



Full wwPDB NMR Structure Validation Report ⓘ

Jun 3, 2023 – 04:56 AM EDT

PDB ID : 5K6P
BMRB ID : 30100
Title : The NMR structure of the m domain tri-helix bundle and C2 of human cardiac Myosin Binding Protein C
Authors : Michie, K.A.; Kwan, A.H.; Tung, C.S.; Guss, J.M.; Trewhella, J.
Deposited on : 2016-05-25

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

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A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

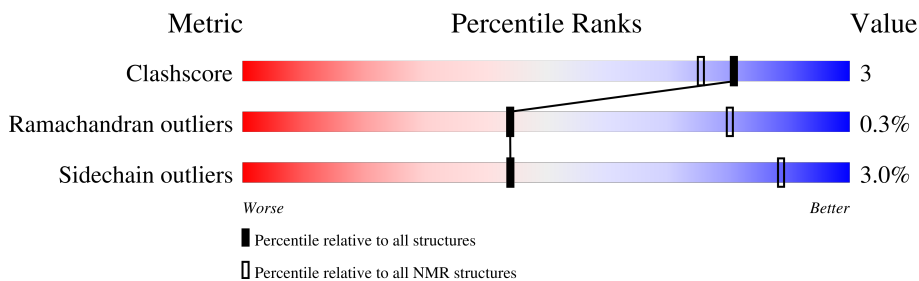
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 92%.

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	137	

2 Ensemble composition and analysis

This entry contains 20 models. Model 20 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:320-A:345 (26)	0.46	12
2	A:363-A:451 (89)	0.60	20

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

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

The models can be grouped into 5 clusters and 4 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2180 atoms, of which 1094 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Myosin-binding protein C, cardiac-type.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	137	2180	682	1094	190	208	6	0

There are 4 discrepancies between the modelled and reference sequences:

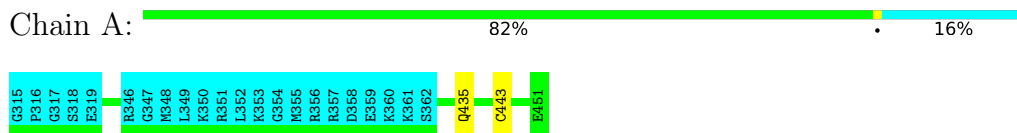
Chain	Residue	Modelled	Actual	Comment	Reference
A	315	GLY	-	expression tag	UNP Q14896
A	316	PRO	-	expression tag	UNP Q14896
A	317	GLY	-	expression tag	UNP Q14896
A	318	SER	-	expression tag	UNP Q14896

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: Myosin-binding protein C, cardiac-type

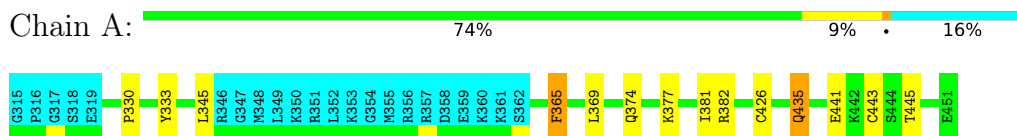


4.2 Scores per residue for each member of the ensemble

Colouring as in section [4.1](#) above.

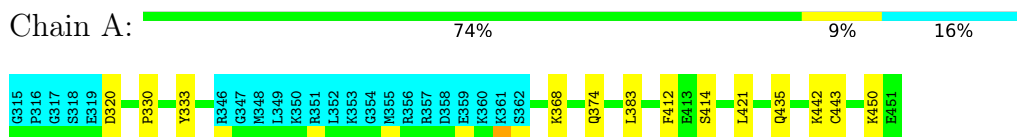
4.2.1 Score per residue for model 1

- Molecule 1: Myosin-binding protein C, cardiac-type



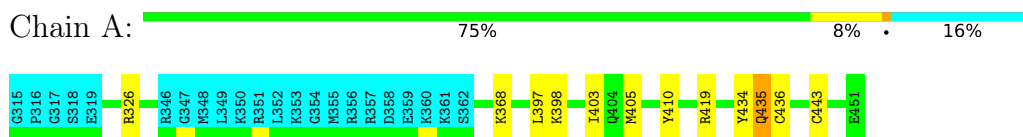
4.2.2 Score per residue for model 2

- Molecule 1: Myosin-binding protein C, cardiac-type



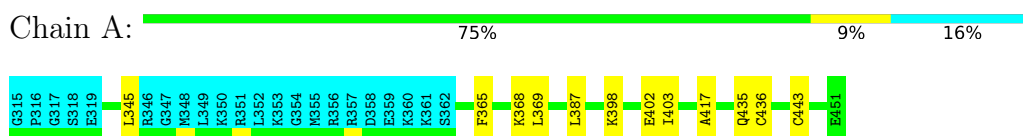
4.2.3 Score per residue for model 3

- Molecule 1: Myosin-binding protein C, cardiac-type



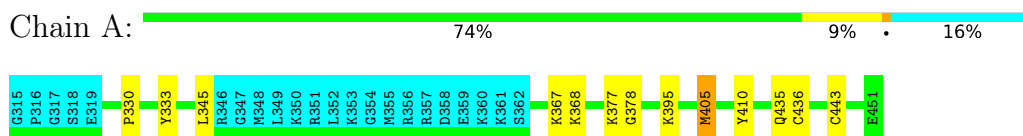
4.2.4 Score per residue for model 4

- Molecule 1: Myosin-binding protein C, cardiac-type



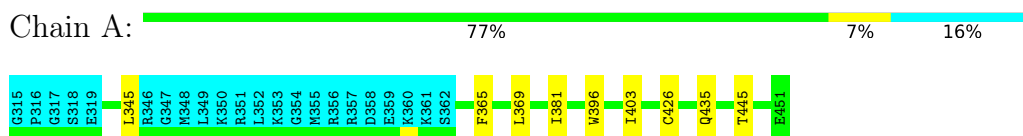
4.2.5 Score per residue for model 5

- Molecule 1: Myosin-binding protein C, cardiac-type



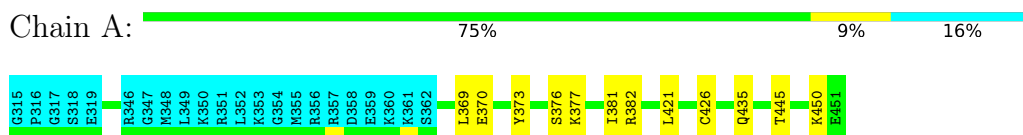
4.2.6 Score per residue for model 6

- Molecule 1: Myosin-binding protein C, cardiac-type



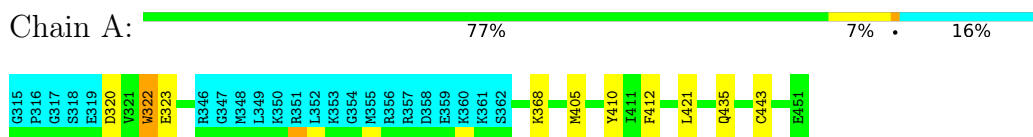
4.2.7 Score per residue for model 7

- Molecule 1: Myosin-binding protein C, cardiac-type



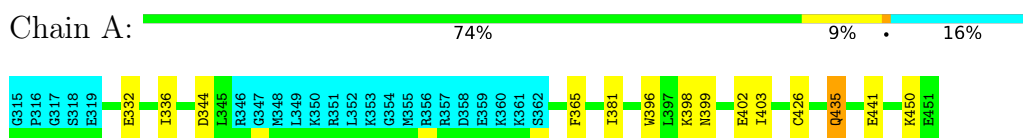
4.2.8 Score per residue for model 8

- Molecule 1: Myosin-binding protein C, cardiac-type



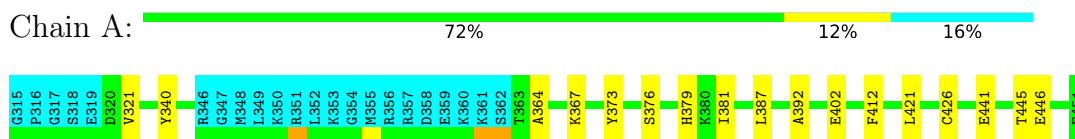
4.2.9 Score per residue for model 9

- Molecule 1: Myosin-binding protein C, cardiac-type



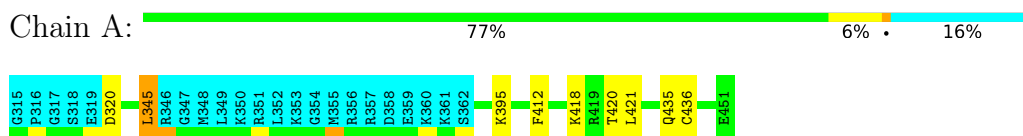
4.2.10 Score per residue for model 10

- Molecule 1: Myosin-binding protein C, cardiac-type



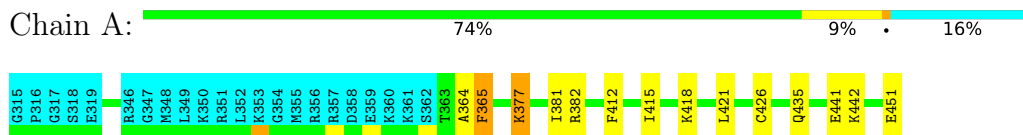
4.2.11 Score per residue for model 11

- Molecule 1: Myosin-binding protein C, cardiac-type



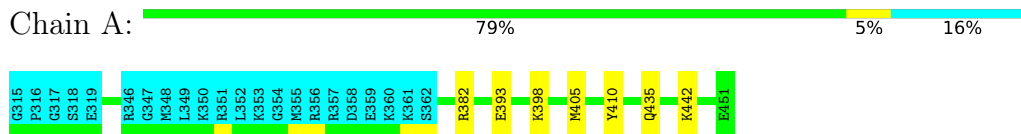
4.2.12 Score per residue for model 12

- Molecule 1: Myosin-binding protein C, cardiac-type



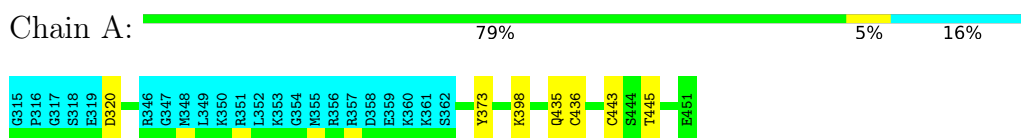
4.2.13 Score per residue for model 13

- Molecule 1: Myosin-binding protein C, cardiac-type



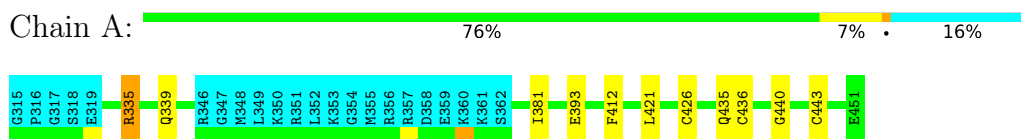
4.2.14 Score per residue for model 14

- Molecule 1: Myosin-binding protein C, cardiac-type



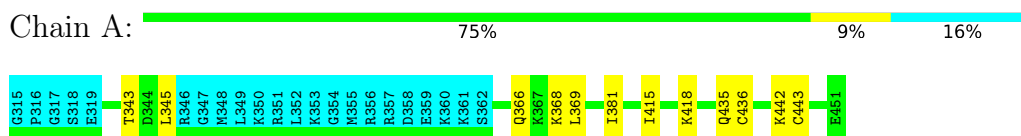
4.2.15 Score per residue for model 15

- Molecule 1: Myosin-binding protein C, cardiac-type



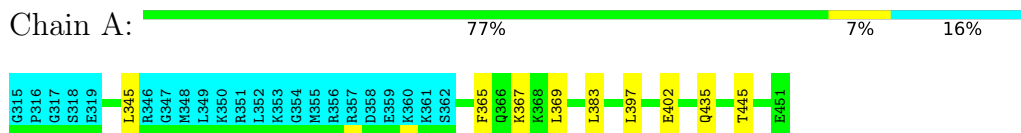
4.2.16 Score per residue for model 16

- Molecule 1: Myosin-binding protein C, cardiac-type



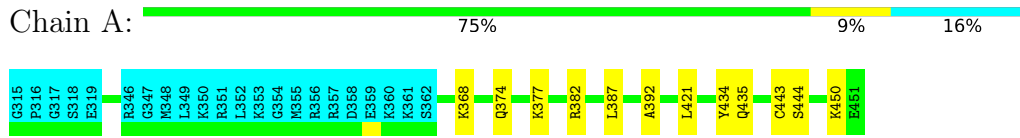
4.2.17 Score per residue for model 17

- Molecule 1: Myosin-binding protein C, cardiac-type



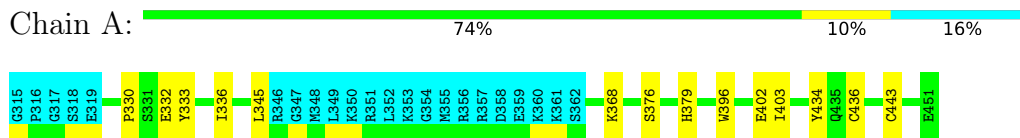
4.2.18 Score per residue for model 18

- Molecule 1: Myosin-binding protein C, cardiac-type



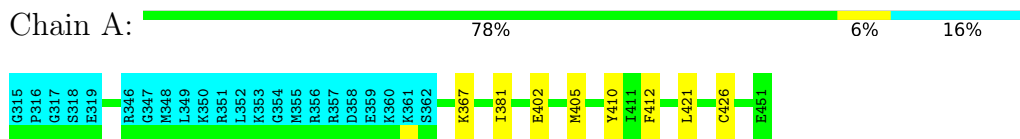
4.2.19 Score per residue for model 19

- Molecule 1: Myosin-binding protein C, cardiac-type



4.2.20 Score per residue for model 20 (medoid)

- Molecule 1: Myosin-binding protein C, cardiac-type



5 Refinement protocol and experimental data overview

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

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

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

Software name	Classification	Version
CYANA	refinement	
CNS	refinement	1.2
CYANA	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	1701
Number of shifts mapped to atoms	1701
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	92%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	0.2±0.5
All	All	0	5

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	382	ARG	Sidechain	2
1	A	326	ARG	Sidechain	1
1	A	419	ARG	Sidechain	1
1	A	335	ARG	Sidechain	1

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	913	903	903	5±2
All	All	18260	18060	18060	95

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 3.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:368:LYS:HB3	1:A:443:CYS:SG	0.67	2.30	3	8
1:A:436:CYS:SG	1:A:443:CYS:HB3	0.61	2.35	5	3
1:A:364:ALA:HB3	1:A:441:GLU:HG3	0.59	1.74	12	2
1:A:381:ILE:HG22	1:A:426:CYS:SG	0.55	2.41	1	8
1:A:330:PRO:HA	1:A:333:TYR:CZ	0.53	2.38	19	3
1:A:396:TRP:HB3	1:A:403:ILE:HD12	0.53	1.79	19	3
1:A:436:CYS:HB2	1:A:443:CYS:SG	0.53	2.44	14	2
1:A:320:ASP:HA	1:A:322:TRP:NE1	0.52	2.20	8	1
1:A:397:LEU:HD23	1:A:402:GLU:HA	0.51	1.82	17	1
1:A:415:ILE:HB	1:A:418:LYS:CG	0.50	2.36	12	1
1:A:435:GLN:HE21	1:A:435:GLN:N	0.49	2.04	1	2
1:A:330:PRO:HA	1:A:333:TYR:CD2	0.49	2.41	5	1
1:A:397:LEU:O	1:A:434:TYR:HA	0.49	2.08	3	1
1:A:415:ILE:O	1:A:418:LYS:HG2	0.47	2.09	16	1
1:A:376:SER:HA	1:A:450:LYS:O	0.47	2.09	7	1
1:A:398:LYS:HG2	1:A:403:ILE:HG12	0.47	1.85	9	2
1:A:387:LEU:HG	1:A:392:ALA:O	0.46	2.10	18	1
1:A:403:ILE:HD11	1:A:434:TYR:HD1	0.46	1.70	19	1
1:A:415:ILE:HB	1:A:418:LYS:HG3	0.46	1.87	12	1
1:A:435:GLN:HA	1:A:443:CYS:O	0.46	2.11	16	3
1:A:434:TYR:O	1:A:444:SER:HA	0.46	2.10	18	1
1:A:369:LEU:HB3	1:A:445:THR:HB	0.45	1.88	7	4
1:A:377:LYS:HD2	1:A:378:GLY:N	0.45	2.26	5	1
1:A:405:MET:HA	1:A:410:TYR:HB2	0.45	1.88	5	1
1:A:398:LYS:HG3	1:A:403:ILE:HG12	0.45	1.87	3	1
1:A:330:PRO:HA	1:A:333:TYR:CE1	0.45	2.46	19	1
1:A:412:PHE:CE1	1:A:421:LEU:HD13	0.45	2.46	2	2
1:A:321:VAL:HB	1:A:340:TYR:CG	0.45	2.46	10	1
1:A:376:SER:HB2	1:A:379:HIS:CD2	0.45	2.47	10	2
1:A:365:PHE:CD2	1:A:441:GLU:HB3	0.44	2.47	9	2
1:A:412:PHE:CE2	1:A:421:LEU:HD13	0.44	2.46	20	5
1:A:387:LEU:HD13	1:A:392:ALA:O	0.44	2.13	10	1
1:A:345:LEU:HD23	1:A:345:LEU:H	0.44	1.73	4	2
1:A:405:MET:HG3	1:A:410:TYR:O	0.44	2.13	3	4
1:A:369:LEU:HD11	1:A:436:CYS:SG	0.44	2.52	4	2
1:A:436:CYS:O	1:A:442:LYS:HA	0.44	2.13	16	1
1:A:396:TRP:CB	1:A:403:ILE:HD12	0.43	2.42	19	1
1:A:395:LYS:O	1:A:436:CYS:HA	0.43	2.13	11	1
1:A:418:LYS:HE2	1:A:420:THR:OG1	0.43	2.13	11	1
1:A:364:ALA:HB3	1:A:441:GLU:CG	0.43	2.43	12	1
1:A:442:LYS:HG2	1:A:443:CYS:N	0.42	2.29	2	1
1:A:387:LEU:O	1:A:417:ALA:HB1	0.42	2.14	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:373:TYR:HD1	1:A:445:THR:OG1	0.42	1.98	10	2
1:A:377:LYS:CB	1:A:451:GLU:HA	0.42	2.45	12	1
1:A:382:ARG:HA	1:A:421:LEU:O	0.42	2.14	7	2
1:A:332:GLU:HB3	1:A:336:ILE:CD1	0.42	2.44	9	1
1:A:335:ARG:O	1:A:339:GLN:HB2	0.42	2.13	15	1
1:A:332:GLU:O	1:A:336:ILE:HG13	0.42	2.14	19	1
1:A:320:ASP:HB3	1:A:323:GLU:HG2	0.41	1.92	8	1
1:A:412:PHE:CD1	1:A:421:LEU:HD13	0.40	2.52	2	1
1:A:370:GLU:HB2	1:A:373:TYR:CE1	0.40	2.51	7	1
1:A:412:PHE:CD2	1:A:421:LEU:HD13	0.40	2.52	15	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	114/137 (83%)	107±2 (94±2%)	7±2 (6±2%)	0±1 (0±1%)	44	80
All	All	2280/2740 (83%)	2136 (94%)	137 (6%)	7 (0%)	44	80

All 3 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	402	GLU	5
1	A	399	ASN	1
1	A	320	ASP	1

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	98/116 (84%)	95±2 (97±2%)	3±2 (3±2%)	44 89
All	All	1960/2320 (84%)	1901 (97%)	59 (3%)	44 89

All 21 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	435	GLN	16
1	A	345	LEU	6
1	A	365	PHE	5
1	A	377	LYS	4
1	A	367	LYS	4
1	A	374	GLN	3
1	A	450	LYS	3
1	A	383	LEU	2
1	A	442	LYS	2
1	A	393	GLU	2
1	A	398	LYS	2
1	A	382	ARG	1
1	A	320	ASP	1
1	A	414	SER	1
1	A	395	LYS	1
1	A	405	MET	1
1	A	322	TRP	1
1	A	446	GLU	1
1	A	343	THR	1
1	A	366	GLN	1
1	A	381	ILE	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 92% for the well-defined parts and 91% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: chinaA_fix_data_160303d_ref_corr

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	1701
Number of shifts mapped to atoms	1701
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	4

7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	136	-0.05 ± 0.07	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	126	0.04 ± 0.09	None needed (< 0.5 ppm)
$^{13}\text{C}'$	129	-0.05 ± 0.11	None needed (< 0.5 ppm)
^{15}N	132	0.00 ± 0.26	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 92%, i.e. 1434 atoms were assigned a chemical shift out of a possible 1562. 0 out of 17 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	570/576 (99%)	234/234 (100%)	224/230 (97%)	112/112 (100%)
Sidechain	792/863 (92%)	539/559 (96%)	241/273 (88%)	12/31 (39%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	72/123 (59%)	45/60 (75%)	25/59 (42%)	2/4 (50%)
Overall	1434/1562 (92%)	818/853 (96%)	490/562 (87%)	126/147 (86%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 91%, i.e. 1700 atoms were assigned a chemical shift out of a possible 1877. 0 out of 19 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	675/688 (98%)	278/281 (99%)	265/274 (97%)	132/133 (99%)
Sidechain	953/1066 (89%)	648/687 (94%)	292/332 (88%)	13/47 (28%)
Aromatic	72/123 (59%)	45/60 (75%)	25/59 (42%)	2/4 (50%)
Overall	1700/1877 (91%)	971/1028 (94%)	582/665 (88%)	147/184 (80%)

7.1.4 Statistically unusual chemical shifts [i](#)

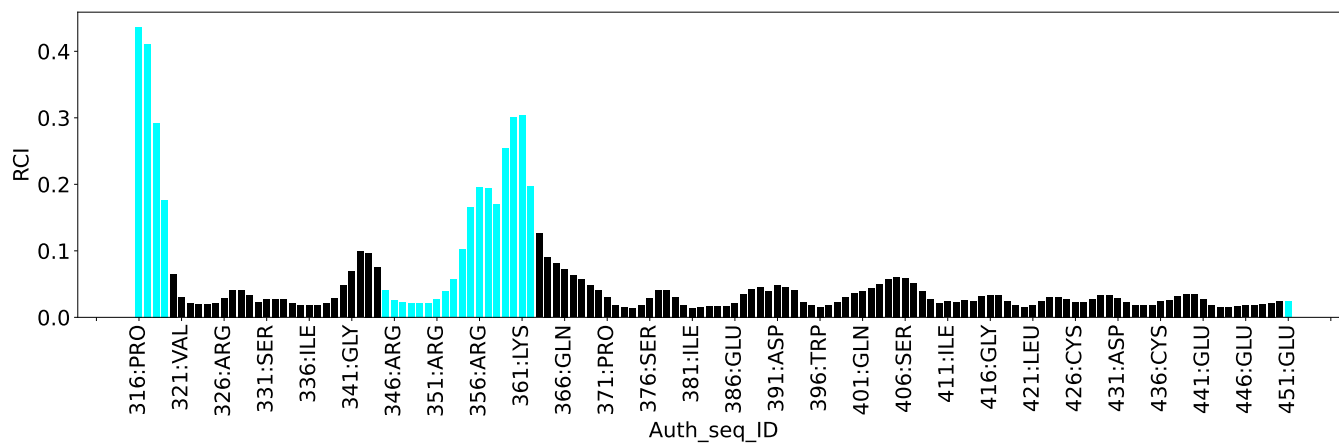
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	421	LEU	HB3	-1.05	-0.26 – 3.31	-7.2
1	A	330	PRO	HA	2.43	2.78 – 6.00	-6.1
1	A	409	LYS	HG2	-0.04	0.13 – 2.61	-5.7
1	A	398	LYS	HD2	0.56	0.58 – 2.64	-5.1

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	3947
Intra-residue ($ i-j =0$)	473
Sequential ($ i-j =1$)	1103
Medium range ($ i-j >1$ and $ i-j <5$)	838
Long range ($ i-j \geq 5$)	1533
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	206
Number of unmapped restraints	0
Number of restraints per residue	30.3
Number of long range restraints per residue ¹	11.2

¹Long range hydrogen bonds and disulfide bonds are counted as long range restraints while calculating the number of long range restraints per residue

8.2 Residual restraint violations

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)	9.4	0.2
0.2-0.5 (Medium)	0.3	0.25
>0.5 (Large)	None	None

8.2.2 Average number of dihedral-angle violations per model [i](#)

Dihedral-angle violations less than 1° are not included in the calculation.

Bins (°)	Average number of violations per model	Max (°)
1.0-10.0 (Small)	4.4	5.5
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis [i](#)

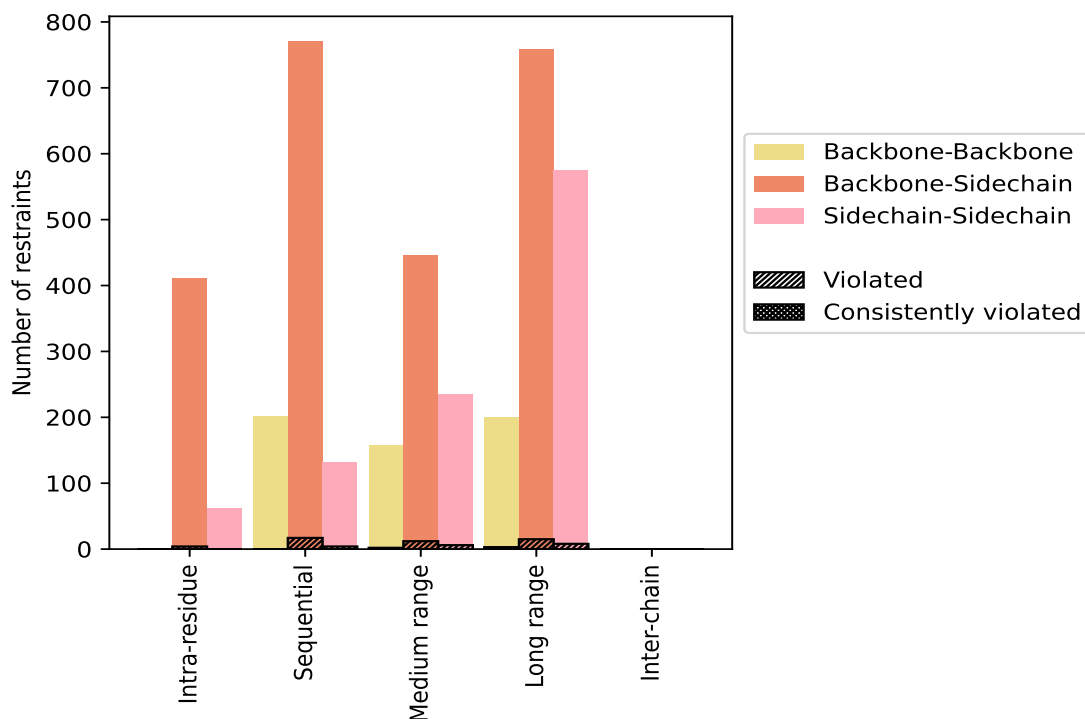
9.1 Summary of distance violations [i](#)

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 ($i-j =0$)	473	12.0	4	0.8	0.1	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	411	10.4	4	1.0	0.1	0	0.0	0.0
Sidechain-Sidechain	62	1.6	0	0.0	0.0	0	0.0	0.0
Sequential ($i-j =1$)	1103	27.9	21	1.9	0.5	0	0.0	0.0
Backbone-Backbone	202	5.1	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	770	19.5	17	2.2	0.4	0	0.0	0.0
Sidechain-Sidechain	131	3.3	4	3.1	0.1	0	0.0	0.0
Medium range ($i-j >1$ & $i-j <5$)	838	21.2	20	2.4	0.5	0	0.0	0.0
Backbone-Backbone	157	4.0	2	1.3	0.1	0	0.0	0.0
Backbone-Sidechain	446	11.3	12	2.7	0.3	0	0.0	0.0
Sidechain-Sidechain	235	6.0	6	2.6	0.2	0	0.0	0.0
Long range ($i-j \geq 5$)	1533	38.8	26	1.7	0.7	0	0.0	0.0
Backbone-Backbone	200	5.1	3	1.5	0.1	0	0.0	0.0
Backbone-Sidechain	759	19.2	15	2.0	0.4	0	0.0	0.0
Sidechain-Sidechain	574	14.5	8	1.4	0.2	0	0.0	0.0
Inter-chain	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Hydrogen bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	3947	100.0	71	1.8	1.8	0	0.0	0.0
Backbone-Backbone	559	14.2	5	0.9	0.1	0	0.0	0.0
Backbone-Sidechain	2386	60.5	48	2.0	1.2	0	0.0	0.0
Sidechain-Sidechain	1002	25.4	18	1.8	0.5	0	0.0	0.0

¹ percentage calculated with respect to the total number of distance restraints, ² percentage calculated with respect to the number of restraints in a particular restraint category, ³ violated in at least one model, ⁴ violated in all the models

9.1.1 Bar chart : Distribution of distance restraints and violations [i](#)



Violated and consistently violated restraints are shown using different hatch patterns in their respective categories. The hydrogen bonds and 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	0	3	2	4	0	9	0.15	0.22	0.04	0.14
2	0	2	2	5	0	9	0.13	0.15	0.02	0.13
3	0	3	2	3	0	8	0.14	0.18	0.03	0.15
4	1	3	3	2	0	9	0.13	0.15	0.01	0.13
5	0	3	3	4	0	10	0.15	0.22	0.03	0.14
6	0	6	3	5	0	14	0.13	0.17	0.02	0.12
7	0	2	0	4	0	6	0.14	0.17	0.03	0.12
8	1	8	5	2	0	16	0.13	0.16	0.02	0.12
9	1	1	2	4	0	8	0.15	0.25	0.04	0.14
10	1	4	2	5	0	12	0.13	0.19	0.03	0.12
11	0	3	1	5	0	9	0.13	0.24	0.04	0.12

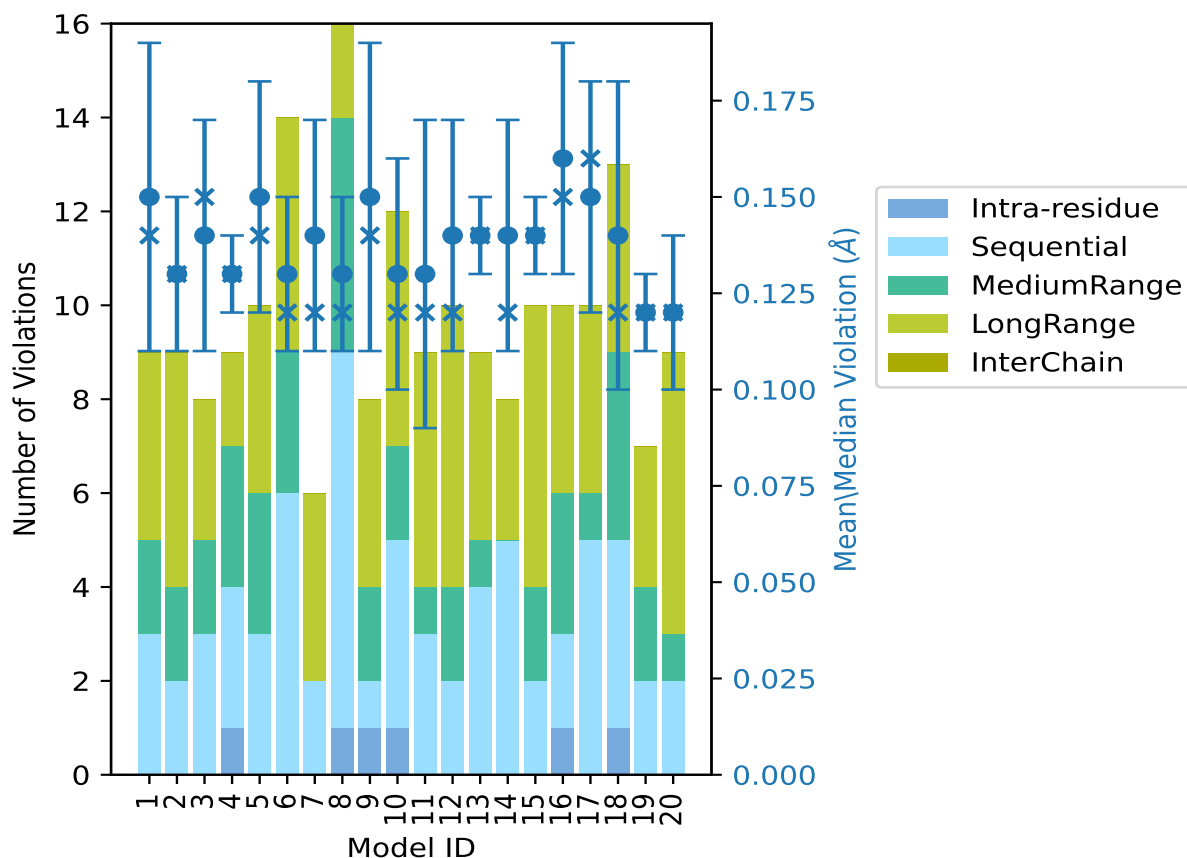
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Model ID	Number of violations					Total	Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵					
12	0	2	2	6	0	10	0.14	0.2	0.03	0.12
13	0	4	1	4	0	9	0.14	0.15	0.01	0.14
14	0	5	0	3	0	8	0.14	0.18	0.03	0.12
15	0	2	2	6	0	10	0.14	0.17	0.01	0.14
16	1	2	3	4	0	10	0.16	0.22	0.03	0.15
17	0	5	1	4	0	10	0.15	0.21	0.03	0.16
18	1	4	4	4	0	13	0.14	0.25	0.04	0.12
19	0	2	2	3	0	7	0.12	0.14	0.01	0.12
20	0	2	1	6	0	9	0.12	0.15	0.02	0.12

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

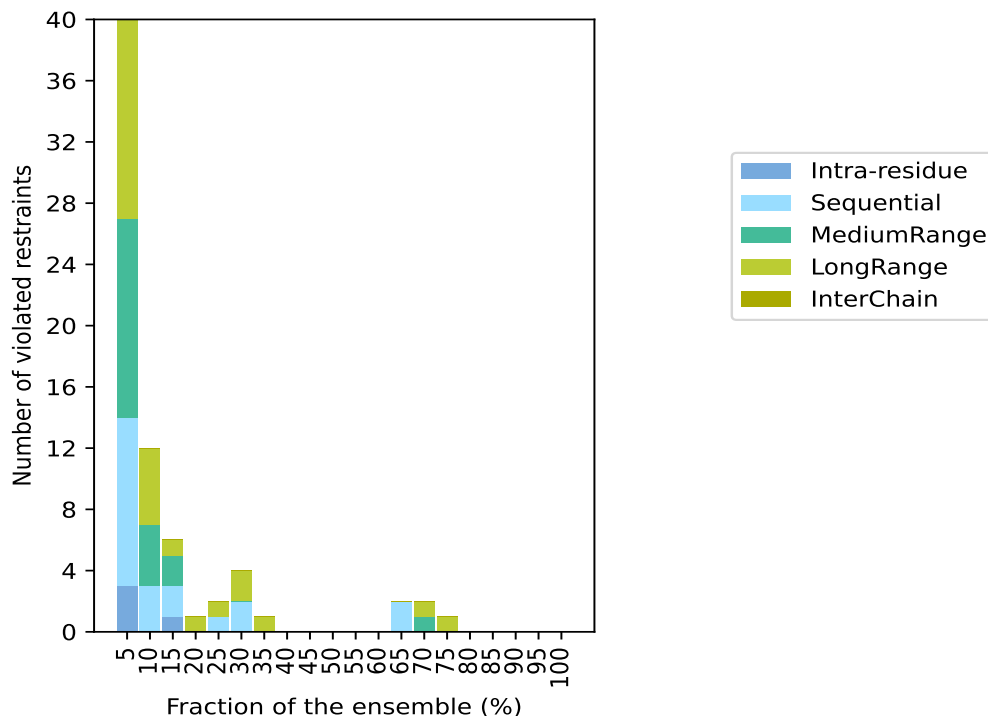
9.3 Distance violation statistics for the ensemble

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, 3876(IR:469, SQ:1082, MR:818, LR:1507, 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	%
3	11	13	13	0	40	1	5.0
0	3	4	5	0	12	2	10.0
1	2	2	1	0	6	3	15.0
0	0	0	1	0	1	4	20.0
0	1	0	1	0	2	5	25.0
0	2	0	2	0	4	6	30.0
0	0	0	1	0	1	7	35.0
0	0	0	0	0	0	8	40.0
0	0	0	0	0	0	9	45.0
0	0	0	0	0	0	10	50.0
0	0	0	0	0	0	11	55.0
0	0	0	0	0	0	12	60.0
0	2	0	0	0	2	13	65.0
0	0	1	1	0	2	14	70.0
0	0	0	1	0	1	15	75.0
0	0	0	0	0	0	16	80.0
0	0	0	0	0	0	17	85.0
0	0	0	0	0	0	18	90.0
0	0	0	0	0	0	19	95.0
0	0	0	0	0	0	20	100.0

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

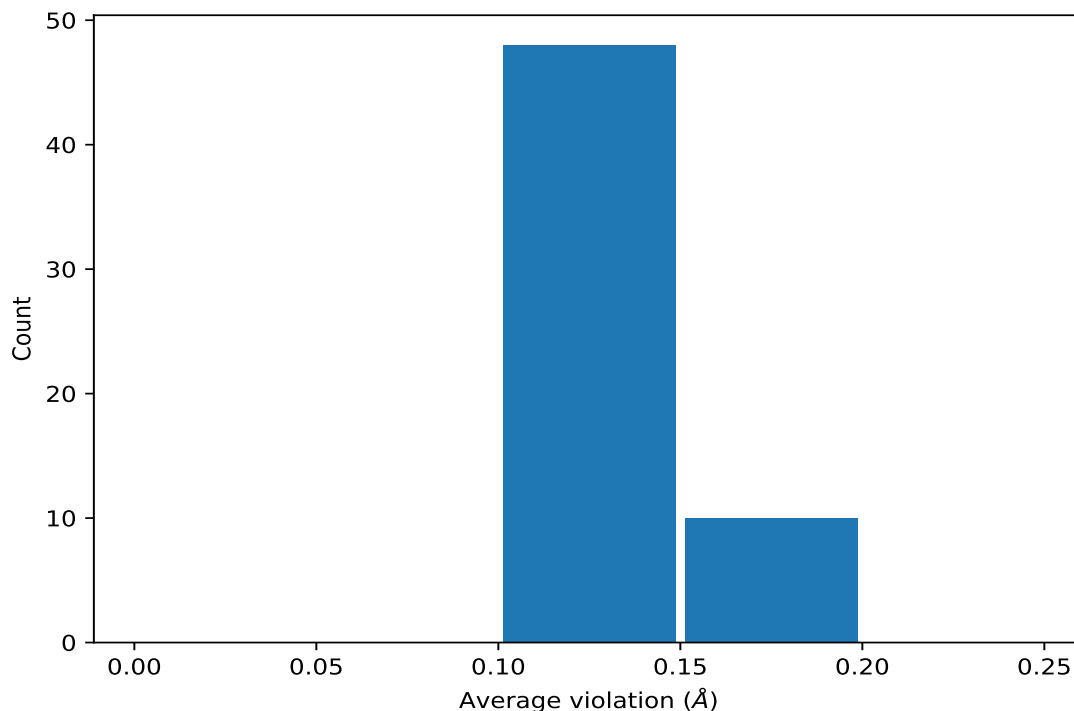
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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)
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD11	15	0.15	0.04	0.14
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD12	15	0.15	0.04	0.14
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD13	15	0.15	0.04	0.14
(1,1316)	1:A:396:TRP:HE1	1:A:412:PHE:HZ	14	0.15	0.02	0.15
(2,760)	1:A:367:LYS:H	1:A:369:LEU:H	14	0.14	0.02	0.14
(1,1208)	1:A:397:LEU:HG	1:A:398:LYS:HA	13	0.13	0.02	0.13
(2,1250)	1:A:342:VAL:HB	1:A:343:THR:HB	13	0.13	0.01	0.13
(2,540)	1:A:365:PHE:HB2	1:A:441:GLU:H	7	0.13	0.02	0.12
(2,257)	1:A:392:ALA:H	1:A:393:GLU:HB3	6	0.16	0.03	0.16
(1,872)	1:A:382:ARG:HA	1:A:383:LEU:HG	6	0.14	0.03	0.12
(2,93)	1:A:398:LYS:HB2	1:A:403:ILE:H	6	0.12	0.01	0.12
(2,157)	1:A:369:LEU:H	1:A:445:THR:HA	6	0.12	0.01	0.12
(2,256)	1:A:392:ALA:H	1:A:393:GLU:HB2	5	0.15	0.03	0.15
(2,560)	1:A:383:LEU:HD21	1:A:445:THR:H	5	0.14	0.01	0.13
(2,560)	1:A:383:LEU:HD22	1:A:445:THR:H	5	0.14	0.01	0.13
(2,560)	1:A:383:LEU:HD23	1:A:445:THR:H	5	0.14	0.01	0.13

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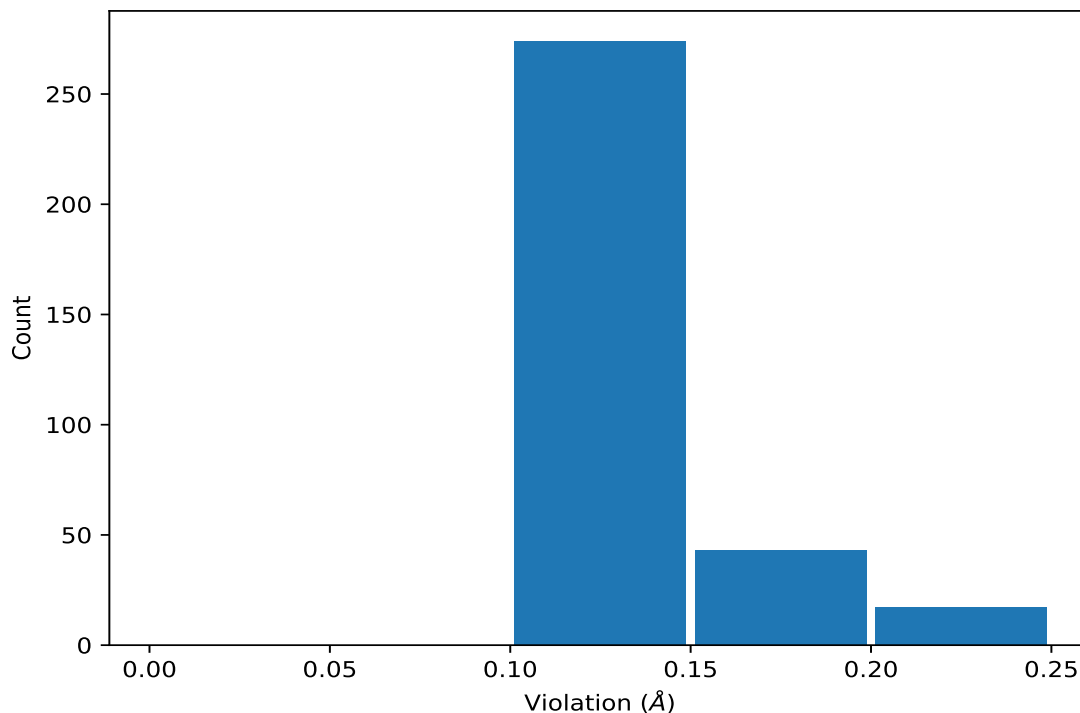
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(2,1608)	1:A:366:GLN:HA	1:A:386:GLU:HG2	4	0.12	0.0	0.12
(2,1608)	1:A:366:GLN:HA	1:A:386:GLU:HG3	4	0.12	0.0	0.12
(1,1287)	1:A:356:ARG:HA	1:A:356:ARG:HD2	3	0.17	0.01	0.16
(2,1766)	1:A:414:SER:H	1:A:419:ARG:HG2	3	0.17	0.02	0.17
(2,1766)	1:A:414:SER:H	1:A:419:ARG:HG3	3	0.17	0.02	0.17
(2,530)	1:A:440:GLY:H	1:A:441:GLU:HG3	3	0.16	0.02	0.15
(2,1442)	1:A:352:LEU:HD21	1:A:355:MET:HA	3	0.16	0.04	0.13
(2,1442)	1:A:352:LEU:HD22	1:A:355:MET:HA	3	0.16	0.04	0.13
(2,1442)	1:A:352:LEU:HD23	1:A:355:MET:HA	3	0.16	0.04	0.13
(2,1777)	1:A:424:SER:H	1:A:425:GLN:HG2	3	0.13	0.01	0.14
(2,1777)	1:A:424:SER:H	1:A:425:GLN:HG3	3	0.13	0.01	0.14
(2,195)	1:A:377:LYS:HG3	1:A:379:HIS:H	3	0.11	0.0	0.11
(2,292)	1:A:400:GLY:H	1:A:434:TYR:HD1	2	0.16	0.01	0.16
(2,292)	1:A:400:GLY:H	1:A:434:TYR:HD2	2	0.16	0.01	0.16
(2,529)	1:A:440:GLY:H	1:A:441:GLU:HG2	2	0.15	0.03	0.15
(2,1695)	1:A:392:ALA:H	1:A:393:GLU:HG2	2	0.14	0.01	0.14
(2,1695)	1:A:392:ALA:H	1:A:393:GLU:HG3	2	0.14	0.01	0.14
(1,1299)	1:A:396:TRP:HD1	1:A:403:ILE:HD11	2	0.14	0.01	0.14
(1,1299)	1:A:396:TRP:HD1	1:A:403:ILE:HD12	2	0.14	0.01	0.14
(1,1299)	1:A:396:TRP:HD1	1:A:403:ILE:HD13	2	0.14	0.01	0.14
(2,1147)	1:A:320:ASP:HA	1:A:324:ILE:HG21	2	0.13	0.01	0.13
(2,1147)	1:A:320:ASP:HA	1:A:324:ILE:HG22	2	0.13	0.01	0.13
(2,1147)	1:A:320:ASP:HA	1:A:324:ILE:HG23	2	0.13	0.01	0.13
(2,1222)	1:A:362:SER:HB2	1:A:365:PHE:HD1	2	0.12	0.01	0.12
(2,1222)	1:A:362:SER:HB2	1:A:365:PHE:HD2	2	0.12	0.01	0.12
(2,1385)	1:A:354:GLY:HA3	1:A:355:MET:HE1	2	0.12	0.01	0.12
(2,1385)	1:A:354:GLY:HA3	1:A:355:MET:HE2	2	0.12	0.01	0.12
(2,1385)	1:A:354:GLY:HA3	1:A:355:MET:HE3	2	0.12	0.01	0.12
(2,820)	1:A:399:ASN:HD22	1:A:433:ALA:HB1	2	0.12	0.0	0.12
(2,820)	1:A:399:ASN:HD22	1:A:433:ALA:HB2	2	0.12	0.0	0.12
(2,820)	1:A:399:ASN:HD22	1:A:433:ALA:HB3	2	0.12	0.0	0.12
(2,1011)	1:A:325:LEU:HD21	1:A:340:TYR:HD1	2	0.12	0.0	0.12
(2,1011)	1:A:325:LEU:HD21	1:A:340:TYR:HD2	2	0.12	0.0	0.12
(2,1011)	1:A:325:LEU:HD22	1:A:340:TYR:HD1	2	0.12	0.0	0.12
(2,1011)	1:A:325:LEU:HD22	1:A:340:TYR:HD2	2	0.12	0.0	0.12
(2,1011)	1:A:325:LEU:HD23	1:A:340:TYR:HD1	2	0.12	0.0	0.12
(2,1011)	1:A:325:LEU:HD23	1:A:340:TYR:HD2	2	0.12	0.0	0.12
(2,1154)	1:A:387:LEU:HA	1:A:394:VAL:HG21	2	0.12	0.0	0.12
(2,1154)	1:A:387:LEU:HA	1:A:394:VAL:HG22	2	0.12	0.0	0.12
(2,1154)	1:A:387:LEU:HA	1:A:394:VAL:HG23	2	0.12	0.0	0.12
(2,595)	1:A:319:GLU:H	1:A:322:TRP:HD1	2	0.11	0.0	0.11
(2,794)	1:A:406:SER:H	1:A:409:LYS:HG2	2	0.11	0.0	0.11

¹Number of violated models, ²Standard deviation

9.5 All violated distance restraints [i](#)

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

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



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

The following table lists the absolute value of the violation for each restraint in the ensemble sorted by its value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint. Rows with same key represent combinatorial or ambiguous restraints and are counted as a single restraint.

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD11	9	0.25
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD12	9	0.25
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD13	9	0.25
(1,1295)	1:A:359:GLU:HA	1:A:359:GLU:HG3	18	0.25
(2,129)	1:A:353:LYS:HA	1:A:356:ARG:H	11	0.24
(2,257)	1:A:392:ALA:H	1:A:393:GLU:HB3	16	0.22
(2,1442)	1:A:352:LEU:HD21	1:A:355:MET:HA	1	0.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,1442)	1:A:352:LEU:HD22	1:A:355:MET:HA	1	0.22
(2,1442)	1:A:352:LEU:HD23	1:A:355:MET:HA	1	0.22
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD11	5	0.22
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD12	5	0.22
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD13	5	0.22
(2,1197)	1:A:397:LEU:HG	1:A:403:ILE:HA	17	0.21
(2,256)	1:A:392:ALA:H	1:A:393:GLU:HB2	1	0.2
(2,132)	1:A:362:SER:H	1:A:364:ALA:HB1	12	0.2
(2,132)	1:A:362:SER:H	1:A:364:ALA:HB2	12	0.2
(2,132)	1:A:362:SER:H	1:A:364:ALA:HB3	12	0.2
(2,530)	1:A:440:GLY:H	1:A:441:GLU:HG3	16	0.19
(2,1766)	1:A:414:SER:H	1:A:419:ARG:HG2	12	0.19
(2,1766)	1:A:414:SER:H	1:A:419:ARG:HG3	12	0.19
(1,1568)	1:A:360:LYS:HA	1:A:360:LYS:HD2	10	0.19
(1,1568)	1:A:360:LYS:HA	1:A:360:LYS:HD3	10	0.19
(1,1316)	1:A:396:TRP:HE1	1:A:412:PHE:HZ	18	0.19
(2,8)	1:A:360:LYS:HE2	1:A:361:LYS:H	5	0.18
(2,760)	1:A:367:LYS:H	1:A:369:LEU:H	3	0.18
(1,872)	1:A:382:ARG:HA	1:A:383:LEU:HG	14	0.18
(1,1316)	1:A:396:TRP:HE1	1:A:412:PHE:HZ	1	0.18
(1,1287)	1:A:356:ARG:HA	1:A:356:ARG:HD2	16	0.18
(2,529)	1:A:440:GLY:H	1:A:441:GLU:HG2	17	0.17
(2,292)	1:A:400:GLY:H	1:A:434:TYR:HD1	15	0.17
(2,292)	1:A:400:GLY:H	1:A:434:TYR:HD2	15	0.17
(2,257)	1:A:392:ALA:H	1:A:393:GLU:HB3	7	0.17
(2,257)	1:A:392:ALA:H	1:A:393:GLU:HB3	14	0.17
(2,1766)	1:A:414:SER:H	1:A:419:ARG:HG2	5	0.17
(2,1766)	1:A:414:SER:H	1:A:419:ARG:HG3	5	0.17
(1,957)	1:A:362:SER:HA	1:A:441:GLU:HG2	6	0.17
(1,872)	1:A:382:ARG:HA	1:A:383:LEU:HG	10	0.17
(1,1316)	1:A:396:TRP:HE1	1:A:412:PHE:HZ	7	0.17
(1,1316)	1:A:396:TRP:HE1	1:A:412:PHE:HZ	17	0.17
(1,1208)	1:A:397:LEU:HG	1:A:398:LYS:HA	3	0.17
(1,1208)	1:A:397:LEU:HG	1:A:398:LYS:HA	9	0.17
(2,760)	1:A:367:LYS:H	1:A:369:LEU:H	16	0.16
(2,560)	1:A:383:LEU:HD21	1:A:445:THR:H	14	0.16
(2,560)	1:A:383:LEU:HD22	1:A:445:THR:H	14	0.16
(2,560)	1:A:383:LEU:HD23	1:A:445:THR:H	14	0.16
(2,540)	1:A:365:PHE:HB2	1:A:441:GLU:H	17	0.16
(2,256)	1:A:392:ALA:H	1:A:393:GLU:HB2	17	0.16
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD11	1	0.16
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD12	1	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD13	1	0.16
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD11	3	0.16
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD12	3	0.16
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD13	3	0.16
(2,1250)	1:A:342:VAL:HB	1:A:343:THR:HB	8	0.16
(1,1353)	1:A:320:ASP:HA	1:A:323:GLU:HB2	8	0.16
(1,1353)	1:A:320:ASP:HA	1:A:323:GLU:HB3	8	0.16
(1,1316)	1:A:396:TRP:HE1	1:A:412:PHE:HZ	8	0.16
(1,1316)	1:A:396:TRP:HE1	1:A:412:PHE:HZ	10	0.16
(1,1287)	1:A:356:ARG:HA	1:A:356:ARG:HD2	8	0.16
(1,1287)	1:A:356:ARG:HA	1:A:356:ARG:HD2	9	0.16
(2,93)	1:A:398:LYS:HB2	1:A:403:ILE:H	15	0.15
(2,760)	1:A:367:LYS:H	1:A:369:LEU:H	13	0.15
(2,560)	1:A:383:LEU:HD21	1:A:445:THR:H	2	0.15
(2,560)	1:A:383:LEU:HD22	1:A:445:THR:H	2	0.15
(2,560)	1:A:383:LEU:HD23	1:A:445:THR:H	2	0.15
(2,530)	1:A:440:GLY:H	1:A:441:GLU:HG3	4	0.15
(2,326)	1:A:397:LEU:HA	1:A:404:GLN:H	15	0.15
(2,292)	1:A:400:GLY:H	1:A:434:TYR:HD1	13	0.15
(2,292)	1:A:400:GLY:H	1:A:434:TYR:HD2	13	0.15
(2,256)	1:A:392:ALA:H	1:A:393:GLU:HB2	8	0.15
(2,1695)	1:A:392:ALA:H	1:A:393:GLU:HG2	13	0.15
(2,1695)	1:A:392:ALA:H	1:A:393:GLU:HG3	13	0.15
(2,1577)	1:A:349:LEU:HD11	1:A:352:LEU:HA	4	0.15
(2,1577)	1:A:349:LEU:HD12	1:A:352:LEU:HA	4	0.15
(2,1577)	1:A:349:LEU:HD13	1:A:352:LEU:HA	4	0.15
(2,1577)	1:A:349:LEU:HD21	1:A:352:LEU:HA	4	0.15
(2,1577)	1:A:349:LEU:HD22	1:A:352:LEU:HA	4	0.15
(2,1577)	1:A:349:LEU:HD23	1:A:352:LEU:HA	4	0.15
(2,154)	1:A:369:LEU:H	1:A:435:GLN:HA	16	0.15
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD11	17	0.15
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD12	17	0.15
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD13	17	0.15
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD11	20	0.15
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD12	20	0.15
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD13	20	0.15
(2,138)	1:A:365:PHE:H	1:A:368:LYS:HD3	18	0.15
(2,1250)	1:A:342:VAL:HB	1:A:343:THR:HB	13	0.15
(1,1598)	1:A:366:GLN:HG2	1:A:367:LYS:HE2	3	0.15
(1,1598)	1:A:366:GLN:HG2	1:A:367:LYS:HE3	3	0.15
(1,1598)	1:A:366:GLN:HG3	1:A:367:LYS:HE2	3	0.15
(1,1598)	1:A:366:GLN:HG3	1:A:367:LYS:HE3	3	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1316)	1:A:396:TRP:HE1	1:A:412:PHE:HZ	2	0.15
(1,1316)	1:A:396:TRP:HE1	1:A:412:PHE:HZ	11	0.15
(1,1316)	1:A:396:TRP:HE1	1:A:412:PHE:HZ	12	0.15
(1,1316)	1:A:396:TRP:HE1	1:A:412:PHE:HZ	20	0.15
(1,1229)	1:A:362:SER:HA	1:A:363:THR:HG21	8	0.15
(1,1229)	1:A:362:SER:HA	1:A:363:THR:HG22	8	0.15
(1,1229)	1:A:362:SER:HA	1:A:363:THR:HG23	8	0.15
(1,1208)	1:A:397:LEU:HG	1:A:398:LYS:HA	6	0.15
(1,1208)	1:A:397:LEU:HG	1:A:398:LYS:HA	17	0.15
(2,821)	1:A:398:LYS:HD3	1:A:399:ASN:HD21	18	0.14
(2,760)	1:A:367:LYS:H	1:A:369:LEU:H	4	0.14
(2,760)	1:A:367:LYS:H	1:A:369:LEU:H	5	0.14
(2,760)	1:A:367:LYS:H	1:A:369:LEU:H	6	0.14
(2,760)	1:A:367:LYS:H	1:A:369:LEU:H	15	0.14
(2,540)	1:A:365:PHE:HB2	1:A:441:GLU:H	9	0.14
(2,530)	1:A:440:GLY:H	1:A:441:GLU:HG3	6	0.14
(2,257)	1:A:392:ALA:H	1:A:393:GLU:HB3	10	0.14
(2,1777)	1:A:424:SER:H	1:A:425:GLN:HG2	13	0.14
(2,1777)	1:A:424:SER:H	1:A:425:GLN:HG3	13	0.14
(2,1777)	1:A:424:SER:H	1:A:425:GLN:HG2	17	0.14
(2,1777)	1:A:424:SER:H	1:A:425:GLN:HG3	17	0.14
(2,1766)	1:A:414:SER:H	1:A:419:ARG:HG2	6	0.14
(2,1766)	1:A:414:SER:H	1:A:419:ARG:HG3	6	0.14
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD11	2	0.14
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD12	2	0.14
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD13	2	0.14
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD11	15	0.14
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD12	15	0.14
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD13	15	0.14
(2,1250)	1:A:342:VAL:HB	1:A:343:THR:HB	3	0.14
(2,1250)	1:A:342:VAL:HB	1:A:343:THR:HB	19	0.14
(2,1147)	1:A:320:ASP:HA	1:A:324:ILE:HG21	5	0.14
(2,1147)	1:A:320:ASP:HA	1:A:324:ILE:HG22	5	0.14
(2,1147)	1:A:320:ASP:HA	1:A:324:ILE:HG23	5	0.14
(1,1578)	1:A:361:LYS:HE2	1:A:363:THR:HG21	16	0.14
(1,1578)	1:A:361:LYS:HE2	1:A:363:THR:HG22	16	0.14
(1,1578)	1:A:361:LYS:HE2	1:A:363:THR:HG23	16	0.14
(1,1578)	1:A:361:LYS:HE3	1:A:363:THR:HG21	16	0.14
(1,1578)	1:A:361:LYS:HE3	1:A:363:THR:HG22	16	0.14
(1,1578)	1:A:361:LYS:HE3	1:A:363:THR:HG23	16	0.14
(1,1299)	1:A:396:TRP:HD1	1:A:403:ILE:HD11	16	0.14
(1,1299)	1:A:396:TRP:HD1	1:A:403:ILE:HD12	16	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1299)	1:A:396:TRP:HD1	1:A:403:ILE:HD13	16	0.14
(1,1208)	1:A:397:LEU:HG	1:A:398:LYS:HA	1	0.14
(1,1208)	1:A:397:LEU:HG	1:A:398:LYS:HA	4	0.14
(2,809)	1:A:396:TRP:HE1	1:A:412:PHE:H	12	0.13
(2,770)	1:A:395:LYS:H	1:A:396:TRP:HE1	18	0.13
(2,760)	1:A:367:LYS:H	1:A:369:LEU:H	2	0.13
(2,760)	1:A:367:LYS:H	1:A:369:LEU:H	19	0.13
(2,560)	1:A:383:LEU:HD21	1:A:445:THR:H	1	0.13
(2,560)	1:A:383:LEU:HD22	1:A:445:THR:H	1	0.13
(2,560)	1:A:383:LEU:HD23	1:A:445:THR:H	1	0.13
(2,560)	1:A:383:LEU:HD21	1:A:445:THR:H	10	0.13
(2,560)	1:A:383:LEU:HD22	1:A:445:THR:H	10	0.13
(2,560)	1:A:383:LEU:HD23	1:A:445:THR:H	10	0.13
(2,560)	1:A:383:LEU:HD21	1:A:445:THR:H	11	0.13
(2,560)	1:A:383:LEU:HD22	1:A:445:THR:H	11	0.13
(2,560)	1:A:383:LEU:HD23	1:A:445:THR:H	11	0.13
(2,540)	1:A:365:PHE:HB2	1:A:441:GLU:H	8	0.13
(2,1695)	1:A:392:ALA:H	1:A:393:GLU:HG2	15	0.13
(2,1695)	1:A:392:ALA:H	1:A:393:GLU:HG3	15	0.13
(2,157)	1:A:369:LEU:H	1:A:445:THR:HA	15	0.13
(2,1442)	1:A:352:LEU:HD21	1:A:355:MET:HA	5	0.13
(2,1442)	1:A:352:LEU:HD22	1:A:355:MET:HA	5	0.13
(2,1442)	1:A:352:LEU:HD23	1:A:355:MET:HA	5	0.13
(2,1442)	1:A:352:LEU:HD21	1:A:355:MET:HA	16	0.13
(2,1442)	1:A:352:LEU:HD22	1:A:355:MET:HA	16	0.13
(2,1442)	1:A:352:LEU:HD23	1:A:355:MET:HA	16	0.13
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD11	4	0.13
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD12	4	0.13
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD13	4	0.13
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD11	13	0.13
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD12	13	0.13
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD13	13	0.13
(2,1398)	1:A:325:LEU:HG	1:A:340:TYR:HD1	9	0.13
(2,1398)	1:A:325:LEU:HG	1:A:340:TYR:HD2	9	0.13
(2,1385)	1:A:354:GLY:HA3	1:A:355:MET:HE1	8	0.13
(2,1385)	1:A:354:GLY:HA3	1:A:355:MET:HE2	8	0.13
(2,1385)	1:A:354:GLY:HA3	1:A:355:MET:HE3	8	0.13
(2,1250)	1:A:342:VAL:HB	1:A:343:THR:HB	2	0.13
(2,1250)	1:A:342:VAL:HB	1:A:343:THR:HB	5	0.13
(2,1250)	1:A:342:VAL:HB	1:A:343:THR:HB	7	0.13
(2,1250)	1:A:342:VAL:HB	1:A:343:THR:HB	10	0.13
(2,1250)	1:A:342:VAL:HB	1:A:343:THR:HB	12	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,1250)	1:A:342:VAL:HB	1:A:343:THR:HB	14	0.13
(2,1222)	1:A:362:SER:HB2	1:A:365:PHE:HD1	18	0.13
(2,1222)	1:A:362:SER:HB2	1:A:365:PHE:HD2	18	0.13
(1,1316)	1:A:396:TRP:HE1	1:A:412:PHE:HZ	5	0.13
(1,1316)	1:A:396:TRP:HE1	1:A:412:PHE:HZ	13	0.13
(1,1299)	1:A:396:TRP:HD1	1:A:403:ILE:HD11	6	0.13
(1,1299)	1:A:396:TRP:HD1	1:A:403:ILE:HD12	6	0.13
(1,1299)	1:A:396:TRP:HD1	1:A:403:ILE:HD13	6	0.13
(1,1208)	1:A:397:LEU:HG	1:A:398:LYS:HA	15	0.13
(1,1208)	1:A:397:LEU:HG	1:A:398:LYS:HA	20	0.13
(2,93)	1:A:398:LYS:HB2	1:A:403:ILE:H	5	0.12
(2,93)	1:A:398:LYS:HB2	1:A:403:ILE:H	6	0.12
(2,93)	1:A:398:LYS:HB2	1:A:403:ILE:H	19	0.12
(2,820)	1:A:399:ASN:HD22	1:A:433:ALA:HB1	18	0.12
(2,820)	1:A:399:ASN:HD22	1:A:433:ALA:HB2	18	0.12
(2,820)	1:A:399:ASN:HD22	1:A:433:ALA:HB3	18	0.12
(2,760)	1:A:367:LYS:H	1:A:369:LEU:H	1	0.12
(2,760)	1:A:367:LYS:H	1:A:369:LEU:H	8	0.12
(2,760)	1:A:367:LYS:H	1:A:369:LEU:H	10	0.12
(2,760)	1:A:367:LYS:H	1:A:369:LEU:H	18	0.12
(2,674)	1:A:319:GLU:H	1:A:321:VAL:HB	18	0.12
(2,664)	1:A:341:GLY:H	1:A:343:THR:HG21	15	0.12
(2,664)	1:A:341:GLY:H	1:A:343:THR:HG22	15	0.12
(2,664)	1:A:341:GLY:H	1:A:343:THR:HG23	15	0.12
(2,600)	1:A:322:TRP:H	1:A:342:VAL:HG11	9	0.12
(2,600)	1:A:322:TRP:H	1:A:342:VAL:HG12	9	0.12
(2,600)	1:A:322:TRP:H	1:A:342:VAL:HG13	9	0.12
(2,540)	1:A:365:PHE:HB2	1:A:441:GLU:H	3	0.12
(2,540)	1:A:365:PHE:HB2	1:A:441:GLU:H	18	0.12
(2,540)	1:A:365:PHE:HB2	1:A:441:GLU:H	19	0.12
(2,529)	1:A:440:GLY:H	1:A:441:GLU:HG2	4	0.12
(2,354)	1:A:410:TYR:HD1	1:A:412:PHE:H	6	0.12
(2,354)	1:A:410:TYR:HD2	1:A:412:PHE:H	6	0.12
(2,257)	1:A:392:ALA:H	1:A:393:GLU:HB3	11	0.12
(2,257)	1:A:392:ALA:H	1:A:393:GLU:HB3	12	0.12
(2,256)	1:A:392:ALA:H	1:A:393:GLU:HB2	20	0.12
(2,1608)	1:A:366:GLN:HA	1:A:386:GLU:HG2	2	0.12
(2,1608)	1:A:366:GLN:HA	1:A:386:GLU:HG3	2	0.12
(2,1608)	1:A:366:GLN:HA	1:A:386:GLU:HG2	11	0.12
(2,1608)	1:A:366:GLN:HA	1:A:386:GLU:HG3	11	0.12
(2,1608)	1:A:366:GLN:HA	1:A:386:GLU:HG2	16	0.12
(2,1608)	1:A:366:GLN:HA	1:A:386:GLU:HG3	16	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,1608)	1:A:366:GLN:HA	1:A:386:GLU:HG2	18	0.12
(2,1608)	1:A:366:GLN:HA	1:A:386:GLU:HG3	18	0.12
(2,157)	1:A:369:LEU:H	1:A:445:THR:HA	4	0.12
(2,157)	1:A:369:LEU:H	1:A:445:THR:HA	12	0.12
(2,157)	1:A:369:LEU:H	1:A:445:THR:HA	19	0.12
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD11	7	0.12
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD12	7	0.12
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD13	7	0.12
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD11	16	0.12
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD12	16	0.12
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD13	16	0.12
(2,1250)	1:A:342:VAL:HB	1:A:343:THR:HB	17	0.12
(2,1154)	1:A:387:LEU:HA	1:A:394:VAL:HG21	20	0.12
(2,1154)	1:A:387:LEU:HA	1:A:394:VAL:HG22	20	0.12
(2,1154)	1:A:387:LEU:HA	1:A:394:VAL:HG23	20	0.12
(2,1147)	1:A:320:ASP:HA	1:A:324:ILE:HG21	12	0.12
(2,1147)	1:A:320:ASP:HA	1:A:324:ILE:HG22	12	0.12
(2,1147)	1:A:320:ASP:HA	1:A:324:ILE:HG23	12	0.12
(2,1011)	1:A:325:LEU:HD21	1:A:340:TYR:HD1	12	0.12
(2,1011)	1:A:325:LEU:HD21	1:A:340:TYR:HD2	12	0.12
(2,1011)	1:A:325:LEU:HD22	1:A:340:TYR:HD1	12	0.12
(2,1011)	1:A:325:LEU:HD22	1:A:340:TYR:HD2	12	0.12
(2,1011)	1:A:325:LEU:HD23	1:A:340:TYR:HD1	12	0.12
(2,1011)	1:A:325:LEU:HD23	1:A:340:TYR:HD2	12	0.12
(1,872)	1:A:382:ARG:HA	1:A:383:LEU:HG	1	0.12
(1,872)	1:A:382:ARG:HA	1:A:383:LEU:HG	11	0.12
(1,574)	1:A:450:LYS:H	1:A:450:LYS:HE2	4	0.12
(1,1983)	1:A:413:GLU:H	1:A:414:SER:HB2	8	0.12
(1,1983)	1:A:413:GLU:H	1:A:414:SER:HB3	8	0.12
(1,1604)	1:A:366:GLN:HE21	1:A:386:GLU:HG2	12	0.12
(1,1604)	1:A:366:GLN:HE21	1:A:386:GLU:HG3	12	0.12
(1,1604)	1:A:366:GLN:HE22	1:A:386:GLU:HG2	12	0.12
(1,1604)	1:A:366:GLN:HE22	1:A:386:GLU:HG3	12	0.12
(1,1519)	1:A:350:LYS:HB2	1:A:351:ARG:H	14	0.12
(1,1519)	1:A:350:LYS:HB3	1:A:351:ARG:H	14	0.12
(1,1316)	1:A:396:TRP:HE1	1:A:412:PHE:HZ	14	0.12
(1,1316)	1:A:396:TRP:HE1	1:A:412:PHE:HZ	15	0.12
(1,1208)	1:A:397:LEU:HG	1:A:398:LYS:HA	8	0.12
(1,1208)	1:A:397:LEU:HG	1:A:398:LYS:HA	13	0.12
(2,93)	1:A:398:LYS:HB2	1:A:403:ILE:H	7	0.11
(2,93)	1:A:398:LYS:HB2	1:A:403:ILE:H	20	0.11
(2,9)	1:A:360:LYS:HE3	1:A:361:LYS:H	5	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,820)	1:A:399:ASN:HD22	1:A:433:ALA:HB1	13	0.11
(2,820)	1:A:399:ASN:HD22	1:A:433:ALA:HB2	13	0.11
(2,820)	1:A:399:ASN:HD22	1:A:433:ALA:HB3	13	0.11
(2,794)	1:A:406:SER:H	1:A:409:LYS:HG2	3	0.11
(2,794)	1:A:406:SER:H	1:A:409:LYS:HG2	8	0.11
(2,780)	1:A:337:ALA:HB1	1:A:348:MET:H	10	0.11
(2,780)	1:A:337:ALA:HB2	1:A:348:MET:H	10	0.11
(2,780)	1:A:337:ALA:HB3	1:A:348:MET:H	10	0.11
(2,760)	1:A:367:LYS:H	1:A:369:LEU:H	20	0.11
(2,730)	1:A:435:GLN:HE21	1:A:444:SER:HB2	20	0.11
(2,686)	1:A:352:LEU:H	1:A:353:LYS:HE2	8	0.11
(2,595)	1:A:319:GLU:H	1:A:322:TRP:HD1	8	0.11
(2,595)	1:A:319:GLU:H	1:A:322:TRP:HD1	19	0.11
(2,540)	1:A:365:PHE:HB2	1:A:441:GLU:H	11	0.11
(2,324)	1:A:398:LYS:HB3	1:A:403:ILE:H	3	0.11
(2,256)	1:A:392:ALA:H	1:A:393:GLU:HB2	18	0.11
(2,195)	1:A:377:LYS:HG3	1:A:379:HIS:H	6	0.11
(2,195)	1:A:377:LYS:HG3	1:A:379:HIS:H	9	0.11
(2,195)	1:A:377:LYS:HG3	1:A:379:HIS:H	10	0.11
(2,1777)	1:A:424:SER:H	1:A:425:GLN:HG2	8	0.11
(2,1777)	1:A:424:SER:H	1:A:425:GLN:HG3	8	0.11
(2,157)	1:A:369:LEU:H	1:A:445:THR:HA	2	0.11
(2,157)	1:A:369:LEU:H	1:A:445:THR:HA	10	0.11
(2,1488)	1:A:320:ASP:HB2	1:A:322:TRP:HE1	2	0.11
(2,1488)	1:A:320:ASP:HB3	1:A:322:TRP:HE1	2	0.11
(2,1467)	1:A:363:THR:HG21	1:A:365:PHE:HD1	8	0.11
(2,1467)	1:A:363:THR:HG21	1:A:365:PHE:HD2	8	0.11
(2,1467)	1:A:363:THR:HG22	1:A:365:PHE:HD1	8	0.11
(2,1467)	1:A:363:THR:HG22	1:A:365:PHE:HD2	8	0.11
(2,1467)	1:A:363:THR:HG23	1:A:365:PHE:HD1	8	0.11
(2,1467)	1:A:363:THR:HG23	1:A:365:PHE:HD2	8	0.11
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD11	6	0.11
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD12	6	0.11
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD13	6	0.11
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD11	11	0.11
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD12	11	0.11
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD13	11	0.11
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD11	14	0.11
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD12	14	0.11
(2,1436)	1:A:331:SER:HA	1:A:336:ILE:HD13	14	0.11
(2,1385)	1:A:354:GLY:HA3	1:A:355:MET:HE1	10	0.11
(2,1385)	1:A:354:GLY:HA3	1:A:355:MET:HE2	10	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,1385)	1:A:354:GLY:HA3	1:A:355:MET:HE3	10	0.11
(2,1250)	1:A:342:VAL:HB	1:A:343:THR:HB	6	0.11
(2,1250)	1:A:342:VAL:HB	1:A:343:THR:HB	18	0.11
(2,1227)	1:A:362:SER:HB2	1:A:368:LYS:HE3	1	0.11
(2,1222)	1:A:362:SER:HB2	1:A:365:PHE:HD1	17	0.11
(2,1222)	1:A:362:SER:HB2	1:A:365:PHE:HD2	17	0.11
(2,1154)	1:A:387:LEU:HA	1:A:394:VAL:HG21	10	0.11
(2,1154)	1:A:387:LEU:HA	1:A:394:VAL:HG22	10	0.11
(2,1154)	1:A:387:LEU:HA	1:A:394:VAL:HG23	10	0.11
(2,1143)	1:A:357:ARG:HD3	1:A:358:ASP:HA	6	0.11
(2,1011)	1:A:325:LEU:HD21	1:A:340:TYR:HD1	7	0.11
(2,1011)	1:A:325:LEU:HD21	1:A:340:TYR:HD2	7	0.11
(2,1011)	1:A:325:LEU:HD22	1:A:340:TYR:HD1	7	0.11
(2,1011)	1:A:325:LEU:HD22	1:A:340:TYR:HD2	7	0.11
(2,1011)	1:A:325:LEU:HD23	1:A:340:TYR:HD1	7	0.11
(2,1011)	1:A:325:LEU:HD23	1:A:340:TYR:HD2	7	0.11
(1,872)	1:A:382:ARG:HA	1:A:383:LEU:HG	2	0.11
(1,872)	1:A:382:ARG:HA	1:A:383:LEU:HG	6	0.11
(1,1959)	1:A:409:LYS:HD2	1:A:410:TYR:HE1	6	0.11
(1,1959)	1:A:409:LYS:HD2	1:A:410:TYR:HE2	6	0.11
(1,1959)	1:A:409:LYS:HD3	1:A:410:TYR:HE1	6	0.11
(1,1959)	1:A:409:LYS:HD3	1:A:410:TYR:HE2	6	0.11
(1,1933)	1:A:401:GLN:HG3	1:A:403:ILE:HG12	9	0.11
(1,1933)	1:A:401:GLN:HG3	1:A:403:ILE:HG13	9	0.11
(1,1739)	1:A:377:LYS:HE2	1:A:451:GLU:HA	20	0.11
(1,1739)	1:A:377:LYS:HE3	1:A:451:GLU:HA	20	0.11
(1,1495)	1:A:346:ARG:HG2	1:A:349:LEU:HB2	4	0.11
(1,1495)	1:A:346:ARG:HG2	1:A:349:LEU:HB3	4	0.11
(1,1495)	1:A:346:ARG:HG3	1:A:349:LEU:HB2	4	0.11
(1,1495)	1:A:346:ARG:HG3	1:A:349:LEU:HB3	4	0.11
(1,1208)	1:A:397:LEU:HG	1:A:398:LYS:HA	11	0.11
(1,1208)	1:A:397:LEU:HG	1:A:398:LYS:HA	14	0.11
(1,1208)	1:A:397:LEU:HG	1:A:398:LYS:HA	19	0.11

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

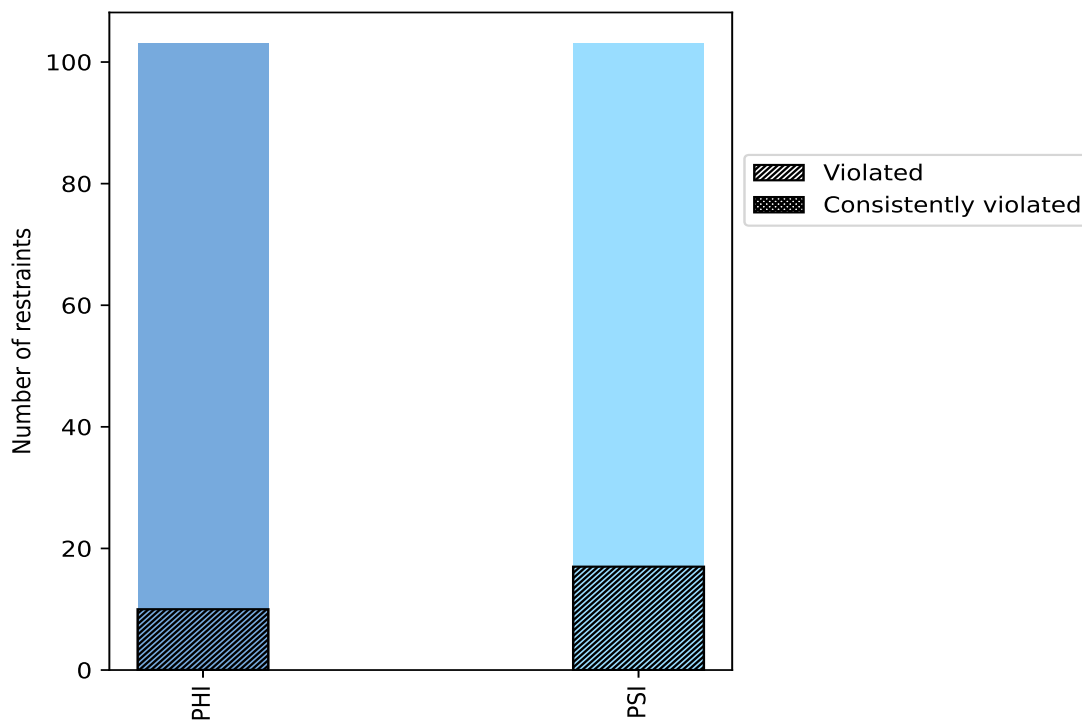
10.1 Summary of dihedral-angle violations [i](#)

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
PHI	103	50.0	10	9.7	4.9	0	0.0	0.0
PSI	103	50.0	17	16.5	8.3	0	0.0	0.0
Total	206	100.0	27	13.1	13.1	0	0.0	0.0

¹ percentage calculated with respect to total number of dihedral-angle restraints, ² percentage calculated with respect to number of restraints in a particular dihedral-angle type, ³ violated in at least one model, ⁴ violated in all the models

10.1.1 Bar chart : Distribution of dihedral-angles and violations [i](#)



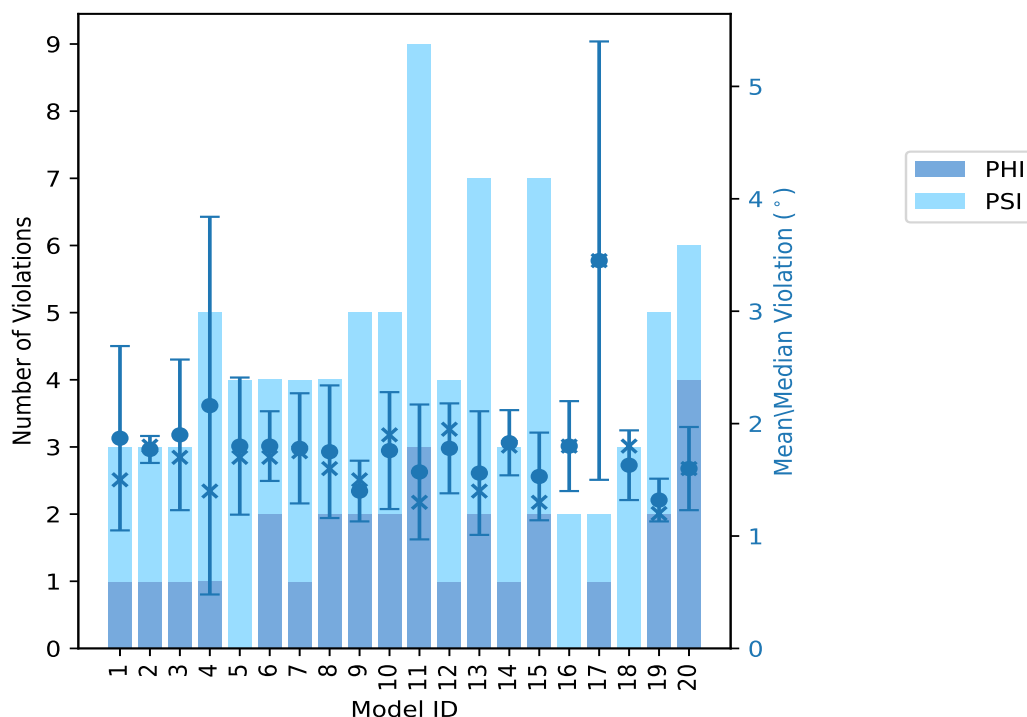
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

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

The following table provides the dihedral-angle violation statistics for each model in the ensemble. Violations less than 1° are not included in the statistics.

Model ID	Number of violations			Mean (°)	Max (°)	SD (°)	Median (°)
	PHI	PSI	Total				
1	1	2	3	1.87	3.0	0.82	1.5
2	1	2	3	1.77	1.9	0.12	1.8
3	1	2	3	1.9	2.8	0.67	1.7
4	1	4	5	2.16	5.5	1.68	1.4
5	0	4	4	1.8	2.7	0.61	1.7
6	2	2	4	1.8	2.3	0.31	1.7
7	1	3	4	1.78	2.4	0.49	1.75
8	2	2	4	1.75	2.7	0.59	1.6
9	2	3	5	1.4	1.8	0.27	1.5
10	2	3	5	1.76	2.4	0.52	1.9
11	3	6	9	1.57	3.1	0.6	1.3
12	1	3	4	1.78	2.1	0.4	1.95
13	2	5	7	1.56	2.8	0.55	1.4
14	1	2	3	1.83	2.2	0.29	1.8
15	2	5	7	1.53	2.1	0.39	1.3
16	0	2	2	1.8	2.2	0.4	1.8
17	1	1	2	3.45	5.4	1.95	3.45
18	0	3	3	1.63	1.9	0.31	1.8
19	2	3	5	1.32	1.7	0.19	1.2
20	4	2	6	1.6	2.1	0.37	1.6

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

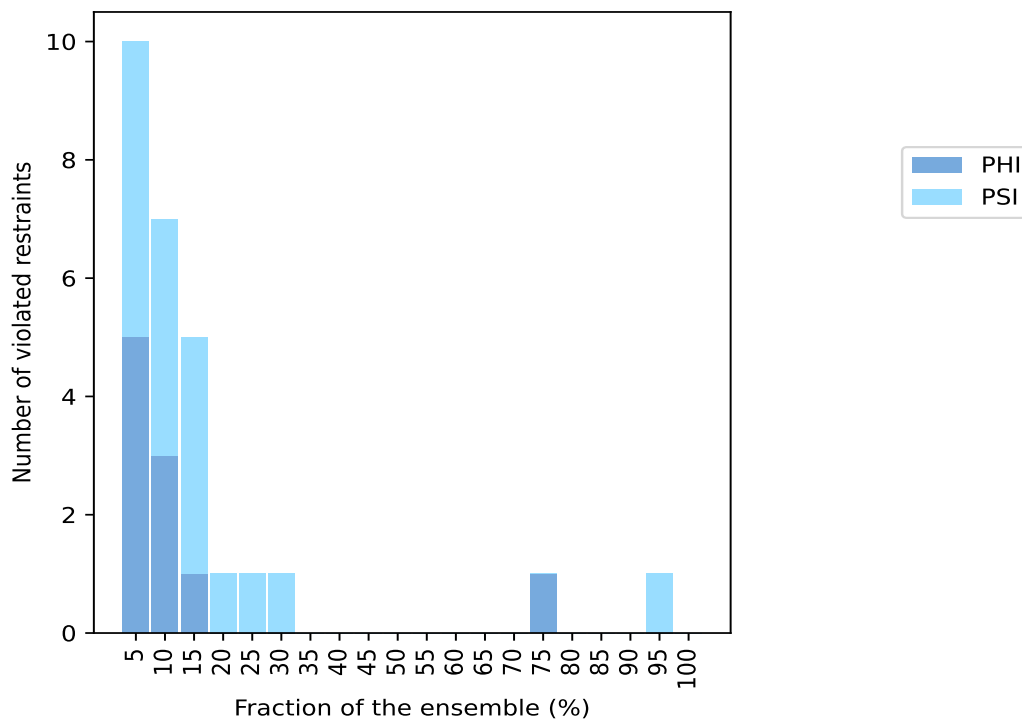
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Number of violated restraints			Fraction of the ensemble	
PHI	PSI	Total	Count ¹	%
0	0	0	12	60.0
0	0	0	13	65.0
0	0	0	14	70.0
1	0	1	15	75.0
0	0	0	16	80.0
0	0	0	17	85.0
0	0	0	18	90.0
0	1	1	19	95.0
0	0	0	20	100.0

¹ Number of models with violations

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

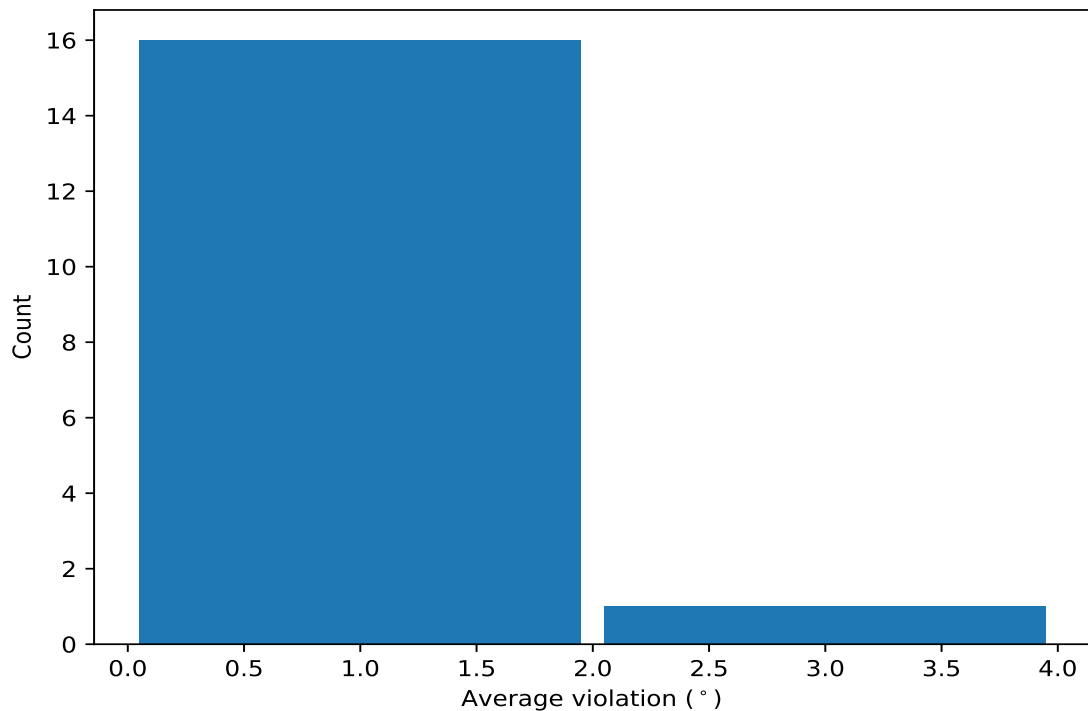


10.4 Most violated dihedral-angle restraints in the ensemble [i](#)

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.

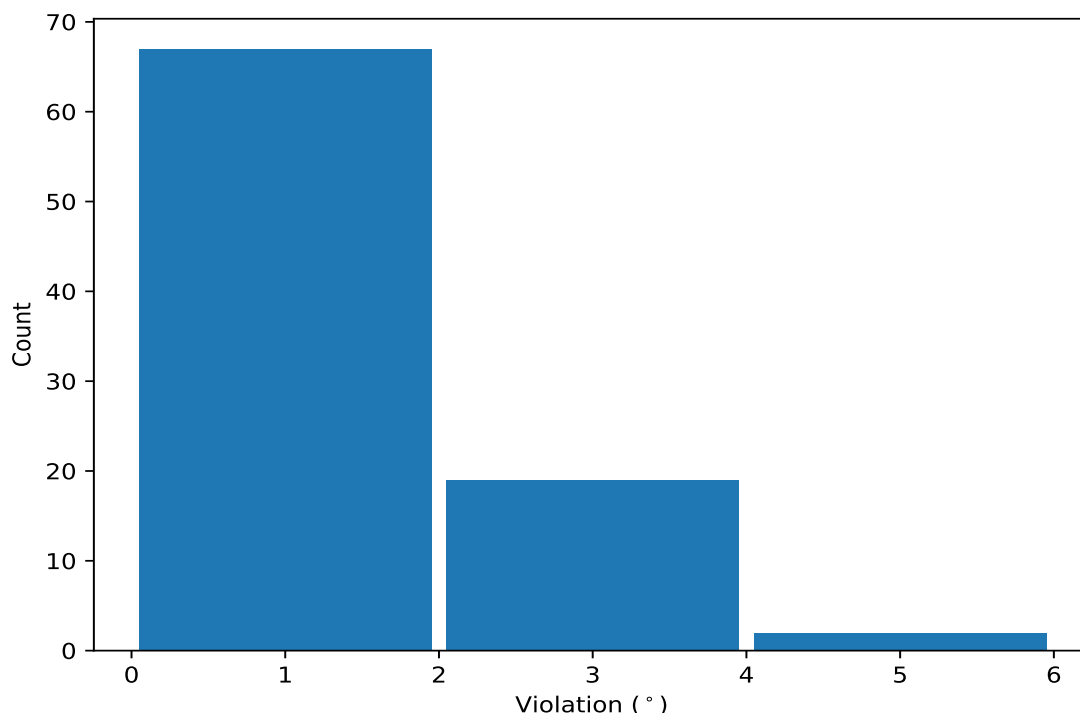
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,186)	1:A:439:GLY:N	1:A:439:GLY:CA	1:A:439:GLY:C	1:A:440:GLY:N	19	2.44	1.15	2.1
(1,137)	1:A:411:ILE:C	1:A:412:PHE:N	1:A:412:PHE:CA	1:A:412:PHE:C	15	1.89	0.4	1.8
(1,188)	1:A:440:GLY:N	1:A:440:GLY:CA	1:A:440:GLY:C	1:A:441:GLU:N	6	1.57	0.18	1.5
(1,44)	1:A:344:ASP:N	1:A:344:ASP:CA	1:A:344:ASP:C	1:A:345:LEU:N	5	1.76	0.52	1.9
(1,140)	1:A:413:GLU:N	1:A:413:GLU:CA	1:A:413:GLU:C	1:A:414:SER:N	4	1.8	0.61	1.7
(1,184)	1:A:438:VAL:N	1:A:438:VAL:CA	1:A:438:VAL:C	1:A:439:GLY:N	3	1.47	0.45	1.2
(1,58)	1:A:351:ARG:N	1:A:351:ARG:CA	1:A:351:ARG:C	1:A:352:LEU:N	3	1.37	0.12	1.4
(1,187)	1:A:439:GLY:C	1:A:440:GLY:N	1:A:440:GLY:CA	1:A:440:GLY:C	3	1.33	0.19	1.2
(1,196)	1:A:445:THR:N	1:A:445:THR:CA	1:A:445:THR:C	1:A:446:GLU:N	3	1.3	0.22	1.2
(1,198)	1:A:446:GLU:N	1:A:446:GLU:CA	1:A:446:GLU:C	1:A:447:LEU:N	3	1.27	0.09	1.2
(1,172)	1:A:432:ALA:N	1:A:432:ALA:CA	1:A:432:ALA:C	1:A:433:ALA:N	2	1.45	0.35	1.45
(1,5)	1:A:322:TRP:C	1:A:323:GLU:N	1:A:323:GLU:CA	1:A:323:GLU:C	2	1.45	0.25	1.45
(1,110)	1:A:391:ASP:N	1:A:391:ASP:CA	1:A:391:ASP:C	1:A:392:ALA:N	2	1.35	0.05	1.35
(1,192)	1:A:443:CYS:N	1:A:443:CYS:CA	1:A:443:CYS:C	1:A:444:SER:N	2	1.2	0.1	1.2
(1,173)	1:A:432:ALA:C	1:A:433:ALA:N	1:A:433:ALA:CA	1:A:433:ALA:C	2	1.2	0.0	1.2
(1,111)	1:A:392:ALA:C	1:A:393:GLU:N	1:A:393:GLU:CA	1:A:393:GLU:C	2	1.15	0.05	1.15
(1,102)	1:A:385:VAL:N	1:A:385:VAL:CA	1:A:385:VAL:C	1:A:386:GLU:N	2	1.1	0.0	1.1

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

10.5 All violated dihedral-angle restraints [i](#)

10.5.1 Histogram : Distribution of violations [i](#)

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



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

The following table lists the absolute value of the violation for each restraint in the ensemble sorted by its value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint.

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,186)	1:A:439:GLY:N	1:A:439:GLY:CA	1:A:439:GLY:C	1:A:440:GLY:N	4	5.5
(1,186)	1:A:439:GLY:N	1:A:439:GLY:CA	1:A:439:GLY:C	1:A:440:GLY:N	17	5.4
(1,137)	1:A:411:ILE:C	1:A:412:PHE:N	1:A:412:PHE:CA	1:A:412:PHE:C	11	3.1
(1,186)	1:A:439:GLY:N	1:A:439:GLY:CA	1:A:439:GLY:C	1:A:440:GLY:N	1	3.0
(1,186)	1:A:439:GLY:N	1:A:439:GLY:CA	1:A:439:GLY:C	1:A:440:GLY:N	3	2.8
(1,186)	1:A:439:GLY:N	1:A:439:GLY:CA	1:A:439:GLY:C	1:A:440:GLY:N	13	2.8
(1,186)	1:A:439:GLY:N	1:A:439:GLY:CA	1:A:439:GLY:C	1:A:440:GLY:N	8	2.7
(1,140)	1:A:413:GLU:N	1:A:413:GLU:CA	1:A:413:GLU:C	1:A:414:SER:N	5	2.7
(1,44)	1:A:344:ASP:N	1:A:344:ASP:CA	1:A:344:ASP:C	1:A:345:LEU:N	7	2.4
(1,186)	1:A:439:GLY:N	1:A:439:GLY:CA	1:A:439:GLY:C	1:A:440:GLY:N	10	2.4
(1,137)	1:A:411:ILE:C	1:A:412:PHE:N	1:A:412:PHE:CA	1:A:412:PHE:C	6	2.3
(1,44)	1:A:344:ASP:N	1:A:344:ASP:CA	1:A:344:ASP:C	1:A:345:LEU:N	10	2.2
(1,186)	1:A:439:GLY:N	1:A:439:GLY:CA	1:A:439:GLY:C	1:A:440:GLY:N	14	2.2
(1,186)	1:A:439:GLY:N	1:A:439:GLY:CA	1:A:439:GLY:C	1:A:440:GLY:N	16	2.2

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,186)	1:A:439:GLY:N	1:A:439:GLY:CA	1:A:439:GLY:C	1:A:440:GLY:N	12	2.1
(1,184)	1:A:438:VAL:N	1:A:438:VAL:CA	1:A:438:VAL:C	1:A:439:GLY:N	20	2.1
(1,137)	1:A:411:ILE:C	1:A:412:PHE:N	1:A:412:PHE:CA	1:A:412:PHE:C	7	2.1
(1,137)	1:A:411:ILE:C	1:A:412:PHE:N	1:A:412:PHE:CA	1:A:412:PHE:C	15	2.1
(1,186)	1:A:439:GLY:N	1:A:439:GLY:CA	1:A:439:GLY:C	1:A:440:GLY:N	5	2.0
(1,186)	1:A:439:GLY:N	1:A:439:GLY:CA	1:A:439:GLY:C	1:A:440:GLY:N	20	2.0
(1,140)	1:A:413:GLU:N	1:A:413:GLU:CA	1:A:413:GLU:C	1:A:414:SER:N	12	2.0
(1,44)	1:A:344:ASP:N	1:A:344:ASP:CA	1:A:344:ASP:C	1:A:345:LEU:N	2	1.9
(1,32)	1:A:338:PHE:N	1:A:338:PHE:CA	1:A:338:PHE:C	1:A:339:GLN:N	11	1.9
(1,188)	1:A:440:GLY:N	1:A:440:GLY:CA	1:A:440:GLY:C	1:A:441:GLU:N	15	1.9
(1,186)	1:A:439:GLY:N	1:A:439:GLY:CA	1:A:439:GLY:C	1:A:440:GLY:N	15	1.9
(1,186)	1:A:439:GLY:N	1:A:439:GLY:CA	1:A:439:GLY:C	1:A:440:GLY:N	18	1.9
(1,137)	1:A:411:ILE:C	1:A:412:PHE:N	1:A:412:PHE:CA	1:A:412:PHE:C	10	1.9
(1,137)	1:A:411:ILE:C	1:A:412:PHE:N	1:A:412:PHE:CA	1:A:412:PHE:C	12	1.9
(1,186)	1:A:439:GLY:N	1:A:439:GLY:CA	1:A:439:GLY:C	1:A:440:GLY:N	2	1.8
(1,186)	1:A:439:GLY:N	1:A:439:GLY:CA	1:A:439:GLY:C	1:A:440:GLY:N	6	1.8
(1,172)	1:A:432:ALA:N	1:A:432:ALA:CA	1:A:432:ALA:C	1:A:433:ALA:N	18	1.8
(1,137)	1:A:411:ILE:C	1:A:412:PHE:N	1:A:412:PHE:CA	1:A:412:PHE:C	9	1.8
(1,137)	1:A:411:ILE:C	1:A:412:PHE:N	1:A:412:PHE:CA	1:A:412:PHE:C	13	1.8
(1,137)	1:A:411:ILE:C	1:A:412:PHE:N	1:A:412:PHE:CA	1:A:412:PHE:C	14	1.8
(1,5)	1:A:322:TRP:C	1:A:323:GLU:N	1:A:323:GLU:CA	1:A:323:GLU:C	20	1.7
(1,188)	1:A:440:GLY:N	1:A:440:GLY:CA	1:A:440:GLY:C	1:A:441:GLU:N	19	1.7
(1,137)	1:A:411:ILE:C	1:A:412:PHE:N	1:A:412:PHE:CA	1:A:412:PHE:C	3	1.7
(1,137)	1:A:411:ILE:C	1:A:412:PHE:N	1:A:412:PHE:CA	1:A:412:PHE:C	8	1.7
(1,46)	1:A:345:LEU:N	1:A:345:LEU:CA	1:A:345:LEU:C	1:A:346:ARG:N	11	1.6
(1,196)	1:A:445:THR:N	1:A:445:THR:CA	1:A:445:THR:C	1:A:446:GLU:N	4	1.6
(1,189)	1:A:441:GLU:C	1:A:442:LYS:N	1:A:442:LYS:CA	1:A:442:LYS:C	11	1.6
(1,187)	1:A:439:GLY:C	1:A:440:GLY:N	1:A:440:GLY:CA	1:A:440:GLY:C	6	1.6
(1,137)	1:A:411:ILE:C	1:A:412:PHE:N	1:A:412:PHE:CA	1:A:412:PHE:C	2	1.6
(1,58)	1:A:351:ARG:N	1:A:351:ARG:CA	1:A:351:ARG:C	1:A:352:LEU:N	8	1.5
(1,188)	1:A:440:GLY:N	1:A:440:GLY:CA	1:A:440:GLY:C	1:A:441:GLU:N	6	1.5
(1,188)	1:A:440:GLY:N	1:A:440:GLY:CA	1:A:440:GLY:C	1:A:441:GLU:N	14	1.5
(1,186)	1:A:439:GLY:N	1:A:439:GLY:CA	1:A:439:GLY:C	1:A:440:GLY:N	9	1.5
(1,137)	1:A:411:ILE:C	1:A:412:PHE:N	1:A:412:PHE:CA	1:A:412:PHE:C	1	1.5
(1,137)	1:A:411:ILE:C	1:A:412:PHE:N	1:A:412:PHE:CA	1:A:412:PHE:C	17	1.5
(1,137)	1:A:411:ILE:C	1:A:412:PHE:N	1:A:412:PHE:CA	1:A:412:PHE:C	20	1.5
(1,122)	1:A:398:LYS:N	1:A:398:LYS:CA	1:A:398:LYS:C	1:A:399:ASN:N	9	1.5
(1,58)	1:A:351:ARG:N	1:A:351:ARG:CA	1:A:351:ARG:C	1:A:352:LEU:N	5	1.4
(1,198)	1:A:446:GLU:N	1:A:446:GLU:CA	1:A:446:GLU:C	1:A:447:LEU:N	7	1.4
(1,188)	1:A:440:GLY:N	1:A:440:GLY:CA	1:A:440:GLY:C	1:A:441:GLU:N	4	1.4
(1,188)	1:A:440:GLY:N	1:A:440:GLY:CA	1:A:440:GLY:C	1:A:441:GLU:N	16	1.4
(1,140)	1:A:413:GLU:N	1:A:413:GLU:CA	1:A:413:GLU:C	1:A:414:SER:N	13	1.4
(1,110)	1:A:391:ASP:N	1:A:391:ASP:CA	1:A:391:ASP:C	1:A:392:ALA:N	13	1.4
(1,93)	1:A:380:LYS:C	1:A:381:ILE:N	1:A:381:ILE:CA	1:A:381:ILE:C	15	1.3
(1,192)	1:A:443:CYS:N	1:A:443:CYS:CA	1:A:443:CYS:C	1:A:444:SER:N	11	1.3
(1,138)	1:A:412:PHE:N	1:A:412:PHE:CA	1:A:412:PHE:C	1:A:413:GLU:N	19	1.3
(1,110)	1:A:391:ASP:N	1:A:391:ASP:CA	1:A:391:ASP:C	1:A:392:ALA:N	15	1.3
(1,58)	1:A:351:ARG:N	1:A:351:ARG:CA	1:A:351:ARG:C	1:A:352:LEU:N	11	1.2
(1,5)	1:A:322:TRP:C	1:A:323:GLU:N	1:A:323:GLU:CA	1:A:323:GLU:C	19	1.2
(1,44)	1:A:344:ASP:N	1:A:344:ASP:CA	1:A:344:ASP:C	1:A:345:LEU:N	19	1.2
(1,198)	1:A:446:GLU:N	1:A:446:GLU:CA	1:A:446:GLU:C	1:A:447:LEU:N	13	1.2

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,198)	1:A:446:GLU:N	1:A:446:GLU:CA	1:A:446:GLU:C	1:A:447:LEU:N	18	1.2
(1,196)	1:A:445:THR:N	1:A:445:THR:CA	1:A:445:THR:C	1:A:446:GLU:N	3	1.2
(1,187)	1:A:439:GLY:C	1:A:440:GLY:N	1:A:440:GLY:CA	1:A:440:GLY:C	11	1.2
(1,187)	1:A:439:GLY:C	1:A:440:GLY:N	1:A:440:GLY:CA	1:A:440:GLY:C	19	1.2
(1,186)	1:A:439:GLY:N	1:A:439:GLY:CA	1:A:439:GLY:C	1:A:440:GLY:N	7	1.2
(1,184)	1:A:438:VAL:N	1:A:438:VAL:CA	1:A:438:VAL:C	1:A:439:GLY:N	10	1.2
(1,173)	1:A:432:ALA:C	1:A:433:ALA:N	1:A:433:ALA:CA	1:A:433:ALA:C	4	1.2
(1,173)	1:A:432:ALA:C	1:A:433:ALA:N	1:A:433:ALA:CA	1:A:433:ALA:C	13	1.2
(1,111)	1:A:392:ALA:C	1:A:393:GLU:N	1:A:393:GLU:CA	1:A:393:GLU:C	20	1.2
(1,59)	1:A:351:ARG:C	1:A:352:LEU:N	1:A:352:LEU:CA	1:A:352:LEU:C	10	1.1
(1,45)	1:A:344:ASP:C	1:A:345:LEU:N	1:A:345:LEU:CA	1:A:345:LEU:C	8	1.1
(1,44)	1:A:344:ASP:N	1:A:344:ASP:CA	1:A:344:ASP:C	1:A:345:LEU:N	1	1.1
(1,196)	1:A:445:THR:N	1:A:445:THR:CA	1:A:445:THR:C	1:A:446:GLU:N	11	1.1
(1,192)	1:A:443:CYS:N	1:A:443:CYS:CA	1:A:443:CYS:C	1:A:444:SER:N	12	1.1
(1,186)	1:A:439:GLY:N	1:A:439:GLY:CA	1:A:439:GLY:C	1:A:440:GLY:N	11	1.1
(1,184)	1:A:438:VAL:N	1:A:438:VAL:CA	1:A:438:VAL:C	1:A:439:GLY:N	5	1.1
(1,172)	1:A:432:ALA:N	1:A:432:ALA:CA	1:A:432:ALA:C	1:A:433:ALA:N	4	1.1
(1,140)	1:A:413:GLU:N	1:A:413:GLU:CA	1:A:413:GLU:C	1:A:414:SER:N	9	1.1
(1,134)	1:A:410:TYR:N	1:A:410:TYR:CA	1:A:410:TYR:C	1:A:411:ILE:N	15	1.1
(1,113)	1:A:393:GLU:C	1:A:394:VAL:N	1:A:394:VAL:CA	1:A:394:VAL:C	20	1.1
(1,111)	1:A:392:ALA:C	1:A:393:GLU:N	1:A:393:GLU:CA	1:A:393:GLU:C	9	1.1
(1,102)	1:A:385:VAL:N	1:A:385:VAL:CA	1:A:385:VAL:C	1:A:386:GLU:N	13	1.1
(1,102)	1:A:385:VAL:N	1:A:385:VAL:CA	1:A:385:VAL:C	1:A:386:GLU:N	15	1.1