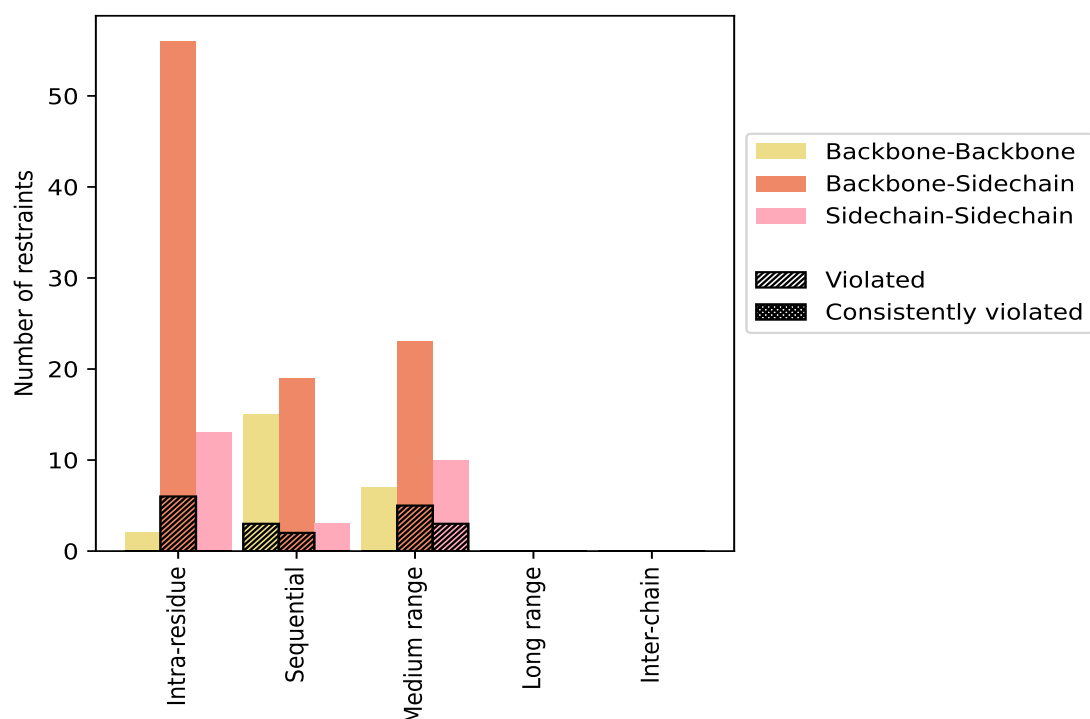
9.1 Summary of distance violations ⓘ

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

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue (i-j =0)	71	48.0	6	8.5	4.1	0	0.0	0.0
Backbone-Backbone	2	1.4	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	56	37.8	6	10.7	4.1	0	0.0	0.0
Sidechain-Sidechain	13	8.8	0	0.0	0.0	0	0.0	0.0
Sequential (i-j =1)	37	25.0	5	13.5	3.4	0	0.0	0.0
Backbone-Backbone	15	10.1	3	20.0	2.0	0	0.0	0.0
Backbone-Sidechain	19	12.8	2	10.5	1.4	0	0.0	0.0
Sidechain-Sidechain	3	2.0	0	0.0	0.0	0	0.0	0.0
Medium range (i-j >1 & i-j <5)	40	27.0	8	20.0	5.4	0	0.0	0.0
Backbone-Backbone	7	4.7	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	23	15.5	5	21.7	3.4	0	0.0	0.0
Sidechain-Sidechain	10	6.8	3	30.0	2.0	0	0.0	0.0
Long range (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
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	148	100.0	19	12.8	12.8	0	0.0	0.0
Backbone-Backbone	24	16.2	3	12.5	2.0	0	0.0	0.0
Backbone-Sidechain	98	66.2	13	13.3	8.8	0	0.0	0.0
Sidechain-Sidechain	26	17.6	3	11.5	2.0	0	0.0	0.0

¹ percentage calculated with respect to the total number of distance restraints, ² percentage calculated with respect to the number of restraints in a particular restraint category, ³ violated in at least one model, ⁴ violated in all the models

9.1.1 Bar chart : Distribution of distance restraints and violations [i](#)



Violated and consistently violated restraints are shown using different hatch patterns in their respective categories. The hydrogen bonds and disulfied bonds are counted in their appropriate category on the x-axis

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

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

Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
1	2	0	3	0	0	5	0.13	0.15	0.01	0.12
2	1	1	3	0	0	5	0.17	0.39	0.11	0.12
3	1	1	4	0	0	6	0.23	0.7	0.21	0.14
4	1	1	3	0	0	5	0.25	0.72	0.24	0.12
5	2	0	2	0	0	4	0.19	0.44	0.14	0.12
6	3	2	3	0	0	8	0.18	0.43	0.11	0.12
7	4	2	1	0	0	7	0.19	0.44	0.11	0.15
8	1	1	1	0	0	3	0.24	0.47	0.16	0.12
9	1	1	5	0	0	7	0.18	0.49	0.13	0.13
10	2	1	1	0	0	4	0.15	0.24	0.05	0.12

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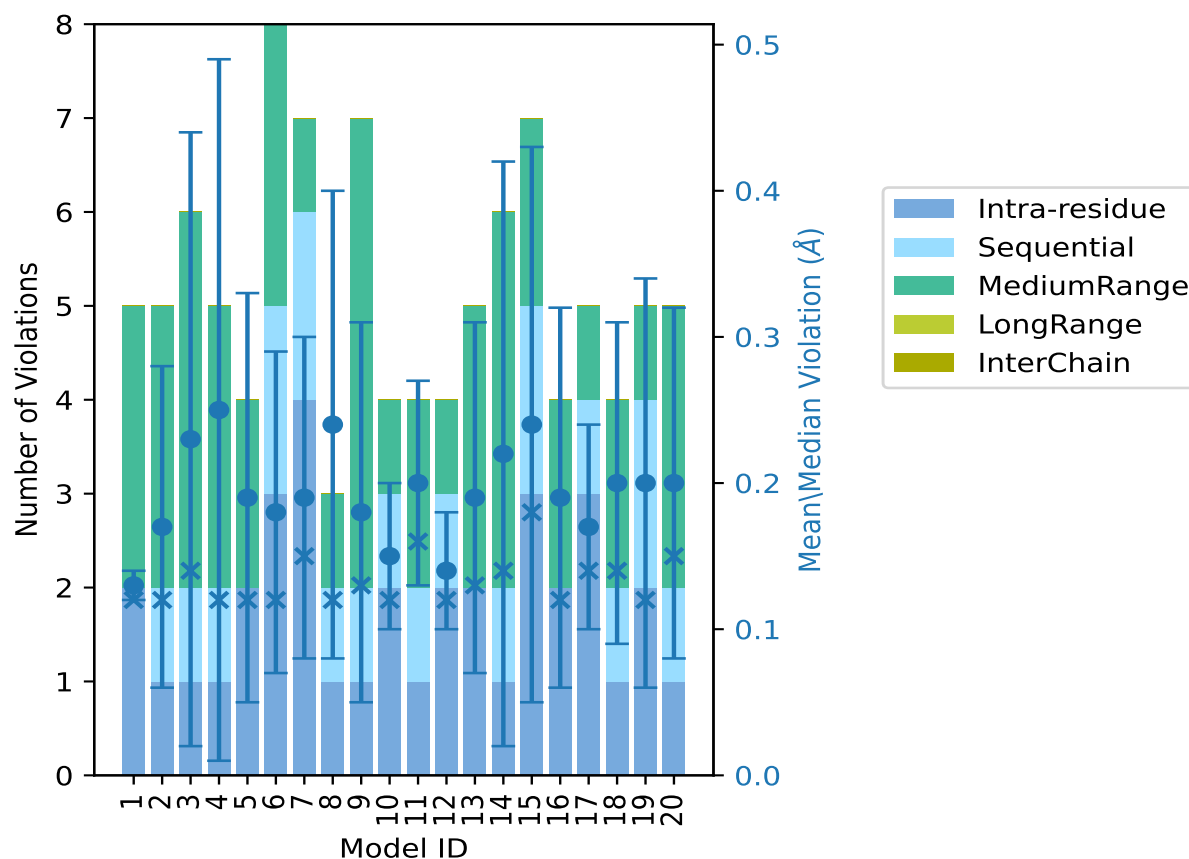
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	1	1	2	0	0	4	0.2	0.31	0.07	0.16
12	2	1	1	0	0	4	0.14	0.21	0.04	0.12
13	2	0	3	0	0	5	0.19	0.43	0.12	0.13
14	1	1	4	0	0	6	0.22	0.66	0.2	0.14
15	3	2	2	0	0	7	0.24	0.69	0.19	0.18
16	2	0	2	0	0	4	0.19	0.42	0.13	0.12
17	3	1	1	0	0	5	0.17	0.3	0.07	0.14
18	1	1	2	0	0	4	0.2	0.39	0.11	0.14
19	2	2	1	0	0	5	0.2	0.47	0.14	0.12
20	1	1	3	0	0	5	0.2	0.43	0.12	0.15

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 ⓘ

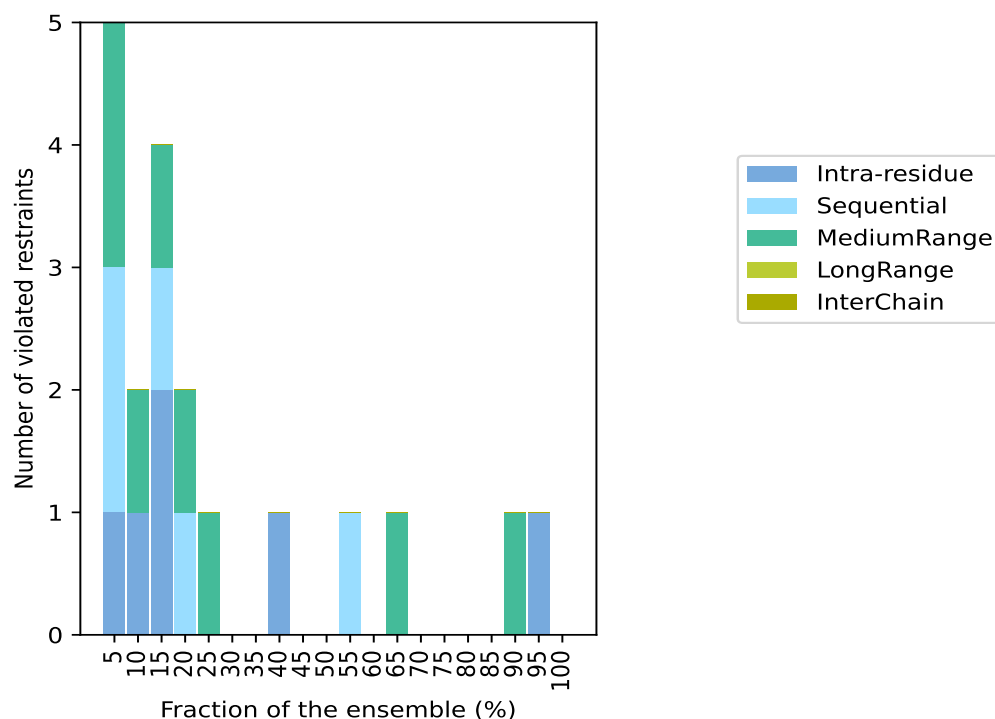
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 129(IR:65, SQ:32, MR:32, LR:0, IC:0) restraints are not violated in the ensemble.

Number of violated restraints						Fraction of the ensemble	
IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total	Count ⁶	%
1	2	2	0	0	5	1	5.0
1	0	1	0	0	2	2	10.0
2	1	1	0	0	4	3	15.0
0	1	1	0	0	2	4	20.0
0	0	1	0	0	1	5	25.0
0	0	0	0	0	0	6	30.0
0	0	0	0	0	0	7	35.0
1	0	0	0	0	1	8	40.0
0	0	0	0	0	0	9	45.0
0	0	0	0	0	0	10	50.0
0	1	0	0	0	1	11	55.0
0	0	0	0	0	0	12	60.0
0	0	1	0	0	1	13	65.0
0	0	0	0	0	0	14	70.0
0	0	0	0	0	0	15	75.0
0	0	0	0	0	0	16	80.0
0	0	0	0	0	0	17	85.0
0	0	1	0	0	1	18	90.0
1	0	0	0	0	1	19	95.0
0	0	0	0	0	0	20	100.0

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

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

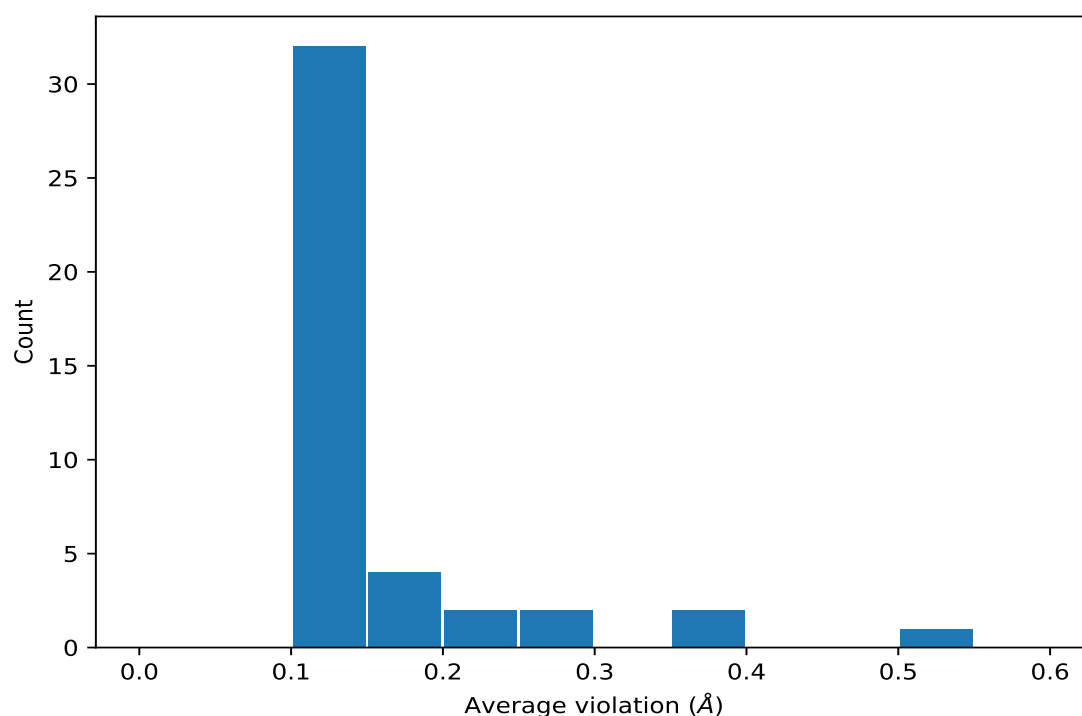
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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)
(1,51)	1:688:A:GLU:HA	1:688:A:GLU:HG2	19	0.12	0.01	0.11
(1,51)	1:688:A:GLU:HA	1:688:A:GLU:HG3	19	0.12	0.01	0.11
(1,38)	1:685:A:VAL:HG21	1:688:A:GLU:HG2	18	0.14	0.02	0.13
(1,38)	1:685:A:VAL:HG21	1:688:A:GLU:HG3	18	0.14	0.02	0.13
(1,38)	1:685:A:VAL:HG22	1:688:A:GLU:HG2	18	0.14	0.02	0.13
(1,38)	1:685:A:VAL:HG22	1:688:A:GLU:HG3	18	0.14	0.02	0.13
(1,38)	1:685:A:VAL:HG23	1:688:A:GLU:HG2	18	0.14	0.02	0.13
(1,38)	1:685:A:VAL:HG23	1:688:A:GLU:HG3	18	0.14	0.02	0.13
(1,101)	1:697:A:VAL:HG21	1:701:A:TYR:HD1	13	0.13	0.03	0.12
(1,101)	1:697:A:VAL:HG21	1:701:A:TYR:HD2	13	0.13	0.03	0.12
(1,101)	1:697:A:VAL:HG22	1:701:A:TYR:HD1	13	0.13	0.03	0.12
(1,101)	1:697:A:VAL:HG22	1:701:A:TYR:HD2	13	0.13	0.03	0.12
(1,101)	1:697:A:VAL:HG23	1:701:A:TYR:HD1	13	0.13	0.03	0.12
(1,101)	1:697:A:VAL:HG23	1:701:A:TYR:HD2	13	0.13	0.03	0.12
(1,2)	1:677:A:LEU:H	1:678:A:GLY:H	11	0.51	0.15	0.47
(1,1)	1:677:A:LEU:H	1:677:A:LEU:HB2	8	0.38	0.09	0.43

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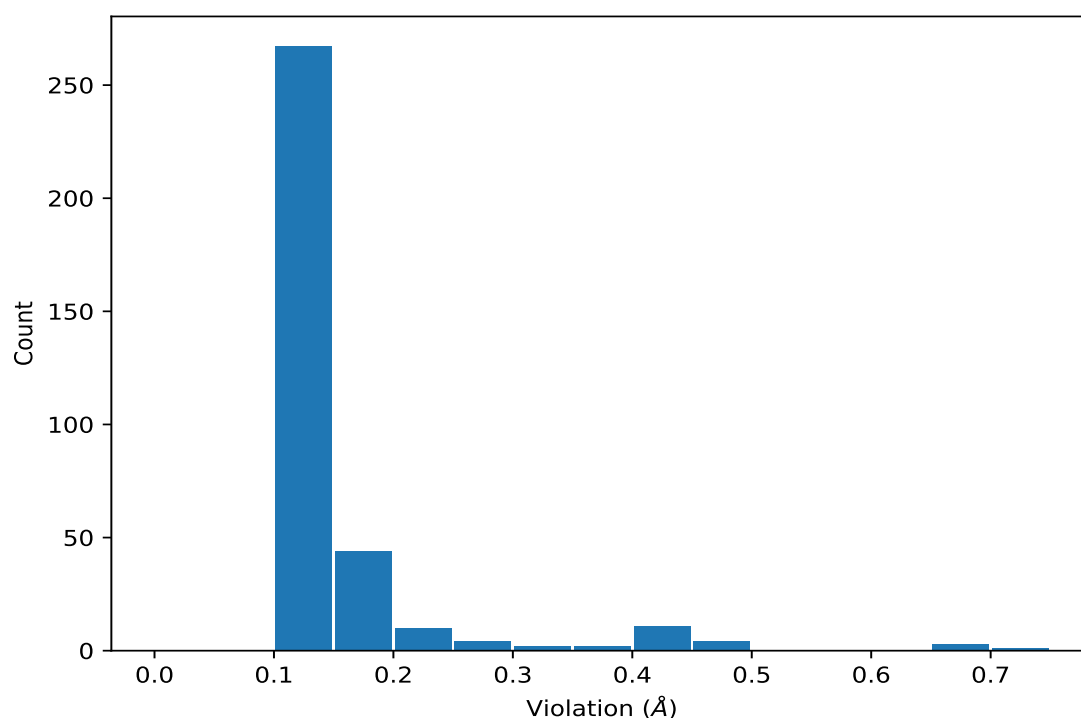
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,1)	1:677:A:LEU:H	1:677:A:LEU:HB3	8	0.38	0.09	0.43
(1,108)	1:698:A:GLU:HA	1:701:A:TYR:HE1	5	0.14	0.02	0.15
(1,108)	1:698:A:GLU:HA	1:701:A:TYR:HE2	5	0.14	0.02	0.15
(1,60)	1:689:A:VAL:HG21	1:692:A:ALA:HB1	4	0.11	0.01	0.12
(1,60)	1:689:A:VAL:HG21	1:692:A:ALA:HB2	4	0.11	0.01	0.12
(1,60)	1:689:A:VAL:HG21	1:692:A:ALA:HB3	4	0.11	0.01	0.12
(1,60)	1:689:A:VAL:HG22	1:692:A:ALA:HB1	4	0.11	0.01	0.12
(1,60)	1:689:A:VAL:HG22	1:692:A:ALA:HB2	4	0.11	0.01	0.12
(1,60)	1:689:A:VAL:HG22	1:692:A:ALA:HB3	4	0.11	0.01	0.12
(1,60)	1:689:A:VAL:HG23	1:692:A:ALA:HB1	4	0.11	0.01	0.12
(1,60)	1:689:A:VAL:HG23	1:692:A:ALA:HB2	4	0.11	0.01	0.12
(1,60)	1:689:A:VAL:HG23	1:692:A:ALA:HB3	4	0.11	0.01	0.12
(1,100)	1:697:A:VAL:HG21	1:698:A:GLU:H	4	0.11	0.01	0.1
(1,100)	1:697:A:VAL:HG22	1:698:A:GLU:H	4	0.11	0.01	0.1
(1,100)	1:697:A:VAL:HG23	1:698:A:GLU:H	4	0.11	0.01	0.1
(1,104)	1:698:A:GLU:H	1:698:A:GLU:HG2	3	0.22	0.01	0.22
(1,104)	1:698:A:GLU:H	1:698:A:GLU:HG3	3	0.22	0.01	0.22
(1,138)	1:704:A:THR:HB	1:705:A:GLU:H	3	0.16	0.03	0.16

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)
(1,2)	1:677:A:LEU:H	1:678:A:GLY:H	4	0.72
(1,2)	1:677:A:LEU:H	1:678:A:GLY:H	3	0.7
(1,2)	1:677:A:LEU:H	1:678:A:GLY:H	15	0.69
(1,2)	1:677:A:LEU:H	1:678:A:GLY:H	14	0.66
(1,2)	1:677:A:LEU:H	1:678:A:GLY:H	9	0.49
(1,2)	1:677:A:LEU:H	1:678:A:GLY:H	8	0.47
(1,1)	1:677:A:LEU:H	1:677:A:LEU:HB2	19	0.47
(1,1)	1:677:A:LEU:H	1:677:A:LEU:HB3	19	0.47
(1,1)	1:677:A:LEU:H	1:677:A:LEU:HB2	5	0.44
(1,1)	1:677:A:LEU:H	1:677:A:LEU:HB3	5	0.44
(1,1)	1:677:A:LEU:H	1:677:A:LEU:HB2	7	0.44
(1,1)	1:677:A:LEU:H	1:677:A:LEU:HB3	7	0.44
(1,2)	1:677:A:LEU:H	1:678:A:GLY:H	20	0.43

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

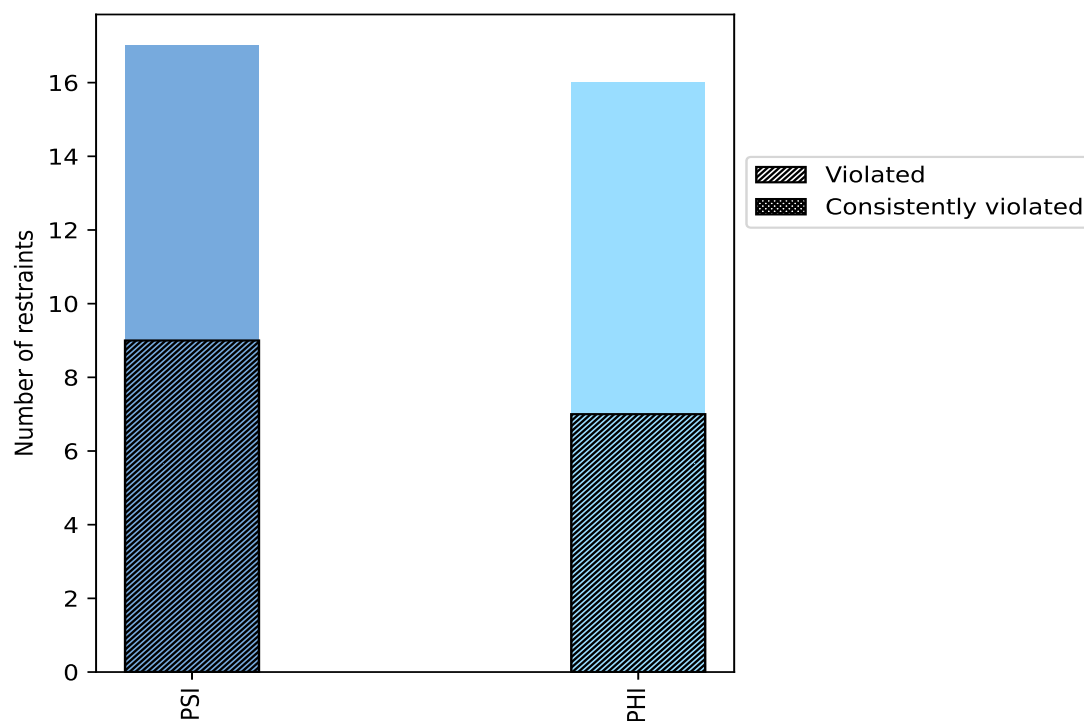
10.1 Summary of dihedral-angle violations [i](#)

The following table provides the summary of dihedral-angle violations in different dihedral-angle types. Violations less than 1° are not included in the calculation.

Angle type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
PSI	17	51.5	9	52.9	27.3	0	0.0	0.0
PHI	16	48.5	7	43.8	21.2	0	0.0	0.0
Total	33	100.0	16	48.5	48.5	0	0.0	0.0

¹ percentage calculated with respect to total number of dihedral-angle restraints, ² percentage calculated with respect to number of restraints in a particular dihedral-angle type, ³ violated in at least one model, ⁴ violated in all the models

10.1.1 Bar chart : Distribution of dihedral-angles and violations [i](#)



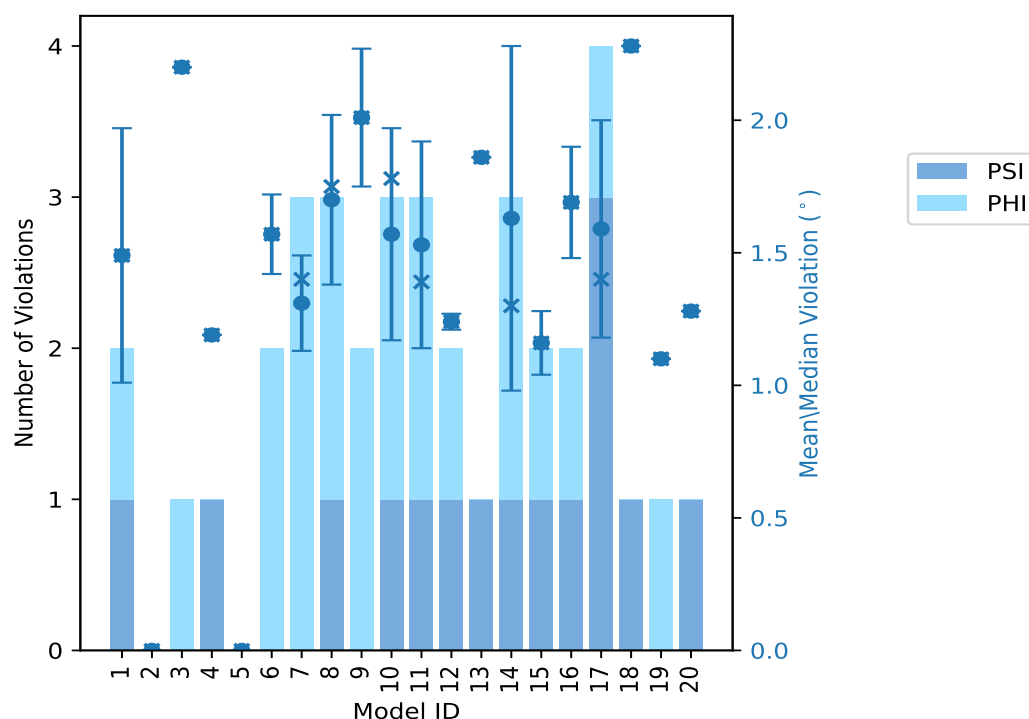
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

10.2 Dihedral-angle violation statistics for each model

The following table provides the dihedral-angle violation statistics for each model in the ensemble. Violations less than 1° are not included in the statistics.

Model ID	Number of violations			Mean (°)	Max (°)	SD (°)	Median (°)
	PSI	PHI	Total				
1	1	1	2	1.49	1.97	0.48	1.49
2	0	0	0	0.0	0.0	0.0	0.0
3	0	1	1	2.2	2.2	0.0	2.2
4	1	0	1	1.19	1.19	0.0	1.19
5	0	0	0	0.0	0.0	0.0	0.0
6	0	2	2	1.57	1.72	0.15	1.57
7	0	3	3	1.31	1.47	0.18	1.4
8	1	2	3	1.7	2.07	0.32	1.75
9	0	2	2	2.01	2.28	0.26	2.01
10	1	2	3	1.57	1.92	0.4	1.78
11	1	2	3	1.53	2.07	0.39	1.39
12	1	1	2	1.24	1.27	0.03	1.24
13	1	0	1	1.86	1.86	0.0	1.86
14	1	2	3	1.63	2.54	0.65	1.3
15	1	1	2	1.16	1.29	0.12	1.16
16	1	1	2	1.69	1.9	0.21	1.69
17	3	1	4	1.59	2.29	0.41	1.4
18	1	0	1	2.28	2.28	0.0	2.28
19	0	1	1	1.1	1.1	0.0	1.1
20	1	0	1	1.28	1.28	0.0	1.28

10.2.1 Bar graph : Dihedral violation statistics for each model [i](#)



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

10.3 Dihedral-angle violation statistics for the ensemble [i](#)

Violation analysis may find that some restraints are violated in very few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of ensemble.

Number of violated restraints			Fraction of the ensemble	
PSI	PHI	Total	Count ¹	%
6	2	8	1	5.0
1	2	3	2	10.0
1	1	2	3	15.0
1	1	2	4	20.0
0	0	0	5	25.0
0	0	0	6	30.0
0	0	0	7	35.0
0	0	0	8	40.0
0	1	1	9	45.0
0	0	0	10	50.0
0	0	0	11	55.0

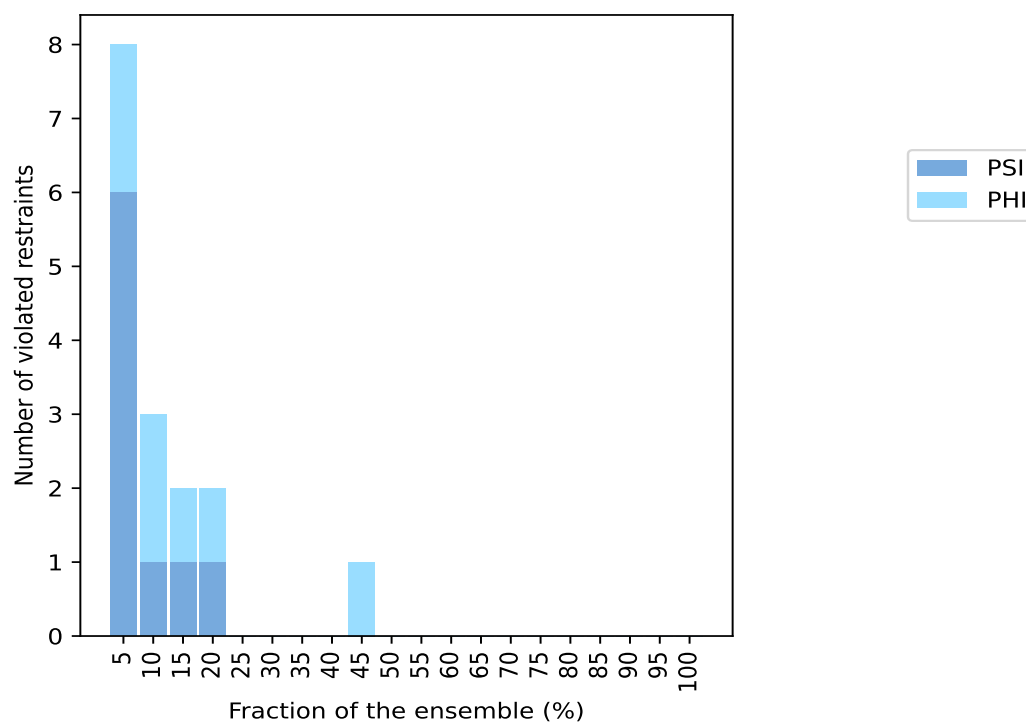
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Number of violated restraints			Fraction of the ensemble	
PSI	PHI	Total	Count ¹	%
0	0	0	12	60.0
0	0	0	13	65.0
0	0	0	14	70.0
0	0	0	15	75.0
0	0	0	16	80.0
0	0	0	17	85.0
0	0	0	18	90.0
0	0	0	19	95.0
0	0	0	20	100.0

¹ Number of models with violations

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

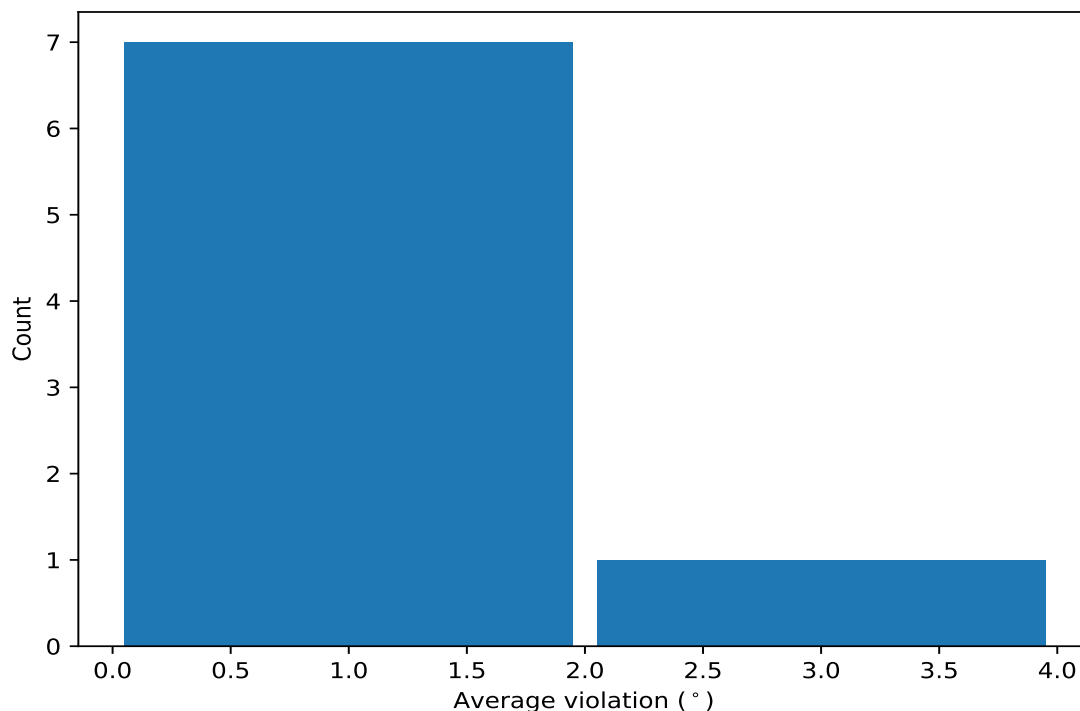


10.4 Most violated dihedral-angle restraints in the ensemble [i](#)

10.4.1 Histogram : Distribution of mean dihedral-angle violations [i](#)

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

in the ensemble



10.4.2 Table: Most violated dihedral-angle restraints [i](#)

The following table provides the mean and the standard deviation of the violation for each restraint sorted by number of violated models and the mean value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint.

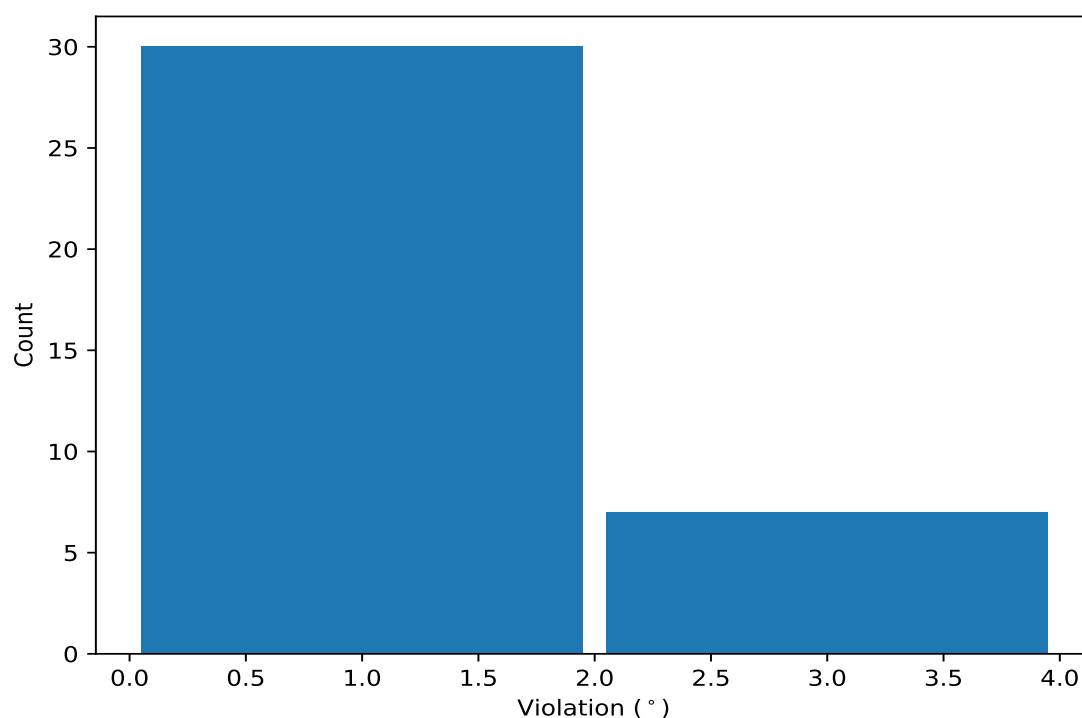
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,19)	1:690:A:ARG:C	1:691:A:LYS:N	1:691:A:LYS:CA	1:691:A:LYS:C	9	1.43	0.34	1.3
(1,11)	1:686:A:TYR:C	1:687:A:SER:N	1:687:A:SER:CA	1:687:A:SER:C	4	1.66	0.36	1.57
(1,31)	1:699:A:SER:N	1:699:A:SER:CA	1:699:A:SER:C	1:700:A:ARG:N	4	1.46	0.38	1.36
(1,1)	1:681:A:ASP:C	1:682:A:THR:N	1:682:A:THR:CA	1:682:A:THR:C	3	2.19	0.33	2.28
(1,18)	1:690:A:ARG:N	1:690:A:ARG:CA	1:690:A:ARG:C	1:691:A:LYS:N	3	1.75	0.45	1.78
(1,32)	1:699:A:SER:C	1:700:A:ARG:N	1:700:A:ARG:CA	1:700:A:ARG:C	2	1.69	0.22	1.69
(1,20)	1:691:A:LYS:N	1:691:A:LYS:CA	1:691:A:LYS:C	1:692:A:ALA:N	2	1.44	0.43	1.44
(1,26)	1:696:A:ALA:C	1:697:A:VAL:N	1:697:A:VAL:CA	1:697:A:VAL:C	2	1.41	0.01	1.41

¹ Number of violated models, ²Standard deviation, All angle values are in degree (°)

10.5 All violated dihedral-angle restraints [i](#)

10.5.1 Histogram : Distribution of violations [i](#)

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



10.5.2 Table: All violated dihedral-angle restraints [i](#)

The following table provides the list of violations for 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.

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,1)	1:681:A:ASP:C	1:682:A:THR:N	1:682:A:THR:CA	1:682:A:THR:C	14	2.54
(1,18)	1:690:A:ARG:N	1:690:A:ARG:CA	1:690:A:ARG:C	1:691:A:LYS:N	17	2.29
(1,2)	1:682:A:THR:N	1:682:A:THR:CA	1:682:A:THR:C	1:683:A:GLU:N	18	2.28
(1,1)	1:681:A:ASP:C	1:682:A:THR:N	1:682:A:THR:CA	1:682:A:THR:C	9	2.28
(1,11)	1:686:A:TYR:C	1:687:A:SER:N	1:687:A:SER:CA	1:687:A:SER:C	3	2.2
(1,31)	1:699:A:SER:N	1:699:A:SER:CA	1:699:A:SER:C	1:700:A:ARG:N	8	2.07
(1,8)	1:685:A:VAL:N	1:685:A:VAL:CA	1:685:A:VAL:C	1:686:A:TYR:N	11	2.07
(1,19)	1:690:A:ARG:C	1:691:A:LYS:N	1:691:A:LYS:CA	1:691:A:LYS:C	1	1.97
(1,32)	1:699:A:SER:C	1:700:A:ARG:N	1:700:A:ARG:CA	1:700:A:ARG:C	10	1.92
(1,19)	1:690:A:ARG:C	1:691:A:LYS:N	1:691:A:LYS:CA	1:691:A:LYS:C	16	1.9