

wwPDB NMR Structure Validation Summary Report (i)

Nov 8, 2023 – 03:22 AM EST

PDB ID	:	6UCO
BMRB ID	:	30673
Title	:	Backbone-modified variant of zinc finger 2 from the transcription factor Sp1
		DNA binding domain: BTD in the metal-binding turn
Authors	:	Rao, S.R.; Horne, W.S.
Deposited on	:	2019-09-17

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 (i) 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 (1)) were used in the production of this report:

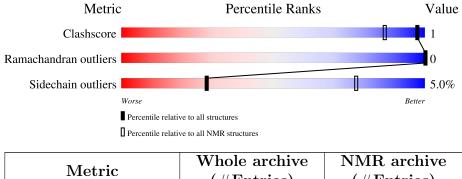
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Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (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)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $SOLUTION\ NMR$

The overall completeness of chemical shifts assignment is 46%.

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	(# Entries)	(#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 <=5%

Mol	Chain	Length	Quality of chain		
		20			
	А	32	69%	•	28%



2 Ensemble composition and analysis (i)

This entry contains 10 models. Model 5 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:3-A:3, A:5-A:7, A:9-A:27	0.19	5			
(23)						

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	2, 3, 4, 9, 10		
2	5, 6, 8		
3	1, 7		



3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 525 atoms, of which 260 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called Transcription factor Sp1.

Mol	Chain	Residues	Atoms				Trace		
1	٨	20	Total	С	Н	Ν	0	S	1
	А	-∂ <i>2</i>	524	162	260	56	43	3	

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	4	NLE	MET	conflict	UNP P08047
А	8	NVA	SER	conflict	UNP P08047
А	9	CYS	TYR	conflict	UNP P08047
А	32	NH2	-	amidation	UNP P08047

• Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	
0	Δ	1	Total Zn	
	A	1	1 1	

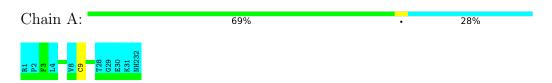


4 Residue-property plots (i)

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: Transcription factor Sp1



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

The representative model is number 5. Colouring as in section 4.1 above.

• Molecule 1: Transcription factor Sp1

Chain A:	66%	6%	28%
R1 F3 V8 C9 C9	R25 128 128 630 830 831 NH232 NH232		



5 Refinement protocol and experimental data overview (i)

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

Of the 10 calculated structures, 10 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
ARIA	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	215
Number of shifts mapped to atoms	215
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	46%



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: NH2, NLE, ZN, NVA

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	А	201	189	189	0 ± 0
All	All	2020	1890	1890	2

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.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
Atom-1	At0111-2	Clash(A)	Distance(A)	Worst	Total
1:A:3:PHE:CE1	1:A:17:SER:HB3	0.41	2.51	7	1
1:A:17:SER:O	1:A:21:GLN:HG2	0.40	2.15	6	1

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

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	Percer	ntiles
1	А	23/32~(72%)	$21 \pm 1 (91 \pm 3\%)$	$2\pm1 (9\pm3\%)$	0±0 (0±0%)	100	100
All	All	230/320~(72%)	210 (91%)	20 (9%)	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 side chain 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 side chain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	А	22/27~(81%)	21 ± 0 (95 $\pm1\%$)	$1\pm0 (5\pm1\%)$	28 77	
All	All	220/270 (81%)	209~(95%)	11 (5%)	28 77	

All 2 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	А	9	CYS	10
1	А	18	ASP	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)

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with |Z| > 2 is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.



Mol	Turne	Chain	Dec	Tiple	Bond lengths		
	Tybe	Chain	nes	es Link	Counts	RMSZ	#Z>2
1	NLE	А	4	1	6,7,8	$0.53 {\pm} 0.01$	0±0 (0±0%)
1	NVA	А	8	1	$5,\!6,\!7$	$0.51 {\pm} 0.03$	0±0 (0±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with |Z| > 2 is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Dog	Link	Bond angles		
	туре	Ullaili	nes	LIIIK	Counts	RMSZ	#Z>2
1	NLE	А	4	1	2,7,9	$0.47 {\pm} 0.01$	0±0 (0±0%)
1	NVA	А	8	1	2,6,8	$0.60 {\pm} 0.08$	0±0 (0±0%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	NLE	А	4	1	-	$0\pm 0,5,6,8$	-
1	NVA	А	8	1	-	$0\pm0,4,5,7$	-

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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 46% for the well-defined parts and 46% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *starch_output*

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	215
Number of shifts mapped to atoms	215
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

7.1.2 Chemical shift referencing (i)

No chemical shift referencing corrections were calculated (not enough data).

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 46%, i.e. 156 atoms were assigned a chemical shift out of a possible 339. 0 out of 1 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^{1}\mathrm{H}$	$^{13}\mathbf{C}$	$^{15}\mathbf{N}$
Backbone	46/116~(40%)	46/47~(98%)	0/46~(0%)	0/23~(0%)
Sidechain	91/177~(51%)	91/111~(82%)	0/51~(0%)	0/15~(0%)
Aromatic	19/46~(41%)	19/24~(79%)	0/19~(0%)	0/3~(0%)
Overall	156/339~(46%)	156/182~(86%)	0/116~(0%)	0/41~(0%)



7.1.4 Statistically unusual chemical shifts (i)

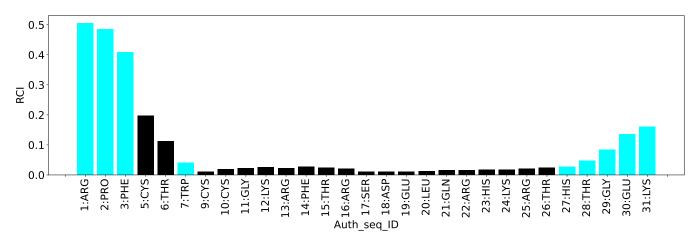
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	А	27	HIS	HB3	1.07	1.18 - 4.91	-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 (i)

8.1 Conformationally restricting restraints (i)

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	559
Intra-residue (i-j =0)	272
Sequential (i-j =1)	106
Medium range ($ i-j >1$ and $ i-j <5$)	60
Long range $(i-j \ge 5)$	91
Inter-chain	0
Hydrogen bond restraints	30
Disulfide bond restraints	0
Total dihedral-angle restraints	8
Number of unmapped restraints	0
Number of restraints per residue	17.2
Number of long range restraints per residue ¹	3.0

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 (i)

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 (i)

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)	14.1	0.2
0.2-0.5 (Medium)	20.3	0.5
>0.5 (Large)	24.3	3.27



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 $(^{\circ})$	Average number of violations per model	Max ($^{\circ}$)
1.0-10.0 (Small)	0.2	1.45
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None



9 Distance violation analysis (i)

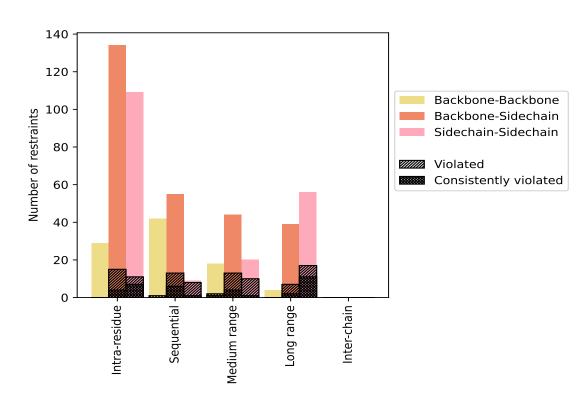
9.1 Summary of distance violations (i)

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.

Destroints trues	Count	$\%^1$	Vi	olated	3	Consis	tently	$\mathbf{Violated}^4$
Restraints type	Count	70-	Count	$\%^2$	$\%^1$	Count	$\%^2$	$\%^1$
Intra-residue (i-j =0)	272	48.7	26	9.6	4.7	11	4.0	2.0
Backbone-Backbone	29	5.2	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	134	24.0	15	11.2	2.7	4	3.0	0.7
Sidechain-Sidechain	109	19.5	11	10.1	2.0	7	6.4	1.3
Sequential (i-j =1)	106	19.0	22	20.8	3.9	7	6.6	1.3
Backbone-Backbone	42	7.5	1	2.4	0.2	0	0.0	0.0
Backbone-Sidechain	55	9.8	13	23.6	2.3	6	10.9	1.1
Sidechain-Sidechain	9	1.6	8	88.9	1.4	1	11.1	0.2
Medium range ($ i-j > 1 \& i-j < 5$)	60	10.7	17	28.3	3.0	4	6.7	0.7
Backbone-Backbone	18	3.2	2	11.1	0.4	1	5.6	0.2
Backbone-Sidechain	22	3.9	5	22.7	0.9	2	9.1	0.4
Sidechain-Sidechain	20	3.6	10	50.0	1.8	1	5.0	0.2
Long range $(i-j \ge 5)$	91	16.3	23	25.3	4.1	12	13.2	2.1
Backbone-Backbone	4	0.7	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	31	5.5	6	19.4	1.1	1	3.2	0.2
Sidechain-Sidechain	56	10.0	17	30.4	3.0	11	19.6	2.0
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	30	5.4	9	30.0	1.6	3	10.0	0.5
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	559	100.0	97	17.4	17.4	37	6.6	6.6
Backbone-Backbone	93	16.6	3	3.2	0.5	1	1.1	0.2
Backbone-Sidechain	272	48.7	48	17.6	8.6	16	5.9	2.9
Sidechain-Sidechain	194	34.7	46	23.7	8.2	20	10.3	3.6

 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)

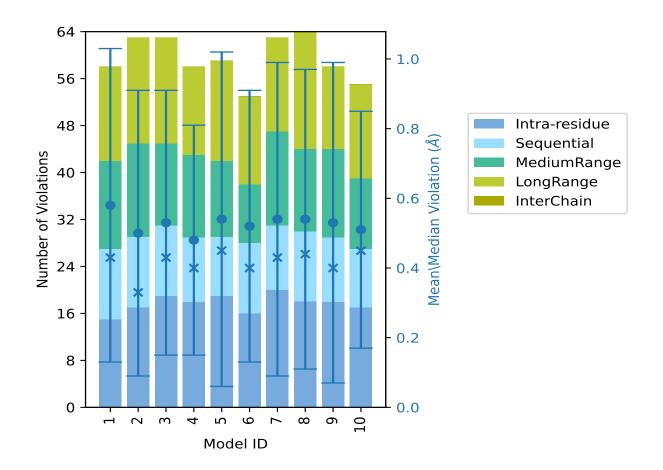
The following table provides the distance violation statistics for each model in the ensemble. Violations less than 0.1 Å are not included in the statistics.

Model ID		Nur	nber o	f viola	ations	5	Mean (Å)	Max (Å)	SD^6 (Å)	Median (Å)
Model ID	IR^1	SQ^2	MR^3	LR^4	$ IC^5 $	Total	Mean (A)	Max (A)	$SD^{*}(A)$	Median (A)
1	15	12	15	16	0	58	0.58	2.36	0.45	0.43
2	17	12	16	18	0	63	0.5	2.14	0.41	0.33
3	19	12	14	18	0	63	0.53	1.77	0.38	0.43
4	18	11	14	15	0	58	0.48	1.48	0.33	0.4
5	19	10	13	17	0	59	0.54	3.27	0.48	0.45
6	16	12	10	15	0	53	0.52	1.7	0.39	0.4
7	20	11	16	16	0	63	0.54	2.77	0.45	0.43
8	18	12	14	20	0	64	0.54	2.75	0.43	0.44
9	18	11	15	14	0	58	0.53	2.99	0.46	0.4
10	17	10	12	16	0	55	0.51	1.65	0.34	0.45

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



⁵Inter-chain restraints, ⁶Standard deviation



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

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

9.3 Distance violation statistics for the ensemble (i)

Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 441(IR:246, SQ:84, MR:43, LR:68, IC:0) restraints are not violated in the ensemble.

Nu	Number of violated restraints						Fraction of the ensemble		
IR^1	SQ^2	MR^3	LR^4	$ IC^5 $	Total	Count^6	%		
5	2	3	4	0	14	1	10.0		
2	6	2	2	0	12	2	20.0		
0	3	2	1	0	6	3	30.0		
1	0	1	1	0	3	4	40.0		

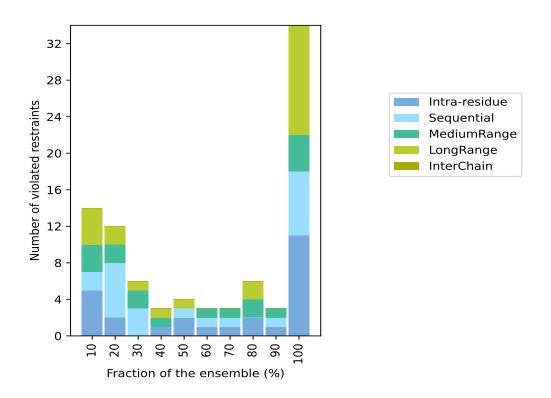
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Nu	mber	of vio	lated	Fraction of the ensemble			
IR^1	SQ^2	MR^3	LR^4	IC ⁵	Total	Count^6	%
2	1	0	1	0	4	5	50.0
1	1	1	0	0	3	6	60.0
1	1	1	0	0	3	7	70.0
2	0	2	2	0	6	8	80.0
1	1	1	0	0	3	9	90.0
11	7	4	12	0	34	10	100.0

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



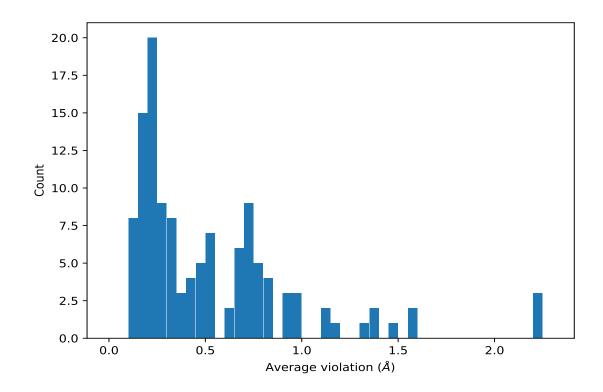
9.3.1 Bar graph : Distance violation statistics for the ensemble (i)

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	\mathbf{Models}^1	Mean (Å)	SD^1 (Å)	Median (Å)
(1,189)	1:14:A:PHE:HB3	1:3:A:PHE:HB3	10	1.49	0.17	1.49
(1,259)	1:20:A:LEU:HB3	1:14:A:PHE:HB3	10	1.33	0.09	1.31
(1,335)	1:20:A:LEU:HB3	1:14:A:PHE:HE1	10	1.15	0.08	1.14
(2,6)	1:3:A:PHE:HB2	1:20:A:LEU:HD13	10	0.94	0.12	0.94
(2,6)	1:3:A:PHE:HB2	1:20:A:LEU:HD11	10	0.94	0.12	0.94
(2,6)	1:3:A:PHE:HB2	1:20:A:LEU:HD12	10	0.94	0.12	0.94
(1,310)	1:13:A:ARG:HG2	1:12:A:LYS:HA	10	0.83	0.18	0.84
(1,246)	1:19:A:GLU:HG3	1:14:A:PHE:HB2	10	0.82	0.18	0.88
(1,246)	1:19:A:GLU:HG2	1:14:A:PHE:HB2	10	0.82	0.18	0.88
(1,70)	1:5:A:CYS:HB3	1:23:A:HIS:HD2	10	0.82	0.13	0.76
(1,251)	1:7:A:TRP:HB2	1:10:A:CYS:HB2	10	0.77	0.15	0.77
(1,147)	1:5:A:CYS:HB3	1:20:A:LEU:HD12	10	0.76	0.08	0.78
(1,147)	1:5:A:CYS:HB3	1:20:A:LEU:HD13	10	0.76	0.08	0.78
(1,147)	1:5:A:CYS:HB3	1:20:A:LEU:HD11	10	0.76	0.08	0.78
(1,2)	1:4:A:NLE:HG3	1:4:A:NLE:HD2	10	0.73	0.0	0.73

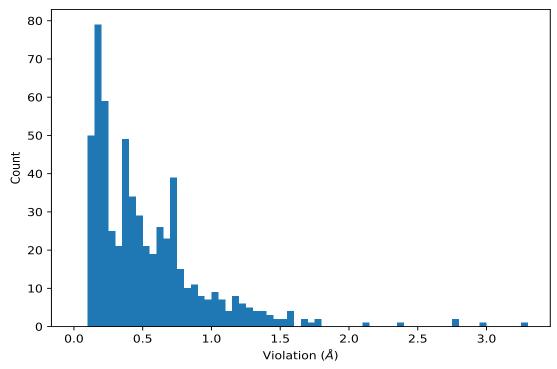


¹Number of violated models, ²Standard deviation

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)
(2,8)	1:24:A:LYS:HE2	1:20:A:LEU:HD12	5	3.27
(2,8)	1:24:A:LYS:HE2	1:20:A:LEU:HD11	9	2.99
(2,8)	1:24:A:LYS:HE2	1:20:A:LEU:HD11	7	2.77
(2,8)	1:24:A:LYS:HE2	1:20:A:LEU:HD11	8	2.75
(2,8)	1:24:A:LYS:HE2	1:20:A:LEU:HD11	1	2.36
(1,387)	1:27:A:HIS:HA	1:28:A:THR:HG22	2	2.14
(1,232)	1:12:A:LYS:HG3	1:14:A:PHE:HE1	1	1.79
(1,189)	1:14:A:PHE:HB3	1:3:A:PHE:HB3	3	1.77

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,232)	1:12:A:LYS:HG3	1:14:A:PHE:HE1	6	1.7
(1,189)	1:14:A:PHE:HB3	1:3:A:PHE:HB3	6	1.65



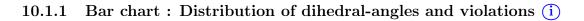
10 Dihedral-angle violation analysis (i)

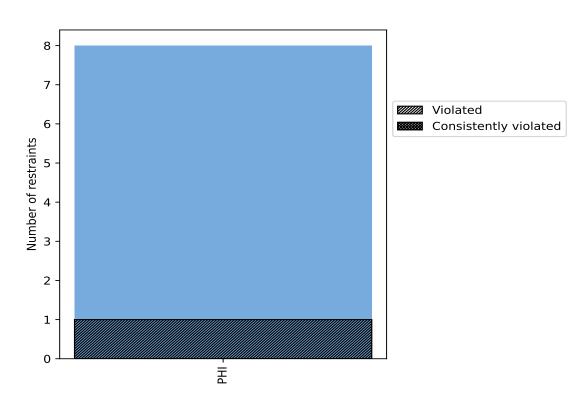
10.1 Summary of dihedral-angle violations (i)

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.

A	C		${f Violated^3}$			Consistently Violated ⁴		
Angle type	Count	$\%^1$	Count	$\%^2$	$\%^1$	Count	$\%^2$	$\%^1$
PHI	8	100.0	1	12.5	12.5	0	0.0	0.0
Total	8	100.0	1	12.5	12.5	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





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

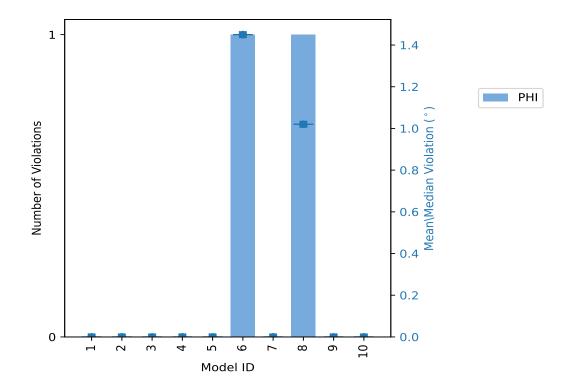


10.2 Dihedral-angle violation statistics for each model (i)

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	Num	ber of violations	Mean (°)	Max (°)	SD (°)	Median (°)
Model ID	PHI	Total	Mean ()	Max ()	SD ()	Median ()
1	0	0	0.0	0.0	0.0	0.0
2	0	0	0.0	0.0	0.0	0.0
3	0	0	0.0	0.0	0.0	0.0
4	0	0	0.0	0.0	0.0	0.0
5	0	0	0.0	0.0	0.0	0.0
6	1	1	1.45	1.45	0.0	1.45
7	0	0	0.0	0.0	0.0	0.0
8	1	1	1.02	1.02	0.0	1.02
9	0	0	0.0	0.0	0.0	0.0
10	0	0	0.0	0.0	0.0	0.0

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 \mathbf{y} axis on the right



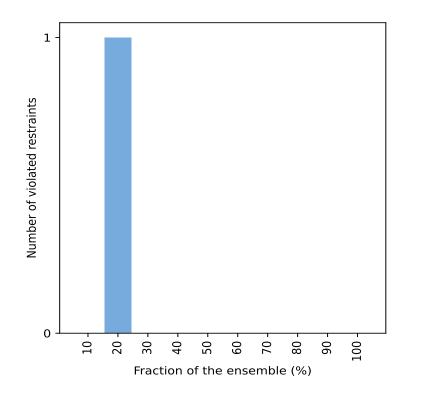
10.3 Dihedral-angle violation statistics for the ensemble (i)

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.

Num	ber of violated restraints	Fractio	n of the ensemble
PHI	Total	Count ¹	%
0	0	1	10.0
1	1	2	20.0
0	0	3	30.0
0	0	4	40.0
0	0	5	50.0
0	0	6	60.0
0	0	7	70.0
0	0	8	80.0
0	0	9	90.0
0	0	10	100.0

¹ Number of models with violations

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



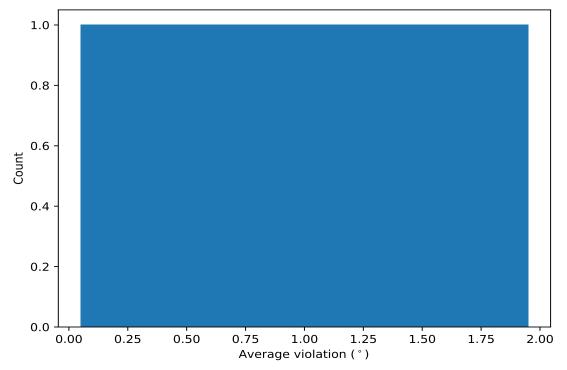


PHI

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	\mathbf{Models}^1	Mean	\mathbf{SD}^2	Median
(1,1)	1:2:A:PRO:C	1:3:A:PHE:N	1:3:A:PHE:CA	1:3:A:PHE:C	2	1.23	0.21	1.23

¹ Number of violated models, ²Standard deviation, All angle values are in degree ($^{\circ}$)

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.

Data insufficient to plot histogram



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

The following table lists the absolute value of the violation for each restraint in the ensemble sorted by its 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)	1:2:A:PRO:C	1:3:A:PHE:N	1:3:A:PHE:CA	1:3:A:PHE:C	6	1.45
(1,1)	1:2:A:PRO:C	1:3:A:PHE:N	1:3:A:PHE:CA	1:3:A:PHE:C	8	1.02

