



Full wwPDB NMR Structure Validation Report ⓘ

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PDB ID : 5O2M / pdb_00005o2m
BMRB ID : 34141
Title : p130Cas SH3 domain
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Deposited on : 2017-05-22

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
BMRB Restraints Analysis : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

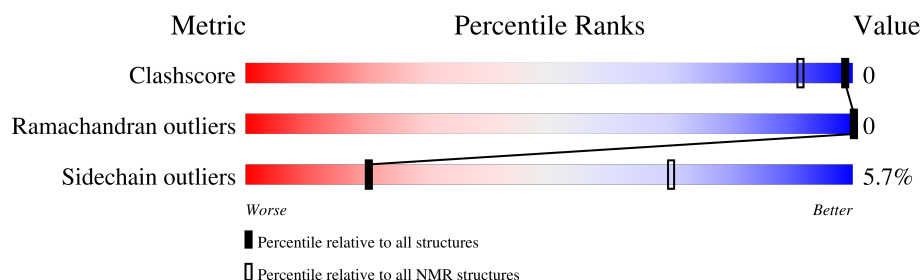
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 91%.

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	81	

2 Ensemble composition and analysis

This entry contains 40 models. Model 23 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:64 (59)	0.38	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 7 clusters and 4 single-model clusters were found.

Cluster number	Models
1	3, 4, 5, 11, 14, 19, 29, 31, 38
2	2, 15, 16, 21, 23, 25, 35, 36
3	6, 8, 12, 13, 20, 37
4	10, 24, 26, 39
5	27, 32, 33
6	7, 9, 18
7	17, 30, 34
Single-model clusters	1; 22; 28; 40

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1274 atoms, of which 639 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Breast cancer anti-estrogen resistance 1.

Mol	Chain	Residues	Atoms						Trace
1	A	81	Total	C	H	N	O	S	0
			1274	404	639	108	119	4	

There are 12 discrepancies between the modelled and reference sequences:

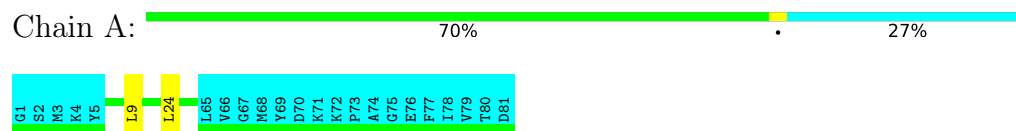
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP Q6P5Z4
A	2	SER	-	expression tag	UNP Q6P5Z4
A	3	MET	-	expression tag	UNP Q6P5Z4
A	4	LYS	-	expression tag	UNP Q6P5Z4
A	5	TYR	-	expression tag	UNP Q6P5Z4
A	37	ARG	GLN	conflict	UNP Q6P5Z4
A	76	GLU	-	expression tag	UNP Q6P5Z4
A	77	PHE	-	expression tag	UNP Q6P5Z4
A	78	ILE	-	expression tag	UNP Q6P5Z4
A	79	VAL	-	expression tag	UNP Q6P5Z4
A	80	THR	-	expression tag	UNP Q6P5Z4
A	81	ASP	-	expression tag	UNP Q6P5Z4

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

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

- Molecule 1: Breast cancer anti-estrogen resistance 1

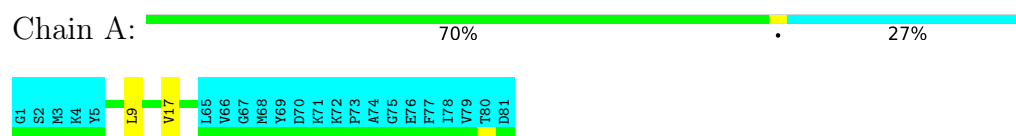


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

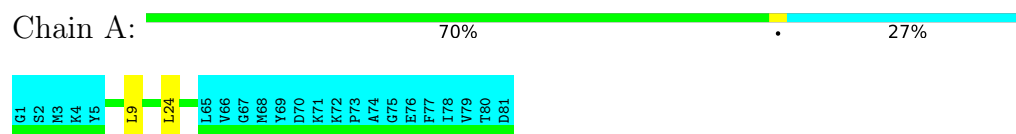
4.2.1 Score per residue for model 1

- Molecule 1: Breast cancer anti-estrogen resistance 1



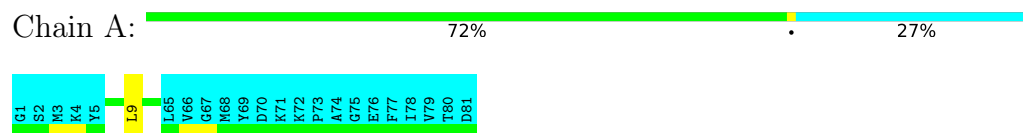
4.2.2 Score per residue for model 2

- Molecule 1: Breast cancer anti-estrogen resistance 1



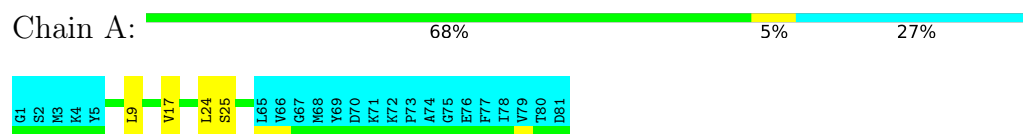
4.2.3 Score per residue for model 3

- Molecule 1: Breast cancer anti-estrogen resistance 1



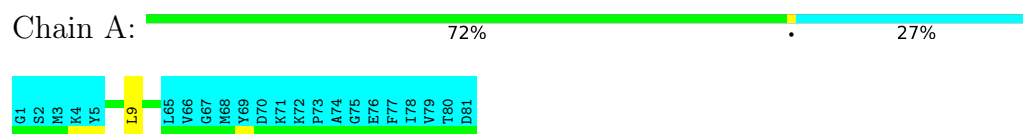
4.2.4 Score per residue for model 4

- Molecule 1: Breast cancer anti-estrogen resistance 1



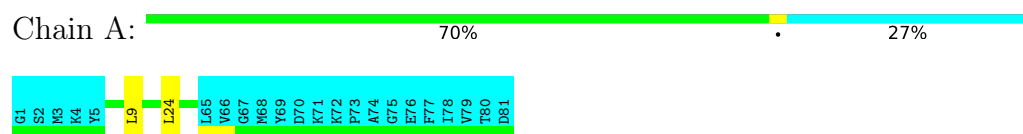
4.2.5 Score per residue for model 5

- Molecule 1: Breast cancer anti-estrogen resistance 1



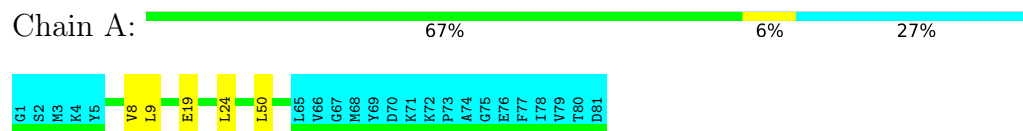
4.2.6 Score per residue for model 6

- Molecule 1: Breast cancer anti-estrogen resistance 1



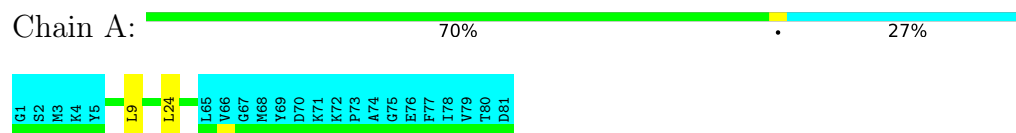
4.2.7 Score per residue for model 7

- Molecule 1: Breast cancer anti-estrogen resistance 1



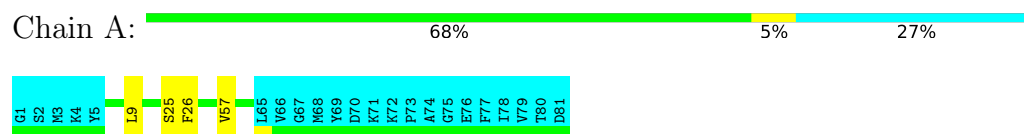
4.2.8 Score per residue for model 8

- Molecule 1: Breast cancer anti-estrogen resistance 1



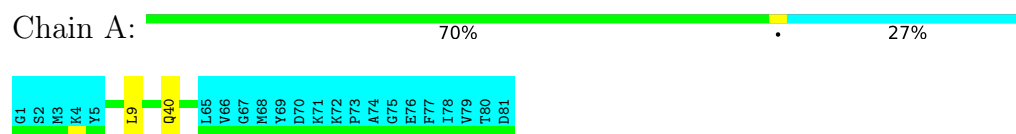
4.2.9 Score per residue for model 9

- Molecule 1: Breast cancer anti-estrogen resistance 1



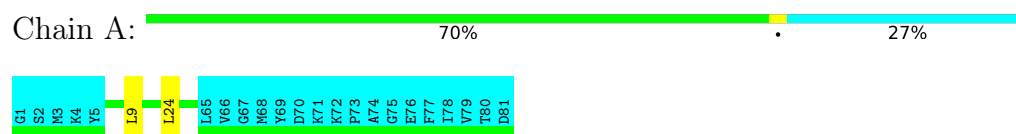
4.2.10 Score per residue for model 10

- Molecule 1: Breast cancer anti-estrogen resistance 1



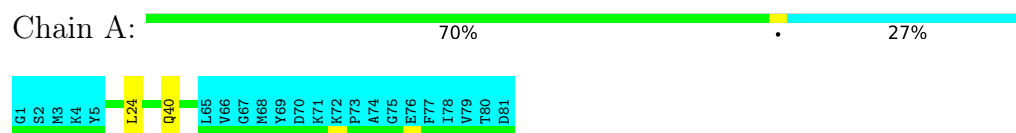
4.2.11 Score per residue for model 11

- Molecule 1: Breast cancer anti-estrogen resistance 1



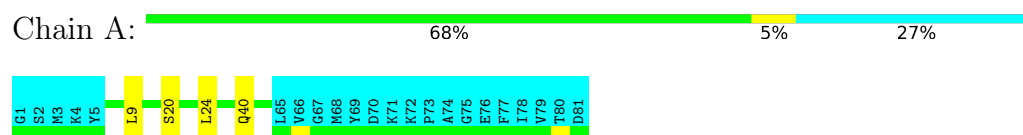
4.2.12 Score per residue for model 12

- Molecule 1: Breast cancer anti-estrogen resistance 1



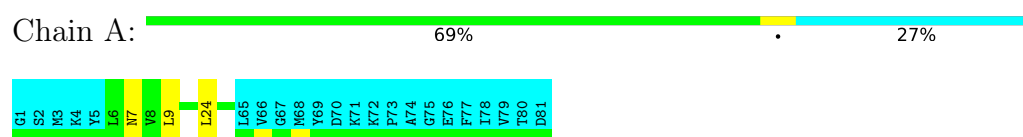
4.2.13 Score per residue for model 13

- Molecule 1: Breast cancer anti-estrogen resistance 1



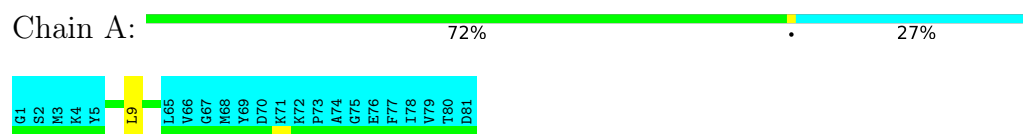
4.2.14 Score per residue for model 14

- Molecule 1: Breast cancer anti-estrogen resistance 1



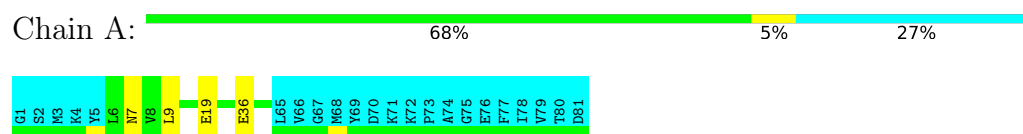
4.2.15 Score per residue for model 15

- Molecule 1: Breast cancer anti-estrogen resistance 1



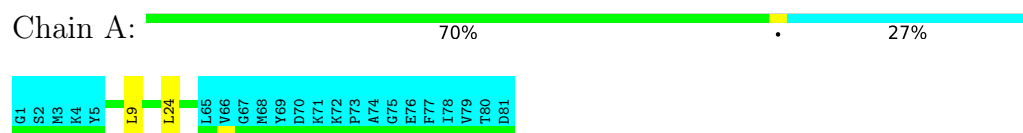
4.2.16 Score per residue for model 16

- Molecule 1: Breast cancer anti-estrogen resistance 1



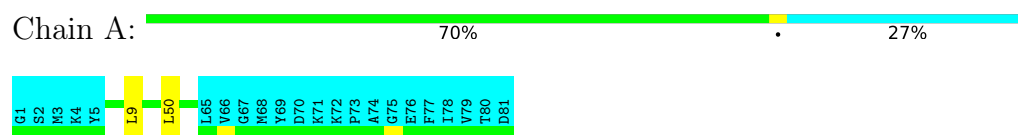
4.2.17 Score per residue for model 17

- Molecule 1: Breast cancer anti-estrogen resistance 1



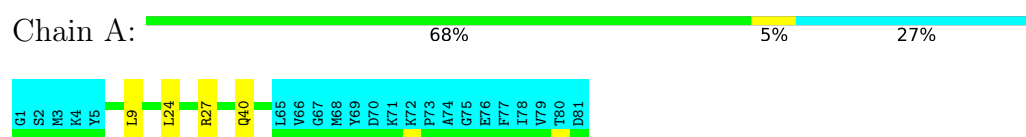
4.2.18 Score per residue for model 18

- Molecule 1: Breast cancer anti-estrogen resistance 1



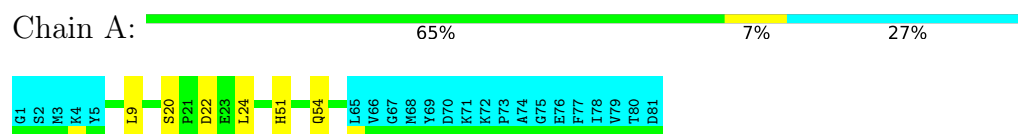
4.2.19 Score per residue for model 19

- Molecule 1: Breast cancer anti-estrogen resistance 1



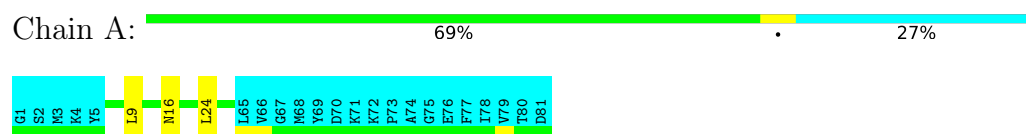
4.2.20 Score per residue for model 20

- Molecule 1: Breast cancer anti-estrogen resistance 1



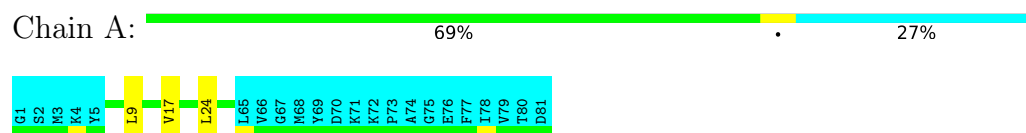
4.2.21 Score per residue for model 21

- Molecule 1: Breast cancer anti-estrogen resistance 1



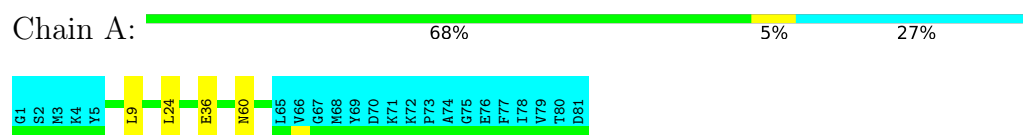
4.2.22 Score per residue for model 22

- Molecule 1: Breast cancer anti-estrogen resistance 1



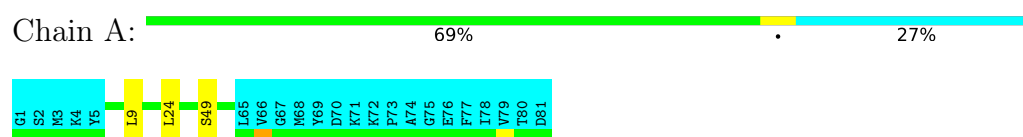
4.2.23 Score per residue for model 23 (medoid)

- Molecule 1: Breast cancer anti-estrogen resistance 1



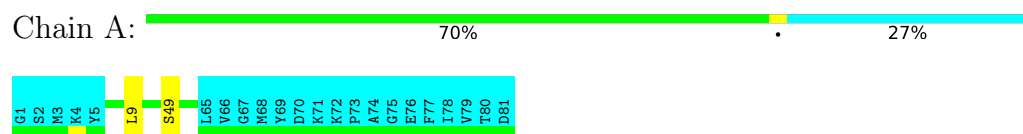
4.2.24 Score per residue for model 24

- Molecule 1: Breast cancer anti-estrogen resistance 1



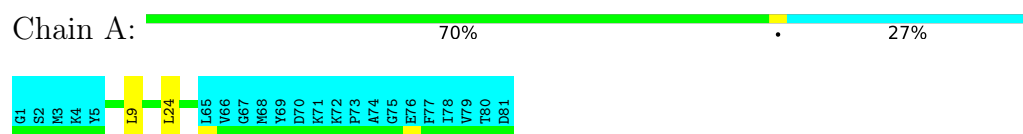
4.2.25 Score per residue for model 25

- Molecule 1: Breast cancer anti-estrogen resistance 1



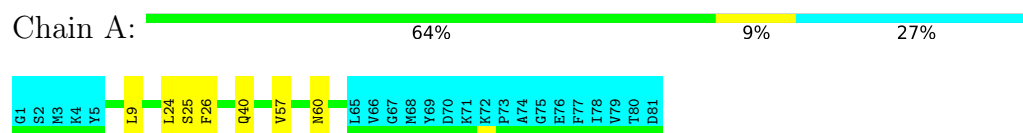
4.2.26 Score per residue for model 26

- Molecule 1: Breast cancer anti-estrogen resistance 1



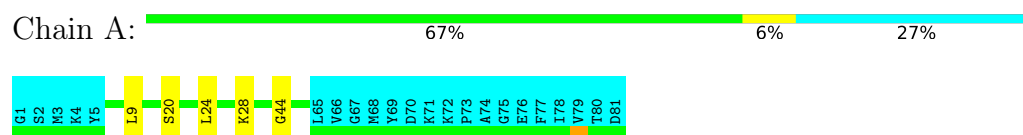
4.2.27 Score per residue for model 27

- Molecule 1: Breast cancer anti-estrogen resistance 1



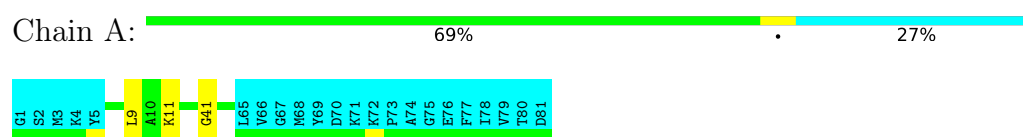
4.2.28 Score per residue for model 28

- Molecule 1: Breast cancer anti-estrogen resistance 1



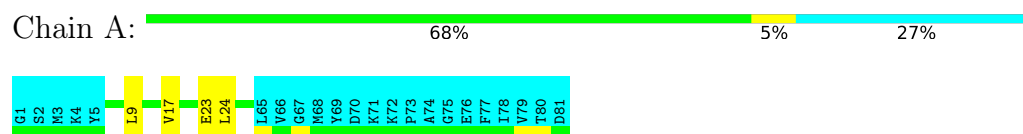
4.2.29 Score per residue for model 29

- Molecule 1: Breast cancer anti-estrogen resistance 1



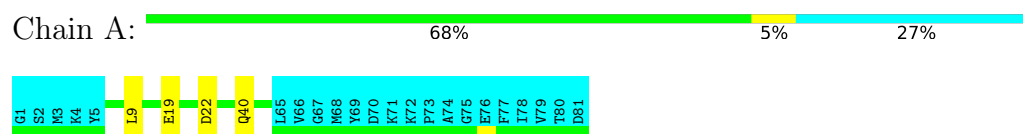
4.2.30 Score per residue for model 30

- Molecule 1: Breast cancer anti-estrogen resistance 1



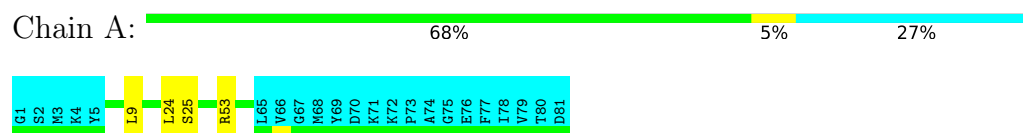
4.2.31 Score per residue for model 31

- Molecule 1: Breast cancer anti-estrogen resistance 1



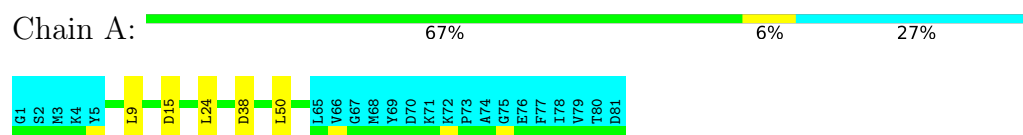
4.2.32 Score per residue for model 32

- Molecule 1: Breast cancer anti-estrogen resistance 1



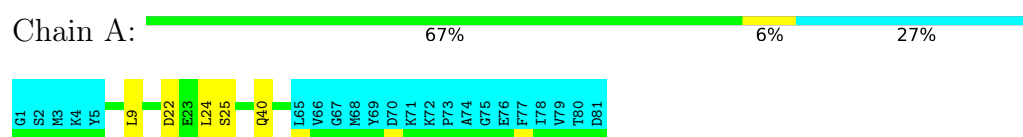
4.2.33 Score per residue for model 33

- Molecule 1: Breast cancer anti-estrogen resistance 1



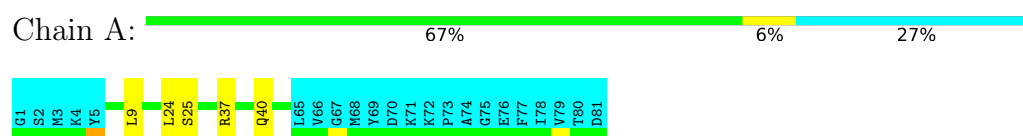
4.2.34 Score per residue for model 34

- Molecule 1: Breast cancer anti-estrogen resistance 1



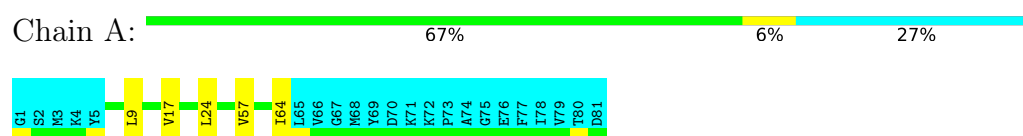
4.2.35 Score per residue for model 35

- Molecule 1: Breast cancer anti-estrogen resistance 1



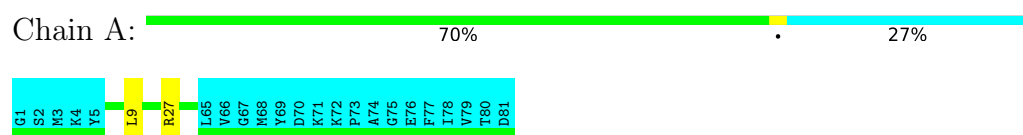
4.2.36 Score per residue for model 36

- Molecule 1: Breast cancer anti-estrogen resistance 1



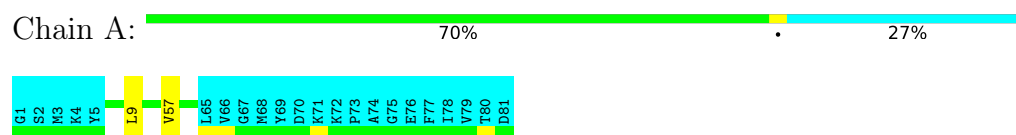
4.2.37 Score per residue for model 37

- Molecule 1: Breast cancer anti-estrogen resistance 1



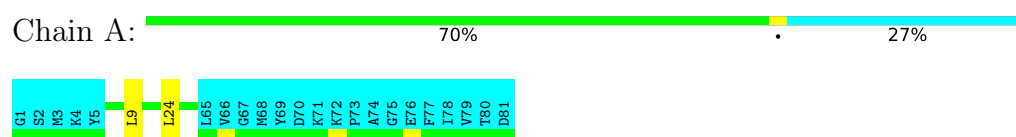
4.2.38 Score per residue for model 38

- Molecule 1: Breast cancer anti-estrogen resistance 1



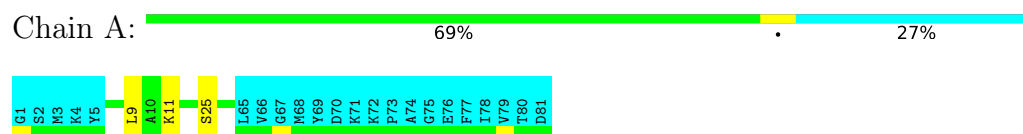
4.2.39 Score per residue for model 39

- Molecule 1: Breast cancer anti-estrogen resistance 1



4.2.40 Score per residue for model 40

- Molecule 1: Breast cancer anti-estrogen resistance 1



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 40 were deposited, based on the following criterion: *structures with the least restraint violations*.

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

Software name	Classification	Version
CYANA	structure calculation	
YASARA	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	965
Number of shifts mapped to atoms	965
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	91%

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	0.78±0.19	0±0/473 (0.0± 0.1%)	0.88±0.09	0±1/641 (0.0± 0.1%)
All	All	0.80	2/18920 (0.0%)	0.89	11/25640 (0.0%)

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	17	VAL	CA-CB	7.35	1.62	1.54	36	1
1	A	64	ILE	CA-CB	6.67	1.61	1.54	36	1

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	57	VAL	CA-C-N	-8.11	111.39	119.90	36	2
1	A	57	VAL	C-N-CA	-8.11	111.39	119.90	36	2
1	A	17	VAL	N-CA-C	-5.79	100.14	108.48	4	3
1	A	44	GLY	N-CA-C	-5.47	108.19	114.69	28	1
1	A	19	GLU	N-CA-C	-5.22	106.59	113.12	31	1
1	A	37	ARG	N-CA-C	-5.07	101.50	109.50	35	1
1	A	41	GLY	N-CA-C	-5.03	108.38	115.32	29	1

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	464	466	466	0±0
All	All	18560	18640	18640	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 0.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:26:PHE:CE1	1:A:57:VAL:HG13	0.45	2.47	27	2

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	59/81 (73%)	59±1 (100±1%)	0±1 (0±1%)	0±0 (0±0%)	100	100
All	All	2360/3240 (73%)	2350 (100%)	10 (0%)	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	50/68 (74%)	47±1 (94±3%)	3±1 (6±3%)	20	70
All	All	2000/2720 (74%)	1887 (94%)	113 (6%)	20	70

All 24 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	9	LEU	39
1	A	24	LEU	26
1	A	40	GLN	8
1	A	25	SER	7
1	A	50	LEU	3
1	A	20	SER	3
1	A	22	ASP	3
1	A	19	GLU	2
1	A	7	ASN	2
1	A	36	GLU	2
1	A	27	ARG	2
1	A	60	ASN	2
1	A	49	SER	2
1	A	11	LYS	2
1	A	8	VAL	1
1	A	51	HIS	1
1	A	54	GLN	1
1	A	16	ASN	1
1	A	28	LYS	1
1	A	17	VAL	1
1	A	23	GLU	1
1	A	53	ARG	1
1	A	15	ASP	1
1	A	38	ASP	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

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 91% for the well-defined parts and 87% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *wt_star.txt*

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	965
Number of shifts mapped to atoms	965
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	4

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
$^{13}\text{C}_\alpha$	79	-0.31 ± 0.13	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	71	0.07 ± 0.28	None needed (< 0.5 ppm)
$^{13}\text{C}'$	79	-0.04 ± 0.09	None needed (< 0.5 ppm)
^{15}N	74	0.08 ± 0.38	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 91%, i.e. 740 atoms were assigned a chemical shift out of a possible 815. 0 out of 13 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	295/297 (99%)	121/122 (99%)	118/118 (100%)	56/57 (98%)
Sidechain	411/468 (88%)	282/304 (93%)	125/144 (87%)	4/20 (20%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	34/50 (68%)	21/25 (84%)	11/22 (50%)	2/3 (67%)
Overall	740/815 (91%)	424/451 (94%)	254/284 (89%)	62/80 (78%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 87%, i.e. 965 atoms were assigned a chemical shift out of a possible 1105. 0 out of 16 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	388/408 (95%)	156/168 (93%)	158/162 (98%)	74/78 (95%)
Sidechain	536/619 (87%)	366/403 (91%)	166/193 (86%)	4/23 (17%)
Aromatic	41/78 (53%)	27/38 (71%)	12/37 (32%)	2/3 (67%)
Overall	965/1105 (87%)	549/609 (90%)	336/392 (86%)	80/104 (77%)

7.1.4 Statistically unusual chemical shifts ⓘ

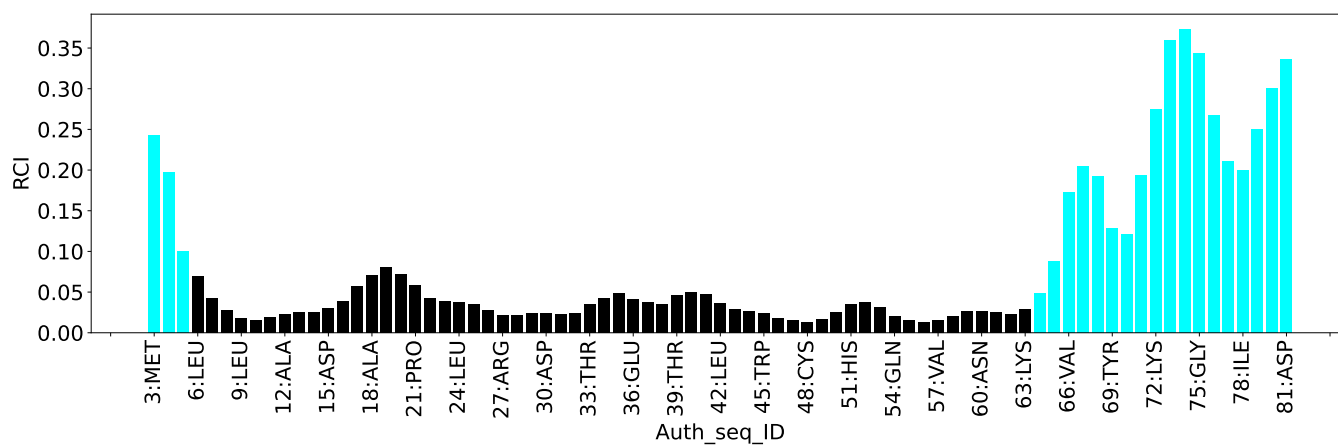
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	37	ARG	HG3	-0.25	0.15 – 2.94	-6.5
1	A	16	ASN	HB3	0.82	1.12 – 4.38	-5.9
1	A	59	GLY	HA2	1.86	2.15 – 5.77	-5.8
1	A	59	GLY	HA3	2.01	2.08 – 5.71	-5.2

7.1.5 Random Coil Index (RCI) plots ⓘ

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

Random coil index (RCI) for chain A:



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	1170
Intra-residue ($ i-j =0$)	212
Sequential ($ i-j =1$)	306
Medium range ($ i-j >1$ and $ i-j <5$)	122
Long range ($ i-j \geq 5$)	530
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	100
Number of unmapped restraints	0
Number of restraints per residue	15.7
Number of long range restraints per residue ¹	6.5

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)	3.2	0.2
0.2-0.5 (Medium)	2.1	0.5
>0.5 (Large)	None	None

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)	2.3	4.97
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis ⓘ

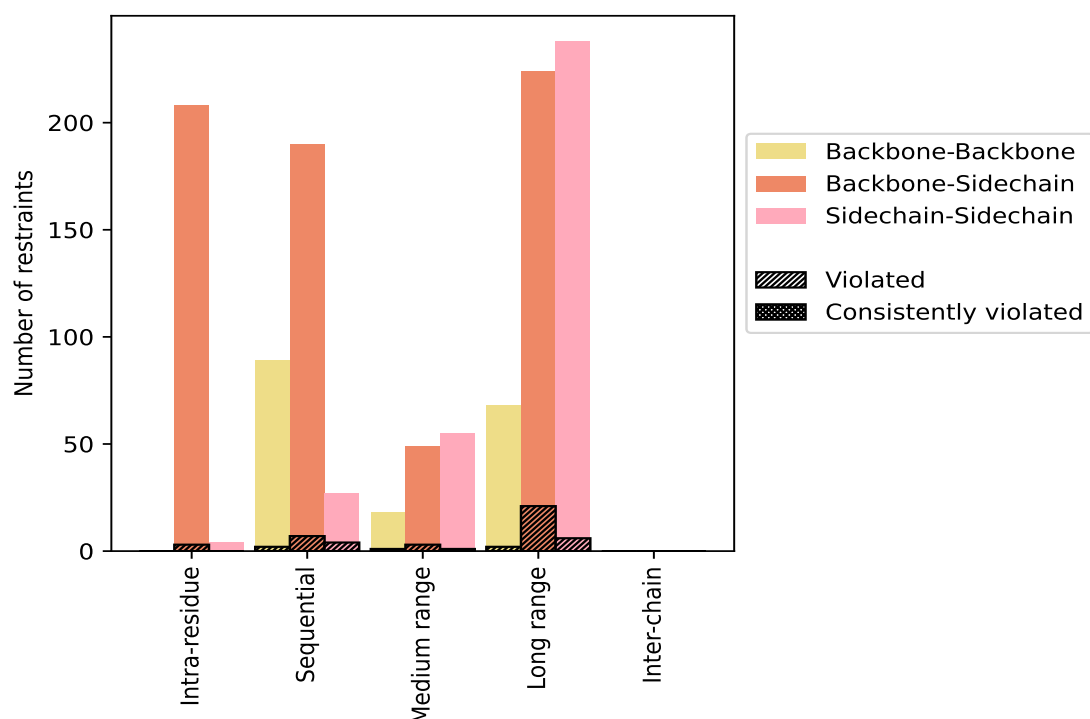
9.1 Summary of distance violations ⓘ

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)	212	18.1	3	1.4	0.3	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	208	17.8	3	1.4	0.3	0	0.0	0.0
Sidechain-Sidechain	4	0.3	0	0.0	0.0	0	0.0	0.0
Sequential (i-j =1)	306	26.2	13	4.2	1.1	0	0.0	0.0
Backbone-Backbone	89	7.6	2	2.2	0.2	0	0.0	0.0
Backbone-Sidechain	190	16.2	7	3.7	0.6	0	0.0	0.0
Sidechain-Sidechain	27	2.3	4	14.8	0.3	0	0.0	0.0
Medium range (i-j >1 & i-j <5)	122	10.4	5	4.1	0.4	0	0.0	0.0
Backbone-Backbone	18	1.5	1	5.6	0.1	0	0.0	0.0
Backbone-Sidechain	49	4.2	3	6.1	0.3	0	0.0	0.0
Sidechain-Sidechain	55	4.7	1	1.8	0.1	0	0.0	0.0
Long range (i-j ≥5)	530	45.3	29	5.5	2.5	0	0.0	0.0
Backbone-Backbone	68	5.8	2	2.9	0.2	0	0.0	0.0
Backbone-Sidechain	224	19.1	21	9.4	1.8	0	0.0	0.0
Sidechain-Sidechain	238	20.3	6	2.5	0.5	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	1170	100.0	50	4.3	4.3	0	0.0	0.0
Backbone-Backbone	175	15.0	5	2.9	0.4	0	0.0	0.0
Backbone-Sidechain	671	57.4	34	5.1	2.9	0	0.0	0.0
Sidechain-Sidechain	324	27.7	11	3.4	0.9	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	0	2	0	1	0	3	0.16	0.21	0.04	0.14
2	0	1	0	2	0	3	0.17	0.21	0.03	0.15
3	0	1	0	2	0	3	0.2	0.32	0.08	0.17
4	0	1	0	2	0	3	0.18	0.19	0.01	0.18
5	0	0	0	3	0	3	0.15	0.19	0.03	0.15
6	0	2	0	3	0	5	0.21	0.3	0.06	0.21
7	0	2	0	3	0	5	0.18	0.31	0.08	0.15
8	0	2	0	2	0	4	0.26	0.49	0.14	0.2
9	0	4	0	3	0	7	0.22	0.34	0.09	0.23
10	0	0	0	4	0	4	0.23	0.48	0.15	0.16

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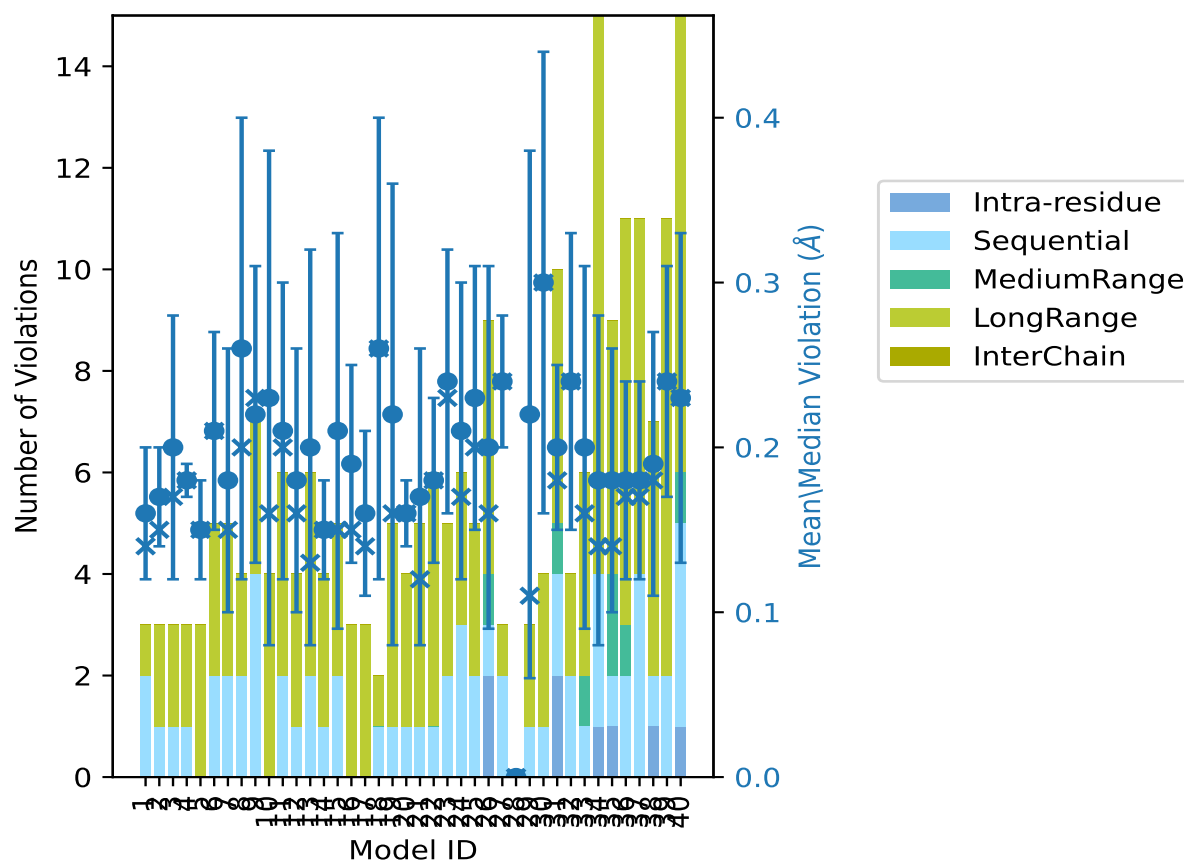
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	0	2	0	4	0	6	0.21	0.37	0.09	0.2
12	0	1	0	3	0	4	0.18	0.3	0.08	0.16
13	0	2	0	4	0	6	0.2	0.43	0.12	0.13
14	0	1	0	3	0	4	0.15	0.19	0.03	0.15
15	0	2	0	3	0	5	0.21	0.43	0.12	0.15
16	0	0	0	3	0	3	0.19	0.27	0.06	0.15
17	0	0	0	3	0	3	0.16	0.23	0.05	0.14
18	0	1	0	1	0	2	0.26	0.4	0.14	0.26
19	0	1	0	4	0	5	0.22	0.49	0.14	0.16
20	0	1	0	3	0	4	0.16	0.19	0.02	0.16
21	0	1	0	4	0	5	0.17	0.35	0.09	0.12
22	0	1	0	5	0	6	0.18	0.24	0.05	0.18
23	0	2	0	3	0	5	0.24	0.39	0.08	0.23
24	0	3	0	3	0	6	0.21	0.37	0.09	0.17
25	0	2	0	3	0	5	0.23	0.38	0.08	0.2
26	2	1	1	5	0	9	0.2	0.44	0.11	0.16
27	0	2	0	1	0	3	0.24	0.3	0.04	0.24
28	0	0	0	0	0	0	0.0	0.0	0.0	0.0
29	0	1	0	2	0	3	0.22	0.45	0.16	0.11
30	0	1	0	3	0	4	0.3	0.5	0.14	0.3
31	2	2	1	5	0	10	0.2	0.29	0.05	0.18
32	0	2	0	2	0	4	0.24	0.37	0.09	0.24
33	0	1	1	4	0	6	0.2	0.45	0.11	0.16
34	1	3	0	11	0	15	0.18	0.47	0.1	0.14
35	1	1	2	5	0	9	0.18	0.32	0.08	0.14
36	0	2	1	8	0	11	0.18	0.31	0.06	0.17
37	0	4	0	7	0	11	0.18	0.31	0.06	0.17
38	1	1	0	5	0	7	0.19	0.37	0.08	0.18
39	0	2	0	9	0	11	0.24	0.4	0.07	0.24
40	1	4	1	9	0	15	0.23	0.4	0.1	0.23

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, 1120(IR:209, SQ:293, MR:117, LR:501, 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	7	3	14	0	25	1	2.5
0	2	2	7	0	11	2	5.0
1	1	0	2	0	4	3	7.5
1	0	0	1	0	2	4	10.0
0	0	0	0	0	0	5	12.5
0	0	0	0	0	0	6	15.0

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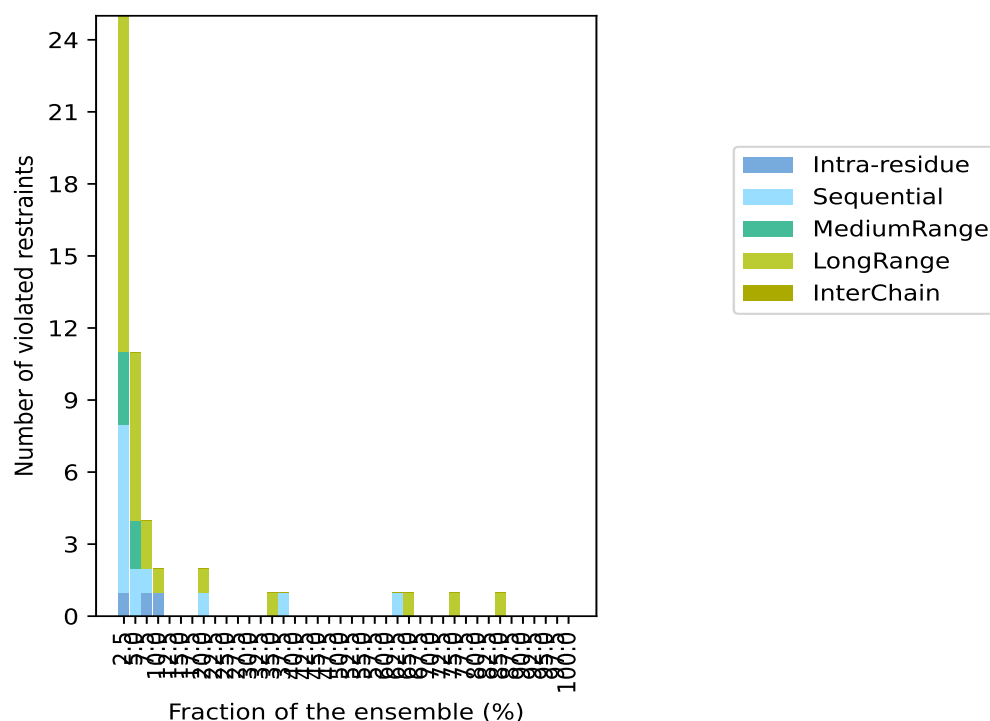
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Number of violated restraints						Fraction of the ensemble	
IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total	Count ⁶	%
0	0	0	0	0	0	7	17.5
0	1	0	1	0	2	8	20.0
0	0	0	0	0	0	9	22.5
0	0	0	0	0	0	10	25.0
0	0	0	0	0	0	11	27.5
0	0	0	0	0	0	12	30.0
0	0	0	0	0	0	13	32.5
0	0	0	1	0	1	14	35.0
0	1	0	0	0	1	15	37.5
0	0	0	0	0	0	16	40.0
0	0	0	0	0	0	17	42.5
0	0	0	0	0	0	18	45.0
0	0	0	0	0	0	19	47.5
0	0	0	0	0	0	20	50.0
0	0	0	0	0	0	21	52.5
0	0	0	0	0	0	22	55.0
0	0	0	0	0	0	23	57.5
0	0	0	0	0	0	24	60.0
0	1	0	0	0	1	25	62.5
0	0	0	1	0	1	26	65.0
0	0	0	0	0	0	27	67.5
0	0	0	0	0	0	28	70.0
0	0	0	0	0	0	29	72.5
0	0	0	1	0	1	30	75.0
0	0	0	0	0	0	31	77.5
0	0	0	0	0	0	32	80.0
0	0	0	0	0	0	33	82.5
0	0	0	1	0	1	34	85.0
0	0	0	0	0	0	35	87.5
0	0	0	0	0	0	36	90.0
0	0	0	0	0	0	37	92.5
0	0	0	0	0	0	38	95.0
0	0	0	0	0	0	39	97.5
0	0	0	0	0	0	40	100.0

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

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

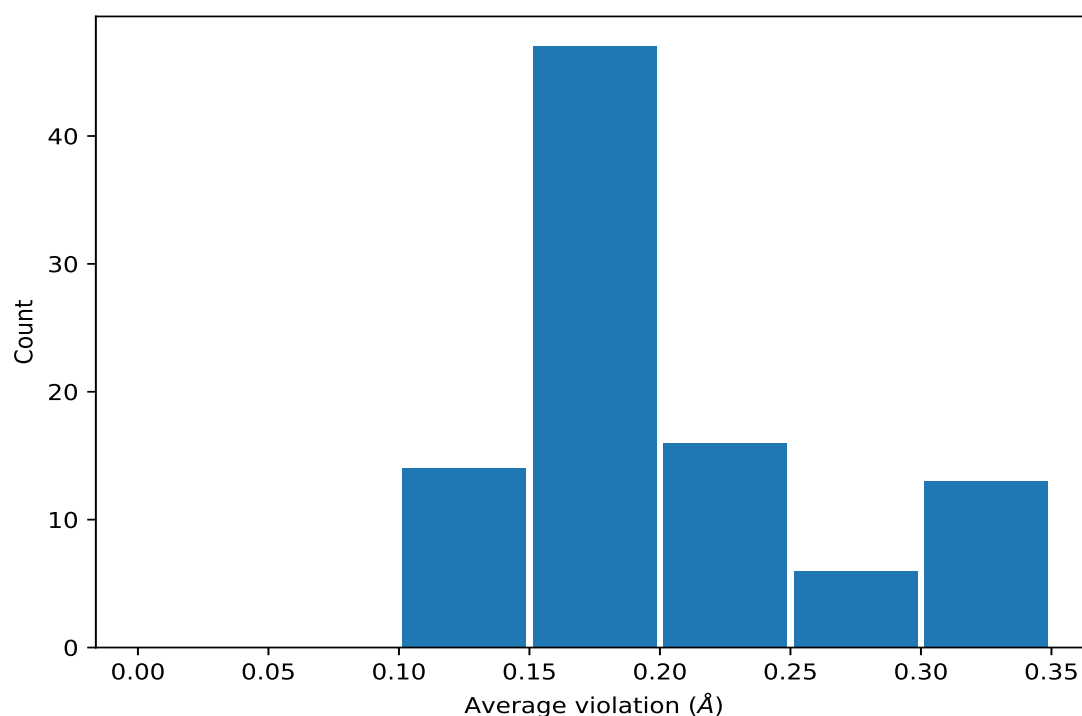
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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 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. 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)
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	34	0.29	0.1	0.3
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	34	0.29	0.1	0.3
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	34	0.29	0.1	0.3
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	34	0.29	0.1	0.3
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	34	0.29	0.1	0.3
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	34	0.29	0.1	0.3
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	30	0.16	0.04	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	30	0.16	0.04	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	30	0.16	0.04	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	30	0.16	0.04	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	30	0.16	0.04	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	30	0.16	0.04	0.15
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	26	0.19	0.09	0.16
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	26	0.19	0.09	0.16
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	26	0.19	0.09	0.16
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	25	0.3	0.1	0.27

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	25	0.3	0.1	0.27
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	25	0.3	0.1	0.27
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	25	0.3	0.1	0.27
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	25	0.3	0.1	0.27
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	25	0.3	0.1	0.27
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	25	0.3	0.1	0.27
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	25	0.3	0.1	0.27
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	25	0.3	0.1	0.27
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	25	0.3	0.1	0.27
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	25	0.3	0.1	0.27
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	25	0.3	0.1	0.27
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB2	15	0.21	0.03	0.21
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB3	15	0.21	0.03	0.21
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB2	15	0.21	0.03	0.21
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB3	15	0.21	0.03	0.21
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD11	14	0.15	0.05	0.14
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD12	14	0.15	0.05	0.14
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD13	14	0.15	0.05	0.14
(1,1014)	1:19:A:GLU:HG2	1:20:A:SER:HB2	8	0.2	0.08	0.18
(1,1014)	1:19:A:GLU:HG2	1:20:A:SER:HB3	8	0.2	0.08	0.18
(1,1014)	1:19:A:GLU:HG3	1:20:A:SER:HB2	8	0.2	0.08	0.18
(1,1014)	1:19:A:GLU:HG3	1:20:A:SER:HB3	8	0.2	0.08	0.18
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD11	8	0.17	0.06	0.16
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD12	8	0.17	0.06	0.16
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD13	8	0.17	0.06	0.16
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD21	8	0.17	0.06	0.16
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD22	8	0.17	0.06	0.16
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD23	8	0.17	0.06	0.16
(1,185)	1:31:A:ILE:H	1:31:A:ILE:HD11	4	0.16	0.02	0.16
(1,185)	1:31:A:ILE:H	1:31:A:ILE:HD12	4	0.16	0.02	0.16
(1,185)	1:31:A:ILE:H	1:31:A:ILE:HD13	4	0.16	0.02	0.16
(1,1142)	1:49:A:SER:HB2	1:54:A:GLN:H	4	0.16	0.04	0.14
(1,1142)	1:49:A:SER:HB3	1:54:A:GLN:H	4	0.16	0.04	0.14
(1,59)	1:12:A:ALA:H	1:31:A:ILE:HD11	3	0.17	0.07	0.13
(1,59)	1:12:A:ALA:H	1:31:A:ILE:HD12	3	0.17	0.07	0.13
(1,59)	1:12:A:ALA:H	1:31:A:ILE:HD13	3	0.17	0.07	0.13
(1,864)	1:71:A:LYS:HA	1:72:A:LYS:HD2	3	0.15	0.04	0.13
(1,864)	1:71:A:LYS:HA	1:72:A:LYS:HD3	3	0.15	0.04	0.13
(1,1049)	1:24:A:LEU:HD11	1:56:A:ILE:H	3	0.15	0.03	0.14
(1,1049)	1:24:A:LEU:HD12	1:56:A:ILE:H	3	0.15	0.03	0.14
(1,1049)	1:24:A:LEU:HD13	1:56:A:ILE:H	3	0.15	0.03	0.14
(1,1049)	1:24:A:LEU:HD21	1:56:A:ILE:H	3	0.15	0.03	0.14

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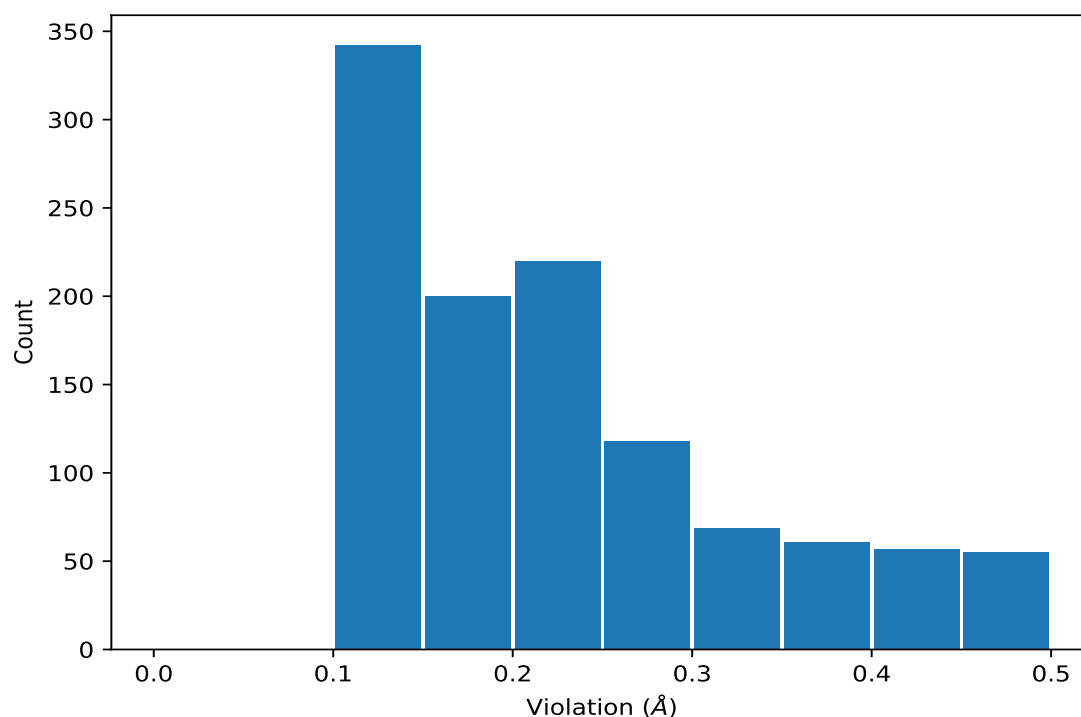
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,1049)	1:24:A:LEU:HD22	1:56:A:ILE:H	3	0.15	0.03	0.14
(1,1049)	1:24:A:LEU:HD23	1:56:A:ILE:H	3	0.15	0.03	0.14
(1,997)	1:16:A:ASN:H	1:16:A:ASN:HD21	3	0.12	0.01	0.12
(1,997)	1:16:A:ASN:H	1:16:A:ASN:HD22	3	0.12	0.01	0.12
(1,438)	1:9:A:LEU:HB2	1:32:A:MET:H	2	0.3	0.18	0.3
(1,86)	1:15:A:ASP:H	1:28:A:LYS:HE2	2	0.23	0.02	0.23
(1,86)	1:15:A:ASP:H	1:28:A:LYS:HE3	2	0.23	0.02	0.23
(1,894)	1:24:A:LEU:HD11	1:53:A:ARG:HD2	2	0.22	0.02	0.22
(1,894)	1:24:A:LEU:HD11	1:53:A:ARG:HD3	2	0.22	0.02	0.22
(1,894)	1:24:A:LEU:HD12	1:53:A:ARG:HD2	2	0.22	0.02	0.22
(1,894)	1:24:A:LEU:HD12	1:53:A:ARG:HD3	2	0.22	0.02	0.22
(1,894)	1:24:A:LEU:HD13	1:53:A:ARG:HD2	2	0.22	0.02	0.22
(1,894)	1:24:A:LEU:HD13	1:53:A:ARG:HD3	2	0.22	0.02	0.22
(1,923)	1:46:A:TRP:HH2	1:64:A:ILE:HG21	2	0.18	0.06	0.18
(1,923)	1:46:A:TRP:HH2	1:64:A:ILE:HG22	2	0.18	0.06	0.18
(1,923)	1:46:A:TRP:HH2	1:64:A:ILE:HG23	2	0.18	0.06	0.18
(1,556)	1:15:A:ASP:HA	1:27:A:ARG:HD2	2	0.17	0.01	0.17
(1,556)	1:15:A:ASP:HA	1:27:A:ARG:HD3	2	0.17	0.01	0.17
(1,764)	1:26:A:PHE:HD1	1:57:A:VAL:HB	2	0.16	0.01	0.16
(1,764)	1:26:A:PHE:HD2	1:57:A:VAL:HB	2	0.16	0.01	0.16
(1,953)	1:8:A:VAL:HG11	1:34:A:VAL:H	2	0.15	0.0	0.15
(1,953)	1:8:A:VAL:HG12	1:34:A:VAL:H	2	0.15	0.0	0.15
(1,953)	1:8:A:VAL:HG13	1:34:A:VAL:H	2	0.15	0.0	0.15
(1,953)	1:8:A:VAL:HG21	1:34:A:VAL:H	2	0.15	0.0	0.15
(1,953)	1:8:A:VAL:HG22	1:34:A:VAL:H	2	0.15	0.0	0.15
(1,953)	1:8:A:VAL:HG23	1:34:A:VAL:H	2	0.15	0.0	0.15
(1,498)	1:11:A:LYS:HE2	1:13:A:LEU:HA	2	0.14	0.01	0.14
(1,498)	1:11:A:LYS:HE3	1:13:A:LEU:HA	2	0.14	0.01	0.14
(1,545)	1:24:A:LEU:HG	1:26:A:PHE:HD1	2	0.14	0.02	0.14
(1,545)	1:24:A:LEU:HG	1:26:A:PHE:HD2	2	0.14	0.02	0.14
(1,329)	1:54:A:GLN:HB2	1:55:A:GLY:H	2	0.11	0.0	0.11
(1,329)	1:54:A:GLN:HB3	1:55:A:GLY:H	2	0.11	0.0	0.11
(1,1160)	1:61:A:ARG:HD2	1:62:A:LEU:HD21	2	0.11	0.0	0.11
(1,1160)	1:61:A:ARG:HD2	1:62:A:LEU:HD22	2	0.11	0.0	0.11
(1,1160)	1:61:A:ARG:HD2	1:62:A:LEU:HD23	2	0.11	0.0	0.11
(1,1160)	1:61:A:ARG:HD3	1:62:A:LEU:HD21	2	0.11	0.0	0.11
(1,1160)	1:61:A:ARG:HD3	1:62:A:LEU:HD22	2	0.11	0.0	0.11
(1,1160)	1:61:A:ARG:HD3	1:62:A:LEU:HD23	2	0.11	0.0	0.11

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 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. 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)
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	30	0.5
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	30	0.5
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	30	0.5
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	30	0.5
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	30	0.5
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	30	0.5
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	30	0.5
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	30	0.5
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	30	0.5
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	30	0.5

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	30	0.5
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	30	0.5
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	19	0.49
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	19	0.49
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	19	0.49
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	19	0.49
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	19	0.49
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	19	0.49
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	8	0.49
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	8	0.49
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	8	0.49
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	8	0.49
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	8	0.49
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	8	0.49
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	8	0.49
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	8	0.49
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	8	0.49
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	8	0.49
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	8	0.49
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	8	0.49
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	10	0.48
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	10	0.48
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	10	0.48
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	10	0.48
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	10	0.48
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	10	0.48
(1,438)	1:9:A:LEU:HB2	1:32:A:MET:H	34	0.47
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	33	0.45
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	33	0.45
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	33	0.45
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	33	0.45
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	33	0.45
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	33	0.45
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	29	0.45
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	29	0.45
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	29	0.45
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	29	0.45
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	29	0.45
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	29	0.45
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	29	0.45
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	29	0.45
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	29	0.45

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	29	0.45
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	29	0.45
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	29	0.45
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	26	0.44
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	26	0.44
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	26	0.44
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	26	0.44
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	26	0.44
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	26	0.44
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	13	0.43
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	13	0.43
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	13	0.43
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	13	0.43
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	13	0.43
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	13	0.43
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	13	0.43
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	13	0.43
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	13	0.43
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	13	0.43
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	13	0.43
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	13	0.43
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	15	0.43
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	15	0.43
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	15	0.43
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	15	0.43
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	15	0.43
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	15	0.43
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	15	0.43
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	15	0.43
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	15	0.43
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	15	0.43
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	15	0.43
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	15	0.43
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	39	0.4
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	39	0.4
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	39	0.4
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	39	0.4
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	39	0.4
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	39	0.4
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	40	0.4
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	40	0.4
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	40	0.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	40	0.4
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	40	0.4
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	40	0.4
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	18	0.4
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	18	0.4
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	18	0.4
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	18	0.4
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	18	0.4
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	18	0.4
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	18	0.4
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	18	0.4
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	18	0.4
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	18	0.4
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	18	0.4
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	18	0.4
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	40	0.4
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	40	0.4
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	40	0.4
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	23	0.39
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	23	0.39
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	23	0.39
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	23	0.39
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	23	0.39
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	23	0.39
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	34	0.39
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	34	0.39
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	34	0.39
(1,1014)	1:19:A:GLU:HG2	1:20:A:SER:HB2	40	0.38
(1,1014)	1:19:A:GLU:HG2	1:20:A:SER:HB3	40	0.38
(1,1014)	1:19:A:GLU:HG3	1:20:A:SER:HB2	40	0.38
(1,1014)	1:19:A:GLU:HG3	1:20:A:SER:HB3	40	0.38
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	25	0.38
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	25	0.38
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	25	0.38
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	25	0.38
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	25	0.38
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	25	0.38
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	11	0.37
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	11	0.37
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	11	0.37
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	11	0.37
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	11	0.37

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	11	0.37
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	30	0.37
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	30	0.37
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	30	0.37
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	30	0.37
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	30	0.37
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	30	0.37
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	38	0.37
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	38	0.37
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	38	0.37
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	38	0.37
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	38	0.37
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	38	0.37
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	24	0.37
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	24	0.37
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	24	0.37
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	24	0.37
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	24	0.37
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	24	0.37
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	24	0.37
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	24	0.37
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	24	0.37
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	24	0.37
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	24	0.37
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	24	0.37
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	32	0.37
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	32	0.37
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	32	0.37
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	32	0.37
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	32	0.37
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	32	0.37
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	32	0.37
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	32	0.37
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	32	0.37
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	32	0.37
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	32	0.37
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	32	0.37
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	21	0.35
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	21	0.35
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	21	0.35
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	21	0.35
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	21	0.35

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	21	0.35
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	9	0.34
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	9	0.34
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	9	0.34
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	9	0.34
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	9	0.34
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	9	0.34
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	9	0.34
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	9	0.34
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	9	0.34
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	9	0.34
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	9	0.34
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	9	0.34
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	9	0.34
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	9	0.34
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	9	0.34
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	9	0.34
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	9	0.34
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	9	0.34
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	26	0.33
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	26	0.33
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	26	0.33
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	35	0.32
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	35	0.32
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	35	0.32
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	35	0.32
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	35	0.32
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	35	0.32
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	3	0.32
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	3	0.32
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	3	0.32
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	3	0.32
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	3	0.32
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	3	0.32
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	3	0.32
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	3	0.32
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	3	0.32
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	3	0.32
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	3	0.32
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	3	0.32
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	36	0.31
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	36	0.31

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	36	0.31
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	36	0.31
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	36	0.31
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	36	0.31
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	7	0.31
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	7	0.31
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	7	0.31
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	7	0.31
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	7	0.31
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	7	0.31
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	7	0.31
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	7	0.31
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	7	0.31
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	7	0.31
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	7	0.31
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	7	0.31
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	35	0.31
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	35	0.31
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	35	0.31
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	37	0.31
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	37	0.31
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	37	0.31
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	6	0.3
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	6	0.3
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	6	0.3
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	6	0.3
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	6	0.3
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	6	0.3
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	12	0.3
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	12	0.3
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	12	0.3
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	12	0.3
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	12	0.3
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	12	0.3
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	13	0.3
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	13	0.3
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	13	0.3
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	13	0.3
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	13	0.3
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	13	0.3
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	27	0.3
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	27	0.3

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	27	0.3
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	27	0.3
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	27	0.3
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	27	0.3
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	27	0.3
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	27	0.3
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	27	0.3
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	27	0.3
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	27	0.3
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	27	0.3
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB2	31	0.29
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB3	31	0.29
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB2	31	0.29
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB3	31	0.29
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	39	0.29
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	39	0.29
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	39	0.29
(1,1014)	1:19:A:GLU:HG2	1:20:A:SER:HB2	39	0.28
(1,1014)	1:19:A:GLU:HG2	1:20:A:SER:HB3	39	0.28
(1,1014)	1:19:A:GLU:HG3	1:20:A:SER:HB2	39	0.28
(1,1014)	1:19:A:GLU:HG3	1:20:A:SER:HB3	39	0.28
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	16	0.27
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	16	0.27
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	16	0.27
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	16	0.27
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	16	0.27
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	16	0.27
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	24	0.27
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	24	0.27
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	24	0.27
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	24	0.27
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	24	0.27
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	24	0.27
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	31	0.27
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	31	0.27
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	31	0.27
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	31	0.27
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	31	0.27
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	31	0.27
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	31	0.27
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	31	0.27
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	31	0.27

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	31	0.27
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	31	0.27
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	31	0.27
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	40	0.27
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	40	0.27
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	40	0.27
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	40	0.27
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	40	0.27
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	40	0.27
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	40	0.27
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	40	0.27
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	40	0.27
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	40	0.27
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	40	0.27
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	40	0.27
(1,59)	1:12:A:ALA:H	1:31:A:ILE:HD11	39	0.27
(1,59)	1:12:A:ALA:H	1:31:A:ILE:HD12	39	0.27
(1,59)	1:12:A:ALA:H	1:31:A:ILE:HD13	39	0.27
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD11	35	0.26
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD12	35	0.26
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD13	35	0.26
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD21	35	0.26
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD22	35	0.26
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD23	35	0.26
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	32	0.26
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	32	0.26
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	32	0.26
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	32	0.26
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	32	0.26
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	32	0.26
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD11	40	0.26
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD12	40	0.26
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD13	40	0.26
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	31	0.25
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	31	0.25
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	31	0.25
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	31	0.25
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	31	0.25
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	31	0.25
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	39	0.25
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	39	0.25
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	39	0.25

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	39	0.25
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	39	0.25
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	39	0.25
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	39	0.25
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	39	0.25
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	39	0.25
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	39	0.25
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	39	0.25
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	39	0.25
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	36	0.25
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	36	0.25
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	36	0.25
(1,86)	1:15:A:ASP:H	1:28:A:LYS:HE2	40	0.25
(1,86)	1:15:A:ASP:H	1:28:A:LYS:HE3	40	0.25
(1,1142)	1:49:A:SER:HB2	1:54:A:GLN:H	40	0.24
(1,1142)	1:49:A:SER:HB3	1:54:A:GLN:H	40	0.24
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD11	22	0.24
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD12	22	0.24
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD13	22	0.24
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD21	22	0.24
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD22	22	0.24
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD23	22	0.24
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	27	0.24
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	27	0.24
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	27	0.24
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	27	0.24
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	27	0.24
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	27	0.24
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	23	0.24
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	23	0.24
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	23	0.24
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	23	0.24
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	23	0.24
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	23	0.24
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	23	0.24
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	23	0.24
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	23	0.24
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	23	0.24
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	23	0.24
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	23	0.24
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	37	0.24
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	37	0.24

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	37	0.24
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	37	0.24
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	37	0.24
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	37	0.24
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	37	0.24
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	37	0.24
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	37	0.24
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	37	0.24
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	37	0.24
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	37	0.24
(1,923)	1:46:A:TRP:HH2	1:64:A:ILE:HG21	39	0.24
(1,923)	1:46:A:TRP:HH2	1:64:A:ILE:HG22	39	0.24
(1,923)	1:46:A:TRP:HH2	1:64:A:ILE:HG23	39	0.24
(1,894)	1:24:A:LEU:HD11	1:53:A:ARG:HD2	9	0.24
(1,894)	1:24:A:LEU:HD11	1:53:A:ARG:HD3	9	0.24
(1,894)	1:24:A:LEU:HD12	1:53:A:ARG:HD2	9	0.24
(1,894)	1:24:A:LEU:HD12	1:53:A:ARG:HD3	9	0.24
(1,894)	1:24:A:LEU:HD13	1:53:A:ARG:HD2	9	0.24
(1,894)	1:24:A:LEU:HD13	1:53:A:ARG:HD3	9	0.24
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD11	39	0.24
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD12	39	0.24
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD13	39	0.24
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	11	0.24
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	11	0.24
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	11	0.24
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	11	0.24
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	11	0.24
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	11	0.24
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD11	34	0.23
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD12	34	0.23
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD13	34	0.23
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD21	34	0.23
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD22	34	0.23
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD23	34	0.23
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB2	7	0.23
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB3	7	0.23
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB2	7	0.23
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB3	7	0.23
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB2	9	0.23
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB3	9	0.23
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB2	9	0.23
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB3	9	0.23

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1014)	1:19:A:GLU:HG2	1:20:A:SER:HB2	23	0.23
(1,1014)	1:19:A:GLU:HG2	1:20:A:SER:HB3	23	0.23
(1,1014)	1:19:A:GLU:HG3	1:20:A:SER:HB2	23	0.23
(1,1014)	1:19:A:GLU:HG3	1:20:A:SER:HB3	23	0.23
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	17	0.23
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	17	0.23
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	17	0.23
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	17	0.23
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	17	0.23
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	17	0.23
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	22	0.23
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	22	0.23
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	22	0.23
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	22	0.23
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	22	0.23
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	22	0.23
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	6	0.23
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	6	0.23
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	6	0.23
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	6	0.23
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	6	0.23
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	6	0.23
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	6	0.23
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	6	0.23
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	6	0.23
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	6	0.23
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	6	0.23
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	6	0.23
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	40	0.23
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	40	0.23
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	40	0.23
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	40	0.23
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	40	0.23
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	40	0.23
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB2	25	0.22
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB3	25	0.22
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB2	25	0.22
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB3	25	0.22
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB2	36	0.22
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB3	36	0.22
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB2	36	0.22
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB3	36	0.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	30	0.22
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	30	0.22
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	30	0.22
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	30	0.22
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	30	0.22
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	30	0.22
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	31	0.22
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	31	0.22
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	31	0.22
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB2	1	0.21
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB3	1	0.21
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB2	1	0.21
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB3	1	0.21
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB2	6	0.21
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB3	6	0.21
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB2	6	0.21
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB3	6	0.21
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB2	12	0.21
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB3	12	0.21
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB2	12	0.21
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB3	12	0.21
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB2	15	0.21
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB3	15	0.21
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB2	15	0.21
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB3	15	0.21
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB2	24	0.21
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB3	24	0.21
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB2	24	0.21
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB3	24	0.21
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB2	32	0.21
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB3	32	0.21
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB2	32	0.21
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB3	32	0.21
(1,1008)	1:18:A:ALA:HA	1:19:A:GLU:HG2	11	0.21
(1,1008)	1:18:A:ALA:HA	1:19:A:GLU:HG3	11	0.21
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	2	0.21
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	2	0.21
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	2	0.21
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	2	0.21
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	2	0.21
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	2	0.21
(1,894)	1:24:A:LEU:HD11	1:53:A:ARG:HD2	36	0.21

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,894)	1:24:A:LEU:HD11	1:53:A:ARG:HD3	36	0.21
(1,894)	1:24:A:LEU:HD12	1:53:A:ARG:HD2	36	0.21
(1,894)	1:24:A:LEU:HD12	1:53:A:ARG:HD3	36	0.21
(1,894)	1:24:A:LEU:HD13	1:53:A:ARG:HD2	36	0.21
(1,894)	1:24:A:LEU:HD13	1:53:A:ARG:HD3	36	0.21
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	26	0.21
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	26	0.21
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	26	0.21
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	26	0.21
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	26	0.21
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	26	0.21
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	38	0.21
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	38	0.21
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	38	0.21
(1,86)	1:15:A:ASP:H	1:28:A:LYS:HE2	37	0.21
(1,86)	1:15:A:ASP:H	1:28:A:LYS:HE3	37	0.21
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB2	8	0.2
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB3	8	0.2
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB2	8	0.2
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB3	8	0.2
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB2	19	0.2
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB3	19	0.2
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB2	19	0.2
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB3	19	0.2
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	11	0.2
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	11	0.2
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	11	0.2
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	11	0.2
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	11	0.2
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	11	0.2
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	11	0.2
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	11	0.2
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	11	0.2
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	11	0.2
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	11	0.2
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	11	0.2
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	25	0.2
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	25	0.2
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	25	0.2
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	25	0.2
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	25	0.2
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	25	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	25	0.2
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	25	0.2
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	25	0.2
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	25	0.2
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	25	0.2
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	25	0.2
(1,864)	1:71:A:LYS:HA	1:72:A:LYS:HD2	37	0.2
(1,864)	1:71:A:LYS:HA	1:72:A:LYS:HD3	37	0.2
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	22	0.2
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	22	0.2
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	22	0.2
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	22	0.2
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	22	0.2
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	22	0.2
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	38	0.2
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	38	0.2
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	38	0.2
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	38	0.2
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	38	0.2
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	38	0.2
(1,480)	1:9:A:LEU:HG	1:10:A:ALA:HA	34	0.2
(1,44)	1:11:A:LYS:H	1:31:A:ILE:HD11	39	0.2
(1,44)	1:11:A:LYS:H	1:31:A:ILE:HD12	39	0.2
(1,44)	1:11:A:LYS:H	1:31:A:ILE:HD13	39	0.2
(1,1049)	1:24:A:LEU:HD11	1:56:A:ILE:H	40	0.19
(1,1049)	1:24:A:LEU:HD12	1:56:A:ILE:H	40	0.19
(1,1049)	1:24:A:LEU:HD13	1:56:A:ILE:H	40	0.19
(1,1049)	1:24:A:LEU:HD21	1:56:A:ILE:H	40	0.19
(1,1049)	1:24:A:LEU:HD22	1:56:A:ILE:H	40	0.19
(1,1049)	1:24:A:LEU:HD23	1:56:A:ILE:H	40	0.19
(1,1014)	1:19:A:GLU:HG2	1:20:A:SER:HB2	27	0.19
(1,1014)	1:19:A:GLU:HG2	1:20:A:SER:HB3	27	0.19
(1,1014)	1:19:A:GLU:HG3	1:20:A:SER:HB2	27	0.19
(1,1014)	1:19:A:GLU:HG3	1:20:A:SER:HB3	27	0.19
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	8	0.19
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	8	0.19
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	8	0.19
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	8	0.19
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	8	0.19
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	8	0.19
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	14	0.19
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	14	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	14	0.19
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	14	0.19
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	14	0.19
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	14	0.19
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	14	0.19
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	14	0.19
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	14	0.19
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	14	0.19
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	14	0.19
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	14	0.19
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	20	0.19
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	20	0.19
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	20	0.19
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	20	0.19
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	20	0.19
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	20	0.19
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	20	0.19
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	20	0.19
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	20	0.19
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	20	0.19
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	20	0.19
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	20	0.19
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	4	0.19
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	4	0.19
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	4	0.19
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	4	0.19
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	4	0.19
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	4	0.19
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	5	0.19
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	5	0.19
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	5	0.19
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	5	0.19
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	5	0.19
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	5	0.19
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	36	0.19
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	36	0.19
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	36	0.19
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	36	0.19
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	36	0.19
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	36	0.19
(1,538)	1:24:A:LEU:HG	1:55:A:GLY:HA2	25	0.19
(1,185)	1:31:A:ILE:H	1:31:A:ILE:HD11	31	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,185)	1:31:A:ILE:H	1:31:A:ILE:HD12	31	0.19
(1,185)	1:31:A:ILE:H	1:31:A:ILE:HD13	31	0.19
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB2	33	0.18
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB3	33	0.18
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB2	33	0.18
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB3	33	0.18
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	4	0.18
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	4	0.18
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	4	0.18
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	4	0.18
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	4	0.18
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	4	0.18
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	34	0.18
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	34	0.18
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	34	0.18
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	34	0.18
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	34	0.18
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	34	0.18
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	34	0.18
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	34	0.18
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	34	0.18
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	34	0.18
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	34	0.18
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	34	0.18
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD11	26	0.18
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD12	26	0.18
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD13	26	0.18
(1,556)	1:15:A:ASP:HA	1:27:A:ARG:HD2	31	0.18
(1,556)	1:15:A:ASP:HA	1:27:A:ARG:HD3	31	0.18
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	10	0.18
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	10	0.18
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	10	0.18
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	33	0.18
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	33	0.18
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	33	0.18
(1,159)	1:27:A:ARG:H	1:50:A:LEU:HD11	38	0.18
(1,159)	1:27:A:ARG:H	1:50:A:LEU:HD12	38	0.18
(1,159)	1:27:A:ARG:H	1:50:A:LEU:HD13	38	0.18
(1,1143)	1:49:A:SER:HB2	1:54:A:GLN:HG2	37	0.17
(1,1143)	1:49:A:SER:HB2	1:54:A:GLN:HG3	37	0.17
(1,1143)	1:49:A:SER:HB3	1:54:A:GLN:HG2	37	0.17
(1,1143)	1:49:A:SER:HB3	1:54:A:GLN:HG3	37	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD11	39	0.17
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD12	39	0.17
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD13	39	0.17
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD21	39	0.17
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD22	39	0.17
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD23	39	0.17
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB2	4	0.17
(1,1017)	1:20:A:SER:HB2	1:21:A:PRO:HB3	4	0.17
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB2	4	0.17
(1,1017)	1:20:A:SER:HB3	1:21:A:PRO:HB3	4	0.17
(1,1014)	1:19:A:GLU:HG2	1:20:A:SER:HB2	22	0.17
(1,1014)	1:19:A:GLU:HG2	1:20:A:SER:HB3	22	0.17
(1,1014)	1:19:A:GLU:HG3	1:20:A:SER:HB2	22	0.17
(1,1014)	1:19:A:GLU:HG3	1:20:A:SER:HB3	22	0.17
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	3	0.17
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	3	0.17
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	3	0.17
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	3	0.17
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	3	0.17
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	3	0.17
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	14	0.17
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	14	0.17
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	14	0.17
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	14	0.17
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	14	0.17
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	14	0.17
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	21	0.17
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	21	0.17
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	21	0.17
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	21	0.17
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	21	0.17
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	21	0.17
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	21	0.17
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	21	0.17
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	21	0.17
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	21	0.17
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	21	0.17
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	21	0.17
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD11	37	0.17
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD12	37	0.17
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD13	37	0.17
(1,764)	1:26:A:PHE:HD1	1:57:A:VAL:HB	36	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,764)	1:26:A:PHE:HD2	1:57:A:VAL:HB	36	0.17
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	23	0.17
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	23	0.17
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	23	0.17
(1,185)	1:31:A:ILE:H	1:31:A:ILE:HD11	34	0.17
(1,185)	1:31:A:ILE:H	1:31:A:ILE:HD12	34	0.17
(1,185)	1:31:A:ILE:H	1:31:A:ILE:HD13	34	0.17
(1,1085)	1:33:A:THR:H	1:49:A:SER:HB2	26	0.16
(1,1085)	1:33:A:THR:H	1:49:A:SER:HB3	26	0.16
(1,1070)	1:30:A:ASP:H	1:31:A:ILE:HG12	40	0.16
(1,1070)	1:30:A:ASP:H	1:31:A:ILE:HG13	40	0.16
(1,999)	1:16:A:ASN:H	1:27:A:ARG:HG2	37	0.16
(1,999)	1:16:A:ASN:H	1:27:A:ARG:HG3	37	0.16
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD11	36	0.16
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD12	36	0.16
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD13	36	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	6	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	6	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	6	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	6	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	6	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	6	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	20	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	20	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	20	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	20	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	20	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	20	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	23	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	23	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	23	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	23	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	23	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	23	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	37	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	37	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	37	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	37	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	37	0.16
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	37	0.16
(1,764)	1:26:A:PHE:HD1	1:57:A:VAL:HB	39	0.16
(1,764)	1:26:A:PHE:HD2	1:57:A:VAL:HB	39	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,556)	1:15:A:ASP:HA	1:27:A:ARG:HD2	36	0.16
(1,556)	1:15:A:ASP:HA	1:27:A:ARG:HD3	36	0.16
(1,545)	1:24:A:LEU:HG	1:26:A:PHE:HD1	31	0.16
(1,545)	1:24:A:LEU:HG	1:26:A:PHE:HD2	31	0.16
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	9	0.16
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	9	0.16
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	9	0.16
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	19	0.16
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	19	0.16
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	19	0.16
(1,185)	1:31:A:ILE:H	1:31:A:ILE:HD11	35	0.16
(1,185)	1:31:A:ILE:H	1:31:A:ILE:HD12	35	0.16
(1,185)	1:31:A:ILE:H	1:31:A:ILE:HD13	35	0.16
(1,101)	1:16:A:ASN:H	1:28:A:LYS:H	40	0.16
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD11	16	0.15
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD12	16	0.15
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD13	16	0.15
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD21	16	0.15
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD22	16	0.15
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD23	16	0.15
(1,1014)	1:19:A:GLU:HG2	1:20:A:SER:HB2	2	0.15
(1,1014)	1:19:A:GLU:HG2	1:20:A:SER:HB3	2	0.15
(1,1014)	1:19:A:GLU:HG3	1:20:A:SER:HB2	2	0.15
(1,1014)	1:19:A:GLU:HG3	1:20:A:SER:HB3	2	0.15
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	5	0.15
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	5	0.15
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	5	0.15
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	5	0.15
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	5	0.15
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	5	0.15
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	7	0.15
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	7	0.15
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	7	0.15
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	7	0.15
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	7	0.15
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	7	0.15
(1,953)	1:8:A:VAL:HG11	1:34:A:VAL:H	20	0.15
(1,953)	1:8:A:VAL:HG12	1:34:A:VAL:H	20	0.15
(1,953)	1:8:A:VAL:HG13	1:34:A:VAL:H	20	0.15
(1,953)	1:8:A:VAL:HG21	1:34:A:VAL:H	20	0.15
(1,953)	1:8:A:VAL:HG22	1:34:A:VAL:H	20	0.15
(1,953)	1:8:A:VAL:HG23	1:34:A:VAL:H	20	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD11	34	0.15
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD12	34	0.15
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD13	34	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	2	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	2	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	2	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	2	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	2	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	2	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	15	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	15	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	15	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	15	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	15	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	15	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	16	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	16	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	16	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	16	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	16	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	16	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	31	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	31	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	31	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	31	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	31	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	31	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	33	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	33	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	33	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	33	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	33	0.15
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	33	0.15
(1,553)	1:16:A:ASN:H	1:27:A:ARG:HD2	36	0.15
(1,553)	1:16:A:ASN:H	1:27:A:ARG:HD3	36	0.15
(1,1142)	1:49:A:SER:HB2	1:54:A:GLN:H	34	0.14
(1,1142)	1:49:A:SER:HB3	1:54:A:GLN:H	34	0.14
(1,1142)	1:49:A:SER:HB2	1:54:A:GLN:H	38	0.14
(1,1142)	1:49:A:SER:HB3	1:54:A:GLN:H	38	0.14
(1,1049)	1:24:A:LEU:HD11	1:56:A:ILE:H	17	0.14
(1,1049)	1:24:A:LEU:HD12	1:56:A:ILE:H	17	0.14
(1,1049)	1:24:A:LEU:HD13	1:56:A:ILE:H	17	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1049)	1:24:A:LEU:HD21	1:56:A:ILE:H	17	0.14
(1,1049)	1:24:A:LEU:HD22	1:56:A:ILE:H	17	0.14
(1,1049)	1:24:A:LEU:HD23	1:56:A:ILE:H	17	0.14
(1,1014)	1:19:A:GLU:HG2	1:20:A:SER:HB2	9	0.14
(1,1014)	1:19:A:GLU:HG2	1:20:A:SER:HB3	9	0.14
(1,1014)	1:19:A:GLU:HG3	1:20:A:SER:HB2	9	0.14
(1,1014)	1:19:A:GLU:HG3	1:20:A:SER:HB3	9	0.14
(1,997)	1:16:A:ASN:H	1:16:A:ASN:HD21	31	0.14
(1,997)	1:16:A:ASN:H	1:16:A:ASN:HD22	31	0.14
(1,953)	1:8:A:VAL:HG11	1:34:A:VAL:H	15	0.14
(1,953)	1:8:A:VAL:HG12	1:34:A:VAL:H	15	0.14
(1,953)	1:8:A:VAL:HG13	1:34:A:VAL:H	15	0.14
(1,953)	1:8:A:VAL:HG21	1:34:A:VAL:H	15	0.14
(1,953)	1:8:A:VAL:HG22	1:34:A:VAL:H	15	0.14
(1,953)	1:8:A:VAL:HG23	1:34:A:VAL:H	15	0.14
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD11	1	0.14
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD12	1	0.14
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD13	1	0.14
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD21	1	0.14
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD22	1	0.14
(1,935)	1:5:A:TYR:HE1	1:6:A:LEU:HD23	1	0.14
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD11	1	0.14
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD12	1	0.14
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD13	1	0.14
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD21	1	0.14
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD22	1	0.14
(1,935)	1:5:A:TYR:HE2	1:6:A:LEU:HD23	1	0.14
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD11	31	0.14
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD12	31	0.14
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD13	31	0.14
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	8	0.14
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	8	0.14
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	8	0.14
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	8	0.14
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	8	0.14
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	8	0.14
(1,498)	1:11:A:LYS:HE2	1:13:A:LEU:HA	33	0.14
(1,498)	1:11:A:LYS:HE3	1:13:A:LEU:HA	33	0.14
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	22	0.14
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	22	0.14
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	22	0.14
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	25	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	25	0.14
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	25	0.14
(1,178)	1:30:A:ASP:H	1:32:A:MET:HE1	35	0.14
(1,178)	1:30:A:ASP:H	1:32:A:MET:HE2	35	0.14
(1,178)	1:30:A:ASP:H	1:32:A:MET:HE3	35	0.14
(1,126)	1:23:A:GLU:H	1:23:A:GLU:HG3	40	0.14
(1,1142)	1:49:A:SER:HB2	1:54:A:GLN:H	39	0.13
(1,1142)	1:49:A:SER:HB3	1:54:A:GLN:H	39	0.13
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD11	18	0.13
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD12	18	0.13
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD13	18	0.13
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD21	18	0.13
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD22	18	0.13
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD23	18	0.13
(1,864)	1:71:A:LYS:HA	1:72:A:LYS:HD2	24	0.13
(1,864)	1:71:A:LYS:HA	1:72:A:LYS:HD3	24	0.13
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD11	13	0.13
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD12	13	0.13
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD13	13	0.13
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD11	35	0.13
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD12	35	0.13
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD13	35	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	7	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	7	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	7	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	7	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	7	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	7	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	10	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	10	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	10	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	10	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	10	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	10	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	13	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	13	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	13	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	13	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	13	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	13	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	14	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	14	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	14	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	14	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	14	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	14	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	24	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	24	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	24	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	24	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	24	0.13
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	24	0.13
(1,498)	1:11:A:LYS:HE2	1:13:A:LEU:HA	26	0.13
(1,498)	1:11:A:LYS:HE3	1:13:A:LEU:HA	26	0.13
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	6	0.13
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	6	0.13
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	6	0.13
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	11	0.13
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	11	0.13
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	11	0.13
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	24	0.13
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	24	0.13
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	24	0.13
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	30	0.13
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	30	0.13
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	30	0.13
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	32	0.13
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	32	0.13
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	32	0.13
(1,323)	1:65:A:LEU:H	1:66:A:VAL:H	34	0.13
(1,185)	1:31:A:ILE:H	1:31:A:ILE:HD11	26	0.13
(1,185)	1:31:A:ILE:H	1:31:A:ILE:HD12	26	0.13
(1,185)	1:31:A:ILE:H	1:31:A:ILE:HD13	26	0.13
(1,59)	1:12:A:ALA:H	1:31:A:ILE:HD11	1	0.13
(1,59)	1:12:A:ALA:H	1:31:A:ILE:HD12	1	0.13
(1,59)	1:12:A:ALA:H	1:31:A:ILE:HD13	1	0.13
(1,1063)	1:28:A:LYS:H	1:30:A:ASP:HB2	35	0.12
(1,1063)	1:28:A:LYS:H	1:30:A:ASP:HB3	35	0.12
(1,997)	1:16:A:ASN:H	1:16:A:ASN:HD21	26	0.12
(1,997)	1:16:A:ASN:H	1:16:A:ASN:HD22	26	0.12
(1,929)	1:5:A:TYR:HE1	1:35:A:LEU:HG	34	0.12
(1,929)	1:5:A:TYR:HE2	1:35:A:LEU:HG	34	0.12
(1,923)	1:46:A:TRP:HH2	1:64:A:ILE:HG21	10	0.12
(1,923)	1:46:A:TRP:HH2	1:64:A:ILE:HG22	10	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,923)	1:46:A:TRP:HH2	1:64:A:ILE:HG23	10	0.12
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD11	19	0.12
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD12	19	0.12
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD13	19	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	3	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	3	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	3	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	3	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	3	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	3	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	12	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	12	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	12	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	12	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	12	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	12	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	19	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	19	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	19	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	19	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	19	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	19	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	34	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	34	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	34	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	34	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	34	0.12
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	34	0.12
(1,453)	1:50:A:LEU:H	1:55:A:GLY:H	34	0.12
(1,448)	1:46:A:TRP:H	1:56:A:ILE:HG21	34	0.12
(1,448)	1:46:A:TRP:H	1:56:A:ILE:HG22	34	0.12
(1,448)	1:46:A:TRP:H	1:56:A:ILE:HG23	34	0.12
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	14	0.12
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	14	0.12
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	14	0.12
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	17	0.12
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	17	0.12
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	17	0.12
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	21	0.12
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	21	0.12
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	21	0.12
(1,438)	1:9:A:LEU:HB2	1:32:A:MET:H	20	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,163)	1:27:A:ARG:HB2	1:28:A:LYS:H	40	0.12
(1,1160)	1:61:A:ARG:HD2	1:62:A:LEU:HD21	38	0.11
(1,1160)	1:61:A:ARG:HD2	1:62:A:LEU:HD22	38	0.11
(1,1160)	1:61:A:ARG:HD2	1:62:A:LEU:HD23	38	0.11
(1,1160)	1:61:A:ARG:HD3	1:62:A:LEU:HD21	38	0.11
(1,1160)	1:61:A:ARG:HD3	1:62:A:LEU:HD22	38	0.11
(1,1160)	1:61:A:ARG:HD3	1:62:A:LEU:HD23	38	0.11
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD11	21	0.11
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD12	21	0.11
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD13	21	0.11
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD21	21	0.11
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD22	21	0.11
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD23	21	0.11
(1,1049)	1:24:A:LEU:HD11	1:56:A:ILE:H	34	0.11
(1,1049)	1:24:A:LEU:HD12	1:56:A:ILE:H	34	0.11
(1,1049)	1:24:A:LEU:HD13	1:56:A:ILE:H	34	0.11
(1,1049)	1:24:A:LEU:HD21	1:56:A:ILE:H	34	0.11
(1,1049)	1:24:A:LEU:HD22	1:56:A:ILE:H	34	0.11
(1,1049)	1:24:A:LEU:HD23	1:56:A:ILE:H	34	0.11
(1,997)	1:16:A:ASN:H	1:16:A:ASN:HD21	38	0.11
(1,997)	1:16:A:ASN:H	1:16:A:ASN:HD22	38	0.11
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	29	0.11
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	29	0.11
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	29	0.11
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	29	0.11
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	29	0.11
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	29	0.11
(1,915)	1:26:A:PHE:HE1	1:62:A:LEU:HD11	37	0.11
(1,915)	1:26:A:PHE:HE1	1:62:A:LEU:HD12	37	0.11
(1,915)	1:26:A:PHE:HE1	1:62:A:LEU:HD13	37	0.11
(1,915)	1:26:A:PHE:HE2	1:62:A:LEU:HD11	37	0.11
(1,915)	1:26:A:PHE:HE2	1:62:A:LEU:HD12	37	0.11
(1,915)	1:26:A:PHE:HE2	1:62:A:LEU:HD13	37	0.11
(1,864)	1:71:A:LYS:HA	1:72:A:LYS:HD2	9	0.11
(1,864)	1:71:A:LYS:HA	1:72:A:LYS:HD3	9	0.11
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD11	5	0.11
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD12	5	0.11
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD13	5	0.11
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD11	21	0.11
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD12	21	0.11
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD13	21	0.11
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD11	22	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD12	22	0.11
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD13	22	0.11
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD11	33	0.11
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD12	33	0.11
(1,834)	1:48:A:CYS:H	1:62:A:LEU:HD13	33	0.11
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	29	0.11
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	29	0.11
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	29	0.11
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	29	0.11
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	29	0.11
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	29	0.11
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG11	35	0.11
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG12	35	0.11
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG13	35	0.11
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG21	35	0.11
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG22	35	0.11
(1,773)	1:46:A:TRP:HA	1:57:A:VAL:HG23	35	0.11
(1,545)	1:24:A:LEU:HG	1:26:A:PHE:HD1	40	0.11
(1,545)	1:24:A:LEU:HG	1:26:A:PHE:HD2	40	0.11
(1,407)	1:65:A:LEU:HD11	1:66:A:VAL:H	37	0.11
(1,407)	1:65:A:LEU:HD12	1:66:A:VAL:H	37	0.11
(1,407)	1:65:A:LEU:HD13	1:66:A:VAL:H	37	0.11
(1,329)	1:54:A:GLN:HB2	1:55:A:GLY:H	35	0.11
(1,329)	1:54:A:GLN:HB3	1:55:A:GLY:H	35	0.11
(1,1160)	1:61:A:ARG:HD2	1:62:A:LEU:HD21	26	0.1
(1,1160)	1:61:A:ARG:HD2	1:62:A:LEU:HD22	26	0.1
(1,1160)	1:61:A:ARG:HD2	1:62:A:LEU:HD23	26	0.1
(1,1160)	1:61:A:ARG:HD3	1:62:A:LEU:HD21	26	0.1
(1,1160)	1:61:A:ARG:HD3	1:62:A:LEU:HD22	26	0.1
(1,1160)	1:61:A:ARG:HD3	1:62:A:LEU:HD23	26	0.1
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD11	7	0.1
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD12	7	0.1
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD13	7	0.1
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD21	7	0.1
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD22	7	0.1
(1,1086)	1:33:A:THR:H	1:50:A:LEU:HD23	7	0.1
(1,1014)	1:19:A:GLU:HG2	1:20:A:SER:HB2	36	0.1
(1,1014)	1:19:A:GLU:HG2	1:20:A:SER:HB3	36	0.1
(1,1014)	1:19:A:GLU:HG3	1:20:A:SER:HB2	36	0.1
(1,1014)	1:19:A:GLU:HG3	1:20:A:SER:HB3	36	0.1
(1,959)	1:9:A:LEU:HD11	1:34:A:VAL:H	15	0.1
(1,959)	1:9:A:LEU:HD12	1:34:A:VAL:H	15	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,959)	1:9:A:LEU:HD13	1:34:A:VAL:H	15	0.1
(1,959)	1:9:A:LEU:HD21	1:34:A:VAL:H	15	0.1
(1,959)	1:9:A:LEU:HD22	1:34:A:VAL:H	15	0.1
(1,959)	1:9:A:LEU:HD23	1:34:A:VAL:H	15	0.1
(1,806)	1:14:A:TYR:H	1:61:A:ARG:HD2	40	0.1
(1,725)	1:49:A:SER:H	1:54:A:GLN:HB2	34	0.1
(1,725)	1:49:A:SER:H	1:54:A:GLN:HB3	34	0.1
(1,457)	1:57:A:VAL:H	1:59:A:GLY:H	36	0.1
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	12	0.1
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	12	0.1
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	12	0.1
(1,447)	1:34:A:VAL:HG21	1:46:A:TRP:H	13	0.1
(1,447)	1:34:A:VAL:HG22	1:46:A:TRP:H	13	0.1
(1,447)	1:34:A:VAL:HG23	1:46:A:TRP:H	13	0.1
(1,436)	1:28:A:LYS:H	1:29:A:GLY:H	37	0.1
(1,329)	1:54:A:GLN:HB2	1:55:A:GLY:H	13	0.1
(1,329)	1:54:A:GLN:HB3	1:55:A:GLY:H	13	0.1
(1,59)	1:12:A:ALA:H	1:31:A:ILE:HD11	11	0.1
(1,59)	1:12:A:ALA:H	1:31:A:ILE:HD12	11	0.1
(1,59)	1:12:A:ALA:H	1:31:A:ILE:HD13	11	0.1

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

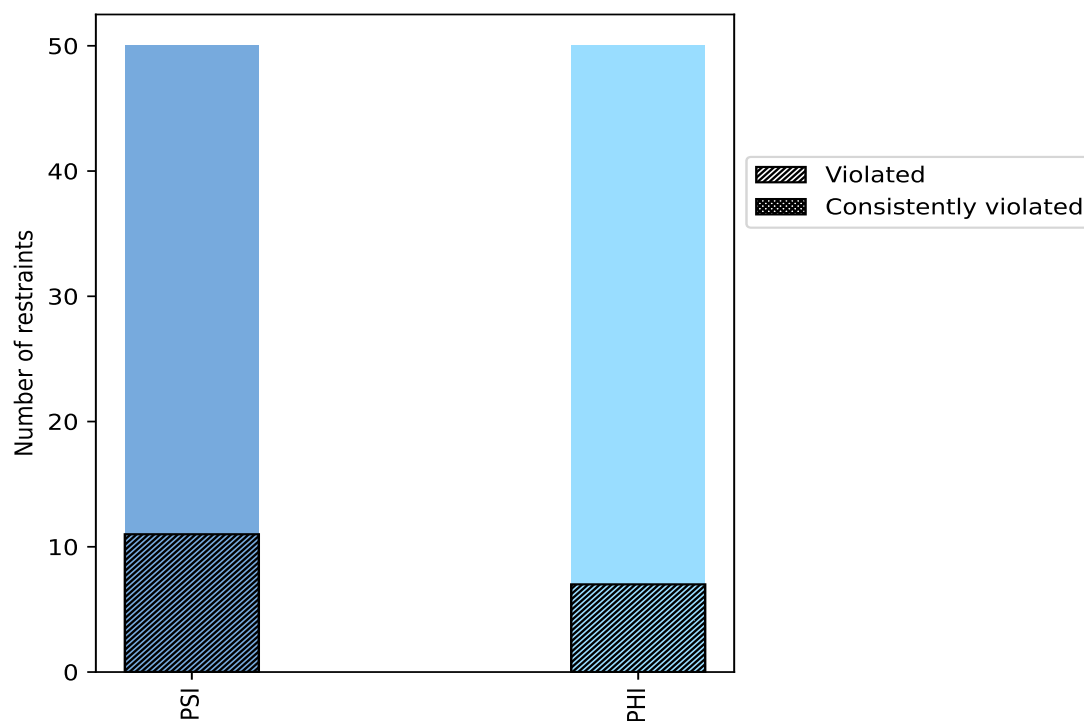
10.1 Summary of dihedral-angle violations [i](#)

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	50	50.0	11	22.0	11.0	0	0.0	0.0
PHI	50	50.0	7	14.0	7.0	0	0.0	0.0
Total	100	100.0	18	18.0	18.0	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 [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.

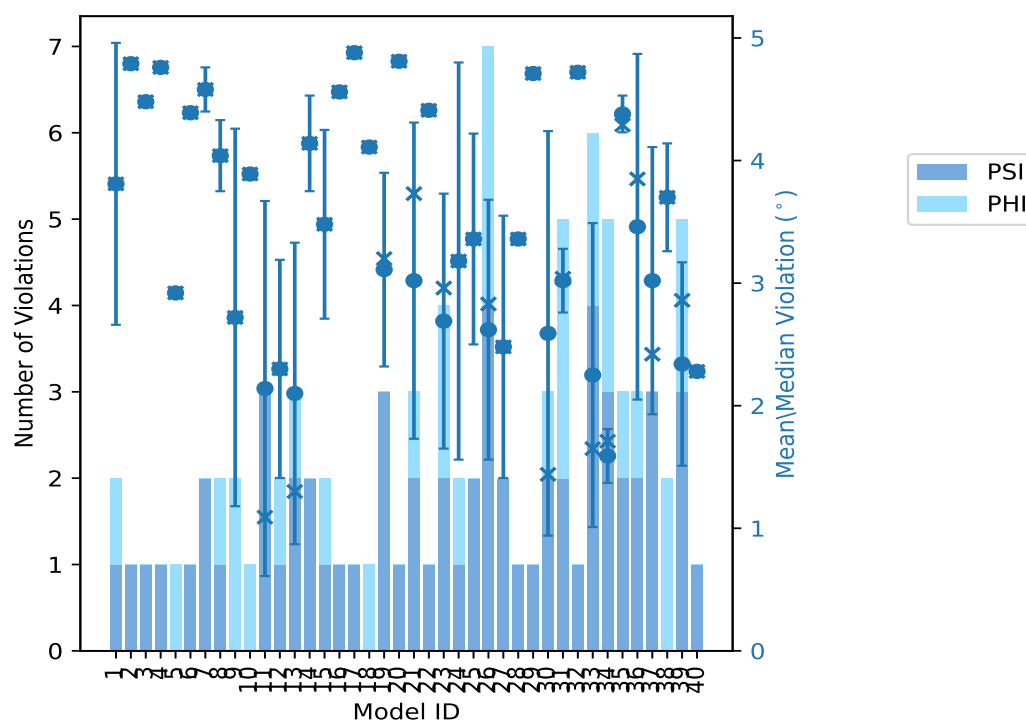
Model ID	Number of violations			Mean (°)	Max (°)	SD (°)	Median (°)
	PSI	PHI	Total				
1	1	1	2	3.81	4.96	1.15	3.81
2	1	0	1	4.79	4.79	0.0	4.79
3	1	0	1	4.48	4.48	0.0	4.48
4	1	0	1	4.76	4.76	0.0	4.76
5	0	1	1	2.92	2.92	0.0	2.92
6	1	0	1	4.39	4.39	0.0	4.39
7	2	0	2	4.58	4.77	0.18	4.58
8	1	1	2	4.04	4.33	0.29	4.04
9	0	2	2	2.72	4.26	1.54	2.72
10	0	1	1	3.89	3.89	0.0	3.89
11	3	0	3	2.14	4.3	1.53	1.09
12	1	1	2	2.3	3.18	0.89	2.3
13	2	1	3	2.1	3.84	1.23	1.3
14	2	0	2	4.14	4.53	0.39	4.14
15	1	1	2	3.48	4.26	0.77	3.48
16	1	0	1	4.56	4.56	0.0	4.56
17	1	0	1	4.88	4.88	0.0	4.88
18	0	1	1	4.11	4.11	0.0	4.11
19	3	0	3	3.11	4.04	0.79	3.2
20	1	0	1	4.81	4.81	0.0	4.81
21	2	1	3	3.02	4.12	1.29	3.73
22	1	0	1	4.41	4.41	0.0	4.41
23	2	2	4	2.69	3.84	1.04	2.96
24	1	1	2	3.18	4.81	1.62	3.18
25	2	0	2	3.36	4.21	0.86	3.36
26	4	3	7	2.62	4.42	1.06	2.83
27	2	0	2	2.48	3.55	1.07	2.48
28	1	0	1	3.36	3.36	0.0	3.36
29	1	0	1	4.71	4.71	0.0	4.71
30	2	1	3	2.59	4.92	1.65	1.44
31	2	3	5	3.02	3.39	0.26	3.04
32	1	0	1	4.72	4.72	0.0	4.72
33	4	2	6	2.25	4.15	1.24	1.65
34	3	2	5	1.59	1.81	0.22	1.71
35	2	1	3	4.38	4.6	0.15	4.29
36	2	1	3	3.46	4.97	1.41	3.85
37	3	0	3	3.02	4.56	1.09	2.42
38	0	2	2	3.7	4.14	0.44	3.7

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Model ID	Number of violations			Mean (°)	Max (°)	SD (°)	Median (°)
	PSI	PHI	Total				
39	3	2	5	2.34	3.1	0.83	2.86
40	1	0	1	2.28	2.28	0.0	2.28

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	%
2	1	3	1	2.5
3	2	5	2	5.0
1	1	2	3	7.5
0	1	1	4	10.0

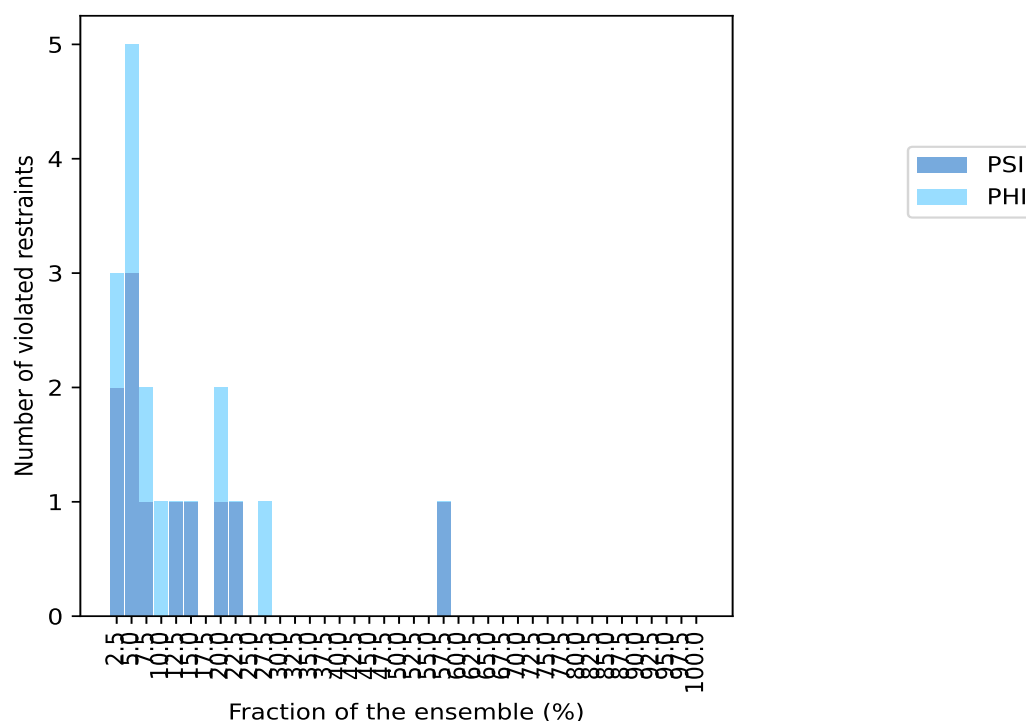
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Number of violated restraints			Fraction of the ensemble	
PSI	PHI	Total	Count ¹	%
1	0	1	5	12.5
1	0	1	6	15.0
0	0	0	7	17.5
1	1	2	8	20.0
1	0	1	9	22.5
0	0	0	10	25.0
0	1	1	11	27.5
0	0	0	12	30.0
0	0	0	13	32.5
0	0	0	14	35.0
0	0	0	15	37.5
0	0	0	16	40.0
0	0	0	17	42.5
0	0	0	18	45.0
0	0	0	19	47.5
0	0	0	20	50.0
0	0	0	21	52.5
0	0	0	22	55.0
1	0	1	23	57.5
0	0	0	24	60.0
0	0	0	25	62.5
0	0	0	26	65.0
0	0	0	27	67.5
0	0	0	28	70.0
0	0	0	29	72.5
0	0	0	30	75.0
0	0	0	31	77.5
0	0	0	32	80.0
0	0	0	33	82.5
0	0	0	34	85.0
0	0	0	35	87.5
0	0	0	36	90.0
0	0	0	37	92.5
0	0	0	38	95.0
0	0	0	39	97.5
0	0	0	40	100.0

¹ Number of models with violations

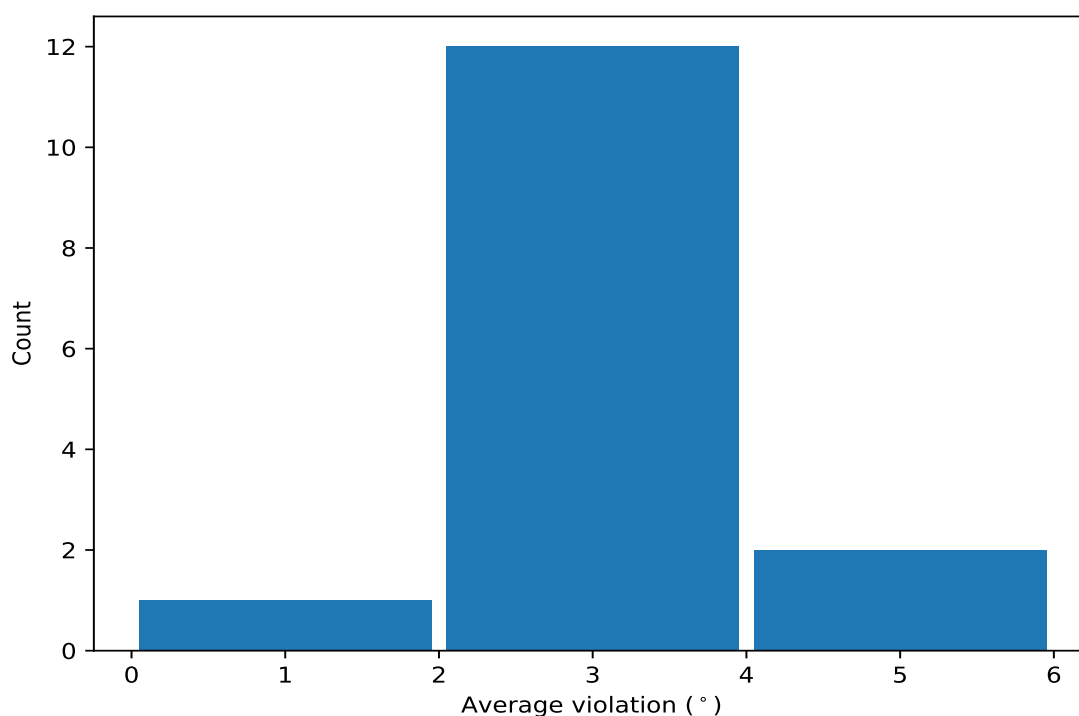
10.3.1 Bar graph : Dihedral-angle Violation statistics for the ensemble [i](#)



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.

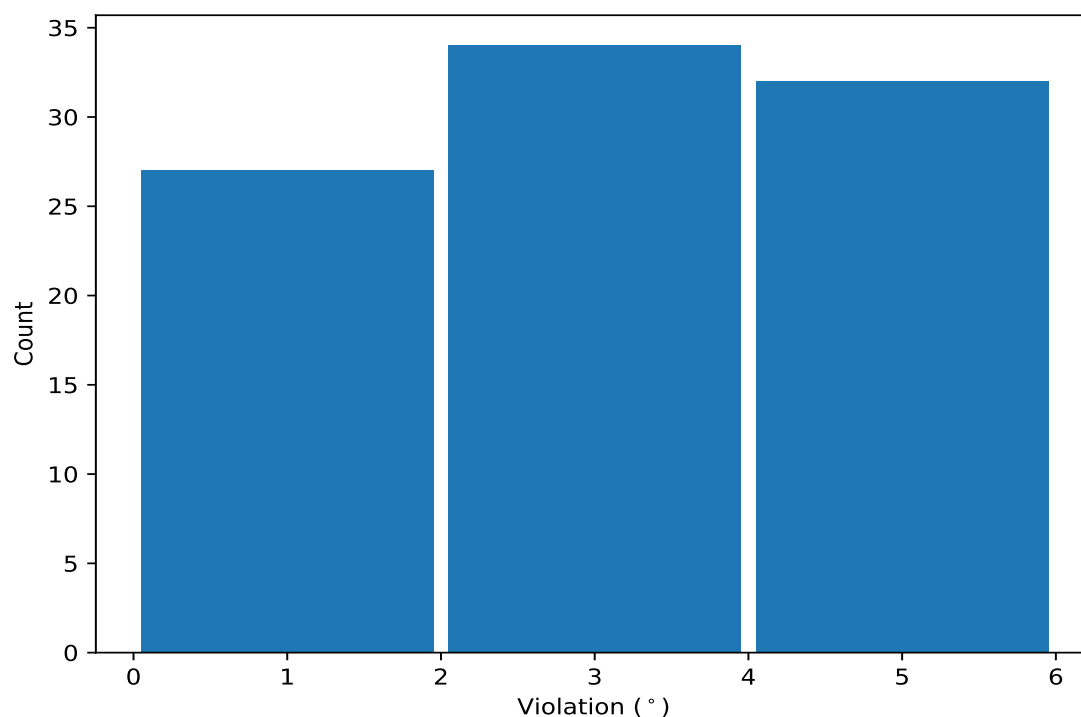
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	23	2.91	1.37	2.71
(1,57)	1:38:A:ASP:C	1:39:A:THR:N	1:39:A:THR:CA	1:39:A:THR:C	11	2.64	1.33	2.74
(1,28)	1:22:A:ASP:N	1:22:A:ASP:CA	1:22:A:ASP:C	1:23:A:GLU:N	9	4.21	0.54	4.21
(1,62)	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	1:43:A:ASP:N	8	4.08	1.22	4.73
(1,15)	1:11:A:LYS:C	1:12:A:ALA:N	1:12:A:ALA:CA	1:12:A:ALA:C	8	2.02	0.96	1.5
(1,96)	1:63:A:LYS:N	1:63:A:LYS:CA	1:63:A:LYS:C	1:64:A:ILE:N	6	3.19	1.01	3.52
(1,2)	1:5:A:TYR:N	1:5:A:TYR:CA	1:5:A:TYR:C	1:6:A:LEU:N	5	3.43	0.88	3.73
(1,99)	1:71:A:LYS:C	1:72:A:LYS:N	1:72:A:LYS:CA	1:72:A:LYS:C	4	3.83	0.42	3.94
(1,24)	1:18:A:ALA:N	1:18:A:ALA:CA	1:18:A:ALA:C	1:19:A:GLU:N	3	3.45	1.27	4.3
(1,67)	1:44:A:GLY:C	1:45:A:TRP:N	1:45:A:TRP:CA	1:45:A:TRP:C	3	2.74	0.83	3.25
(1,13)	1:10:A:ALA:C	1:11:A:LYS:N	1:11:A:LYS:CA	1:11:A:LYS:C	2	3.86	0.4	3.86
(1,56)	1:37:A:ARG:N	1:37:A:ARG:CA	1:37:A:ARG:C	1:38:A:ASP:N	2	3.43	0.34	3.43
(1,34)	1:25:A:SER:N	1:25:A:SER:CA	1:25:A:SER:C	1:26:A:PHE:N	2	3.42	1.14	3.42
(1,1)	1:4:A:LYS:C	1:5:A:TYR:N	1:5:A:TYR:CA	1:5:A:TYR:C	2	2.82	0.1	2.82
(1,58)	1:39:A:THR:N	1:39:A:THR:CA	1:39:A:THR:C	1:40:A:GLN:N	2	1.44	0.07	1.44

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 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 (°)
(1,28)	1:22:A:ASP:N	1:22:A:ASP:CA	1:22:A:ASP:C	1:23:A:GLU:N	36	4.97
(1,57)	1:38:A:ASP:C	1:39:A:THR:N	1:39:A:THR:CA	1:39:A:THR:C	1	4.96
(1,28)	1:22:A:ASP:N	1:22:A:ASP:CA	1:22:A:ASP:C	1:23:A:GLU:N	30	4.92
(1,62)	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	1:43:A:ASP:N	17	4.88
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	20	4.81
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	24	4.81
(1,62)	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	1:43:A:ASP:N	2	4.79
(1,62)	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	1:43:A:ASP:N	7	4.77
(1,62)	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	1:43:A:ASP:N	4	4.76
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	32	4.72
(1,62)	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	1:43:A:ASP:N	29	4.71
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	35	4.6
(1,34)	1:25:A:SER:N	1:25:A:SER:CA	1:25:A:SER:C	1:26:A:PHE:N	37	4.56
(1,2)	1:5:A:TYR:N	1:5:A:TYR:CA	1:5:A:TYR:C	1:6:A:LEU:N	16	4.56

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	14	4.53
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	3	4.48
(1,96)	1:63:A:LYS:N	1:63:A:LYS:CA	1:63:A:LYS:C	1:64:A:ILE:N	26	4.42
(1,28)	1:22:A:ASP:N	1:22:A:ASP:CA	1:22:A:ASP:C	1:23:A:GLU:N	22	4.41
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	7	4.4
(1,24)	1:18:A:ALA:N	1:18:A:ALA:CA	1:18:A:ALA:C	1:19:A:GLU:N	6	4.39
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	8	4.33
(1,24)	1:18:A:ALA:N	1:18:A:ALA:CA	1:18:A:ALA:C	1:19:A:GLU:N	11	4.3
(1,28)	1:22:A:ASP:N	1:22:A:ASP:CA	1:22:A:ASP:C	1:23:A:GLU:N	35	4.29
(1,99)	1:71:A:LYS:C	1:72:A:LYS:N	1:72:A:LYS:CA	1:72:A:LYS:C	15	4.26
(1,57)	1:38:A:ASP:C	1:39:A:THR:N	1:39:A:THR:CA	1:39:A:THR:C	35	4.26
(1,13)	1:10:A:ALA:C	1:11:A:LYS:N	1:11:A:LYS:CA	1:11:A:LYS:C	9	4.26
(1,28)	1:22:A:ASP:N	1:22:A:ASP:CA	1:22:A:ASP:C	1:23:A:GLU:N	25	4.21
(1,28)	1:22:A:ASP:N	1:22:A:ASP:CA	1:22:A:ASP:C	1:23:A:GLU:N	33	4.15
(1,57)	1:38:A:ASP:C	1:39:A:THR:N	1:39:A:THR:CA	1:39:A:THR:C	38	4.14
(1,62)	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	1:43:A:ASP:N	21	4.12
(1,99)	1:71:A:LYS:C	1:72:A:LYS:N	1:72:A:LYS:CA	1:72:A:LYS:C	18	4.11
(1,28)	1:22:A:ASP:N	1:22:A:ASP:CA	1:22:A:ASP:C	1:23:A:GLU:N	19	4.04
(1,15)	1:11:A:LYS:C	1:12:A:ALA:N	1:12:A:ALA:CA	1:12:A:ALA:C	10	3.89
(1,96)	1:63:A:LYS:N	1:63:A:LYS:CA	1:63:A:LYS:C	1:64:A:ILE:N	36	3.85
(1,96)	1:63:A:LYS:N	1:63:A:LYS:CA	1:63:A:LYS:C	1:64:A:ILE:N	13	3.84
(1,28)	1:22:A:ASP:N	1:22:A:ASP:CA	1:22:A:ASP:C	1:23:A:GLU:N	23	3.84
(1,56)	1:37:A:ARG:N	1:37:A:ARG:CA	1:37:A:ARG:C	1:38:A:ASP:N	33	3.78
(1,99)	1:71:A:LYS:C	1:72:A:LYS:N	1:72:A:LYS:CA	1:72:A:LYS:C	8	3.76
(1,2)	1:5:A:TYR:N	1:5:A:TYR:CA	1:5:A:TYR:C	1:6:A:LEU:N	14	3.75
(1,2)	1:5:A:TYR:N	1:5:A:TYR:CA	1:5:A:TYR:C	1:6:A:LEU:N	21	3.73
(1,62)	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	1:43:A:ASP:N	27	3.55
(1,13)	1:10:A:ALA:C	1:11:A:LYS:N	1:11:A:LYS:CA	1:11:A:LYS:C	26	3.46
(1,67)	1:44:A:GLY:C	1:45:A:TRP:N	1:45:A:TRP:CA	1:45:A:TRP:C	31	3.39
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	28	3.36
(1,67)	1:44:A:GLY:C	1:45:A:TRP:N	1:45:A:TRP:CA	1:45:A:TRP:C	38	3.25
(1,96)	1:63:A:LYS:N	1:63:A:LYS:CA	1:63:A:LYS:C	1:64:A:ILE:N	19	3.2
(1,2)	1:5:A:TYR:N	1:5:A:TYR:CA	1:5:A:TYR:C	1:6:A:LEU:N	31	3.2
(1,99)	1:71:A:LYS:C	1:72:A:LYS:N	1:72:A:LYS:CA	1:72:A:LYS:C	12	3.18
(1,57)	1:38:A:ASP:C	1:39:A:THR:N	1:39:A:THR:CA	1:39:A:THR:C	39	3.1
(1,57)	1:38:A:ASP:C	1:39:A:THR:N	1:39:A:THR:CA	1:39:A:THR:C	23	3.09
(1,56)	1:37:A:ARG:N	1:37:A:ARG:CA	1:37:A:ARG:C	1:38:A:ASP:N	39	3.09
(1,28)	1:22:A:ASP:N	1:22:A:ASP:CA	1:22:A:ASP:C	1:23:A:GLU:N	31	3.04
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	26	2.96
(1,1)	1:4:A:LYS:C	1:5:A:TYR:N	1:5:A:TYR:CA	1:5:A:TYR:C	5	2.92
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	39	2.86
(1,15)	1:11:A:LYS:C	1:12:A:ALA:N	1:12:A:ALA:CA	1:12:A:ALA:C	26	2.83
(1,15)	1:11:A:LYS:C	1:12:A:ALA:N	1:12:A:ALA:CA	1:12:A:ALA:C	23	2.82
(1,57)	1:38:A:ASP:C	1:39:A:THR:N	1:39:A:THR:CA	1:39:A:THR:C	31	2.74
(1,1)	1:4:A:LYS:C	1:5:A:TYR:N	1:5:A:TYR:CA	1:5:A:TYR:C	31	2.72
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	15	2.71
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	1	2.66
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	25	2.5
(1,96)	1:63:A:LYS:N	1:63:A:LYS:CA	1:63:A:LYS:C	1:64:A:ILE:N	37	2.42
(1,34)	1:25:A:SER:N	1:25:A:SER:CA	1:25:A:SER:C	1:26:A:PHE:N	40	2.28
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	19	2.1

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	37	2.09
(1,2)	1:5:A:TYR:N	1:5:A:TYR:CA	1:5:A:TYR:C	1:6:A:LEU:N	26	1.89
(1,60)	1:41:A:GLY:N	1:41:A:GLY:CA	1:41:A:GLY:C	1:42:A:LEU:N	34	1.81
(1,57)	1:38:A:ASP:C	1:39:A:THR:N	1:39:A:THR:CA	1:39:A:THR:C	33	1.78
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	34	1.73
(1,68)	1:45:A:TRP:N	1:45:A:TRP:CA	1:45:A:TRP:C	1:46:A:TRP:N	34	1.71
(1,24)	1:18:A:ALA:N	1:18:A:ALA:CA	1:18:A:ALA:C	1:19:A:GLU:N	26	1.65
(1,67)	1:44:A:GLY:C	1:45:A:TRP:N	1:45:A:TRP:CA	1:45:A:TRP:C	36	1.57
(1,15)	1:11:A:LYS:C	1:12:A:ALA:N	1:12:A:ALA:CA	1:12:A:ALA:C	24	1.56
(1,58)	1:39:A:THR:N	1:39:A:THR:CA	1:39:A:THR:C	1:40:A:GLN:N	33	1.52
(1,57)	1:38:A:ASP:C	1:39:A:THR:N	1:39:A:THR:CA	1:39:A:THR:C	34	1.51
(1,15)	1:11:A:LYS:C	1:12:A:ALA:N	1:12:A:ALA:CA	1:12:A:ALA:C	30	1.44
(1,96)	1:63:A:LYS:N	1:63:A:LYS:CA	1:63:A:LYS:C	1:64:A:ILE:N	30	1.42
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	12	1.41
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	27	1.41
(1,58)	1:39:A:THR:N	1:39:A:THR:CA	1:39:A:THR:C	1:40:A:GLN:N	39	1.37
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	13	1.3
(1,81)	1:52:A:GLY:C	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	39	1.3
(1,15)	1:11:A:LYS:C	1:12:A:ALA:N	1:12:A:ALA:CA	1:12:A:ALA:C	33	1.21
(1,15)	1:11:A:LYS:C	1:12:A:ALA:N	1:12:A:ALA:CA	1:12:A:ALA:C	21	1.2
(1,15)	1:11:A:LYS:C	1:12:A:ALA:N	1:12:A:ALA:CA	1:12:A:ALA:C	34	1.2
(1,57)	1:38:A:ASP:C	1:39:A:THR:N	1:39:A:THR:CA	1:39:A:THR:C	9	1.18
(1,57)	1:38:A:ASP:C	1:39:A:THR:N	1:39:A:THR:CA	1:39:A:THR:C	13	1.16
(1,57)	1:38:A:ASP:C	1:39:A:THR:N	1:39:A:THR:CA	1:39:A:THR:C	26	1.11
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	11	1.09
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	33	1.06
(1,62)	1:42:A:LEU:N	1:42:A:LEU:CA	1:42:A:LEU:C	1:43:A:ASP:N	11	1.04
(1,82)	1:53:A:ARG:N	1:53:A:ARG:CA	1:53:A:ARG:C	1:54:A:GLN:N	23	1.02