



Full wwPDB NMR Structure Validation Report ⓘ

Mar 28, 2024 – 12:09 pm GMT

PDB ID : 8PXW
BMRB ID : 34839
Title : Structure of the WW domain tandem of PRPF40A
Authors : Martinez-Lumbreras, S.; Sattler, M.
Deposited on : 2023-07-24

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:

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

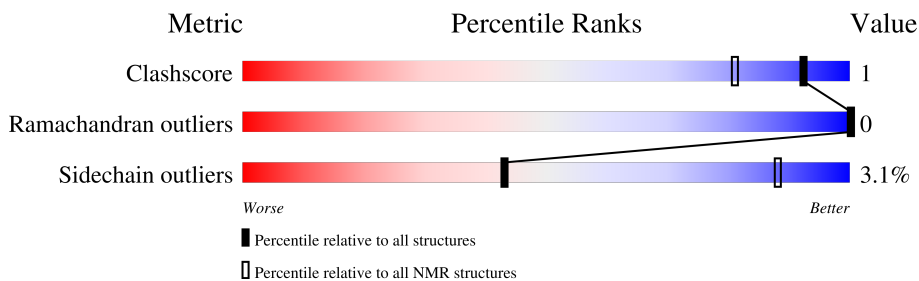
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 93%.

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	99	

2 Ensemble composition and analysis i

This entry contains 20 models. Model 5 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:145-A:171 (27)	0.20	10
2	A:186-A:215 (30)	0.18	5

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 4 clusters. No single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1582 atoms, of which 776 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Pre-mRNA-processing factor 40 homolog A.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	99	1582	508	776	132	163	3	0

There are 3 discrepancies between the modelled and reference sequences:

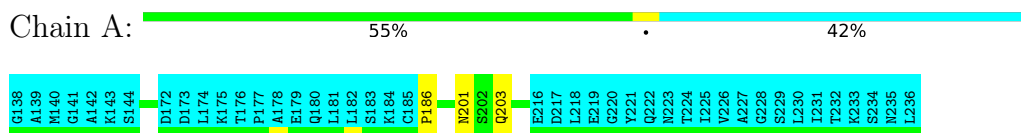
Chain	Residue	Modelled	Actual	Comment	Reference
A	138	GLY	-	expression tag	UNP O75400
A	139	ALA	-	expression tag	UNP O75400
A	140	MET	-	expression tag	UNP O75400

4 Residue-property plots i

4.1 Average score per residue in the NMR ensemble

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

- Molecule 1: Pre-mRNA-processing factor 40 homolog A

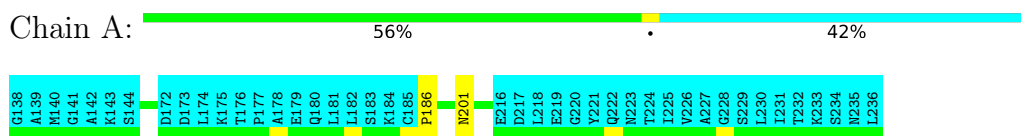


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

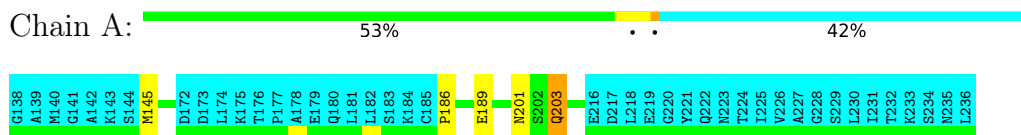
4.2.1 Score per residue for model 1

- Molecule 1: Pre-mRNA-processing factor 40 homolog A



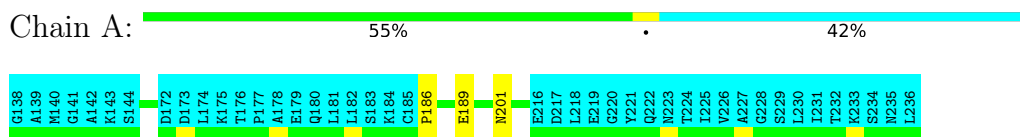
4.2.2 Score per residue for model 2

- Molecule 1: Pre-mRNA-processing factor 40 homolog A



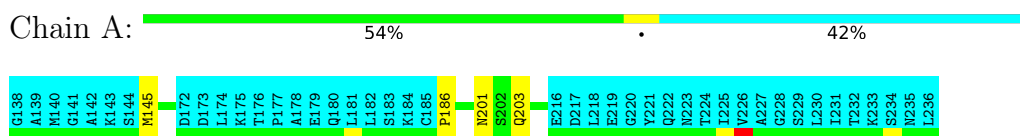
4.2.3 Score per residue for model 3

- Molecule 1: Pre-mRNA-processing factor 40 homolog A



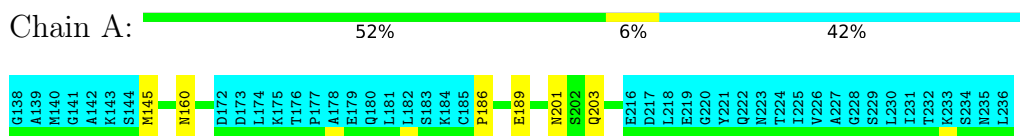
4.2.4 Score per residue for model 4

- Molecule 1: Pre-mRNA-processing factor 40 homolog A



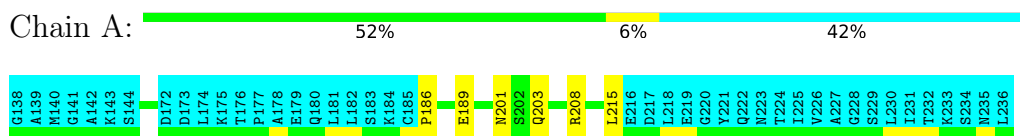
4.2.5 Score per residue for model 5 (medoid)

- Molecule 1: Pre-mRNA-processing factor 40 homolog A



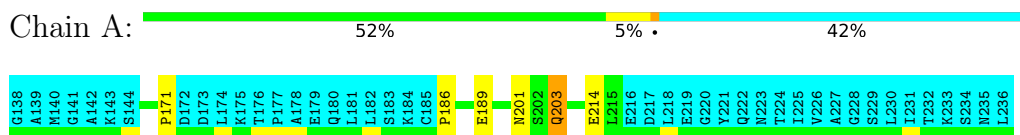
4.2.6 Score per residue for model 6

- Molecule 1: Pre-mRNA-processing factor 40 homolog A



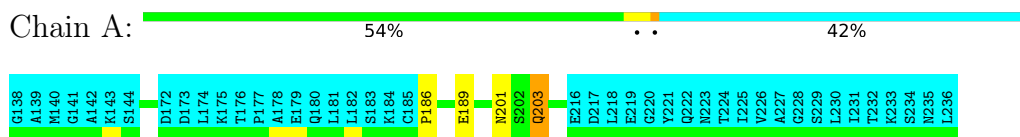
4.2.7 Score per residue for model 7

- Molecule 1: Pre-mRNA-processing factor 40 homolog A



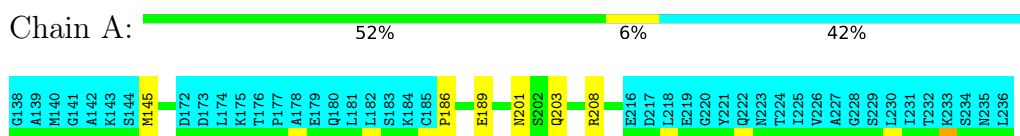
4.2.8 Score per residue for model 8

- Molecule 1: Pre-mRNA-processing factor 40 homolog A



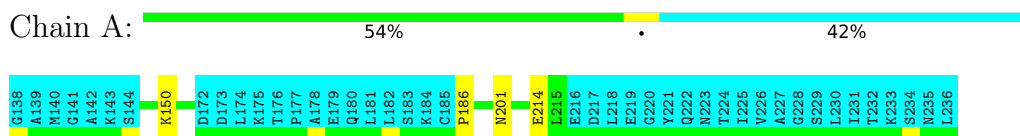
4.2.9 Score per residue for model 9

- Molecule 1: Pre-mRNA-processing factor 40 homolog A



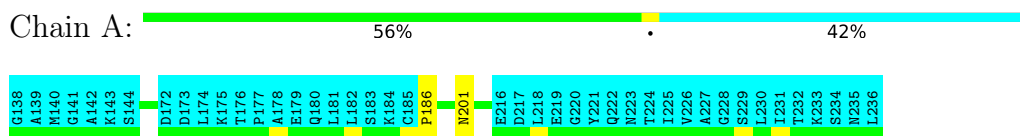
4.2.10 Score per residue for model 10

- Molecule 1: Pre-mRNA-processing factor 40 homolog A



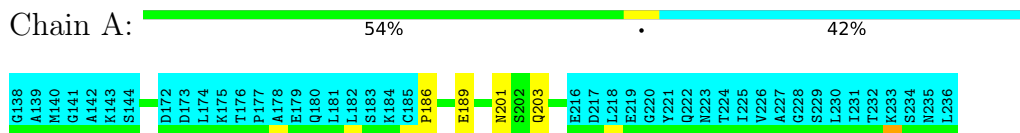
4.2.11 Score per residue for model 11

- Molecule 1: Pre-mRNA-processing factor 40 homolog A



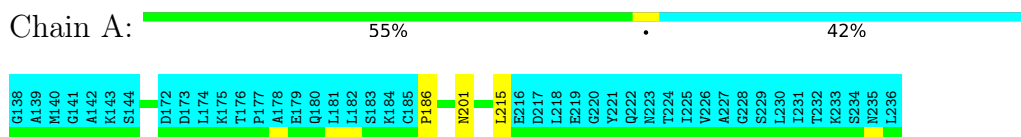
4.2.12 Score per residue for model 12

- Molecule 1: Pre-mRNA-processing factor 40 homolog A



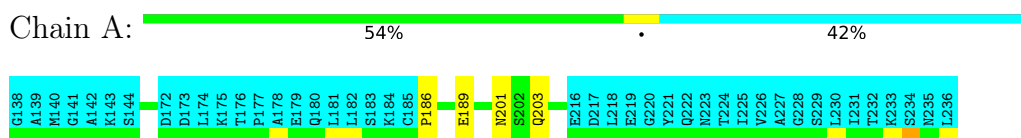
4.2.13 Score per residue for model 13

- Molecule 1: Pre-mRNA-processing factor 40 homolog A



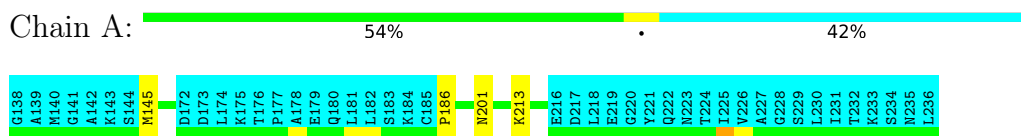
4.2.14 Score per residue for model 14

- Molecule 1: Pre-mRNA-processing factor 40 homolog A



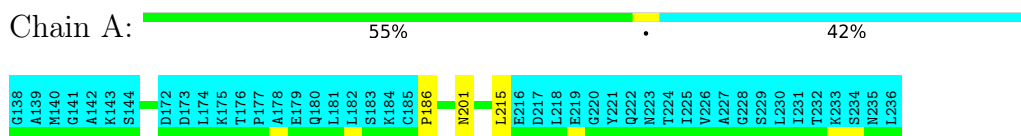
4.2.15 Score per residue for model 15

- Molecule 1: Pre-mRNA-processing factor 40 homolog A



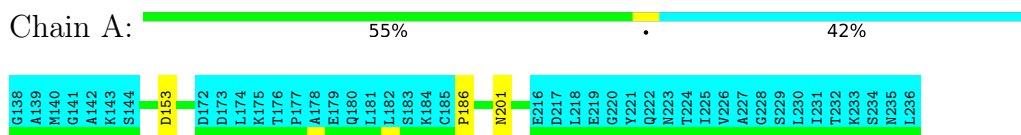
4.2.16 Score per residue for model 16

- Molecule 1: Pre-mRNA-processing factor 40 homolog A



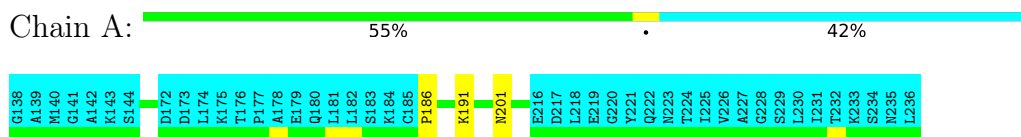
4.2.17 Score per residue for model 17

- Molecule 1: Pre-mRNA-processing factor 40 homolog A



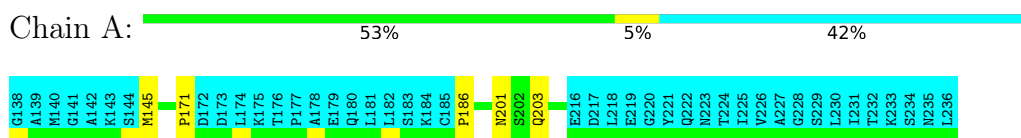
4.2.18 Score per residue for model 18

- Molecule 1: Pre-mRNA-processing factor 40 homolog A



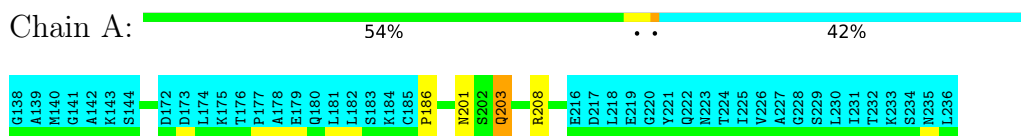
4.2.19 Score per residue for model 19

- Molecule 1: Pre-mRNA-processing factor 40 homolog A



4.2.20 Score per residue for model 20

- Molecule 1: Pre-mRNA-processing factor 40 homolog A



5 Refinement protocol and experimental data overview

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

Of the 200 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
ARIA	structure calculation	

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

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1315
Number of shifts mapped to atoms	1315
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	93%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	499	464	463	1±0
All	All	9980	9280	9260	26

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:186:PRO:O	1:A:201:ASN:HA	0.62	1.95	1	20
1:A:203:GLN:HA	1:A:203:GLN:HE21	0.46	1.71	20	3
1:A:145:MET:O	1:A:160:ASN:HA	0.42	2.12	5	1
1:A:203:GLN:HE21	1:A:203:GLN:HA	0.41	1.75	8	1
1:A:215:LEU:O	1:A:215:LEU:HG	0.40	2.16	13	1

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	57/99 (58%)	57±0 (100±1%)	0±0 (0±1%)	0±0 (0±0%)	100	100
All	All	1140/1980 (58%)	1137 (100%)	3 (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	54/88 (61%)	52±1 (97±2%)	2±1 (3±2%)	43	88
All	All	1080/1760 (61%)	1046 (97%)	34 (3%)	43	88

All 9 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	203	GLN	11
1	A	189	GLU	9
1	A	145	MET	5
1	A	208	ARG	3
1	A	214	GLU	2
1	A	150	LYS	1
1	A	213	LYS	1
1	A	153	ASP	1
1	A	191	LYS	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation i

The completeness of assignment taking into account all chemical shift lists is 93% for the well-defined parts and 94% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chemical_shifts_1*

7.1.1 Bookkeeping i

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1315
Number of shifts mapped to atoms	1315
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	9

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

- Chemical shift has been reported more than once. All 72 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	139	ALA	HB2	1.340	0.000	1
1	A	139	ALA	HB3	1.340	0.000	1
1	A	140	MET	HE2	2.032	0.000	1
1	A	140	MET	HE3	2.032	0.000	1
1	A	142	ALA	HB2	1.340	0.000	1
1	A	142	ALA	HB3	1.340	0.000	1
1	A	145	MET	HE2	1.965	0.000	1
1	A	145	MET	HE3	1.965	0.000	1
1	A	147	THR	HG22	1.189	0.000	1
1	A	147	THR	HG23	1.189	0.000	1
1	A	156	THR	HG22	0.824	0.000	1
1	A	156	THR	HG23	0.824	0.000	1
1	A	161	THR	HG22	1.345	0.000	1
1	A	161	THR	HG23	1.345	0.000	1
1	A	163	THR	HG22	0.916	0.009	1

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	163	THR	HG23	0.916	0.009	1
1	A	167	THR	HG22	1.192	0.000	1
1	A	167	THR	HG23	1.192	0.000	1
1	A	174	LEU	HD12	0.806	0.000	2
1	A	174	LEU	HD13	0.806	0.000	2
1	A	174	LEU	HD22	0.686	0.000	2
1	A	174	LEU	HD23	0.686	0.000	2
1	A	176	THR	HG22	1.272	0.000	1
1	A	176	THR	HG23	1.272	0.000	1
1	A	178	ALA	HB2	1.308	0.000	1
1	A	178	ALA	HB3	1.308	0.000	1
1	A	181	LEU	HD12	0.809	0.000	2
1	A	181	LEU	HD13	0.809	0.000	2
1	A	181	LEU	HD22	0.794	0.000	2
1	A	181	LEU	HD23	0.794	0.000	2
1	A	182	LEU	HD12	0.862	0.000	2
1	A	182	LEU	HD13	0.862	0.000	2
1	A	182	LEU	HD22	0.843	0.000	2
1	A	182	LEU	HD23	0.843	0.000	2
1	A	204	THR	HG22	0.924	0.000	1
1	A	204	THR	HG23	0.924	0.000	1
1	A	210	ALA	HB2	1.210	0.000	1
1	A	210	ALA	HB3	1.210	0.000	1
1	A	215	LEU	HD12	0.887	0.000	2
1	A	215	LEU	HD13	0.887	0.000	2
1	A	215	LEU	HD22	0.840	0.000	2
1	A	215	LEU	HD23	0.840	0.000	2
1	A	218	LEU	HD12	0.941	0.000	2
1	A	218	LEU	HD13	0.941	0.000	2
1	A	218	LEU	HD22	0.874	0.000	2
1	A	218	LEU	HD23	0.874	0.000	2
1	A	224	THR	HG22	1.129	0.000	1
1	A	224	THR	HG23	1.129	0.000	1
1	A	225	ILE	HD12	0.735	0.000	1
1	A	225	ILE	HD13	0.735	0.000	1
1	A	225	ILE	HG22	0.779	0.000	1
1	A	225	ILE	HG23	0.779	0.000	1
1	A	226	VAL	HG12	0.871	0.000	2
1	A	226	VAL	HG13	0.871	0.000	2
1	A	226	VAL	HG22	0.858	0.000	2
1	A	226	VAL	HG23	0.858	0.000	2

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	227	ALA	HB2	1.340	0.000	1
1	A	227	ALA	HB3	1.340	0.000	1
1	A	230	LEU	HD12	0.839	0.000	2
1	A	230	LEU	HD13	0.839	0.000	2
1	A	230	LEU	HD22	0.777	0.000	2
1	A	230	LEU	HD23	0.777	0.000	2
1	A	231	ILE	HD12	0.775	0.000	1
1	A	231	ILE	HD13	0.775	0.000	1
1	A	231	ILE	HG22	0.827	0.000	1
1	A	231	ILE	HG23	0.827	0.000	1
1	A	232	THR	HG22	1.129	0.000	1
1	A	232	THR	HG23	1.129	0.000	1
1	A	236	LEU	HD12	0.828	0.000	2
1	A	236	LEU	HD13	0.828	0.000	2
1	A	236	LEU	HD22	0.786	0.000	2
1	A	236	LEU	HD23	0.786	0.000	2

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
$^{13}\text{C}_\alpha$	99	0.39 ± 0.15	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	92	0.34 ± 0.08	None needed (< 0.5 ppm)
$^{13}\text{C}'$	97	0.47 ± 0.10	None needed (< 0.5 ppm)
^{15}N	91	0.06 ± 0.43	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 93%, i.e. 736 atoms were assigned a chemical shift out of a possible 795. 0 out of 1 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	275/277 (99%)	110/111 (99%)	113/114 (99%)	52/52 (100%)
Sidechain	353/399 (88%)	233/251 (93%)	114/129 (88%)	6/19 (32%)
Aromatic	108/119 (91%)	54/56 (96%)	50/57 (88%)	4/6 (67%)
Overall	736/795 (93%)	397/418 (95%)	277/300 (92%)	62/77 (81%)

The following table shows the completeness of the chemical shift assignments for the full structure.

The overall completeness is 94%, i.e. 1242 atoms were assigned a chemical shift out of a possible 1320. 0 out of 8 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	482/489 (99%)	195/198 (98%)	196/198 (99%)	91/93 (98%)
Sidechain	644/703 (92%)	429/449 (96%)	205/227 (90%)	10/27 (37%)
Aromatic	116/128 (91%)	58/60 (97%)	54/62 (87%)	4/6 (67%)
Overall	1242/1320 (94%)	682/707 (96%)	455/487 (93%)	105/126 (83%)

7.1.4 Statistically unusual chemical shifts [i](#)

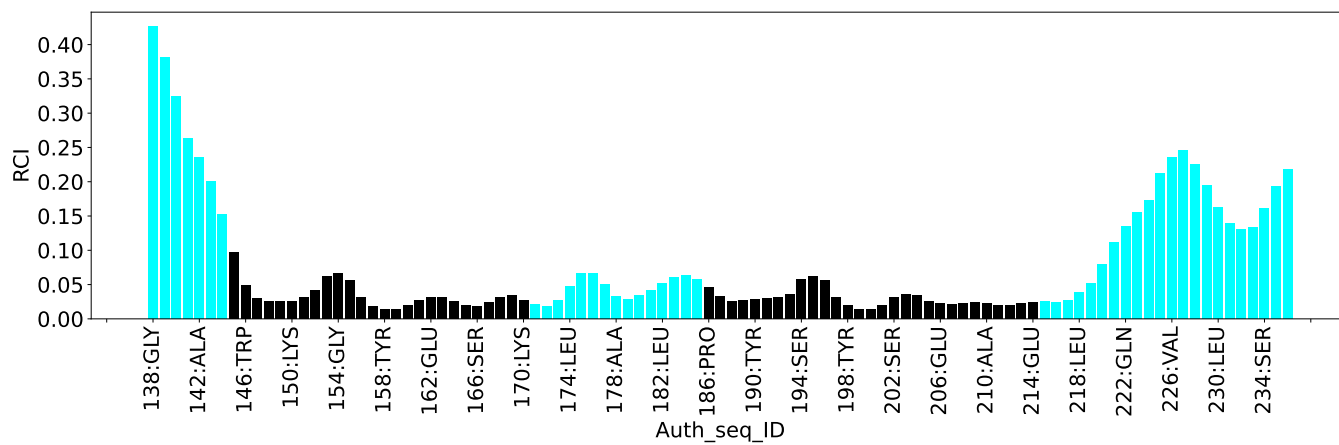
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	163	THR	HG1	5.20	0.08 – 2.19	19.3
1	A	201	ASN	HB3	-0.49	1.12 – 4.38	-9.9
1	A	160	ASN	HB3	-0.00	1.12 – 4.38	-8.4
1	A	171	PRO	HG3	-0.01	0.33 – 3.48	-6.1
1	A	212	PRO	HG3	0.09	0.33 – 3.48	-5.8
1	A	171	PRO	HG2	0.19	0.41 – 3.45	-5.7
1	A	149	HIS	HB3	1.01	1.18 – 4.91	-5.5
1	A	212	PRO	HG2	0.27	0.41 – 3.45	-5.5
1	A	190	TYR	HB2	1.09	1.09 – 4.72	-5.0

7.1.5 Random Coil Index (RCI) plots [i](#)

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

Random coil index (RCI) for chain A:



8 NMR restraints analysis

8.1 Conformationally restricting restraints

The following table provides the summary of experimentally observed NMR restraints in different categories. Restraints are classified into different categories based on the sequence separation of the atoms involved.

Description	Value
Total distance restraints	2409
Intra-residue ($ i-j =0$)	914
Sequential ($ i-j =1$)	513
Medium range ($ i-j >1$ and $ i-j <5$)	352
Long range ($ i-j \geq 5$)	630
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	142
Number of unmapped restraints	0
Number of restraints per residue	25.8
Number of long range restraints per residue ¹	6.4

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)	20.8	0.2
0.2-0.5 (Medium)	19.1	0.5
>0.5 (Large)	3.8	1.95

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)	15.9	8.27
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis [i](#)

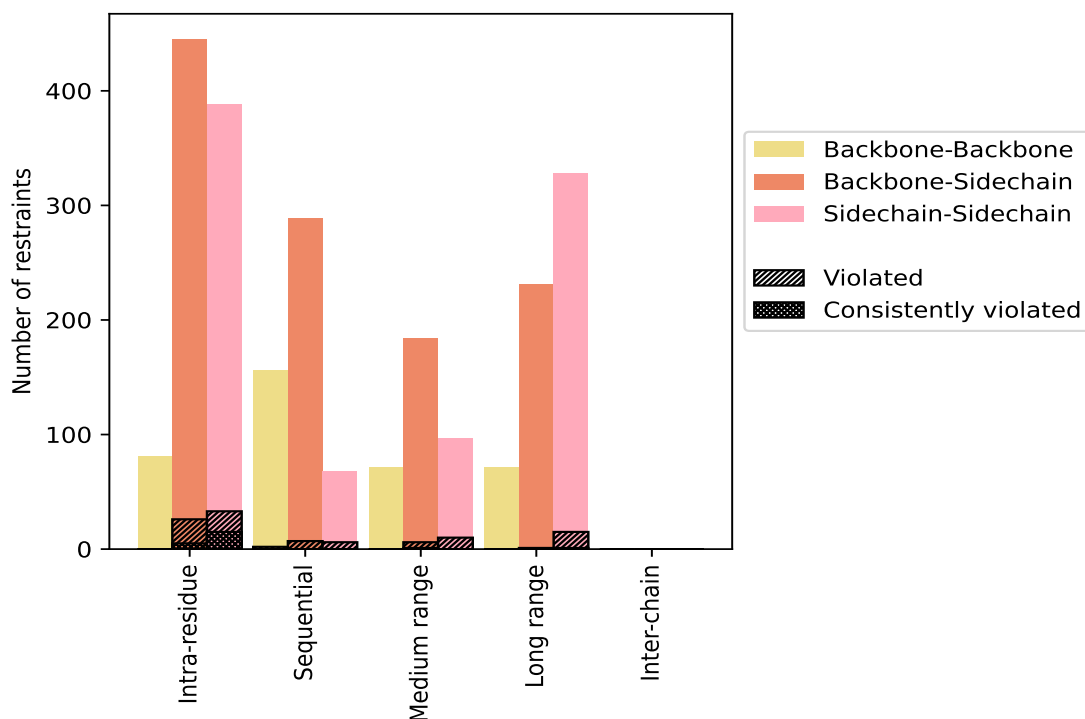
9.1 Summary of distance violations [i](#)

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

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue ($i-j =0$)	914	37.9	59	6.5	2.4	20	2.2	0.8
Backbone-Backbone	81	3.4	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	445	18.5	26	5.8	1.1	5	1.1	0.2
Sidechain-Sidechain	388	16.1	33	8.5	1.4	15	3.9	0.6
Sequential ($i-j =1$)	513	21.3	15	2.9	0.6	0	0.0	0.0
Backbone-Backbone	156	6.5	2	1.3	0.1	0	0.0	0.0
Backbone-Sidechain	289	12.0	7	2.4	0.3	0	0.0	0.0
Sidechain-Sidechain	68	2.8	6	8.8	0.2	0	0.0	0.0
Medium range ($i-j >1$ & $i-j <5$)	352	14.6	16	4.5	0.7	1	0.3	0.0
Backbone-Backbone	71	2.9	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	184	7.6	6	3.3	0.2	1	0.5	0.0
Sidechain-Sidechain	97	4.0	10	10.3	0.4	0	0.0	0.0
Long range ($i-j \geq 5$)	630	26.2	16	2.5	0.7	1	0.2	0.0
Backbone-Backbone	71	2.9	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	231	9.6	1	0.4	0.0	0	0.0	0.0
Sidechain-Sidechain	328	13.6	15	4.6	0.6	1	0.3	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	2409	100.0	106	4.4	4.4	22	0.9	0.9
Backbone-Backbone	379	15.7	2	0.5	0.1	0	0.0	0.0
Backbone-Sidechain	1149	47.7	40	3.5	1.7	6	0.5	0.2
Sidechain-Sidechain	881	36.6	64	7.3	2.7	16	1.8	0.7

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 disulfid 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	37	3	1	6	0	47	0.26	0.63	0.14	0.22
2	34	2	1	4	0	41	0.25	0.89	0.15	0.21
3	35	1	2	1	0	39	0.26	0.9	0.16	0.21
4	33	3	2	3	0	41	0.23	0.53	0.1	0.2
5	34	0	1	3	0	38	0.27	0.85	0.17	0.24
6	38	1	5	5	0	49	0.23	0.52	0.12	0.19
7	37	2	5	4	0	48	0.29	1.23	0.23	0.22
8	37	3	3	2	0	45	0.26	0.8	0.16	0.21
9	37	2	1	4	0	44	0.25	0.86	0.15	0.19
10	35	4	4	4	0	47	0.27	1.1	0.19	0.21
11	37	3	2	6	0	48	0.29	1.02	0.2	0.21

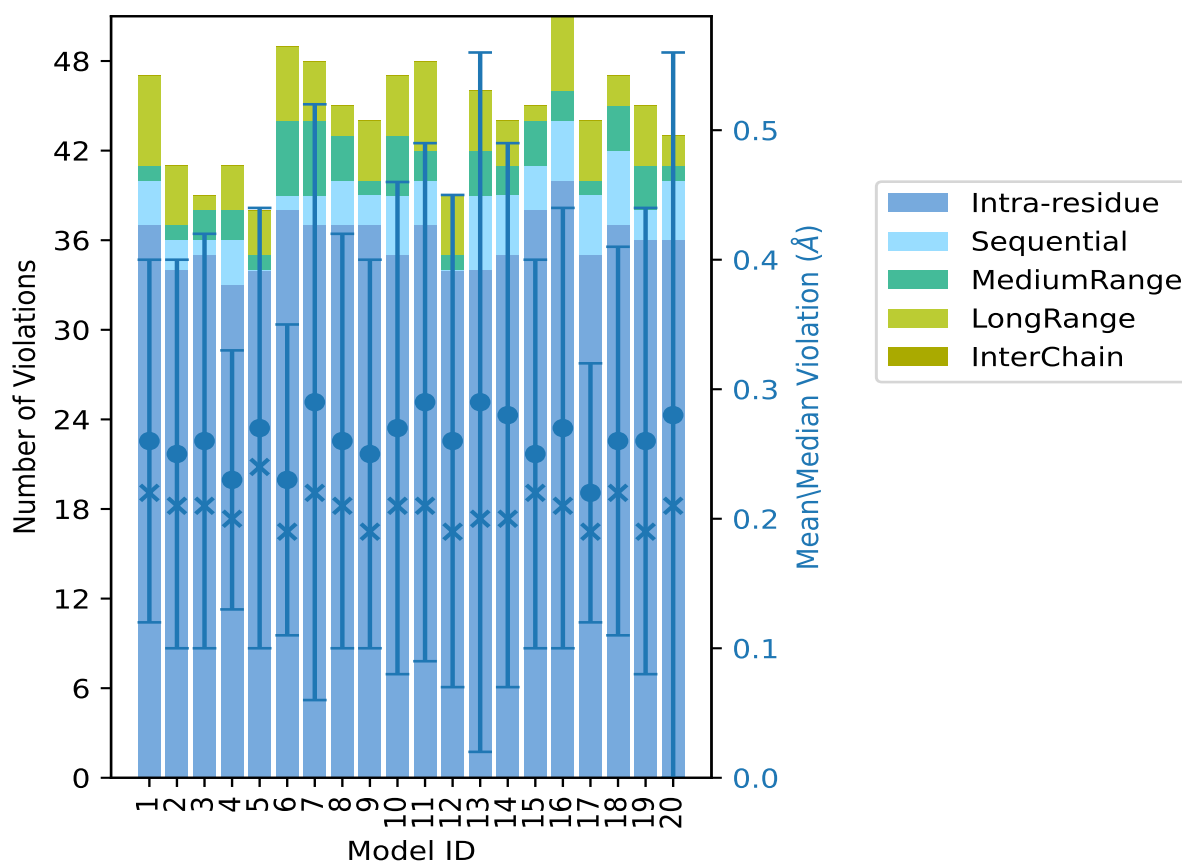
Continued on next page...

Continued from previous page...

Model ID	Number of violations					Total	Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵					
12	34	0	1	4	0	39	0.26	1.0	0.19	0.19
13	34	5	3	4	0	46	0.29	1.74	0.27	0.2
14	35	4	2	3	0	44	0.28	1.07	0.21	0.2
15	38	3	3	1	0	45	0.25	0.89	0.15	0.22
16	40	4	2	5	0	51	0.27	0.89	0.17	0.21
17	35	4	1	4	0	44	0.22	0.5	0.1	0.19
18	37	5	3	2	0	47	0.26	0.94	0.15	0.22
19	36	2	3	4	0	45	0.26	1.13	0.18	0.19
20	36	4	1	2	0	43	0.28	1.95	0.28	0.21

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

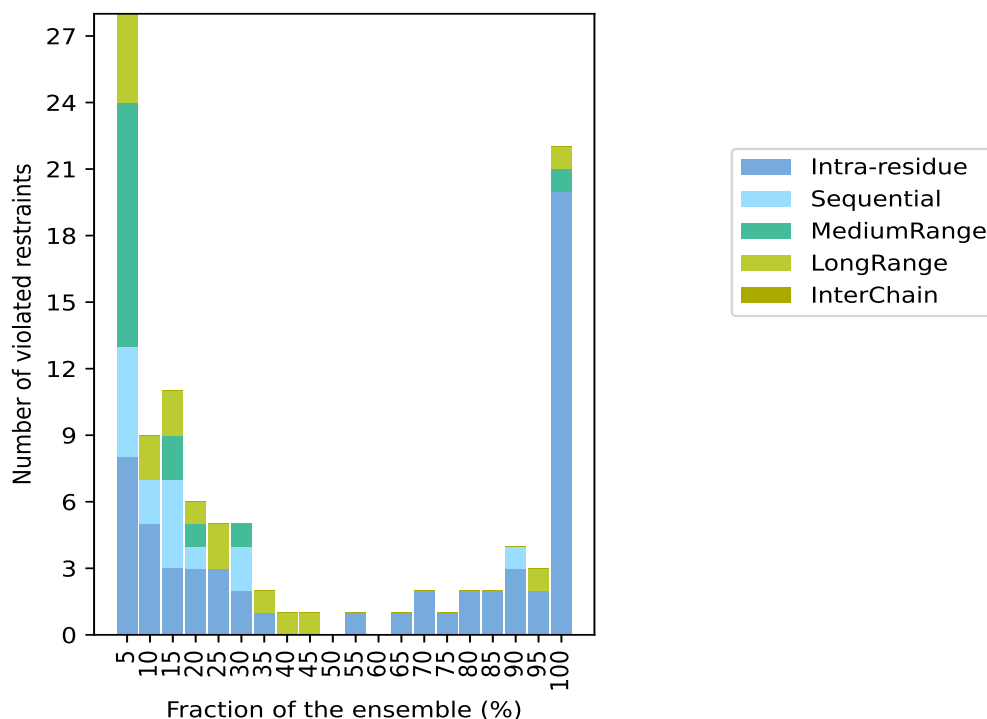
9.3 Distance violation statistics for the ensemble

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, 2303(IR:855, SQ:498, MR:336, LR:614, 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	%
8	5	11	4	0	28	1	5.0
5	2	0	2	0	9	2	10.0
3	4	2	2	0	11	3	15.0
3	1	1	1	0	6	4	20.0
3	0	0	2	0	5	5	25.0
2	2	1	0	0	5	6	30.0
1	0	0	1	0	2	7	35.0
0	0	0	1	0	1	8	40.0
0	0	0	1	0	1	9	45.0
0	0	0	0	0	0	10	50.0
1	0	0	0	0	1	11	55.0
0	0	0	0	0	0	12	60.0
1	0	0	0	0	1	13	65.0
2	0	0	0	0	2	14	70.0
1	0	0	0	0	1	15	75.0
2	0	0	0	0	2	16	80.0
2	0	0	0	0	2	17	85.0
3	1	0	0	0	4	18	90.0
2	0	0	1	0	3	19	95.0
20	0	1	1	0	22	20	100.0

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

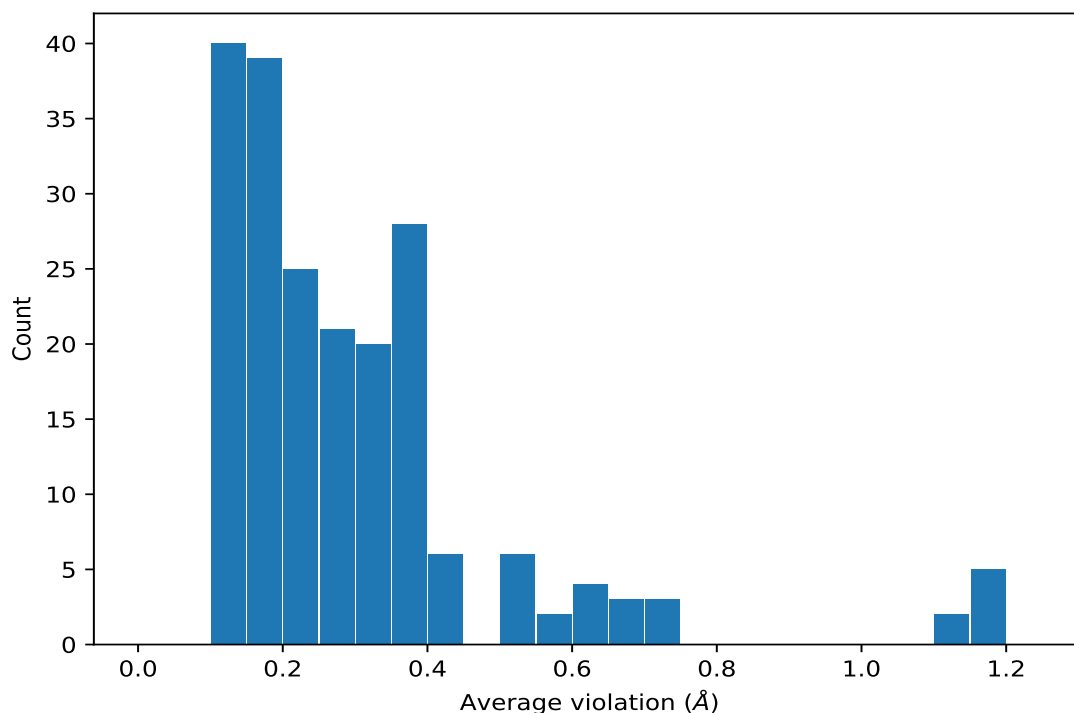
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



9.4 Most violated distance restraints in the ensemble [i](#)

9.4.1 Histogram : Distribution of mean distance violations [i](#)

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



9.4.2 Table: Most violated distance restraints [i](#)

The following table provides the mean and the standard deviation of the 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)
(1,1104)	1:179:A:GLU:HA	1:182:A:LEU:HD23	20	0.74	0.23	0.86
(1,1104)	1:179:A:GLU:HA	1:182:A:LEU:HD21	20	0.74	0.23	0.86
(1,1104)	1:179:A:GLU:HA	1:182:A:LEU:HD22	20	0.74	0.23	0.86
(1,1453)	1:182:A:LEU:HG	1:182:A:LEU:HD11	20	0.42	0.02	0.42
(1,1453)	1:182:A:LEU:HG	1:182:A:LEU:HD13	20	0.42	0.02	0.42
(1,1453)	1:182:A:LEU:HG	1:182:A:LEU:HD12	20	0.42	0.02	0.42
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD23	20	0.37	0.01	0.37
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD21	20	0.37	0.01	0.37
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD12	20	0.37	0.01	0.37
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD11	20	0.37	0.01	0.37
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD22	20	0.37	0.01	0.37
(1,1438)	1:204:A:THR:HB	1:204:A:THR:HG21	20	0.37	0.01	0.37
(1,1438)	1:204:A:THR:HB	1:204:A:THR:HG23	20	0.37	0.01	0.37
(1,1438)	1:204:A:THR:HB	1:204:A:THR:HG22	20	0.37	0.01	0.37
(1,2358)	1:182:A:LEU:HG	1:182:A:LEU:HD11	20	0.35	0.02	0.36
(1,2358)	1:182:A:LEU:HG	1:182:A:LEU:HD13	20	0.35	0.02	0.36

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,2358)	1:182:A:LEU:HD21	1:182:A:LEU:HG	20	0.35	0.02	0.36
(1,2358)	1:182:A:LEU:HD23	1:182:A:LEU:HG	20	0.35	0.02	0.36
(1,2358)	1:182:A:LEU:HG	1:182:A:LEU:HD12	20	0.35	0.02	0.36
(1,2358)	1:182:A:LEU:HD22	1:182:A:LEU:HG	20	0.35	0.02	0.36
(1,2279)	1:184:A:LYS:HD3	1:184:A:LYS:HA	20	0.35	0.07	0.34
(1,2279)	1:184:A:LYS:HD2	1:184:A:LYS:HA	20	0.35	0.07	0.34
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG22	20	0.31	0.01	0.31
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG12	20	0.31	0.01	0.31
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG23	20	0.31	0.01	0.31
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG21	20	0.31	0.01	0.31
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG11	20	0.31	0.01	0.31
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG13	20	0.31	0.01	0.31
(1,637)	1:224:A:THR:H	1:224:A:THR:HG22	20	0.25	0.04	0.26
(1,637)	1:224:A:THR:H	1:224:A:THR:HG23	20	0.25	0.04	0.26
(1,637)	1:224:A:THR:H	1:224:A:THR:HG21	20	0.25	0.04	0.26
(1,1105)	1:181:A:LEU:HG	1:181:A:LEU:HD21	20	0.25	0.02	0.25
(1,1105)	1:181:A:LEU:HG	1:181:A:LEU:HD23	20	0.25	0.02	0.25
(1,1105)	1:181:A:LEU:HG	1:181:A:LEU:HD22	20	0.25	0.02	0.25
(1,1422)	1:163:A:THR:HG21	1:163:A:THR:HB	20	0.25	0.01	0.25
(1,1422)	1:163:A:THR:HG23	1:163:A:THR:HB	20	0.25	0.01	0.25
(1,1422)	1:163:A:THR:HG22	1:163:A:THR:HB	20	0.25	0.01	0.25
(1,1713)	1:181:A:LEU:HD13	1:181:A:LEU:HG	20	0.23	0.01	0.24
(1,1713)	1:181:A:LEU:HD11	1:181:A:LEU:HG	20	0.23	0.01	0.24
(1,1713)	1:181:A:LEU:HD12	1:181:A:LEU:HG	20	0.23	0.01	0.24
(1,2334)	1:203:A:GLN:HB2	1:203:A:GLN:HG2	20	0.21	0.07	0.24
(1,2063)	1:218:A:LEU:HG	1:218:A:LEU:HD23	20	0.21	0.02	0.21
(1,2063)	1:218:A:LEU:HG	1:218:A:LEU:HD21	20	0.21	0.02	0.21
(1,2063)	1:218:A:LEU:HG	1:218:A:LEU:HD22	20	0.21	0.02	0.21
(1,1442)	1:224:A:THR:HB	1:224:A:THR:HG23	20	0.2	0.01	0.2
(1,1442)	1:224:A:THR:HB	1:224:A:THR:HG22	20	0.2	0.01	0.2
(1,1442)	1:224:A:THR:HB	1:224:A:THR:HG21	20	0.2	0.01	0.2
(1,1033)	1:142:A:ALA:HB2	1:142:A:ALA:HA	20	0.19	0.01	0.19
(1,1033)	1:142:A:ALA:HB3	1:142:A:ALA:HA	20	0.19	0.01	0.19
(1,1033)	1:142:A:ALA:HB1	1:142:A:ALA:HA	20	0.19	0.01	0.19
(1,1426)	1:225:A:ILE:HB	1:225:A:ILE:HG23	20	0.18	0.01	0.18
(1,1426)	1:225:A:ILE:HB	1:225:A:ILE:HG22	20	0.18	0.01	0.18
(1,1426)	1:225:A:ILE:HB	1:225:A:ILE:HG21	20	0.18	0.01	0.18
(1,1605)	1:227:A:ALA:HA	1:227:A:ALA:HB3	20	0.15	0.01	0.15
(1,1605)	1:227:A:ALA:HA	1:227:A:ALA:HB1	20	0.15	0.01	0.15
(1,1605)	1:227:A:ALA:HA	1:227:A:ALA:HB2	20	0.15	0.01	0.15
(1,1188)	1:218:A:LEU:HG	1:218:A:LEU:HD23	20	0.14	0.02	0.14
(1,1188)	1:218:A:LEU:HG	1:218:A:LEU:HD21	20	0.14	0.02	0.14

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,1188)	1:218:A:LEU:HG	1:218:A:LEU:HD22	20	0.14	0.02	0.14
(1,779)	1:203:A:GLN:HE21	1:203:A:GLN:HE22	20	0.13	0.0	0.13
(1,1042)	1:210:A:ALA:HA	1:210:A:ALA:HB1	20	0.13	0.01	0.14
(1,1042)	1:210:A:ALA:HA	1:210:A:ALA:HB2	20	0.13	0.01	0.14
(1,1042)	1:210:A:ALA:HA	1:210:A:ALA:HB3	20	0.13	0.01	0.14
(1,1028)	1:147:A:THR:HB	1:147:A:THR:HG23	20	0.12	0.01	0.12
(1,1028)	1:147:A:THR:HB	1:147:A:THR:HG21	20	0.12	0.01	0.12
(1,1028)	1:147:A:THR:HB	1:147:A:THR:HG22	20	0.12	0.01	0.12
(1,501)	1:222:A:GLN:HE22	1:222:A:GLN:HE21	20	0.12	0.0	0.12
(1,1026)	1:159:A:TYR:HE1	1:147:A:THR:HG23	19	0.38	0.13	0.38
(1,1026)	1:159:A:TYR:HE1	1:147:A:THR:HG21	19	0.38	0.13	0.38
(1,1026)	1:159:A:TYR:HE2	1:147:A:THR:HG22	19	0.38	0.13	0.38
(1,1026)	1:159:A:TYR:HE2	1:147:A:THR:HG21	19	0.38	0.13	0.38
(1,1026)	1:159:A:TYR:HE1	1:147:A:THR:HG22	19	0.38	0.13	0.38
(1,1026)	1:159:A:TYR:HE2	1:147:A:THR:HG23	19	0.38	0.13	0.38
(1,1034)	1:178:A:ALA:HA	1:178:A:ALA:HB2	19	0.16	0.02	0.17
(1,1034)	1:178:A:ALA:HA	1:178:A:ALA:HB1	19	0.16	0.02	0.17
(1,1034)	1:178:A:ALA:HA	1:178:A:ALA:HB3	19	0.16	0.02	0.17
(1,2073)	1:218:A:LEU:HB2	1:218:A:LEU:HD12	19	0.15	0.02	0.16
(1,2073)	1:218:A:LEU:HG	1:218:A:LEU:HD13	19	0.15	0.02	0.16
(1,2073)	1:218:A:LEU:HG	1:218:A:LEU:HD12	19	0.15	0.02	0.16
(1,2073)	1:218:A:LEU:HB2	1:218:A:LEU:HD11	19	0.15	0.02	0.16
(1,2073)	1:218:A:LEU:HB2	1:218:A:LEU:HD13	19	0.15	0.02	0.16
(1,2073)	1:218:A:LEU:HG	1:218:A:LEU:HD11	19	0.15	0.02	0.16
(1,1847)	1:205:A:LYS:H	1:205:A:LYS:HD2	18	0.24	0.05	0.24
(1,1847)	1:205:A:LYS:H	1:205:A:LYS:HD3	18	0.24	0.05	0.24
(1,1441)	1:203:A:GLN:HG3	1:204:A:THR:HG23	18	0.2	0.06	0.19
(1,1441)	1:203:A:GLN:HG3	1:204:A:THR:HG22	18	0.2	0.06	0.19
(1,1441)	1:203:A:GLN:HG3	1:204:A:THR:HG21	18	0.2	0.06	0.19
(1,1048)	1:225:A:ILE:HG13	1:225:A:ILE:HG21	18	0.19	0.02	0.19
(1,1048)	1:225:A:ILE:HG13	1:225:A:ILE:HG23	18	0.19	0.02	0.19
(1,1048)	1:225:A:ILE:HG13	1:225:A:ILE:HG22	18	0.19	0.02	0.19
(1,2351)	1:205:A:LYS:HE2	1:205:A:LYS:HD3	18	0.13	0.02	0.14
(1,2351)	1:205:A:LYS:HE2	1:205:A:LYS:HD2	18	0.13	0.02	0.14
(1,2351)	1:205:A:LYS:HE3	1:205:A:LYS:HD2	18	0.13	0.02	0.14
(1,1558)	1:174:A:LEU:HD23	1:174:A:LEU:HA	17	0.52	0.04	0.52
(1,1558)	1:174:A:LEU:HD21	1:174:A:LEU:HA	17	0.52	0.04	0.52
(1,1558)	1:174:A:LEU:HD22	1:174:A:LEU:HA	17	0.52	0.04	0.52
(1,1669)	1:174:A:LEU:HD13	1:174:A:LEU:HB3	17	0.22	0.03	0.22
(1,1669)	1:174:A:LEU:HD11	1:174:A:LEU:HB3	17	0.22	0.03	0.22
(1,1669)	1:174:A:LEU:HD12	1:174:A:LEU:HB3	17	0.22	0.03	0.22
(1,2298)	1:205:A:LYS:HB3	1:205:A:LYS:HE3	16	0.19	0.05	0.2

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,2298)	1:205:A:LYS:HB3	1:205:A:LYS:HE2	16	0.19	0.05	0.2
(1,2298)	1:205:A:LYS:HB2	1:205:A:LYS:HE3	16	0.19	0.05	0.2
(1,2298)	1:205:A:LYS:HB2	1:205:A:LYS:HE2	16	0.19	0.05	0.2
(1,1844)	1:164:A:LYS:H	1:164:A:LYS:HD2	16	0.18	0.03	0.18
(1,1844)	1:164:A:LYS:H	1:164:A:LYS:HD3	16	0.18	0.03	0.18
(1,2297)	1:164:A:LYS:HB2	1:164:A:LYS:HE2	15	0.18	0.07	0.17
(1,2297)	1:164:A:LYS:HB2	1:164:A:LYS:HE3	15	0.18	0.07	0.17
(1,2297)	1:164:A:LYS:HB3	1:164:A:LYS:HE3	15	0.18	0.07	0.17
(1,2297)	1:164:A:LYS:HB3	1:164:A:LYS:HE2	15	0.18	0.07	0.17
(1,1058)	1:231:A:ILE:HD11	1:231:A:ILE:HA	14	0.37	0.18	0.49
(1,1058)	1:231:A:ILE:HD13	1:231:A:ILE:HA	14	0.37	0.18	0.49
(1,1058)	1:231:A:ILE:HD12	1:231:A:ILE:HA	14	0.37	0.18	0.49
(1,1719)	1:215:A:LEU:HG	1:215:A:LEU:HD23	14	0.12	0.02	0.12
(1,1719)	1:215:A:LEU:HG	1:215:A:LEU:HD21	14	0.12	0.02	0.12
(1,1719)	1:215:A:LEU:HG	1:215:A:LEU:HD22	14	0.12	0.02	0.12
(1,1428)	1:145:A:MET:HG2	1:145:A:MET:HE2	13	0.18	0.01	0.18
(1,1428)	1:145:A:MET:HG2	1:145:A:MET:HE1	13	0.18	0.01	0.18
(1,1428)	1:145:A:MET:HG2	1:145:A:MET:HE3	13	0.18	0.01	0.18
(1,1187)	1:218:A:LEU:HG	1:218:A:LEU:HD13	11	0.11	0.01	0.12
(1,1187)	1:218:A:LEU:HG	1:218:A:LEU:HD12	11	0.11	0.01	0.12
(1,1187)	1:218:A:LEU:HG	1:218:A:LEU:HD11	11	0.11	0.01	0.12
(1,1068)	1:147:A:THR:HB	1:161:A:THR:HG21	9	0.16	0.02	0.15
(1,1068)	1:147:A:THR:HB	1:161:A:THR:HG23	9	0.16	0.02	0.15
(1,1068)	1:147:A:THR:HB	1:161:A:THR:HG22	9	0.16	0.02	0.15
(1,2319)	1:215:A:LEU:HD22	1:189:A:GLU:HG3	8	0.29	0.14	0.26
(1,2319)	1:215:A:LEU:HD21	1:189:A:GLU:HG3	8	0.29	0.14	0.26
(1,2319)	1:215:A:LEU:HD13	1:189:A:GLU:HG3	8	0.29	0.14	0.26
(1,2319)	1:215:A:LEU:HD23	1:189:A:GLU:HG3	8	0.29	0.14	0.26
(1,2253)	1:182:A:LEU:HD23	1:221:A:TYR:HB3	7	0.41	0.2	0.35
(1,2253)	1:182:A:LEU:HD21	1:221:A:TYR:HB3	7	0.41	0.2	0.35
(1,2253)	1:182:A:LEU:HD22	1:221:A:TYR:HB3	7	0.41	0.2	0.35
(1,2141)	1:169:A:GLU:HA	1:169:A:GLU:HG3	7	0.18	0.03	0.17
(1,2376)	1:226:A:VAL:HG12	1:227:A:ALA:HB2	6	1.16	0.52	1.04
(1,2376)	1:226:A:VAL:HG13	1:227:A:ALA:HB2	6	1.16	0.52	1.04
(1,2376)	1:226:A:VAL:HG22	1:227:A:ALA:HB2	6	1.16	0.52	1.04
(1,2376)	1:226:A:VAL:HG12	1:227:A:ALA:HB1	6	1.16	0.52	1.04
(1,2376)	1:226:A:VAL:HG12	1:227:A:ALA:HB3	6	1.16	0.52	1.04
(1,2394)	1:181:A:LEU:HD21	1:181:A:LEU:HB2	6	0.63	0.17	0.66
(1,2394)	1:184:A:LYS:HB2	1:181:A:LEU:HD22	6	0.63	0.17	0.66
(1,1298)	1:218:A:LEU:HB2	1:218:A:LEU:HD21	6	0.52	0.01	0.52
(1,1298)	1:218:A:LEU:HB2	1:218:A:LEU:HD22	6	0.52	0.01	0.52
(1,1298)	1:218:A:LEU:HB2	1:218:A:LEU:HD23	6	0.52	0.01	0.52

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,1269)	1:163:A:THR:HG22	1:162:A:GLU:HG3	6	0.36	0.06	0.38
(1,1269)	1:163:A:THR:HG21	1:162:A:GLU:HG3	6	0.36	0.06	0.38
(1,1269)	1:163:A:THR:HG23	1:162:A:GLU:HG3	6	0.36	0.06	0.38
(1,1429)	1:145:A:MET:HG3	1:145:A:MET:HE2	6	0.14	0.01	0.14
(1,1429)	1:145:A:MET:HG3	1:145:A:MET:HE1	6	0.14	0.01	0.14
(1,1429)	1:145:A:MET:HG3	1:145:A:MET:HE3	6	0.14	0.01	0.14
(1,1534)	1:218:A:LEU:HD22	1:185:A:CYS:HB3	5	0.31	0.17	0.26
(1,1534)	1:218:A:LEU:HD23	1:185:A:CYS:HB3	5	0.31	0.17	0.26
(1,2113)	1:213:A:LYS:HE2	1:213:A:LYS:HB2	5	0.26	0.09	0.24
(1,2113)	1:213:A:LYS:HE3	1:213:A:LYS:HB2	5	0.26	0.09	0.24
(1,2299)	1:184:A:LYS:HB2	1:184:A:LYS:HE3	5	0.16	0.03	0.17
(1,641)	1:225:A:ILE:H	1:225:A:ILE:HG22	5	0.14	0.03	0.13
(1,641)	1:225:A:ILE:H	1:225:A:ILE:HG23	5	0.14	0.03	0.13
(1,641)	1:225:A:ILE:H	1:225:A:ILE:HG21	5	0.14	0.03	0.13
(1,1446)	1:149:A:HIS:HA	1:156:A:THR:HG23	5	0.13	0.02	0.13
(1,1446)	1:149:A:HIS:HA	1:156:A:THR:HG21	5	0.13	0.02	0.13
(1,1446)	1:149:A:HIS:HA	1:156:A:THR:HG22	5	0.13	0.02	0.13
(1,47)	1:144:A:SER:H	1:145:A:MET:HE1	4	0.68	0.35	0.62
(1,47)	1:144:A:SER:H	1:145:A:MET:HE2	4	0.68	0.35	0.62
(1,47)	1:144:A:SER:H	1:145:A:MET:HE3	4	0.68	0.35	0.62
(1,1531)	1:232:A:THR:HG22	1:232:A:THR:HA	4	0.59	0.02	0.6
(1,1531)	1:232:A:THR:HG23	1:232:A:THR:HA	4	0.59	0.02	0.6
(1,2264)	1:181:A:LEU:HD22	1:178:A:ALA:HA	4	0.38	0.11	0.34
(1,2264)	1:181:A:LEU:HD11	1:178:A:ALA:HA	4	0.38	0.11	0.34
(1,1825)	1:145:A:MET:H	1:145:A:MET:HB2	4	0.24	0.02	0.24
(1,1210)	1:187:A:TRP:HD1	1:214:A:GLU:HB2	4	0.17	0.05	0.16
(1,651)	1:231:A:ILE:H	1:231:A:ILE:HG22	4	0.16	0.06	0.15
(1,651)	1:231:A:ILE:H	1:231:A:ILE:HG21	4	0.16	0.06	0.15
(1,651)	1:231:A:ILE:H	1:231:A:ILE:HG23	4	0.16	0.06	0.15
(1,2060)	1:171:A:PRO:HD2	1:174:A:LEU:HD23	3	1.12	0.02	1.13
(1,2060)	1:171:A:PRO:HD2	1:174:A:LEU:HD21	3	1.12	0.02	1.13
(1,1586)	1:171:A:PRO:HD2	1:174:A:LEU:HD23	3	0.64	0.02	0.65
(1,1586)	1:171:A:PRO:HD2	1:174:A:LEU:HD21	3	0.64	0.02	0.65
(1,1099)	1:146:A:TRP:HD1	1:174:A:LEU:HD13	3	0.39	0.06	0.38
(1,1099)	1:146:A:TRP:HD1	1:174:A:LEU:HD12	3	0.39	0.06	0.38
(1,1947)	1:231:A:ILE:H	1:230:A:LEU:HB3	3	0.37	0.09	0.41
(1,1947)	1:231:A:ILE:H	1:230:A:LEU:HB2	3	0.37	0.09	0.41
(1,682)	1:143:A:LYS:H	1:142:A:ALA:HB3	3	0.33	0.16	0.32
(1,682)	1:143:A:LYS:H	1:142:A:ALA:HB1	3	0.33	0.16	0.32
(1,1094)	1:174:A:LEU:HB2	1:174:A:LEU:HD22	3	0.3	0.01	0.3
(1,1094)	1:174:A:LEU:HB2	1:174:A:LEU:HD23	3	0.3	0.01	0.3
(1,1432)	1:140:A:MET:HA	1:139:A:ALA:HB3	3	0.27	0.07	0.22

Continued on next page...

Continued from previous page...

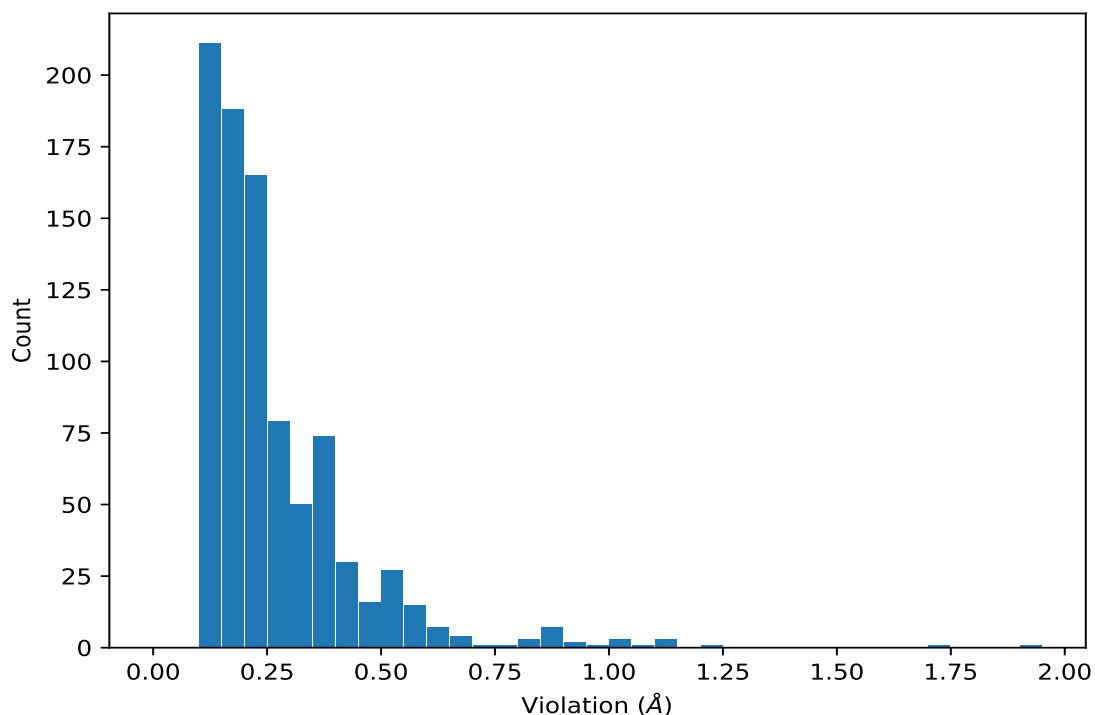
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,1432)	1:140:A:MET:HA	1:139:A:ALA:HB2	3	0.27	0.07	0.22
(1,1817)	1:218:A:LEU:HD12	1:185:A:CYS:HB3	3	0.2	0.04	0.19
(1,1866)	1:173:A:ASP:H	1:172:A:ASP:HB2	3	0.2	0.07	0.19
(1,1866)	1:173:A:ASP:H	1:172:A:ASP:HB3	3	0.2	0.07	0.19
(1,2291)	1:164:A:LYS:HD3	1:164:A:LYS:HA	3	0.17	0.0	0.17
(1,1451)	1:174:A:LEU:HB2	1:174:A:LEU:HD11	3	0.12	0.01	0.12
(1,1451)	1:174:A:LEU:HB2	1:174:A:LEU:HD12	3	0.12	0.01	0.12
(1,1110)	1:236:A:LEU:HA	1:236:A:LEU:HD11	2	0.39	0.18	0.39
(1,1110)	1:236:A:LEU:HA	1:236:A:LEU:HD13	2	0.39	0.18	0.39
(1,2378)	1:182:A:LEU:HD23	1:221:A:TYR:HD2	2	0.32	0.05	0.32
(1,2378)	1:182:A:LEU:HD21	1:221:A:TYR:HD1	2	0.32	0.05	0.32
(1,1957)	1:143:A:LYS:H	1:143:A:LYS:HB2	2	0.28	0.02	0.28
(1,2380)	1:181:A:LEU:HD11	1:180:A:GLN:HB2	2	0.26	0.04	0.26
(1,1482)	1:178:A:ALA:HB1	1:221:A:TYR:HD1	2	0.24	0.02	0.24
(1,1482)	1:178:A:ALA:HB2	1:221:A:TYR:HD1	2	0.24	0.02	0.24
(1,1206)	1:213:A:LYS:HA	1:213:A:LYS:HD3	2	0.24	0.0	0.24
(1,1083)	1:232:A:THR:HA	1:232:A:THR:HB	2	0.17	0.0	0.17
(1,646)	1:227:A:ALA:H	1:227:A:ALA:HB3	2	0.17	0.04	0.17
(1,2240)	1:184:A:LYS:HD2	1:183:A:SER:HB2	2	0.16	0.04	0.16
(1,2240)	1:184:A:LYS:HD3	1:183:A:SER:HB2	2	0.16	0.04	0.16

¹Number of violated models, ²Standard deviation

9.5 All violated distance restraints [i](#)

9.5.1 Histogram : Distribution of distance violations [i](#)

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



9.5.2 Table : All distance violations [i](#)

The following table 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)
(1,2376)	1:226:A:VAL:HG12	1:227:A:ALA:HB3	20	1.95
(1,2376)	1:226:A:VAL:HG13	1:227:A:ALA:HB2	13	1.74
(1,47)	1:144:A:SER:H	1:145:A:MET:HE3	7	1.23
(1,2060)	1:171:A:PRO:HD2	1:174:A:LEU:HD21	7	1.14
(1,2060)	1:171:A:PRO:HD2	1:174:A:LEU:HD21	19	1.13
(1,2060)	1:171:A:PRO:HD2	1:174:A:LEU:HD23	10	1.1
(1,2376)	1:226:A:VAL:HG22	1:227:A:ALA:HB2	14	1.07
(1,2376)	1:226:A:VAL:HG13	1:227:A:ALA:HB2	11	1.02
(1,1104)	1:179:A:GLU:HA	1:182:A:LEU:HD21	14	1.01
(1,1104)	1:179:A:GLU:HA	1:182:A:LEU:HD21	12	1.0
(1,1104)	1:179:A:GLU:HA	1:182:A:LEU:HD23	11	0.95
(1,1104)	1:179:A:GLU:HA	1:182:A:LEU:HD22	18	0.94
(1,1104)	1:179:A:GLU:HA	1:182:A:LEU:HD23	3	0.9
(1,1104)	1:179:A:GLU:HA	1:182:A:LEU:HD21	2	0.89
(1,1104)	1:179:A:GLU:HA	1:182:A:LEU:HD21	15	0.89
(1,1104)	1:179:A:GLU:HA	1:182:A:LEU:HD23	16	0.89

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1104)	1:179:A:GLU:HA	1:182:A:LEU:HD23	10	0.87
(1,1104)	1:179:A:GLU:HA	1:182:A:LEU:HD23	9	0.86
(1,1104)	1:179:A:GLU:HA	1:182:A:LEU:HD23	13	0.86
(1,1104)	1:179:A:GLU:HA	1:182:A:LEU:HD23	5	0.85
(1,2394)	1:181:A:LEU:HD21	1:181:A:LEU:HB2	5	0.82
(1,2253)	1:182:A:LEU:HD21	1:221:A:TYR:HB3	12	0.81
(1,1104)	1:179:A:GLU:HA	1:182:A:LEU:HD22	8	0.8
(1,2394)	1:184:A:LYS:HB2	1:181:A:LEU:HD22	14	0.79
(1,2394)	1:184:A:LYS:HB2	1:181:A:LEU:HD22	11	0.71
(1,1586)	1:171:A:PRO:HD2	1:174:A:LEU:HD21	7	0.66
(1,1586)	1:171:A:PRO:HD2	1:174:A:LEU:HD21	19	0.65
(1,1026)	1:159:A:TYR:HE1	1:147:A:THR:HG22	13	0.65
(1,47)	1:144:A:SER:H	1:145:A:MET:HE2	13	0.65
(1,1104)	1:179:A:GLU:HA	1:182:A:LEU:HD23	1	0.63
(1,2394)	1:184:A:LYS:HB2	1:181:A:LEU:HD22	16	0.62
(1,2376)	1:226:A:VAL:HG12	1:227:A:ALA:HB1	16	0.62
(1,1586)	1:171:A:PRO:HD2	1:174:A:LEU:HD23	10	0.62
(1,1675)	1:176:A:THR:HG21	1:179:A:GLU:HG3	8	0.61
(1,1531)	1:232:A:THR:HG22	1:232:A:THR:HA	3	0.6
(1,1531)	1:232:A:THR:HG23	1:232:A:THR:HA	7	0.6
(1,2376)	1:226:A:VAL:HG12	1:227:A:ALA:HB2	8	0.59
(1,1558)	1:174:A:LEU:HD21	1:174:A:LEU:HA	9	0.59
(1,1531)	1:232:A:THR:HG23	1:232:A:THR:HA	18	0.59
(1,1026)	1:159:A:TYR:HE1	1:147:A:THR:HG21	2	0.59
(1,47)	1:144:A:SER:H	1:145:A:MET:HE1	20	0.59
(1,2319)	1:215:A:LEU:HD13	1:189:A:GLU:HG3	11	0.58
(1,1104)	1:179:A:GLU:HA	1:182:A:LEU:HD23	19	0.58
(1,2264)	1:181:A:LEU:HD11	1:178:A:ALA:HA	7	0.57
(1,1110)	1:236:A:LEU:HA	1:236:A:LEU:HD13	1	0.57
(1,1531)	1:232:A:THR:HG22	1:232:A:THR:HA	8	0.56
(1,1026)	1:159:A:TYR:HE1	1:147:A:THR:HG23	1	0.56
(1,2394)	1:184:A:LYS:HB2	1:181:A:LEU:HD22	8	0.55
(1,1558)	1:174:A:LEU:HD21	1:174:A:LEU:HA	2	0.55
(1,1558)	1:174:A:LEU:HD22	1:174:A:LEU:HA	8	0.55
(1,1558)	1:174:A:LEU:HD23	1:174:A:LEU:HA	11	0.55
(1,1558)	1:174:A:LEU:HD21	1:174:A:LEU:HA	15	0.54
(1,1558)	1:174:A:LEU:HD21	1:174:A:LEU:HA	18	0.54
(1,1298)	1:218:A:LEU:HB2	1:218:A:LEU:HD22	16	0.54
(1,1058)	1:231:A:ILE:HD11	1:231:A:ILE:HA	5	0.54
(1,1058)	1:231:A:ILE:HD12	1:231:A:ILE:HA	7	0.54
(1,2279)	1:184:A:LYS:HD3	1:184:A:LYS:HA	4	0.53
(1,1558)	1:174:A:LEU:HD23	1:174:A:LEU:HA	1	0.53

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1298)	1:218:A:LEU:HB2	1:218:A:LEU:HD23	11	0.53
(1,1058)	1:231:A:ILE:HD12	1:231:A:ILE:HA	19	0.53
(1,682)	1:143:A:LYS:H	1:142:A:ALA:HB3	16	0.53
(1,1558)	1:174:A:LEU:HD21	1:174:A:LEU:HA	3	0.52
(1,1558)	1:174:A:LEU:HD21	1:174:A:LEU:HA	16	0.52
(1,1534)	1:218:A:LEU:HD22	1:185:A:CYS:HB3	16	0.52
(1,1298)	1:218:A:LEU:HB2	1:218:A:LEU:HD21	1	0.52
(1,1298)	1:218:A:LEU:HB2	1:218:A:LEU:HD22	6	0.52
(1,1298)	1:218:A:LEU:HB2	1:218:A:LEU:HD22	9	0.52
(1,1298)	1:218:A:LEU:HB2	1:218:A:LEU:HD21	12	0.52
(1,2253)	1:182:A:LEU:HD23	1:221:A:TYR:HB3	1	0.51
(1,2253)	1:182:A:LEU:HD23	1:221:A:TYR:HB3	13	0.51
(1,1558)	1:174:A:LEU:HD23	1:174:A:LEU:HA	12	0.51
(1,1558)	1:174:A:LEU:HD22	1:174:A:LEU:HA	13	0.51
(1,1558)	1:174:A:LEU:HD22	1:174:A:LEU:HA	14	0.51
(1,1534)	1:218:A:LEU:HD23	1:185:A:CYS:HB3	6	0.51
(1,1058)	1:231:A:ILE:HD13	1:231:A:ILE:HA	16	0.51
(1,1026)	1:159:A:TYR:HE2	1:147:A:THR:HG21	15	0.51
(1,1058)	1:231:A:ILE:HD11	1:231:A:ILE:HA	11	0.5
(1,1058)	1:231:A:ILE:HD11	1:231:A:ILE:HA	17	0.5
(1,1104)	1:179:A:GLU:HA	1:182:A:LEU:HD22	6	0.49
(1,1058)	1:231:A:ILE:HD13	1:231:A:ILE:HA	3	0.49
(1,1058)	1:231:A:ILE:HD11	1:231:A:ILE:HA	13	0.49
(1,1558)	1:174:A:LEU:HD21	1:174:A:LEU:HA	5	0.48
(1,1558)	1:174:A:LEU:HD23	1:174:A:LEU:HA	6	0.48
(1,1026)	1:159:A:TYR:HE1	1:147:A:THR:HG21	14	0.48
(1,1929)	1:216:A:GLU:H	1:216:A:GLU:HG2	10	0.47
(1,1558)	1:174:A:LEU:HD22	1:174:A:LEU:HA	20	0.47
(1,1058)	1:231:A:ILE:HD11	1:231:A:ILE:HA	14	0.47
(1,1947)	1:231:A:ILE:H	1:230:A:LEU:HB3	18	0.46
(1,1558)	1:174:A:LEU:HD23	1:174:A:LEU:HA	4	0.46
(1,1099)	1:146:A:TRP:HD1	1:174:A:LEU:HD12	19	0.46
(1,1026)	1:159:A:TYR:HE2	1:147:A:THR:HG21	9	0.46
(1,2279)	1:184:A:LYS:HD3	1:184:A:LYS:HA	6	0.45
(1,1558)	1:174:A:LEU:HD22	1:174:A:LEU:HA	17	0.45
(1,643)	1:226:A:VAL:H	1:225:A:ILE:HG23	15	0.45
(1,2319)	1:215:A:LEU:HD22	1:189:A:GLU:HG3	7	0.44
(1,1453)	1:182:A:LEU:HG	1:182:A:LEU:HD12	5	0.44
(1,1453)	1:182:A:LEU:HG	1:182:A:LEU:HD11	9	0.44
(1,1453)	1:182:A:LEU:HG	1:182:A:LEU:HD12	12	0.44
(1,1104)	1:179:A:GLU:HA	1:182:A:LEU:HD23	7	0.44
(1,1026)	1:159:A:TYR:HE1	1:147:A:THR:HG23	6	0.44

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1453)	1:182:A:LEU:HG	1:182:A:LEU:HD13	2	0.43
(1,1453)	1:182:A:LEU:HG	1:182:A:LEU:HD13	11	0.43
(1,1453)	1:182:A:LEU:HG	1:182:A:LEU:HD11	13	0.43
(1,1453)	1:182:A:LEU:HG	1:182:A:LEU:HD12	14	0.43
(1,1453)	1:182:A:LEU:HG	1:182:A:LEU:HD11	18	0.43
(1,1269)	1:163:A:THR:HG23	1:162:A:GLU:HG3	10	0.43
(1,1104)	1:179:A:GLU:HA	1:182:A:LEU:HD23	20	0.43
(1,2279)	1:184:A:LYS:HD3	1:184:A:LYS:HA	10	0.42
(1,2279)	1:184:A:LYS:HD3	1:184:A:LYS:HA	19	0.42
(1,1453)	1:182:A:LEU:HG	1:182:A:LEU:HD12	8	0.42
(1,1453)	1:182:A:LEU:HG	1:182:A:LEU:HD13	10	0.42
(1,1453)	1:182:A:LEU:HG	1:182:A:LEU:HD12	15	0.42
(1,2113)	1:213:A:LYS:HE3	1:213:A:LYS:HB2	15	0.41
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD23	16	0.41
(1,1947)	1:231:A:ILE:H	1:230:A:LEU:HB2	11	0.41
(1,1453)	1:182:A:LEU:HG	1:182:A:LEU:HD13	3	0.41
(1,1453)	1:182:A:LEU:HG	1:182:A:LEU:HD13	6	0.41
(1,1453)	1:182:A:LEU:HG	1:182:A:LEU:HD13	20	0.41
(1,2279)	1:184:A:LYS:HD3	1:184:A:LYS:HA	16	0.4
(1,1453)	1:182:A:LEU:HG	1:182:A:LEU:HD11	1	0.4
(1,1453)	1:182:A:LEU:HG	1:182:A:LEU:HD13	4	0.4
(1,1453)	1:182:A:LEU:HG	1:182:A:LEU:HD12	16	0.4
(1,1453)	1:182:A:LEU:HG	1:182:A:LEU:HD13	17	0.4
(1,1453)	1:182:A:LEU:HG	1:182:A:LEU:HD13	19	0.4
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD12	5	0.39
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD12	11	0.39
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD21	17	0.39
(1,1453)	1:182:A:LEU:HG	1:182:A:LEU:HD12	7	0.39
(1,1269)	1:163:A:THR:HG21	1:162:A:GLU:HG3	8	0.39
(1,1026)	1:159:A:TYR:HE1	1:147:A:THR:HG21	3	0.39
(1,2358)	1:182:A:LEU:HD22	1:182:A:LEU:HG	12	0.38
(1,2279)	1:184:A:LYS:HD3	1:184:A:LYS:HA	20	0.38
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD23	1	0.38
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD21	4	0.38
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD23	8	0.38
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD23	12	0.38
(1,1438)	1:204:A:THR:HB	1:204:A:THR:HG22	17	0.38
(1,1438)	1:204:A:THR:HB	1:204:A:THR:HG22	18	0.38
(1,1269)	1:163:A:THR:HG21	1:162:A:GLU:HG3	17	0.38
(1,1099)	1:146:A:TRP:HD1	1:174:A:LEU:HD13	10	0.38
(1,1026)	1:159:A:TYR:HE2	1:147:A:THR:HG22	11	0.38
(1,1026)	1:159:A:TYR:HE2	1:147:A:THR:HG22	18	0.38

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2378)	1:182:A:LEU:HD23	1:221:A:TYR:HD2	1	0.37
(1,2358)	1:182:A:LEU:HG	1:182:A:LEU:HD13	2	0.37
(1,2358)	1:182:A:LEU:HD21	1:182:A:LEU:HG	9	0.37
(1,2358)	1:182:A:LEU:HG	1:182:A:LEU:HD13	11	0.37
(1,2358)	1:182:A:LEU:HG	1:182:A:LEU:HD11	13	0.37
(1,2358)	1:182:A:LEU:HG	1:182:A:LEU:HD12	14	0.37
(1,2358)	1:182:A:LEU:HD23	1:182:A:LEU:HG	18	0.37
(1,2279)	1:184:A:LYS:HD3	1:184:A:LYS:HA	1	0.37
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD23	3	0.37
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD12	6	0.37
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD23	7	0.37
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD11	9	0.37
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD22	10	0.37
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD21	14	0.37
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD21	15	0.37
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD21	19	0.37
(1,1438)	1:204:A:THR:HB	1:204:A:THR:HG23	2	0.37
(1,1438)	1:204:A:THR:HB	1:204:A:THR:HG22	5	0.37
(1,1438)	1:204:A:THR:HB	1:204:A:THR:HG23	8	0.37
(1,1438)	1:204:A:THR:HB	1:204:A:THR:HG21	9	0.37
(1,1438)	1:204:A:THR:HB	1:204:A:THR:HG21	10	0.37
(1,1438)	1:204:A:THR:HB	1:204:A:THR:HG22	11	0.37
(1,1438)	1:204:A:THR:HB	1:204:A:THR:HG23	13	0.37
(1,1438)	1:204:A:THR:HB	1:204:A:THR:HG22	16	0.37
(1,1438)	1:204:A:THR:HB	1:204:A:THR:HG22	19	0.37
(1,1438)	1:204:A:THR:HB	1:204:A:THR:HG23	20	0.37
(1,1432)	1:140:A:MET:HA	1:139:A:ALA:HB3	1	0.37
(1,1269)	1:163:A:THR:HG23	1:162:A:GLU:HG3	20	0.37
(1,2358)	1:182:A:LEU:HD23	1:182:A:LEU:HG	5	0.36
(1,2358)	1:182:A:LEU:HG	1:182:A:LEU:HD12	8	0.36
(1,2358)	1:182:A:LEU:HG	1:182:A:LEU:HD13	10	0.36
(1,2358)	1:182:A:LEU:HG	1:182:A:LEU:HD12	15	0.36
(1,2279)	1:184:A:LYS:HD3	1:184:A:LYS:HA	8	0.36
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD21	2	0.36
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD21	20	0.36
(1,1438)	1:204:A:THR:HB	1:204:A:THR:HG21	1	0.36
(1,1438)	1:204:A:THR:HB	1:204:A:THR:HG22	4	0.36
(1,1438)	1:204:A:THR:HB	1:204:A:THR:HG22	6	0.36
(1,1438)	1:204:A:THR:HB	1:204:A:THR:HG21	7	0.36
(1,1438)	1:204:A:THR:HB	1:204:A:THR:HG21	12	0.36
(1,1438)	1:204:A:THR:HB	1:204:A:THR:HG22	14	0.36
(1,1438)	1:204:A:THR:HB	1:204:A:THR:HG21	15	0.36

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1104)	1:179:A:GLU:HA	1:182:A:LEU:HD23	4	0.36
(1,1026)	1:159:A:TYR:HE1	1:147:A:THR:HG21	16	0.36
(1,2358)	1:182:A:LEU:HG	1:182:A:LEU:HD13	3	0.35
(1,2358)	1:182:A:LEU:HG	1:182:A:LEU:HD13	6	0.35
(1,2358)	1:182:A:LEU:HG	1:182:A:LEU:HD13	20	0.35
(1,2279)	1:184:A:LYS:HD3	1:184:A:LYS:HA	5	0.35
(1,2279)	1:184:A:LYS:HD3	1:184:A:LYS:HA	12	0.35
(1,2264)	1:181:A:LEU:HD22	1:178:A:ALA:HA	18	0.35
(1,2253)	1:182:A:LEU:HD23	1:221:A:TYR:HB3	9	0.35
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD22	13	0.35
(1,2061)	1:215:A:LEU:HG	1:215:A:LEU:HD23	18	0.35
(1,1438)	1:204:A:THR:HB	1:204:A:THR:HG21	3	0.35
(1,1269)	1:163:A:THR:HG22	1:162:A:GLU:HG3	2	0.35
(1,1026)	1:159:A:TYR:HE1	1:147:A:THR:HG23	10	0.35
(1,2358)	1:182:A:LEU:HG	1:182:A:LEU:HD11	1	0.34
(1,2358)	1:182:A:LEU:HG	1:182:A:LEU:HD13	17	0.34
(1,2358)	1:182:A:LEU:HG	1:182:A:LEU:HD13	19	0.34
(1,2297)	1:164:A:LYS:HB2	1:164:A:LYS:HE2	3	0.34
(1,2279)	1:184:A:LYS:HD3	1:184:A:LYS:HA	11	0.34
(1,1441)	1:203:A:GLN:HG3	1:204:A:THR:HG21	11	0.34
(1,1026)	1:159:A:TYR:HE1	1:147:A:THR:HG23	20	0.34
(1,2358)	1:182:A:LEU:HG	1:182:A:LEU:HD12	7	0.33
(1,2358)	1:182:A:LEU:HD21	1:182:A:LEU:HG	16	0.33
(1,2279)	1:184:A:LYS:HD3	1:184:A:LYS:HA	15	0.33
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG12	8	0.33
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG22	11	0.33
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG23	12	0.33
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG11	13	0.33
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG12	20	0.33
(1,1847)	1:205:A:LYS:H	1:205:A:LYS:HD2	3	0.33
(1,637)	1:224:A:THR:H	1:224:A:THR:HG22	5	0.33
(1,637)	1:224:A:THR:H	1:224:A:THR:HG22	9	0.33
(1,2358)	1:182:A:LEU:HD21	1:182:A:LEU:HG	4	0.32
(1,2279)	1:184:A:LYS:HD3	1:184:A:LYS:HA	17	0.32
(1,2264)	1:181:A:LEU:HD22	1:178:A:ALA:HA	6	0.32
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG22	9	0.32
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG22	14	0.32
(1,1847)	1:205:A:LYS:H	1:205:A:LYS:HD2	18	0.32
(1,1099)	1:146:A:TRP:HD1	1:174:A:LEU:HD12	7	0.32
(1,682)	1:143:A:LYS:H	1:142:A:ALA:HB1	18	0.32
(1,637)	1:224:A:THR:H	1:224:A:THR:HG21	15	0.32
(1,2394)	1:184:A:LYS:HB2	1:181:A:LEU:HD22	13	0.31

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2279)	1:184:A:LYS:HD3	1:184:A:LYS:HA	7	0.31
(1,2279)	1:184:A:LYS:HD3	1:184:A:LYS:HA	14	0.31
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG22	1	0.31
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG12	2	0.31
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG12	3	0.31
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG23	4	0.31
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG23	5	0.31
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG12	7	0.31
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG22	10	0.31
(1,1441)	1:203:A:GLN:HG3	1:204:A:THR:HG23	15	0.31
(1,1094)	1:174:A:LEU:HB2	1:174:A:LEU:HD22	10	0.31
(1,2389)	1:167:A:THR:HB	1:165:A:GLN:HG3	15	0.3
(1,2380)	1:181:A:LEU:HD11	1:180:A:GLN:HB2	13	0.3
(1,2319)	1:215:A:LEU:HD23	1:189:A:GLU:HG3	20	0.3
(1,2279)	1:184:A:LYS:HD3	1:184:A:LYS:HA	2	0.3
(1,2279)	1:184:A:LYS:HD3	1:184:A:LYS:HA	18	0.3
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG13	16	0.3
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG11	17	0.3
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG13	19	0.3
(1,1957)	1:143:A:LYS:H	1:143:A:LYS:HB2	16	0.3
(1,1847)	1:205:A:LYS:H	1:205:A:LYS:HD2	11	0.3
(1,1094)	1:174:A:LEU:HB2	1:174:A:LEU:HD23	7	0.3
(1,2334)	1:203:A:GLN:HB2	1:203:A:GLN:HG2	5	0.29
(1,2334)	1:203:A:GLN:HB2	1:203:A:GLN:HG2	12	0.29
(1,2334)	1:203:A:GLN:HB2	1:203:A:GLN:HG2	19	0.29
(1,2113)	1:213:A:LYS:HE3	1:213:A:LYS:HB2	18	0.29
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG22	15	0.29
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG11	18	0.29
(1,1866)	1:173:A:ASP:H	1:172:A:ASP:HB2	4	0.29
(1,1026)	1:159:A:TYR:HE1	1:147:A:THR:HG23	7	0.29
(1,637)	1:224:A:THR:H	1:224:A:THR:HG21	14	0.29
(1,2334)	1:203:A:GLN:HB2	1:203:A:GLN:HG2	6	0.28
(1,2319)	1:215:A:LEU:HD22	1:189:A:GLU:HG3	16	0.28
(1,2298)	1:205:A:LYS:HB3	1:205:A:LYS:HE3	5	0.28
(1,2279)	1:184:A:LYS:HD3	1:184:A:LYS:HA	3	0.28
(1,2264)	1:181:A:LEU:HD22	1:178:A:ALA:HA	15	0.28
(1,2056)	1:226:A:VAL:HB	1:226:A:VAL:HG21	6	0.28
(1,1094)	1:174:A:LEU:HB2	1:174:A:LEU:HD23	19	0.28
(1,637)	1:224:A:THR:H	1:224:A:THR:HG23	3	0.28
(1,637)	1:224:A:THR:H	1:224:A:THR:HG21	7	0.28
(1,2334)	1:203:A:GLN:HB2	1:203:A:GLN:HG2	4	0.27
(1,2334)	1:203:A:GLN:HB2	1:203:A:GLN:HG2	9	0.27

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2334)	1:203:A:GLN:HB2	1:203:A:GLN:HG2	14	0.27
(1,2298)	1:205:A:LYS:HB3	1:205:A:LYS:HE3	18	0.27
(1,2297)	1:164:A:LYS:HB3	1:164:A:LYS:HE3	14	0.27
(1,1847)	1:205:A:LYS:H	1:205:A:LYS:HD2	1	0.27
(1,1825)	1:145:A:MET:H	1:145:A:MET:HB2	9	0.27
(1,1105)	1:181:A:LEU:HG	1:181:A:LEU:HD23	3	0.27
(1,1105)	1:181:A:LEU:HG	1:181:A:LEU:HD21	17	0.27
(1,1105)	1:181:A:LEU:HG	1:181:A:LEU:HD23	20	0.27
(1,637)	1:224:A:THR:H	1:224:A:THR:HG21	13	0.27
(1,637)	1:224:A:THR:H	1:224:A:THR:HG21	16	0.27
(1,47)	1:144:A:SER:H	1:145:A:MET:HE1	1	0.27
(1,2378)	1:182:A:LEU:HD21	1:221:A:TYR:HD1	12	0.26
(1,2334)	1:203:A:GLN:HB2	1:203:A:GLN:HG2	2	0.26
(1,2334)	1:203:A:GLN:HB2	1:203:A:GLN:HG2	8	0.26
(1,2279)	1:184:A:LYS:HD2	1:184:A:LYS:HA	9	0.26
(1,2138)	1:150:A:LYS:HE2	1:150:A:LYS:HB2	10	0.26
(1,1847)	1:205:A:LYS:H	1:205:A:LYS:HD2	5	0.26
(1,1825)	1:145:A:MET:H	1:145:A:MET:HB2	1	0.26
(1,1534)	1:218:A:LEU:HD23	1:185:A:CYS:HB3	9	0.26
(1,1482)	1:178:A:ALA:HB1	1:221:A:TYR:HD1	13	0.26
(1,1105)	1:181:A:LEU:HG	1:181:A:LEU:HD23	2	0.26
(1,1105)	1:181:A:LEU:HG	1:181:A:LEU:HD21	6	0.26
(1,1105)	1:181:A:LEU:HG	1:181:A:LEU:HD23	12	0.26
(1,1105)	1:181:A:LEU:HG	1:181:A:LEU:HD22	13	0.26
(1,1105)	1:181:A:LEU:HG	1:181:A:LEU:HD22	14	0.26
(1,1105)	1:181:A:LEU:HG	1:181:A:LEU:HD22	19	0.26
(1,1026)	1:159:A:TYR:HE2	1:147:A:THR:HG22	4	0.26
(1,637)	1:224:A:THR:H	1:224:A:THR:HG21	12	0.26
(1,637)	1:224:A:THR:H	1:224:A:THR:HG21	19	0.26
(1,2334)	1:203:A:GLN:HB2	1:203:A:GLN:HG2	7	0.25
(1,2319)	1:215:A:LEU:HD21	1:189:A:GLU:HG3	10	0.25
(1,2297)	1:164:A:LYS:HB2	1:164:A:LYS:HE2	16	0.25
(1,1957)	1:143:A:LYS:H	1:143:A:LYS:HB2	19	0.25
(1,1947)	1:231:A:ILE:H	1:230:A:LEU:HB2	13	0.25
(1,1847)	1:205:A:LYS:H	1:205:A:LYS:HD2	8	0.25
(1,1847)	1:205:A:LYS:H	1:205:A:LYS:HD3	15	0.25
(1,1817)	1:218:A:LEU:HD12	1:185:A:CYS:HB3	5	0.25
(1,1713)	1:181:A:LEU:HD12	1:181:A:LEU:HG	10	0.25
(1,1713)	1:181:A:LEU:HD11	1:181:A:LEU:HG	18	0.25
(1,1669)	1:174:A:LEU:HD12	1:174:A:LEU:HB3	8	0.25
(1,1422)	1:163:A:THR:HG21	1:163:A:THR:HB	1	0.25
(1,1422)	1:163:A:THR:HG21	1:163:A:THR:HB	2	0.25

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1422)	1:163:A:THR:HG21	1:163:A:THR:HB	3	0.25
(1,1422)	1:163:A:THR:HG23	1:163:A:THR:HB	6	0.25
(1,1422)	1:163:A:THR:HG22	1:163:A:THR:HB	7	0.25
(1,1422)	1:163:A:THR:HG22	1:163:A:THR:HB	12	0.25
(1,1422)	1:163:A:THR:HG23	1:163:A:THR:HB	13	0.25
(1,1422)	1:163:A:THR:HG23	1:163:A:THR:HB	14	0.25
(1,1422)	1:163:A:THR:HG23	1:163:A:THR:HB	18	0.25
(1,1422)	1:163:A:THR:HG21	1:163:A:THR:HB	19	0.25
(1,1422)	1:163:A:THR:HG22	1:163:A:THR:HB	20	0.25
(1,1105)	1:181:A:LEU:HG	1:181:A:LEU:HD23	9	0.25
(1,1105)	1:181:A:LEU:HG	1:181:A:LEU:HD22	10	0.25
(1,1105)	1:181:A:LEU:HG	1:181:A:LEU:HD21	15	0.25
(1,1105)	1:181:A:LEU:HG	1:181:A:LEU:HD21	18	0.25
(1,1104)	1:179:A:GLU:HA	1:182:A:LEU:HD22	17	0.25
(1,651)	1:231:A:ILE:H	1:231:A:ILE:HG23	20	0.25
(1,637)	1:224:A:THR:H	1:224:A:THR:HG22	2	0.25
(1,637)	1:224:A:THR:H	1:224:A:THR:HG21	11	0.25
(1,2334)	1:203:A:GLN:HB2	1:203:A:GLN:HG2	20	0.24
(1,2319)	1:215:A:LEU:HD23	1:189:A:GLU:HG3	19	0.24
(1,2297)	1:164:A:LYS:HB2	1:164:A:LYS:HE2	1	0.24
(1,2279)	1:184:A:LYS:HD2	1:184:A:LYS:HA	13	0.24
(1,2253)	1:182:A:LEU:HD23	1:221:A:TYR:HB3	11	0.24
(1,2157)	1:172:A:ASP:HA	1:175:A:LYS:HE3	10	0.24
(1,2113)	1:213:A:LYS:HE2	1:213:A:LYS:HB2	6	0.24
(1,2063)	1:218:A:LEU:HG	1:218:A:LEU:HD21	5	0.24
(1,2063)	1:218:A:LEU:HG	1:218:A:LEU:HD21	7	0.24
(1,2063)	1:218:A:LEU:HG	1:218:A:LEU:HD21	8	0.24
(1,1847)	1:205:A:LYS:H	1:205:A:LYS:HD2	10	0.24
(1,1847)	1:205:A:LYS:H	1:205:A:LYS:HD2	14	0.24
(1,1847)	1:205:A:LYS:H	1:205:A:LYS:HD2	16	0.24
(1,1713)	1:181:A:LEU:HD13	1:181:A:LEU:HG	1	0.24
(1,1713)	1:181:A:LEU:HD13	1:181:A:LEU:HG	3	0.24
(1,1713)	1:181:A:LEU:HD11	1:181:A:LEU:HG	5	0.24
(1,1713)	1:181:A:LEU:HD13	1:181:A:LEU:HG	6	0.24
(1,1713)	1:181:A:LEU:HD11	1:181:A:LEU:HG	7	0.24
(1,1713)	1:181:A:LEU:HD11	1:181:A:LEU:HG	8	0.24
(1,1713)	1:181:A:LEU:HD11	1:181:A:LEU:HG	9	0.24
(1,1713)	1:181:A:LEU:HD13	1:181:A:LEU:HG	11	0.24
(1,1713)	1:181:A:LEU:HD12	1:181:A:LEU:HG	12	0.24
(1,1713)	1:181:A:LEU:HD12	1:181:A:LEU:HG	15	0.24
(1,1713)	1:181:A:LEU:HD13	1:181:A:LEU:HG	16	0.24
(1,1713)	1:181:A:LEU:HD11	1:181:A:LEU:HG	19	0.24

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1669)	1:174:A:LEU:HD11	1:174:A:LEU:HB3	5	0.24
(1,1669)	1:174:A:LEU:HD13	1:174:A:LEU:HB3	6	0.24
(1,1669)	1:174:A:LEU:HD12	1:174:A:LEU:HB3	14	0.24
(1,1669)	1:174:A:LEU:HD11	1:174:A:LEU:HB3	17	0.24
(1,1669)	1:174:A:LEU:HD13	1:174:A:LEU:HB3	18	0.24
(1,1441)	1:203:A:GLN:HG3	1:204:A:THR:HG22	13	0.24
(1,1441)	1:203:A:GLN:HG3	1:204:A:THR:HG21	18	0.24
(1,1422)	1:163:A:THR:HG23	1:163:A:THR:HB	4	0.24
(1,1422)	1:163:A:THR:HG23	1:163:A:THR:HB	5	0.24
(1,1422)	1:163:A:THR:HG23	1:163:A:THR:HB	8	0.24
(1,1422)	1:163:A:THR:HG21	1:163:A:THR:HB	9	0.24
(1,1422)	1:163:A:THR:HG22	1:163:A:THR:HB	10	0.24
(1,1422)	1:163:A:THR:HG23	1:163:A:THR:HB	11	0.24
(1,1422)	1:163:A:THR:HG22	1:163:A:THR:HB	15	0.24
(1,1422)	1:163:A:THR:HG23	1:163:A:THR:HB	17	0.24
(1,1210)	1:187:A:TRP:HD1	1:214:A:GLU:HB2	17	0.24
(1,1206)	1:213:A:LYS:HA	1:213:A:LYS:HD3	18	0.24
(1,1105)	1:181:A:LEU:HG	1:181:A:LEU:HD21	1	0.24
(1,1105)	1:181:A:LEU:HG	1:181:A:LEU:HD21	4	0.24
(1,1105)	1:181:A:LEU:HG	1:181:A:LEU:HD23	5	0.24
(1,1105)	1:181:A:LEU:HG	1:181:A:LEU:HD22	11	0.24
(1,1026)	1:159:A:TYR:HE2	1:147:A:THR:HG22	12	0.24
(1,1026)	1:159:A:TYR:HE1	1:147:A:THR:HG21	17	0.24
(1,637)	1:224:A:THR:H	1:224:A:THR:HG23	8	0.24
(1,2392)	1:182:A:LEU:HG	1:178:A:ALA:HB1	4	0.23
(1,2298)	1:205:A:LYS:HB2	1:205:A:LYS:HE2	17	0.23
(1,2141)	1:169:A:GLU:HA	1:169:A:GLU:HG3	9	0.23
(1,2063)	1:218:A:LEU:HG	1:218:A:LEU:HD21	3	0.23
(1,1847)	1:205:A:LYS:H	1:205:A:LYS:HD3	2	0.23
(1,1847)	1:205:A:LYS:H	1:205:A:LYS:HD2	20	0.23
(1,1844)	1:164:A:LYS:H	1:164:A:LYS:HD3	17	0.23
(1,1825)	1:145:A:MET:H	1:145:A:MET:HB2	20	0.23
(1,1713)	1:181:A:LEU:HD13	1:181:A:LEU:HG	4	0.23
(1,1669)	1:174:A:LEU:HD13	1:174:A:LEU:HB3	1	0.23
(1,1669)	1:174:A:LEU:HD13	1:174:A:LEU:HB3	12	0.23
(1,1441)	1:203:A:GLN:HG3	1:204:A:THR:HG23	7	0.23
(1,1441)	1:203:A:GLN:HG3	1:204:A:THR:HG23	9	0.23
(1,1422)	1:163:A:THR:HG22	1:163:A:THR:HB	16	0.23
(1,1269)	1:163:A:THR:HG23	1:162:A:GLU:HG3	15	0.23
(1,1206)	1:213:A:LYS:HA	1:213:A:LYS:HD3	15	0.23
(1,1105)	1:181:A:LEU:HG	1:181:A:LEU:HD22	16	0.23
(1,637)	1:224:A:THR:H	1:224:A:THR:HG22	1	0.23

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2380)	1:181:A:LEU:HD11	1:180:A:GLN:HB2	14	0.22
(1,2298)	1:205:A:LYS:HB3	1:205:A:LYS:HE2	4	0.22
(1,2141)	1:169:A:GLU:HA	1:169:A:GLU:HG3	3	0.22
(1,2072)	1:219:A:GLU:HB2	1:215:A:LEU:HD12	6	0.22
(1,2064)	1:219:A:GLU:HG2	1:215:A:LEU:HD13	6	0.22
(1,2063)	1:218:A:LEU:HG	1:218:A:LEU:HD23	16	0.22
(1,2063)	1:218:A:LEU:HG	1:218:A:LEU:HD23	17	0.22
(1,2063)	1:218:A:LEU:HG	1:218:A:LEU:HD22	18	0.22
(1,2063)	1:218:A:LEU:HG	1:218:A:LEU:HD23	19	0.22
(1,1847)	1:205:A:LYS:H	1:205:A:LYS:HD2	4	0.22
(1,1844)	1:164:A:LYS:H	1:164:A:LYS:HD2	18	0.22
(1,1844)	1:164:A:LYS:H	1:164:A:LYS:HD3	20	0.22
(1,1825)	1:145:A:MET:H	1:145:A:MET:HB2	7	0.22
(1,1713)	1:181:A:LEU:HD13	1:181:A:LEU:HG	2	0.22
(1,1713)	1:181:A:LEU:HD12	1:181:A:LEU:HG	13	0.22
(1,1713)	1:181:A:LEU:HD12	1:181:A:LEU:HG	14	0.22
(1,1669)	1:174:A:LEU:HD13	1:174:A:LEU:HB3	2	0.22
(1,1669)	1:174:A:LEU:HD11	1:174:A:LEU:HB3	4	0.22
(1,1669)	1:174:A:LEU:HD13	1:174:A:LEU:HB3	15	0.22
(1,1669)	1:174:A:LEU:HD12	1:174:A:LEU:HB3	16	0.22
(1,1669)	1:174:A:LEU:HD13	1:174:A:LEU:HB3	20	0.22
(1,1482)	1:178:A:ALA:HB2	1:221:A:TYR:HD1	7	0.22
(1,1442)	1:224:A:THR:HB	1:224:A:THR:HG23	1	0.22
(1,1442)	1:224:A:THR:HB	1:224:A:THR:HG21	8	0.22
(1,1442)	1:224:A:THR:HB	1:224:A:THR:HG23	15	0.22
(1,1432)	1:140:A:MET:HA	1:139:A:ALA:HB2	18	0.22
(1,1105)	1:181:A:LEU:HG	1:181:A:LEU:HD22	8	0.22
(1,1048)	1:225:A:ILE:HG13	1:225:A:ILE:HG23	2	0.22
(1,2312)	1:171:A:PRO:HB3	1:174:A:LEU:HB2	13	0.21
(1,2298)	1:205:A:LYS:HB3	1:205:A:LYS:HE3	8	0.21
(1,2298)	1:205:A:LYS:HB2	1:205:A:LYS:HE3	9	0.21
(1,2298)	1:205:A:LYS:HB2	1:205:A:LYS:HE2	16	0.21
(1,2298)	1:205:A:LYS:HB3	1:205:A:LYS:HE3	20	0.21
(1,2297)	1:164:A:LYS:HB2	1:164:A:LYS:HE2	6	0.21
(1,2253)	1:182:A:LEU:HD21	1:221:A:TYR:HB3	2	0.21
(1,2253)	1:182:A:LEU:HD22	1:221:A:TYR:HB3	5	0.21
(1,2063)	1:218:A:LEU:HG	1:218:A:LEU:HD23	2	0.21
(1,2063)	1:218:A:LEU:HG	1:218:A:LEU:HD21	4	0.21
(1,2063)	1:218:A:LEU:HG	1:218:A:LEU:HD21	20	0.21
(1,1847)	1:205:A:LYS:H	1:205:A:LYS:HD2	7	0.21
(1,1844)	1:164:A:LYS:H	1:164:A:LYS:HD2	11	0.21
(1,1713)	1:181:A:LEU:HD11	1:181:A:LEU:HG	17	0.21

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1713)	1:181:A:LEU:HD11	1:181:A:LEU:HG	20	0.21
(1,1669)	1:174:A:LEU:HD12	1:174:A:LEU:HB3	11	0.21
(1,1442)	1:224:A:THR:HB	1:224:A:THR:HG22	3	0.21
(1,1442)	1:224:A:THR:HB	1:224:A:THR:HG23	5	0.21
(1,1442)	1:224:A:THR:HB	1:224:A:THR:HG22	10	0.21
(1,1442)	1:224:A:THR:HB	1:224:A:THR:HG22	11	0.21
(1,1442)	1:224:A:THR:HB	1:224:A:THR:HG21	17	0.21
(1,1442)	1:224:A:THR:HB	1:224:A:THR:HG22	19	0.21
(1,1442)	1:224:A:THR:HB	1:224:A:THR:HG21	20	0.21
(1,1432)	1:140:A:MET:HA	1:139:A:ALA:HB3	10	0.21
(1,1110)	1:236:A:LEU:HA	1:236:A:LEU:HD11	16	0.21
(1,1105)	1:181:A:LEU:HG	1:181:A:LEU:HD23	7	0.21
(1,1068)	1:147:A:THR:HB	1:161:A:THR:HG22	16	0.21
(1,1048)	1:225:A:ILE:HG13	1:225:A:ILE:HG23	11	0.21
(1,1048)	1:225:A:ILE:HG13	1:225:A:ILE:HG22	14	0.21
(1,1048)	1:225:A:ILE:HG13	1:225:A:ILE:HG22	18	0.21
(1,646)	1:227:A:ALA:H	1:227:A:ALA:HB3	2	0.21
(1,637)	1:224:A:THR:H	1:224:A:THR:HG21	4	0.21
(1,637)	1:224:A:THR:H	1:224:A:THR:HG22	6	0.21
(1,637)	1:224:A:THR:H	1:224:A:THR:HG21	10	0.21
(1,637)	1:224:A:THR:H	1:224:A:THR:HG23	20	0.21
(1,2304)	1:184:A:LYS:HG3	1:184:A:LYS:HE2	4	0.2
(1,2299)	1:184:A:LYS:HB2	1:184:A:LYS:HE3	5	0.2
(1,2297)	1:164:A:LYS:HB2	1:164:A:LYS:HE2	12	0.2
(1,2113)	1:213:A:LYS:HE2	1:213:A:LYS:HB2	14	0.2
(1,2063)	1:218:A:LEU:HG	1:218:A:LEU:HD23	10	0.2
(1,2063)	1:218:A:LEU:HG	1:218:A:LEU:HD21	15	0.2
(1,1877)	1:178:A:ALA:H	1:181:A:LEU:HD21	7	0.2
(1,1847)	1:205:A:LYS:H	1:205:A:LYS:HD2	19	0.2
(1,1844)	1:164:A:LYS:H	1:164:A:LYS:HD2	2	0.2
(1,1442)	1:224:A:THR:HB	1:224:A:THR:HG23	2	0.2
(1,1442)	1:224:A:THR:HB	1:224:A:THR:HG22	4	0.2
(1,1442)	1:224:A:THR:HB	1:224:A:THR:HG23	6	0.2
(1,1442)	1:224:A:THR:HB	1:224:A:THR:HG22	7	0.2
(1,1442)	1:224:A:THR:HB	1:224:A:THR:HG22	13	0.2
(1,1442)	1:224:A:THR:HB	1:224:A:THR:HG22	14	0.2
(1,1442)	1:224:A:THR:HB	1:224:A:THR:HG22	18	0.2
(1,1441)	1:203:A:GLN:HG3	1:204:A:THR:HG21	14	0.2
(1,1426)	1:225:A:ILE:HB	1:225:A:ILE:HG22	4	0.2
(1,1426)	1:225:A:ILE:HB	1:225:A:ILE:HG22	13	0.2
(1,1426)	1:225:A:ILE:HB	1:225:A:ILE:HG21	15	0.2
(1,1048)	1:225:A:ILE:HG13	1:225:A:ILE:HG21	3	0.2

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1048)	1:225:A:ILE:HG13	1:225:A:ILE:HG23	4	0.2
(1,1048)	1:225:A:ILE:HG13	1:225:A:ILE:HG23	10	0.2
(1,1048)	1:225:A:ILE:HG13	1:225:A:ILE:HG22	15	0.2
(1,1033)	1:142:A:ALA:HB2	1:142:A:ALA:HA	1	0.2
(1,1033)	1:142:A:ALA:HB2	1:142:A:ALA:HA	3	0.2
(1,1033)	1:142:A:ALA:HB3	1:142:A:ALA:HA	6	0.2
(1,1033)	1:142:A:ALA:HB2	1:142:A:ALA:HA	8	0.2
(1,1033)	1:142:A:ALA:HB2	1:142:A:ALA:HA	10	0.2
(1,1033)	1:142:A:ALA:HB1	1:142:A:ALA:HA	13	0.2
(1,1033)	1:142:A:ALA:HB3	1:142:A:ALA:HA	14	0.2
(1,1033)	1:142:A:ALA:HB1	1:142:A:ALA:HA	15	0.2
(1,1033)	1:142:A:ALA:HB1	1:142:A:ALA:HA	17	0.2
(1,641)	1:225:A:ILE:H	1:225:A:ILE:HG23	15	0.2
(1,637)	1:224:A:THR:H	1:224:A:THR:HG23	17	0.2
(1,2240)	1:184:A:LYS:HD3	1:183:A:SER:HB2	9	0.19
(1,2063)	1:218:A:LEU:HG	1:218:A:LEU:HD22	11	0.19
(1,2063)	1:218:A:LEU:HG	1:218:A:LEU:HD23	13	0.19
(1,1866)	1:173:A:ASP:H	1:172:A:ASP:HB3	14	0.19
(1,1844)	1:164:A:LYS:H	1:164:A:LYS:HD2	5	0.19
(1,1844)	1:164:A:LYS:H	1:164:A:LYS:HD2	19	0.19
(1,1817)	1:218:A:LEU:HD12	1:185:A:CYS:HB3	4	0.19
(1,1669)	1:174:A:LEU:HD11	1:174:A:LEU:HB3	9	0.19
(1,1442)	1:224:A:THR:HB	1:224:A:THR:HG23	9	0.19
(1,1442)	1:224:A:THR:HB	1:224:A:THR:HG22	12	0.19
(1,1442)	1:224:A:THR:HB	1:224:A:THR:HG22	16	0.19
(1,1441)	1:203:A:GLN:HG3	1:204:A:THR:HG23	1	0.19
(1,1441)	1:203:A:GLN:HG3	1:204:A:THR:HG22	2	0.19
(1,1441)	1:203:A:GLN:HG3	1:204:A:THR:HG21	16	0.19
(1,1428)	1:145:A:MET:HG2	1:145:A:MET:HE2	3	0.19
(1,1428)	1:145:A:MET:HG2	1:145:A:MET:HE2	6	0.19
(1,1428)	1:145:A:MET:HG2	1:145:A:MET:HE2	8	0.19
(1,1428)	1:145:A:MET:HG2	1:145:A:MET:HE1	11	0.19
(1,1428)	1:145:A:MET:HG2	1:145:A:MET:HE3	14	0.19
(1,1428)	1:145:A:MET:HG2	1:145:A:MET:HE3	16	0.19
(1,1426)	1:225:A:ILE:HB	1:225:A:ILE:HG22	2	0.19
(1,1426)	1:225:A:ILE:HB	1:225:A:ILE:HG21	14	0.19
(1,1426)	1:225:A:ILE:HB	1:225:A:ILE:HG21	18	0.19
(1,1210)	1:187:A:TRP:HD1	1:214:A:GLU:HB2	9	0.19
(1,1048)	1:225:A:ILE:HG13	1:225:A:ILE:HG23	6	0.19
(1,1048)	1:225:A:ILE:HG13	1:225:A:ILE:HG23	7	0.19
(1,1033)	1:142:A:ALA:HB3	1:142:A:ALA:HA	2	0.19
(1,1033)	1:142:A:ALA:HB1	1:142:A:ALA:HA	4	0.19

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1033)	1:142:A:ALA:HB3	1:142:A:ALA:HA	5	0.19
(1,1033)	1:142:A:ALA:HB2	1:142:A:ALA:HA	7	0.19
(1,1033)	1:142:A:ALA:HB2	1:142:A:ALA:HA	9	0.19
(1,1033)	1:142:A:ALA:HB1	1:142:A:ALA:HA	11	0.19
(1,1033)	1:142:A:ALA:HB1	1:142:A:ALA:HA	12	0.19
(1,1033)	1:142:A:ALA:HB2	1:142:A:ALA:HA	19	0.19
(1,1033)	1:142:A:ALA:HB3	1:142:A:ALA:HA	20	0.19
(1,1026)	1:159:A:TYR:HE2	1:147:A:THR:HG21	8	0.19
(1,637)	1:224:A:THR:H	1:224:A:THR:HG21	18	0.19
(1,491)	1:222:A:GLN:HE22	1:215:A:LEU:HD21	6	0.19
(1,2299)	1:184:A:LYS:HB2	1:184:A:LYS:HE3	14	0.18
(1,2298)	1:205:A:LYS:HB3	1:205:A:LYS:HE3	14	0.18
(1,2141)	1:169:A:GLU:HA	1:169:A:GLU:HG3	4	0.18
(1,2073)	1:218:A:LEU:HG	1:218:A:LEU:HD13	7	0.18
(1,2073)	1:218:A:LEU:HG	1:218:A:LEU:HD11	14	0.18
(1,2073)	1:218:A:LEU:HG	1:218:A:LEU:HD13	15	0.18
(1,2063)	1:218:A:LEU:HG	1:218:A:LEU:HD21	6	0.18
(1,2063)	1:218:A:LEU:HG	1:218:A:LEU:HD21	9	0.18
(1,2063)	1:218:A:LEU:HG	1:218:A:LEU:HD23	12	0.18
(1,2063)	1:218:A:LEU:HG	1:218:A:LEU:HD21	14	0.18
(1,1946)	1:230:A:LEU:H	1:230:A:LEU:HB2	9	0.18
(1,1847)	1:205:A:LYS:H	1:205:A:LYS:HD2	17	0.18
(1,1844)	1:164:A:LYS:H	1:164:A:LYS:HD2	13	0.18
(1,1844)	1:164:A:LYS:H	1:164:A:LYS:HD3	15	0.18
(1,1844)	1:164:A:LYS:H	1:164:A:LYS:HD2	16	0.18
(1,1428)	1:145:A:MET:HG2	1:145:A:MET:HE1	10	0.18
(1,1428)	1:145:A:MET:HG2	1:145:A:MET:HE2	13	0.18
(1,1428)	1:145:A:MET:HG2	1:145:A:MET:HE2	20	0.18
(1,1426)	1:225:A:ILE:HB	1:225:A:ILE:HG22	6	0.18
(1,1426)	1:225:A:ILE:HB	1:225:A:ILE:HG21	8	0.18
(1,1426)	1:225:A:ILE:HB	1:225:A:ILE:HG22	10	0.18
(1,1426)	1:225:A:ILE:HB	1:225:A:ILE:HG22	11	0.18
(1,1068)	1:147:A:THR:HB	1:161:A:THR:HG21	11	0.18
(1,1048)	1:225:A:ILE:HG13	1:225:A:ILE:HG21	1	0.18
(1,1048)	1:225:A:ILE:HG13	1:225:A:ILE:HG23	16	0.18
(1,1048)	1:225:A:ILE:HG13	1:225:A:ILE:HG21	20	0.18
(1,1034)	1:178:A:ALA:HA	1:178:A:ALA:HB2	3	0.18
(1,1034)	1:178:A:ALA:HA	1:178:A:ALA:HB2	10	0.18
(1,1034)	1:178:A:ALA:HA	1:178:A:ALA:HB1	11	0.18
(1,1034)	1:178:A:ALA:HA	1:178:A:ALA:HB3	14	0.18
(1,1034)	1:178:A:ALA:HA	1:178:A:ALA:HB1	15	0.18
(1,1034)	1:178:A:ALA:HA	1:178:A:ALA:HB3	18	0.18

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1033)	1:142:A:ALA:HB2	1:142:A:ALA:HA	16	0.18
(1,1033)	1:142:A:ALA:HB1	1:142:A:ALA:HA	18	0.18
(1,2334)	1:203:A:GLN:HB2	1:203:A:GLN:HG2	1	0.17
(1,2299)	1:184:A:LYS:HB2	1:184:A:LYS:HE3	3	0.17
(1,2298)	1:205:A:LYS:HB3	1:205:A:LYS:HE3	1	0.17
(1,2298)	1:205:A:LYS:HB3	1:205:A:LYS:HE2	10	0.17
(1,2297)	1:164:A:LYS:HB2	1:164:A:LYS:HE2	4	0.17
(1,2297)	1:164:A:LYS:HB2	1:164:A:LYS:HE2	8	0.17
(1,2291)	1:164:A:LYS:HD3	1:164:A:LYS:HA	17	0.17
(1,2291)	1:164:A:LYS:HD3	1:164:A:LYS:HA	20	0.17
(1,2141)	1:169:A:GLU:HA	1:169:A:GLU:HG3	12	0.17
(1,2073)	1:218:A:LEU:HG	1:218:A:LEU:HD12	10	0.17
(1,2073)	1:218:A:LEU:HG	1:218:A:LEU:HD12	13	0.17
(1,2073)	1:218:A:LEU:HG	1:218:A:LEU:HD11	16	0.17
(1,2063)	1:218:A:LEU:HG	1:218:A:LEU:HD23	1	0.17
(1,1844)	1:164:A:LYS:H	1:164:A:LYS:HD2	12	0.17
(1,1446)	1:149:A:HIS:HA	1:156:A:THR:HG22	11	0.17
(1,1441)	1:203:A:GLN:HG3	1:204:A:THR:HG21	17	0.17
(1,1441)	1:203:A:GLN:HG3	1:204:A:THR:HG21	19	0.17
(1,1428)	1:145:A:MET:HG2	1:145:A:MET:HE2	1	0.17
(1,1428)	1:145:A:MET:HG2	1:145:A:MET:HE2	17	0.17
(1,1428)	1:145:A:MET:HG2	1:145:A:MET:HE1	18	0.17
(1,1426)	1:225:A:ILE:HB	1:225:A:ILE:HG23	1	0.17
(1,1426)	1:225:A:ILE:HB	1:225:A:ILE:HG23	3	0.17
(1,1426)	1:225:A:ILE:HB	1:225:A:ILE:HG23	5	0.17
(1,1426)	1:225:A:ILE:HB	1:225:A:ILE:HG22	7	0.17
(1,1426)	1:225:A:ILE:HB	1:225:A:ILE:HG22	16	0.17
(1,1426)	1:225:A:ILE:HB	1:225:A:ILE:HG22	19	0.17
(1,1426)	1:225:A:ILE:HB	1:225:A:ILE:HG23	20	0.17
(1,1188)	1:218:A:LEU:HG	1:218:A:LEU:HD21	5	0.17
(1,1188)	1:218:A:LEU:HG	1:218:A:LEU:HD21	7	0.17
(1,1188)	1:218:A:LEU:HG	1:218:A:LEU:HD21	8	0.17
(1,1083)	1:232:A:THR:HA	1:232:A:THR:HB	19	0.17
(1,1083)	1:232:A:THR:HA	1:232:A:THR:HB	20	0.17
(1,1068)	1:147:A:THR:HB	1:161:A:THR:HG23	4	0.17
(1,1068)	1:147:A:THR:HB	1:161:A:THR:HG22	14	0.17
(1,1058)	1:231:A:ILE:HD13	1:231:A:ILE:HA	20	0.17
(1,1048)	1:225:A:ILE:HG13	1:225:A:ILE:HG23	17	0.17
(1,1034)	1:178:A:ALA:HA	1:178:A:ALA:HB2	12	0.17
(1,1034)	1:178:A:ALA:HA	1:178:A:ALA:HB3	16	0.17
(1,1034)	1:178:A:ALA:HA	1:178:A:ALA:HB2	17	0.17
(1,1034)	1:178:A:ALA:HA	1:178:A:ALA:HB3	19	0.17

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1034)	1:178:A:ALA:HA	1:178:A:ALA:HB2	20	0.17
(1,651)	1:231:A:ILE:H	1:231:A:ILE:HG21	6	0.17
(1,2351)	1:205:A:LYS:HE2	1:205:A:LYS:HD3	6	0.16
(1,2299)	1:184:A:LYS:HB2	1:184:A:LYS:HE3	17	0.16
(1,2298)	1:205:A:LYS:HB2	1:205:A:LYS:HE3	6	0.16
(1,2298)	1:205:A:LYS:HB3	1:205:A:LYS:HE2	19	0.16
(1,2291)	1:164:A:LYS:HD3	1:164:A:LYS:HA	15	0.16
(1,2141)	1:169:A:GLU:HA	1:169:A:GLU:HG3	1	0.16
(1,2141)	1:169:A:GLU:HA	1:169:A:GLU:HG3	15	0.16
(1,2113)	1:213:A:LYS:HE2	1:213:A:LYS:HB2	7	0.16
(1,2096)	1:195:A:GLY:HA2	1:191:A:LYS:HD2	18	0.16
(1,2073)	1:218:A:LEU:HB2	1:218:A:LEU:HD12	1	0.16
(1,2073)	1:218:A:LEU:HG	1:218:A:LEU:HD13	2	0.16
(1,2073)	1:218:A:LEU:HG	1:218:A:LEU:HD13	3	0.16
(1,2073)	1:218:A:LEU:HB2	1:218:A:LEU:HD11	11	0.16
(1,1847)	1:205:A:LYS:H	1:205:A:LYS:HD2	13	0.16
(1,1844)	1:164:A:LYS:H	1:164:A:LYS:HD2	3	0.16
(1,1817)	1:218:A:LEU:HD12	1:185:A:CYS:HB3	17	0.16
(1,1605)	1:227:A:ALA:HA	1:227:A:ALA:HB3	1	0.16
(1,1605)	1:227:A:ALA:HA	1:227:A:ALA:HB2	3	0.16
(1,1605)	1:227:A:ALA:HA	1:227:A:ALA:HB3	6	0.16
(1,1605)	1:227:A:ALA:HA	1:227:A:ALA:HB1	7	0.16
(1,1605)	1:227:A:ALA:HA	1:227:A:ALA:HB2	11	0.16
(1,1605)	1:227:A:ALA:HA	1:227:A:ALA:HB2	13	0.16
(1,1605)	1:227:A:ALA:HA	1:227:A:ALA:HB1	19	0.16
(1,1534)	1:218:A:LEU:HD22	1:185:A:CYS:HB3	1	0.16
(1,1441)	1:203:A:GLN:HG3	1:204:A:THR:HG23	10	0.16
(1,1428)	1:145:A:MET:HG2	1:145:A:MET:HE1	7	0.16
(1,1426)	1:225:A:ILE:HB	1:225:A:ILE:HG22	9	0.16
(1,1426)	1:225:A:ILE:HB	1:225:A:ILE:HG22	12	0.16
(1,1426)	1:225:A:ILE:HB	1:225:A:ILE:HG22	17	0.16
(1,1188)	1:218:A:LEU:HG	1:218:A:LEU:HD21	3	0.16
(1,1188)	1:218:A:LEU:HG	1:218:A:LEU:HD23	16	0.16
(1,1048)	1:225:A:ILE:HG13	1:225:A:ILE:HG23	9	0.16
(1,1048)	1:225:A:ILE:HG13	1:225:A:ILE:HG23	12	0.16
(1,1035)	1:176:A:THR:HB	1:178:A:ALA:HB1	6	0.16
(1,1034)	1:178:A:ALA:HA	1:178:A:ALA:HB2	2	0.16
(1,1034)	1:178:A:ALA:HA	1:178:A:ALA:HB2	8	0.16
(1,1034)	1:178:A:ALA:HA	1:178:A:ALA:HB3	13	0.16
(1,2351)	1:205:A:LYS:HE2	1:205:A:LYS:HD3	9	0.15
(1,2351)	1:205:A:LYS:HE2	1:205:A:LYS:HD3	13	0.15
(1,2334)	1:203:A:GLN:HB2	1:203:A:GLN:HG2	3	0.15

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2334)	1:203:A:GLN:HB2	1:203:A:GLN:HG2	16	0.15
(1,2319)	1:215:A:LEU:HD22	1:189:A:GLU:HG3	1	0.15
(1,2298)	1:205:A:LYS:HB3	1:205:A:LYS:HE2	11	0.15
(1,2073)	1:218:A:LEU:HG	1:218:A:LEU:HD12	5	0.15
(1,2073)	1:218:A:LEU:HG	1:218:A:LEU:HD13	8	0.15
(1,2073)	1:218:A:LEU:HG	1:218:A:LEU:HD13	18	0.15
(1,2065)	1:187:A:TRP:HB3	1:215:A:LEU:HD23	6	0.15
(1,1719)	1:215:A:LEU:HG	1:215:A:LEU:HD21	5	0.15
(1,1719)	1:215:A:LEU:HG	1:215:A:LEU:HD21	6	0.15
(1,1605)	1:227:A:ALA:HA	1:227:A:ALA:HB1	2	0.15
(1,1605)	1:227:A:ALA:HA	1:227:A:ALA:HB1	5	0.15
(1,1605)	1:227:A:ALA:HA	1:227:A:ALA:HB1	8	0.15
(1,1605)	1:227:A:ALA:HA	1:227:A:ALA:HB2	10	0.15
(1,1605)	1:227:A:ALA:HA	1:227:A:ALA:HB2	12	0.15
(1,1605)	1:227:A:ALA:HA	1:227:A:ALA:HB2	16	0.15
(1,1605)	1:227:A:ALA:HA	1:227:A:ALA:HB3	17	0.15
(1,1605)	1:227:A:ALA:HA	1:227:A:ALA:HB3	18	0.15
(1,1605)	1:227:A:ALA:HA	1:227:A:ALA:HB1	20	0.15
(1,1446)	1:149:A:HIS:HA	1:156:A:THR:HG22	18	0.15
(1,1441)	1:203:A:GLN:HG3	1:204:A:THR:HG23	3	0.15
(1,1441)	1:203:A:GLN:HG3	1:204:A:THR:HG21	4	0.15
(1,1429)	1:145:A:MET:HG3	1:145:A:MET:HE1	15	0.15
(1,1429)	1:145:A:MET:HG3	1:145:A:MET:HE3	19	0.15
(1,1188)	1:218:A:LEU:HG	1:218:A:LEU:HD21	4	0.15
(1,1188)	1:218:A:LEU:HG	1:218:A:LEU:HD23	17	0.15
(1,1188)	1:218:A:LEU:HG	1:218:A:LEU:HD22	18	0.15
(1,1188)	1:218:A:LEU:HG	1:218:A:LEU:HD23	19	0.15
(1,1068)	1:147:A:THR:HB	1:161:A:THR:HG21	2	0.15
(1,1068)	1:147:A:THR:HB	1:161:A:THR:HG22	5	0.15
(1,1068)	1:147:A:THR:HB	1:161:A:THR:HG21	12	0.15
(1,1048)	1:225:A:ILE:HG13	1:225:A:ILE:HG23	19	0.15
(1,1034)	1:178:A:ALA:HA	1:178:A:ALA:HB1	4	0.15
(1,1034)	1:178:A:ALA:HA	1:178:A:ALA:HB1	7	0.15
(1,687)	1:233:A:LYS:H	1:232:A:THR:HA	17	0.15
(1,2398)	1:209:A:TRP:HZ3	1:196:A:LYS:HE2	2	0.14
(1,2351)	1:205:A:LYS:HE3	1:205:A:LYS:HD2	4	0.14
(1,2351)	1:205:A:LYS:HE3	1:205:A:LYS:HD2	7	0.14
(1,2351)	1:205:A:LYS:HE2	1:205:A:LYS:HD3	8	0.14
(1,2351)	1:205:A:LYS:HE2	1:205:A:LYS:HD3	14	0.14
(1,2351)	1:205:A:LYS:HE3	1:205:A:LYS:HD2	16	0.14
(1,2351)	1:205:A:LYS:HE3	1:205:A:LYS:HD2	17	0.14
(1,2351)	1:205:A:LYS:HE3	1:205:A:LYS:HD2	19	0.14

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2334)	1:203:A:GLN:HB2	1:203:A:GLN:HG2	13	0.14
(1,2334)	1:203:A:GLN:HB2	1:203:A:GLN:HG2	17	0.14
(1,2297)	1:164:A:LYS:HB3	1:164:A:LYS:HE3	9	0.14
(1,2297)	1:164:A:LYS:HB2	1:164:A:LYS:HE3	18	0.14
(1,2141)	1:169:A:GLU:HA	1:169:A:GLU:HG3	13	0.14
(1,2073)	1:218:A:LEU:HB2	1:218:A:LEU:HD11	9	0.14
(1,2073)	1:218:A:LEU:HG	1:218:A:LEU:HD13	19	0.14
(1,1959)	1:225:A:ILE:H	1:224:A:THR:HA	19	0.14
(1,1844)	1:164:A:LYS:H	1:164:A:LYS:HD2	8	0.14
(1,1844)	1:164:A:LYS:H	1:164:A:LYS:HD2	10	0.14
(1,1719)	1:215:A:LEU:HG	1:215:A:LEU:HD23	16	0.14
(1,1669)	1:174:A:LEU:HD11	1:174:A:LEU:HB3	3	0.14
(1,1605)	1:227:A:ALA:HA	1:227:A:ALA:HB2	4	0.14
(1,1605)	1:227:A:ALA:HA	1:227:A:ALA:HB3	15	0.14
(1,1441)	1:203:A:GLN:HG3	1:204:A:THR:HG22	8	0.14
(1,1429)	1:145:A:MET:HG3	1:145:A:MET:HE2	2	0.14
(1,1429)	1:145:A:MET:HG3	1:145:A:MET:HE2	12	0.14
(1,1188)	1:218:A:LEU:HG	1:218:A:LEU:HD23	2	0.14
(1,1188)	1:218:A:LEU:HG	1:218:A:LEU:HD21	20	0.14
(1,1068)	1:147:A:THR:HB	1:161:A:THR:HG21	10	0.14
(1,1048)	1:225:A:ILE:HG13	1:225:A:ILE:HG21	5	0.14
(1,1042)	1:210:A:ALA:HA	1:210:A:ALA:HB1	1	0.14
(1,1042)	1:210:A:ALA:HA	1:210:A:ALA:HB1	2	0.14
(1,1042)	1:210:A:ALA:HA	1:210:A:ALA:HB1	4	0.14
(1,1042)	1:210:A:ALA:HA	1:210:A:ALA:HB3	5	0.14
(1,1042)	1:210:A:ALA:HA	1:210:A:ALA:HB2	8	0.14
(1,1042)	1:210:A:ALA:HA	1:210:A:ALA:HB2	11	0.14
(1,1042)	1:210:A:ALA:HA	1:210:A:ALA:HB1	13	0.14
(1,1042)	1:210:A:ALA:HA	1:210:A:ALA:HB3	14	0.14
(1,1042)	1:210:A:ALA:HA	1:210:A:ALA:HB3	16	0.14
(1,1042)	1:210:A:ALA:HA	1:210:A:ALA:HB2	18	0.14
(1,1034)	1:178:A:ALA:HA	1:178:A:ALA:HB3	5	0.14
(1,1034)	1:178:A:ALA:HA	1:178:A:ALA:HB2	9	0.14
(1,1028)	1:147:A:THR:HB	1:147:A:THR:HG21	3	0.14
(1,1028)	1:147:A:THR:HB	1:147:A:THR:HG21	17	0.14
(1,1026)	1:159:A:TYR:HE2	1:147:A:THR:HG23	19	0.14
(1,779)	1:203:A:GLN:HE21	1:203:A:GLN:HE22	1	0.14
(1,779)	1:203:A:GLN:HE21	1:203:A:GLN:HE22	3	0.14
(1,779)	1:203:A:GLN:HE21	1:203:A:GLN:HE22	10	0.14
(1,779)	1:203:A:GLN:HE21	1:203:A:GLN:HE22	11	0.14
(1,779)	1:203:A:GLN:HE21	1:203:A:GLN:HE22	13	0.14
(1,779)	1:203:A:GLN:HE21	1:203:A:GLN:HE22	15	0.14

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,779)	1:203:A:GLN:HE21	1:203:A:GLN:HE22	16	0.14
(1,779)	1:203:A:GLN:HE21	1:203:A:GLN:HE22	17	0.14
(1,779)	1:203:A:GLN:HE21	1:203:A:GLN:HE22	18	0.14
(1,641)	1:225:A:ILE:H	1:225:A:ILE:HG22	7	0.14
(1,2351)	1:205:A:LYS:HE3	1:205:A:LYS:HD2	10	0.13
(1,2351)	1:205:A:LYS:HE2	1:205:A:LYS:HD3	20	0.13
(1,2334)	1:203:A:GLN:HB2	1:203:A:GLN:HG2	10	0.13
(1,2298)	1:205:A:LYS:HB2	1:205:A:LYS:HE2	7	0.13
(1,2297)	1:164:A:LYS:HB2	1:164:A:LYS:HE3	2	0.13
(1,2297)	1:164:A:LYS:HB3	1:164:A:LYS:HE2	10	0.13
(1,2073)	1:218:A:LEU:HG	1:218:A:LEU:HD13	20	0.13
(1,1847)	1:205:A:LYS:H	1:205:A:LYS:HD2	6	0.13
(1,1844)	1:164:A:LYS:H	1:164:A:LYS:HD2	1	0.13
(1,1719)	1:215:A:LEU:HG	1:215:A:LEU:HD22	11	0.13
(1,1638)	1:143:A:LYS:HB3	1:143:A:LYS:HA	6	0.13
(1,1605)	1:227:A:ALA:HA	1:227:A:ALA:HB1	9	0.13
(1,1605)	1:227:A:ALA:HA	1:227:A:ALA:HB2	14	0.13
(1,1530)	1:227:A:ALA:HB1	1:224:A:THR:HA	3	0.13
(1,1451)	1:174:A:LEU:HB2	1:174:A:LEU:HD11	8	0.13
(1,1446)	1:149:A:HIS:HA	1:156:A:THR:HG22	19	0.13
(1,1441)	1:203:A:GLN:HG3	1:204:A:THR:HG22	20	0.13
(1,1429)	1:145:A:MET:HG3	1:145:A:MET:HE2	4	0.13
(1,1188)	1:218:A:LEU:HG	1:218:A:LEU:HD23	10	0.13
(1,1188)	1:218:A:LEU:HG	1:218:A:LEU:HD21	15	0.13
(1,1187)	1:218:A:LEU:HG	1:218:A:LEU:HD13	1	0.13
(1,1187)	1:218:A:LEU:HG	1:218:A:LEU:HD11	11	0.13
(1,1068)	1:147:A:THR:HB	1:161:A:THR:HG22	8	0.13
(1,1058)	1:231:A:ILE:HD11	1:231:A:ILE:HA	15	0.13
(1,1042)	1:210:A:ALA:HA	1:210:A:ALA:HB2	3	0.13
(1,1042)	1:210:A:ALA:HA	1:210:A:ALA:HB3	6	0.13
(1,1042)	1:210:A:ALA:HA	1:210:A:ALA:HB1	9	0.13
(1,1042)	1:210:A:ALA:HA	1:210:A:ALA:HB2	10	0.13
(1,1042)	1:210:A:ALA:HA	1:210:A:ALA:HB2	17	0.13
(1,1042)	1:210:A:ALA:HA	1:210:A:ALA:HB1	19	0.13
(1,1034)	1:178:A:ALA:HA	1:178:A:ALA:HB3	6	0.13
(1,1028)	1:147:A:THR:HB	1:147:A:THR:HG21	5	0.13
(1,1028)	1:147:A:THR:HB	1:147:A:THR:HG23	6	0.13
(1,1028)	1:147:A:THR:HB	1:147:A:THR:HG23	7	0.13
(1,1028)	1:147:A:THR:HB	1:147:A:THR:HG21	9	0.13
(1,1028)	1:147:A:THR:HB	1:147:A:THR:HG21	14	0.13
(1,1028)	1:147:A:THR:HB	1:147:A:THR:HG22	18	0.13
(1,1028)	1:147:A:THR:HB	1:147:A:THR:HG22	19	0.13

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,779)	1:203:A:GLN:HE21	1:203:A:GLN:HE22	2	0.13
(1,779)	1:203:A:GLN:HE21	1:203:A:GLN:HE22	4	0.13
(1,779)	1:203:A:GLN:HE21	1:203:A:GLN:HE22	5	0.13
(1,779)	1:203:A:GLN:HE21	1:203:A:GLN:HE22	6	0.13
(1,779)	1:203:A:GLN:HE21	1:203:A:GLN:HE22	7	0.13
(1,779)	1:203:A:GLN:HE21	1:203:A:GLN:HE22	8	0.13
(1,779)	1:203:A:GLN:HE21	1:203:A:GLN:HE22	9	0.13
(1,779)	1:203:A:GLN:HE21	1:203:A:GLN:HE22	12	0.13
(1,779)	1:203:A:GLN:HE21	1:203:A:GLN:HE22	14	0.13
(1,779)	1:203:A:GLN:HE21	1:203:A:GLN:HE22	19	0.13
(1,779)	1:203:A:GLN:HE21	1:203:A:GLN:HE22	20	0.13
(1,682)	1:143:A:LYS:H	1:142:A:ALA:HB1	4	0.13
(1,646)	1:227:A:ALA:H	1:227:A:ALA:HB3	8	0.13
(1,641)	1:225:A:ILE:H	1:225:A:ILE:HG2	16	0.13
(1,613)	1:219:A:GLU:H	1:219:A:GLU:HG2	16	0.13
(1,501)	1:222:A:GLN:HE22	1:222:A:GLN:HE21	14	0.13
(1,2351)	1:205:A:LYS:HE2	1:205:A:LYS:HD2	3	0.12
(1,2351)	1:205:A:LYS:HE2	1:205:A:LYS:HD3	5	0.12
(1,2351)	1:205:A:LYS:HE3	1:205:A:LYS:HD2	11	0.12
(1,2334)	1:203:A:GLN:HB2	1:203:A:GLN:HG2	15	0.12
(1,2297)	1:164:A:LYS:HB3	1:164:A:LYS:HE2	19	0.12
(1,2280)	1:143:A:LYS:HG2	1:143:A:LYS:HA	2	0.12
(1,2240)	1:184:A:LYS:HD2	1:183:A:SER:HB2	16	0.12
(1,2073)	1:218:A:LEU:HB2	1:218:A:LEU:HD12	6	0.12
(1,2073)	1:218:A:LEU:HG	1:218:A:LEU:HD12	17	0.12
(1,1844)	1:164:A:LYS:H	1:164:A:LYS:HD2	7	0.12
(1,1719)	1:215:A:LEU:HG	1:215:A:LEU:HD21	9	0.12
(1,1719)	1:215:A:LEU:HG	1:215:A:LEU:HD23	12	0.12
(1,1719)	1:215:A:LEU:HG	1:215:A:LEU:HD21	17	0.12
(1,1669)	1:174:A:LEU:HD11	1:174:A:LEU:HB3	13	0.12
(1,1451)	1:174:A:LEU:HB2	1:174:A:LEU:HD11	11	0.12
(1,1441)	1:203:A:GLN:HG3	1:204:A:THR:HG21	6	0.12
(1,1210)	1:187:A:TRP:HD1	1:214:A:GLU:HB2	11	0.12
(1,1210)	1:187:A:TRP:HD1	1:214:A:GLU:HB2	16	0.12
(1,1188)	1:218:A:LEU:HG	1:218:A:LEU:HD21	9	0.12
(1,1188)	1:218:A:LEU:HG	1:218:A:LEU:HD22	11	0.12
(1,1188)	1:218:A:LEU:HG	1:218:A:LEU:HD23	12	0.12
(1,1188)	1:218:A:LEU:HG	1:218:A:LEU:HD23	13	0.12
(1,1187)	1:218:A:LEU:HG	1:218:A:LEU:HD13	6	0.12
(1,1187)	1:218:A:LEU:HG	1:218:A:LEU:HD13	7	0.12
(1,1187)	1:218:A:LEU:HG	1:218:A:LEU:HD12	9	0.12
(1,1187)	1:218:A:LEU:HG	1:218:A:LEU:HD11	14	0.12

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1058)	1:231:A:ILE:HD12	1:231:A:ILE:HA	8	0.12
(1,1042)	1:210:A:ALA:HA	1:210:A:ALA:HB3	12	0.12
(1,1042)	1:210:A:ALA:HA	1:210:A:ALA:HB2	15	0.12
(1,1042)	1:210:A:ALA:HA	1:210:A:ALA:HB3	20	0.12
(1,1028)	1:147:A:THR:HB	1:147:A:THR:HG21	2	0.12
(1,1028)	1:147:A:THR:HB	1:147:A:THR:HG22	4	0.12
(1,1028)	1:147:A:THR:HB	1:147:A:THR:HG21	8	0.12
(1,1028)	1:147:A:THR:HB	1:147:A:THR:HG23	10	0.12
(1,1028)	1:147:A:THR:HB	1:147:A:THR:HG22	11	0.12
(1,1028)	1:147:A:THR:HB	1:147:A:THR:HG22	12	0.12
(1,1028)	1:147:A:THR:HB	1:147:A:THR:HG22	13	0.12
(1,1028)	1:147:A:THR:HB	1:147:A:THR:HG21	15	0.12
(1,1028)	1:147:A:THR:HB	1:147:A:THR:HG21	16	0.12
(1,1028)	1:147:A:THR:HB	1:147:A:THR:HG23	20	0.12
(1,651)	1:231:A:ILE:H	1:231:A:ILE:HG21	2	0.12
(1,501)	1:222:A:GLN:HE22	1:222:A:GLN:HE21	1	0.12
(1,501)	1:222:A:GLN:HE22	1:222:A:GLN:HE21	2	0.12
(1,501)	1:222:A:GLN:HE22	1:222:A:GLN:HE21	3	0.12
(1,501)	1:222:A:GLN:HE22	1:222:A:GLN:HE21	4	0.12
(1,501)	1:222:A:GLN:HE22	1:222:A:GLN:HE21	5	0.12
(1,501)	1:222:A:GLN:HE22	1:222:A:GLN:HE21	6	0.12
(1,501)	1:222:A:GLN:HE22	1:222:A:GLN:HE21	7	0.12
(1,501)	1:222:A:GLN:HE22	1:222:A:GLN:HE21	8	0.12
(1,501)	1:222:A:GLN:HE22	1:222:A:GLN:HE21	9	0.12
(1,501)	1:222:A:GLN:HE22	1:222:A:GLN:HE21	10	0.12
(1,501)	1:222:A:GLN:HE22	1:222:A:GLN:HE21	11	0.12
(1,501)	1:222:A:GLN:HE22	1:222:A:GLN:HE21	12	0.12
(1,501)	1:222:A:GLN:HE22	1:222:A:GLN:HE21	13	0.12
(1,501)	1:222:A:GLN:HE22	1:222:A:GLN:HE21	15	0.12
(1,501)	1:222:A:GLN:HE22	1:222:A:GLN:HE21	16	0.12
(1,501)	1:222:A:GLN:HE22	1:222:A:GLN:HE21	17	0.12
(1,501)	1:222:A:GLN:HE22	1:222:A:GLN:HE21	18	0.12
(1,501)	1:222:A:GLN:HE22	1:222:A:GLN:HE21	19	0.12
(1,501)	1:222:A:GLN:HE22	1:222:A:GLN:HE21	20	0.12
(1,91)	1:228:A:GLY:H	1:227:A:ALA:HA	17	0.12
(1,2351)	1:205:A:LYS:HE2	1:205:A:LYS:HD3	18	0.11
(1,2343)	1:170:A:LYS:HE2	1:170:A:LYS:HB2	9	0.11
(1,2334)	1:203:A:GLN:HB2	1:203:A:GLN:HG2	11	0.11
(1,2334)	1:203:A:GLN:HB2	1:203:A:GLN:HG2	18	0.11
(1,2321)	1:215:A:LEU:HD22	1:216:A:GLU:HG3	10	0.11
(1,2298)	1:205:A:LYS:HB3	1:205:A:LYS:HE2	13	0.11
(1,2297)	1:164:A:LYS:HB2	1:164:A:LYS:HE2	11	0.11

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1866)	1:173:A:ASP:H	1:172:A:ASP:HB2	18	0.11
(1,1719)	1:215:A:LEU:HG	1:215:A:LEU:HD23	1	0.11
(1,1719)	1:215:A:LEU:HG	1:215:A:LEU:HD21	4	0.11
(1,1719)	1:215:A:LEU:HG	1:215:A:LEU:HD23	8	0.11
(1,1534)	1:218:A:LEU:HD23	1:185:A:CYS:HB3	17	0.11
(1,1521)	1:147:A:THR:HG22	1:161:A:THR:HB	14	0.11
(1,1446)	1:149:A:HIS:HA	1:156:A:THR:HG23	1	0.11
(1,1446)	1:149:A:HIS:HA	1:156:A:THR:HG21	6	0.11
(1,1429)	1:145:A:MET:HG3	1:145:A:MET:HE2	9	0.11
(1,1188)	1:218:A:LEU:HG	1:218:A:LEU:HD21	6	0.11
(1,1188)	1:218:A:LEU:HG	1:218:A:LEU:HD21	14	0.11
(1,1187)	1:218:A:LEU:HG	1:218:A:LEU:HD13	15	0.11
(1,1058)	1:231:A:ILE:HD11	1:231:A:ILE:HA	12	0.11
(1,1042)	1:210:A:ALA:HA	1:210:A:ALA:HB2	7	0.11
(1,1028)	1:147:A:THR:HB	1:147:A:THR:HG23	1	0.11
(1,651)	1:231:A:ILE:H	1:231:A:ILE:HG22	8	0.11
(1,641)	1:225:A:ILE:H	1:225:A:ILE:HG21	18	0.11
(1,2351)	1:205:A:LYS:HE2	1:205:A:LYS:HD3	1	0.1
(1,2351)	1:205:A:LYS:HE2	1:205:A:LYS:HD2	15	0.1
(1,2319)	1:215:A:LEU:HD13	1:189:A:GLU:HG3	13	0.1
(1,2299)	1:184:A:LYS:HB2	1:184:A:LYS:HE3	19	0.1
(1,2297)	1:164:A:LYS:HB2	1:164:A:LYS:HE2	13	0.1
(1,2073)	1:218:A:LEU:HB2	1:218:A:LEU:HD13	12	0.1
(1,1719)	1:215:A:LEU:HG	1:215:A:LEU:HD23	7	0.1
(1,1719)	1:215:A:LEU:HG	1:215:A:LEU:HD22	10	0.1
(1,1719)	1:215:A:LEU:HG	1:215:A:LEU:HD21	15	0.1
(1,1719)	1:215:A:LEU:HG	1:215:A:LEU:HD21	19	0.1
(1,1451)	1:174:A:LEU:HB2	1:174:A:LEU:HD12	18	0.1
(1,1188)	1:218:A:LEU:HG	1:218:A:LEU:HD23	1	0.1
(1,1187)	1:218:A:LEU:HG	1:218:A:LEU:HD12	10	0.1
(1,1187)	1:218:A:LEU:HG	1:218:A:LEU:HD11	12	0.1
(1,1187)	1:218:A:LEU:HG	1:218:A:LEU:HD12	13	0.1
(1,1187)	1:218:A:LEU:HG	1:218:A:LEU:HD11	16	0.1
(1,1058)	1:231:A:ILE:HD11	1:231:A:ILE:HA	2	0.1
(1,641)	1:225:A:ILE:H	1:225:A:ILE:HG22	6	0.1

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

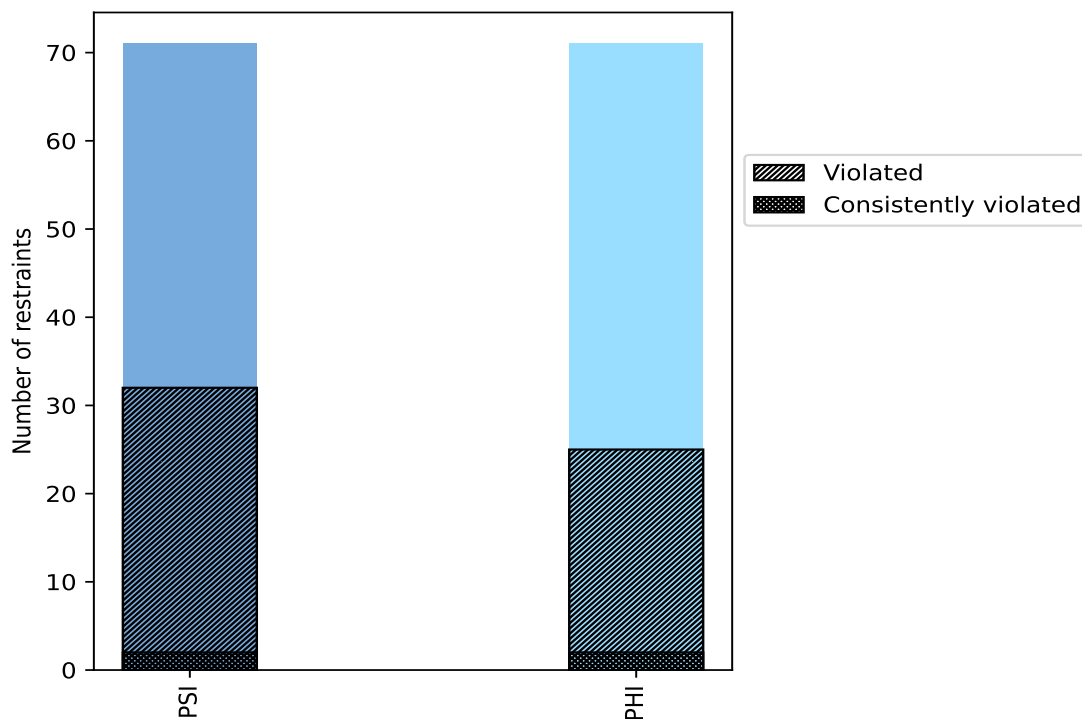
10.1 Summary of dihedral-angle violations [i](#)

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	71	50.0	32	45.1	22.5	2	2.8	1.4
PHI	71	50.0	25	35.2	17.6	2	2.8	1.4
Total	142	100.0	57	40.1	40.1	4	2.8	2.8

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](#)



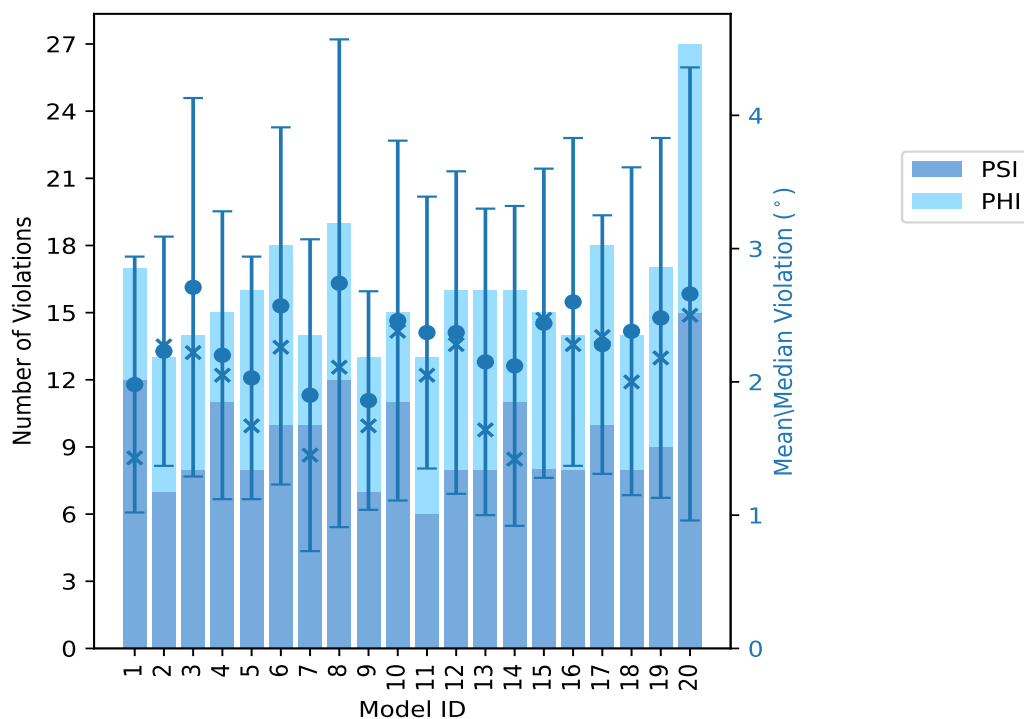
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

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	12	5	17	1.98	4.18	0.96	1.43
2	7	6	13	2.23	4.33	0.86	2.27
3	8	6	14	2.71	6.2	1.42	2.22
4	11	4	15	2.2	4.37	1.08	2.05
5	8	8	16	2.03	4.15	0.91	1.67
6	10	8	18	2.57	6.02	1.34	2.26
7	10	4	14	1.9	5.35	1.17	1.45
8	12	7	19	2.74	8.26	1.83	2.11
9	7	6	13	1.86	3.99	0.82	1.67
10	11	4	15	2.46	6.24	1.35	2.38
11	6	7	13	2.37	4.54	1.02	2.05
12	8	8	16	2.37	5.97	1.21	2.28
13	8	8	16	2.15	4.89	1.15	1.64
14	11	5	16	2.12	4.81	1.2	1.42
15	8	7	15	2.44	4.72	1.16	2.47
16	8	6	14	2.6	5.3	1.23	2.28
17	10	8	18	2.28	4.7	0.97	2.34
18	8	6	14	2.38	5.88	1.23	2.0
19	9	8	17	2.48	6.87	1.35	2.18
20	15	12	27	2.66	8.27	1.7	2.5

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	%
9	7	16	1	5.0
5	3	8	2	10.0
3	5	8	3	15.0
2	2	4	4	20.0
2	2	4	5	25.0
0	1	1	6	30.0
1	1	2	7	35.0
1	0	1	8	40.0
1	0	1	9	45.0
1	0	1	10	50.0
2	0	2	11	55.0

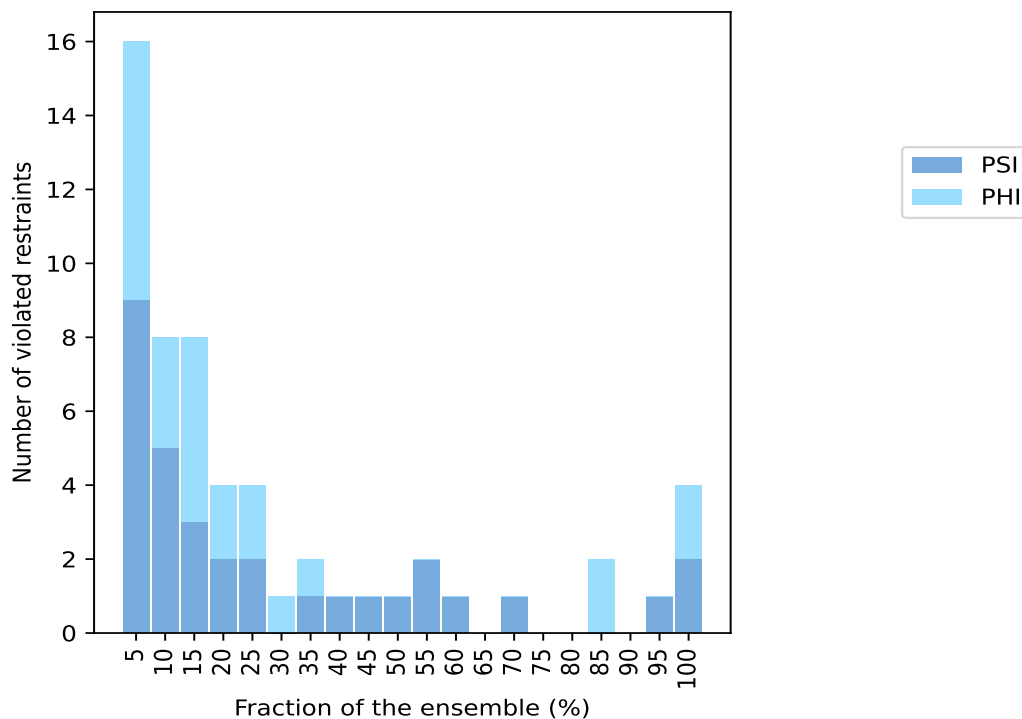
Continued on next page...

Continued from previous page...

Number of violated restraints			Fraction of the ensemble	
PSI	PHI	Total	Count ¹	%
1	0	1	12	60.0
0	0	0	13	65.0
1	0	1	14	70.0
0	0	0	15	75.0
0	0	0	16	80.0
0	2	2	17	85.0
0	0	0	18	90.0
1	0	1	19	95.0
2	2	4	20	100.0

¹ Number of models with violations

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

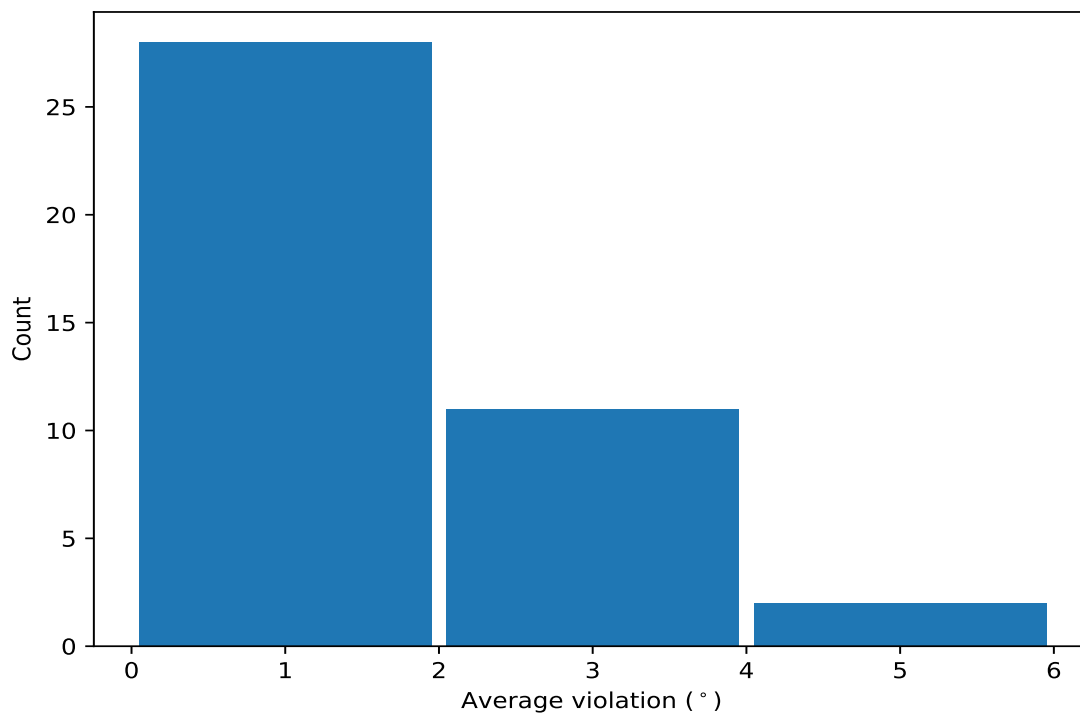


10.4 Most violated dihedral-angle restraints in the ensemble [i](#)

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

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

in the ensemble



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

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

Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,48)	1:170:A:LYS:N	1:170:A:LYS:CA	1:170:A:LYS:C	1:171:A:PRO:N	20	4.44	0.7	4.37
(1,79)	1:186:A:PRO:C	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	20	3.25	0.49	3.18
(1,126)	1:211:A:LYS:N	1:211:A:LYS:CA	1:211:A:LYS:C	1:212:A:PRO:N	20	3.15	0.85	3.26
(1,101)	1:197:A:PRO:C	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	20	2.61	0.48	2.58
(1,98)	1:196:A:LYS:N	1:196:A:LYS:CA	1:196:A:LYS:C	1:197:A:PRO:N	19	1.84	0.44	1.82
(1,127)	1:211:A:LYS:C	1:212:A:PRO:N	1:212:A:PRO:CA	1:212:A:PRO:C	17	2.46	0.71	2.47
(1,13)	1:151:A:SER:C	1:152:A:PRO:N	1:152:A:PRO:CA	1:152:A:PRO:C	17	1.61	0.4	1.43
(1,124)	1:210:A:ALA:N	1:210:A:ALA:CA	1:210:A:ALA:C	1:211:A:LYS:N	14	2.44	0.46	2.44
(1,78)	1:185:A:CYS:N	1:185:A:CYS:CA	1:185:A:CYS:C	1:186:A:PRO:N	12	5.32	2.07	5.59
(1,58)	1:175:A:LYS:N	1:175:A:LYS:CA	1:175:A:LYS:C	1:176:A:THR:N	11	2.96	1.88	2.15
(1,72)	1:182:A:LEU:N	1:182:A:LEU:CA	1:182:A:LEU:C	1:183:A:SER:N	11	2.47	0.85	2.43
(1,34)	1:162:A:GLU:N	1:162:A:GLU:CA	1:162:A:GLU:C	1:163:A:THR:N	10	1.55	0.26	1.56
(1,92)	1:193:A:ASP:N	1:193:A:ASP:CA	1:193:A:ASP:C	1:194:A:SER:N	9	1.56	0.45	1.4
(1,108)	1:201:A:ASN:N	1:201:A:ASN:CA	1:201:A:ASN:C	1:202:A:SER:N	8	1.36	0.18	1.31
(1,73)	1:182:A:LEU:C	1:183:A:SER:N	1:183:A:SER:CA	1:183:A:SER:C	7	2.77	1.05	2.57
(1,102)	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	1:199:A:TYR:N	7	1.22	0.17	1.23
(1,77)	1:184:A:LYS:C	1:185:A:CYS:N	1:185:A:CYS:CA	1:185:A:CYS:C	6	1.93	0.55	1.86
(1,91)	1:192:A:SER:C	1:193:A:ASP:N	1:193:A:ASP:CA	1:193:A:ASP:C	5	1.43	0.26	1.5
(1,8)	1:149:A:HIS:N	1:149:A:HIS:CA	1:149:A:HIS:C	1:150:A:LYS:N	5	1.4	0.34	1.22
(1,61)	1:176:A:THR:C	1:177:A:PRO:N	1:177:A:PRO:CA	1:177:A:PRO:C	5	1.27	0.13	1.3

Continued on next page...

Continued from previous page...

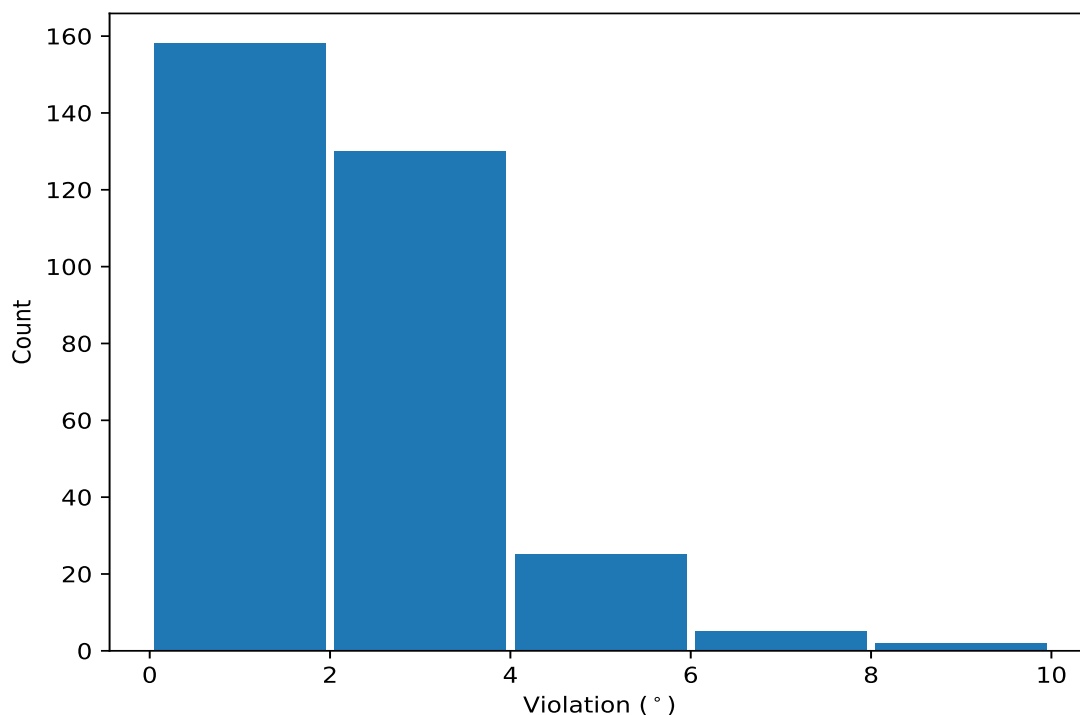
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,94)	1:194:A:SER:N	1:194:A:SER:CA	1:194:A:SER:C	1:195:A:GLY:N	5	1.26	0.13	1.2
(1,54)	1:173:A:ASP:N	1:173:A:ASP:CA	1:173:A:ASP:C	1:174:A:LEU:N	4	1.73	0.52	1.72
(1,41)	1:165:A:GLN:C	1:166:A:SER:N	1:166:A:SER:CA	1:166:A:SER:C	4	1.33	0.28	1.32
(1,85)	1:189:A:GLU:C	1:190:A:TYR:N	1:190:A:TYR:CA	1:190:A:TYR:C	4	1.28	0.18	1.27
(1,114)	1:204:A:THR:N	1:204:A:THR:CA	1:204:A:THR:C	1:205:A:LYS:N	4	1.08	0.05	1.07
(1,56)	1:174:A:LEU:N	1:174:A:LEU:CA	1:174:A:LEU:C	1:175:A:LYS:N	3	2.75	1.02	2.88
(1,59)	1:175:A:LYS:C	1:176:A:THR:N	1:176:A:THR:CA	1:176:A:THR:C	3	2.74	0.23	2.6
(1,57)	1:174:A:LEU:C	1:175:A:LYS:N	1:175:A:LYS:CA	1:175:A:LYS:C	3	2.21	0.6	2.6
(1,75)	1:183:A:SER:C	1:184:A:LYS:N	1:184:A:LYS:CA	1:184:A:LYS:C	3	1.95	0.39	1.97
(1,14)	1:152:A:PRO:N	1:152:A:PRO:CA	1:152:A:PRO:C	1:153:A:ASP:N	3	1.63	0.6	1.28
(1,93)	1:193:A:ASP:C	1:194:A:SER:N	1:194:A:SER:CA	1:194:A:SER:C	3	1.61	0.26	1.71
(1,84)	1:189:A:GLU:N	1:189:A:GLU:CA	1:189:A:GLU:C	1:190:A:TYR:N	3	1.44	0.22	1.59
(1,23)	1:156:A:THR:C	1:157:A:TYR:N	1:157:A:TYR:CA	1:157:A:TYR:C	3	1.09	0.04	1.07
(1,70)	1:181:A:LEU:N	1:181:A:LEU:CA	1:181:A:LEU:C	1:182:A:LEU:N	2	1.92	0.42	1.92
(1,111)	1:202:A:SER:C	1:203:A:GLN:N	1:203:A:GLN:CA	1:203:A:GLN:C	2	1.56	0.27	1.56
(1,80)	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	1:188:A:LYS:N	2	1.48	0.17	1.48
(1,68)	1:180:A:GLN:N	1:180:A:GLN:CA	1:180:A:GLN:C	1:181:A:LEU:N	2	1.48	0.33	1.48
(1,121)	1:207:A:SER:C	1:208:A:ARG:N	1:208:A:ARG:CA	1:208:A:ARG:C	2	1.42	0.19	1.42
(1,141)	1:218:A:LEU:C	1:219:A:GLU:N	1:219:A:GLU:CA	1:219:A:GLU:C	2	1.32	0.1	1.32
(1,76)	1:184:A:LYS:N	1:184:A:LYS:CA	1:184:A:LYS:C	1:185:A:CYS:N	2	1.27	0.22	1.27
(1,90)	1:192:A:SER:N	1:192:A:SER:CA	1:192:A:SER:C	1:193:A:ASP:N	2	1.24	0.12	1.24

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

10.5 All violated dihedral-angle restraints

10.5.1 Histogram : Distribution of violations

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 (°)
(1,78)	1:185:A:CYS:N	1:185:A:CYS:CA	1:185:A:CYS:C	1:186:A:PRO:N	20	8.27
(1,78)	1:185:A:CYS:N	1:185:A:CYS:CA	1:185:A:CYS:C	1:186:A:PRO:N	8	8.26
(1,78)	1:185:A:CYS:N	1:185:A:CYS:CA	1:185:A:CYS:C	1:186:A:PRO:N	19	6.87
(1,58)	1:175:A:LYS:N	1:175:A:LYS:CA	1:175:A:LYS:C	1:176:A:THR:N	8	6.28
(1,78)	1:185:A:CYS:N	1:185:A:CYS:CA	1:185:A:CYS:C	1:186:A:PRO:N	10	6.24
(1,78)	1:185:A:CYS:N	1:185:A:CYS:CA	1:185:A:CYS:C	1:186:A:PRO:N	3	6.2
(1,58)	1:175:A:LYS:N	1:175:A:LYS:CA	1:175:A:LYS:C	1:176:A:THR:N	6	6.02
(1,48)	1:170:A:LYS:N	1:170:A:LYS:CA	1:170:A:LYS:C	1:171:A:PRO:N	12	5.97
(1,78)	1:185:A:CYS:N	1:185:A:CYS:CA	1:185:A:CYS:C	1:186:A:PRO:N	18	5.88
(1,48)	1:170:A:LYS:N	1:170:A:LYS:CA	1:170:A:LYS:C	1:171:A:PRO:N	7	5.35
(1,78)	1:185:A:CYS:N	1:185:A:CYS:CA	1:185:A:CYS:C	1:186:A:PRO:N	16	5.3
(1,48)	1:170:A:LYS:N	1:170:A:LYS:CA	1:170:A:LYS:C	1:171:A:PRO:N	20	5.26
(1,48)	1:170:A:LYS:N	1:170:A:LYS:CA	1:170:A:LYS:C	1:171:A:PRO:N	6	5.15
(1,48)	1:170:A:LYS:N	1:170:A:LYS:CA	1:170:A:LYS:C	1:171:A:PRO:N	3	5.06
(1,58)	1:175:A:LYS:N	1:175:A:LYS:CA	1:175:A:LYS:C	1:176:A:THR:N	20	5.02
(1,73)	1:182:A:LEU:C	1:183:A:SER:N	1:183:A:SER:CA	1:183:A:SER:C	20	4.97
(1,48)	1:170:A:LYS:N	1:170:A:LYS:CA	1:170:A:LYS:C	1:171:A:PRO:N	16	4.93
(1,126)	1:211:A:LYS:N	1:211:A:LYS:CA	1:211:A:LYS:C	1:212:A:PRO:N	13	4.89
(1,78)	1:185:A:CYS:N	1:185:A:CYS:CA	1:185:A:CYS:C	1:186:A:PRO:N	14	4.81
(1,48)	1:170:A:LYS:N	1:170:A:LYS:CA	1:170:A:LYS:C	1:171:A:PRO:N	13	4.72
(1,48)	1:170:A:LYS:N	1:170:A:LYS:CA	1:170:A:LYS:C	1:171:A:PRO:N	15	4.72

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,78)	1:185:A:CYS:N	1:185:A:CYS:CA	1:185:A:CYS:C	1:186:A:PRO:N	17	4.7
(1,48)	1:170:A:LYS:N	1:170:A:LYS:CA	1:170:A:LYS:C	1:171:A:PRO:N	11	4.54
(1,48)	1:170:A:LYS:N	1:170:A:LYS:CA	1:170:A:LYS:C	1:171:A:PRO:N	8	4.41
(1,79)	1:186:A:PRO:C	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	4	4.37
(1,48)	1:170:A:LYS:N	1:170:A:LYS:CA	1:170:A:LYS:C	1:171:A:PRO:N	2	4.33
(1,48)	1:170:A:LYS:N	1:170:A:LYS:CA	1:170:A:LYS:C	1:171:A:PRO:N	1	4.18
(1,126)	1:211:A:LYS:N	1:211:A:LYS:CA	1:211:A:LYS:C	1:212:A:PRO:N	4	4.15
(1,48)	1:170:A:LYS:N	1:170:A:LYS:CA	1:170:A:LYS:C	1:171:A:PRO:N	5	4.15
(1,48)	1:170:A:LYS:N	1:170:A:LYS:CA	1:170:A:LYS:C	1:171:A:PRO:N	4	4.07
(1,78)	1:185:A:CYS:N	1:185:A:CYS:CA	1:185:A:CYS:C	1:186:A:PRO:N	15	4.05
(1,48)	1:170:A:LYS:N	1:170:A:LYS:CA	1:170:A:LYS:C	1:171:A:PRO:N	14	4.03
(1,48)	1:170:A:LYS:N	1:170:A:LYS:CA	1:170:A:LYS:C	1:171:A:PRO:N	9	3.99
(1,126)	1:211:A:LYS:N	1:211:A:LYS:CA	1:211:A:LYS:C	1:212:A:PRO:N	11	3.98
(1,56)	1:174:A:LEU:N	1:174:A:LEU:CA	1:174:A:LEU:C	1:175:A:LYS:N	6	3.93
(1,72)	1:182:A:LEU:N	1:182:A:LEU:CA	1:182:A:LEU:C	1:183:A:SER:N	20	3.92
(1,79)	1:186:A:PRO:C	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	8	3.91
(1,127)	1:211:A:LYS:C	1:212:A:PRO:N	1:212:A:PRO:CA	1:212:A:PRO:C	14	3.9
(1,79)	1:186:A:PRO:C	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	18	3.88
(1,126)	1:211:A:LYS:N	1:211:A:LYS:CA	1:211:A:LYS:C	1:212:A:PRO:N	3	3.81
(1,126)	1:211:A:LYS:N	1:211:A:LYS:CA	1:211:A:LYS:C	1:212:A:PRO:N	20	3.81
(1,48)	1:170:A:LYS:N	1:170:A:LYS:CA	1:170:A:LYS:C	1:171:A:PRO:N	10	3.75
(1,58)	1:175:A:LYS:N	1:175:A:LYS:CA	1:175:A:LYS:C	1:176:A:THR:N	12	3.71
(1,126)	1:211:A:LYS:N	1:211:A:LYS:CA	1:211:A:LYS:C	1:212:A:PRO:N	5	3.67
(1,79)	1:186:A:PRO:C	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	6	3.67
(1,48)	1:170:A:LYS:N	1:170:A:LYS:CA	1:170:A:LYS:C	1:171:A:PRO:N	19	3.67
(1,79)	1:186:A:PRO:C	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	20	3.66
(1,126)	1:211:A:LYS:N	1:211:A:LYS:CA	1:211:A:LYS:C	1:212:A:PRO:N	15	3.63
(1,126)	1:211:A:LYS:N	1:211:A:LYS:CA	1:211:A:LYS:C	1:212:A:PRO:N	12	3.61
(1,79)	1:186:A:PRO:C	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	19	3.6
(1,79)	1:186:A:PRO:C	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	3	3.45
(1,127)	1:211:A:LYS:C	1:212:A:PRO:N	1:212:A:PRO:CA	1:212:A:PRO:C	10	3.38
(1,126)	1:211:A:LYS:N	1:211:A:LYS:CA	1:211:A:LYS:C	1:212:A:PRO:N	1	3.38
(1,101)	1:197:A:PRO:C	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	20	3.37
(1,101)	1:197:A:PRO:C	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	15	3.35
(1,48)	1:170:A:LYS:N	1:170:A:LYS:CA	1:170:A:LYS:C	1:171:A:PRO:N	18	3.35
(1,79)	1:186:A:PRO:C	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	10	3.34
(1,79)	1:186:A:PRO:C	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	1	3.3
(1,72)	1:182:A:LEU:N	1:182:A:LEU:CA	1:182:A:LEU:C	1:183:A:SER:N	17	3.3
(1,126)	1:211:A:LYS:N	1:211:A:LYS:CA	1:211:A:LYS:C	1:212:A:PRO:N	17	3.29
(1,101)	1:197:A:PRO:C	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	19	3.28
(1,101)	1:197:A:PRO:C	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	14	3.26
(1,72)	1:182:A:LEU:N	1:182:A:LEU:CA	1:182:A:LEU:C	1:183:A:SER:N	16	3.25
(1,126)	1:211:A:LYS:N	1:211:A:LYS:CA	1:211:A:LYS:C	1:212:A:PRO:N	10	3.24
(1,79)	1:186:A:PRO:C	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	16	3.22
(1,73)	1:182:A:LEU:C	1:183:A:SER:N	1:183:A:SER:CA	1:183:A:SER:C	8	3.17
(1,48)	1:170:A:LYS:N	1:170:A:LYS:CA	1:170:A:LYS:C	1:171:A:PRO:N	17	3.16
(1,124)	1:210:A:ALA:N	1:210:A:ALA:CA	1:210:A:ALA:C	1:211:A:LYS:N	1	3.15
(1,73)	1:182:A:LEU:C	1:183:A:SER:N	1:183:A:SER:CA	1:183:A:SER:C	6	3.14
(1,79)	1:186:A:PRO:C	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	7	3.13
(1,79)	1:186:A:PRO:C	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	15	3.13
(1,127)	1:211:A:LYS:C	1:212:A:PRO:N	1:212:A:PRO:CA	1:212:A:PRO:C	3	3.12

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,79)	1:186:A:PRO:C	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	17	3.11
(1,127)	1:211:A:LYS:C	1:212:A:PRO:N	1:212:A:PRO:CA	1:212:A:PRO:C	15	3.1
(1,101)	1:197:A:PRO:C	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	11	3.09
(1,79)	1:186:A:PRO:C	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	11	3.09
(1,59)	1:175:A:LYS:C	1:176:A:THR:N	1:176:A:THR:CA	1:176:A:THR:C	8	3.06
(1,101)	1:197:A:PRO:C	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	7	3.05
(1,127)	1:211:A:LYS:C	1:212:A:PRO:N	1:212:A:PRO:CA	1:212:A:PRO:C	5	3.04
(1,72)	1:182:A:LEU:N	1:182:A:LEU:CA	1:182:A:LEU:C	1:183:A:SER:N	8	3.03
(1,124)	1:210:A:ALA:N	1:210:A:ALA:CA	1:210:A:ALA:C	1:211:A:LYS:N	16	3.02
(1,124)	1:210:A:ALA:N	1:210:A:ALA:CA	1:210:A:ALA:C	1:211:A:LYS:N	2	2.97
(1,126)	1:211:A:LYS:N	1:211:A:LYS:CA	1:211:A:LYS:C	1:212:A:PRO:N	18	2.96
(1,79)	1:186:A:PRO:C	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	14	2.94
(1,126)	1:211:A:LYS:N	1:211:A:LYS:CA	1:211:A:LYS:C	1:212:A:PRO:N	19	2.9
(1,79)	1:186:A:PRO:C	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	9	2.9
(1,56)	1:174:A:LEU:N	1:174:A:LEU:CA	1:174:A:LEU:C	1:175:A:LYS:N	20	2.88
(1,126)	1:211:A:LYS:N	1:211:A:LYS:CA	1:211:A:LYS:C	1:212:A:PRO:N	2	2.83
(1,126)	1:211:A:LYS:N	1:211:A:LYS:CA	1:211:A:LYS:C	1:212:A:PRO:N	16	2.83
(1,124)	1:210:A:ALA:N	1:210:A:ALA:CA	1:210:A:ALA:C	1:211:A:LYS:N	15	2.81
(1,17)	1:153:A:ASP:C	1:154:A:GLY:N	1:154:A:GLY:CA	1:154:A:GLY:C	19	2.76
(1,79)	1:186:A:PRO:C	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	13	2.75
(1,127)	1:211:A:LYS:C	1:212:A:PRO:N	1:212:A:PRO:CA	1:212:A:PRO:C	13	2.74
(1,98)	1:196:A:LYS:N	1:196:A:LYS:CA	1:196:A:LYS:C	1:197:A:PRO:N	20	2.72
(1,72)	1:182:A:LEU:N	1:182:A:LEU:CA	1:182:A:LEU:C	1:183:A:SER:N	6	2.72
(1,124)	1:210:A:ALA:N	1:210:A:ALA:CA	1:210:A:ALA:C	1:211:A:LYS:N	20	2.71
(1,101)	1:197:A:PRO:C	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	17	2.68
(1,57)	1:174:A:LEU:C	1:175:A:LYS:N	1:175:A:LYS:CA	1:175:A:LYS:C	20	2.67
(1,127)	1:211:A:LYS:C	1:212:A:PRO:N	1:212:A:PRO:CA	1:212:A:PRO:C	11	2.64
(1,79)	1:186:A:PRO:C	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	5	2.64
(1,77)	1:184:A:LYS:C	1:185:A:CYS:N	1:185:A:CYS:CA	1:185:A:CYS:C	13	2.64
(1,77)	1:184:A:LYS:C	1:185:A:CYS:N	1:185:A:CYS:CA	1:185:A:CYS:C	2	2.63
(1,101)	1:197:A:PRO:C	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	12	2.62
(1,124)	1:210:A:ALA:N	1:210:A:ALA:CA	1:210:A:ALA:C	1:211:A:LYS:N	12	2.6
(1,59)	1:175:A:LYS:C	1:176:A:THR:N	1:176:A:THR:CA	1:176:A:THR:C	6	2.6
(1,57)	1:174:A:LEU:C	1:175:A:LYS:N	1:175:A:LYS:CA	1:175:A:LYS:C	6	2.6
(1,101)	1:197:A:PRO:C	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	8	2.59
(1,101)	1:197:A:PRO:C	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	13	2.59
(1,73)	1:182:A:LEU:C	1:183:A:SER:N	1:183:A:SER:CA	1:183:A:SER:C	17	2.57
(1,127)	1:211:A:LYS:C	1:212:A:PRO:N	1:212:A:PRO:CA	1:212:A:PRO:C	16	2.56
(1,101)	1:197:A:PRO:C	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	1	2.56
(1,59)	1:175:A:LYS:C	1:176:A:THR:N	1:176:A:THR:CA	1:176:A:THR:C	20	2.55
(1,79)	1:186:A:PRO:C	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	2	2.52
(1,124)	1:210:A:ALA:N	1:210:A:ALA:CA	1:210:A:ALA:C	1:211:A:LYS:N	4	2.5
(1,92)	1:193:A:ASP:N	1:193:A:ASP:CA	1:193:A:ASP:C	1:194:A:SER:N	20	2.5
(1,127)	1:211:A:LYS:C	1:212:A:PRO:N	1:212:A:PRO:CA	1:212:A:PRO:C	2	2.47
(1,98)	1:196:A:LYS:N	1:196:A:LYS:CA	1:196:A:LYS:C	1:197:A:PRO:N	15	2.47
(1,54)	1:173:A:ASP:N	1:173:A:ASP:CA	1:173:A:ASP:C	1:174:A:LEU:N	12	2.47
(1,14)	1:152:A:PRO:N	1:152:A:PRO:CA	1:152:A:PRO:C	1:153:A:ASP:N	20	2.47
(1,101)	1:197:A:PRO:C	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	5	2.46
(1,101)	1:197:A:PRO:C	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	6	2.45
(1,79)	1:186:A:PRO:C	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	12	2.44
(1,72)	1:182:A:LEU:N	1:182:A:LEU:CA	1:182:A:LEU:C	1:183:A:SER:N	10	2.43

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,126)	1:211:A:LYS:N	1:211:A:LYS:CA	1:211:A:LYS:C	1:212:A:PRO:N	8	2.42
(1,101)	1:197:A:PRO:C	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	10	2.42
(1,75)	1:183:A:SER:C	1:184:A:LYS:N	1:184:A:LYS:CA	1:184:A:LYS:C	17	2.42
(1,126)	1:211:A:LYS:N	1:211:A:LYS:CA	1:211:A:LYS:C	1:212:A:PRO:N	9	2.41
(1,124)	1:210:A:ALA:N	1:210:A:ALA:CA	1:210:A:ALA:C	1:211:A:LYS:N	10	2.38
(1,58)	1:175:A:LYS:N	1:175:A:LYS:CA	1:175:A:LYS:C	1:176:A:THR:N	5	2.37
(1,127)	1:211:A:LYS:C	1:212:A:PRO:N	1:212:A:PRO:CA	1:212:A:PRO:C	12	2.36
(1,101)	1:197:A:PRO:C	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	3	2.36
(1,101)	1:197:A:PRO:C	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	18	2.35
(1,13)	1:151:A:SER:C	1:152:A:PRO:N	1:152:A:PRO:CA	1:152:A:PRO:C	17	2.35
(1,124)	1:210:A:ALA:N	1:210:A:ALA:CA	1:210:A:ALA:C	1:211:A:LYS:N	19	2.34
(1,70)	1:181:A:LEU:N	1:181:A:LEU:CA	1:181:A:LEU:C	1:182:A:LEU:N	17	2.34
(1,98)	1:196:A:LYS:N	1:196:A:LYS:CA	1:196:A:LYS:C	1:197:A:PRO:N	3	2.28
(1,98)	1:196:A:LYS:N	1:196:A:LYS:CA	1:196:A:LYS:C	1:197:A:PRO:N	10	2.28
(1,126)	1:211:A:LYS:N	1:211:A:LYS:CA	1:211:A:LYS:C	1:212:A:PRO:N	7	2.27
(1,101)	1:197:A:PRO:C	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	2	2.27
(1,72)	1:182:A:LEU:N	1:182:A:LEU:CA	1:182:A:LEU:C	1:183:A:SER:N	19	2.24
(1,98)	1:196:A:LYS:N	1:196:A:LYS:CA	1:196:A:LYS:C	1:197:A:PRO:N	12	2.2
(1,127)	1:211:A:LYS:C	1:212:A:PRO:N	1:212:A:PRO:CA	1:212:A:PRO:C	4	2.19
(1,127)	1:211:A:LYS:C	1:212:A:PRO:N	1:212:A:PRO:CA	1:212:A:PRO:C	19	2.18
(1,124)	1:210:A:ALA:N	1:210:A:ALA:CA	1:210:A:ALA:C	1:211:A:LYS:N	3	2.17
(1,58)	1:175:A:LYS:N	1:175:A:LYS:CA	1:175:A:LYS:C	1:176:A:THR:N	1	2.15
(1,13)	1:151:A:SER:C	1:152:A:PRO:N	1:152:A:PRO:CA	1:152:A:PRO:C	11	2.15
(1,13)	1:151:A:SER:C	1:152:A:PRO:N	1:152:A:PRO:CA	1:152:A:PRO:C	3	2.12
(1,127)	1:211:A:LYS:C	1:212:A:PRO:N	1:212:A:PRO:CA	1:212:A:PRO:C	8	2.11
(1,124)	1:210:A:ALA:N	1:210:A:ALA:CA	1:210:A:ALA:C	1:211:A:LYS:N	9	2.11
(1,78)	1:185:A:CYS:N	1:185:A:CYS:CA	1:185:A:CYS:C	1:186:A:PRO:N	1	2.11
(1,73)	1:182:A:LEU:C	1:183:A:SER:N	1:183:A:SER:CA	1:183:A:SER:C	4	2.1
(1,72)	1:182:A:LEU:N	1:182:A:LEU:CA	1:182:A:LEU:C	1:183:A:SER:N	4	2.07
(1,72)	1:182:A:LEU:N	1:182:A:LEU:CA	1:182:A:LEU:C	1:183:A:SER:N	18	2.07
(1,13)	1:151:A:SER:C	1:152:A:PRO:N	1:152:A:PRO:CA	1:152:A:PRO:C	12	2.07
(1,98)	1:196:A:LYS:N	1:196:A:LYS:CA	1:196:A:LYS:C	1:197:A:PRO:N	6	2.06
(1,124)	1:210:A:ALA:N	1:210:A:ALA:CA	1:210:A:ALA:C	1:211:A:LYS:N	17	2.05
(1,98)	1:196:A:LYS:N	1:196:A:LYS:CA	1:196:A:LYS:C	1:197:A:PRO:N	11	2.05
(1,8)	1:149:A:HIS:N	1:149:A:HIS:CA	1:149:A:HIS:C	1:150:A:LYS:N	4	2.05
(1,13)	1:151:A:SER:C	1:152:A:PRO:N	1:152:A:PRO:CA	1:152:A:PRO:C	19	2.03
(1,98)	1:196:A:LYS:N	1:196:A:LYS:CA	1:196:A:LYS:C	1:197:A:PRO:N	16	2.01
(1,92)	1:193:A:ASP:N	1:193:A:ASP:CA	1:193:A:ASP:C	1:194:A:SER:N	18	2.01
(1,124)	1:210:A:ALA:N	1:210:A:ALA:CA	1:210:A:ALA:C	1:211:A:LYS:N	11	2.0
(1,101)	1:197:A:PRO:C	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	9	1.99
(1,98)	1:196:A:LYS:N	1:196:A:LYS:CA	1:196:A:LYS:C	1:197:A:PRO:N	18	1.99
(1,75)	1:183:A:SER:C	1:184:A:LYS:N	1:184:A:LYS:CA	1:184:A:LYS:C	19	1.97
(1,58)	1:175:A:LYS:N	1:175:A:LYS:CA	1:175:A:LYS:C	1:176:A:THR:N	2	1.95
(1,34)	1:162:A:GLU:N	1:162:A:GLU:CA	1:162:A:GLU:C	1:163:A:THR:N	14	1.93
(1,63)	1:177:A:PRO:C	1:178:A:ALA:N	1:178:A:ALA:CA	1:178:A:ALA:C	20	1.92
(1,93)	1:193:A:ASP:C	1:194:A:SER:N	1:194:A:SER:CA	1:194:A:SER:C	11	1.87
(1,92)	1:193:A:ASP:N	1:193:A:ASP:CA	1:193:A:ASP:C	1:194:A:SER:N	2	1.87
(1,77)	1:184:A:LYS:C	1:185:A:CYS:N	1:185:A:CYS:CA	1:185:A:CYS:C	15	1.87
(1,34)	1:162:A:GLU:N	1:162:A:GLU:CA	1:162:A:GLU:C	1:163:A:THR:N	6	1.87
(1,127)	1:211:A:LYS:C	1:212:A:PRO:N	1:212:A:PRO:CA	1:212:A:PRO:C	17	1.86
(1,77)	1:184:A:LYS:C	1:185:A:CYS:N	1:185:A:CYS:CA	1:185:A:CYS:C	11	1.84

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,111)	1:202:A:SER:C	1:203:A:GLN:N	1:203:A:GLN:CA	1:203:A:GLN:C	6	1.83
(1,73)	1:182:A:LEU:C	1:183:A:SER:N	1:183:A:SER:CA	1:183:A:SER:C	16	1.83
(1,98)	1:196:A:LYS:N	1:196:A:LYS:CA	1:196:A:LYS:C	1:197:A:PRO:N	9	1.82
(1,98)	1:196:A:LYS:N	1:196:A:LYS:CA	1:196:A:LYS:C	1:197:A:PRO:N	8	1.81
(1,54)	1:173:A:ASP:N	1:173:A:ASP:CA	1:173:A:ASP:C	1:174:A:LEU:N	1	1.81
(1,68)	1:180:A:GLN:N	1:180:A:GLN:CA	1:180:A:GLN:C	1:181:A:LEU:N	8	1.8
(1,101)	1:197:A:PRO:C	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	4	1.78
(1,34)	1:162:A:GLU:N	1:162:A:GLU:CA	1:162:A:GLU:C	1:163:A:THR:N	16	1.78
(1,13)	1:151:A:SER:C	1:152:A:PRO:N	1:152:A:PRO:CA	1:152:A:PRO:C	18	1.77
(1,91)	1:192:A:SER:C	1:193:A:ASP:N	1:193:A:ASP:CA	1:193:A:ASP:C	13	1.76
(1,108)	1:201:A:ASN:N	1:201:A:ASN:CA	1:201:A:ASN:C	1:202:A:SER:N	18	1.73
(1,13)	1:151:A:SER:C	1:152:A:PRO:N	1:152:A:PRO:CA	1:152:A:PRO:C	13	1.72
(1,93)	1:193:A:ASP:C	1:194:A:SER:N	1:194:A:SER:CA	1:194:A:SER:C	5	1.71
(1,101)	1:197:A:PRO:C	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	16	1.7
(1,98)	1:196:A:LYS:N	1:196:A:LYS:CA	1:196:A:LYS:C	1:197:A:PRO:N	5	1.7
(1,127)	1:211:A:LYS:C	1:212:A:PRO:N	1:212:A:PRO:CA	1:212:A:PRO:C	9	1.67
(1,82)	1:188:A:LYS:N	1:188:A:LYS:CA	1:188:A:LYS:C	1:189:A:GLU:N	18	1.66
(1,80)	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	1:188:A:LYS:N	6	1.65
(1,41)	1:165:A:GLN:C	1:166:A:SER:N	1:166:A:SER:CA	1:166:A:SER:C	5	1.65
(1,73)	1:182:A:LEU:C	1:183:A:SER:N	1:183:A:SER:CA	1:183:A:SER:C	19	1.64
(1,54)	1:173:A:ASP:N	1:173:A:ASP:CA	1:173:A:ASP:C	1:174:A:LEU:N	4	1.62
(1,121)	1:207:A:SER:C	1:208:A:ARG:N	1:208:A:ARG:CA	1:208:A:ARG:C	3	1.61
(1,84)	1:189:A:GLU:N	1:189:A:GLU:CA	1:189:A:GLU:C	1:190:A:TYR:N	7	1.6
(1,34)	1:162:A:GLU:N	1:162:A:GLU:CA	1:162:A:GLU:C	1:163:A:THR:N	3	1.6
(1,91)	1:192:A:SER:C	1:193:A:ASP:N	1:193:A:ASP:CA	1:193:A:ASP:C	3	1.59
(1,84)	1:189:A:GLU:N	1:189:A:GLU:CA	1:189:A:GLU:C	1:190:A:TYR:N	19	1.59
(1,13)	1:151:A:SER:C	1:152:A:PRO:N	1:152:A:PRO:CA	1:152:A:PRO:C	10	1.59
(1,126)	1:211:A:LYS:N	1:211:A:LYS:CA	1:211:A:LYS:C	1:212:A:PRO:N	6	1.56
(1,98)	1:196:A:LYS:N	1:196:A:LYS:CA	1:196:A:LYS:C	1:197:A:PRO:N	13	1.56
(1,98)	1:196:A:LYS:N	1:196:A:LYS:CA	1:196:A:LYS:C	1:197:A:PRO:N	19	1.56
(1,41)	1:165:A:GLN:C	1:166:A:SER:N	1:166:A:SER:CA	1:166:A:SER:C	12	1.56
(1,34)	1:162:A:GLU:N	1:162:A:GLU:CA	1:162:A:GLU:C	1:163:A:THR:N	5	1.56
(1,34)	1:162:A:GLU:N	1:162:A:GLU:CA	1:162:A:GLU:C	1:163:A:THR:N	9	1.56
(1,108)	1:201:A:ASN:N	1:201:A:ASN:CA	1:201:A:ASN:C	1:202:A:SER:N	6	1.53
(1,92)	1:193:A:ASP:N	1:193:A:ASP:CA	1:193:A:ASP:C	1:194:A:SER:N	13	1.53
(1,94)	1:194:A:SER:N	1:194:A:SER:CA	1:194:A:SER:C	1:195:A:GLY:N	14	1.5
(1,91)	1:192:A:SER:C	1:193:A:ASP:N	1:193:A:ASP:CA	1:193:A:ASP:C	7	1.5
(1,102)	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	1:199:A:TYR:N	11	1.49
(1,98)	1:196:A:LYS:N	1:196:A:LYS:CA	1:196:A:LYS:C	1:197:A:PRO:N	2	1.49
(1,85)	1:189:A:GLU:C	1:190:A:TYR:N	1:190:A:TYR:CA	1:190:A:TYR:C	15	1.49
(1,76)	1:184:A:LYS:N	1:184:A:LYS:CA	1:184:A:LYS:C	1:185:A:CYS:N	13	1.49
(1,70)	1:181:A:LEU:N	1:181:A:LEU:CA	1:181:A:LEU:C	1:182:A:LEU:N	20	1.49
(1,34)	1:162:A:GLU:N	1:162:A:GLU:CA	1:162:A:GLU:C	1:163:A:THR:N	7	1.48
(1,58)	1:175:A:LYS:N	1:175:A:LYS:CA	1:175:A:LYS:C	1:176:A:THR:N	9	1.47
(1,75)	1:183:A:SER:C	1:184:A:LYS:N	1:184:A:LYS:CA	1:184:A:LYS:C	13	1.46
(1,34)	1:162:A:GLU:N	1:162:A:GLU:CA	1:162:A:GLU:C	1:163:A:THR:N	4	1.46
(1,61)	1:176:A:THR:C	1:177:A:PRO:N	1:177:A:PRO:CA	1:177:A:PRO:C	12	1.45
(1,56)	1:174:A:LEU:N	1:174:A:LEU:CA	1:174:A:LEU:C	1:175:A:LYS:N	8	1.45
(1,60)	1:176:A:THR:N	1:176:A:THR:CA	1:176:A:THR:C	1:177:A:PRO:N	8	1.44
(1,13)	1:151:A:SER:C	1:152:A:PRO:N	1:152:A:PRO:CA	1:152:A:PRO:C	1	1.43
(1,13)	1:151:A:SER:C	1:152:A:PRO:N	1:152:A:PRO:CA	1:152:A:PRO:C	8	1.43

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,8)	1:149:A:HIS:N	1:149:A:HIS:CA	1:149:A:HIS:C	1:150:A:LYS:N	10	1.43
(1,141)	1:218:A:LEU:C	1:219:A:GLU:N	1:219:A:GLU:CA	1:219:A:GLU:C	14	1.42
(1,108)	1:201:A:ASN:N	1:201:A:ASN:CA	1:201:A:ASN:C	1:202:A:SER:N	14	1.42
(1,77)	1:184:A:LYS:C	1:185:A:CYS:N	1:185:A:CYS:CA	1:185:A:CYS:C	5	1.42
(1,13)	1:151:A:SER:C	1:152:A:PRO:N	1:152:A:PRO:CA	1:152:A:PRO:C	7	1.42
(1,13)	1:151:A:SER:C	1:152:A:PRO:N	1:152:A:PRO:CA	1:152:A:PRO:C	16	1.42
(1,98)	1:196:A:LYS:N	1:196:A:LYS:CA	1:196:A:LYS:C	1:197:A:PRO:N	1	1.41
(1,85)	1:189:A:GLU:C	1:190:A:TYR:N	1:190:A:TYR:CA	1:190:A:TYR:C	5	1.41
(1,92)	1:193:A:ASP:N	1:193:A:ASP:CA	1:193:A:ASP:C	1:194:A:SER:N	14	1.4
(1,98)	1:196:A:LYS:N	1:196:A:LYS:CA	1:196:A:LYS:C	1:197:A:PRO:N	17	1.39
(1,124)	1:210:A:ALA:N	1:210:A:ALA:CA	1:210:A:ALA:C	1:211:A:LYS:N	8	1.38
(1,102)	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	1:199:A:TYR:N	8	1.37
(1,57)	1:174:A:LEU:C	1:175:A:LYS:N	1:175:A:LYS:CA	1:175:A:LYS:C	2	1.37
(1,90)	1:192:A:SER:N	1:192:A:SER:CA	1:192:A:SER:C	1:193:A:ASP:N	19	1.36
(1,139)	1:217:A:ASP:C	1:218:A:LEU:N	1:218:A:LEU:CA	1:218:A:LEU:C	15	1.35
(1,126)	1:211:A:LYS:N	1:211:A:LYS:CA	1:211:A:LYS:C	1:212:A:PRO:N	14	1.35
(1,108)	1:201:A:ASN:N	1:201:A:ASN:CA	1:201:A:ASN:C	1:202:A:SER:N	13	1.34
(1,66)	1:179:A:GLU:N	1:179:A:GLU:CA	1:179:A:GLU:C	1:180:A:GLN:N	17	1.34
(1,61)	1:176:A:THR:C	1:177:A:PRO:N	1:177:A:PRO:CA	1:177:A:PRO:C	1	1.33
(1,92)	1:193:A:ASP:N	1:193:A:ASP:CA	1:193:A:ASP:C	1:194:A:SER:N	3	1.32
(1,102)	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	1:199:A:TYR:N	20	1.31
(1,80)	1:187:A:TRP:N	1:187:A:TRP:CA	1:187:A:TRP:C	1:188:A:LYS:N	7	1.31
(1,61)	1:176:A:THR:C	1:177:A:PRO:N	1:177:A:PRO:CA	1:177:A:PRO:C	16	1.3
(1,13)	1:151:A:SER:C	1:152:A:PRO:N	1:152:A:PRO:CA	1:152:A:PRO:C	6	1.3
(1,111)	1:202:A:SER:C	1:203:A:GLN:N	1:203:A:GLN:CA	1:203:A:GLN:C	20	1.29
(1,94)	1:194:A:SER:N	1:194:A:SER:CA	1:194:A:SER:C	1:195:A:GLY:N	3	1.28
(1,14)	1:152:A:PRO:N	1:152:A:PRO:CA	1:152:A:PRO:C	1:153:A:ASP:N	14	1.28
(1,13)	1:151:A:SER:C	1:152:A:PRO:N	1:152:A:PRO:CA	1:152:A:PRO:C	20	1.28
(1,108)	1:201:A:ASN:N	1:201:A:ASN:CA	1:201:A:ASN:C	1:202:A:SER:N	15	1.27
(1,58)	1:175:A:LYS:N	1:175:A:LYS:CA	1:175:A:LYS:C	1:176:A:THR:N	4	1.27
(1,127)	1:211:A:LYS:C	1:212:A:PRO:N	1:212:A:PRO:CA	1:212:A:PRO:C	18	1.26
(1,91)	1:192:A:SER:C	1:193:A:ASP:N	1:193:A:ASP:CA	1:193:A:ASP:C	12	1.26
(1,135)	1:215:A:LEU:C	1:216:A:GLU:N	1:216:A:GLU:CA	1:216:A:GLU:C	18	1.25
(1,93)	1:193:A:ASP:C	1:194:A:SER:N	1:194:A:SER:CA	1:194:A:SER:C	17	1.25
(1,121)	1:207:A:SER:C	1:208:A:ARG:N	1:208:A:ARG:CA	1:208:A:ARG:C	20	1.23
(1,108)	1:201:A:ASN:N	1:201:A:ASN:CA	1:201:A:ASN:C	1:202:A:SER:N	4	1.23
(1,102)	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	1:199:A:TYR:N	1	1.23
(1,141)	1:218:A:LEU:C	1:219:A:GLU:N	1:219:A:GLU:CA	1:219:A:GLU:C	18	1.22
(1,8)	1:149:A:HIS:N	1:149:A:HIS:CA	1:149:A:HIS:C	1:150:A:LYS:N	5	1.22
(1,108)	1:201:A:ASN:N	1:201:A:ASN:CA	1:201:A:ASN:C	1:202:A:SER:N	5	1.21
(1,98)	1:196:A:LYS:N	1:196:A:LYS:CA	1:196:A:LYS:C	1:197:A:PRO:N	7	1.21
(1,92)	1:193:A:ASP:N	1:193:A:ASP:CA	1:193:A:ASP:C	1:194:A:SER:N	16	1.21
(1,77)	1:184:A:LYS:C	1:185:A:CYS:N	1:185:A:CYS:CA	1:185:A:CYS:C	12	1.21
(1,8)	1:149:A:HIS:N	1:149:A:HIS:CA	1:149:A:HIS:C	1:150:A:LYS:N	14	1.21
(1,94)	1:194:A:SER:N	1:194:A:SER:CA	1:194:A:SER:C	1:195:A:GLY:N	12	1.2
(1,16)	1:153:A:ASP:N	1:153:A:ASP:CA	1:153:A:ASP:C	1:154:A:GLY:N	14	1.2
(1,127)	1:211:A:LYS:C	1:212:A:PRO:N	1:212:A:PRO:CA	1:212:A:PRO:C	1	1.19
(1,55)	1:173:A:ASP:C	1:174:A:LEU:N	1:174:A:LEU:CA	1:174:A:LEU:C	20	1.19
(1,94)	1:194:A:SER:N	1:194:A:SER:CA	1:194:A:SER:C	1:195:A:GLY:N	8	1.18
(1,34)	1:162:A:GLU:N	1:162:A:GLU:CA	1:162:A:GLU:C	1:163:A:THR:N	12	1.18
(1,13)	1:151:A:SER:C	1:152:A:PRO:N	1:152:A:PRO:CA	1:152:A:PRO:C	14	1.18

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,78)	1:185:A:CYS:N	1:185:A:CYS:CA	1:185:A:CYS:C	1:186:A:PRO:N	13	1.17
(1,114)	1:204:A:THR:N	1:204:A:THR:CA	1:204:A:THR:C	1:205:A:LYS:N	1	1.16
(1,61)	1:176:A:THR:C	1:177:A:PRO:N	1:177:A:PRO:CA	1:177:A:PRO:C	17	1.16
(1,58)	1:175:A:LYS:N	1:175:A:LYS:CA	1:175:A:LYS:C	1:176:A:THR:N	19	1.16
(1,94)	1:194:A:SER:N	1:194:A:SER:CA	1:194:A:SER:C	1:195:A:GLY:N	20	1.15
(1,68)	1:180:A:GLN:N	1:180:A:GLN:CA	1:180:A:GLN:C	1:181:A:LEU:N	4	1.15
(1,23)	1:156:A:THR:C	1:157:A:TYR:N	1:157:A:TYR:CA	1:157:A:TYR:C	6	1.15
(1,108)	1:201:A:ASN:N	1:201:A:ASN:CA	1:201:A:ASN:C	1:202:A:SER:N	10	1.14
(1,29)	1:159:A:TYR:C	1:160:A:ASN:N	1:160:A:ASN:CA	1:160:A:ASN:C	5	1.14
(1,14)	1:152:A:PRO:N	1:152:A:PRO:CA	1:152:A:PRO:C	1:153:A:ASP:N	2	1.14
(1,92)	1:193:A:ASP:N	1:193:A:ASP:CA	1:193:A:ASP:C	1:194:A:SER:N	7	1.13
(1,85)	1:189:A:GLU:C	1:190:A:TYR:N	1:190:A:TYR:CA	1:190:A:TYR:C	9	1.12
(1,84)	1:189:A:GLU:N	1:189:A:GLU:CA	1:189:A:GLU:C	1:190:A:TYR:N	15	1.12
(1,72)	1:182:A:LEU:N	1:182:A:LEU:CA	1:182:A:LEU:C	1:183:A:SER:N	15	1.12
(1,90)	1:192:A:SER:N	1:192:A:SER:CA	1:192:A:SER:C	1:193:A:ASP:N	1	1.11
(1,58)	1:175:A:LYS:N	1:175:A:LYS:CA	1:175:A:LYS:C	1:176:A:THR:N	10	1.11
(1,30)	1:160:A:ASN:N	1:160:A:ASN:CA	1:160:A:ASN:C	1:161:A:THR:N	7	1.1
(1,8)	1:149:A:HIS:N	1:149:A:HIS:CA	1:149:A:HIS:C	1:150:A:LYS:N	20	1.1
(1,92)	1:193:A:ASP:N	1:193:A:ASP:CA	1:193:A:ASP:C	1:194:A:SER:N	10	1.09
(1,85)	1:189:A:GLU:C	1:190:A:TYR:N	1:190:A:TYR:CA	1:190:A:TYR:C	13	1.09
(1,61)	1:176:A:THR:C	1:177:A:PRO:N	1:177:A:PRO:CA	1:177:A:PRO:C	2	1.09
(1,114)	1:204:A:THR:N	1:204:A:THR:CA	1:204:A:THR:C	1:205:A:LYS:N	10	1.08
(1,41)	1:165:A:GLN:C	1:166:A:SER:N	1:166:A:SER:CA	1:166:A:SER:C	9	1.08
(1,34)	1:162:A:GLU:N	1:162:A:GLU:CA	1:162:A:GLU:C	1:163:A:THR:N	1	1.07
(1,23)	1:156:A:THR:C	1:157:A:TYR:N	1:157:A:TYR:CA	1:157:A:TYR:C	20	1.07
(1,13)	1:151:A:SER:C	1:152:A:PRO:N	1:152:A:PRO:CA	1:152:A:PRO:C	15	1.07
(1,114)	1:204:A:THR:N	1:204:A:THR:CA	1:204:A:THR:C	1:205:A:LYS:N	20	1.06
(1,65)	1:178:A:ALA:C	1:179:A:GLU:N	1:179:A:GLU:CA	1:179:A:GLU:C	11	1.06
(1,52)	1:172:A:ASP:N	1:172:A:ASP:CA	1:172:A:ASP:C	1:173:A:ASP:N	5	1.06
(1,32)	1:161:A:THR:N	1:161:A:THR:CA	1:161:A:THR:C	1:162:A:GLU:N	9	1.06
(1,102)	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	1:199:A:TYR:N	7	1.05
(1,102)	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	1:199:A:TYR:N	17	1.05
(1,76)	1:184:A:LYS:N	1:184:A:LYS:CA	1:184:A:LYS:C	1:185:A:CYS:N	6	1.05
(1,23)	1:156:A:THR:C	1:157:A:TYR:N	1:157:A:TYR:CA	1:157:A:TYR:C	8	1.05
(1,102)	1:198:A:TYR:N	1:198:A:TYR:CA	1:198:A:TYR:C	1:199:A:TYR:N	14	1.04
(1,72)	1:182:A:LEU:N	1:182:A:LEU:CA	1:182:A:LEU:C	1:183:A:SER:N	7	1.04
(1,91)	1:192:A:SER:C	1:193:A:ASP:N	1:193:A:ASP:CA	1:193:A:ASP:C	20	1.03
(1,46)	1:169:A:GLU:N	1:169:A:GLU:CA	1:169:A:GLU:C	1:170:A:LYS:N	1	1.03
(1,114)	1:204:A:THR:N	1:204:A:THR:CA	1:204:A:THR:C	1:205:A:LYS:N	17	1.02
(1,54)	1:173:A:ASP:N	1:173:A:ASP:CA	1:173:A:ASP:C	1:174:A:LEU:N	13	1.02
(1,41)	1:165:A:GLN:C	1:166:A:SER:N	1:166:A:SER:CA	1:166:A:SER:C	19	1.02
(1,13)	1:151:A:SER:C	1:152:A:PRO:N	1:152:A:PRO:CA	1:152:A:PRO:C	9	1.02
(1,96)	1:195:A:GLY:N	1:195:A:GLY:CA	1:195:A:GLY:C	1:196:A:LYS:N	11	1.01
(1,98)	1:196:A:LYS:N	1:196:A:LYS:CA	1:196:A:LYS:C	1:197:A:PRO:N	4	1.0