

wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	7RY6
BMRB ID	:	30943
Title	:	Solution NMR structural bundle of the first cyclization domain from yersini-
		abactin synthetase (Cy1) impacted by dynamics
Authors	:	Kancherla, A.K.; Mishra, S.H.; Marincin, K.A.; Nerli, S.; Sgourakis, N.G.;
		Dowling, D.P.; Bouvignies, G.; Frueh, D.P.
Deposited on	:	2021-08-24

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:

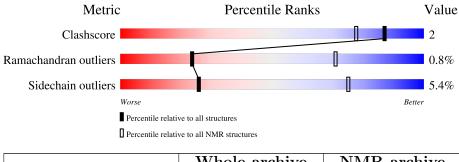
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.33

1 Overall quality at a glance (i)

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

The overall completeness of chemical shifts assignment is 52%.

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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f NMR} { m archive} \ (\#{ m Entries})$
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		
1	А	453	90%	•	8%



2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 1 is the overall representative, medoid model (most similar to other models).

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

Well-defined (core) protein residues							
Well-defined core	Residue rang	ge (total)	Backbone RMSD (Å)	Medoid model			
1	A:11-A:35, A:374-A:382, (417)	/	1.90	1			

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 4 single-model clusters were found.

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



3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 7223 atoms, of which 3560 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called HMWP2 nonribosomal peptide synthetase.

Mol	Chain	Residues	Atoms					Trace	
1	٨	452	Total	С	Н	Ν	0	S	0
	A	A 453 7223	2326	3560	658	663	16	0	

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	1	MET	-	initiating methionine	UNP A0A5P8YEQ8
А	446	LEU	-	expression tag	UNP A0A5P8YEQ8
А	447	GLU	-	expression tag	UNP A0A5P8YEQ8
А	448	HIS	-	expression tag	UNP A0A5P8YEQ8
А	449	HIS	-	expression tag	UNP A0A5P8YEQ8
А	450	HIS	-	expression tag	UNP A0A5P8YEQ8
А	451	HIS	-	expression tag	UNP A0A5P8YEQ8
А	452	HIS	-	expression tag	UNP A0A5P8YEQ8
А	453	HIS	-	expression tag	UNP A0A5P8YEQ8

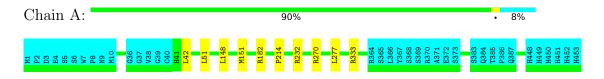


4 Residue-property plots (i)

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.

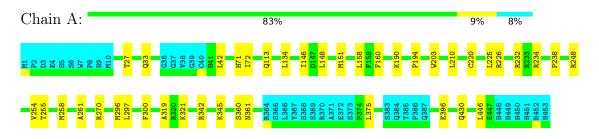
• Molecule 1: HMWP2 nonribosomal peptide synthetase



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

The representative model is number 1. Colouring as in section 4.1 above.

• Molecule 1: HMWP2 nonribosomal peptide synthetase





5 Refinement protocol and experimental data overview (i)

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

Of the 500 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
CYANA	structure calculation	3.98.13
CNS	refinement	1.3

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	3219
Number of shifts mapped to atoms	3219
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	52%



6 Model quality (i)

6.1 Standard geometry (i)

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	3378	3307	3288	13 ± 4
All	All	67560	66140	65760	268

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 2.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models		
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total	
1:A:245:PHE:HE2	1:A:432:CYS:HG	0.68	1.31	16	1	
1:A:391:ASP:HB3	1:A:406:ASP:HB3	0.62	1.70	16	1	
1:A:180:ASP:HB2	1:A:182:ARG:HG2	0.62	1.69	15	5	
1:A:245:PHE:HB2	1:A:432:CYS:SG	0.61	2.35	18	2	
1:A:293:VAL:HA	1:A:296:MET:HB3	0.57	1.77	7	1	

5 of 225 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	P	erce	ntiles
1	А	417/453~(92%)	$392\pm3(94\pm1\%)$	$21 \pm 3 (5 \pm 1\%)$	$3\pm1~(1\pm0\%)$		24	71
All	All	8340/9060~(92%)	7849 (94%)	428 (5%)	63 (1%)		24	71

5 of 28 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	А	374	PRO	7
1	А	66	ARG	5
1	А	51	LEU	5
1	А	300	PHE	4
1	А	21	VAL	4

6.3.2 Protein sidechains (i)

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	361/393~(92%)	$341 \pm 4 \ (95 \pm 1\%)$	$20{\pm}4~(5{\pm}1\%)$	26 75
All	All	7220/7860~(92%)	6827~(95%)	393~(5%)	26 75

5 of 141 unique residues with a non-rotameric side chain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	А	232	ARG	11
1	А	42	LEU	10
1	А	151	MET	9
1	А	342	ARG	9
1	А	333	ARG	9

6.3.3 RNA (i)

There are no RNA molecules in this entry.



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

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

6.5 Carbohydrates (i)

There are no monosaccharides in this entry.

6.6 Ligand geometry (i)

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 52% for the well-defined parts and 51% 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	3219
Number of shifts mapped to atoms	3219
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	3

The following errors were found when reading this chemical shift list.

• Chemical shift has been reported more than once. First 5 (of 0) occurrences are reported below.

	Chain	Dec	Trune	Atom		Shift Dat	a
List ID	Chain	Res	Type	Atom	Value	Uncertainty	Ambiguity
1	А	274	LEU	HD13	1.071	0.020	•
1	А	318	LEU	HD11	0.729	0.020	•
1	А	318	LEU	HD12	0.729	0.020	•
1	А	318	LEU	HD13	0.729	0.020	•
1	А	166	LEU	HD11	0.841	0.020	•
1	А	166	LEU	HD12	0.841	0.020	•
1	А	166	LEU	HD13	0.841	0.020	•
1	А	210	LEU	HD11	1.028	0.020	•
1	А	210	LEU	HD12	1.028	0.020	•
1	А	210	LEU	HD13	1.028	0.020	•
1	А	225	LEU	HD11	0.733	0.020	•
1	А	225	LEU	HD12	0.733	0.020	•
1	А	225	LEU	HD13	0.733	0.020	•
1	А	83	LEU	HD11	0.787	0.020	

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List ID	Chain	Res Type	Atom	Shift Data			
	Chain	nes	Type	Atom	Value	Uncertainty	Ambiguity
1	А	83	LEU	HD12	0.787	0.020	•
1	А	83	LEU	HD13	0.787	0.020	•
1	А	393	LEU	HD11	0.774	0.020	•
1	А	393	LEU	HD12	0.774	0.020	•
1	А	393	LEU	HD13	0.774	0.020	•

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7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	$\textbf{Correction} \pm \textbf{precision}, \textit{ppm}$	Suggested action
$^{13}C_{\alpha}$	426	0.34 ± 0.06	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	399	0.99 ± 0.10	Should be checked
$^{13}C'$	420	0.07 ± 0.05	None needed (< 0.5 ppm)
¹⁵ N	381	0.23 ± 0.14	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 52%, i.e. 3078 atoms were assigned a chemical shift out of a possible 5877. 0 out of 81 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^{1}\mathrm{H}$	$^{13}\mathrm{C}$	$^{15}\mathbf{N}$
Backbone	1914/2050~(93%)	745/826~(90%)	805/834~(97%)	364/390~(93%)
Sidechain	1122/3251~(35%)	567/2122~(27%)	555/996~(56%)	0/133~(0%)
Aromatic	42/576~(7%)	31/283~(11%)	0/243~(0%)	11/50~(22%)
Overall	3078/5877~(52%)	1343/3231~(42%)	1360/2073~(66%)	375/573~(65%)

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.

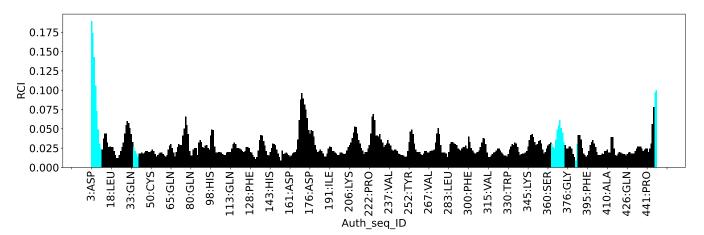
List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	А	292	ALA	Н	12.18	5.31 - 11.08	6.9
1	А	10	MET	Н	11.73	5.39 - 11.10	6.1
1	А	68	PRO	CA	54.76	55.85 - 70.84	-5.7



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	4848
Intra-residue (i-j =0)	324
Sequential (i-j =1)	1016
Medium range ($ i-j >1$ and $ i-j <5$)	1348
Long range $(i-j \ge 5)$	1574
Inter-chain	0
Hydrogen bond restraints	586
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	10.7
Number of long range restraints per residue ¹	3.7

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 (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)	89.8	0.2
0.2-0.5 (Medium)	189.5	0.5
>0.5 (Large)	84.5	1.12



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 (i)

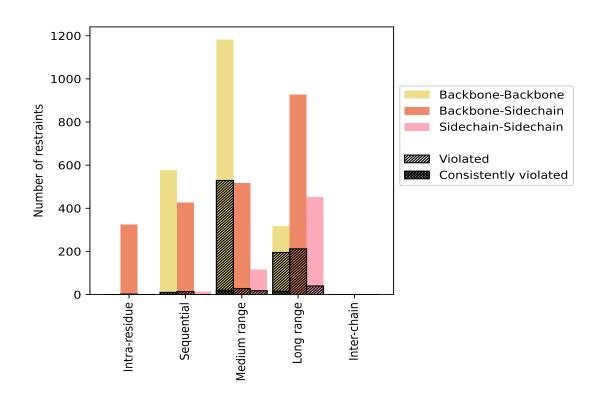
9.1 Summary of distance violations (i)

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 type	Count	$\%^1$	${f Violated}^3$			Consis	tently	V Violated ⁴
Restraints type	Count		Count	$\%^2$	$\%^{1}$	Count	$\%^2$	$\%^1$
Intra-residue (i-j =0)	324	6.7	2	0.6	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	324	6.7	2	0.6	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sequential (i-j =1)	1016	21.0	24	2.4	0.5	2	0.2	0.0
Backbone-Backbone	576	11.9	10	1.7	0.2	2	0.3	0.0
Backbone-Sidechain	426	8.8	14	3.3	0.3	0	0.0	0.0
Sidechain-Sidechain	14	0.3	0	0.0	0.0	0	0.0	0.0
Medium range ($ i-j > 1 \& i-j < 5$)	1348	27.8	184	13.6	3.8	6	0.4	0.1
Backbone-Backbone	716	14.8	138	19.3	2.8	6	0.8	0.1
Backbone-Sidechain	516	10.6	28	5.4	0.6	0	0.0	0.0
Sidechain-Sidechain	116	2.4	18	15.5	0.4	0	0.0	0.0
Long range $(i-j \ge 5)$	1574	32.5	352	22.4	7.3	2	0.1	0.0
Backbone-Backbone	196	4.0	100	51.0	2.1	2	1.0	0.0
Backbone-Sidechain	926	19.1	212	22.9	4.4	0	0.0	0.0
Sidechain-Sidechain	452	9.3	40	8.8	0.8	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	586	12.1	486	82.9	10.0	27	4.6	0.6
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	4848	100.0	1048	21.6	21.6	37	0.8	0.8
Backbone-Backbone	2074	42.8	734	35.4	15.1	37	1.8	0.8
Backbone-Sidechain	2192	45.2	256	11.7	5.3	0	0.0	0.0
Sidechain-Sidechain	582	12.0	58	10.0	1.2	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.

Madal ID		Nun	nber o	f viola	ations	5	Mean (Å)	Mor (Å)	SD^6 (Å)	Median (Å)
Model ID	IR^1	SQ^2	MR^3	LR^4	$ IC^5 $	Total	Mean (A)	Max (Å)	$SD^{*}(A)$	Median (A)
1	0	2	220	134	0	356	0.36	0.95	0.19	0.31
2	0	4	208	140	0	352	0.38	1.01	0.22	0.32
3	2	2	206	124	0	334	0.37	0.96	0.19	0.33
4	2	4	219	143	0	368	0.37	1.03	0.21	0.31
5	0	2	231	146	0	379	0.36	1.03	0.2	0.32
6	0	2	221	127	0	350	0.35	1.01	0.2	0.29
7	0	6	215	137	0	358	0.38	1.12	0.21	0.34
8	2	4	226	131	0	363	0.37	1.04	0.2	0.32
9	2	2	223	137	0	364	0.37	0.93	0.19	0.34
10	0	2	230	154	0	386	0.36	1.0	0.2	0.32
11	0	4	231	140	0	375	0.36	1.02	0.21	0.32

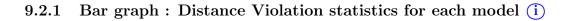
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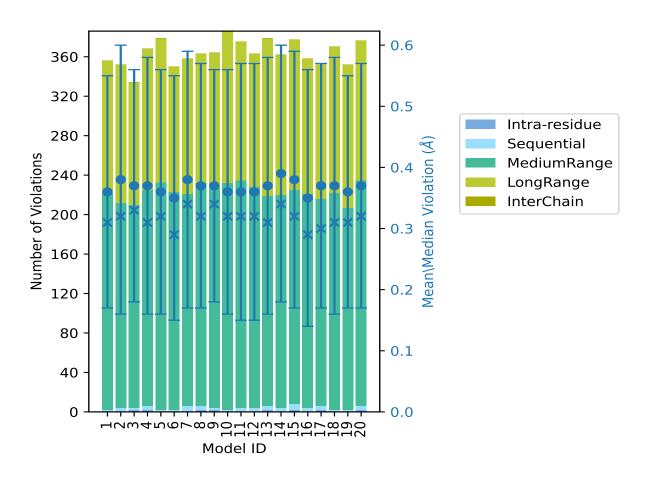


Madal ID		Nun	nber o	f viola	ations	5	Mean (Å)	Mar (Å)	\mathbf{SD}^{6} (Å)	Median (Å)
Model ID	IR^{1}	SQ^2	MR^3	LR^4	$ IC^5 $	Total		Max (Å)		
12	0	4	224	135	0	363	0.36	1.08	0.21	0.32
13	2	4	213	160	0	379	0.37	1.04	0.21	0.31
14	0	4	216	142	0	362	0.39	1.0	0.21	0.34
15	2	6	217	152	0	377	0.38	1.08	0.21	0.32
16	0	4	217	137	0	358	0.35	1.01	0.21	0.29
17	2	4	210	136	0	352	0.37	1.12	0.2	0.3
18	0	2	220	148	0	370	0.37	1.03	0.21	0.31
19	0	2	205	145	0	352	0.36	0.87	0.19	0.31
20	2	4	229	141	0	376	0.37	0.89	0.2	0.32

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 1 Intra-residue restraints, 2 Sequential restraints, 3 Medium range restraints, 4 Long range restraints, 5 Inter-chain restraints, 6 Standard deviation





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, 3700(IR:322, SQ:992, MR:1164, LR:1222, IC:0) restraints are not violated in the ensemble.

Nu	Number of violated restraints						n of the ensemble
IR^1	SQ^2	MR^3	LR ⁴	IC ⁵	Total	Count^6	%
0	16	62	120	0	198	1	5.0
0	6	32	50	0	88	2	10.0
0	0	14	46	0	60	3	15.0
0	0	16	26	0	42	4	20.0
0	0	4	12	0	16	5	25.0
0	0	0	6	0	6	6	30.0
0	0	6	8	0	14	7	35.0
2	0	4	12	0	18	8	40.0
0	0	10	10	0	20	9	45.0
0	0	10	4	0	14	10	50.0
0	0	2	12	0	14	11	55.0
0	0	2	4	0	6	12	60.0
0	0	0	2	0	2	13	65.0
0	0	6	6	0	12	14	70.0
0	0	4	4	0	8	15	75.0
0	0	0	6	0	6	16	80.0
0	0	6	10	0	16	17	85.0
0	0	0	6	0	6	18	90.0
0	0	0	6	0	6	19	95.0
0	2	6	2	0	10	20	100.0

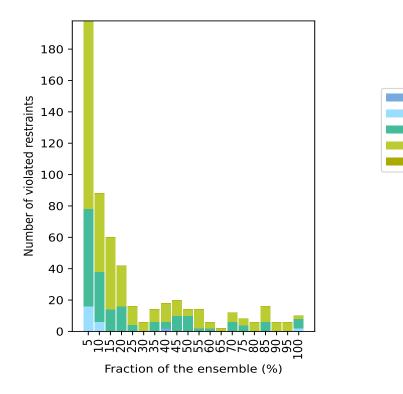
 1 Intra-residue restraints, 2 Sequential restraints, 3 Medium range restraints, 4 Long range restraints, 5 Inter-chain restraints, 6 Number of models with violations



Intra-residue

Sequential MediumRange

LongRange InterChain



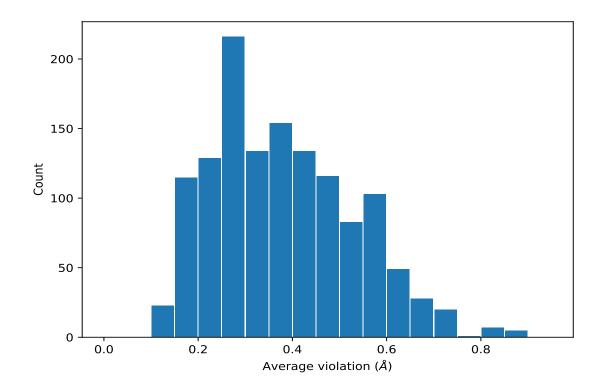
9.3.1 Bar graph : Distance violation statistics for the ensemble (i)

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)
(2,92)	1:A:253:GLY:H	1:A:257:THR:H	20	0.85	0.15	0.84
(5,92)	1:A:253:GLY:H	1:A:257:THR:H	20	0.85	0.15	0.84
(6,254)	1:A:92:THR:O	1:A:132:LEU:N	20	0.83	0.14	0.84
(6,253)	1:A:92:THR:O	1:A:132:LEU:H	20	0.73	0.16	0.76
(6,287)	1:A:393:LEU:O	1:A:404:GLN:N	20	0.71	0.07	0.72
(6,242)	1:A:73:ALA:N	1:A:81:VAL:O	20	0.68	0.06	0.7
(2,114)	1:A:278:LEU:H	1:A:306:LEU:H	20	0.66	0.15	0.68
(5,114)	1:A:278:LEU:H	1:A:306:LEU:H	20	0.66	0.15	0.68
(6,244)	1:A:75:ARG:N	1:A:79:GLN:O	20	0.65	0.11	0.68
(6,14)	1:A:359:THR:N	1:A:392:HIS:O	20	0.64	0.14	0.66

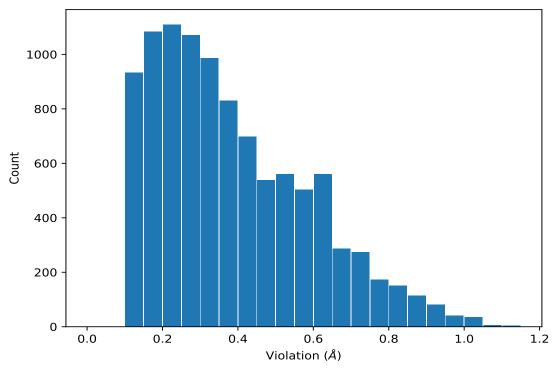
 $^1\mathrm{Number}$ of violated models, $^2\mathrm{Standard}$ deviation



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)
(5,3)	1:A:11:THR:H	1:A:186:LEU:H	7	1.12
(5,163)	1:A:213:ALA:H	1:A:346:ARG:H	17	1.12
(2,3)	1:A:11:THR:H	1:A:186:LEU:H	7	1.12
(2,163)	1:A:213:ALA:H	1:A:346:ARG:H	17	1.12
(5,92)	1:A:253:GLY:H	1:A:257:THR:H	12	1.08
(5,30)	1:A:95:ASP:H	1:A:107:TYR:H	15	1.08
(2,92)	1:A:253:GLY:H	1:A:257:THR:H	12	1.08
(2,30)	1:A:95:ASP:H	1:A:107:TYR:H	15	1.08
(5,30)	1:A:95:ASP:H	1:A:107:TYR:H	12	1.05
(2,30)	1:A:95:ASP:H	1:A:107:TYR:H	12	1.05



10 Dihedral-angle violation analysis (i)

Dihedral angle analysis failed due to data error in the dihedral angle restraints, possibly missing target value

