

wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	2LXO
BMRB ID	:	18684
Title	:	Identification of the Structural Traits Mediating the Antimicrobial Activity of
		a Chimeric Peptide of HBD2 and HBD3
Authors	:	Spudy, B.; Soennichsen, F.D.; Waetzig, G.H.; Grotzinger, J.; Jung, S.
Deposited on	:	2012-08-30
Authors	:	a Chimeric Peptide of HBD2 and HBD3 Spudy, B.; Soennichsen, F.D.; Waetzig, G.H.; Grotzinger, J.; Jung, S.

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:

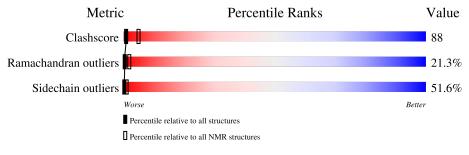
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 34%.

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	44	5%	34%	25%	7%	30%



2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 9 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:6-A:11, A:18-A:42 (31) 0.73 9						

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

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

The models can be grouped into 2 clusters. No single-model clusters were found.

Cluster number	Models
1	$\begin{array}{c} 1, 2, 4, 5, 6, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, \\ 19, 20 \end{array}$
2	3, 7



3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 704 atoms, of which 360 are hydrogens and 0 are deuteriums.

• Molecule 1 is a protein called Chimeric Peptide.

Mol	Chain	Residues	Atoms				Trace		
1	۸	4.4	Total	С	Η	Ν	Ο	S	0
	A	44	704	219	360	66	53	6	0



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: Chimeric Peptide

Chain A: 5%	34%	25% 79	% 30%
61 12 13 13 13 13 14 13 13 13 13 13 13 13 13 13 13 13 13 13	V13 R14 R14 A16 117 C18 H19 P20 V21 V21 C23 C23 C23 P24 R26 R26	Y27 Y28 129 130 132 132 132 133 133 133 133 133 133 133	C41 K42 K43 P44

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

The representative model is number 9. Colouring as in section 4.1 above.

• Molecule 1: Chimeric Peptide

Chain A:	14%	23%	25%	9%	30%
61 12 13 13 15 15 16 16 17 17 17 17 17 17 17 17 17 17 17 17 17	K8 Y9 C11 R12 R12 V13 R14	615 117 117 117 117 117 117 117 117 117 1	R26 Y27 K28 K28 Q29 Q29 G31 T32 C33 C33 C33 C33 C33 C33 C33 C33 C33 C	K39 C40 C41 K42 K43 P44	



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *simulated annealing, torsion angle dynamics.*

Of the 200 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
CYANA	refinement	

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

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	144
Number of shifts mapped to atoms	144
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	34%



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	247	248	247	43 ± 6
All	All	4940	4960	4940	866

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 88.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models		
Atom-1	Atom-2	Clash(A)	Distance(A)	Worst	Total	
1:A:6:LEU:HD12	1:A:7:GLN:N	0.94	1.77	8	6	
1:A:34:GLY:C	1:A:35:LEU:HD13	0.89	1.87	20	2	
1:A:18:CYS:SG	1:A:38:THR:HG22	0.87	2.09	7	6	
1:A:6:LEU:HD21	1:A:30:ILE:HG22	0.86	1.47	10	2	
1:A:19:HIS:O	1:A:38:THR:HG23	0.82	1.74	8	6	

5 of 174 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	Percentiles
1	А	31/44~(70%)	$15\pm1 (48\pm4\%)$	$10\pm2~(31\pm5\%)$	7 ± 1 (21 $\pm4\%$)	0 2
All	All	620/880~(70%)	298 (48%)	190 (31%)	132 (21%)	0 2

5 of 13 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	8	LYS	20
1	А	24	PRO	20
1	А	27	TYR	20
1	А	28	LYS	20
1	А	9	TYR	12

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	28/38~(74%)	$14\pm1~(48\pm5\%)$	$14 \pm 1 (52 \pm 5\%)$	0 1
All	All	560/760~(74%)	271 (48%)	289 (52%)	0 1

5 of 23 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	8	LYS	20
1	А	10	TYR	20
1	А	22	PHE	20
1	А	27	TYR	20
1	А	39	LYS	20

6.3.3 RNA (i)

There are no RNA molecules in this entry.



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

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

6.5 Carbohydrates (i)

There are no monosaccharides in this entry.

6.6 Ligand geometry (i)

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 34% for the well-defined parts and 23% 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 (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	144
Number of shifts mapped to atoms	144
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)

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 34%, i.e. 144 atoms were assigned a chemical shift out of a possible 426. 0 out of 3 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^{1}\mathrm{H}$	$^{13}\mathrm{C}$	15 N
Backbone	56/152~(37%)	56/62~(90%)	0/62~(0%)	0/28~(0%)
Sidechain	77/229~(34%)	77/148~(52%)	0/69~(0%)	0/12~(0%)
Aromatic	11/45~(24%)	11/21~(52%)	0/22~(0%)	0/2~(0%)
Overall	144/426~(34%)	144/231~(62%)	0/153~(0%)	0/42~(0%)

7.1.4 Statistically unusual chemical shifts (i)

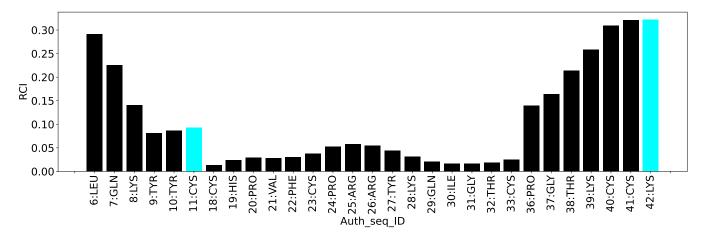
There are no statistically unusual chemical shifts.



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 (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	471
Intra-residue (i-j =0)	108
Sequential (i-j =1)	139
Medium range ($ i-j >1$ and $ i-j <5$)	75
Long range $(i-j \ge 5)$	125
Inter-chain	0
Hydrogen bond restraints	18
Disulfide bond restraints	6
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	3.2

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)	21.9	0.2
0.2-0.5 (Medium)	14.4	0.5
>0.5 (Large)	7.0	3.86



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)

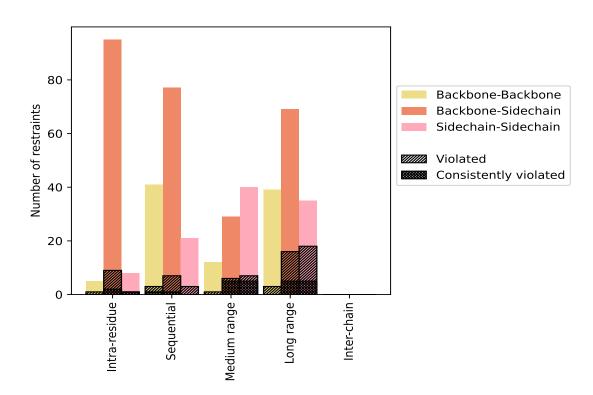
9.1 Summary of distance violations (i)

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	$\%^1$	Vi	olated	3	Consis	tently	$Violated^4$
Restraints type	Count	70	Count	$\%^2$	$\%^1$	Count	$\%^2$	$\%^1$
Intra-residue (i-j =0)	108	22.9	11	10.2	2.3	3	2.8	0.6
Backbone-Backbone	5	1.1	1	20.0	0.2	0	0.0	0.0
Backbone-Sidechain	95	20.2	9	9.5	1.9	2	2.1	0.4
Sidechain-Sidechain	8	1.7	1	12.5	0.2	1	12.5	0.2
Sequential (i-j =1)	139	29.5	13	9.4	2.8	2	1.4	0.4
Backbone-Backbone	41	8.7	3	7.3	0.6	1	2.4	0.2
Backbone-Sidechain	77	16.3	7	9.1	1.5	1	1.3	0.2
Sidechain-Sidechain	21	4.5	3	14.3	0.6	0	0.0	0.0
Medium range ($ i-j > 1 \& i-j < 5$)	75	15.9	9	12.0	1.9	6	8.0	1.3
Backbone-Backbone	12	2.5	1	8.3	0.2	0	0.0	0.0
Backbone-Sidechain	23	4.9	1	4.3	0.2	1	4.3	0.2
Sidechain-Sidechain	40	8.5	7	17.5	1.5	5	12.5	1.1
Long range $(i-j \ge 5)$	125	26.5	25	20.0	5.3	7	5.6	1.5
Backbone-Backbone	39	8.3	3	7.7	0.6	0	0.0	0.0
Backbone-Sidechain	57	12.1	8	14.0	1.7	2	3.5	0.4
Sidechain-Sidechain	29	6.2	14	48.3	3.0	5	17.2	1.1
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	18	3.8	13	72.2	2.8	7	38.9	1.5
Disulfide bond	6	1.3	4	66.7	0.8	0	0.0	0.0
Total	471	100.0	75	15.9	15.9	25	5.3	5.3
Backbone-Backbone	97	20.6	8	8.2	1.7	1	1.0	0.2
Backbone-Sidechain	270	57.3	38	14.1	8.1	13	4.8	2.8
Sidechain-Sidechain	104	22.1	29	27.9	6.2	11	10.6	2.3

 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.

MadalID	Number of violations						Maan (Å)	Mor (Å)	SD^6 (Å)	Madian (Å)
Model ID	IR^1	SQ^2	MR^3	LR^4	IC^5	Total	Mean (Å)	Max (Å)	$SD^{*}(A)$	Median (Å)
1	5	6	13	18	0	42	0.49	3.65	0.74	0.21
2	4	9	13	20	0	46	0.47	3.62	0.69	0.2
3	5	8	13	19	0	45	0.46	3.55	0.7	0.19
4	5	7	13	18	0	43	0.5	3.73	0.75	0.2
5	7	5	13	16	0	41	0.51	3.64	0.75	0.2
6	4	5	13	19	0	41	0.51	3.65	0.76	0.2
7	4	6	12	17	0	39	0.53	3.58	0.76	0.18
8	5	6	13	16	0	40	0.52	3.73	0.76	0.22
9	7	8	12	20	0	47	0.46	3.63	0.7	0.19
10	4	9	13	22	0	48	0.45	3.55	0.68	0.2
11	5	6	13	22	0	46	0.48	3.7	0.72	0.19

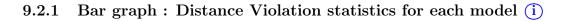
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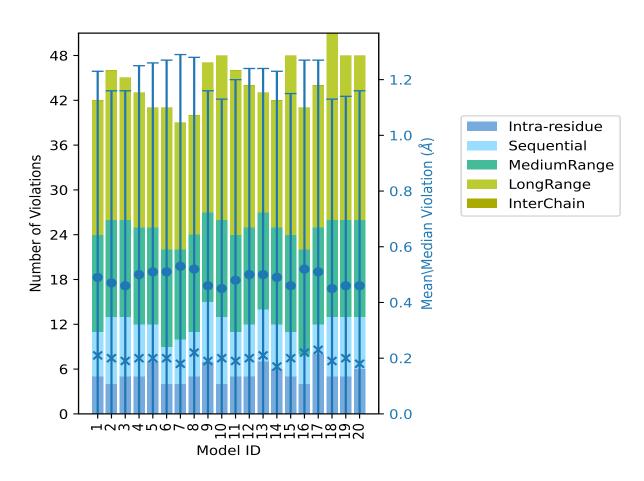


		Nun	nber o	f viola	ations	5	Mean (Å)	$M_{orr}(\lambda)$	SD^6 (Å)	Median (Å)
Model ID	IR^{1}	SQ^2	MR^3	LR^4	$ IC^5 $	Total	Mean (A)	Max (Å)	$SD^*(A)$	Median (A)
12	5	7	13	19	0	44	0.5	3.8	0.74	0.2
13	7	7	13	16	0	43	0.5	3.53	0.74	0.21
14	6	6	13	17	0	42	0.49	3.71	0.74	0.17
15	5	6	13	24	0	48	0.46	3.61	0.69	0.2
16	4	4	14	19	0	41	0.52	3.67	0.75	0.22
17	8	4	13	19	0	44	0.51	3.86	0.76	0.23
18	5	8	13	25	0	51	0.45	3.69	0.68	0.19
19	5	8	13	22	0	48	0.46	3.54	0.68	0.2
20	6	7	13	22	0	48	0.46	3.64	0.7	0.18

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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



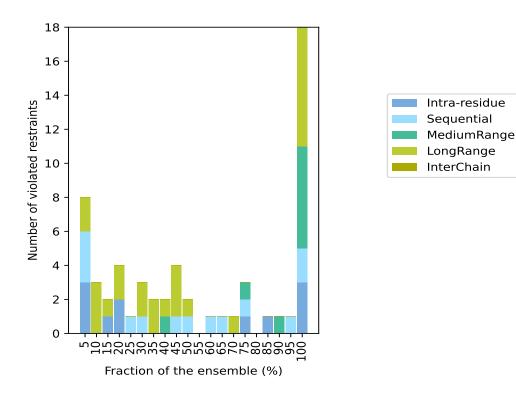
9.3 Distance violation statistics for the ensemble (i)

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, 389(IR:97, SQ:126, MR:66, LR:100, IC:0) restraints are not violated in the ensemble.

Nu	mber	of vio	lated	restra	aints	Fractio	n of the ensemble
IR^1	SQ^2	MR^3	LR ⁴	IC ⁵	Total	Count^6	%
3	3	0	2	0	8	1	5.0
0	0	0	3	0	3	2	10.0
1	0	0	1	0	2	3	15.0
2	0	0	2	0	4	4	20.0
0	1	0	0	0	1	5	25.0
0	1	0	2	0	3	6	30.0
0	0	0	2	0	2	7	35.0
0	0	1	1	0	2	8	40.0
0	1	0	3	0	4	9	45.0
0	1	0	1	0	2	10	50.0
0	0	0	0	0	0	11	55.0
0	1	0	0	0	1	12	60.0
0	1	0	0	0	1	13	65.0
0	0	0	1	0	1	14	70.0
1	1	1	0	0	3	15	75.0
0	0	0	0	0	0	16	80.0
1	0	0	0	0	1	17	85.0
0	0	1	0	0	1	18	90.0
0	1	0	0	0	1	19	95.0
3	2	6	7	0	18	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





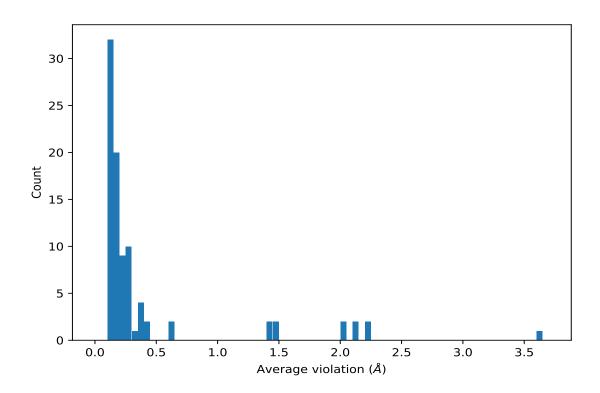
9.3.1 Bar graph : Distance violation statistics for the ensemble (i)

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)
(1,103)	1:27:A:TYR:HE1	1:39:A:LYS:H	20	3.65	0.08	3.64
(1,191)	1:24:A:PRO:HG2	1:27:A:TYR:HD1	20	2.24	0.04	2.24
(1,191)	1:24:A:PRO:HG3	1:27:A:TYR:HD1	20	2.24	0.04	2.24
(1,189)	1:24:A:PRO:HB2	1:27:A:TYR:HE1	20	2.13	0.04	2.12
(1,189)	1:24:A:PRO:HB3	1:27:A:TYR:HE1	20	2.13	0.04	2.12
(1,199)	1:27:A:TYR:HD1	1:39:A:LYS:HG2	20	2.01	0.16	2.01
(1,199)	1:27:A:TYR:HD1	1:39:A:LYS:HG3	20	2.01	0.16	2.01
(1,188)	1:24:A:PRO:HB2	1:27:A:TYR:HD1	20	1.48	0.03	1.48
(1,188)	1:24:A:PRO:HB3	1:27:A:TYR:HD1	20	1.48	0.03	1.48
(1,203)	1:27:A:TYR:HE1	1:41:A:CYS:HB2	20	1.42	0.14	1.48
(1,203)	1:27:A:TYR:HE1	1:41:A:CYS:HB3	20	1.42	0.14	1.48
(1,201)	1:27:A:TYR:HD1	1:41:A:CYS:HB2	20	0.64	0.06	0.64
(1,201)	1:27:A:TYR:HD1	1:41:A:CYS:HB3	20	0.64	0.06	0.64
(4,13)	1:35:A:LEU:O	1:38:A:THR:N	20	0.44	0.02	0.44
(4,16)	1:19:A:HIS:N	1:39:A:LYS:O	20	0.41	0.03	0.42
(4,17)	1:33:A:CYS:N	1:38:A:THR:O	20	0.39	0.05	0.4

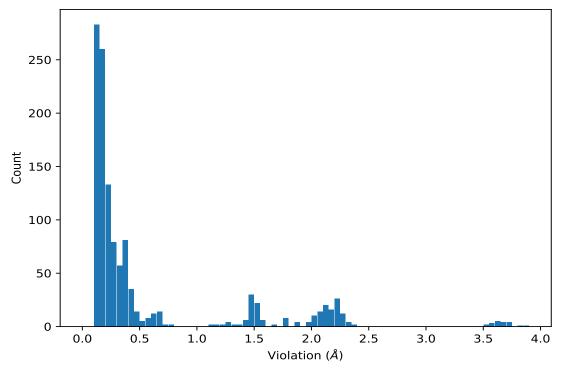


¹Number of violated models, ²Standard deviation

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)
(1,103)	1:27:A:TYR:HE1	1:39:A:LYS:H	17	3.86
(1,103)	1:27:A:TYR:HE1	1:39:A:LYS:H	12	3.8
(1,103)	1:27:A:TYR:HE1	1:39:A:LYS:H	4	3.73
(1,103)	1:27:A:TYR:HE1	1:39:A:LYS:H	8	3.73
(1,103)	1:27:A:TYR:HE1	1:39:A:LYS:H	14	3.71
(1,103)	1:27:A:TYR:HE1	1:39:A:LYS:H	11	3.7
(1,103)	1:27:A:TYR:HE1	1:39:A:LYS:H	18	3.69
(1,103)	1:27:A:TYR:HE1	1:39:A:LYS:H	16	3.67

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,103)	1:27:A:TYR:HE1	1:39:A:LYS:H	1	3.65
(1,103)	1:27:A:TYR:HE1	1:39:A:LYS:H	6	3.65



10 Dihedral-angle violation analysis (i)

No dihedral-angle restraints found

