



Full wwPDB NMR Structure Validation Report ⓘ

Jun 4, 2023 – 12:26 AM EDT

PDB ID : 2KW7
BMRB ID : 16810
Title : Solution NMR Structure of the N-terminal domain of protein PG_0361 from P.gingivalis, Northeast Structural Genomics Consortium Target PgR37A
Authors : Eletsky, A.; Mills, J.L.; Lee, D.; Ciccocanti, C.; Hamilton, K.; Acton, T.B.; Xiao, R.; Everett, J.K.; Montelione, G.T.; Szyperski, T.; Northeast Structural Genomics Consortium (NESG)
Deposited on : 2010-03-31

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-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

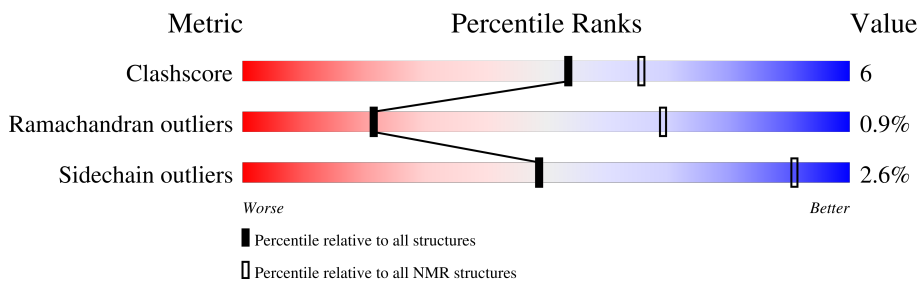
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 93%.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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

Mol	Chain	Length	Quality of chain
1	A	157	 85% . . . 10%

2 Ensemble composition and analysis

This entry contains 20 models. Model 12 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:3-A:77, A:82-A:147 (141)	0.68	12

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 3 clusters and 7 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2462 atoms, of which 1226 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Conserved domain protein.

Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		S
1	A	157	2462	772	1226	229	232	3	0

There are 9 discrepancies between the modelled and reference sequences:

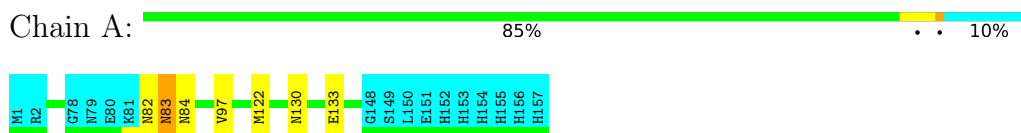
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q7MX54
A	150	LEU	-	expression tag	UNP Q7MX54
A	151	GLU	-	expression tag	UNP Q7MX54
A	152	HIS	-	expression tag	UNP Q7MX54
A	153	HIS	-	expression tag	UNP Q7MX54
A	154	HIS	-	expression tag	UNP Q7MX54
A	155	HIS	-	expression tag	UNP Q7MX54
A	156	HIS	-	expression tag	UNP Q7MX54
A	157	HIS	-	expression tag	UNP Q7MX54

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: Conserved domain protein

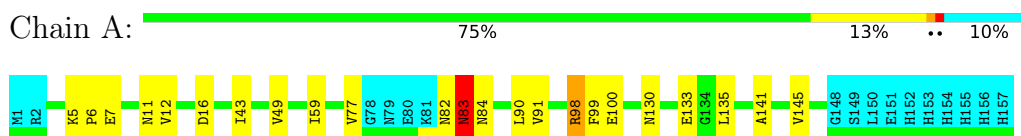


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

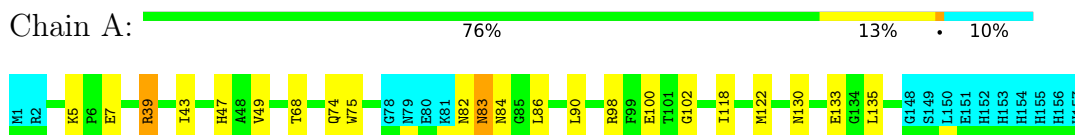
4.2.1 Score per residue for model 1

- Molecule 1: Conserved domain protein



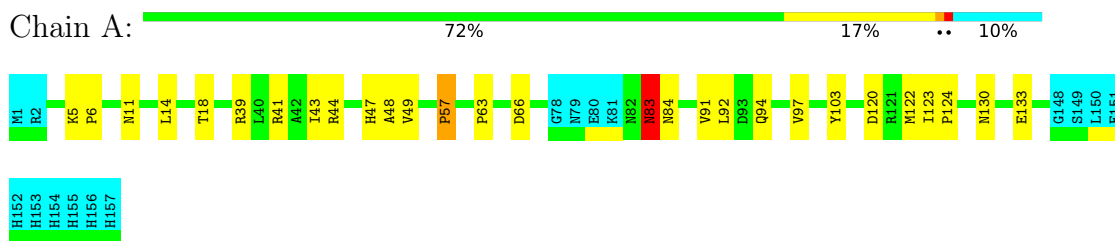
4.2.2 Score per residue for model 2

- Molecule 1: Conserved domain protein



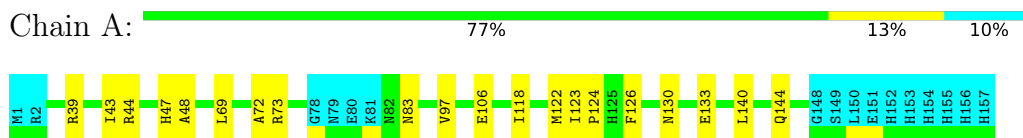
4.2.3 Score per residue for model 3

- Molecule 1: Conserved domain protein



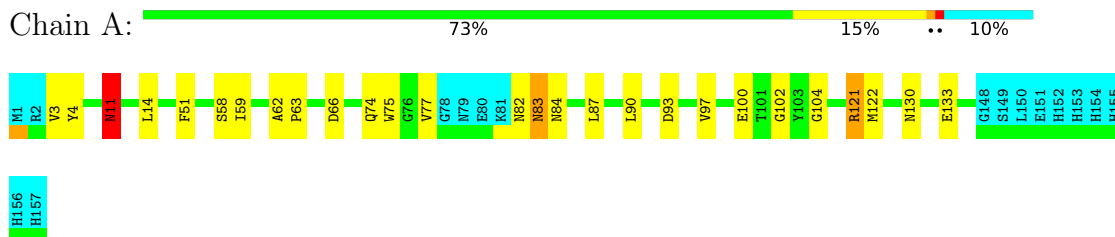
4.2.4 Score per residue for model 4

- Molecule 1: Conserved domain protein



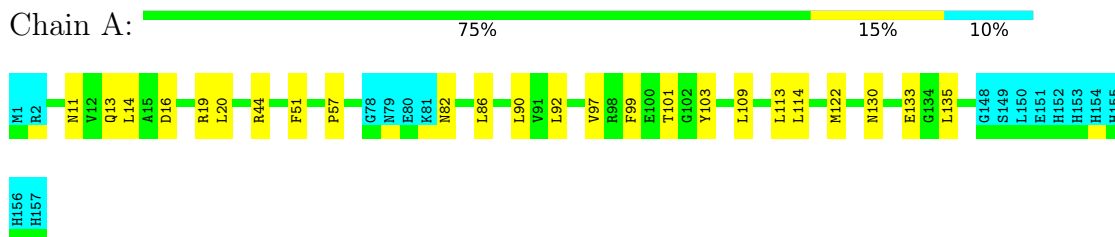
4.2.5 Score per residue for model 5

- Molecule 1: Conserved domain protein



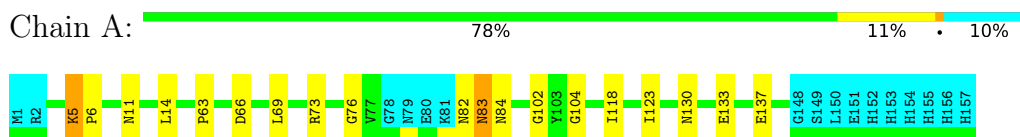
4.2.6 Score per residue for model 6

- Molecule 1: Conserved domain protein



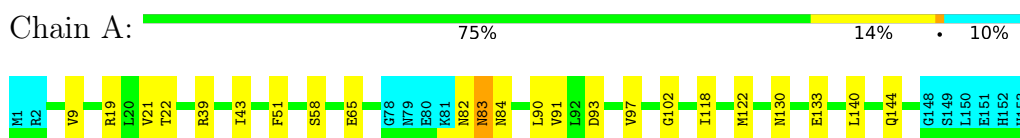
4.2.7 Score per residue for model 7

- Molecule 1: Conserved domain protein



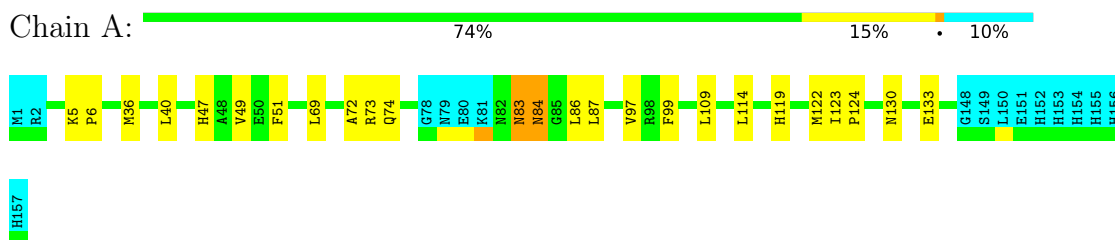
4.2.8 Score per residue for model 8

- Molecule 1: Conserved domain protein



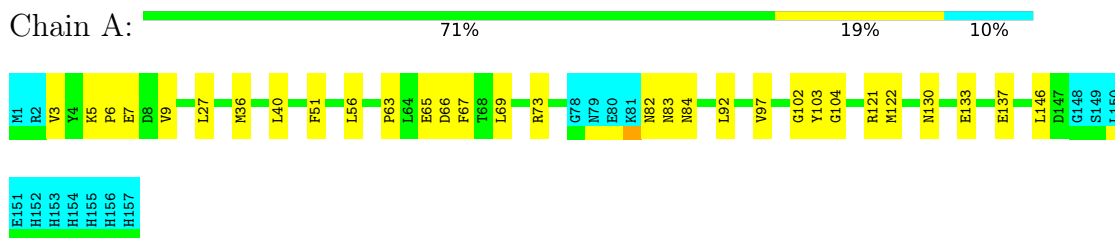
4.2.9 Score per residue for model 9

- Molecule 1: Conserved domain protein



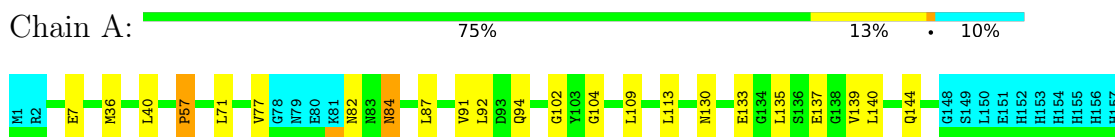
4.2.10 Score per residue for model 10

- Molecule 1: Conserved domain protein



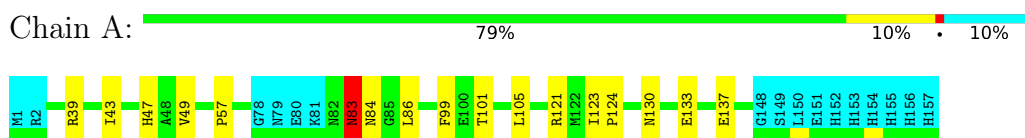
4.2.11 Score per residue for model 11

- Molecule 1: Conserved domain protein



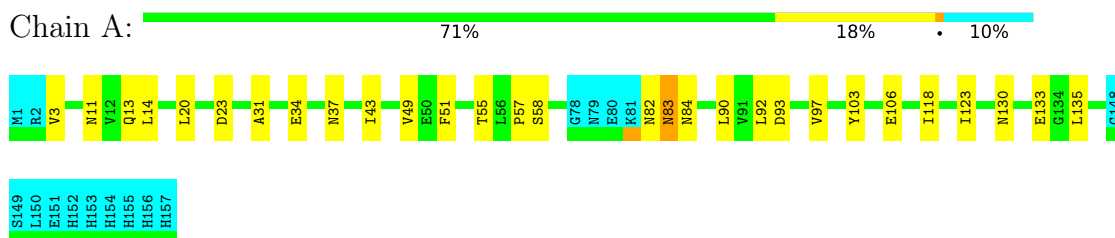
4.2.12 Score per residue for model 12 (medoid)

- Molecule 1: Conserved domain protein



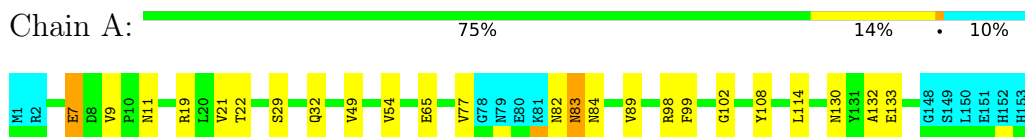
4.2.13 Score per residue for model 13

- Molecule 1: Conserved domain protein



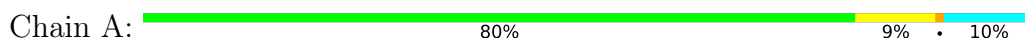
4.2.14 Score per residue for model 14

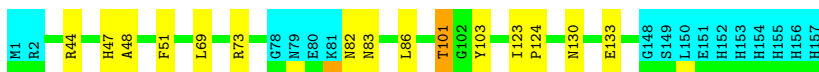
- Molecule 1: Conserved domain protein



4.2.15 Score per residue for model 15

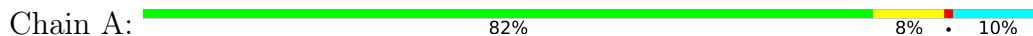
- Molecule 1: Conserved domain protein





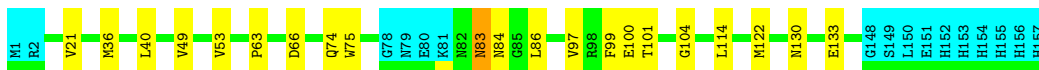
4.2.16 Score per residue for model 16

- Molecule 1: Conserved domain protein



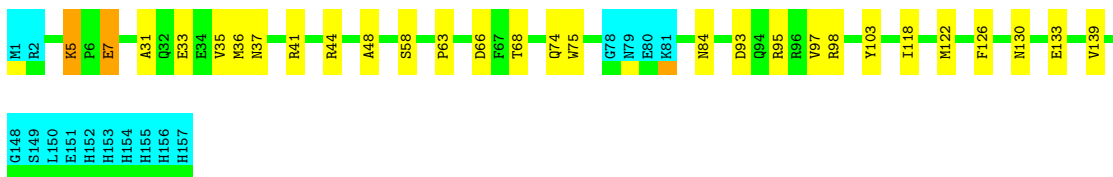
4.2.17 Score per residue for model 17

- Molecule 1: Conserved domain protein



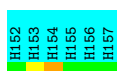
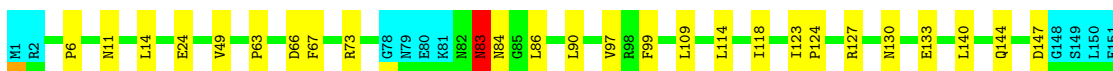
4.2.18 Score per residue for model 18

- Molecule 1: Conserved domain protein



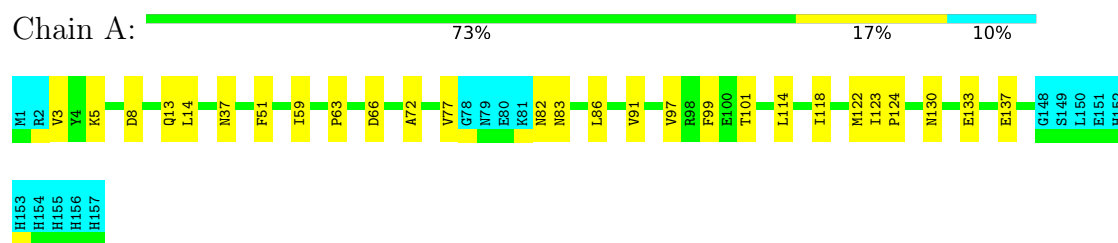
4.2.19 Score per residue for model 19

- Molecule 1: Conserved domain protein



4.2.20 Score per residue for model 20

- Molecule 1: Conserved domain protein



5 Refinement protocol and experimental data overview

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

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
CNS	refinement	1.2
CNS	structure solution	1.2
CNS	geometry optimization	1.2
CYANA	structure solution	3.0
AutoStructure	structure solution	2.2.1

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	1937
Number of shifts mapped to atoms	1937
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	93%

6 Model quality

6.1 Standard geometry

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

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	1099	1101	1100	12±3
All	All	21980	22020	22000	243

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 6.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:130:ASN:HB3	1:A:133:GLU:HB3	0.74	1.60	20	6
1:A:58:SER:HA	1:A:93:ASP:HB2	0.71	1.60	8	4
1:A:84:ASN:H	1:A:104:GLY:HA3	0.70	1.45	10	2
1:A:49:VAL:HA	1:A:84:ASN:HB3	0.66	1.67	19	8
1:A:97:VAL:HG21	1:A:122:MET:SD	0.66	2.30	20	11
1:A:130:ASN:HB3	1:A:133:GLU:HB2	0.64	1.68	14	14
1:A:90:LEU:HD22	1:A:135:LEU:HD11	0.64	1.70	2	3
1:A:36:MET:SD	1:A:139:VAL:HG21	0.60	2.37	18	1
1:A:83:ASN:HD22	1:A:83:ASN:N	0.58	1.97	17	8
1:A:91:VAL:HG11	1:A:94:GLN:HE21	0.58	1.58	3	1
1:A:118:ILE:O	1:A:122:MET:HB2	0.57	1.99	2	3
1:A:11:ASN:HD22	1:A:14:LEU:HB2	0.56	1.60	7	1
1:A:11:ASN:HB3	1:A:14:LEU:HB3	0.56	1.77	3	1
1:A:82:ASN:O	1:A:102:GLY:HA3	0.55	2.02	14	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:65:GLU:HG2	1:A:98:ARG:HD3	0.55	1.77	14	1
1:A:5:LYS:HB3	1:A:6:PRO:HD2	0.54	1.78	1	5
1:A:69:LEU:O	1:A:73:ARG:HG3	0.54	2.02	10	5
1:A:83:ASN:ND2	1:A:84:ASN:H	0.52	2.02	14	10
1:A:99:PHE:HB2	1:A:114:LEU:HB3	0.52	1.80	20	2
1:A:63:PRO:HG2	1:A:66:ASP:HB2	0.52	1.80	3	8
1:A:86:LEU:HD11	1:A:99:PHE:HB3	0.51	1.82	9	5
1:A:99:PHE:HB2	1:A:114:LEU:HD13	0.51	1.82	19	1
1:A:99:PHE:HB3	1:A:114:LEU:HD13	0.51	1.83	14	2
1:A:13:GLN:O	1:A:14:LEU:HB2	0.50	2.07	20	1
1:A:39:ARG:NH1	1:A:140:LEU:HD13	0.49	2.21	4	1
1:A:123:ILE:HB	1:A:124:PRO:HD3	0.49	1.82	19	3
1:A:68:THR:OG1	1:A:98:ARG:NH1	0.49	2.44	18	2
1:A:5:LYS:H	1:A:8:ASP:HB3	0.49	1.67	20	1
1:A:90:LEU:HA	1:A:97:VAL:HG12	0.49	1.83	19	4
1:A:72:ALA:HB1	1:A:77:VAL:O	0.49	2.07	20	1
1:A:49:VAL:HG22	1:A:84:ASN:HD22	0.49	1.68	12	1
1:A:123:ILE:N	1:A:124:PRO:HD2	0.48	2.24	12	5
1:A:121:ARG:HB3	1:A:137:GLU:HB3	0.48	1.84	12	1
1:A:16:ASP:HB3	1:A:19:ARG:HB3	0.48	1.83	6	1
1:A:6:PRO:HB2	1:A:74:GLN:NE2	0.48	2.24	9	1
1:A:83:ASN:HA	1:A:104:GLY:N	0.48	2.24	5	2
1:A:49:VAL:HG22	1:A:84:ASN:HB2	0.48	1.85	9	1
1:A:77:VAL:HA	1:A:82:ASN:HD22	0.48	1.68	14	1
1:A:121:ARG:HE	1:A:121:ARG:HA	0.48	1.69	5	1
1:A:11:ASN:HD22	1:A:14:LEU:HB3	0.47	1.68	5	1
1:A:31:ALA:O	1:A:35:VAL:HG23	0.47	2.09	18	1
1:A:36:MET:O	1:A:40:LEU:HG	0.47	2.09	10	4
1:A:5:LYS:NZ	1:A:5:LYS:HB2	0.46	2.24	1	2
1:A:39:ARG:O	1:A:43:ILE:HG13	0.46	2.10	12	5
1:A:9:VAL:HG13	1:A:22:THR:HG21	0.46	1.87	14	2
1:A:44:ARG:O	1:A:48:ALA:HA	0.46	2.09	4	4
1:A:72:ALA:HB2	1:A:87:LEU:HD22	0.46	1.88	9	1
1:A:57:PRO:HA	1:A:92:LEU:HB3	0.46	1.86	6	4
1:A:98:ARG:NH1	1:A:99:PHE:O	0.46	2.48	1	1
1:A:12:VAL:O	1:A:16:ASP:N	0.46	2.48	1	1
1:A:122:MET:HB3	1:A:126:PHE:CE2	0.46	2.44	16	3
1:A:87:LEU:HB3	1:A:100:GLU:HB3	0.46	1.87	5	1
1:A:109:LEU:HB3	1:A:114:LEU:HD21	0.46	1.86	9	2
1:A:43:ILE:HG22	1:A:49:VAL:HB	0.46	1.88	13	2
1:A:118:ILE:O	1:A:123:ILE:HG12	0.46	2.11	19	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:83:ASN:ND2	1:A:84:ASN:N	0.46	2.64	12	1
1:A:83:ASN:HD22	1:A:84:ASN:N	0.45	2.09	12	3
1:A:37:ASN:HB3	1:A:41:ARG:NH2	0.45	2.26	18	1
1:A:83:ASN:HA	1:A:104:GLY:H	0.45	1.71	17	2
1:A:54:VAL:HB	1:A:89:VAL:HG22	0.45	1.89	14	1
1:A:13:GLN:HE22	1:A:20:LEU:HG	0.44	1.71	13	2
1:A:97:VAL:HG22	1:A:118:ILE:HG23	0.44	1.89	8	1
1:A:140:LEU:O	1:A:144:GLN:HG2	0.44	2.12	19	3
1:A:7:GLU:HA	1:A:74:GLN:HE22	0.44	1.73	18	1
1:A:77:VAL:O	1:A:82:ASN:HB3	0.44	2.12	11	3
1:A:82:ASN:O	1:A:103:TYR:N	0.44	2.51	15	2
1:A:19:ARG:HG3	1:A:21:VAL:H	0.44	1.73	14	1
1:A:86:LEU:HD13	1:A:101:THR:HG23	0.44	1.88	15	2
1:A:49:VAL:HA	1:A:84:ASN:HD22	0.44	1.72	9	1
1:A:31:ALA:HA	1:A:34:GLU:HG2	0.44	1.89	13	1
1:A:74:GLN:HG3	1:A:75:TRP:CD1	0.44	2.47	2	3
1:A:91:VAL:HG11	1:A:94:GLN:NE2	0.44	2.28	11	2
1:A:90:LEU:HB2	1:A:135:LEU:HD21	0.43	1.90	13	1
1:A:74:GLN:HG3	1:A:75:TRP:HD1	0.43	1.72	2	2
1:A:32:GLN:HG2	1:A:132:ALA:HB1	0.43	1.91	14	1
1:A:56:LEU:HD11	1:A:67:PHE:CZ	0.43	2.49	10	1
1:A:19:ARG:HD2	1:A:21:VAL:O	0.43	2.14	8	1
1:A:11:ASN:OD1	1:A:14:LEU:HB3	0.43	2.13	19	1
1:A:11:ASN:ND2	1:A:14:LEU:HD13	0.43	2.29	13	1
1:A:101:THR:HG23	1:A:114:LEU:HD11	0.42	1.91	6	2
1:A:71:LEU:HD23	1:A:87:LEU:HD21	0.42	1.90	11	1
1:A:140:LEU:O	1:A:144:GLN:HG3	0.42	2.14	4	1
1:A:21:VAL:HA	1:A:53:VAL:O	0.42	2.14	17	1
1:A:49:VAL:HG13	1:A:105:LEU:HD11	0.42	1.90	12	1
1:A:4:TYR:HB2	1:A:58:SER:O	0.42	2.15	5	1
1:A:91:VAL:HG12	1:A:93:ASP:HB3	0.41	1.91	8	1
1:A:141:ALA:O	1:A:145:VAL:HG23	0.41	2.15	1	1
1:A:86:LEU:HA	1:A:100:GLU:O	0.41	2.15	2	1
1:A:23:ASP:HA	1:A:55:THR:OG1	0.41	2.15	13	1
1:A:6:PRO:HD3	1:A:67:PHE:CE2	0.41	2.49	19	1
1:A:109:LEU:HA	1:A:113:LEU:HD23	0.41	1.92	11	2
1:A:29:SER:HB2	1:A:32:GLN:OE1	0.41	2.14	14	1
1:A:59:ILE:HG12	1:A:91:VAL:HG11	0.41	1.93	20	2
1:A:18:THR:O	1:A:41:ARG:HD3	0.41	2.15	3	1
1:A:9:VAL:HG22	1:A:56:LEU:HD21	0.41	1.91	10	1
1:A:77:VAL:HA	1:A:82:ASN:HB3	0.41	1.92	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:83:ASN:N	1:A:83:ASN:ND2	0.41	2.67	17	2
1:A:59:ILE:HD12	1:A:62:ALA:O	0.40	2.16	5	1
1:A:95:ARG:NH2	1:A:126:PHE:O	0.40	2.54	18	1
1:A:11:ASN:ND2	1:A:14:LEU:HB2	0.40	2.29	7	1
1:A:123:ILE:O	1:A:127:ARG:HG3	0.40	2.17	19	1
1:A:27:LEU:HD21	1:A:92:LEU:HD22	0.40	1.93	10	1
1:A:65:GLU:H	1:A:65:GLU:CD	0.40	2.19	10	1
1:A:135:LEU:O	1:A:139:VAL:HG23	0.40	2.17	11	1
1:A:82:ASN:OD1	1:A:83:ASN:ND2	0.40	2.55	5	1
1:A:119:HIS:HA	1:A:123:ILE:CG1	0.40	2.47	9	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	141/157 (90%)	131±2 (93±1%)	8±2 (6±1%)	1±1 (1±1%)	21	69
All	All	2820/3140 (90%)	2628 (93%)	166 (6%)	26 (1%)	21	69

All 9 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	83	ASN	8
1	A	3	VAL	4
1	A	11	ASN	3
1	A	7	GLU	3
1	A	57	PRO	3
1	A	84	ASN	2
1	A	14	LEU	1
1	A	82	ASN	1
1	A	103	TYR	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	119/133 (89%)	116±1 (97±1%)	3±1 (3±1%)	49 91
All	All	2380/2660 (89%)	2319 (97%)	61 (3%)	49 91

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	83	ASN	16
1	A	51	PHE	8
1	A	7	GLU	4
1	A	137	GLU	4
1	A	5	LYS	3
1	A	103	TYR	3
1	A	121	ARG	3
1	A	84	ASN	2
1	A	100	GLU	2
1	A	106	GLU	2
1	A	11	ASN	2
1	A	101	THR	2
1	A	37	ASN	2
1	A	98	ARG	1
1	A	39	ARG	1
1	A	120	ASP	1
1	A	44	ARG	1
1	A	65	GLU	1
1	A	33	GLU	1
1	A	24	GLU	1
1	A	147	ASP	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation (i)

The completeness of assignment taking into account all chemical shift lists is 93% for the well-defined parts and 89% 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	1937
Number of shifts mapped to atoms	1937
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	3

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
$^{13}\text{C}_\alpha$	152	-0.44 ± 0.11	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	138	0.33 ± 0.13	None needed (< 0.5 ppm)
$^{13}\text{C}'$	145	-0.24 ± 0.15	None needed (< 0.5 ppm)
^{15}N	139	0.28 ± 0.37	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments (i)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 93%, i.e. 1813 atoms were assigned a chemical shift out of a possible 1948. 0 out of 36 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	695/705 (99%)	287/288 (100%)	277/282 (98%)	131/135 (97%)
Sidechain	1016/1131 (90%)	692/738 (94%)	302/345 (88%)	22/48 (46%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	102/112 (91%)	48/54 (89%)	47/51 (92%)	7/7 (100%)
Overall	1813/1948 (93%)	1027/1080 (95%)	626/678 (92%)	160/190 (84%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 89%, i.e. 1933 atoms were assigned a chemical shift out of a possible 2174. 0 out of 37 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	746/787 (95%)	310/322 (96%)	297/314 (95%)	139/151 (92%)
Sidechain	1085/1227 (88%)	739/799 (92%)	323/375 (86%)	23/53 (43%)
Aromatic	102/160 (64%)	48/78 (62%)	47/63 (75%)	7/19 (37%)
Overall	1933/2174 (89%)	1097/1199 (91%)	667/752 (89%)	169/223 (76%)

7.1.4 Statistically unusual chemical shifts [i](#)

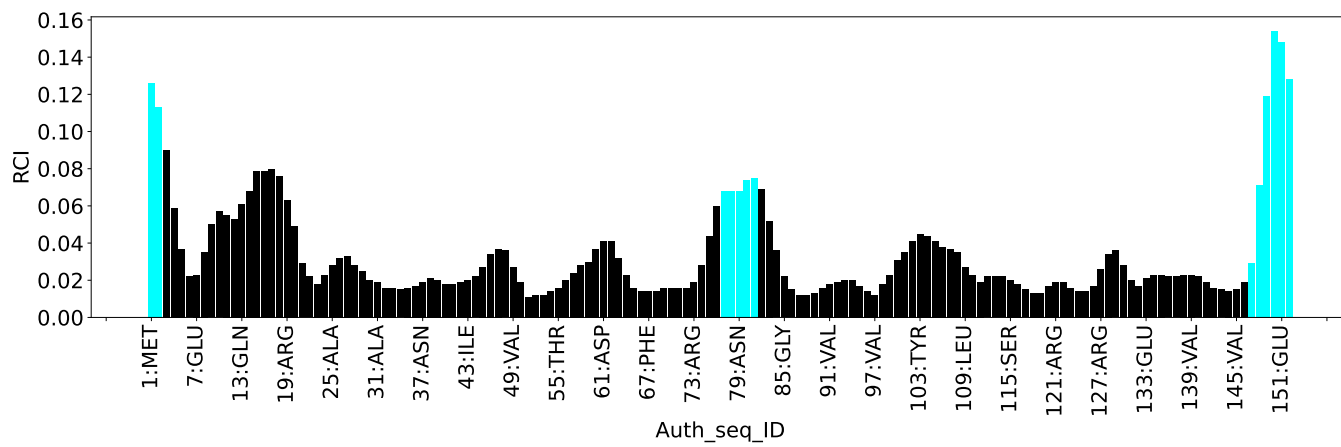
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	22	THR	HG1	7.12	0.08 – 2.19	28.4
1	A	55	THR	HG1	6.71	0.08 – 2.19	26.4
1	A	68	THR	HG1	6.01	0.08 – 2.19	23.1

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	8078
Intra-residue ($ i-j =0$)	1274
Sequential ($ i-j =1$)	1874
Medium range ($ i-j >1$ and $ i-j <5$)	2024
Long range ($ i-j \geq 5$)	2906
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	154
Number of unmapped restraints	0
Number of restraints per residue	52.4
Number of long range restraints per residue ¹	18.5

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

8.2 Residual restraint violations

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

8.2.1 Average number of distance violations per model

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

Bins (Å)	Average number of violations per model	Max (Å)
0.1-0.2 (Small)	15.1	0.2
0.2-0.5 (Medium)	1.6	0.29
>0.5 (Large)	None	None

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

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

Bins (°)	Average number of violations per model	Max (°)
1.0-10.0 (Small)	2.6	2.7
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis [i](#)

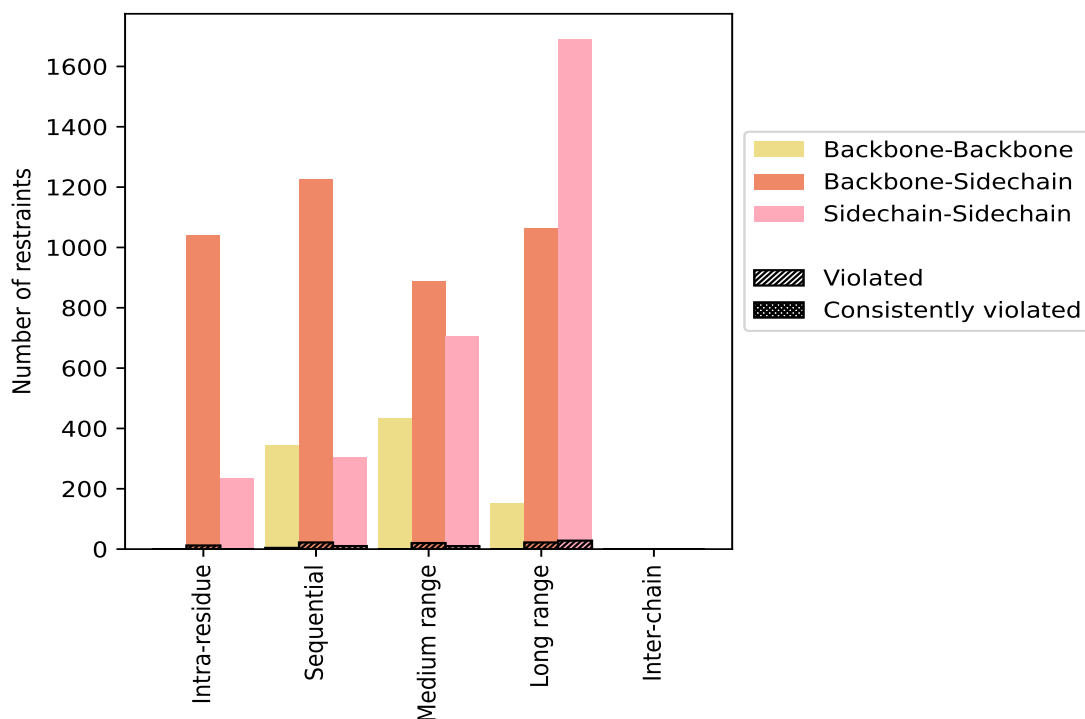
9.1 Summary of distance violations [i](#)

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 ($i-j =0$)	1274	15.8	12	0.9	0.1	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	1040	12.9	12	1.2	0.1	0	0.0	0.0
Sidechain-Sidechain	234	2.9	0	0.0	0.0	0	0.0	0.0
Sequential ($i-j =1$)	1874	23.2	36	1.9	0.4	0	0.0	0.0
Backbone-Backbone	344	4.3	4	1.2	0.0	0	0.0	0.0
Backbone-Sidechain	1226	15.2	22	1.8	0.3	0	0.0	0.0
Sidechain-Sidechain	304	3.8	10	3.3	0.1	0	0.0	0.0
Medium range ($i-j >1$ & $i-j <5$)	2024	25.1	30	1.5	0.4	0	0.0	0.0
Backbone-Backbone	432	5.3	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	886	11.0	20	2.3	0.2	0	0.0	0.0
Sidechain-Sidechain	706	8.7	10	1.4	0.1	0	0.0	0.0
Long range ($i-j \geq 5$)	2906	36.0	50	1.7	0.6	0	0.0	0.0
Backbone-Backbone	152	1.9	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	1064	13.2	22	2.1	0.3	0	0.0	0.0
Sidechain-Sidechain	1690	20.9	28	1.7	0.3	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	8078	100.0	128	1.6	1.6	0	0.0	0.0
Backbone-Backbone	928	11.5	4	0.4	0.0	0	0.0	0.0
Backbone-Sidechain	4216	52.2	76	1.8	0.9	0	0.0	0.0
Sidechain-Sidechain	2934	36.3	48	1.6	0.6	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	6	2	8	0	16	0.14	0.18	0.03	0.14
2	0	4	4	10	0	18	0.14	0.21	0.03	0.14
3	0	2	2	8	0	12	0.13	0.18	0.02	0.12
4	0	8	0	12	0	20	0.14	0.2	0.03	0.13
5	0	2	4	10	0	16	0.15	0.25	0.05	0.14
6	2	2	0	6	0	10	0.14	0.21	0.03	0.14
7	0	2	2	14	0	18	0.16	0.24	0.04	0.13
8	2	2	6	8	0	18	0.13	0.21	0.03	0.12
9	0	4	8	10	0	22	0.14	0.18	0.03	0.13
10	0	4	4	8	0	16	0.16	0.29	0.05	0.16
11	0	6	6	12	0	24	0.14	0.25	0.04	0.12

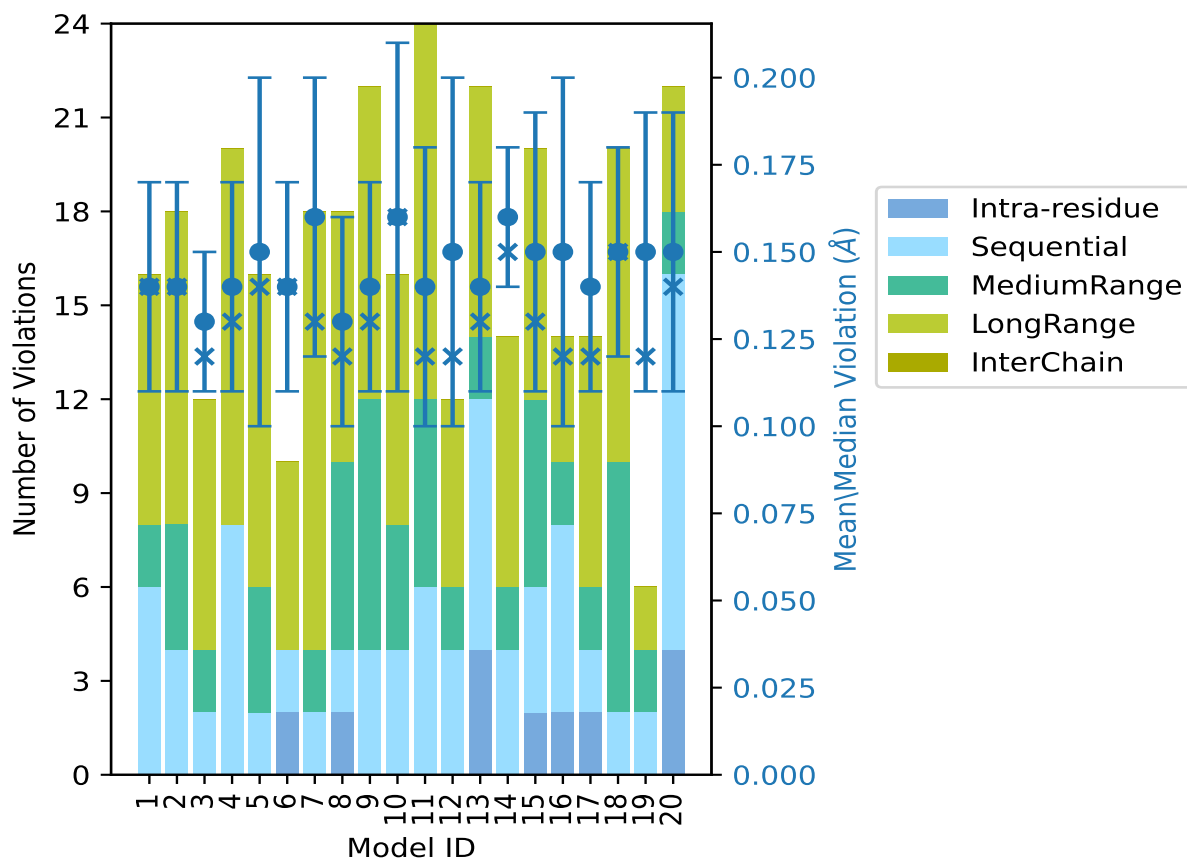
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Model ID	Number of violations					Total	Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵					
12	0	4	2	6	0	12	0.15	0.25	0.05	0.12
13	4	8	2	8	0	22	0.14	0.2	0.03	0.13
14	0	4	2	8	0	14	0.16	0.2	0.02	0.15
15	2	4	6	8	0	20	0.15	0.22	0.04	0.13
16	2	6	2	4	0	14	0.15	0.24	0.05	0.12
17	2	2	2	8	0	14	0.14	0.2	0.03	0.12
18	0	2	8	10	0	20	0.15	0.21	0.03	0.15
19	0	2	2	2	0	6	0.15	0.21	0.04	0.12
20	4	12	2	4	0	22	0.15	0.22	0.04	0.14

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

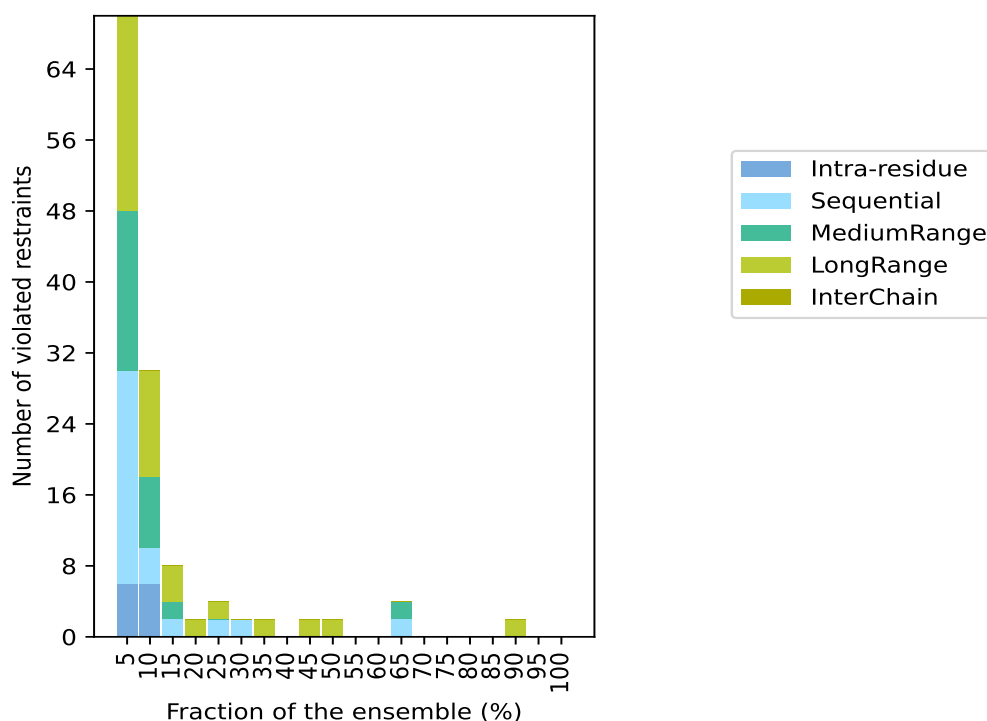
9.3 Distance violation statistics for the ensemble

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, 7950(IR:1262, SQ:1838, MR:1994, LR:2856, 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	%
6	24	18	22	0	70	1	5.0
6	4	8	12	0	30	2	10.0
0	2	2	4	0	8	3	15.0
0	0	0	2	0	2	4	20.0
0	2	0	2	0	4	5	25.0
0	2	0	0	0	2	6	30.0
0	0	0	2	0	2	7	35.0
0	0	0	0	0	0	8	40.0
0	0	0	2	0	2	9	45.0
0	0	0	2	0	2	10	50.0
0	0	0	0	0	0	11	55.0
0	0	0	0	0	0	12	60.0
0	2	2	0	0	4	13	65.0
0	0	0	0	0	0	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	2	0	2	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

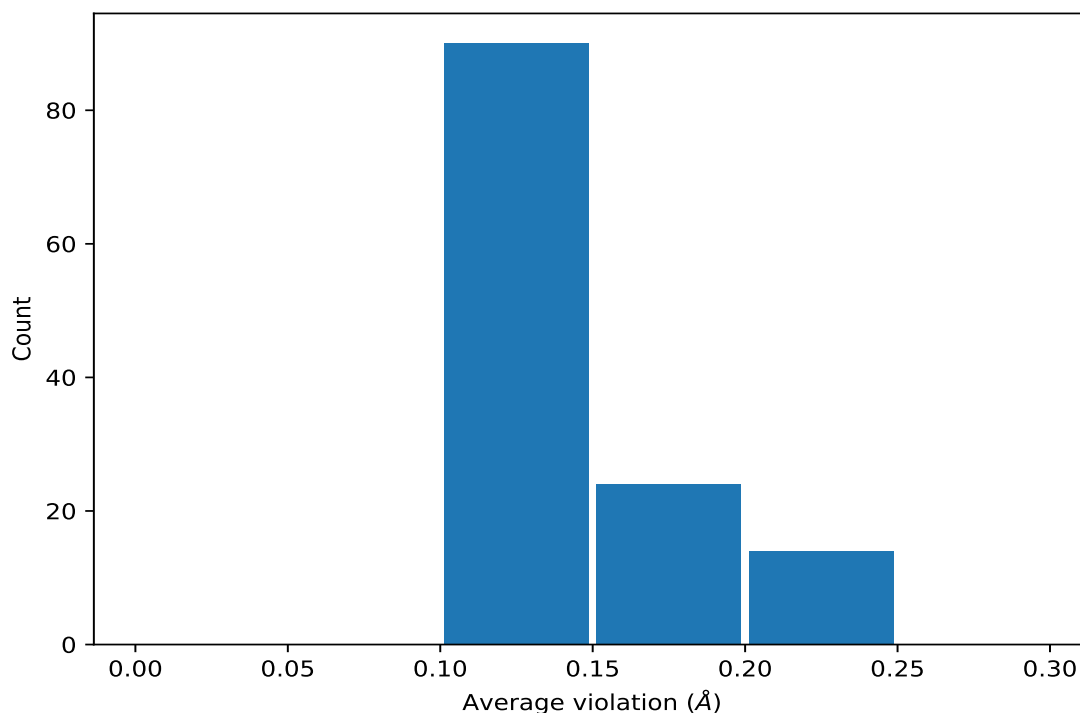
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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)
(1,2081)	1:A:90:LEU:HG	1:A:97:VAL:HB	18	0.15	0.02	0.15
(1,5570)	1:A:90:LEU:HG	1:A:97:VAL:HB	18	0.15	0.02	0.15
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	13	0.2	0.05	0.21
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	13	0.2	0.05	0.21
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	13	0.2	0.05	0.21
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	13	0.2	0.05	0.21
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	13	0.2	0.05	0.21
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	13	0.2	0.05	0.21
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	13	0.2	0.05	0.21
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	13	0.2	0.05	0.21
(1,750)	1:A:101:THR:HG21	1:A:104:GLY:H	13	0.13	0.02	0.13
(1,750)	1:A:101:THR:HG22	1:A:104:GLY:H	13	0.13	0.02	0.13
(1,750)	1:A:101:THR:HG23	1:A:104:GLY:H	13	0.13	0.02	0.13
(1,4239)	1:A:101:THR:HG21	1:A:104:GLY:H	13	0.13	0.02	0.13
(1,4239)	1:A:101:THR:HG22	1:A:104:GLY:H	13	0.13	0.02	0.13
(1,4239)	1:A:101:THR:HG23	1:A:104:GLY:H	13	0.13	0.02	0.13

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,3259)	1:A:83:ASN:HD21	1:A:104:GLY:HA2	10	0.17	0.04	0.17
(1,3259)	1:A:83:ASN:HD22	1:A:104:GLY:HA2	10	0.17	0.04	0.17
(1,6748)	1:A:83:ASN:HD21	1:A:104:GLY:HA2	10	0.17	0.04	0.17
(1,6748)	1:A:83:ASN:HD22	1:A:104:GLY:HA2	10	0.17	0.04	0.17
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD21	9	0.14	0.03	0.12
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD22	9	0.14	0.03	0.12
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD23	9	0.14	0.03	0.12
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD21	9	0.14	0.03	0.12
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD22	9	0.14	0.03	0.12
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD23	9	0.14	0.03	0.12
(1,113)	1:A:25:ALA:H	1:A:56:LEU:HB3	7	0.12	0.01	0.12
(1,3602)	1:A:25:ALA:H	1:A:56:LEU:HB3	7	0.12	0.01	0.12
(1,701)	1:A:96:ARG:HG3	1:A:97:VAL:H	6	0.12	0.01	0.12
(1,4190)	1:A:96:ARG:HG3	1:A:97:VAL:H	6	0.12	0.01	0.12
(1,3250)	1:A:80:GLU:HB2	1:A:81:LYS:HD2	5	0.16	0.03	0.16
(1,3250)	1:A:80:GLU:HB2	1:A:81:LYS:HD3	5	0.16	0.03	0.16
(1,3250)	1:A:80:GLU:HB3	1:A:81:LYS:HD2	5	0.16	0.03	0.16
(1,3250)	1:A:80:GLU:HB3	1:A:81:LYS:HD3	5	0.16	0.03	0.16
(1,6739)	1:A:80:GLU:HB2	1:A:81:LYS:HD2	5	0.16	0.03	0.16
(1,6739)	1:A:80:GLU:HB2	1:A:81:LYS:HD3	5	0.16	0.03	0.16
(1,6739)	1:A:80:GLU:HB3	1:A:81:LYS:HD2	5	0.16	0.03	0.16
(1,6739)	1:A:80:GLU:HB3	1:A:81:LYS:HD3	5	0.16	0.03	0.16
(1,743)	1:A:83:ASN:HB2	1:A:103:TYR:H	5	0.14	0.03	0.13
(1,743)	1:A:83:ASN:HB3	1:A:103:TYR:H	5	0.14	0.03	0.13
(1,4232)	1:A:83:ASN:HB2	1:A:103:TYR:H	5	0.14	0.03	0.13
(1,4232)	1:A:83:ASN:HB3	1:A:103:TYR:H	5	0.14	0.03	0.13
(1,1130)	1:A:51:PHE:HZ	1:A:143:GLN:H	4	0.12	0.01	0.12
(1,4619)	1:A:51:PHE:HZ	1:A:143:GLN:H	4	0.12	0.01	0.12
(1,3241)	1:A:77:VAL:HA	1:A:83:ASN:HD21	3	0.19	0.04	0.21
(1,3241)	1:A:77:VAL:HA	1:A:83:ASN:HD22	3	0.19	0.04	0.21
(1,6730)	1:A:77:VAL:HA	1:A:83:ASN:HD21	3	0.19	0.04	0.21
(1,6730)	1:A:77:VAL:HA	1:A:83:ASN:HD22	3	0.19	0.04	0.21
(1,8)	1:A:2:ARG:HA	1:A:3:VAL:H	3	0.19	0.02	0.18
(1,3497)	1:A:2:ARG:HA	1:A:3:VAL:H	3	0.19	0.02	0.18
(1,3256)	1:A:81:LYS:HE2	1:A:102:GLY:HA2	3	0.14	0.01	0.14
(1,3256)	1:A:81:LYS:HE2	1:A:102:GLY:HA3	3	0.14	0.01	0.14
(1,3256)	1:A:81:LYS:HE3	1:A:102:GLY:HA2	3	0.14	0.01	0.14
(1,3256)	1:A:81:LYS:HE3	1:A:102:GLY:HA3	3	0.14	0.01	0.14
(1,6745)	1:A:81:LYS:HE2	1:A:102:GLY:HA2	3	0.14	0.01	0.14
(1,6745)	1:A:81:LYS:HE2	1:A:102:GLY:HA3	3	0.14	0.01	0.14
(1,6745)	1:A:81:LYS:HE3	1:A:102:GLY:HA2	3	0.14	0.01	0.14
(1,6745)	1:A:81:LYS:HE3	1:A:102:GLY:HA3	3	0.14	0.01	0.14

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,1971)	1:A:82:ASN:HB3	1:A:84:ASN:H	3	0.13	0.0	0.13
(1,5460)	1:A:82:ASN:HB3	1:A:84:ASN:H	3	0.13	0.0	0.13
(1,2655)	1:A:103:TYR:HA	1:A:103:TYR:HD1	2	0.22	0.02	0.22
(1,2655)	1:A:103:TYR:HA	1:A:103:TYR:HD2	2	0.22	0.02	0.22
(1,6144)	1:A:103:TYR:HA	1:A:103:TYR:HD1	2	0.22	0.02	0.22
(1,6144)	1:A:103:TYR:HA	1:A:103:TYR:HD2	2	0.22	0.02	0.22
(2,271)	1:A:81:LYS:HA	1:A:82:ASN:HB3	2	0.2	0.01	0.2
(2,821)	1:A:81:LYS:HA	1:A:82:ASN:HB3	2	0.2	0.01	0.2
(1,98)	1:A:20:LEU:H	1:A:21:VAL:HB	2	0.16	0.02	0.16
(1,3587)	1:A:20:LEU:H	1:A:21:VAL:HB	2	0.16	0.02	0.16
(1,718)	1:A:68:THR:HB	1:A:98:ARG:HE	2	0.16	0.05	0.16
(1,4207)	1:A:68:THR:HB	1:A:98:ARG:HE	2	0.16	0.05	0.16
(1,558)	1:A:77:VAL:HB	1:A:82:ASN:HD22	2	0.14	0.03	0.14
(1,1341)	1:A:19:ARG:HB3	1:A:21:VAL:HG21	2	0.14	0.01	0.14
(1,1341)	1:A:19:ARG:HB3	1:A:21:VAL:HG22	2	0.14	0.01	0.14
(1,1341)	1:A:19:ARG:HB3	1:A:21:VAL:HG23	2	0.14	0.01	0.14
(1,4047)	1:A:77:VAL:HB	1:A:82:ASN:HD22	2	0.14	0.03	0.14
(1,4830)	1:A:19:ARG:HB3	1:A:21:VAL:HG21	2	0.14	0.01	0.14
(1,4830)	1:A:19:ARG:HB3	1:A:21:VAL:HG22	2	0.14	0.01	0.14
(1,4830)	1:A:19:ARG:HB3	1:A:21:VAL:HG23	2	0.14	0.01	0.14
(1,5)	1:A:3:VAL:H	1:A:3:VAL:HB	2	0.14	0.01	0.14
(1,993)	1:A:130:ASN:HD22	1:A:133:GLU:HG3	2	0.14	0.02	0.14
(1,3494)	1:A:3:VAL:H	1:A:3:VAL:HB	2	0.14	0.01	0.14
(1,4482)	1:A:130:ASN:HD22	1:A:133:GLU:HG3	2	0.14	0.02	0.14
(1,1474)	1:A:31:ALA:HA	1:A:34:GLU:HB2	2	0.13	0.0	0.13
(1,4963)	1:A:31:ALA:HA	1:A:34:GLU:HB2	2	0.13	0.0	0.13
(1,60)	1:A:12:VAL:H	1:A:71:LEU:HD11	2	0.12	0.01	0.12
(1,60)	1:A:12:VAL:H	1:A:71:LEU:HD12	2	0.12	0.01	0.12
(1,60)	1:A:12:VAL:H	1:A:71:LEU:HD13	2	0.12	0.01	0.12
(1,3549)	1:A:12:VAL:H	1:A:71:LEU:HD11	2	0.12	0.01	0.12
(1,3549)	1:A:12:VAL:H	1:A:71:LEU:HD12	2	0.12	0.01	0.12
(1,3549)	1:A:12:VAL:H	1:A:71:LEU:HD13	2	0.12	0.01	0.12
(1,1329)	1:A:13:GLN:HG3	1:A:17:SER:HA	2	0.12	0.0	0.12
(1,2653)	1:A:103:TYR:H	1:A:103:TYR:HD1	2	0.12	0.0	0.12
(1,2653)	1:A:103:TYR:H	1:A:103:TYR:HD2	2	0.12	0.0	0.12
(1,3276)	1:A:91:VAL:HG11	1:A:96:ARG:HD2	2	0.12	0.0	0.12
(1,3276)	1:A:91:VAL:HG11	1:A:96:ARG:HD3	2	0.12	0.0	0.12
(1,3276)	1:A:91:VAL:HG12	1:A:96:ARG:HD2	2	0.12	0.0	0.12
(1,3276)	1:A:91:VAL:HG12	1:A:96:ARG:HD3	2	0.12	0.0	0.12
(1,3276)	1:A:91:VAL:HG13	1:A:96:ARG:HD2	2	0.12	0.0	0.12
(1,3276)	1:A:91:VAL:HG13	1:A:96:ARG:HD3	2	0.12	0.0	0.12
(1,4818)	1:A:13:GLN:HG3	1:A:17:SER:HA	2	0.12	0.0	0.12

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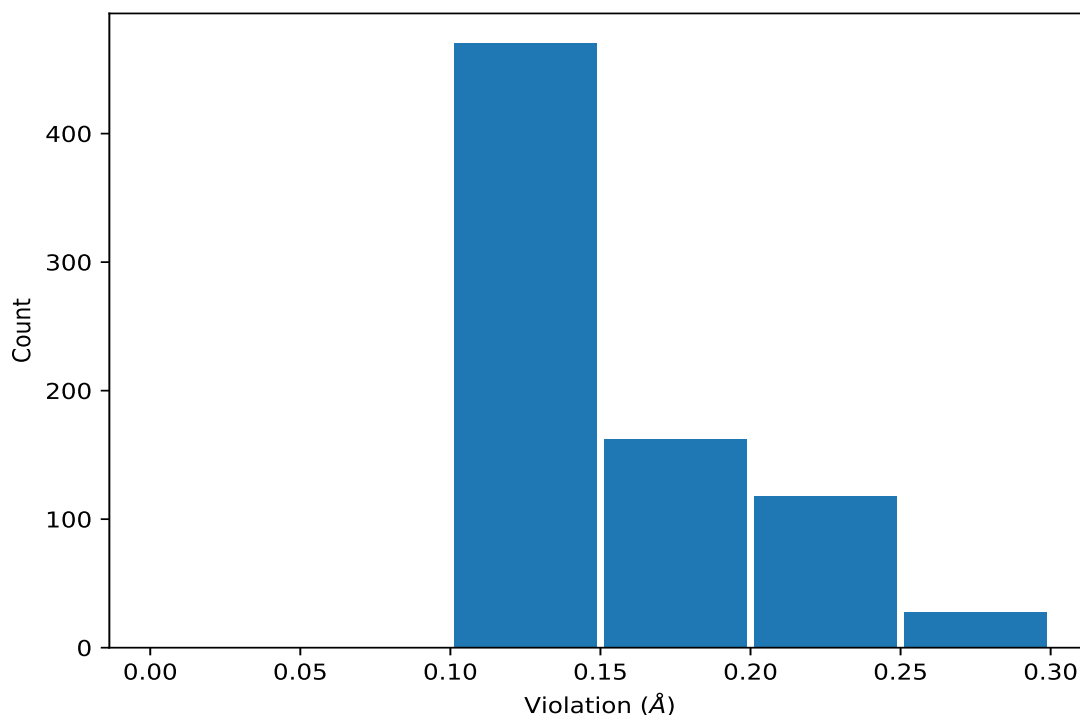
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,6142)	1:A:103:TYR:H	1:A:103:TYR:HD1	2	0.12	0.0	0.12
(1,6142)	1:A:103:TYR:H	1:A:103:TYR:HD2	2	0.12	0.0	0.12
(1,6765)	1:A:91:VAL:HG11	1:A:96:ARG:HD2	2	0.12	0.0	0.12
(1,6765)	1:A:91:VAL:HG11	1:A:96:ARG:HD3	2	0.12	0.0	0.12
(1,6765)	1:A:91:VAL:HG12	1:A:96:ARG:HD2	2	0.12	0.0	0.12
(1,6765)	1:A:91:VAL:HG12	1:A:96:ARG:HD3	2	0.12	0.0	0.12
(1,6765)	1:A:91:VAL:HG13	1:A:96:ARG:HD2	2	0.12	0.0	0.12
(1,6765)	1:A:91:VAL:HG13	1:A:96:ARG:HD3	2	0.12	0.0	0.12
(1,2663)	1:A:83:ASN:HB2	1:A:103:TYR:HE1	2	0.11	0.0	0.11
(1,2663)	1:A:83:ASN:HB2	1:A:103:TYR:HE2	2	0.11	0.0	0.11
(1,2663)	1:A:83:ASN:HB3	1:A:103:TYR:HE1	2	0.11	0.0	0.11
(1,2663)	1:A:83:ASN:HB3	1:A:103:TYR:HE2	2	0.11	0.0	0.11
(1,3244)	1:A:77:VAL:HG11	1:A:83:ASN:HD21	2	0.11	0.0	0.11
(1,3244)	1:A:77:VAL:HG11	1:A:83:ASN:HD22	2	0.11	0.0	0.11
(1,3244)	1:A:77:VAL:HG12	1:A:83:ASN:HD21	2	0.11	0.0	0.11
(1,3244)	1:A:77:VAL:HG12	1:A:83:ASN:HD22	2	0.11	0.0	0.11
(1,3244)	1:A:77:VAL:HG13	1:A:83:ASN:HD21	2	0.11	0.0	0.11
(1,3244)	1:A:77:VAL:HG13	1:A:83:ASN:HD22	2	0.11	0.0	0.11
(1,6152)	1:A:83:ASN:HB2	1:A:103:TYR:HE1	2	0.11	0.0	0.11
(1,6152)	1:A:83:ASN:HB2	1:A:103:TYR:HE2	2	0.11	0.0	0.11
(1,6152)	1:A:83:ASN:HB3	1:A:103:TYR:HE1	2	0.11	0.0	0.11
(1,6152)	1:A:83:ASN:HB3	1:A:103:TYR:HE2	2	0.11	0.0	0.11
(1,6733)	1:A:77:VAL:HG11	1:A:83:ASN:HD21	2	0.11	0.0	0.11
(1,6733)	1:A:77:VAL:HG11	1:A:83:ASN:HD22	2	0.11	0.0	0.11
(1,6733)	1:A:77:VAL:HG12	1:A:83:ASN:HD21	2	0.11	0.0	0.11
(1,6733)	1:A:77:VAL:HG12	1:A:83:ASN:HD22	2	0.11	0.0	0.11
(1,6733)	1:A:77:VAL:HG13	1:A:83:ASN:HD21	2	0.11	0.0	0.11
(1,6733)	1:A:77:VAL:HG13	1:A:83:ASN:HD22	2	0.11	0.0	0.11

¹Number of violated models, ²Standard deviation

9.5 All violated distance restraints [i](#)

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

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



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

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

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,6748)	1:A:83:ASN:HD21	1:A:104:GLY:HA2	10	0.29
(1,6748)	1:A:83:ASN:HD22	1:A:104:GLY:HA2	10	0.29
(1,3259)	1:A:83:ASN:HD21	1:A:104:GLY:HA2	10	0.29
(1,3259)	1:A:83:ASN:HD22	1:A:104:GLY:HA2	10	0.29
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	5	0.25
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	5	0.25
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	5	0.25
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	5	0.25
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	11	0.25
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	11	0.25
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	11	0.25
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	11	0.25
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	12	0.25
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	12	0.25
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	12	0.25
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	12	0.25

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	5	0.25
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	5	0.25
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	5	0.25
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	5	0.25
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	11	0.25
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	11	0.25
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	11	0.25
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	11	0.25
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	12	0.25
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	12	0.25
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	12	0.25
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	12	0.25
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	7	0.24
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	7	0.24
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	7	0.24
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	7	0.24
(1,6144)	1:A:103:TYR:HA	1:A:103:TYR:HD1	16	0.24
(1,6144)	1:A:103:TYR:HA	1:A:103:TYR:HD2	16	0.24
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	7	0.24
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	7	0.24
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	7	0.24
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	7	0.24
(1,2655)	1:A:103:TYR:HA	1:A:103:TYR:HD1	16	0.24
(1,2655)	1:A:103:TYR:HA	1:A:103:TYR:HD2	16	0.24
(1,8)	1:A:2:ARG:HA	1:A:3:VAL:H	20	0.22
(1,6730)	1:A:77:VAL:HA	1:A:83:ASN:HD21	7	0.22
(1,6730)	1:A:77:VAL:HA	1:A:83:ASN:HD22	7	0.22
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	15	0.22
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	15	0.22
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	15	0.22
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	15	0.22
(1,6080)	1:A:14:LEU:HD21	1:A:15:ALA:HB1	20	0.22
(1,6080)	1:A:14:LEU:HD21	1:A:15:ALA:HB2	20	0.22
(1,6080)	1:A:14:LEU:HD21	1:A:15:ALA:HB3	20	0.22
(1,6080)	1:A:14:LEU:HD22	1:A:15:ALA:HB1	20	0.22
(1,6080)	1:A:14:LEU:HD22	1:A:15:ALA:HB2	20	0.22
(1,6080)	1:A:14:LEU:HD22	1:A:15:ALA:HB3	20	0.22
(1,6080)	1:A:14:LEU:HD23	1:A:15:ALA:HB1	20	0.22
(1,6080)	1:A:14:LEU:HD23	1:A:15:ALA:HB2	20	0.22
(1,6080)	1:A:14:LEU:HD23	1:A:15:ALA:HB3	20	0.22
(1,3497)	1:A:2:ARG:HA	1:A:3:VAL:H	20	0.22
(1,3241)	1:A:77:VAL:HA	1:A:83:ASN:HD21	7	0.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,3241)	1:A:77:VAL:HA	1:A:83:ASN:HD22	7	0.22
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	15	0.22
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	15	0.22
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	15	0.22
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	15	0.22
(1,2591)	1:A:14:LEU:HD21	1:A:15:ALA:HB1	20	0.22
(1,2591)	1:A:14:LEU:HD21	1:A:15:ALA:HB2	20	0.22
(1,2591)	1:A:14:LEU:HD21	1:A:15:ALA:HB3	20	0.22
(1,2591)	1:A:14:LEU:HD22	1:A:15:ALA:HB1	20	0.22
(1,2591)	1:A:14:LEU:HD22	1:A:15:ALA:HB2	20	0.22
(1,2591)	1:A:14:LEU:HD22	1:A:15:ALA:HB3	20	0.22
(1,2591)	1:A:14:LEU:HD23	1:A:15:ALA:HB1	20	0.22
(1,2591)	1:A:14:LEU:HD23	1:A:15:ALA:HB2	20	0.22
(1,2591)	1:A:14:LEU:HD23	1:A:15:ALA:HB3	20	0.22
(2,821)	1:A:81:LYS:HA	1:A:82:ASN:HB3	18	0.21
(2,271)	1:A:81:LYS:HA	1:A:82:ASN:HB3	18	0.21
(1,6730)	1:A:77:VAL:HA	1:A:83:ASN:HD21	5	0.21
(1,6730)	1:A:77:VAL:HA	1:A:83:ASN:HD22	5	0.21
(1,6602)	1:A:44:ARG:HG2	1:A:45:SER:HB2	6	0.21
(1,6602)	1:A:44:ARG:HG2	1:A:45:SER:HB3	6	0.21
(1,6602)	1:A:44:ARG:HG3	1:A:45:SER:HB2	6	0.21
(1,6602)	1:A:44:ARG:HG3	1:A:45:SER:HB3	6	0.21
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	2	0.21
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	2	0.21
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	2	0.21
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	2	0.21
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	19	0.21
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	19	0.21
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	19	0.21
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	19	0.21
(1,6144)	1:A:103:TYR:HA	1:A:103:TYR:HD1	8	0.21
(1,6144)	1:A:103:TYR:HA	1:A:103:TYR:HD2	8	0.21
(1,3241)	1:A:77:VAL:HA	1:A:83:ASN:HD21	5	0.21
(1,3241)	1:A:77:VAL:HA	1:A:83:ASN:HD22	5	0.21
(1,3113)	1:A:44:ARG:HG2	1:A:45:SER:HB2	6	0.21
(1,3113)	1:A:44:ARG:HG2	1:A:45:SER:HB3	6	0.21
(1,3113)	1:A:44:ARG:HG3	1:A:45:SER:HB2	6	0.21
(1,3113)	1:A:44:ARG:HG3	1:A:45:SER:HB3	6	0.21
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	2	0.21
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	2	0.21
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	2	0.21
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	2	0.21

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	19	0.21
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	19	0.21
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	19	0.21
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	19	0.21
(1,2655)	1:A:103:TYR:HA	1:A:103:TYR:HD1	8	0.21
(1,2655)	1:A:103:TYR:HA	1:A:103:TYR:HD2	8	0.21
(1,718)	1:A:68:THR:HB	1:A:98:ARG:HE	18	0.2
(1,6914)	1:A:126:PHE:HD1	1:A:127:ARG:HG2	16	0.2
(1,6914)	1:A:126:PHE:HD1	1:A:127:ARG:HG3	16	0.2
(1,6914)	1:A:126:PHE:HD2	1:A:127:ARG:HG2	16	0.2
(1,6914)	1:A:126:PHE:HD2	1:A:127:ARG:HG3	16	0.2
(1,6748)	1:A:83:ASN:HD21	1:A:104:GLY:HA2	17	0.2
(1,6748)	1:A:83:ASN:HD22	1:A:104:GLY:HA2	17	0.2
(1,6739)	1:A:80:GLU:HB2	1:A:81:LYS:HD2	4	0.2
(1,6739)	1:A:80:GLU:HB2	1:A:81:LYS:HD3	4	0.2
(1,6739)	1:A:80:GLU:HB3	1:A:81:LYS:HD2	4	0.2
(1,6739)	1:A:80:GLU:HB3	1:A:81:LYS:HD3	4	0.2
(1,6560)	1:A:39:ARG:H	1:A:39:ARG:HG2	15	0.2
(1,6560)	1:A:39:ARG:H	1:A:39:ARG:HG3	15	0.2
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	13	0.2
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	13	0.2
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	13	0.2
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	13	0.2
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD21	14	0.2
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD22	14	0.2
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD23	14	0.2
(1,4207)	1:A:68:THR:HB	1:A:98:ARG:HE	18	0.2
(1,3425)	1:A:126:PHE:HD1	1:A:127:ARG:HG2	16	0.2
(1,3425)	1:A:126:PHE:HD1	1:A:127:ARG:HG3	16	0.2
(1,3425)	1:A:126:PHE:HD2	1:A:127:ARG:HG2	16	0.2
(1,3425)	1:A:126:PHE:HD2	1:A:127:ARG:HG3	16	0.2
(1,3259)	1:A:83:ASN:HD21	1:A:104:GLY:HA2	17	0.2
(1,3259)	1:A:83:ASN:HD22	1:A:104:GLY:HA2	17	0.2
(1,3250)	1:A:80:GLU:HB2	1:A:81:LYS:HD2	4	0.2
(1,3250)	1:A:80:GLU:HB2	1:A:81:LYS:HD3	4	0.2
(1,3250)	1:A:80:GLU:HB3	1:A:81:LYS:HD2	4	0.2
(1,3250)	1:A:80:GLU:HB3	1:A:81:LYS:HD3	4	0.2
(1,3071)	1:A:39:ARG:H	1:A:39:ARG:HG2	15	0.2
(1,3071)	1:A:39:ARG:H	1:A:39:ARG:HG3	15	0.2
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	13	0.2
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	13	0.2
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	13	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	13	0.2
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD21	14	0.2
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD22	14	0.2
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD23	14	0.2
(2,821)	1:A:81:LYS:HA	1:A:82:ASN:HB3	20	0.19
(2,271)	1:A:81:LYS:HA	1:A:82:ASN:HB3	20	0.19
(1,750)	1:A:101:THR:HG21	1:A:104:GLY:H	7	0.19
(1,750)	1:A:101:THR:HG22	1:A:104:GLY:H	7	0.19
(1,750)	1:A:101:THR:HG23	1:A:104:GLY:H	7	0.19
(1,6787)	1:A:95:ARG:HG2	1:A:96:ARG:HG2	4	0.19
(1,6787)	1:A:95:ARG:HG2	1:A:96:ARG:HG3	4	0.19
(1,6787)	1:A:95:ARG:HG3	1:A:96:ARG:HG2	4	0.19
(1,6787)	1:A:95:ARG:HG3	1:A:96:ARG:HG3	4	0.19
(1,5570)	1:A:90:LEU:HG	1:A:97:VAL:HB	12	0.19
(1,4239)	1:A:101:THR:HG21	1:A:104:GLY:H	7	0.19
(1,4239)	1:A:101:THR:HG22	1:A:104:GLY:H	7	0.19
(1,4239)	1:A:101:THR:HG23	1:A:104:GLY:H	7	0.19
(1,3298)	1:A:95:ARG:HG2	1:A:96:ARG:HG2	4	0.19
(1,3298)	1:A:95:ARG:HG2	1:A:96:ARG:HG3	4	0.19
(1,3298)	1:A:95:ARG:HG3	1:A:96:ARG:HG2	4	0.19
(1,3298)	1:A:95:ARG:HG3	1:A:96:ARG:HG3	4	0.19
(1,2081)	1:A:90:LEU:HG	1:A:97:VAL:HB	12	0.19
(1,98)	1:A:20:LEU:H	1:A:21:VAL:HB	11	0.18
(1,8)	1:A:2:ARG:HA	1:A:3:VAL:H	10	0.18
(1,743)	1:A:83:ASN:HB2	1:A:103:TYR:H	13	0.18
(1,743)	1:A:83:ASN:HB3	1:A:103:TYR:H	13	0.18
(1,6748)	1:A:83:ASN:HD21	1:A:104:GLY:HA2	3	0.18
(1,6748)	1:A:83:ASN:HD22	1:A:104:GLY:HA2	3	0.18
(1,6739)	1:A:80:GLU:HB2	1:A:81:LYS:HD2	1	0.18
(1,6739)	1:A:80:GLU:HB2	1:A:81:LYS:HD3	1	0.18
(1,6739)	1:A:80:GLU:HB3	1:A:81:LYS:HD2	1	0.18
(1,6739)	1:A:80:GLU:HB3	1:A:81:LYS:HD3	1	0.18
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	9	0.18
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	9	0.18
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	9	0.18
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	9	0.18
(1,5570)	1:A:90:LEU:HG	1:A:97:VAL:HB	9	0.18
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD21	10	0.18
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD22	10	0.18
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD23	10	0.18
(1,4232)	1:A:83:ASN:HB2	1:A:103:TYR:H	13	0.18
(1,4232)	1:A:83:ASN:HB3	1:A:103:TYR:H	13	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,3587)	1:A:20:LEU:H	1:A:21:VAL:HB	11	0.18
(1,3497)	1:A:2:ARG:HA	1:A:3:VAL:H	10	0.18
(1,3259)	1:A:83:ASN:HD21	1:A:104:GLY:HA2	3	0.18
(1,3259)	1:A:83:ASN:HD22	1:A:104:GLY:HA2	3	0.18
(1,3250)	1:A:80:GLU:HB2	1:A:81:LYS:HD2	1	0.18
(1,3250)	1:A:80:GLU:HB2	1:A:81:LYS:HD3	1	0.18
(1,3250)	1:A:80:GLU:HB3	1:A:81:LYS:HD2	1	0.18
(1,3250)	1:A:80:GLU:HB3	1:A:81:LYS:HD3	1	0.18
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	9	0.18
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	9	0.18
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	9	0.18
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	9	0.18
(1,2081)	1:A:90:LEU:HG	1:A:97:VAL:HB	9	0.18
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD21	10	0.18
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD22	10	0.18
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD23	10	0.18
(1,743)	1:A:83:ASN:HB2	1:A:103:TYR:H	9	0.17
(1,743)	1:A:83:ASN:HB3	1:A:103:TYR:H	9	0.17
(1,6748)	1:A:83:ASN:HD21	1:A:104:GLY:HA2	1	0.17
(1,6748)	1:A:83:ASN:HD22	1:A:104:GLY:HA2	1	0.17
(1,6748)	1:A:83:ASN:HD21	1:A:104:GLY:HA2	4	0.17
(1,6748)	1:A:83:ASN:HD22	1:A:104:GLY:HA2	4	0.17
(1,6748)	1:A:83:ASN:HD21	1:A:104:GLY:HA2	14	0.17
(1,6748)	1:A:83:ASN:HD22	1:A:104:GLY:HA2	14	0.17
(1,5664)	1:A:72:ALA:HB1	1:A:100:GLU:HG3	20	0.17
(1,5664)	1:A:72:ALA:HB2	1:A:100:GLU:HG3	20	0.17
(1,5664)	1:A:72:ALA:HB3	1:A:100:GLU:HG3	20	0.17
(1,558)	1:A:77:VAL:HB	1:A:82:ASN:HD22	14	0.17
(1,5570)	1:A:90:LEU:HG	1:A:97:VAL:HB	15	0.17
(1,5570)	1:A:90:LEU:HG	1:A:97:VAL:HB	18	0.17
(1,4232)	1:A:83:ASN:HB2	1:A:103:TYR:H	9	0.17
(1,4232)	1:A:83:ASN:HB3	1:A:103:TYR:H	9	0.17
(1,4047)	1:A:77:VAL:HB	1:A:82:ASN:HD22	14	0.17
(1,3762)	1:A:45:SER:H	1:A:46:SER:HB2	11	0.17
(1,3259)	1:A:83:ASN:HD21	1:A:104:GLY:HA2	1	0.17
(1,3259)	1:A:83:ASN:HD22	1:A:104:GLY:HA2	1	0.17
(1,3259)	1:A:83:ASN:HD21	1:A:104:GLY:HA2	4	0.17
(1,3259)	1:A:83:ASN:HD22	1:A:104:GLY:HA2	4	0.17
(1,3259)	1:A:83:ASN:HD21	1:A:104:GLY:HA2	14	0.17
(1,3259)	1:A:83:ASN:HD22	1:A:104:GLY:HA2	14	0.17
(1,273)	1:A:45:SER:H	1:A:46:SER:HB2	11	0.17
(1,2175)	1:A:72:ALA:HB1	1:A:100:GLU:HG3	20	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2175)	1:A:72:ALA:HB2	1:A:100:GLU:HG3	20	0.17
(1,2175)	1:A:72:ALA:HB3	1:A:100:GLU:HG3	20	0.17
(1,2081)	1:A:90:LEU:HG	1:A:97:VAL:HB	15	0.17
(1,2081)	1:A:90:LEU:HG	1:A:97:VAL:HB	18	0.17
(1,8)	1:A:2:ARG:HA	1:A:3:VAL:H	13	0.16
(1,6739)	1:A:80:GLU:HB2	1:A:81:LYS:HD2	10	0.16
(1,6739)	1:A:80:GLU:HB2	1:A:81:LYS:HD3	10	0.16
(1,6739)	1:A:80:GLU:HB3	1:A:81:LYS:HD2	10	0.16
(1,6739)	1:A:80:GLU:HB3	1:A:81:LYS:HD3	10	0.16
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	20	0.16
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	20	0.16
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	20	0.16
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	20	0.16
(1,5570)	1:A:90:LEU:HG	1:A:97:VAL:HB	1	0.16
(1,5570)	1:A:90:LEU:HG	1:A:97:VAL:HB	10	0.16
(1,5570)	1:A:90:LEU:HG	1:A:97:VAL:HB	13	0.16
(1,547)	1:A:77:VAL:H	1:A:77:VAL:HB	17	0.16
(1,4036)	1:A:77:VAL:H	1:A:77:VAL:HB	17	0.16
(1,3497)	1:A:2:ARG:HA	1:A:3:VAL:H	13	0.16
(1,3250)	1:A:80:GLU:HB2	1:A:81:LYS:HD2	10	0.16
(1,3250)	1:A:80:GLU:HB2	1:A:81:LYS:HD3	10	0.16
(1,3250)	1:A:80:GLU:HB3	1:A:81:LYS:HD2	10	0.16
(1,3250)	1:A:80:GLU:HB3	1:A:81:LYS:HD3	10	0.16
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	20	0.16
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	20	0.16
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	20	0.16
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	20	0.16
(1,2081)	1:A:90:LEU:HG	1:A:97:VAL:HB	1	0.16
(1,2081)	1:A:90:LEU:HG	1:A:97:VAL:HB	10	0.16
(1,2081)	1:A:90:LEU:HG	1:A:97:VAL:HB	13	0.16
(1,993)	1:A:130:ASN:HD22	1:A:133:GLU:HG3	8	0.15
(1,98)	1:A:20:LEU:H	1:A:21:VAL:HB	15	0.15
(1,750)	1:A:101:THR:HG21	1:A:104:GLY:H	2	0.15
(1,750)	1:A:101:THR:HG22	1:A:104:GLY:H	2	0.15
(1,750)	1:A:101:THR:HG23	1:A:104:GLY:H	2	0.15
(1,6748)	1:A:83:ASN:HD21	1:A:104:GLY:HA2	2	0.15
(1,6748)	1:A:83:ASN:HD22	1:A:104:GLY:HA2	2	0.15
(1,6748)	1:A:83:ASN:HD21	1:A:104:GLY:HA2	5	0.15
(1,6748)	1:A:83:ASN:HD22	1:A:104:GLY:HA2	5	0.15
(1,6745)	1:A:81:LYS:HE2	1:A:102:GLY:HA2	18	0.15
(1,6745)	1:A:81:LYS:HE2	1:A:102:GLY:HA3	18	0.15
(1,6745)	1:A:81:LYS:HE3	1:A:102:GLY:HA2	18	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,6745)	1:A:81:LYS:HE3	1:A:102:GLY:HA3	18	0.15
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	1	0.15
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	1	0.15
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	1	0.15
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	1	0.15
(1,5570)	1:A:90:LEU:HG	1:A:97:VAL:HB	4	0.15
(1,5570)	1:A:90:LEU:HG	1:A:97:VAL:HB	5	0.15
(1,5570)	1:A:90:LEU:HG	1:A:97:VAL:HB	7	0.15
(1,5570)	1:A:90:LEU:HG	1:A:97:VAL:HB	11	0.15
(1,5570)	1:A:90:LEU:HG	1:A:97:VAL:HB	14	0.15
(1,4830)	1:A:19:ARG:HB3	1:A:21:VAL:HG21	17	0.15
(1,4830)	1:A:19:ARG:HB3	1:A:21:VAL:HG22	17	0.15
(1,4830)	1:A:19:ARG:HB3	1:A:21:VAL:HG23	17	0.15
(1,4482)	1:A:130:ASN:HD22	1:A:133:GLU:HG3	8	0.15
(1,4239)	1:A:101:THR:HG21	1:A:104:GLY:H	2	0.15
(1,4239)	1:A:101:THR:HG22	1:A:104:GLY:H	2	0.15
(1,4239)	1:A:101:THR:HG23	1:A:104:GLY:H	2	0.15
(1,3728)	1:A:36:MET:HG2	1:A:40:LEU:H	18	0.15
(1,3587)	1:A:20:LEU:H	1:A:21:VAL:HB	15	0.15
(1,3259)	1:A:83:ASN:HD21	1:A:104:GLY:HA2	2	0.15
(1,3259)	1:A:83:ASN:HD22	1:A:104:GLY:HA2	2	0.15
(1,3259)	1:A:83:ASN:HD21	1:A:104:GLY:HA2	5	0.15
(1,3259)	1:A:83:ASN:HD22	1:A:104:GLY:HA2	5	0.15
(1,3256)	1:A:81:LYS:HE2	1:A:102:GLY:HA2	18	0.15
(1,3256)	1:A:81:LYS:HE2	1:A:102:GLY:HA3	18	0.15
(1,3256)	1:A:81:LYS:HE3	1:A:102:GLY:HA2	18	0.15
(1,3256)	1:A:81:LYS:HE3	1:A:102:GLY:HA3	18	0.15
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	1	0.15
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	1	0.15
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	1	0.15
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	1	0.15
(1,239)	1:A:36:MET:HG2	1:A:40:LEU:H	18	0.15
(1,2081)	1:A:90:LEU:HG	1:A:97:VAL:HB	4	0.15
(1,2081)	1:A:90:LEU:HG	1:A:97:VAL:HB	5	0.15
(1,2081)	1:A:90:LEU:HG	1:A:97:VAL:HB	7	0.15
(1,2081)	1:A:90:LEU:HG	1:A:97:VAL:HB	11	0.15
(1,2081)	1:A:90:LEU:HG	1:A:97:VAL:HB	14	0.15
(1,1341)	1:A:19:ARG:HB3	1:A:21:VAL:HG21	17	0.15
(1,1341)	1:A:19:ARG:HB3	1:A:21:VAL:HG22	17	0.15
(1,1341)	1:A:19:ARG:HB3	1:A:21:VAL:HG23	17	0.15
(2,572)	1:A:44:ARG:HE	1:A:45:SER:HA	4	0.14
(2,22)	1:A:44:ARG:HE	1:A:45:SER:HA	4	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,750)	1:A:101:THR:HG21	1:A:104:GLY:H	11	0.14
(1,750)	1:A:101:THR:HG22	1:A:104:GLY:H	11	0.14
(1,750)	1:A:101:THR:HG23	1:A:104:GLY:H	11	0.14
(1,750)	1:A:101:THR:HG21	1:A:104:GLY:H	18	0.14
(1,750)	1:A:101:THR:HG22	1:A:104:GLY:H	18	0.14
(1,750)	1:A:101:THR:HG23	1:A:104:GLY:H	18	0.14
(1,701)	1:A:96:ARG:HG3	1:A:97:VAL:H	13	0.14
(1,6745)	1:A:81:LYS:HE2	1:A:102:GLY:HA2	6	0.14
(1,6745)	1:A:81:LYS:HE2	1:A:102:GLY:HA3	6	0.14
(1,6745)	1:A:81:LYS:HE3	1:A:102:GLY:HA2	6	0.14
(1,6745)	1:A:81:LYS:HE3	1:A:102:GLY:HA3	6	0.14
(1,6739)	1:A:80:GLU:HB2	1:A:81:LYS:HD2	14	0.14
(1,6739)	1:A:80:GLU:HB2	1:A:81:LYS:HD3	14	0.14
(1,6739)	1:A:80:GLU:HB3	1:A:81:LYS:HD2	14	0.14
(1,6739)	1:A:80:GLU:HB3	1:A:81:LYS:HD3	14	0.14
(1,5570)	1:A:90:LEU:HG	1:A:97:VAL:HB	6	0.14
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD21	2	0.14
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD22	2	0.14
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD23	2	0.14
(1,5)	1:A:3:VAL:H	1:A:3:VAL:HB	20	0.14
(1,4239)	1:A:101:THR:HG21	1:A:104:GLY:H	11	0.14
(1,4239)	1:A:101:THR:HG22	1:A:104:GLY:H	11	0.14
(1,4239)	1:A:101:THR:HG23	1:A:104:GLY:H	11	0.14
(1,4239)	1:A:101:THR:HG21	1:A:104:GLY:H	18	0.14
(1,4239)	1:A:101:THR:HG22	1:A:104:GLY:H	18	0.14
(1,4239)	1:A:101:THR:HG23	1:A:104:GLY:H	18	0.14
(1,4190)	1:A:96:ARG:HG3	1:A:97:VAL:H	13	0.14
(1,3602)	1:A:25:ALA:H	1:A:56:LEU:HB3	2	0.14
(1,3494)	1:A:3:VAL:H	1:A:3:VAL:HB	20	0.14
(1,3256)	1:A:81:LYS:HE2	1:A:102:GLY:HA2	6	0.14
(1,3256)	1:A:81:LYS:HE2	1:A:102:GLY:HA3	6	0.14
(1,3256)	1:A:81:LYS:HE3	1:A:102:GLY:HA2	6	0.14
(1,3256)	1:A:81:LYS:HE3	1:A:102:GLY:HA3	6	0.14
(1,3250)	1:A:80:GLU:HB2	1:A:81:LYS:HD2	14	0.14
(1,3250)	1:A:80:GLU:HB2	1:A:81:LYS:HD3	14	0.14
(1,3250)	1:A:80:GLU:HB3	1:A:81:LYS:HD2	14	0.14
(1,3250)	1:A:80:GLU:HB3	1:A:81:LYS:HD3	14	0.14
(1,2081)	1:A:90:LEU:HG	1:A:97:VAL:HB	6	0.14
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD21	2	0.14
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD22	2	0.14
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD23	2	0.14
(1,113)	1:A:25:ALA:H	1:A:56:LEU:HB3	2	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,750)	1:A:101:THR:HG21	1:A:104:GLY:H	8	0.13
(1,750)	1:A:101:THR:HG22	1:A:104:GLY:H	8	0.13
(1,750)	1:A:101:THR:HG23	1:A:104:GLY:H	8	0.13
(1,750)	1:A:101:THR:HG21	1:A:104:GLY:H	9	0.13
(1,750)	1:A:101:THR:HG22	1:A:104:GLY:H	9	0.13
(1,750)	1:A:101:THR:HG23	1:A:104:GLY:H	9	0.13
(1,750)	1:A:101:THR:HG21	1:A:104:GLY:H	10	0.13
(1,750)	1:A:101:THR:HG22	1:A:104:GLY:H	10	0.13
(1,750)	1:A:101:THR:HG23	1:A:104:GLY:H	10	0.13
(1,750)	1:A:101:THR:HG21	1:A:104:GLY:H	14	0.13
(1,750)	1:A:101:THR:HG22	1:A:104:GLY:H	14	0.13
(1,750)	1:A:101:THR:HG23	1:A:104:GLY:H	14	0.13
(1,750)	1:A:101:THR:HG21	1:A:104:GLY:H	15	0.13
(1,750)	1:A:101:THR:HG22	1:A:104:GLY:H	15	0.13
(1,750)	1:A:101:THR:HG23	1:A:104:GLY:H	15	0.13
(1,743)	1:A:83:ASN:HB2	1:A:103:TYR:H	18	0.13
(1,743)	1:A:83:ASN:HB3	1:A:103:TYR:H	18	0.13
(1,701)	1:A:96:ARG:HG3	1:A:97:VAL:H	16	0.13
(1,6753)	1:A:84:ASN:HD21	1:A:105:LEU:HD11	18	0.13
(1,6753)	1:A:84:ASN:HD21	1:A:105:LEU:HD12	18	0.13
(1,6753)	1:A:84:ASN:HD21	1:A:105:LEU:HD13	18	0.13
(1,6753)	1:A:84:ASN:HD22	1:A:105:LEU:HD11	18	0.13
(1,6753)	1:A:84:ASN:HD22	1:A:105:LEU:HD12	18	0.13
(1,6753)	1:A:84:ASN:HD22	1:A:105:LEU:HD13	18	0.13
(1,6748)	1:A:83:ASN:HD21	1:A:104:GLY:HA2	7	0.13
(1,6748)	1:A:83:ASN:HD22	1:A:104:GLY:HA2	7	0.13
(1,6745)	1:A:81:LYS:HE2	1:A:102:GLY:HA2	13	0.13
(1,6745)	1:A:81:LYS:HE2	1:A:102:GLY:HA3	13	0.13
(1,6745)	1:A:81:LYS:HE3	1:A:102:GLY:HA2	13	0.13
(1,6745)	1:A:81:LYS:HE3	1:A:102:GLY:HA3	13	0.13
(1,6730)	1:A:77:VAL:HA	1:A:83:ASN:HD21	20	0.13
(1,6730)	1:A:77:VAL:HA	1:A:83:ASN:HD22	20	0.13
(1,6635)	1:A:50:GLU:HG3	1:A:84:ASN:HD21	12	0.13
(1,6635)	1:A:50:GLU:HG3	1:A:84:ASN:HD22	12	0.13
(1,6447)	1:A:17:SER:HB2	1:A:20:LEU:HD21	9	0.13
(1,6447)	1:A:17:SER:HB2	1:A:20:LEU:HD22	9	0.13
(1,6447)	1:A:17:SER:HB2	1:A:20:LEU:HD23	9	0.13
(1,6447)	1:A:17:SER:HB3	1:A:20:LEU:HD21	9	0.13
(1,6447)	1:A:17:SER:HB3	1:A:20:LEU:HD22	9	0.13
(1,6447)	1:A:17:SER:HB3	1:A:20:LEU:HD23	9	0.13
(1,6393)	1:A:6:PRO:HG2	1:A:7:GLU:H	14	0.13
(1,6393)	1:A:6:PRO:HG3	1:A:7:GLU:H	14	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,60)	1:A:12:VAL:H	1:A:71:LEU:HD11	7	0.13
(1,60)	1:A:12:VAL:H	1:A:71:LEU:HD12	7	0.13
(1,60)	1:A:12:VAL:H	1:A:71:LEU:HD13	7	0.13
(1,5570)	1:A:90:LEU:HG	1:A:97:VAL:HB	2	0.13
(1,5460)	1:A:82:ASN:HB3	1:A:84:ASN:H	9	0.13
(1,5460)	1:A:82:ASN:HB3	1:A:84:ASN:H	15	0.13
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD21	13	0.13
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD22	13	0.13
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD23	13	0.13
(1,5)	1:A:3:VAL:H	1:A:3:VAL:HB	13	0.13
(1,4963)	1:A:31:ALA:HA	1:A:34:GLU:HB2	13	0.13
(1,4963)	1:A:31:ALA:HA	1:A:34:GLU:HB2	15	0.13
(1,4830)	1:A:19:ARG:HB3	1:A:21:VAL:HG21	18	0.13
(1,4830)	1:A:19:ARG:HB3	1:A:21:VAL:HG22	18	0.13
(1,4830)	1:A:19:ARG:HB3	1:A:21:VAL:HG23	18	0.13
(1,4619)	1:A:51:PHE:HZ	1:A:143:GLN:H	7	0.13
(1,4239)	1:A:101:THR:HG21	1:A:104:GLY:H	8	0.13
(1,4239)	1:A:101:THR:HG22	1:A:104:GLY:H	8	0.13
(1,4239)	1:A:101:THR:HG23	1:A:104:GLY:H	8	0.13
(1,4239)	1:A:101:THR:HG21	1:A:104:GLY:H	9	0.13
(1,4239)	1:A:101:THR:HG22	1:A:104:GLY:H	9	0.13
(1,4239)	1:A:101:THR:HG23	1:A:104:GLY:H	9	0.13
(1,4239)	1:A:101:THR:HG21	1:A:104:GLY:H	10	0.13
(1,4239)	1:A:101:THR:HG22	1:A:104:GLY:H	10	0.13
(1,4239)	1:A:101:THR:HG23	1:A:104:GLY:H	10	0.13
(1,4239)	1:A:101:THR:HG21	1:A:104:GLY:H	14	0.13
(1,4239)	1:A:101:THR:HG22	1:A:104:GLY:H	14	0.13
(1,4239)	1:A:101:THR:HG23	1:A:104:GLY:H	14	0.13
(1,4239)	1:A:101:THR:HG21	1:A:104:GLY:H	15	0.13
(1,4239)	1:A:101:THR:HG22	1:A:104:GLY:H	15	0.13
(1,4239)	1:A:101:THR:HG23	1:A:104:GLY:H	15	0.13
(1,4232)	1:A:83:ASN:HB2	1:A:103:TYR:H	18	0.13
(1,4232)	1:A:83:ASN:HB3	1:A:103:TYR:H	18	0.13
(1,4190)	1:A:96:ARG:HG3	1:A:97:VAL:H	16	0.13
(1,3602)	1:A:25:ALA:H	1:A:56:LEU:HB3	3	0.13
(1,3549)	1:A:12:VAL:H	1:A:71:LEU:HD11	7	0.13
(1,3549)	1:A:12:VAL:H	1:A:71:LEU:HD12	7	0.13
(1,3549)	1:A:12:VAL:H	1:A:71:LEU:HD13	7	0.13
(1,3494)	1:A:3:VAL:H	1:A:3:VAL:HB	13	0.13
(1,3264)	1:A:84:ASN:HD21	1:A:105:LEU:HD11	18	0.13
(1,3264)	1:A:84:ASN:HD21	1:A:105:LEU:HD12	18	0.13
(1,3264)	1:A:84:ASN:HD21	1:A:105:LEU:HD13	18	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,3264)	1:A:84:ASN:HD22	1:A:105:LEU:HD11	18	0.13
(1,3264)	1:A:84:ASN:HD22	1:A:105:LEU:HD12	18	0.13
(1,3264)	1:A:84:ASN:HD22	1:A:105:LEU:HD13	18	0.13
(1,3259)	1:A:83:ASN:HD21	1:A:104:GLY:HA2	7	0.13
(1,3259)	1:A:83:ASN:HD22	1:A:104:GLY:HA2	7	0.13
(1,3256)	1:A:81:LYS:HE2	1:A:102:GLY:HA2	13	0.13
(1,3256)	1:A:81:LYS:HE2	1:A:102:GLY:HA3	13	0.13
(1,3256)	1:A:81:LYS:HE3	1:A:102:GLY:HA2	13	0.13
(1,3256)	1:A:81:LYS:HE3	1:A:102:GLY:HA3	13	0.13
(1,3241)	1:A:77:VAL:HA	1:A:83:ASN:HD21	20	0.13
(1,3241)	1:A:77:VAL:HA	1:A:83:ASN:HD22	20	0.13
(1,3146)	1:A:50:GLU:HG3	1:A:84:ASN:HD21	12	0.13
(1,3146)	1:A:50:GLU:HG3	1:A:84:ASN:HD22	12	0.13
(1,2958)	1:A:17:SER:HB2	1:A:20:LEU:HD21	9	0.13
(1,2958)	1:A:17:SER:HB2	1:A:20:LEU:HD22	9	0.13
(1,2958)	1:A:17:SER:HB2	1:A:20:LEU:HD23	9	0.13
(1,2958)	1:A:17:SER:HB3	1:A:20:LEU:HD21	9	0.13
(1,2958)	1:A:17:SER:HB3	1:A:20:LEU:HD22	9	0.13
(1,2958)	1:A:17:SER:HB3	1:A:20:LEU:HD23	9	0.13
(1,2904)	1:A:6:PRO:HG2	1:A:7:GLU:H	14	0.13
(1,2904)	1:A:6:PRO:HG3	1:A:7:GLU:H	14	0.13
(1,2081)	1:A:90:LEU:HG	1:A:97:VAL:HB	2	0.13
(1,1971)	1:A:82:ASN:HB3	1:A:84:ASN:H	9	0.13
(1,1971)	1:A:82:ASN:HB3	1:A:84:ASN:H	15	0.13
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD21	13	0.13
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD22	13	0.13
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD23	13	0.13
(1,1474)	1:A:31:ALA:HA	1:A:34:GLU:HB2	13	0.13
(1,1474)	1:A:31:ALA:HA	1:A:34:GLU:HB2	15	0.13
(1,1341)	1:A:19:ARG:HB3	1:A:21:VAL:HG21	18	0.13
(1,1341)	1:A:19:ARG:HB3	1:A:21:VAL:HG22	18	0.13
(1,1341)	1:A:19:ARG:HB3	1:A:21:VAL:HG23	18	0.13
(1,1130)	1:A:51:PHE:HZ	1:A:143:GLN:H	7	0.13
(1,113)	1:A:25:ALA:H	1:A:56:LEU:HB3	3	0.13
(1,993)	1:A:130:ASN:HD22	1:A:133:GLU:HG3	20	0.12
(1,750)	1:A:101:THR:HG21	1:A:104:GLY:H	3	0.12
(1,750)	1:A:101:THR:HG22	1:A:104:GLY:H	3	0.12
(1,750)	1:A:101:THR:HG23	1:A:104:GLY:H	3	0.12
(1,750)	1:A:101:THR:HG21	1:A:104:GLY:H	5	0.12
(1,750)	1:A:101:THR:HG22	1:A:104:GLY:H	5	0.12
(1,750)	1:A:101:THR:HG23	1:A:104:GLY:H	5	0.12
(1,743)	1:A:83:ASN:HB2	1:A:103:TYR:H	11	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,743)	1:A:83:ASN:HB3	1:A:103:TYR:H	11	0.12
(1,743)	1:A:83:ASN:HB2	1:A:103:TYR:H	15	0.12
(1,743)	1:A:83:ASN:HB3	1:A:103:TYR:H	15	0.12
(1,701)	1:A:96:ARG:HG3	1:A:97:VAL:H	1	0.12
(1,6878)	1:A:120:ASP:HB2	1:A:141:ALA:HB1	11	0.12
(1,6878)	1:A:120:ASP:HB2	1:A:141:ALA:HB2	11	0.12
(1,6878)	1:A:120:ASP:HB2	1:A:141:ALA:HB3	11	0.12
(1,6878)	1:A:120:ASP:HB3	1:A:141:ALA:HB1	11	0.12
(1,6878)	1:A:120:ASP:HB3	1:A:141:ALA:HB2	11	0.12
(1,6878)	1:A:120:ASP:HB3	1:A:141:ALA:HB3	11	0.12
(1,6815)	1:A:101:THR:HG21	1:A:106:GLU:HG2	4	0.12
(1,6815)	1:A:101:THR:HG21	1:A:106:GLU:HG3	4	0.12
(1,6815)	1:A:101:THR:HG22	1:A:106:GLU:HG2	4	0.12
(1,6815)	1:A:101:THR:HG22	1:A:106:GLU:HG3	4	0.12
(1,6815)	1:A:101:THR:HG23	1:A:106:GLU:HG2	4	0.12
(1,6815)	1:A:101:THR:HG23	1:A:106:GLU:HG3	4	0.12
(1,6765)	1:A:91:VAL:HG11	1:A:96:ARG:HD2	9	0.12
(1,6765)	1:A:91:VAL:HG11	1:A:96:ARG:HD3	9	0.12
(1,6765)	1:A:91:VAL:HG12	1:A:96:ARG:HD2	9	0.12
(1,6765)	1:A:91:VAL:HG12	1:A:96:ARG:HD3	9	0.12
(1,6765)	1:A:91:VAL:HG13	1:A:96:ARG:HD2	9	0.12
(1,6765)	1:A:91:VAL:HG13	1:A:96:ARG:HD3	9	0.12
(1,6748)	1:A:83:ASN:HD21	1:A:104:GLY:HA2	8	0.12
(1,6748)	1:A:83:ASN:HD22	1:A:104:GLY:HA2	8	0.12
(1,6185)	1:A:92:LEU:HB2	1:A:131:TYR:HE1	5	0.12
(1,6185)	1:A:92:LEU:HB2	1:A:131:TYR:HE2	5	0.12
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	17	0.12
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	17	0.12
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	17	0.12
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	17	0.12
(1,6142)	1:A:103:TYR:H	1:A:103:TYR:HD1	6	0.12
(1,6142)	1:A:103:TYR:H	1:A:103:TYR:HD2	6	0.12
(1,5570)	1:A:90:LEU:HG	1:A:97:VAL:HB	3	0.12
(1,5570)	1:A:90:LEU:HG	1:A:97:VAL:HB	16	0.12
(1,5570)	1:A:90:LEU:HG	1:A:97:VAL:HB	17	0.12
(1,5570)	1:A:90:LEU:HG	1:A:97:VAL:HB	19	0.12
(1,5460)	1:A:82:ASN:HB3	1:A:84:ASN:H	11	0.12
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD21	8	0.12
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD22	8	0.12
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD23	8	0.12
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD21	9	0.12
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD22	9	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD23	9	0.12
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD21	12	0.12
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD22	12	0.12
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD23	12	0.12
(1,4818)	1:A:13:GLN:HG3	1:A:17:SER:HA	11	0.12
(1,4690)	1:A:150:LEU:HD21	1:A:151:GLU:H	13	0.12
(1,4690)	1:A:150:LEU:HD22	1:A:151:GLU:H	13	0.12
(1,4690)	1:A:150:LEU:HD23	1:A:151:GLU:H	13	0.12
(1,4689)	1:A:150:LEU:H	1:A:151:GLU:H	9	0.12
(1,4623)	1:A:42:ALA:HB1	1:A:143:GLN:HE21	7	0.12
(1,4623)	1:A:42:ALA:HB2	1:A:143:GLN:HE21	7	0.12
(1,4623)	1:A:42:ALA:HB3	1:A:143:GLN:HE21	7	0.12
(1,4619)	1:A:51:PHE:HZ	1:A:143:GLN:H	4	0.12
(1,4482)	1:A:130:ASN:HD22	1:A:133:GLU:HG3	20	0.12
(1,4239)	1:A:101:THR:HG21	1:A:104:GLY:H	3	0.12
(1,4239)	1:A:101:THR:HG22	1:A:104:GLY:H	3	0.12
(1,4239)	1:A:101:THR:HG23	1:A:104:GLY:H	3	0.12
(1,4239)	1:A:101:THR:HG21	1:A:104:GLY:H	5	0.12
(1,4239)	1:A:101:THR:HG22	1:A:104:GLY:H	5	0.12
(1,4239)	1:A:101:THR:HG23	1:A:104:GLY:H	5	0.12
(1,4232)	1:A:83:ASN:HB2	1:A:103:TYR:H	11	0.12
(1,4232)	1:A:83:ASN:HB3	1:A:103:TYR:H	11	0.12
(1,4232)	1:A:83:ASN:HB2	1:A:103:TYR:H	15	0.12
(1,4232)	1:A:83:ASN:HB3	1:A:103:TYR:H	15	0.12
(1,4190)	1:A:96:ARG:HG3	1:A:97:VAL:H	1	0.12
(1,3602)	1:A:25:ALA:H	1:A:56:LEU:HB3	1	0.12
(1,3602)	1:A:25:ALA:H	1:A:56:LEU:HB3	8	0.12
(1,3602)	1:A:25:ALA:H	1:A:56:LEU:HB3	11	0.12
(1,3389)	1:A:120:ASP:HB2	1:A:141:ALA:HB1	11	0.12
(1,3389)	1:A:120:ASP:HB2	1:A:141:ALA:HB2	11	0.12
(1,3389)	1:A:120:ASP:HB2	1:A:141:ALA:HB3	11	0.12
(1,3389)	1:A:120:ASP:HB3	1:A:141:ALA:HB1	11	0.12
(1,3389)	1:A:120:ASP:HB3	1:A:141:ALA:HB2	11	0.12
(1,3389)	1:A:120:ASP:HB3	1:A:141:ALA:HB3	11	0.12
(1,3326)	1:A:101:THR:HG21	1:A:106:GLU:HG2	4	0.12
(1,3326)	1:A:101:THR:HG21	1:A:106:GLU:HG3	4	0.12
(1,3326)	1:A:101:THR:HG22	1:A:106:GLU:HG2	4	0.12
(1,3326)	1:A:101:THR:HG22	1:A:106:GLU:HG3	4	0.12
(1,3326)	1:A:101:THR:HG23	1:A:106:GLU:HG2	4	0.12
(1,3326)	1:A:101:THR:HG23	1:A:106:GLU:HG3	4	0.12
(1,3276)	1:A:91:VAL:HG11	1:A:96:ARG:HD2	9	0.12
(1,3276)	1:A:91:VAL:HG11	1:A:96:ARG:HD3	9	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,3276)	1:A:91:VAL:HG12	1:A:96:ARG:HD2	9	0.12
(1,3276)	1:A:91:VAL:HG12	1:A:96:ARG:HD3	9	0.12
(1,3276)	1:A:91:VAL:HG13	1:A:96:ARG:HD2	9	0.12
(1,3276)	1:A:91:VAL:HG13	1:A:96:ARG:HD3	9	0.12
(1,3259)	1:A:83:ASN:HD21	1:A:104:GLY:HA2	8	0.12
(1,3259)	1:A:83:ASN:HD22	1:A:104:GLY:HA2	8	0.12
(1,2696)	1:A:92:LEU:HB2	1:A:131:TYR:HE1	5	0.12
(1,2696)	1:A:92:LEU:HB2	1:A:131:TYR:HE2	5	0.12
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	17	0.12
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	17	0.12
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	17	0.12
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	17	0.12
(1,2653)	1:A:103:TYR:H	1:A:103:TYR:HD1	6	0.12
(1,2653)	1:A:103:TYR:H	1:A:103:TYR:HD2	6	0.12
(1,2081)	1:A:90:LEU:HG	1:A:97:VAL:HB	3	0.12
(1,2081)	1:A:90:LEU:HG	1:A:97:VAL:HB	16	0.12
(1,2081)	1:A:90:LEU:HG	1:A:97:VAL:HB	17	0.12
(1,2081)	1:A:90:LEU:HG	1:A:97:VAL:HB	19	0.12
(1,1971)	1:A:82:ASN:HB3	1:A:84:ASN:H	11	0.12
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD21	8	0.12
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD22	8	0.12
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD23	8	0.12
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD21	9	0.12
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD22	9	0.12
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD23	9	0.12
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD21	12	0.12
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD22	12	0.12
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD23	12	0.12
(1,1329)	1:A:13:GLN:HG3	1:A:17:SER:HA	11	0.12
(1,1201)	1:A:150:LEU:HD21	1:A:151:GLU:H	13	0.12
(1,1201)	1:A:150:LEU:HD22	1:A:151:GLU:H	13	0.12
(1,1201)	1:A:150:LEU:HD23	1:A:151:GLU:H	13	0.12
(1,1200)	1:A:150:LEU:H	1:A:151:GLU:H	9	0.12
(1,1134)	1:A:42:ALA:HB1	1:A:143:GLN:HE21	7	0.12
(1,1134)	1:A:42:ALA:HB2	1:A:143:GLN:HE21	7	0.12
(1,1134)	1:A:42:ALA:HB3	1:A:143:GLN:HE21	7	0.12
(1,1130)	1:A:51:PHE:HZ	1:A:143:GLN:H	4	0.12
(1,113)	1:A:25:ALA:H	1:A:56:LEU:HB3	1	0.12
(1,113)	1:A:25:ALA:H	1:A:56:LEU:HB3	8	0.12
(1,113)	1:A:25:ALA:H	1:A:56:LEU:HB3	11	0.12
(2,7)	1:A:19:ARG:HE	1:A:21:VAL:HG11	9	0.11
(2,7)	1:A:19:ARG:HE	1:A:21:VAL:HG12	9	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,7)	1:A:19:ARG:HE	1:A:21:VAL:HG13	9	0.11
(2,557)	1:A:19:ARG:HE	1:A:21:VAL:HG11	9	0.11
(2,557)	1:A:19:ARG:HE	1:A:21:VAL:HG12	9	0.11
(2,557)	1:A:19:ARG:HE	1:A:21:VAL:HG13	9	0.11
(1,994)	1:A:130:ASN:HD22	1:A:133:GLU:HG2	12	0.11
(1,750)	1:A:101:THR:HG21	1:A:104:GLY:H	1	0.11
(1,750)	1:A:101:THR:HG22	1:A:104:GLY:H	1	0.11
(1,750)	1:A:101:THR:HG23	1:A:104:GLY:H	1	0.11
(1,750)	1:A:101:THR:HG21	1:A:104:GLY:H	19	0.11
(1,750)	1:A:101:THR:HG22	1:A:104:GLY:H	19	0.11
(1,750)	1:A:101:THR:HG23	1:A:104:GLY:H	19	0.11
(1,718)	1:A:68:THR:HB	1:A:98:ARG:HE	2	0.11
(1,703)	1:A:96:ARG:HG2	1:A:97:VAL:H	4	0.11
(1,701)	1:A:96:ARG:HG3	1:A:97:VAL:H	2	0.11
(1,701)	1:A:96:ARG:HG3	1:A:97:VAL:H	8	0.11
(1,701)	1:A:96:ARG:HG3	1:A:97:VAL:H	12	0.11
(1,6765)	1:A:91:VAL:HG11	1:A:96:ARG:HD2	6	0.11
(1,6765)	1:A:91:VAL:HG11	1:A:96:ARG:HD3	6	0.11
(1,6765)	1:A:91:VAL:HG12	1:A:96:ARG:HD2	6	0.11
(1,6765)	1:A:91:VAL:HG12	1:A:96:ARG:HD3	6	0.11
(1,6765)	1:A:91:VAL:HG13	1:A:96:ARG:HD2	6	0.11
(1,6765)	1:A:91:VAL:HG13	1:A:96:ARG:HD3	6	0.11
(1,6739)	1:A:80:GLU:HB2	1:A:81:LYS:HD2	16	0.11
(1,6739)	1:A:80:GLU:HB2	1:A:81:LYS:HD3	16	0.11
(1,6739)	1:A:80:GLU:HB3	1:A:81:LYS:HD2	16	0.11
(1,6739)	1:A:80:GLU:HB3	1:A:81:LYS:HD3	16	0.11
(1,6733)	1:A:77:VAL:HG11	1:A:83:ASN:HD21	10	0.11
(1,6733)	1:A:77:VAL:HG11	1:A:83:ASN:HD22	10	0.11
(1,6733)	1:A:77:VAL:HG12	1:A:83:ASN:HD21	10	0.11
(1,6733)	1:A:77:VAL:HG12	1:A:83:ASN:HD22	10	0.11
(1,6733)	1:A:77:VAL:HG13	1:A:83:ASN:HD21	10	0.11
(1,6733)	1:A:77:VAL:HG13	1:A:83:ASN:HD22	10	0.11
(1,6733)	1:A:77:VAL:HG11	1:A:83:ASN:HD21	15	0.11
(1,6733)	1:A:77:VAL:HG11	1:A:83:ASN:HD22	15	0.11
(1,6733)	1:A:77:VAL:HG12	1:A:83:ASN:HD21	15	0.11
(1,6733)	1:A:77:VAL:HG12	1:A:83:ASN:HD22	15	0.11
(1,6733)	1:A:77:VAL:HG13	1:A:83:ASN:HD21	15	0.11
(1,6733)	1:A:77:VAL:HG13	1:A:83:ASN:HD22	15	0.11
(1,6728)	1:A:76:GLY:HA2	1:A:82:ASN:HD21	3	0.11
(1,6728)	1:A:76:GLY:HA2	1:A:82:ASN:HD22	3	0.11
(1,6728)	1:A:76:GLY:HA3	1:A:82:ASN:HD21	3	0.11
(1,6728)	1:A:76:GLY:HA3	1:A:82:ASN:HD22	3	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,6605)	1:A:44:ARG:HD2	1:A:48:ALA:HA	8	0.11
(1,6605)	1:A:44:ARG:HD3	1:A:48:ALA:HA	8	0.11
(1,6332)	1:A:125:HIS:HD2	1:A:137:GLU:HB2	9	0.11
(1,6152)	1:A:83:ASN:HB2	1:A:103:TYR:HE1	7	0.11
(1,6152)	1:A:83:ASN:HB2	1:A:103:TYR:HE2	7	0.11
(1,6152)	1:A:83:ASN:HB3	1:A:103:TYR:HE1	7	0.11
(1,6152)	1:A:83:ASN:HB3	1:A:103:TYR:HE2	7	0.11
(1,6152)	1:A:83:ASN:HB2	1:A:103:TYR:HE1	11	0.11
(1,6152)	1:A:83:ASN:HB2	1:A:103:TYR:HE2	11	0.11
(1,6152)	1:A:83:ASN:HB3	1:A:103:TYR:HE1	11	0.11
(1,6152)	1:A:83:ASN:HB3	1:A:103:TYR:HE2	11	0.11
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	3	0.11
(1,6151)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	3	0.11
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	3	0.11
(1,6151)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	3	0.11
(1,6142)	1:A:103:TYR:H	1:A:103:TYR:HD1	20	0.11
(1,6142)	1:A:103:TYR:H	1:A:103:TYR:HD2	20	0.11
(1,6130)	1:A:4:TYR:HE1	1:A:56:LEU:HA	5	0.11
(1,6130)	1:A:4:TYR:HE2	1:A:56:LEU:HA	5	0.11
(1,6129)	1:A:4:TYR:HD1	1:A:8:ASP:H	5	0.11
(1,6129)	1:A:4:TYR:HD2	1:A:8:ASP:H	5	0.11
(1,6074)	1:A:151:GLU:H	1:A:152:HIS:HB3	20	0.11
(1,60)	1:A:12:VAL:H	1:A:71:LEU:HD11	17	0.11
(1,60)	1:A:12:VAL:H	1:A:71:LEU:HD12	17	0.11
(1,60)	1:A:12:VAL:H	1:A:71:LEU:HD13	17	0.11
(1,6)	1:A:1:MET:HB2	1:A:3:VAL:H	18	0.11
(1,6)	1:A:1:MET:HB3	1:A:3:VAL:H	18	0.11
(1,558)	1:A:77:VAL:HB	1:A:82:ASN:HD22	16	0.11
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD21	4	0.11
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD22	4	0.11
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD23	4	0.11
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD21	11	0.11
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD22	11	0.11
(1,5228)	1:A:5:LYS:HA	1:A:56:LEU:HD23	11	0.11
(1,4988)	1:A:31:ALA:HA	1:A:34:GLU:HG2	16	0.11
(1,4988)	1:A:31:ALA:HA	1:A:34:GLU:HG3	16	0.11
(1,4854)	1:A:20:LEU:HA	1:A:20:LEU:HD21	13	0.11
(1,4854)	1:A:20:LEU:HA	1:A:20:LEU:HD22	13	0.11
(1,4854)	1:A:20:LEU:HA	1:A:20:LEU:HD23	13	0.11
(1,4818)	1:A:13:GLN:HG3	1:A:17:SER:HA	2	0.11
(1,4619)	1:A:51:PHE:HZ	1:A:143:GLN:H	8	0.11
(1,4619)	1:A:51:PHE:HZ	1:A:143:GLN:H	17	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,4556)	1:A:122:MET:HG3	1:A:138:GLY:H	1	0.11
(1,4483)	1:A:130:ASN:HD22	1:A:133:GLU:HG2	12	0.11
(1,4239)	1:A:101:THR:HG21	1:A:104:GLY:H	1	0.11
(1,4239)	1:A:101:THR:HG22	1:A:104:GLY:H	1	0.11
(1,4239)	1:A:101:THR:HG23	1:A:104:GLY:H	1	0.11
(1,4239)	1:A:101:THR:HG21	1:A:104:GLY:H	19	0.11
(1,4239)	1:A:101:THR:HG22	1:A:104:GLY:H	19	0.11
(1,4239)	1:A:101:THR:HG23	1:A:104:GLY:H	19	0.11
(1,4207)	1:A:68:THR:HB	1:A:98:ARG:HE	2	0.11
(1,4192)	1:A:96:ARG:HG2	1:A:97:VAL:H	4	0.11
(1,4190)	1:A:96:ARG:HG3	1:A:97:VAL:H	2	0.11
(1,4190)	1:A:96:ARG:HG3	1:A:97:VAL:H	8	0.11
(1,4190)	1:A:96:ARG:HG3	1:A:97:VAL:H	12	0.11
(1,4047)	1:A:77:VAL:HB	1:A:82:ASN:HD22	16	0.11
(1,4)	1:A:2:ARG:HG3	1:A:3:VAL:H	20	0.11
(1,3695)	1:A:35:VAL:HB	1:A:37:ASN:H	10	0.11
(1,3602)	1:A:25:ALA:H	1:A:56:LEU:HB3	4	0.11
(1,3602)	1:A:25:ALA:H	1:A:56:LEU:HB3	15	0.11
(1,3549)	1:A:12:VAL:H	1:A:71:LEU:HD11	17	0.11
(1,3549)	1:A:12:VAL:H	1:A:71:LEU:HD12	17	0.11
(1,3549)	1:A:12:VAL:H	1:A:71:LEU:HD13	17	0.11
(1,3495)	1:A:1:MET:HB2	1:A:3:VAL:H	18	0.11
(1,3495)	1:A:1:MET:HB3	1:A:3:VAL:H	18	0.11
(1,3493)	1:A:2:ARG:HG3	1:A:3:VAL:H	20	0.11
(1,3276)	1:A:91:VAL:HG11	1:A:96:ARG:HD2	6	0.11
(1,3276)	1:A:91:VAL:HG11	1:A:96:ARG:HD3	6	0.11
(1,3276)	1:A:91:VAL:HG12	1:A:96:ARG:HD2	6	0.11
(1,3276)	1:A:91:VAL:HG12	1:A:96:ARG:HD3	6	0.11
(1,3276)	1:A:91:VAL:HG13	1:A:96:ARG:HD2	6	0.11
(1,3276)	1:A:91:VAL:HG13	1:A:96:ARG:HD3	6	0.11
(1,3250)	1:A:80:GLU:HB2	1:A:81:LYS:HD2	16	0.11
(1,3250)	1:A:80:GLU:HB2	1:A:81:LYS:HD3	16	0.11
(1,3250)	1:A:80:GLU:HB3	1:A:81:LYS:HD2	16	0.11
(1,3250)	1:A:80:GLU:HB3	1:A:81:LYS:HD3	16	0.11
(1,3244)	1:A:77:VAL:HG11	1:A:83:ASN:HD21	10	0.11
(1,3244)	1:A:77:VAL:HG11	1:A:83:ASN:HD22	10	0.11
(1,3244)	1:A:77:VAL:HG12	1:A:83:ASN:HD21	10	0.11
(1,3244)	1:A:77:VAL:HG12	1:A:83:ASN:HD22	10	0.11
(1,3244)	1:A:77:VAL:HG13	1:A:83:ASN:HD21	10	0.11
(1,3244)	1:A:77:VAL:HG13	1:A:83:ASN:HD22	10	0.11
(1,3244)	1:A:77:VAL:HG11	1:A:83:ASN:HD21	15	0.11
(1,3244)	1:A:77:VAL:HG11	1:A:83:ASN:HD22	15	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,3244)	1:A:77:VAL:HG12	1:A:83:ASN:HD21	15	0.11
(1,3244)	1:A:77:VAL:HG12	1:A:83:ASN:HD22	15	0.11
(1,3244)	1:A:77:VAL:HG13	1:A:83:ASN:HD21	15	0.11
(1,3244)	1:A:77:VAL:HG13	1:A:83:ASN:HD22	15	0.11
(1,3239)	1:A:76:GLY:HA2	1:A:82:ASN:HD21	3	0.11
(1,3239)	1:A:76:GLY:HA2	1:A:82:ASN:HD22	3	0.11
(1,3239)	1:A:76:GLY:HA3	1:A:82:ASN:HD21	3	0.11
(1,3239)	1:A:76:GLY:HA3	1:A:82:ASN:HD22	3	0.11
(1,3116)	1:A:44:ARG:HD2	1:A:48:ALA:HA	8	0.11
(1,3116)	1:A:44:ARG:HD3	1:A:48:ALA:HA	8	0.11
(1,2843)	1:A:125:HIS:HD2	1:A:137:GLU:HB2	9	0.11
(1,2663)	1:A:83:ASN:HB2	1:A:103:TYR:HE1	7	0.11
(1,2663)	1:A:83:ASN:HB2	1:A:103:TYR:HE2	7	0.11
(1,2663)	1:A:83:ASN:HB3	1:A:103:TYR:HE1	7	0.11
(1,2663)	1:A:83:ASN:HB3	1:A:103:TYR:HE2	7	0.11
(1,2663)	1:A:83:ASN:HB2	1:A:103:TYR:HE1	11	0.11
(1,2663)	1:A:83:ASN:HB2	1:A:103:TYR:HE2	11	0.11
(1,2663)	1:A:83:ASN:HB3	1:A:103:TYR:HE1	11	0.11
(1,2663)	1:A:83:ASN:HB3	1:A:103:TYR:HE2	11	0.11
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD1	3	0.11
(1,2662)	1:A:102:GLY:HA2	1:A:103:TYR:HD2	3	0.11
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD1	3	0.11
(1,2662)	1:A:102:GLY:HA3	1:A:103:TYR:HD2	3	0.11
(1,2653)	1:A:103:TYR:H	1:A:103:TYR:HD1	20	0.11
(1,2653)	1:A:103:TYR:H	1:A:103:TYR:HD2	20	0.11
(1,2641)	1:A:4:TYR:HE1	1:A:56:LEU:HA	5	0.11
(1,2641)	1:A:4:TYR:HE2	1:A:56:LEU:HA	5	0.11
(1,2640)	1:A:4:TYR:HD1	1:A:8:ASP:H	5	0.11
(1,2640)	1:A:4:TYR:HD2	1:A:8:ASP:H	5	0.11
(1,2585)	1:A:151:GLU:H	1:A:152:HIS:HB3	20	0.11
(1,206)	1:A:35:VAL:HB	1:A:37:ASN:H	10	0.11
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD21	4	0.11
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD22	4	0.11
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD23	4	0.11
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD21	11	0.11
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD22	11	0.11
(1,1739)	1:A:5:LYS:HA	1:A:56:LEU:HD23	11	0.11
(1,1499)	1:A:31:ALA:HA	1:A:34:GLU:HG2	16	0.11
(1,1499)	1:A:31:ALA:HA	1:A:34:GLU:HG3	16	0.11
(1,1365)	1:A:20:LEU:HA	1:A:20:LEU:HD21	13	0.11
(1,1365)	1:A:20:LEU:HA	1:A:20:LEU:HD22	13	0.11
(1,1365)	1:A:20:LEU:HA	1:A:20:LEU:HD23	13	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1329)	1:A:13:GLN:HG3	1:A:17:SER:HA	2	0.11
(1,1130)	1:A:51:PHE:HZ	1:A:143:GLN:H	8	0.11
(1,1130)	1:A:51:PHE:HZ	1:A:143:GLN:H	17	0.11
(1,113)	1:A:25:ALA:H	1:A:56:LEU:HB3	4	0.11
(1,113)	1:A:25:ALA:H	1:A:56:LEU:HB3	15	0.11
(1,1067)	1:A:122:MET:HG3	1:A:138:GLY:H	1	0.11

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

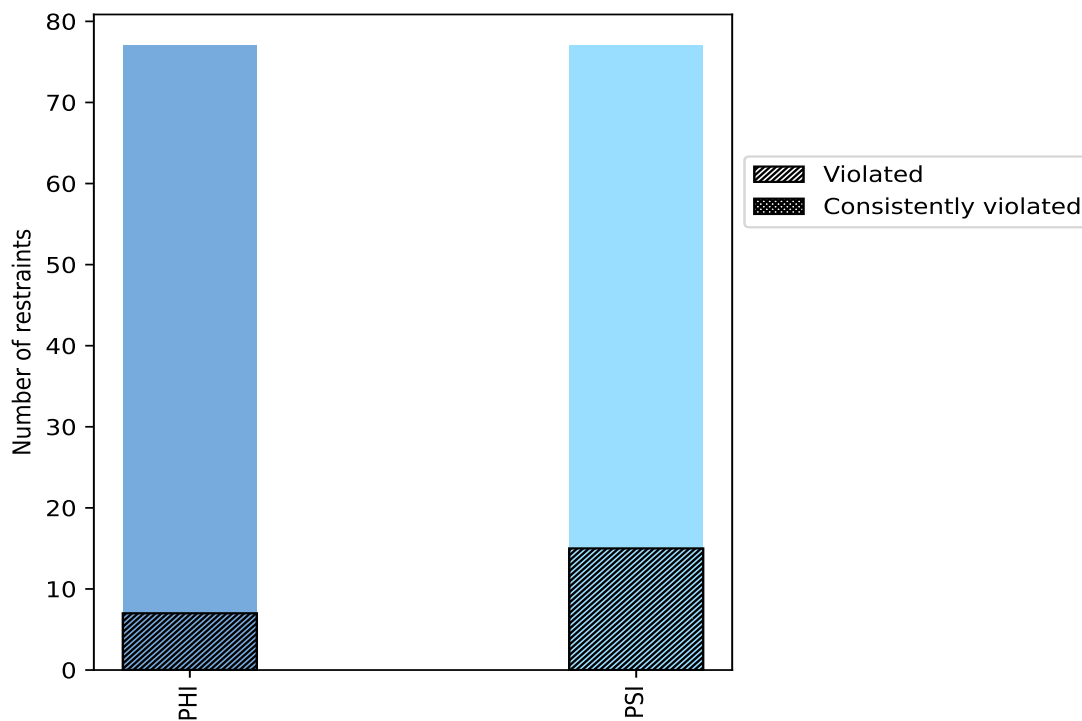
10.1 Summary of dihedral-angle violations [i](#)

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	77	50.0	7	9.1	4.5	0	0.0	0.0
PSI	77	50.0	15	19.5	9.7	0	0.0	0.0
Total	154	100.0	22	14.3	14.3	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](#)



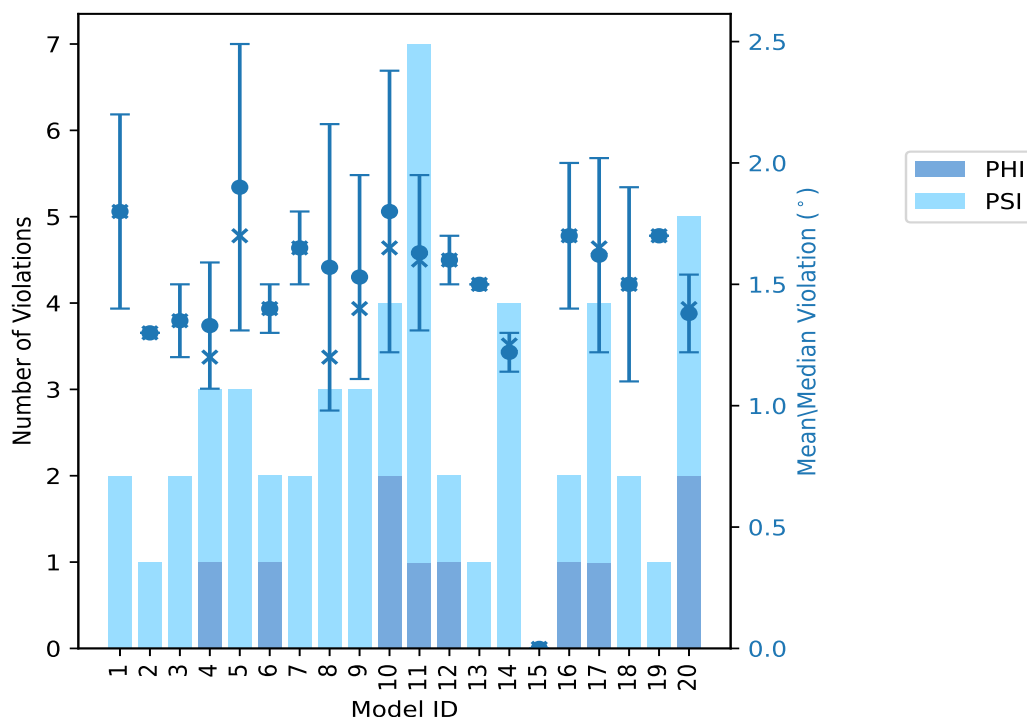
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

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	0	2	2	1.8	2.2	0.4	1.8
2	0	1	1	1.3	1.3	0.0	1.3
3	0	2	2	1.35	1.5	0.15	1.35
4	1	2	3	1.33	1.7	0.26	1.2
5	0	3	3	1.9	2.7	0.59	1.7
6	1	1	2	1.4	1.5	0.1	1.4
7	0	2	2	1.65	1.8	0.15	1.65
8	0	3	3	1.57	2.4	0.59	1.2
9	0	3	3	1.53	2.1	0.42	1.4
10	2	2	4	1.8	2.7	0.58	1.65
11	1	6	7	1.63	2.1	0.32	1.6
12	1	1	2	1.6	1.7	0.1	1.6
13	0	1	1	1.5	1.5	0.0	1.5
14	0	4	4	1.22	1.3	0.08	1.25
15	0	0	0	0.0	0.0	0.0	0.0
16	1	1	2	1.7	2.0	0.3	1.7
17	1	3	4	1.62	2.1	0.4	1.65
18	0	2	2	1.5	1.9	0.4	1.5
19	0	1	1	1.7	1.7	0.0	1.7
20	2	3	5	1.38	1.6	0.16	1.4

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
1	4	5	2	10.0
1	2	3	3	15.0
0	2	2	4	20.0
0	1	1	5	25.0
0	0	0	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	1	1	11	55.0

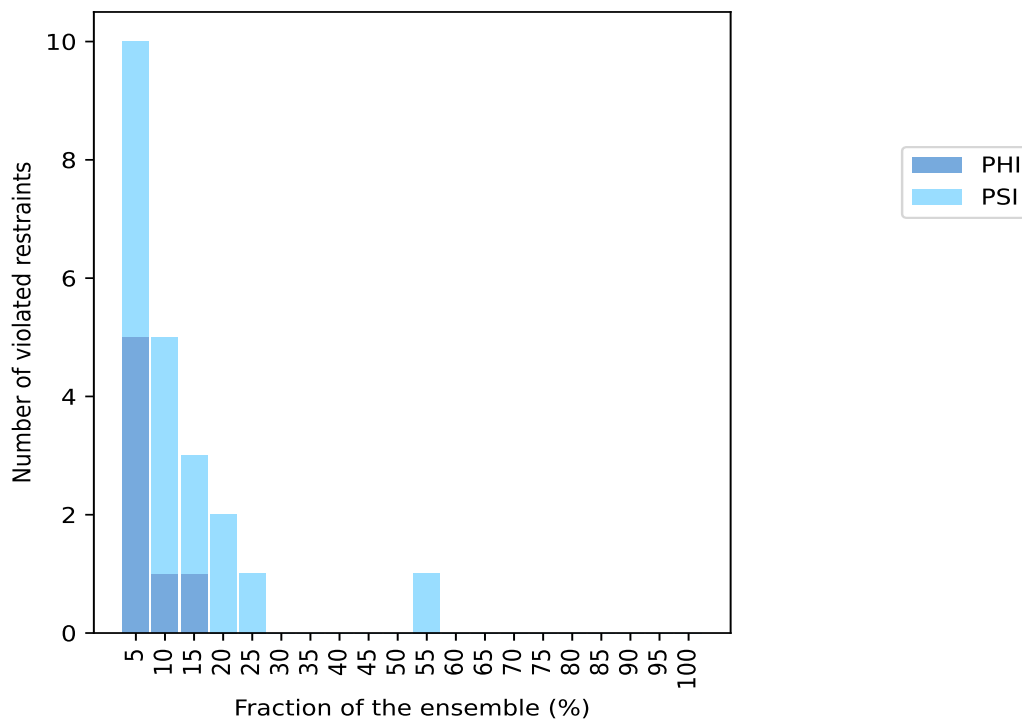
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Number of violated restraints			Fraction of the ensemble	
PHI	PSI	Total	Count ¹	%
0	0	0	12	60.0
0	0	0	13	65.0
0	0	0	14	70.0
0	0	0	15	75.0
0	0	0	16	80.0
0	0	0	17	85.0
0	0	0	18	90.0
0	0	0	19	95.0
0	0	0	20	100.0

¹ Number of models with violations

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

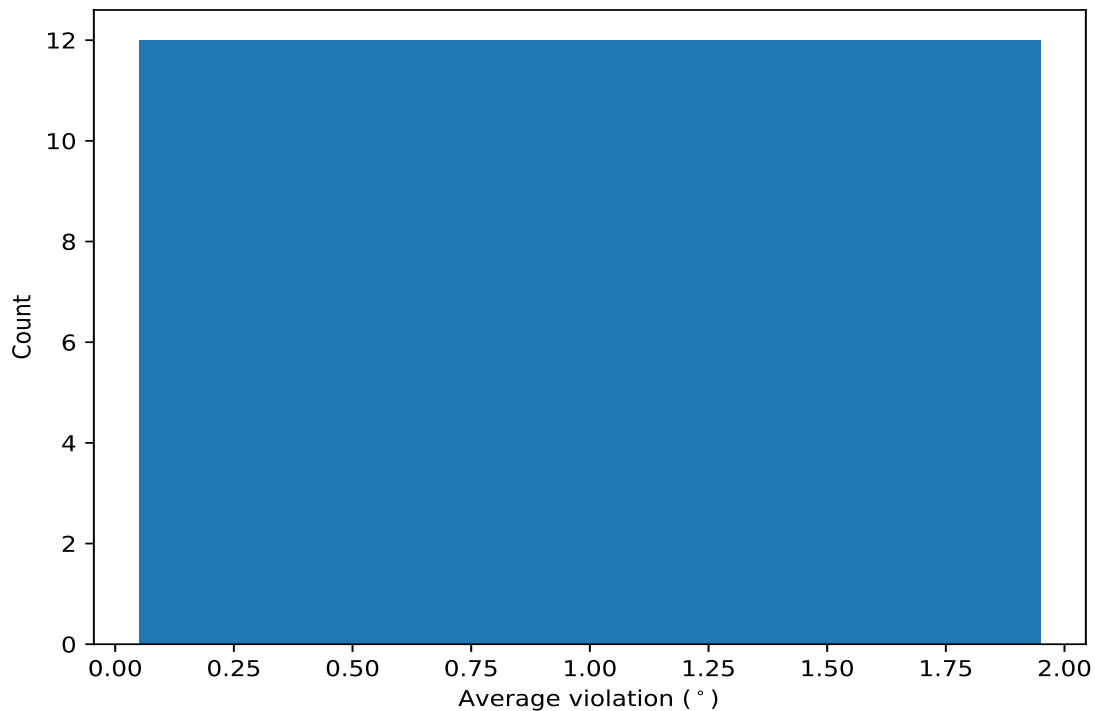


10.4 Most violated dihedral-angle restraints in the ensemble [i](#)

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.

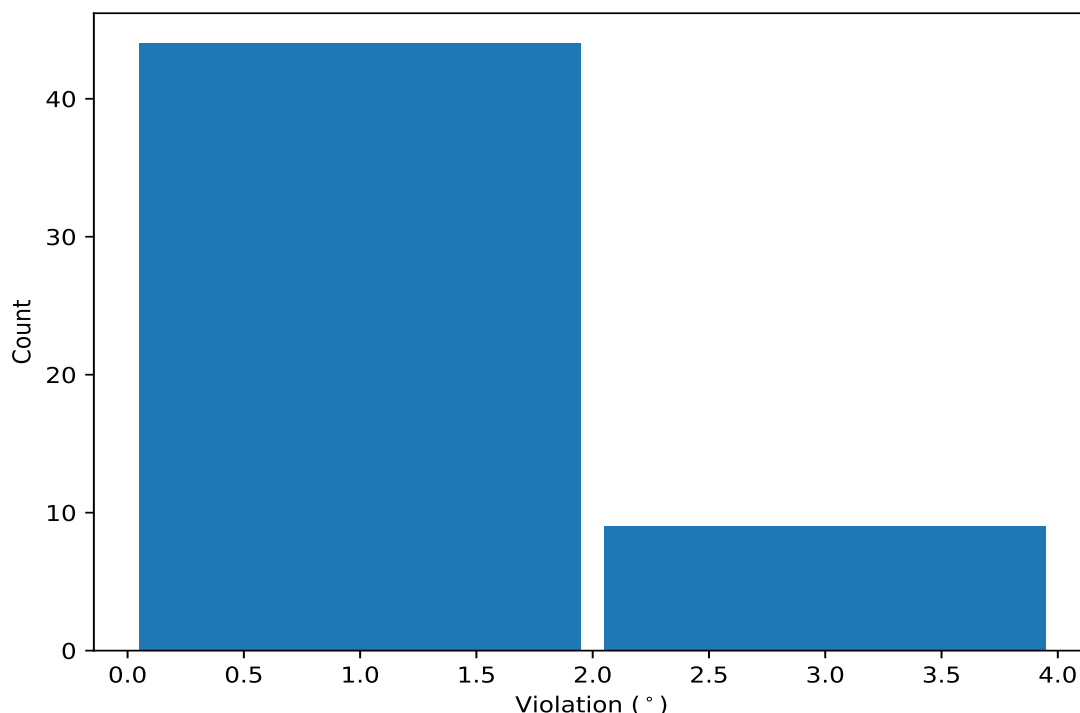
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,38)	1:A:50:GLU:N	1:A:50:GLU:CA	1:A:50:GLU:C	1:A:51:PHE:N	11	1.6	0.35	1.5
(1,92)	1:A:100:GLU:N	1:A:100:GLU:CA	1:A:100:GLU:C	1:A:101:THR:N	5	1.38	0.22	1.3
(1,36)	1:A:44:ARG:N	1:A:44:ARG:CA	1:A:44:ARG:C	1:A:45:SER:N	4	1.9	0.38	1.9
(1,112)	1:A:118:ILE:N	1:A:118:ILE:CA	1:A:118:ILE:C	1:A:119:HIS:N	4	1.48	0.25	1.5
(1,48)	1:A:55:THR:N	1:A:55:THR:CA	1:A:55:THR:C	1:A:56:LEU:N	3	1.87	0.6	1.6
(1,152)	1:A:146:LEU:N	1:A:146:LEU:CA	1:A:146:LEU:C	1:A:147:ASP:N	3	1.8	0.22	1.9
(1,121)	1:A:130:ASN:C	1:A:131:TYR:N	1:A:131:TYR:CA	1:A:131:TYR:C	3	1.1	0.0	1.1
(1,68)	1:A:75:TRP:N	1:A:75:TRP:CA	1:A:75:TRP:C	1:A:76:GLY:N	2	2.0	0.1	2.0
(1,26)	1:A:39:ARG:N	1:A:39:ARG:CA	1:A:39:ARG:C	1:A:40:LEU:N	2	1.4	0.3	1.4
(1,153)	1:A:146:LEU:C	1:A:147:ASP:N	1:A:147:ASP:CA	1:A:147:ASP:C	2	1.35	0.15	1.35
(1,20)	1:A:36:MET:N	1:A:36:MET:CA	1:A:36:MET:C	1:A:37:ASN:N	2	1.25	0.15	1.25
(1,86)	1:A:97:VAL:N	1:A:97:VAL:CA	1:A:97:VAL:C	1:A:98:ARG:N	2	1.25	0.05	1.25

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 (°)
(1,56)	1:A:69:LEU:N	1:A:69:LEU:CA	1:A:69:LEU:C	1:A:70:LYS:N	10	2.7
(1,48)	1:A:55:THR:N	1:A:55:THR:CA	1:A:55:THR:C	1:A:56:LEU:N	5	2.7
(1,36)	1:A:44:ARG:N	1:A:44:ARG:CA	1:A:44:ARG:C	1:A:45:SER:N	8	2.4
(1,38)	1:A:50:GLU:N	1:A:50:GLU:CA	1:A:50:GLU:C	1:A:51:PHE:N	1	2.2
(1,68)	1:A:75:TRP:N	1:A:75:TRP:CA	1:A:75:TRP:C	1:A:76:GLY:N	9	2.1
(1,38)	1:A:50:GLU:N	1:A:50:GLU:CA	1:A:50:GLU:C	1:A:51:PHE:N	17	2.1
(1,36)	1:A:44:ARG:N	1:A:44:ARG:CA	1:A:44:ARG:C	1:A:45:SER:N	11	2.1
(1,38)	1:A:50:GLU:N	1:A:50:GLU:CA	1:A:50:GLU:C	1:A:51:PHE:N	16	2.0
(1,152)	1:A:146:LEU:N	1:A:146:LEU:CA	1:A:146:LEU:C	1:A:147:ASP:N	11	2.0
(1,68)	1:A:75:TRP:N	1:A:75:TRP:CA	1:A:75:TRP:C	1:A:76:GLY:N	18	1.9
(1,152)	1:A:146:LEU:N	1:A:146:LEU:CA	1:A:146:LEU:C	1:A:147:ASP:N	17	1.9
(1,109)	1:A:116:ARG:C	1:A:117:ILE:N	1:A:117:ILE:CA	1:A:117:ILE:C	10	1.9
(1,92)	1:A:100:GLU:N	1:A:100:GLU:CA	1:A:100:GLU:C	1:A:101:THR:N	7	1.8
(1,112)	1:A:118:ILE:N	1:A:118:ILE:CA	1:A:118:ILE:C	1:A:119:HIS:N	11	1.8

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,38)	1:A:50:GLU:N	1:A:50:GLU:CA	1:A:50:GLU:C	1:A:51:PHE:N	4	1.7
(1,38)	1:A:50:GLU:N	1:A:50:GLU:CA	1:A:50:GLU:C	1:A:51:PHE:N	5	1.7
(1,36)	1:A:44:ARG:N	1:A:44:ARG:CA	1:A:44:ARG:C	1:A:45:SER:N	19	1.7
(1,26)	1:A:39:ARG:N	1:A:39:ARG:CA	1:A:39:ARG:C	1:A:40:LEU:N	12	1.7
(1,48)	1:A:55:THR:N	1:A:55:THR:CA	1:A:55:THR:C	1:A:56:LEU:N	20	1.6
(1,14)	1:A:33:GLU:N	1:A:33:GLU:CA	1:A:33:GLU:C	1:A:34:GLU:N	11	1.6
(1,38)	1:A:50:GLU:N	1:A:50:GLU:CA	1:A:50:GLU:C	1:A:51:PHE:N	3	1.5
(1,153)	1:A:146:LEU:C	1:A:147:ASP:N	1:A:147:ASP:CA	1:A:147:ASP:C	12	1.5
(1,152)	1:A:146:LEU:N	1:A:146:LEU:CA	1:A:146:LEU:C	1:A:147:ASP:N	6	1.5
(1,112)	1:A:118:ILE:N	1:A:118:ILE:CA	1:A:118:ILE:C	1:A:119:HIS:N	7	1.5
(1,112)	1:A:118:ILE:N	1:A:118:ILE:CA	1:A:118:ILE:C	1:A:119:HIS:N	13	1.5
(1,92)	1:A:100:GLU:N	1:A:100:GLU:CA	1:A:100:GLU:C	1:A:101:THR:N	1	1.4
(1,45)	1:A:53:VAL:C	1:A:54:VAL:N	1:A:54:VAL:CA	1:A:54:VAL:C	20	1.4
(1,38)	1:A:50:GLU:N	1:A:50:GLU:CA	1:A:50:GLU:C	1:A:51:PHE:N	10	1.4
(1,38)	1:A:50:GLU:N	1:A:50:GLU:CA	1:A:50:GLU:C	1:A:51:PHE:N	20	1.4
(1,36)	1:A:44:ARG:N	1:A:44:ARG:CA	1:A:44:ARG:C	1:A:45:SER:N	20	1.4
(1,20)	1:A:36:MET:N	1:A:36:MET:CA	1:A:36:MET:C	1:A:37:ASN:N	17	1.4
(1,148)	1:A:144:GLN:N	1:A:144:GLN:CA	1:A:144:GLN:C	1:A:145:VAL:N	11	1.4
(1,132)	1:A:136:SER:N	1:A:136:SER:CA	1:A:136:SER:C	1:A:137:GLU:N	9	1.4
(1,117)	1:A:124:PRO:C	1:A:125:HIS:N	1:A:125:HIS:CA	1:A:125:HIS:C	16	1.4
(1,92)	1:A:100:GLU:N	1:A:100:GLU:CA	1:A:100:GLU:C	1:A:101:THR:N	11	1.3
(1,86)	1:A:97:VAL:N	1:A:97:VAL:CA	1:A:97:VAL:C	1:A:98:ARG:N	5	1.3
(1,72)	1:A:86:LEU:N	1:A:86:LEU:CA	1:A:86:LEU:C	1:A:87:LEU:N	14	1.3
(1,48)	1:A:55:THR:N	1:A:55:THR:CA	1:A:55:THR:C	1:A:56:LEU:N	14	1.3
(1,38)	1:A:50:GLU:N	1:A:50:GLU:CA	1:A:50:GLU:C	1:A:51:PHE:N	2	1.3
(1,133)	1:A:136:SER:C	1:A:137:GLU:N	1:A:137:GLU:CA	1:A:137:GLU:C	6	1.3
(1,92)	1:A:100:GLU:N	1:A:100:GLU:CA	1:A:100:GLU:C	1:A:101:THR:N	3	1.2
(1,92)	1:A:100:GLU:N	1:A:100:GLU:CA	1:A:100:GLU:C	1:A:101:THR:N	8	1.2
(1,86)	1:A:97:VAL:N	1:A:97:VAL:CA	1:A:97:VAL:C	1:A:98:ARG:N	4	1.2
(1,38)	1:A:50:GLU:N	1:A:50:GLU:CA	1:A:50:GLU:C	1:A:51:PHE:N	14	1.2
(1,153)	1:A:146:LEU:C	1:A:147:ASP:N	1:A:147:ASP:CA	1:A:147:ASP:C	10	1.2
(1,113)	1:A:118:ILE:C	1:A:119:HIS:N	1:A:119:HIS:CA	1:A:119:HIS:C	11	1.2
(1,38)	1:A:50:GLU:N	1:A:50:GLU:CA	1:A:50:GLU:C	1:A:51:PHE:N	9	1.1
(1,26)	1:A:39:ARG:N	1:A:39:ARG:CA	1:A:39:ARG:C	1:A:40:LEU:N	18	1.1
(1,20)	1:A:36:MET:N	1:A:36:MET:CA	1:A:36:MET:C	1:A:37:ASN:N	14	1.1
(1,121)	1:A:130:ASN:C	1:A:131:TYR:N	1:A:131:TYR:CA	1:A:131:TYR:C	4	1.1
(1,121)	1:A:130:ASN:C	1:A:131:TYR:N	1:A:131:TYR:CA	1:A:131:TYR:C	17	1.1
(1,121)	1:A:130:ASN:C	1:A:131:TYR:N	1:A:131:TYR:CA	1:A:131:TYR:C	20	1.1
(1,112)	1:A:118:ILE:N	1:A:118:ILE:CA	1:A:118:ILE:C	1:A:119:HIS:N	8	1.1