Full wwPDB NMR Structure Validation Report (i)

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PDB ID	:	2MA7
BMRB ID	:	19331
Title	:	Solution NMR Structure of Zinc finger protein Eos from Homo sapiens, Northeast Structural Genomics Consortium (NESG) Target HR7992A
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Deposited on	:	2013-06-28

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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

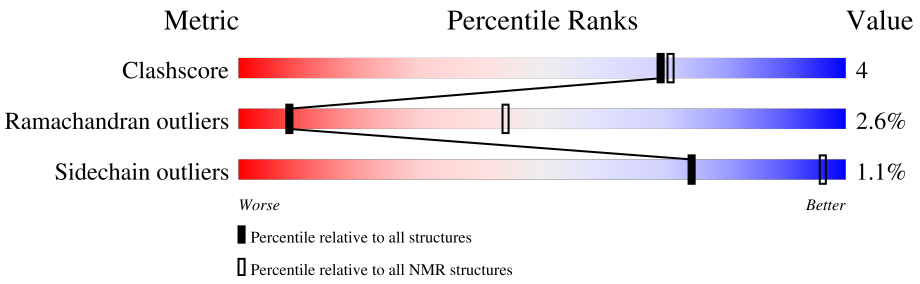
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal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

1 Overall quality at a glance (i)

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

The overall completeness of chemical shifts assignment is 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 <=5%

Mol	Chain	Length	Quality of chain
1	A	73	40% • 58%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 2 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:30-A:37 (8)	0.29	5
2	A:44-A:66 (23)	0.77	2

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 2 single-model clusters were found.

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

3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 1148 atoms, of which 572 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Zinc finger protein Eos.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	73	1147	355	572	119	92	9	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP Q9H2S9
A	2	GLY	-	expression tag	UNP Q9H2S9
A	3	HIS	-	expression tag	UNP Q9H2S9
A	4	HIS	-	expression tag	UNP Q9H2S9
A	5	HIS	-	expression tag	UNP Q9H2S9
A	6	HIS	-	expression tag	UNP Q9H2S9
A	7	HIS	-	expression tag	UNP Q9H2S9
A	8	HIS	-	expression tag	UNP Q9H2S9
A	9	SER	-	expression tag	UNP Q9H2S9
A	10	HIS	-	expression tag	UNP Q9H2S9
A	11	MET	-	expression tag	UNP Q9H2S9

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	
			Total	Zn
2	A	1	1	1

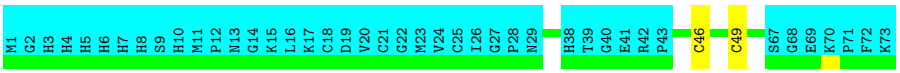
4 Residue-property plots (i)

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: Zinc finger protein Eos

Chain A:



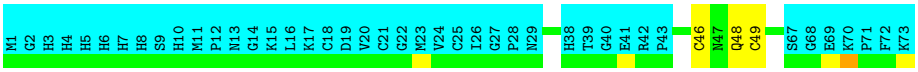
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: Zinc finger protein Eos

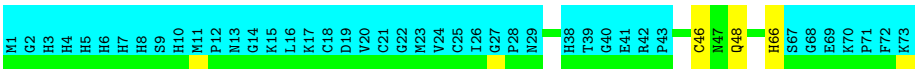
Chain A:



4.2.2 Score per residue for model 2 (medoid)

• Molecule 1: Zinc finger protein Eos

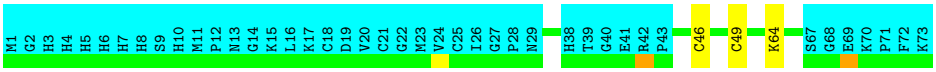
Chain A:



4.2.3 Score per residue for model 3

- Molecule 1: Zinc finger protein Eos

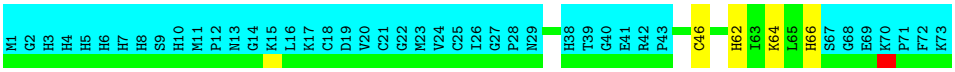
Chain A: 38% • 58%



4.2.4 Score per residue for model 4

- Molecule 1: Zinc finger protein Eos

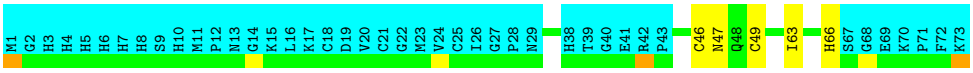
Chain A: 37% 5% 58%



4.2.5 Score per residue for model 5

- Molecule 1: Zinc finger protein Eos

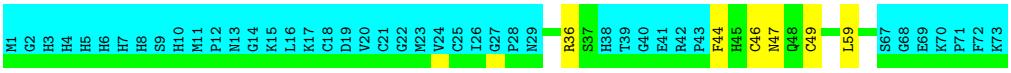
Chain A: 36% 7% 58%



4.2.6 Score per residue for model 6

- Molecule 1: Zinc finger protein Eos

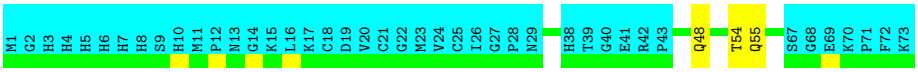
Chain A: 34% 8% 58%



4.2.7 Score per residue for model 7

- Molecule 1: Zinc finger protein Eos

Chain A: 38% • 58%



4.2.8 Score per residue for model 8

- Molecule 1: Zinc finger protein Eos

Chain A: 40% 58%

M1 G2 H3 H4 H5 H6 H7 H8 S9 H10 M11 P12 N13 G14 K15 L16 K17 C18 D19 V20 C21 G22 M23 V24 C25 I26 G27 P28 N29 H38 T39 G40 E41 R42 P43 C46 C49 S67 G68 E69 K70 P71 F72 K73

4.2.9 Score per residue for model 9

- Molecule 1: Zinc finger protein Eos

Chain A: 37% 58%

M1 G2 H3 H4 H5 H6 H7 H8 S9 H10 M11 P12 N13 G14 K15 L16 K17 C18 D19 V20 C21 G22 M23 V24 C25 I26 G27 P28 N29 H38 T39 G40 E41 R42 P43 C46 N47 H62 T63 K64 S67 G68 E69 K70 P71 F72 K73

4.2.10 Score per residue for model 10

- Molecule 1: Zinc finger protein Eos

Chain A: 38% 58%

M1 G2 H3 H4 H5 H6 H7 H8 S9 H10 M11 P12 N13 G14 K15 L16 K17 C18 D19 V20 C21 G22 M23 V24 C25 I26 G27 P28 N29 R36 S37 H38 T39 G40 E41 R42 P43 Q48 C49 S67 G68 E69 K70 P71 F72 K73

4.2.11 Score per residue for model 11

- Molecule 1: Zinc finger protein Eos

Chain A: 37% 5% 58%

M1 G2 H3 H4 H5 H6 H7 H8 S9 H10 M11 P12 N13 G14 K15 L16 K17 C18 D19 V20 C21 G22 M23 V24 C25 I26 G27 P28 N29 M32 K35 H38 T39 G40 E41 R42 P43 C49 H62 S67 G68 E69 K70 P71 F72 K73

4.2.12 Score per residue for model 12

- Molecule 1: Zinc finger protein Eos

Chain A: 41% 58%

M1 G2 H3 H4 H5 H6 H7 H8 S9 H10 M11 P12 N13 G14 K15 L16 K17 C18 D19 V20 C21 G22 M23 V24 C25 I26 G27 P28 N29 H38 T39 G40 E41 R42 P43 R61 S67 G68 E69 K70 P71 F72 K73

4.2.13 Score per residue for model 13

- Molecule 1: Zinc finger protein Eos

Chain A: 37% 58%

M1 G2 H3 H4 H5 H6 H7 H8 S9 H10 M11 P12 N13 G14 K15 L16 K17 C18 D19 V20 C21 G22 M23 V24 C25 I26 G27 P28 N29 H38 T39 G40 E41 R42 P43 F44 C49 F53 K56 S67 G68 E69 K70 P71 F72 K73

4.2.14 Score per residue for model 14

- Molecule 1: Zinc finger protein Eos

Chain A: 40% 58%

M1 G2 H3 H4 H5 H6 H7 H8 S9 H10 M11 P12 N13 G14 K15 L16 K17 C18 D19 V20 C21 G22 M23 V24 C25 I26 G27 P28 N29 H38 T39 G40 E41 R42 P43 C46 H66 S67 G68 E69 K70 P71 F72 K73

4.2.15 Score per residue for model 15

- Molecule 1: Zinc finger protein Eos

Chain A: 38% 58%

M1 G2 H3 H4 H5 H6 H7 H8 S9 H10 M11 P12 N13 G14 K15 L16 K17 C18 D19 V20 C21 G22 M23 V24 C25 I26 G27 P28 N29 H38 T39 G40 E41 R42 P43 C46 K64 L65 H66 S67 G68 E69 K70 P71 F72 K73

4.2.16 Score per residue for model 16

- Molecule 1: Zinc finger protein Eos

Chain A: 38% 58%

M1 G2 H3 H4 H5 H6 H7 H8 S9 H10 M11 P12 N13 G14 K15 L16 K17 C18 D19 V20 C21 G22 M23 V24 C25 I26 G27 P28 N29 H38 T39 G40 E41 R42 P43 F44 C49 L59 S67 G68 E69 K70 P71 F72 K73

4.2.17 Score per residue for model 17

- Molecule 1: Zinc finger protein Eos

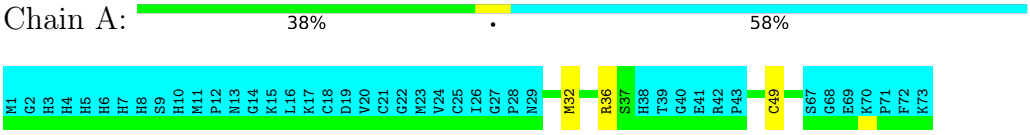
Chain A: 40% 58%

M1 G2 H3 H4 H5 H6 H7 H8 S9 H10 M11 P12 N13 G14 K15 L16 K17 C18 D19 V20 C21 G22 M23 V24 C25 I26 G27 P28 N29 H38 T39 G40 E41 R42 P43 C46 H66 S67 G68 E69 K70 P71 F72 K73

4.2.18 Score per residue for model 18

- Molecule 1: Zinc finger protein Eos

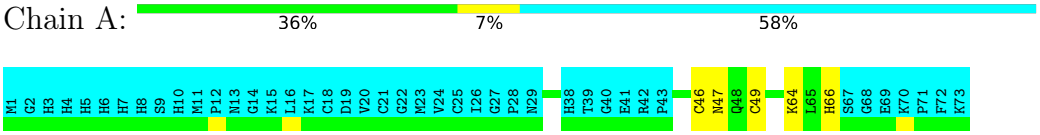
Chain A:



4.2.19 Score per residue for model 19

- Molecule 1: Zinc finger protein Eos

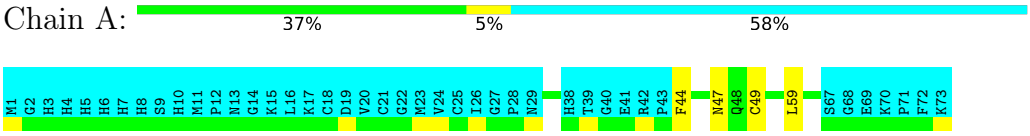
Chain A:



4.2.20 Score per residue for model 20

- Molecule 1: Zinc finger protein Eos

Chain A:



5 Refinement protocol and experimental data overview (i)

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

Of the 100 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
TALOS+	geometry optimization	
CYANA	refinement	

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

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	766
Number of shifts mapped to atoms	766
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)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	251	259	257	2±1
2	A	1	0	0	1±1
All	All	5040	5180	5161	38

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 4.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:46:CYS:HG	2:A:101:ZN:ZN	0.90	0.71	9	5
1:A:49:CYS:HG	2:A:101:ZN:ZN	0.79	0.85	3	2
1:A:46:CYS:SG	1:A:49:CYS:SG	0.71	2.89	5	5
1:A:46:CYS:SG	2:A:101:ZN:ZN	0.63	1.85	3	4
1:A:46:CYS:SG	1:A:62:HIS:CD2	0.52	3.01	4	2
1:A:46:CYS:SG	1:A:66:HIS:NE2	0.52	2.82	19	7
1:A:46:CYS:SG	1:A:66:HIS:CE1	0.47	3.06	19	3
1:A:44:PHE:HA	1:A:59:LEU:HD22	0.47	1.85	20	1
1:A:46:CYS:SG	1:A:63:ILE:HG22	0.46	2.50	5	1
1:A:32:MET:SD	1:A:35:LYS:NZ	0.44	2.89	11	1
1:A:44:PHE:HB2	1:A:53:PHE:HB2	0.44	1.88	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:49:CYS:SG	1:A:62:HIS:NE2	0.43	2.91	11	1
1:A:56:LYS:HD3	1:A:56:LYS:H	0.42	1.75	13	1
1:A:54:THR:HG23	1:A:55:GLN:HG2	0.42	1.92	7	1
1:A:44:PHE:HB3	1:A:59:LEU:HD22	0.41	1.91	6	2
1:A:32:MET:O	1:A:36:ARG:HG2	0.40	2.16	18	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	31/73 (42%)	28±1 (92±3%)	2±1 (6±4%)	1±1 (3±2%)	8	44
All	All	620/1460 (42%)	568 (92%)	36 (6%)	16 (3%)	8	44

All 4 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	49	CYS	5
1	A	47	ASN	5
1	A	48	GLN	3
1	A	46	CYS	3

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	28/64 (44%)	28±0 (99±2%)	0±0 (1±2%)	74	96
All	All	560/1280 (44%)	554 (99%)	6 (1%)	74	96

All 5 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	36	ARG	2
1	A	48	GLN	1
1	A	61	ARG	1
1	A	56	LYS	1
1	A	64	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)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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 77% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping (i)

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

Total number of shifts	766
Number of shifts mapped to atoms	766
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	62	-0.65 ± 0.27	Should be checked
$^{13}C_{\beta}$	55	0.62 ± 0.13	Should be checked
$^{13}C'$	58	-0.15 ± 0.21	None needed (< 0.5 ppm)
^{15}N	58	-0.46 ± 0.38	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments (i)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 92%, i.e. 417 atoms were assigned a chemical shift out of a possible 453. 0 out of 6 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	157/157 (100%)	64/64 (100%)	62/62 (100%)	31/31 (100%)
Sidechain	220/244 (90%)	148/159 (93%)	65/72 (90%)	7/13 (54%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	40/52 (77%)	17/26 (65%)	16/18 (89%)	7/8 (88%)
Overall	417/453 (92%)	229/249 (92%)	143/152 (94%)	45/52 (87%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 77%, i.e. 765 atoms were assigned a chemical shift out of a possible 997. 0 out of 9 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	305/365 (84%)	127/150 (85%)	120/146 (82%)	58/69 (84%)
Sidechain	411/506 (81%)	276/329 (84%)	125/155 (81%)	10/22 (45%)
Aromatic	49/126 (39%)	21/63 (33%)	20/39 (51%)	8/24 (33%)
Overall	765/997 (77%)	424/542 (78%)	265/340 (78%)	76/115 (66%)

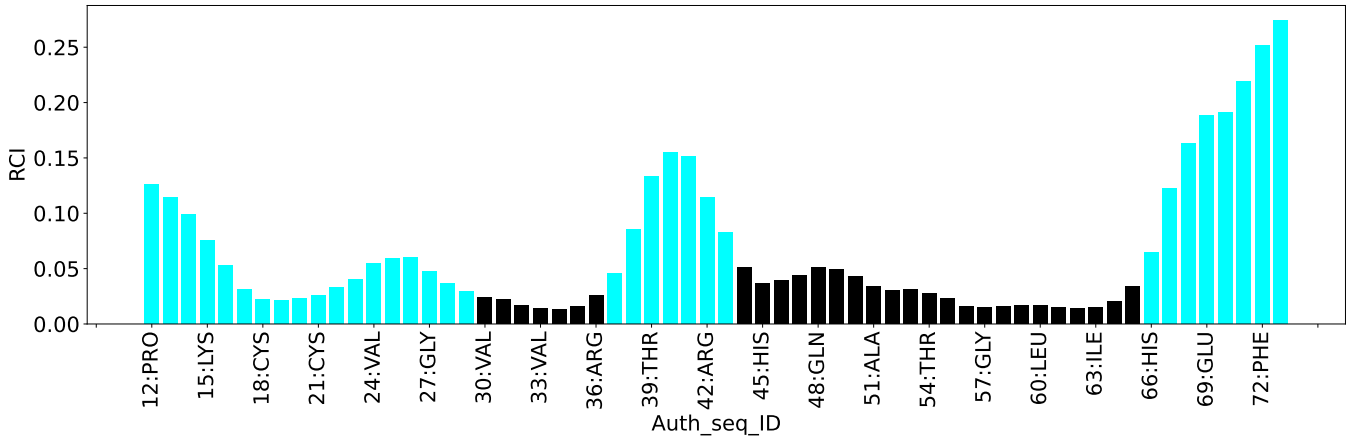
7.1.4 Statistically unusual chemical shifts (i)

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots (i)

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

Random coil index (RCI) for chain A:



8 NMR restraints analysis (i)

8.1 Conformationally restricting restraints (i)

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

Description	Value
Total distance restraints	373
Intra-residue (|i-j|=0)	94
Sequential (|i-j|=1)	135
Medium range (|i-j|>1 and |i-j|<5)	95
Long range (|i-j|≥5)	46
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	3
Total dihedral-angle restraints	46
Number of unmapped restraints	0
Number of restraints per residue	5.7
Number of long range restraints per residue[1]	0.7

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

8.2 Residual restraint violations (i)

This section provides the overview of the restraint violations analysis. The violations are binned as small, medium and large violations based on its absolute value. Average number of violations per model is calculated by dividing the total number of violations in each bin by the size of the ensemble.

8.2.1 Average number of distance violations per model (i)

Distance violations less than 0.1 Å are not included in the calculation.

Bins (Å)	Average number of violations per model	Max (Å)
0.1-0.2 (Small)	3.8	0.2
0.2-0.5 (Medium)	0.8	0.3
>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)	3.9	8.4
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis (i)

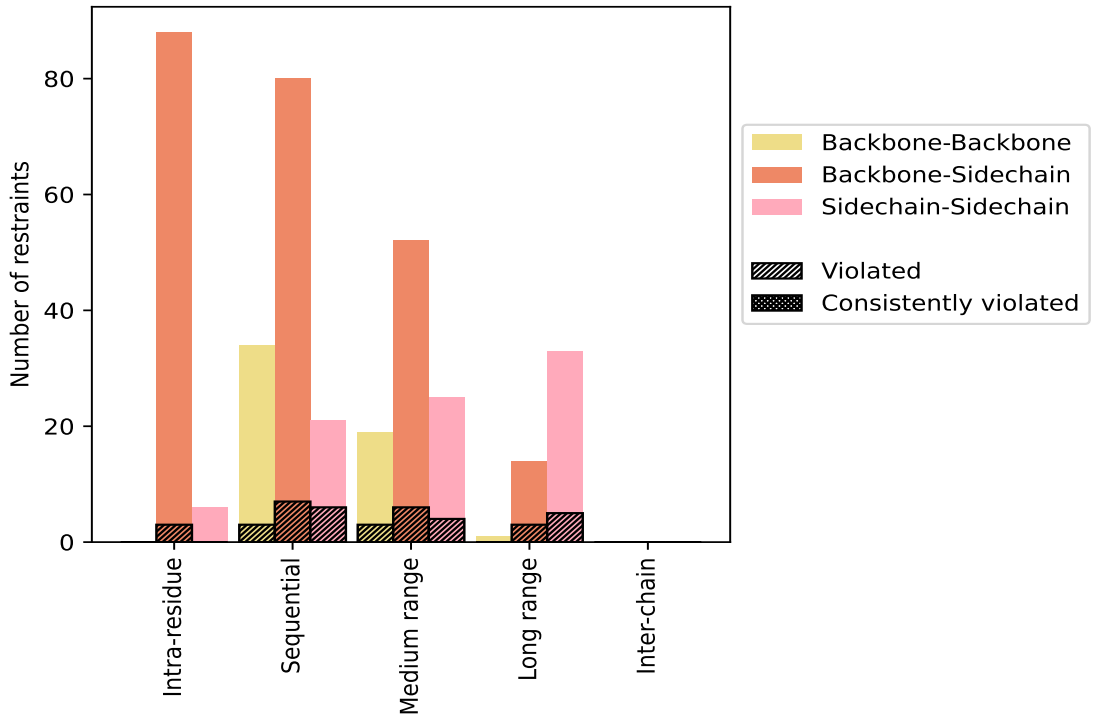
9.1 Summary of distance violations (i)

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.

Restraints type	Count	%[1]	Violated[3]			Consistently Violated[4]		
			Count	%[2]	%[1]	Count	%[2]	%[1]
Intra-residue (|i-j|=0)	94	25.2	3	3.2	0.8	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	88	23.6	3	3.4	0.8	0	0.0	0.0
Sidechain-Sidechain	6	1.6	0	0.0	0.0	0	0.0	0.0
Sequential (|i-j|=1)	135	36.2	16	11.9	4.3	0	0.0	0.0
Backbone-Backbone	34	9.1	3	8.8	0.8	0	0.0	0.0
Backbone-Sidechain	80	21.4	7	8.8	1.9	0	0.0	0.0
Sidechain-Sidechain	21	5.6	6	28.6	1.6	0	0.0	0.0
Medium range (|i-j|>1 & |i-j|<5)	95	25.5	13	13.7	3.5	0	0.0	0.0
Backbone-Backbone	19	5.1	3	15.8	0.8	0	0.0	0.0
Backbone-Sidechain	52	13.9	6	11.5	1.6	0	0.0	0.0
Sidechain-Sidechain	24	6.4	4	16.7	1.1	0	0.0	0.0
Long range (|i-j|≥5)	46	12.3	7	15.2	1.9	0	0.0	0.0
Backbone-Backbone	1	0.3	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	14	3.8	3	21.4	0.8	0	0.0	0.0
Sidechain-Sidechain	31	8.3	4	12.9	1.1	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	3	0.8	1	33.3	0.3	0	0.0	0.0
Total	373	100.0	40	10.7	10.7	0	0.0	0.0
Backbone-Backbone	54	14.5	6	11.1	1.6	0	0.0	0.0
Backbone-Sidechain	234	62.7	19	8.1	5.1	0	0.0	0.0
Sidechain-Sidechain	85	22.8	15	17.6	4.0	0	0.0	0.0

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

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



Violated and consistently violated restraints are shown using different hatch patterns in their respective categories. The hydrogen bonds and disulfied bonds are counted in their appropriate category on the x-axis

9.2 Distance violation statistics for each model (i)

The following table provides the distance violation statistics for each model in the ensemble. Violations less than 0.1 Å are not included in the statistics.

Model ID	Number of violations						Mean (Å)	Max (Å)	SD[6] (Å)	Median (Å)
	IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total				
1	1	1	3	4	0	9	0.18	0.29	0.05	0.15
2	0	3	1	0	0	4	0.15	0.19	0.03	0.15
3	0	1	1	0	0	2	0.18	0.19	0.02	0.18
4	0	2	2	1	0	5	0.21	0.3	0.07	0.19
5	0	2	0	0	0	2	0.21	0.22	0.01	0.21
6	0	3	4	0	0	7	0.13	0.16	0.02	0.13
7	1	3	0	1	0	5	0.17	0.28	0.06	0.16
8	1	1	0	0	0	2	0.15	0.15	0.0	0.15
9	1	2	2	1	0	6	0.14	0.19	0.03	0.14
10	1	1	1	1	0	4	0.14	0.18	0.03	0.15
11	0	1	1	0	0	2	0.17	0.19	0.02	0.17

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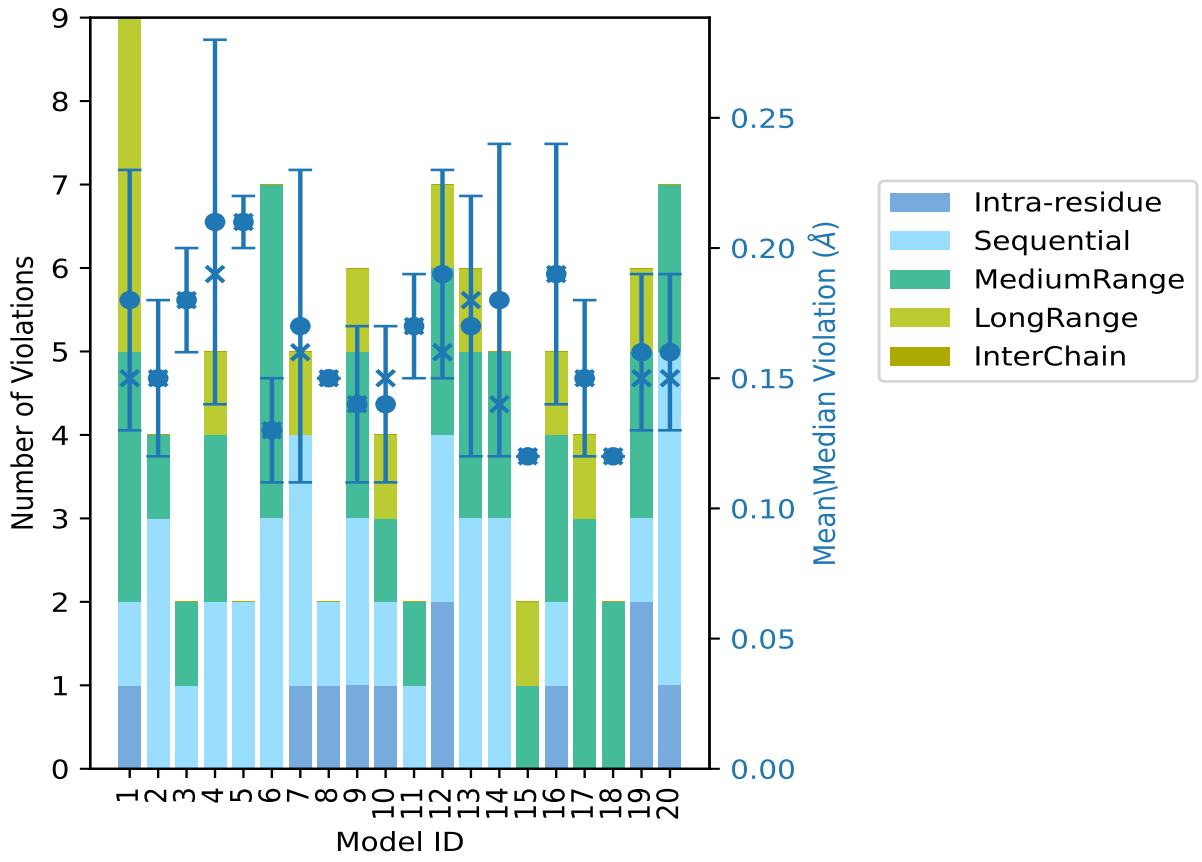
Model ID	Number of violations						Mean (Å)	Max (Å)	SD[6] (Å)	Median (Å)
	IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total				
12	2	2	2	1	0	7	0.19	0.25	0.04	0.16
13	0	3	2	1	0	6	0.17	0.26	0.05	0.18
14	0	3	2	0	0	5	0.18	0.28	0.06	0.14
15	0	0	1	1	0	2	0.12	0.12	0.0	0.12
16	1	1	2	1	0	5	0.19	0.26	0.05	0.19
17	0	0	3	1	0	4	0.15	0.19	0.03	0.15
18	0	0	2	0	0	2	0.12	0.12	0.0	0.12
19	2	1	2	1	0	6	0.16	0.21	0.03	0.15
20	1	4	2	0	0	7	0.16	0.23	0.03	0.15

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

9.2.1 Bar graph : Distance Violation statistics for each model (i)



The mean(dot),median(x) and the standard deviation are shown in blue with respect to the y axis on the right

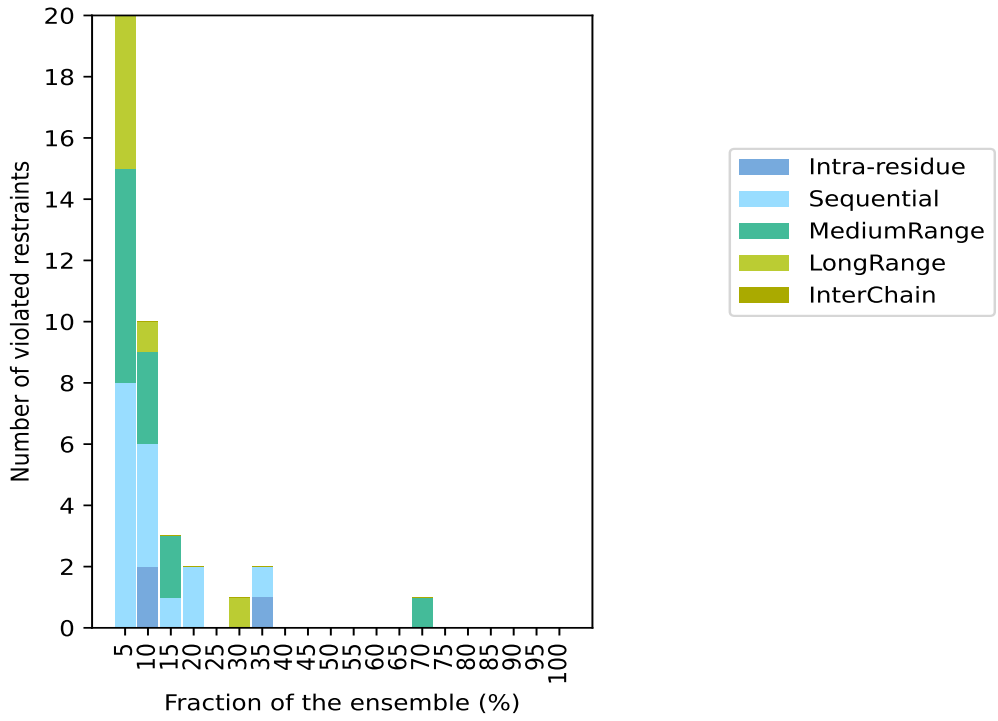
9.3 Distance violation statistics for the ensemble (i)

Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 331(IR:91, SQ:119, MR:82, LR:39, 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]	%
0	8	7	5	0	20	1	5.0
2	4	3	1	0	10	2	10.0
0	1	2	0	0	3	3	15.0
0	2	0	0	0	2	4	20.0
0	0	0	0	0	0	5	25.0
0	0	0	1	0	1	6	30.0
1	1	0	0	0	2	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	0	0	0	0	0	13	65.0
0	0	1	0	0	1	14	70.0
0	0	0	0	0	0	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

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

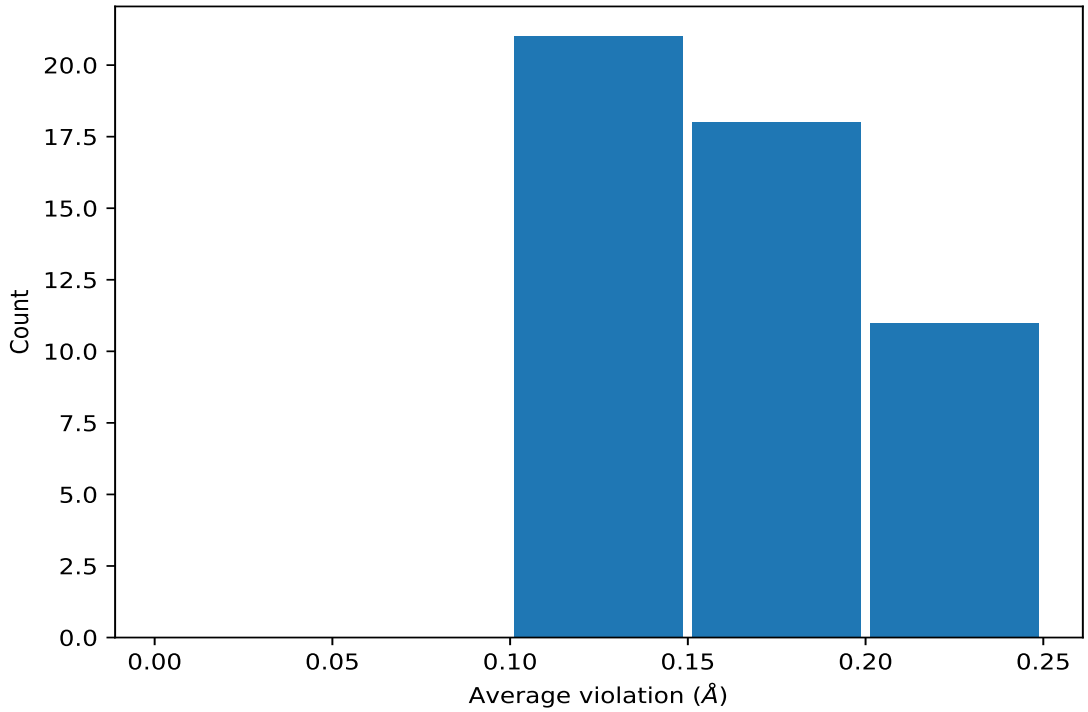
9.3.1 Bar graph : Distance violation statistics for the ensemble (i)



9.4 Most violated distance restraints in the ensemble (i)

9.4.1 Histogram : Distribution of mean distance violations (i)

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



9.4.2 Table: Most violated distance restraints (i)

The following table provides the mean and the standard deviation of the 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)
(2,12)	1:A:56:LYS:HA	1:A:60:LEU:HB3	14	0.18	0.05	0.18
(1,190)	1:A:70:LYS:HG2	1:A:71:PRO:HG2	7	0.16	0.04	0.15
(1,190)	1:A:70:LYS:HG2	1:A:71:PRO:HG3	7	0.16	0.04	0.15
(1,190)	1:A:70:LYS:HG3	1:A:71:PRO:HG2	7	0.16	0.04	0.15
(1,190)	1:A:70:LYS:HG3	1:A:71:PRO:HG3	7	0.16	0.04	0.15
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD21	7	0.15	0.02	0.15
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD22	7	0.15	0.02	0.15
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD23	7	0.15	0.02	0.15
(1,299)	1:A:49:CYS:HB2	1:A:66:HIS:HE1	6	0.18	0.03	0.19
(1,299)	1:A:49:CYS:HB3	1:A:66:HIS:HE1	6	0.18	0.03	0.19
(1,148)	1:A:15:LYS:HA	1:A:16:LEU:HD21	4	0.2	0.04	0.19
(1,148)	1:A:15:LYS:HA	1:A:16:LEU:HD22	4	0.2	0.04	0.19
(1,148)	1:A:15:LYS:HA	1:A:16:LEU:HD23	4	0.2	0.04	0.19
(1,331)	1:A:69:GLU:H	1:A:70:LYS:HB2	4	0.16	0.04	0.16
(1,331)	1:A:69:GLU:H	1:A:70:LYS:HB3	4	0.16	0.04	0.16
(1,187)	1:A:72:PHE:HD1	1:A:73:LYS:HE2	3	0.2	0.07	0.2

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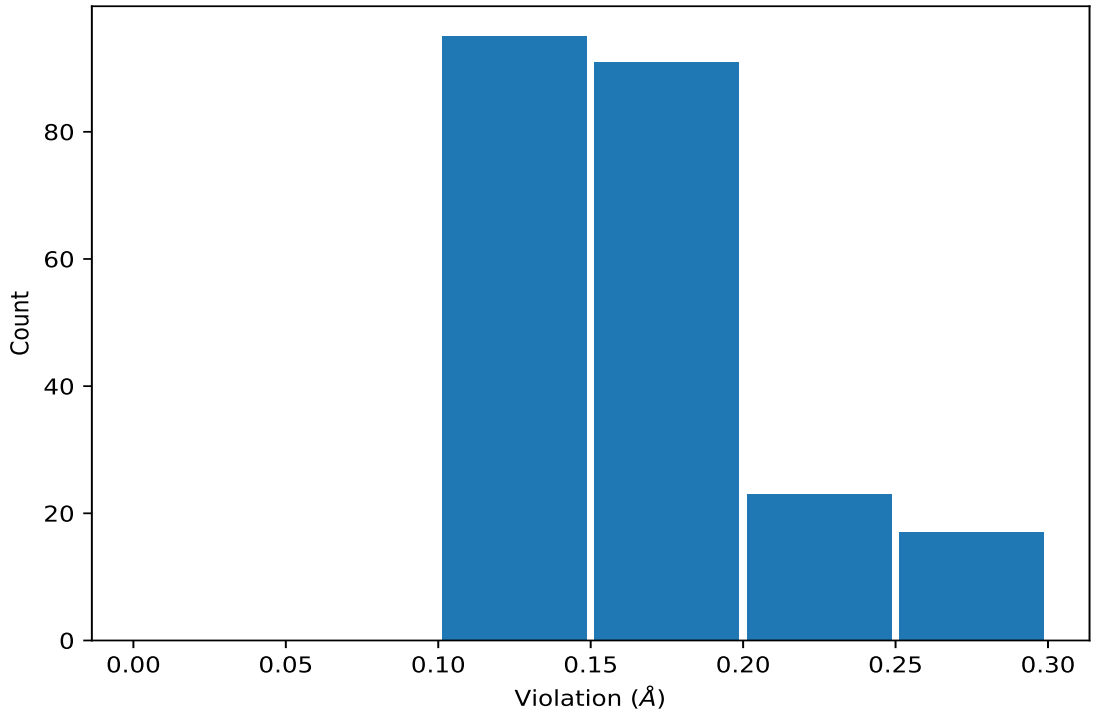
Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(1,187)	1:A:72:PHE:HD1	1:A:73:LYS:HE3	3	0.2	0.07	0.2
(1,187)	1:A:72:PHE:HD2	1:A:73:LYS:HE2	3	0.2	0.07	0.2
(1,187)	1:A:72:PHE:HD2	1:A:73:LYS:HE3	3	0.2	0.07	0.2
(1,336)	1:A:71:PRO:HB2	1:A:73:LYS:H	3	0.14	0.02	0.12
(1,336)	1:A:71:PRO:HB3	1:A:73:LYS:H	3	0.14	0.02	0.12
(1,145)	1:A:66:HIS:H	1:A:70:LYS:HD2	3	0.12	0.01	0.13
(1,145)	1:A:66:HIS:H	1:A:70:LYS:HD3	3	0.12	0.01	0.13
(2,30)	1:A:71:PRO:HG2	1:A:72:PHE:HB2	2	0.2	0.09	0.2
(2,30)	1:A:71:PRO:HG2	1:A:72:PHE:HB3	2	0.2	0.09	0.2
(2,30)	1:A:71:PRO:HG3	1:A:72:PHE:HB2	2	0.2	0.09	0.2
(2,30)	1:A:71:PRO:HG3	1:A:72:PHE:HB3	2	0.2	0.09	0.2
(1,115)	1:A:46:CYS:HB2	1:A:50:GLY:H	2	0.18	0.03	0.18
(2,15)	1:A:61:ARG:HA	1:A:63:ILE:HG21	2	0.16	0.01	0.16
(2,15)	1:A:61:ARG:HA	1:A:63:ILE:HG22	2	0.16	0.01	0.16
(2,15)	1:A:61:ARG:HA	1:A:63:ILE:HG23	2	0.16	0.01	0.16
(1,62)	1:A:72:PHE:H	1:A:73:LYS:H	2	0.16	0.01	0.16
(1,325)	1:A:64:LYS:HB2	1:A:70:LYS:HD2	2	0.16	0.01	0.16
(1,325)	1:A:64:LYS:HB2	1:A:70:LYS:HD3	2	0.16	0.01	0.16
(1,325)	1:A:64:LYS:HB3	1:A:70:LYS:HD2	2	0.16	0.01	0.16
(1,325)	1:A:64:LYS:HB3	1:A:70:LYS:HD3	2	0.16	0.01	0.16
(1,60)	1:A:70:LYS:H	1:A:70:LYS:HD2	2	0.15	0.01	0.15
(1,60)	1:A:70:LYS:H	1:A:70:LYS:HD3	2	0.15	0.01	0.15
(1,298)	1:A:48:GLN:H	1:A:48:GLN:HE21	2	0.14	0.02	0.14
(1,298)	1:A:48:GLN:H	1:A:48:GLN:HE22	2	0.14	0.02	0.14
(1,180)	1:A:32:MET:HB2	1:A:33:VAL:HG11	2	0.13	0.0	0.13
(1,180)	1:A:32:MET:HB2	1:A:33:VAL:HG12	2	0.13	0.0	0.13
(1,180)	1:A:32:MET:HB2	1:A:33:VAL:HG13	2	0.13	0.0	0.13
(1,180)	1:A:32:MET:HB3	1:A:33:VAL:HG11	2	0.13	0.0	0.13
(1,180)	1:A:32:MET:HB3	1:A:33:VAL:HG12	2	0.13	0.0	0.13
(1,180)	1:A:32:MET:HB3	1:A:33:VAL:HG13	2	0.13	0.0	0.13
(1,73)	1:A:55:GLN:H	1:A:58:ASN:H	2	0.12	0.01	0.12
(1,222)	1:A:62:HIS:HD2	1:A:63:ILE:HD11	2	0.11	0.0	0.11
(1,222)	1:A:62:HIS:HD2	1:A:63:ILE:HD12	2	0.11	0.0	0.11
(1,222)	1:A:62:HIS:HD2	1:A:63:ILE:HD13	2	0.11	0.0	0.11

[1]Number of violated models, [2]Standard deviation

9.5 All violated distance restraints (i)

9.5.1 Histogram : Distribution of distance violations (i)

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



9.5.2 Table : All distance violations (i)

The following table 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)
(1,340)	1:A:49:CYS:SG	1:A:62:HIS:NE2	4	0.3
(1,252)	1:A:15:LYS:H	1:A:16:LEU:HB2	1	0.29
(1,252)	1:A:15:LYS:H	1:A:16:LEU:HB3	1	0.29
(2,30)	1:A:71:PRO:HG2	1:A:72:PHE:HB2	4	0.28
(2,30)	1:A:71:PRO:HG2	1:A:72:PHE:HB3	4	0.28
(2,30)	1:A:71:PRO:HG3	1:A:72:PHE:HB2	4	0.28
(2,30)	1:A:71:PRO:HG3	1:A:72:PHE:HB3	4	0.28
(2,12)	1:A:56:LYS:HA	1:A:60:LEU:HB3	14	0.28
(1,187)	1:A:72:PHE:HD1	1:A:73:LYS:HE2	7	0.28
(1,187)	1:A:72:PHE:HD1	1:A:73:LYS:HE3	7	0.28

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,187)	1:A:72:PHE:HD2	1:A:73:LYS:HE2	7	0.28
(1,187)	1:A:72:PHE:HD2	1:A:73:LYS:HE3	7	0.28
(2,12)	1:A:56:LYS:HA	1:A:60:LEU:HB3	16	0.26
(1,148)	1:A:15:LYS:HA	1:A:16:LEU:HD21	13	0.26
(1,148)	1:A:15:LYS:HA	1:A:16:LEU:HD22	13	0.26
(1,148)	1:A:15:LYS:HA	1:A:16:LEU:HD23	13	0.26
(2,12)	1:A:56:LYS:HA	1:A:60:LEU:HB3	12	0.25
(1,99)	1:A:29:ASN:HD21	1:A:32:MET:HG2	14	0.23
(1,99)	1:A:29:ASN:HD21	1:A:32:MET:HG3	14	0.23
(1,299)	1:A:49:CYS:HB2	1:A:66:HIS:HE1	16	0.23
(1,299)	1:A:49:CYS:HB3	1:A:66:HIS:HE1	16	0.23
(1,260)	1:A:72:PHE:HD1	1:A:73:LYS:H	20	0.23
(1,260)	1:A:72:PHE:HD2	1:A:73:LYS:H	20	0.23
(1,190)	1:A:70:LYS:HG2	1:A:71:PRO:HG2	12	0.23
(1,190)	1:A:70:LYS:HG2	1:A:71:PRO:HG3	12	0.23
(1,190)	1:A:70:LYS:HG3	1:A:71:PRO:HG2	12	0.23
(1,190)	1:A:70:LYS:HG3	1:A:71:PRO:HG3	12	0.23
(2,12)	1:A:56:LYS:HA	1:A:60:LEU:HB3	1	0.22
(1,148)	1:A:15:LYS:HA	1:A:16:LEU:HD21	5	0.22
(1,148)	1:A:15:LYS:HA	1:A:16:LEU:HD22	5	0.22
(1,148)	1:A:15:LYS:HA	1:A:16:LEU:HD23	5	0.22
(1,331)	1:A:69:GLU:H	1:A:70:LYS:HB2	13	0.21
(1,331)	1:A:69:GLU:H	1:A:70:LYS:HB3	13	0.21
(1,299)	1:A:49:CYS:HB2	1:A:66:HIS:HE1	19	0.21
(1,299)	1:A:49:CYS:HB3	1:A:66:HIS:HE1	19	0.21
(1,115)	1:A:46:CYS:HB2	1:A:50:GLY:H	12	0.21
(1,187)	1:A:72:PHE:HD1	1:A:73:LYS:HE2	5	0.2
(1,187)	1:A:72:PHE:HD1	1:A:73:LYS:HE3	5	0.2
(1,187)	1:A:72:PHE:HD2	1:A:73:LYS:HE2	5	0.2
(1,187)	1:A:72:PHE:HD2	1:A:73:LYS:HE3	5	0.2
(2,12)	1:A:56:LYS:HA	1:A:60:LEU:HB3	3	0.19
(2,12)	1:A:56:LYS:HA	1:A:60:LEU:HB3	11	0.19
(1,331)	1:A:69:GLU:H	1:A:70:LYS:HB2	19	0.19
(1,331)	1:A:69:GLU:H	1:A:70:LYS:HB3	19	0.19
(1,299)	1:A:49:CYS:HB2	1:A:66:HIS:HE1	1	0.19
(1,299)	1:A:49:CYS:HB3	1:A:66:HIS:HE1	1	0.19
(1,299)	1:A:49:CYS:HB2	1:A:66:HIS:HE1	17	0.19
(1,299)	1:A:49:CYS:HB3	1:A:66:HIS:HE1	17	0.19
(1,227)	1:A:61:ARG:HD2	1:A:65:LEU:HD11	16	0.19
(1,227)	1:A:61:ARG:HD2	1:A:65:LEU:HD12	16	0.19
(1,227)	1:A:61:ARG:HD2	1:A:65:LEU:HD13	16	0.19
(1,227)	1:A:61:ARG:HD3	1:A:65:LEU:HD11	16	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,227)	1:A:61:ARG:HD3	1:A:65:LEU:HD12	16	0.19
(1,227)	1:A:61:ARG:HD3	1:A:65:LEU:HD13	16	0.19
(1,190)	1:A:70:LYS:HG2	1:A:71:PRO:HG2	2	0.19
(1,190)	1:A:70:LYS:HG2	1:A:71:PRO:HG3	2	0.19
(1,190)	1:A:70:LYS:HG3	1:A:71:PRO:HG2	2	0.19
(1,190)	1:A:70:LYS:HG3	1:A:71:PRO:HG3	2	0.19
(1,185)	1:A:64:LYS:H	1:A:70:LYS:HD2	1	0.19
(1,185)	1:A:64:LYS:H	1:A:70:LYS:HD3	1	0.19
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD21	9	0.19
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD22	9	0.19
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD23	9	0.19
(1,112)	1:A:49:CYS:H	1:A:51:ALA:H	4	0.19
(2,12)	1:A:56:LYS:HA	1:A:60:LEU:HB3	10	0.18
(2,12)	1:A:56:LYS:HA	1:A:60:LEU:HB3	13	0.18
(2,15)	1:A:61:ARG:HA	1:A:63:ILE:HG21	13	0.17
(2,15)	1:A:61:ARG:HA	1:A:63:ILE:HG22	13	0.17
(2,15)	1:A:61:ARG:HA	1:A:63:ILE:HG23	13	0.17
(1,336)	1:A:71:PRO:HB2	1:A:73:LYS:H	20	0.17
(1,336)	1:A:71:PRO:HB3	1:A:73:LYS:H	20	0.17
(1,299)	1:A:49:CYS:HB2	1:A:66:HIS:HE1	10	0.17
(1,299)	1:A:49:CYS:HB3	1:A:66:HIS:HE1	10	0.17
(2,15)	1:A:61:ARG:HA	1:A:63:ILE:HG21	6	0.16
(2,15)	1:A:61:ARG:HA	1:A:63:ILE:HG22	6	0.16
(2,15)	1:A:61:ARG:HA	1:A:63:ILE:HG23	6	0.16
(2,12)	1:A:56:LYS:HA	1:A:60:LEU:HB3	4	0.16
(1,62)	1:A:72:PHE:H	1:A:73:LYS:H	12	0.16
(1,60)	1:A:70:LYS:H	1:A:70:LYS:HD2	12	0.16
(1,60)	1:A:70:LYS:H	1:A:70:LYS:HD3	12	0.16
(1,325)	1:A:64:LYS:HB2	1:A:70:LYS:HD2	7	0.16
(1,325)	1:A:64:LYS:HB2	1:A:70:LYS:HD3	7	0.16
(1,325)	1:A:64:LYS:HB3	1:A:70:LYS:HD2	7	0.16
(1,325)	1:A:64:LYS:HB3	1:A:70:LYS:HD3	7	0.16
(1,298)	1:A:48:GLN:H	1:A:48:GLN:HE21	19	0.16
(1,298)	1:A:48:GLN:H	1:A:48:GLN:HE22	19	0.16
(1,190)	1:A:70:LYS:HG2	1:A:71:PRO:HG2	9	0.16
(1,190)	1:A:70:LYS:HG2	1:A:71:PRO:HG3	9	0.16
(1,190)	1:A:70:LYS:HG3	1:A:71:PRO:HG2	9	0.16
(1,190)	1:A:70:LYS:HG3	1:A:71:PRO:HG3	9	0.16
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD21	20	0.16
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD22	20	0.16
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD23	20	0.16
(1,148)	1:A:15:LYS:HA	1:A:16:LEU:HD21	3	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,148)	1:A:15:LYS:HA	1:A:16:LEU:HD22	3	0.16
(1,148)	1:A:15:LYS:HA	1:A:16:LEU:HD23	3	0.16
(1,148)	1:A:15:LYS:HA	1:A:16:LEU:HD21	7	0.16
(1,148)	1:A:15:LYS:HA	1:A:16:LEU:HD22	7	0.16
(1,148)	1:A:15:LYS:HA	1:A:16:LEU:HD23	7	0.16
(2,12)	1:A:56:LYS:HA	1:A:60:LEU:HB3	17	0.15
(1,62)	1:A:72:PHE:H	1:A:73:LYS:H	11	0.15
(1,325)	1:A:64:LYS:HB2	1:A:70:LYS:HD2	1	0.15
(1,325)	1:A:64:LYS:HB2	1:A:70:LYS:HD3	1	0.15
(1,325)	1:A:64:LYS:HB3	1:A:70:LYS:HD2	1	0.15
(1,325)	1:A:64:LYS:HB3	1:A:70:LYS:HD3	1	0.15
(1,307)	1:A:56:LYS:HD2	1:A:57:GLY:HA2	2	0.15
(1,307)	1:A:56:LYS:HD2	1:A:57:GLY:HA3	2	0.15
(1,307)	1:A:56:LYS:HD3	1:A:57:GLY:HA2	2	0.15
(1,307)	1:A:56:LYS:HD3	1:A:57:GLY:HA3	2	0.15
(1,270)	1:A:53:PHE:HE1	1:A:58:ASN:HB2	12	0.15
(1,270)	1:A:53:PHE:HE2	1:A:58:ASN:HB2	12	0.15
(1,239)	1:A:29:ASN:H	1:A:30:VAL:HG21	2	0.15
(1,239)	1:A:29:ASN:H	1:A:30:VAL:HG22	2	0.15
(1,239)	1:A:29:ASN:H	1:A:30:VAL:HG23	2	0.15
(1,190)	1:A:70:LYS:HG2	1:A:71:PRO:HG2	6	0.15
(1,190)	1:A:70:LYS:HG2	1:A:71:PRO:HG3	6	0.15
(1,190)	1:A:70:LYS:HG3	1:A:71:PRO:HG2	6	0.15
(1,190)	1:A:70:LYS:HG3	1:A:71:PRO:HG3	6	0.15
(1,190)	1:A:70:LYS:HG2	1:A:71:PRO:HG2	20	0.15
(1,190)	1:A:70:LYS:HG2	1:A:71:PRO:HG3	20	0.15
(1,190)	1:A:70:LYS:HG3	1:A:71:PRO:HG2	20	0.15
(1,190)	1:A:70:LYS:HG3	1:A:71:PRO:HG3	20	0.15
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD21	1	0.15
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD22	1	0.15
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD23	1	0.15
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD21	7	0.15
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD22	7	0.15
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD23	7	0.15
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD21	8	0.15
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD22	8	0.15
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD23	8	0.15
(2,11)	1:A:44:PHE:HD1	1:A:59:LEU:HA	9	0.14
(2,11)	1:A:44:PHE:HD2	1:A:59:LEU:HA	9	0.14
(1,60)	1:A:70:LYS:H	1:A:70:LYS:HD2	19	0.14
(1,60)	1:A:70:LYS:H	1:A:70:LYS:HD3	19	0.14
(1,332)	1:A:69:GLU:HA	1:A:70:LYS:HB2	6	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,332)	1:A:69:GLU:HA	1:A:70:LYS:HB3	6	0.14
(1,331)	1:A:69:GLU:H	1:A:70:LYS:HB2	8	0.14
(1,331)	1:A:69:GLU:H	1:A:70:LYS:HB3	8	0.14
(1,177)	1:A:64:LYS:HE2	1:A:65:LEU:HD11	14	0.14
(1,177)	1:A:64:LYS:HE2	1:A:65:LEU:HD12	14	0.14
(1,177)	1:A:64:LYS:HE2	1:A:65:LEU:HD13	14	0.14
(1,177)	1:A:64:LYS:HE3	1:A:65:LEU:HD11	14	0.14
(1,177)	1:A:64:LYS:HE3	1:A:65:LEU:HD12	14	0.14
(1,177)	1:A:64:LYS:HE3	1:A:65:LEU:HD13	14	0.14
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD21	12	0.14
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD22	12	0.14
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD23	12	0.14
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD21	16	0.14
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD22	16	0.14
(1,154)	1:A:65:LEU:HA	1:A:65:LEU:HD23	16	0.14
(1,115)	1:A:46:CYS:HB2	1:A:50:GLY:H	17	0.14
(1,10)	1:A:71:PRO:HA	1:A:72:PHE:H	20	0.14
(2,12)	1:A:56:LYS:HA	1:A:60:LEU:HB3	6	0.13
(2,12)	1:A:56:LYS:HA	1:A:60:LEU:HB3	19	0.13
(1,73)	1:A:55:GLN:H	1:A:58:ASN:H	1	0.13
(1,243)	1:A:36:ARG:HA	1:A:39:THR:HG21	19	0.13
(1,243)	1:A:36:ARG:HA	1:A:39:THR:HG22	19	0.13
(1,243)	1:A:36:ARG:HA	1:A:39:THR:HG23	19	0.13
(1,190)	1:A:70:LYS:HG2	1:A:71:PRO:HG2	14	0.13
(1,190)	1:A:70:LYS:HG2	1:A:71:PRO:HG3	14	0.13
(1,190)	1:A:70:LYS:HG3	1:A:71:PRO:HG2	14	0.13
(1,190)	1:A:70:LYS:HG3	1:A:71:PRO:HG3	14	0.13
(1,180)	1:A:32:MET:HB2	1:A:33:VAL:HG11	4	0.13
(1,180)	1:A:32:MET:HB2	1:A:33:VAL:HG12	4	0.13
(1,180)	1:A:32:MET:HB2	1:A:33:VAL:HG13	4	0.13
(1,180)	1:A:32:MET:HB3	1:A:33:VAL:HG11	4	0.13
(1,180)	1:A:32:MET:HB3	1:A:33:VAL:HG12	4	0.13
(1,180)	1:A:32:MET:HB3	1:A:33:VAL:HG13	4	0.13
(1,180)	1:A:32:MET:HB2	1:A:33:VAL:HG11	14	0.13
(1,180)	1:A:32:MET:HB2	1:A:33:VAL:HG12	14	0.13
(1,180)	1:A:32:MET:HB2	1:A:33:VAL:HG13	14	0.13
(1,180)	1:A:32:MET:HB3	1:A:33:VAL:HG11	14	0.13
(1,180)	1:A:32:MET:HB3	1:A:33:VAL:HG12	14	0.13
(1,180)	1:A:32:MET:HB3	1:A:33:VAL:HG13	14	0.13
(1,176)	1:A:64:LYS:HA	1:A:70:LYS:HD2	1	0.13
(1,176)	1:A:64:LYS:HA	1:A:70:LYS:HD3	1	0.13
(1,145)	1:A:66:HIS:H	1:A:70:LYS:HD2	1	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,145)	1:A:66:HIS:H	1:A:70:LYS:HD3	1	0.13
(1,145)	1:A:66:HIS:H	1:A:70:LYS:HD2	9	0.13
(1,145)	1:A:66:HIS:H	1:A:70:LYS:HD3	9	0.13
(2,12)	1:A:56:LYS:HA	1:A:60:LEU:HB3	20	0.12
(1,336)	1:A:71:PRO:HB2	1:A:73:LYS:H	6	0.12
(1,336)	1:A:71:PRO:HB3	1:A:73:LYS:H	6	0.12
(1,336)	1:A:71:PRO:HB2	1:A:73:LYS:H	18	0.12
(1,336)	1:A:71:PRO:HB3	1:A:73:LYS:H	18	0.12
(1,331)	1:A:69:GLU:H	1:A:70:LYS:HB2	16	0.12
(1,331)	1:A:69:GLU:H	1:A:70:LYS:HB3	16	0.12
(1,299)	1:A:49:CYS:HB2	1:A:66:HIS:HE1	15	0.12
(1,299)	1:A:49:CYS:HB3	1:A:66:HIS:HE1	15	0.12
(1,298)	1:A:48:GLN:H	1:A:48:GLN:HE21	10	0.12
(1,298)	1:A:48:GLN:H	1:A:48:GLN:HE22	10	0.12
(1,248)	1:A:36:ARG:HD2	1:A:39:THR:HG21	17	0.12
(1,248)	1:A:36:ARG:HD2	1:A:39:THR:HG22	17	0.12
(1,248)	1:A:36:ARG:HD2	1:A:39:THR:HG23	17	0.12
(1,248)	1:A:36:ARG:HD3	1:A:39:THR:HG21	17	0.12
(1,248)	1:A:36:ARG:HD3	1:A:39:THR:HG22	17	0.12
(1,248)	1:A:36:ARG:HD3	1:A:39:THR:HG23	17	0.12
(1,187)	1:A:72:PHE:HD1	1:A:73:LYS:HE2	20	0.12
(1,187)	1:A:72:PHE:HD1	1:A:73:LYS:HE3	20	0.12
(1,187)	1:A:72:PHE:HD2	1:A:73:LYS:HE2	20	0.12
(1,187)	1:A:72:PHE:HD2	1:A:73:LYS:HE3	20	0.12
(2,30)	1:A:71:PRO:HG2	1:A:72:PHE:HB2	9	0.11
(2,30)	1:A:71:PRO:HG2	1:A:72:PHE:HB3	9	0.11
(2,30)	1:A:71:PRO:HG3	1:A:72:PHE:HB2	9	0.11
(2,30)	1:A:71:PRO:HG3	1:A:72:PHE:HB3	9	0.11
(2,12)	1:A:56:LYS:HA	1:A:60:LEU:HB3	9	0.11
(1,74)	1:A:55:GLN:HA	1:A:58:ASN:H	6	0.11
(1,73)	1:A:55:GLN:H	1:A:58:ASN:H	15	0.11
(1,59)	1:A:69:GLU:HA	1:A:70:LYS:H	6	0.11
(1,275)	1:A:53:PHE:HE1	1:A:62:HIS:HD2	13	0.11
(1,275)	1:A:53:PHE:HE2	1:A:62:HIS:HD2	13	0.11
(1,222)	1:A:62:HIS:HD2	1:A:63:ILE:HD11	7	0.11
(1,222)	1:A:62:HIS:HD2	1:A:63:ILE:HD12	7	0.11
(1,222)	1:A:62:HIS:HD2	1:A:63:ILE:HD13	7	0.11
(1,222)	1:A:62:HIS:HD2	1:A:63:ILE:HD11	10	0.11
(1,222)	1:A:62:HIS:HD2	1:A:63:ILE:HD12	10	0.11
(1,222)	1:A:62:HIS:HD2	1:A:63:ILE:HD13	10	0.11
(1,2)	1:A:29:ASN:HD22	1:A:32:MET:HG2	18	0.11
(1,2)	1:A:29:ASN:HD22	1:A:32:MET:HG3	18	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,190)	1:A:70:LYS:HG2	1:A:71:PRO:HG2	13	0.11
(1,190)	1:A:70:LYS:HG2	1:A:71:PRO:HG3	13	0.11
(1,190)	1:A:70:LYS:HG3	1:A:71:PRO:HG2	13	0.11
(1,190)	1:A:70:LYS:HG3	1:A:71:PRO:HG3	13	0.11
(1,145)	1:A:66:HIS:H	1:A:70:LYS:HD2	2	0.11
(1,145)	1:A:66:HIS:H	1:A:70:LYS:HD3	2	0.11

10 Dihedral-angle violation analysis (i)

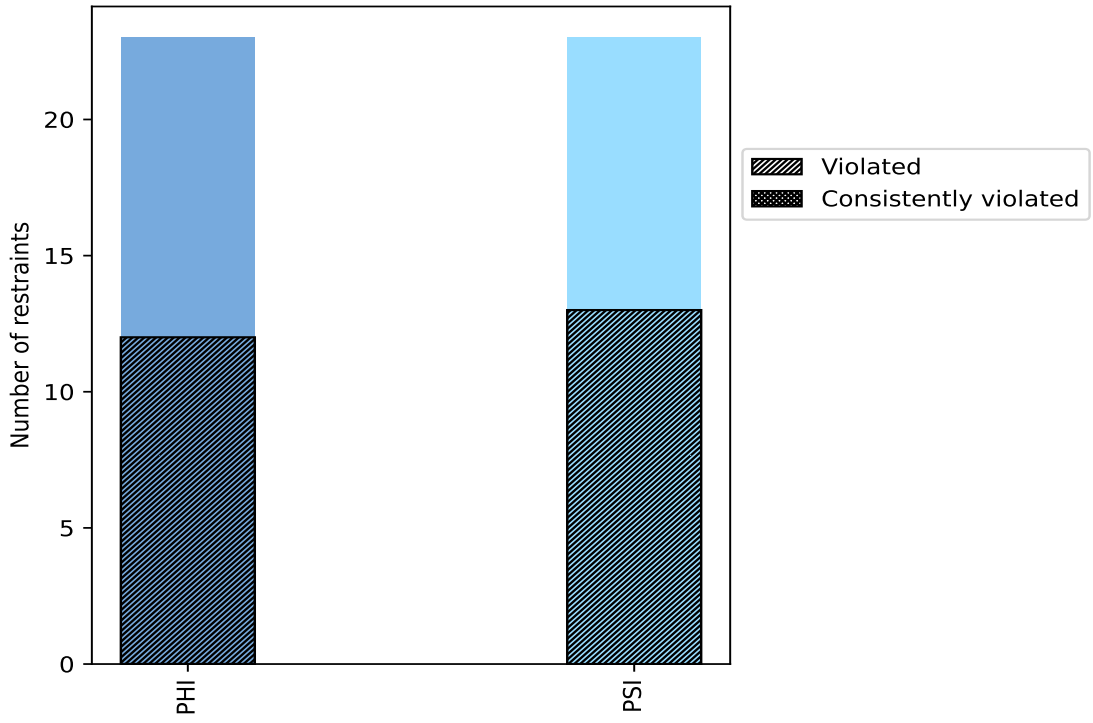
10.1 Summary of dihedral-angle violations (i)

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	23	50.0	12	52.2	26.1	0	0.0	0.0
PSI	23	50.0	13	56.5	28.3	0	0.0	0.0
Total	46	100.0	25	54.3	54.3	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)



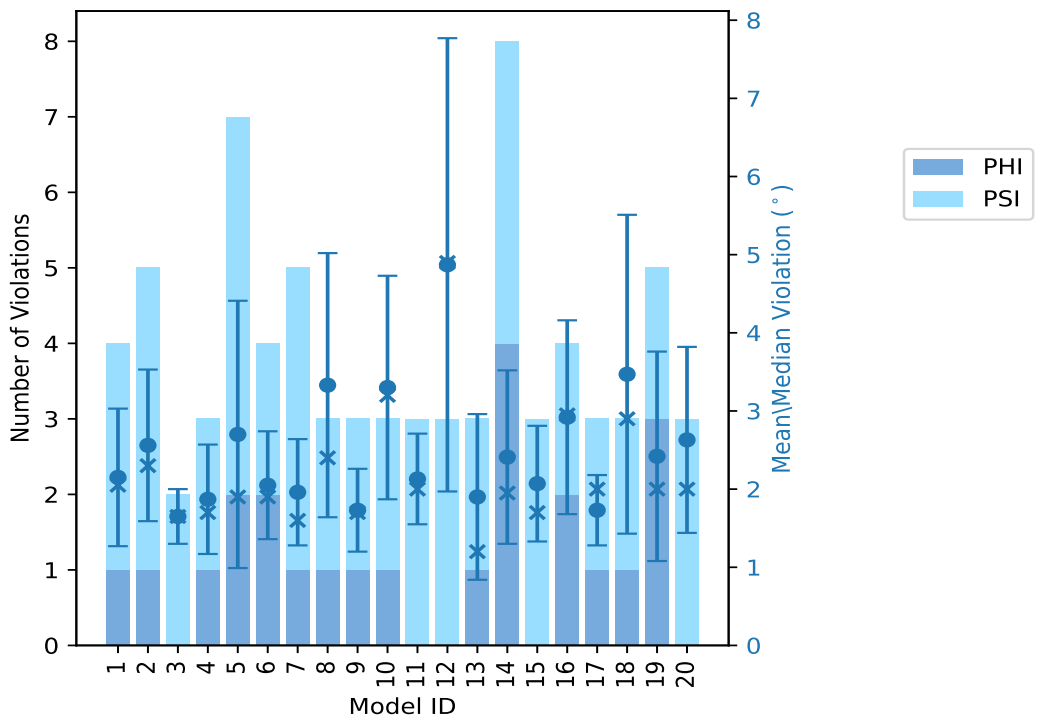
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

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	3	4	2.15	3.4	0.88	2.05
2	1	4	5	2.56	3.9	0.97	2.3
3	0	2	2	1.65	2.0	0.35	1.65
4	1	2	3	1.87	2.8	0.7	1.7
5	2	5	7	2.7	6.1	1.71	1.9
6	2	2	4	2.05	3.1	0.69	1.9
7	1	4	5	1.96	2.9	0.68	1.6
8	1	2	3	3.33	5.7	1.69	2.4
9	1	2	3	1.73	2.4	0.53	1.7
10	1	2	3	3.3	5.1	1.43	3.2
11	0	3	3	2.13	2.9	0.58	2.0
12	0	3	3	4.87	8.4	2.9	4.9
13	1	2	3	1.9	3.4	1.06	1.2
14	4	4	8	2.41	4.7	1.11	1.95
15	0	3	3	2.07	3.1	0.74	1.7
16	2	2	4	2.92	4.3	1.24	2.95
17	1	2	3	1.73	2.1	0.45	2.0
18	1	2	3	3.47	6.2	2.04	2.9
19	3	2	5	2.42	4.5	1.34	2.0
20	0	3	3	2.63	4.3	1.19	2.0

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

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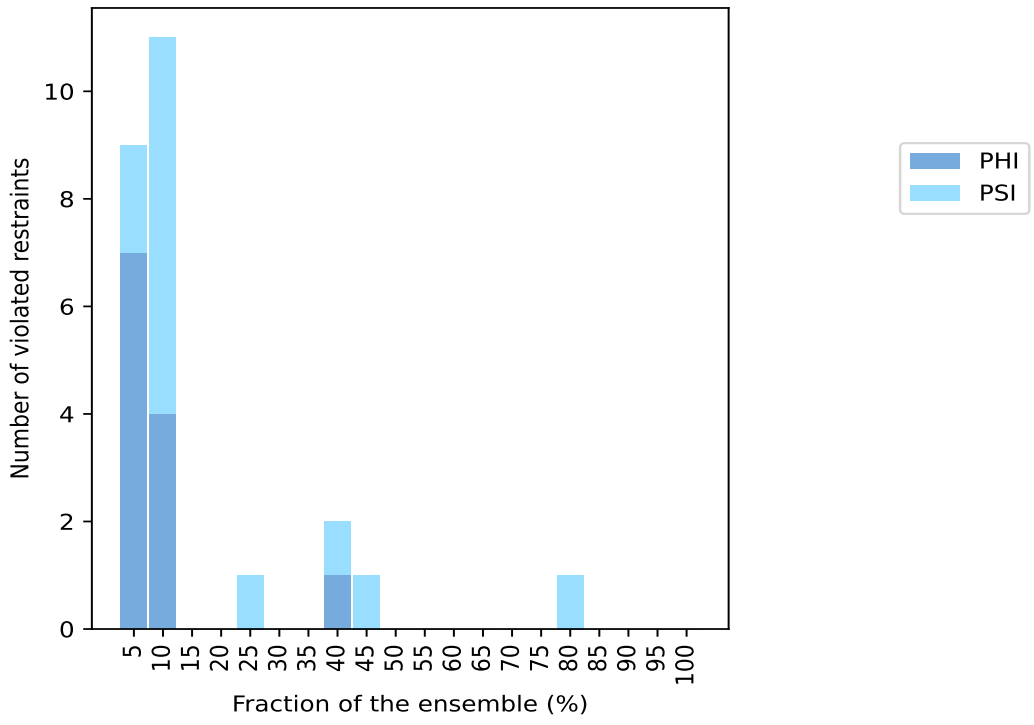
Number of violated restraints			Fraction of the ensemble	
PHI	PSI	Total	Count[1]	%
0	0	0	12	60.0
0	0	0	13	65.0
0	0	0	14	70.0
0	0	0	15	75.0
0	1	1	16	80.0
0	0	0	17	85.0
0	0	0	18	90.0
0	0	0	19	95.0
0	0	0	20	100.0

[1] Number of models with violations

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

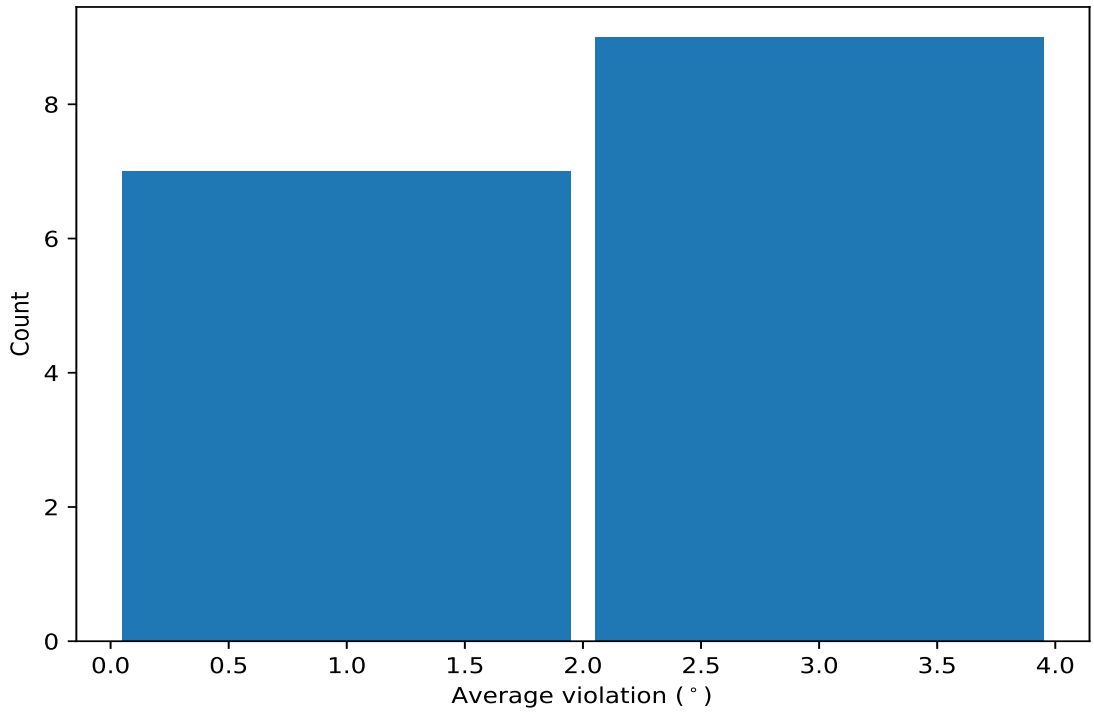


10.4 Most violated dihedral-angle restraints in the ensemble (i)

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.

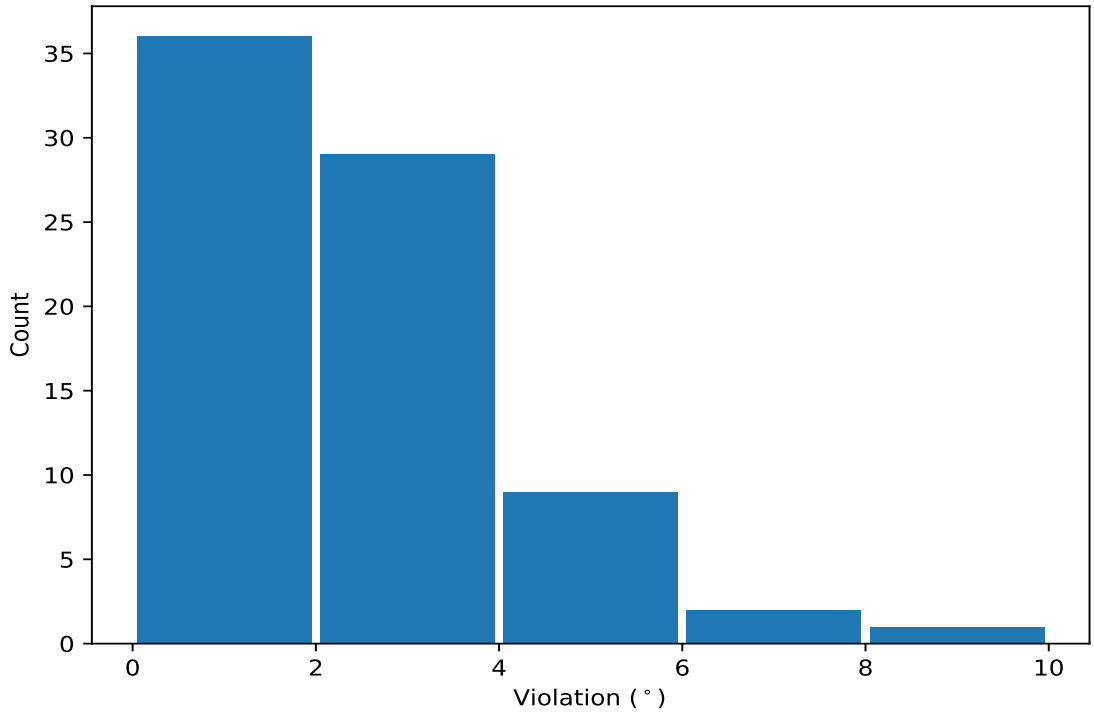
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models[1]	Mean	SD[2]	Median
(1,40)	1:A:63:ILE:N	1:A:63:ILE:CA	1:A:63:ILE:C	1:A:64:LYS:N	16	3.41	1.18	3.2
(1,24)	1:A:52:SER:N	1:A:52:SER:CA	1:A:52:SER:C	1:A:53:PHE:N	9	2.44	2.16	1.7
(1,19)	1:A:44:PHE:C	1:A:45:HIS:N	1:A:45:HIS:CA	1:A:45:HIS:C	8	2.92	1.51	2.3
(1,2)	1:A:30:VAL:N	1:A:30:VAL:CA	1:A:30:VAL:C	1:A:31:LEU:N	8	2.19	1.07	1.8
(1,8)	1:A:33:VAL:N	1:A:33:VAL:CA	1:A:33:VAL:C	1:A:34:HIS:N	5	2.74	1.02	2.8
(1,18)	1:A:42:ARG:N	1:A:42:ARG:CA	1:A:42:ARG:C	1:A:43:PRO:N	2	3.9	2.3	3.9
(1,17)	1:A:41:GLU:C	1:A:42:ARG:N	1:A:42:ARG:CA	1:A:42:ARG:C	2	2.75	1.65	2.75
(1,35)	1:A:60:LEU:C	1:A:61:ARG:N	1:A:61:ARG:CA	1:A:61:ARG:C	2	2.45	0.95	2.45
(1,32)	1:A:59:LEU:N	1:A:59:LEU:CA	1:A:59:LEU:C	1:A:60:LEU:N	2	2.35	0.45	2.35
(1,6)	1:A:32:MET:N	1:A:32:MET:CA	1:A:32:MET:C	1:A:33:VAL:N	2	1.95	0.35	1.95
(1,44)	1:A:65:LEU:N	1:A:65:LEU:CA	1:A:65:LEU:C	1:A:66:HIS:N	2	1.8	0.2	1.8
(1,21)	1:A:50:GLY:C	1:A:51:ALA:N	1:A:51:ALA:CA	1:A:51:ALA:C	2	1.45	0.25	1.45
(1,20)	1:A:45:HIS:N	1:A:45:HIS:CA	1:A:45:HIS:C	1:A:46:CYS:N	2	1.4	0.3	1.4
(1,10)	1:A:34:HIS:N	1:A:34:HIS:CA	1:A:34:HIS:C	1:A:35:LYS:N	2	1.35	0.15	1.35
(1,12)	1:A:35:LYS:N	1:A:35:LYS:CA	1:A:35:LYS:C	1:A:36:ARG:N	2	1.35	0.25	1.35
(1,29)	1:A:57:GLY:C	1:A:58:ASN:N	1:A:58:ASN:CA	1:A:58:ASN:C	2	1.35	0.25	1.35

[1] Number of violated models, [2]Standard 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 (°)
(1,24)	1:A:52:SER:N	1:A:52:SER:CA	1:A:52:SER:C	1:A:53:PHE:N	12	8.4
(1,18)	1:A:42:ARG:N	1:A:42:ARG:CA	1:A:42:ARG:C	1:A:43:PRO:N	18	6.2
(1,19)	1:A:44:PHE:C	1:A:45:HIS:N	1:A:45:HIS:CA	1:A:45:HIS:C	5	6.1
(1,40)	1:A:63:ILE:N	1:A:63:ILE:CA	1:A:63:ILE:C	1:A:64:LYS:N	8	5.7
(1,40)	1:A:63:ILE:N	1:A:63:ILE:CA	1:A:63:ILE:C	1:A:64:LYS:N	10	5.1
(1,40)	1:A:63:ILE:N	1:A:63:ILE:CA	1:A:63:ILE:C	1:A:64:LYS:N	12	4.9
(1,40)	1:A:63:ILE:N	1:A:63:ILE:CA	1:A:63:ILE:C	1:A:64:LYS:N	14	4.7
(1,19)	1:A:44:PHE:C	1:A:45:HIS:N	1:A:45:HIS:CA	1:A:45:HIS:C	19	4.5
(1,17)	1:A:41:GLU:C	1:A:42:ARG:N	1:A:42:ARG:CA	1:A:42:ARG:C	5	4.4
(1,8)	1:A:33:VAL:N	1:A:33:VAL:CA	1:A:33:VAL:C	1:A:34:HIS:N	20	4.3
(1,40)	1:A:63:ILE:N	1:A:63:ILE:CA	1:A:63:ILE:C	1:A:64:LYS:N	16	4.3
(1,2)	1:A:30:VAL:N	1:A:30:VAL:CA	1:A:30:VAL:C	1:A:31:LEU:N	16	4.0
(1,2)	1:A:30:VAL:N	1:A:30:VAL:CA	1:A:30:VAL:C	1:A:31:LEU:N	2	3.9
(1,13)	1:A:35:LYS:C	1:A:36:ARG:N	1:A:36:ARG:CA	1:A:36:ARG:C	14	3.5

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,40)	1:A:63:ILE:N	1:A:63:ILE:CA	1:A:63:ILE:C	1:A:64:LYS:N	13	3.4
(1,40)	1:A:63:ILE:N	1:A:63:ILE:CA	1:A:63:ILE:C	1:A:64:LYS:N	19	3.4
(1,35)	1:A:60:LEU:C	1:A:61:ARG:N	1:A:61:ARG:CA	1:A:61:ARG:C	1	3.4
(1,40)	1:A:63:ILE:N	1:A:63:ILE:CA	1:A:63:ILE:C	1:A:64:LYS:N	2	3.3
(1,19)	1:A:44:PHE:C	1:A:45:HIS:N	1:A:45:HIS:CA	1:A:45:HIS:C	10	3.2
(1,40)	1:A:63:ILE:N	1:A:63:ILE:CA	1:A:63:ILE:C	1:A:64:LYS:N	6	3.1
(1,40)	1:A:63:ILE:N	1:A:63:ILE:CA	1:A:63:ILE:C	1:A:64:LYS:N	15	3.1
(1,8)	1:A:33:VAL:N	1:A:33:VAL:CA	1:A:33:VAL:C	1:A:34:HIS:N	11	2.9
(1,40)	1:A:63:ILE:N	1:A:63:ILE:CA	1:A:63:ILE:C	1:A:64:LYS:N	7	2.9
(1,40)	1:A:63:ILE:N	1:A:63:ILE:CA	1:A:63:ILE:C	1:A:64:LYS:N	18	2.9
(1,8)	1:A:33:VAL:N	1:A:33:VAL:CA	1:A:33:VAL:C	1:A:34:HIS:N	14	2.8
(1,32)	1:A:59:LEU:N	1:A:59:LEU:CA	1:A:59:LEU:C	1:A:60:LEU:N	4	2.8
(1,8)	1:A:33:VAL:N	1:A:33:VAL:CA	1:A:33:VAL:C	1:A:34:HIS:N	7	2.6
(1,24)	1:A:52:SER:N	1:A:52:SER:CA	1:A:52:SER:C	1:A:53:PHE:N	1	2.5
(1,24)	1:A:52:SER:N	1:A:52:SER:CA	1:A:52:SER:C	1:A:53:PHE:N	8	2.4
(1,19)	1:A:44:PHE:C	1:A:45:HIS:N	1:A:45:HIS:CA	1:A:45:HIS:C	9	2.4
(1,6)	1:A:32:MET:N	1:A:32:MET:CA	1:A:32:MET:C	1:A:33:VAL:N	5	2.3
(1,46)	1:A:66:HIS:N	1:A:66:HIS:CA	1:A:66:HIS:C	1:A:67:SER:N	2	2.3
(1,2)	1:A:30:VAL:N	1:A:30:VAL:CA	1:A:30:VAL:C	1:A:31:LEU:N	6	2.2
(1,19)	1:A:44:PHE:C	1:A:45:HIS:N	1:A:45:HIS:CA	1:A:45:HIS:C	2	2.2
(1,40)	1:A:63:ILE:N	1:A:63:ILE:CA	1:A:63:ILE:C	1:A:64:LYS:N	17	2.1
(1,14)	1:A:36:ARG:N	1:A:36:ARG:CA	1:A:36:ARG:C	1:A:37:SER:N	14	2.1
(1,44)	1:A:65:LEU:N	1:A:65:LEU:CA	1:A:65:LEU:C	1:A:66:HIS:N	19	2.0
(1,40)	1:A:63:ILE:N	1:A:63:ILE:CA	1:A:63:ILE:C	1:A:64:LYS:N	3	2.0
(1,40)	1:A:63:ILE:N	1:A:63:ILE:CA	1:A:63:ILE:C	1:A:64:LYS:N	20	2.0
(1,24)	1:A:52:SER:N	1:A:52:SER:CA	1:A:52:SER:C	1:A:53:PHE:N	17	2.0
(1,2)	1:A:30:VAL:N	1:A:30:VAL:CA	1:A:30:VAL:C	1:A:31:LEU:N	11	2.0
(1,33)	1:A:59:LEU:C	1:A:60:LEU:N	1:A:60:LEU:CA	1:A:60:LEU:C	16	1.9
(1,32)	1:A:59:LEU:N	1:A:59:LEU:CA	1:A:59:LEU:C	1:A:60:LEU:N	5	1.9
(1,19)	1:A:44:PHE:C	1:A:45:HIS:N	1:A:45:HIS:CA	1:A:45:HIS:C	8	1.9
(1,7)	1:A:32:MET:C	1:A:33:VAL:N	1:A:33:VAL:CA	1:A:33:VAL:C	14	1.8
(1,40)	1:A:63:ILE:N	1:A:63:ILE:CA	1:A:63:ILE:C	1:A:64:LYS:N	9	1.7
(1,24)	1:A:52:SER:N	1:A:52:SER:CA	1:A:52:SER:C	1:A:53:PHE:N	4	1.7
(1,21)	1:A:50:GLY:C	1:A:51:ALA:N	1:A:51:ALA:CA	1:A:51:ALA:C	14	1.7
(1,20)	1:A:45:HIS:N	1:A:45:HIS:CA	1:A:45:HIS:C	1:A:46:CYS:N	15	1.7
(1,6)	1:A:32:MET:N	1:A:32:MET:CA	1:A:32:MET:C	1:A:33:VAL:N	20	1.6
(1,44)	1:A:65:LEU:N	1:A:65:LEU:CA	1:A:65:LEU:C	1:A:66:HIS:N	1	1.6
(1,29)	1:A:57:GLY:C	1:A:58:ASN:N	1:A:58:ASN:CA	1:A:58:ASN:C	6	1.6
(1,2)	1:A:30:VAL:N	1:A:30:VAL:CA	1:A:30:VAL:C	1:A:31:LEU:N	10	1.6
(1,19)	1:A:44:PHE:C	1:A:45:HIS:N	1:A:45:HIS:CA	1:A:45:HIS:C	7	1.6
(1,18)	1:A:42:ARG:N	1:A:42:ARG:CA	1:A:42:ARG:C	1:A:43:PRO:N	5	1.6
(1,12)	1:A:35:LYS:N	1:A:35:LYS:CA	1:A:35:LYS:C	1:A:36:ARG:N	7	1.6
(1,35)	1:A:60:LEU:C	1:A:61:ARG:N	1:A:61:ARG:CA	1:A:61:ARG:C	16	1.5
(1,24)	1:A:52:SER:N	1:A:52:SER:CA	1:A:52:SER:C	1:A:53:PHE:N	5	1.5
(1,19)	1:A:44:PHE:C	1:A:45:HIS:N	1:A:45:HIS:CA	1:A:45:HIS:C	14	1.5
(1,10)	1:A:34:HIS:N	1:A:34:HIS:CA	1:A:34:HIS:C	1:A:35:LYS:N	11	1.5
(1,2)	1:A:30:VAL:N	1:A:30:VAL:CA	1:A:30:VAL:C	1:A:31:LEU:N	15	1.4
(1,41)	1:A:63:ILE:C	1:A:64:LYS:N	1:A:64:LYS:CA	1:A:64:LYS:C	6	1.3
(1,37)	1:A:61:ARG:C	1:A:62:HIS:N	1:A:62:HIS:CA	1:A:62:HIS:C	18	1.3
(1,24)	1:A:52:SER:N	1:A:52:SER:CA	1:A:52:SER:C	1:A:53:PHE:N	3	1.3
(1,2)	1:A:30:VAL:N	1:A:30:VAL:CA	1:A:30:VAL:C	1:A:31:LEU:N	12	1.3

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,21)	1:A:50:GLY:C	1:A:51:ALA:N	1:A:51:ALA:CA	1:A:51:ALA:C	13	1.2
(1,10)	1:A:34:HIS:N	1:A:34:HIS:CA	1:A:34:HIS:C	1:A:35:LYS:N	14	1.2
(1,8)	1:A:33:VAL:N	1:A:33:VAL:CA	1:A:33:VAL:C	1:A:34:HIS:N	5	1.1
(1,31)	1:A:58:ASN:C	1:A:59:LEU:N	1:A:59:LEU:CA	1:A:59:LEU:C	17	1.1
(1,29)	1:A:57:GLY:C	1:A:58:ASN:N	1:A:58:ASN:CA	1:A:58:ASN:C	19	1.1
(1,24)	1:A:52:SER:N	1:A:52:SER:CA	1:A:52:SER:C	1:A:53:PHE:N	7	1.1
(1,24)	1:A:52:SER:N	1:A:52:SER:CA	1:A:52:SER:C	1:A:53:PHE:N	9	1.1
(1,20)	1:A:45:HIS:N	1:A:45:HIS:CA	1:A:45:HIS:C	1:A:46:CYS:N	13	1.1
(1,2)	1:A:30:VAL:N	1:A:30:VAL:CA	1:A:30:VAL:C	1:A:31:LEU:N	1	1.1
(1,17)	1:A:41:GLU:C	1:A:42:ARG:N	1:A:42:ARG:CA	1:A:42:ARG:C	19	1.1
(1,12)	1:A:35:LYS:N	1:A:35:LYS:CA	1:A:35:LYS:C	1:A:36:ARG:N	2	1.1
(1,1)	1:A:29:ASN:C	1:A:30:VAL:N	1:A:30:VAL:CA	1:A:30:VAL:C	4	1.1