



Full wwPDB NMR Structure Validation Report ⓘ

Dec 24, 2024 – 11:43 AM EST

PDB ID : 2HWT
BMRB ID : 7112
Title : NMR solution structure of the Master-Rep protein nuclease domain (2-95)
from the Faba Bean Necrotic Yellow Virus
Authors : Vega-Rocha, S.; Gronenborn, B.; Gronenborn, A.M.; Campos-Olivas, R.
Deposited on : 2006-08-02

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 : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.40

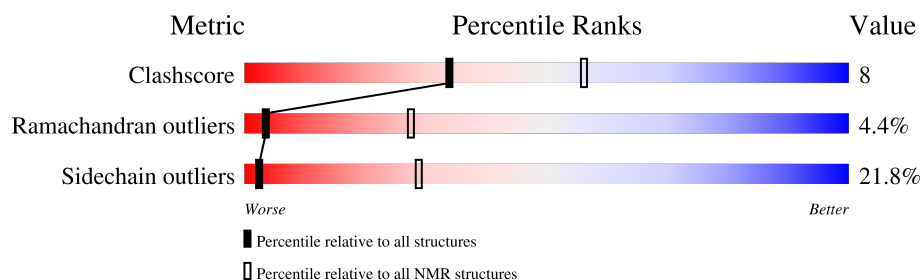
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR


The overall completeness of chemical shifts assignment is 91%.

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



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	210492	14027
Ramachandran outliers	207382	12486
Sidechain outliers	206894	12463

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	94	 71% 26% ..

2 Ensemble composition and analysis

This entry contains 31 models. Model 1 is the overall representative, medoid model (most similar to other models).

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:95 (93)	0.56	1

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 3 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1502 atoms, of which 743 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Putative replicase-associated protein.

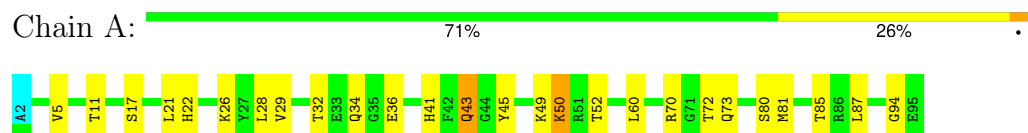
Mol	Chain	Residues	Atoms						Trace
1	A	94	Total	C	H	N	O	S	0
			1502	479	743	135	139	6	

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: Putative replicase-associated protein

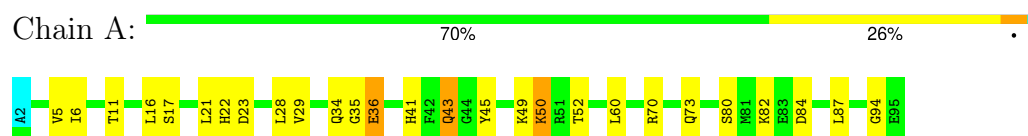


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

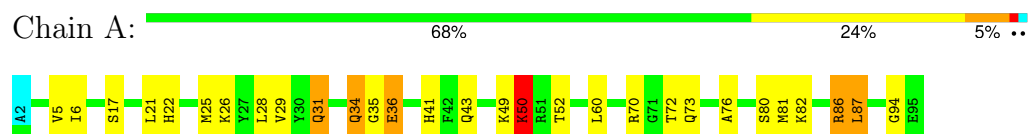
4.2.1 Score per residue for model 1 (medoid)

- Molecule 1: Putative replicase-associated protein



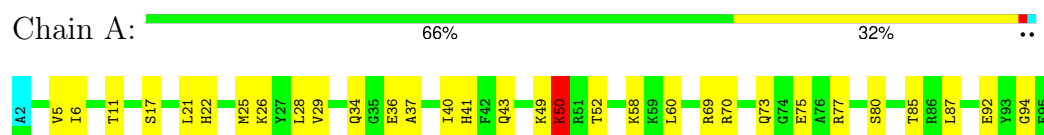
4.2.2 Score per residue for model 2

- Molecule 1: Putative replicase-associated protein



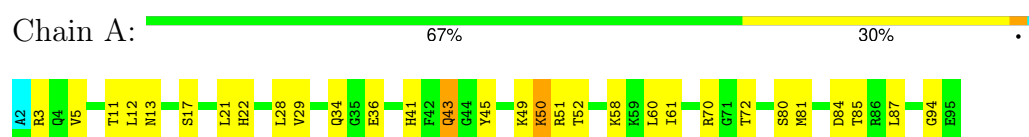
4.2.3 Score per residue for model 3

- Molecule 1: Putative replicase-associated protein



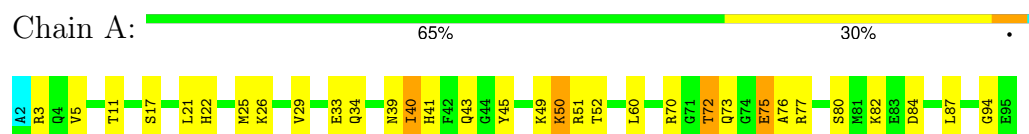
4.2.4 Score per residue for model 4

- Molecule 1: Putative replicase-associated protein



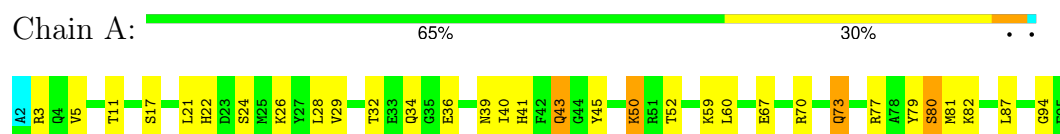
4.2.5 Score per residue for model 5

- Molecule 1: Putative replicase-associated protein



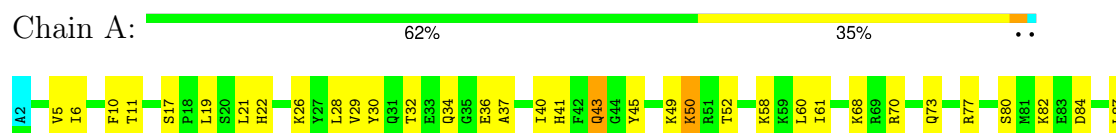
4.2.6 Score per residue for model 6

- Molecule 1: Putative replicase-associated protein



4.2.7 Score per residue for model 7

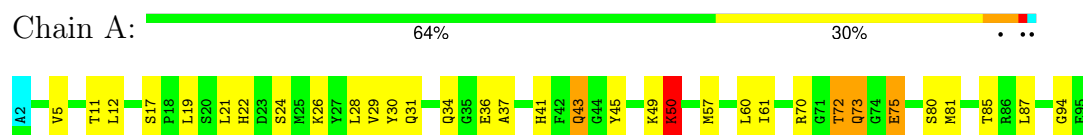
- Molecule 1: Putative replicase-associated protein





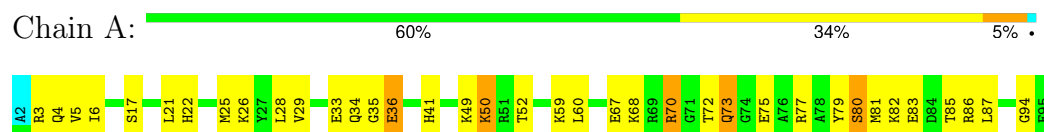
4.2.8 Score per residue for model 8

- Molecule 1: Putative replicase-associated protein



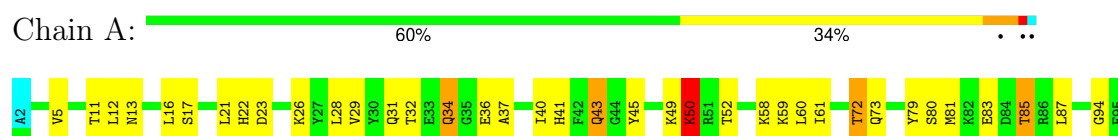
4.2.9 Score per residue for model 9

- Molecule 1: Putative replicase-associated protein



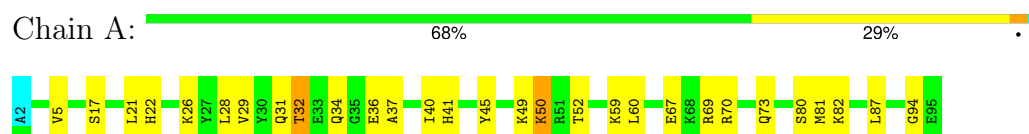
4.2.10 Score per residue for model 10

- Molecule 1: Putative replicase-associated protein



4.2.11 Score per residue for model 11

- Molecule 1: Putative replicase-associated protein



4.2.12 Score per residue for model 12

- Molecule 1: Putative replicase-associated protein

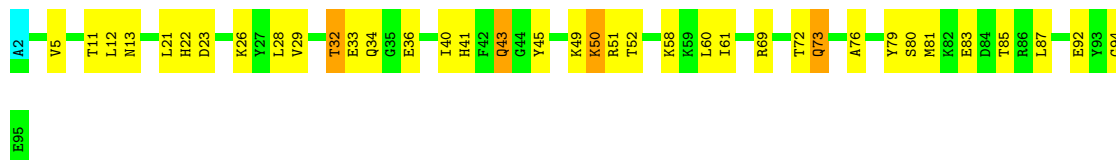




4.2.13 Score per residue for model 13

- Molecule 1: Putative replicase-associated protein

Chain A: 60% 35% ..



4.2.14 Score per residue for model 14

- Molecule 1: Putative replicase-associated protein

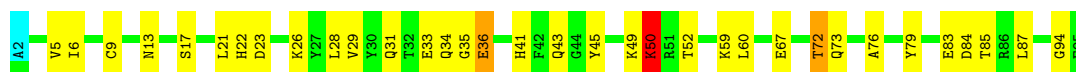
Chain A: 66% 30% ..



4.2.15 Score per residue for model 15

- Molecule 1: Putative replicase-associated protein

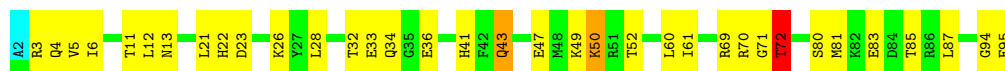
Chain A: 63% 33% ...



4.2.16 Score per residue for model 16

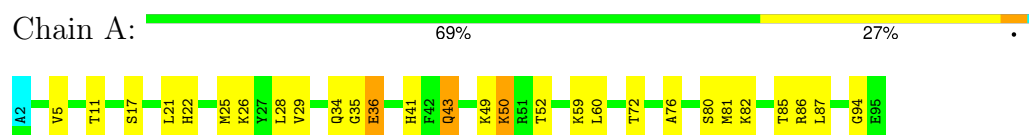
- Molecule 1: Putative replicase-associated protein

Chain A: 62% 34% ...



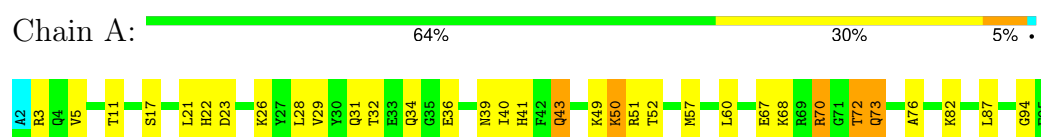
4.2.17 Score per residue for model 17

- Molecule 1: Putative replicase-associated protein



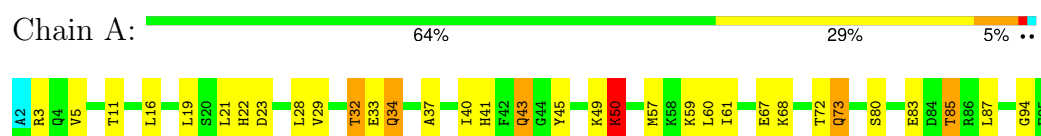
4.2.18 Score per residue for model 18

- Molecule 1: Putative replicase-associated protein



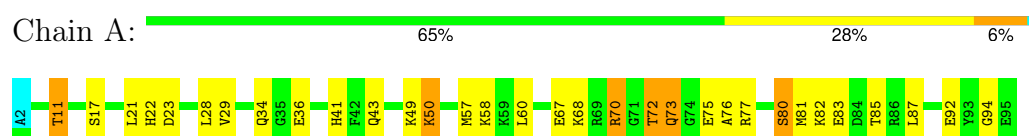
4.2.19 Score per residue for model 19

- Molecule 1: Putative replicase-associated protein



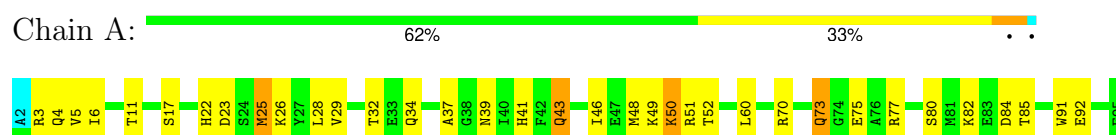
4.2.20 Score per residue for model 20

- Molecule 1: Putative replicase-associated protein



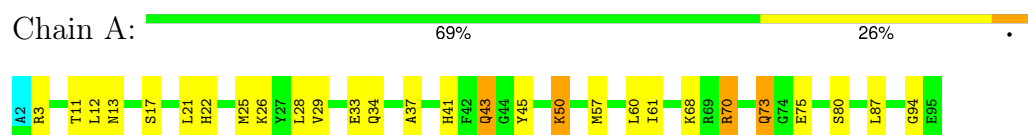
4.2.21 Score per residue for model 21

- Molecule 1: Putative replicase-associated protein



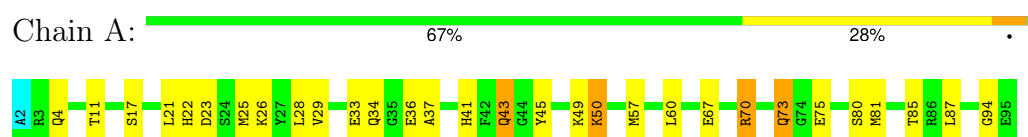
4.2.22 Score per residue for model 22

- Molecule 1: Putative replicase-associated protein



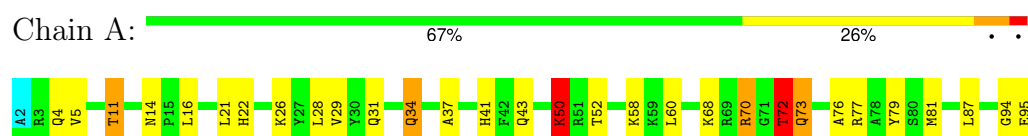
4.2.23 Score per residue for model 23

- Molecule 1: Putative replicase-associated protein



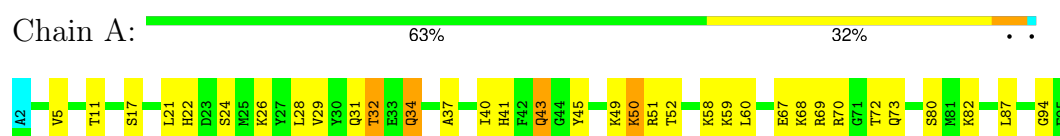
4.2.24 Score per residue for model 24

- Molecule 1: Putative replicase-associated protein



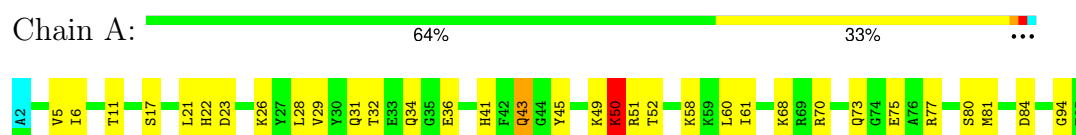
4.2.25 Score per residue for model 25

- Molecule 1: Putative replicase-associated protein



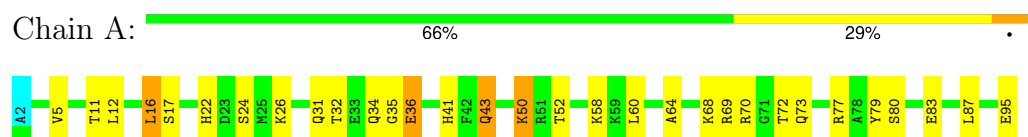
4.2.26 Score per residue for model 26

- Molecule 1: Putative replicase-associated protein



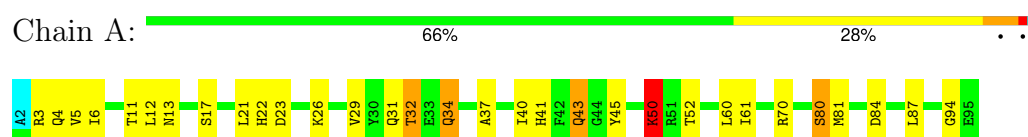
4.2.27 Score per residue for model 27

- Molecule 1: Putative replicase-associated protein



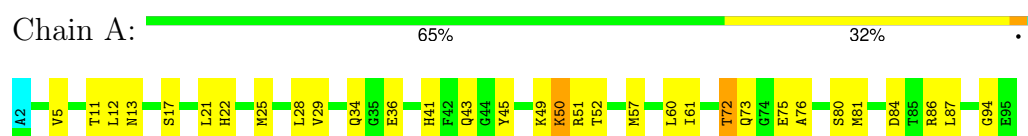
4.2.28 Score per residue for model 28

- Molecule 1: Putative replicase-associated protein



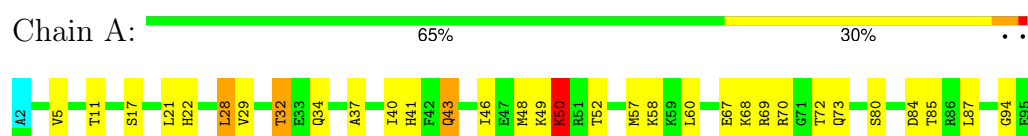
4.2.29 Score per residue for model 29

- Molecule 1: Putative replicase-associated protein



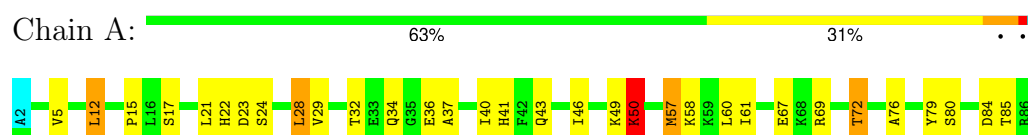
4.2.30 Score per residue for model 30

- Molecule 1: Putative replicase-associated protein



4.2.31 Score per residue for model 31

- Molecule 1: Putative replicase-associated protein



5 Refinement protocol and experimental data overview

The models were refined using the following method: *30 conformers calculated using simulated annealing in torsion angle space with CYANA 2.1 (Models 2-31) and average structure after CYANA variable target function minimisation (Model 1).*

Of the 300 calculated structures, 31 were deposited, based on the following criterion: *target function.*

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

Software name	Classification	Version
CYANA	structure solution	2.1
CYANA	refinement	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	1179
Number of shifts mapped to atoms	1179
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	91%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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	754	738	738	12±3
All	All	23374	22878	22878	371

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 8.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:72:THR:HG23	1:A:76:ALA:HB2	0.84	1.49	15	1
1:A:32:THR:HG21	1:A:40:ILE:HD12	0.73	1.59	28	7
1:A:12:LEU:HD11	1:A:61:ILE:HG21	0.71	1.59	31	1
1:A:22:HIS:CE1	1:A:60:LEU:HD11	0.67	2.23	8	24
1:A:22:HIS:HB2	1:A:60:LEU:HD21	0.66	1.67	19	31
1:A:72:THR:CG2	1:A:76:ALA:HB2	0.65	2.22	20	3
1:A:32:THR:CG2	1:A:40:ILE:HD12	0.64	2.22	13	11
1:A:22:HIS:CG	1:A:60:LEU:HD21	0.63	2.28	8	19
1:A:5:VAL:HG23	1:A:47:GLU:OE1	0.63	1.93	16	1
1:A:21:LEU:HD22	1:A:94:GLY:HA2	0.63	1.70	16	29
1:A:72:THR:HB	1:A:76:ALA:HB2	0.62	1.70	18	2
1:A:11:THR:HG23	1:A:43:GLN:CG	0.62	2.25	29	12
1:A:29:VAL:HG11	1:A:45:TYR:CZ	0.62	2.30	8	13
1:A:5:VAL:HG11	1:A:50:LYS:HA	0.62	1.71	21	28

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:6:ILE:HG21	1:A:70:ARG:HB3	0.61	1.73	9	1
1:A:72:THR:CB	1:A:76:ALA:HB2	0.61	2.26	18	2
1:A:72:THR:O	1:A:76:ALA:HB3	0.60	1.96	17	2
1:A:12:LEU:CD1	1:A:61:ILE:HG21	0.59	2.26	31	1
1:A:11:THR:HG23	1:A:43:GLN:CD	0.59	2.18	13	17
1:A:11:THR:HG23	1:A:43:GLN:HG3	0.58	1.73	21	11
1:A:6:ILE:HG23	1:A:73:GLN:HG3	0.57	1.76	15	2
1:A:28:LEU:HD12	1:A:29:VAL:N	0.57	2.15	22	24
1:A:6:ILE:HG23	1:A:73:GLN:CG	0.56	2.31	2	2
1:A:72:THR:HG22	1:A:75:GLU:CB	0.55	2.31	5	2
1:A:45:TYR:CE2	1:A:76:ALA:HB1	0.55	2.35	15	1
1:A:29:VAL:HG11	1:A:45:TYR:CE2	0.54	2.37	10	4
1:A:12:LEU:HD12	1:A:13:ASN:N	0.54	2.18	13	7
1:A:12:LEU:HD13	1:A:61:ILE:CG2	0.54	2.33	8	1
1:A:60:LEU:C	1:A:61:ILE:HD13	0.54	2.23	22	2
1:A:34:GLN:HG3	1:A:87:LEU:HD11	0.53	1.79	25	2
1:A:12:LEU:HD22	1:A:15:PRO:HB3	0.53	1.81	31	1
1:A:6:ILE:HG21	1:A:70:ARG:HG2	0.53	1.80	16	7
1:A:21:LEU:HD22	1:A:94:GLY:CA	0.52	2.34	31	4
1:A:29:VAL:HG11	1:A:45:TYR:CE1	0.52	2.40	25	5
1:A:19:LEU:HD12	1:A:30:TYR:CB	0.52	2.35	7	2
1:A:29:VAL:HG21	1:A:45:TYR:CZ	0.51	2.40	29	1
1:A:35:GLY:O	1:A:36:GLU:C	0.51	2.49	14	7
1:A:34:GLN:O	1:A:85:THR:HG22	0.50	2.06	19	2
1:A:22:HIS:HB2	1:A:25:MET:HE3	0.50	1.84	22	8
1:A:46:ILE:HD13	1:A:57:MET:HE1	0.49	1.84	30	1
1:A:34:GLN:CD	1:A:87:LEU:HD11	0.48	2.28	19	3
1:A:11:THR:HG23	1:A:43:GLN:NE2	0.48	2.24	30	7
1:A:11:THR:HG23	1:A:43:GLN:HG2	0.48	1.86	20	3
1:A:22:HIS:CB	1:A:60:LEU:HD21	0.48	2.39	29	10
1:A:22:HIS:CG	1:A:60:LEU:HD11	0.47	2.44	14	2
1:A:60:LEU:CB	1:A:61:ILE:HD12	0.47	2.40	12	8
1:A:16:LEU:O	1:A:16:LEU:HD23	0.46	2.10	27	1
1:A:21:LEU:HD13	1:A:94:GLY:HA3	0.46	1.87	7	2
1:A:31:GLN:HG3	1:A:81:MET:HE3	0.46	1.87	8	2
1:A:19:LEU:HD12	1:A:30:TYR:HB3	0.46	1.86	7	1
1:A:72:THR:OG1	1:A:76:ALA:HB2	0.45	2.10	31	2
1:A:46:ILE:HG21	1:A:57:MET:HE1	0.45	1.87	31	1
1:A:21:LEU:HD13	1:A:94:GLY:CA	0.45	2.41	8	1
1:A:60:LEU:O	1:A:61:ILE:HD13	0.44	2.12	22	1
1:A:45:TYR:CD2	1:A:76:ALA:HB1	0.44	2.47	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:31:GLN:HE22	1:A:86:ARG:NE	0.44	2.10	2	1
1:A:22:HIS:ND1	1:A:60:LEU:HD11	0.44	2.27	17	6
1:A:29:VAL:HG21	1:A:45:TYR:CE1	0.43	2.48	8	1
1:A:22:HIS:CD2	1:A:60:LEU:HD11	0.43	2.49	14	3
1:A:12:LEU:CD1	1:A:64:ALA:HB2	0.42	2.45	27	1
1:A:19:LEU:HD22	1:A:61:ILE:HD11	0.42	1.91	19	1
1:A:72:THR:HG22	1:A:75:GLU:HB3	0.42	1.92	5	1
1:A:72:THR:HG22	1:A:75:GLU:HB2	0.42	1.91	8	1
1:A:32:THR:HG23	1:A:40:ILE:HD12	0.42	1.92	31	1
1:A:29:VAL:HG22	1:A:92:GLU:HG3	0.42	1.91	20	1
1:A:29:VAL:HG13	1:A:91:TRP:O	0.41	2.15	21	1
1:A:6:ILE:HG21	1:A:70:ARG:CG	0.41	2.44	16	1
1:A:71:GLY:O	1:A:72:THR:HG23	0.41	2.14	16	1
1:A:19:LEU:HD12	1:A:30:TYR:CG	0.41	2.50	8	1
1:A:79:TYR:O	1:A:81:MET:N	0.41	2.54	6	1
1:A:10:PHE:CE2	1:A:61:ILE:HG21	0.41	2.51	7	1
1:A:25:MET:CE	1:A:46:ILE:HG21	0.40	2.46	21	1
1:A:33:GLU:O	1:A:40:ILE:HG22	0.40	2.17	5	1

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

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	92/94 (98%)	79±2 (86±2%)	9±2 (10±2%)	4±1 (4±1%)	3	27
All	All	2852/2914 (98%)	2442 (86%)	284 (10%)	126 (4%)	3	27

All 11 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	50	LYS	31
1	A	80	SER	23
1	A	73	GLN	20
1	A	36	GLU	19

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Mol	Chain	Res	Type	Models (Total)
1	A	37	ALA	14
1	A	70	ARG	8
1	A	72	THR	6
1	A	81	MET	2
1	A	82	LYS	1
1	A	3	ARG	1
1	A	39	ASN	1

6.3.2 Protein sidechains ⓘ

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	79/79 (100%)	62±3 (78±4%)	17±3 (22±4%)	2	29
All	All	2449/2449 (100%)	1916 (78%)	533 (22%)	2	29

All 50 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	34	GLN	31
1	A	41	HIS	31
1	A	17	SER	27
1	A	49	LYS	25
1	A	52	THR	25
1	A	87	LEU	24
1	A	26	LYS	24
1	A	43	GLN	23
1	A	85	THR	15
1	A	23	ASP	14
1	A	50	LYS	14
1	A	70	ARG	14
1	A	72	THR	14
1	A	73	GLN	14
1	A	58	LYS	12
1	A	68	LYS	12
1	A	82	LYS	11
1	A	84	ASP	11

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Mol	Chain	Res	Type	Models (Total)
1	A	31	GLN	11
1	A	81	MET	11
1	A	75	GLU	11
1	A	3	ARG	11
1	A	67	GLU	11
1	A	32	THR	11
1	A	77	ARG	10
1	A	80	SER	9
1	A	51	ARG	9
1	A	69	ARG	8
1	A	59	LYS	8
1	A	57	MET	8
1	A	83	GLU	8
1	A	33	GLU	7
1	A	79	TYR	7
1	A	24	SER	6
1	A	4	GLN	6
1	A	16	LEU	5
1	A	86	ARG	5
1	A	28	LEU	5
1	A	39	ASN	4
1	A	36	GLU	4
1	A	92	GLU	3
1	A	95	GLU	3
1	A	40	ILE	2
1	A	11	THR	2
1	A	48	MET	2
1	A	9	CYS	1
1	A	13	ASN	1
1	A	25	MET	1
1	A	14	ASN	1
1	A	12	LEU	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no oligosaccharides 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

The completeness of assignment taking into account all chemical shift lists is 91% for the well-defined parts and 91% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping

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	1179
Number of shifts mapped to atoms	1179
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	4

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	94	-0.01 ± 0.24	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	85	-0.56 ± 0.13	Should be checked
$^{13}\text{C}'$	93	0.19 ± 0.20	None needed (< 0.5 ppm)
^{15}N	83	0.01 ± 0.38	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 91%, i.e. 1172 atoms were assigned a chemical shift out of a possible 1292. 0 out of 10 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	453/466 (97%)	185/191 (97%)	185/186 (99%)	83/89 (93%)
Sidechain	623/703 (89%)	423/453 (93%)	192/217 (88%)	8/33 (24%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	96/123 (78%)	53/59 (90%)	35/56 (62%)	8/8 (100%)
Overall	1172/1292 (91%)	661/703 (94%)	412/459 (90%)	99/130 (76%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 91%, i.e. 1179 atoms were assigned a chemical shift out of a possible 1301. 0 out of 10 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	456/471 (97%)	186/193 (96%)	187/188 (99%)	83/90 (92%)
Sidechain	627/707 (89%)	426/456 (93%)	193/218 (89%)	8/33 (24%)
Aromatic	96/123 (78%)	53/59 (90%)	35/56 (62%)	8/8 (100%)
Overall	1179/1301 (91%)	665/708 (94%)	415/462 (90%)	99/131 (76%)

7.1.4 Statistically unusual chemical shifts ⓘ

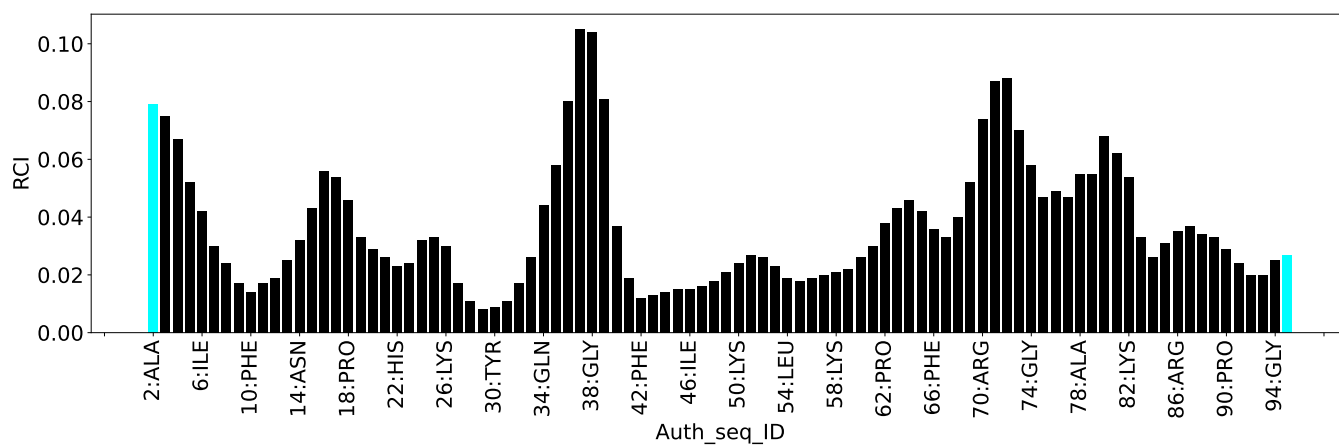
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	57	MET	HG2	-0.41	0.65 – 4.19	-8.0
1	A	57	MET	HB3	-0.44	0.33 – 3.66	-7.3
1	A	89	GLY	HA3	1.44	2.08 – 5.71	-6.8
1	A	15	PRO	HG2	0.29	0.41 – 3.45	-5.4

7.1.5 Random Coil Index (RCI) plots ⓘ

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

Random coil index (RCI) for chain A:



8 NMR restraints analysis

8.1 Conformationally restricting restraints

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

Description	Value
Total distance restraints	1144
Intra-residue ($ i-j =0$)	133
Sequential ($ i-j =1$)	300
Medium range ($ i-j >1$ and $ i-j <5$)	158
Long range ($ i-j \geq 5$)	553
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	110
Number of unmapped restraints	0
Number of restraints per residue	13.3
Number of long range restraints per residue ¹	5.9

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)	12.3	0.2
0.2-0.5 (Medium)	0.5	0.34
>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)	19.6	8.11
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis [i](#)

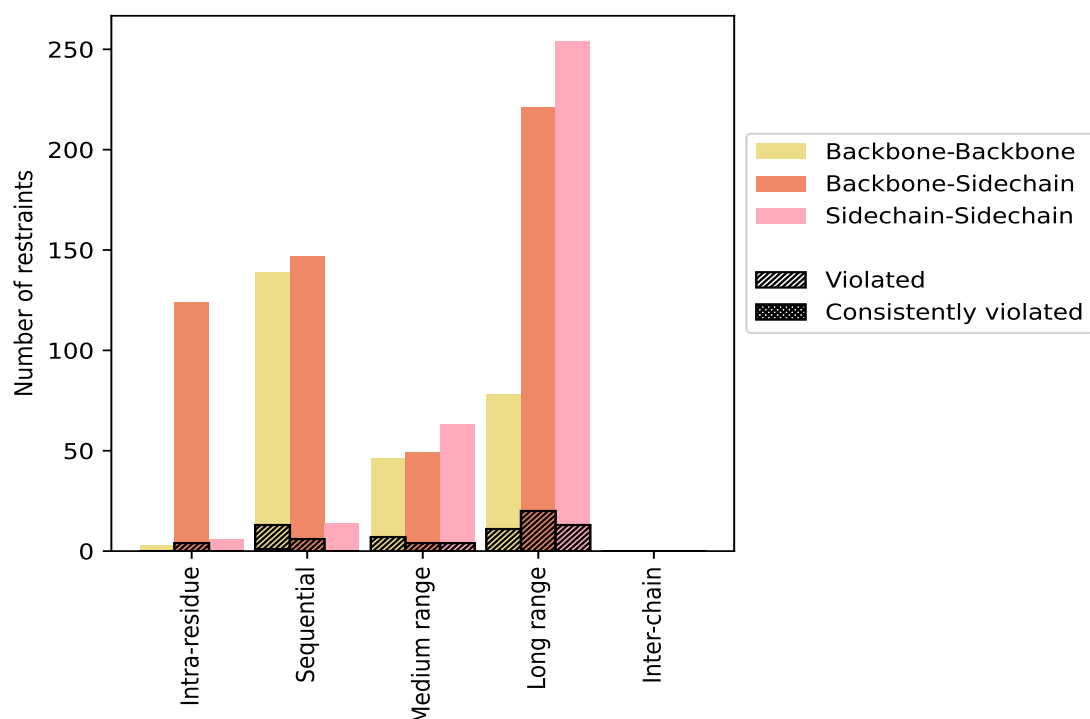
9.1 Summary of distance violations [i](#)

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 ($i-j =0$)	133	11.6	4	3.0	0.3	0	0.0	0.0
Backbone-Backbone	3	0.3	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	124	10.8	4	3.2	0.3	0	0.0	0.0
Sidechain-Sidechain	6	0.5	0	0.0	0.0	0	0.0	0.0
Sequential ($i-j =1$)	300	26.2	19	6.3	1.7	1	0.3	0.1
Backbone-Backbone	139	12.2	13	9.4	1.1	1	0.7	0.1
Backbone-Sidechain	147	12.8	6	4.1	0.5	0	0.0	0.0
Sidechain-Sidechain	14	1.2	0	0.0	0.0	0	0.0	0.0
Medium range ($i-j >1$ & $i-j <5$)	158	13.8	15	9.5	1.3	0	0.0	0.0
Backbone-Backbone	46	4.0	7	15.2	0.6	0	0.0	0.0
Backbone-Sidechain	49	4.3	4	8.2	0.3	0	0.0	0.0
Sidechain-Sidechain	63	5.5	4	6.3	0.3	0	0.0	0.0
Long range ($i-j \geq 5$)	553	48.3	44	8.0	3.8	0	0.0	0.0
Backbone-Backbone	78	6.8	11	14.1	1.0	0	0.0	0.0
Backbone-Sidechain	221	19.3	20	9.0	1.7	0	0.0	0.0
Sidechain-Sidechain	254	22.2	13	5.1	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	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	1144	100.0	82	7.2	7.2	1	0.1	0.1
Backbone-Backbone	266	23.3	31	11.7	2.7	1	0.4	0.1
Backbone-Sidechain	541	47.3	34	6.3	3.0	0	0.0	0.0
Sidechain-Sidechain	337	29.5	17	5.0	1.5	0	0.0	0.0

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

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



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

9.2 Distance violation statistics for each model [i](#)

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

Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
1	0	2	1	1	0	4	0.14	0.2	0.03	0.13
2	0	5	2	8	0	15	0.12	0.2	0.02	0.11
3	0	1	2	3	0	6	0.14	0.2	0.04	0.12
4	0	3	2	3	0	8	0.12	0.2	0.03	0.12
5	1	2	1	5	0	9	0.12	0.2	0.03	0.11
6	1	2	1	5	0	9	0.14	0.2	0.03	0.13
7	0	3	2	6	0	11	0.13	0.2	0.04	0.11
8	0	5	4	7	0	16	0.13	0.2	0.02	0.12
9	0	2	0	4	0	6	0.14	0.2	0.03	0.13
10	0	3	1	6	0	10	0.14	0.24	0.04	0.13

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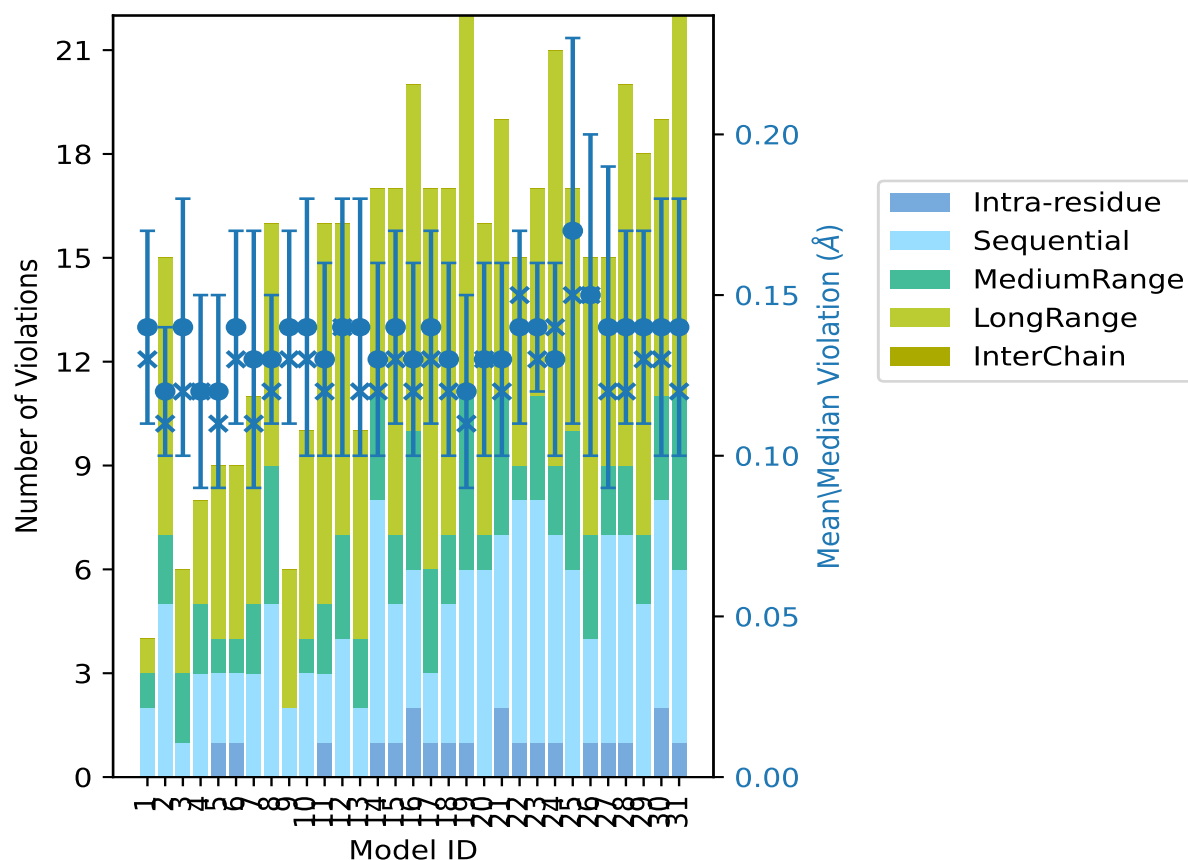
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	1	2	2	11	0	16	0.13	0.2	0.03	0.12
12	0	4	3	9	0	16	0.14	0.26	0.04	0.14
13	0	2	2	6	0	10	0.14	0.21	0.04	0.12
14	1	7	3	6	0	17	0.13	0.2	0.03	0.12
15	1	4	2	10	0	17	0.14	0.2	0.03	0.13
16	2	4	4	10	0	20	0.13	0.2	0.03	0.12
17	1	2	3	11	0	17	0.14	0.22	0.03	0.13
18	1	4	2	10	0	17	0.13	0.2	0.03	0.12
19	1	5	5	11	0	22	0.12	0.2	0.03	0.11
20	0	6	1	9	0	16	0.13	0.2	0.03	0.13
21	2	5	4	8	0	19	0.13	0.2	0.03	0.12
22	1	7	1	6	0	15	0.14	0.2	0.03	0.15
23	1	7	3	6	0	17	0.14	0.2	0.02	0.13
24	1	6	2	12	0	21	0.13	0.2	0.03	0.14
25	0	6	4	7	0	17	0.17	0.34	0.06	0.15
26	1	3	3	8	0	15	0.15	0.29	0.05	0.15
27	1	6	2	6	0	15	0.14	0.26	0.05	0.12
28	1	6	2	11	0	20	0.14	0.2	0.03	0.12
29	0	5	2	11	0	18	0.14	0.22	0.03	0.13
30	2	6	3	8	0	19	0.14	0.28	0.04	0.13
31	1	5	5	11	0	22	0.14	0.25	0.04	0.12

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

⁵Inter-chain restraints, ⁶Standard deviation

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



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

9.3 Distance violation statistics for the ensemble [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, 1062(IR:129, SQ:281, MR:143, LR:509, IC:0) restraints are not violated in the ensemble.

Number of violated restraints						Fraction of the ensemble	
IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total	Count ⁶	%
1	7	3	8	0	19	1	3.2
0	2	2	10	0	14	2	6.5
1	1	1	8	0	11	3	9.7
0	1	3	4	0	8	4	12.9
1	0	3	0	0	4	5	16.1
0	0	1	3	0	4	6	19.4

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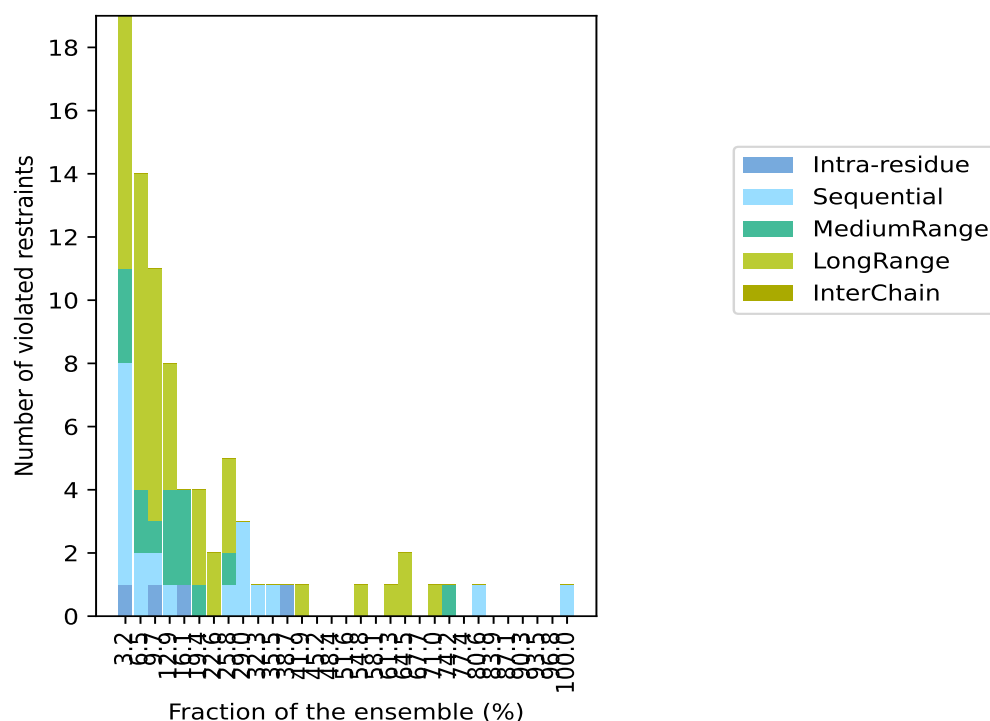
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Number of violated restraints						Fraction of the ensemble	
IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total	Count ⁶	%
0	0	0	2	0	2	7	22.6
0	1	1	3	0	5	8	25.8
0	3	0	0	0	3	9	29.0
0	1	0	0	0	1	10	32.3
0	1	0	0	0	1	11	35.5
1	0	0	0	0	1	12	38.7
0	0	0	1	0	1	13	41.9
0	0	0	0	0	0	14	45.2
0	0	0	0	0	0	15	48.4
0	0	0	0	0	0	16	51.6
0	0	0	1	0	1	17	54.8
0	0	0	0	0	0	18	58.1
0	0	0	1	0	1	19	61.3
0	0	0	2	0	2	20	64.5
0	0	0	0	0	0	21	67.7
0	0	0	1	0	1	22	71.0
0	0	1	0	0	1	23	74.2
0	0	0	0	0	0	24	77.4
0	1	0	0	0	1	25	80.6
0	0	0	0	0	0	26	83.9
0	0	0	0	0	0	27	87.1
0	0	0	0	0	0	28	90.3
0	0	0	0	0	0	29	93.5
0	0	0	0	0	0	30	96.8
0	1	0	0	0	1	31	100.0

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

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

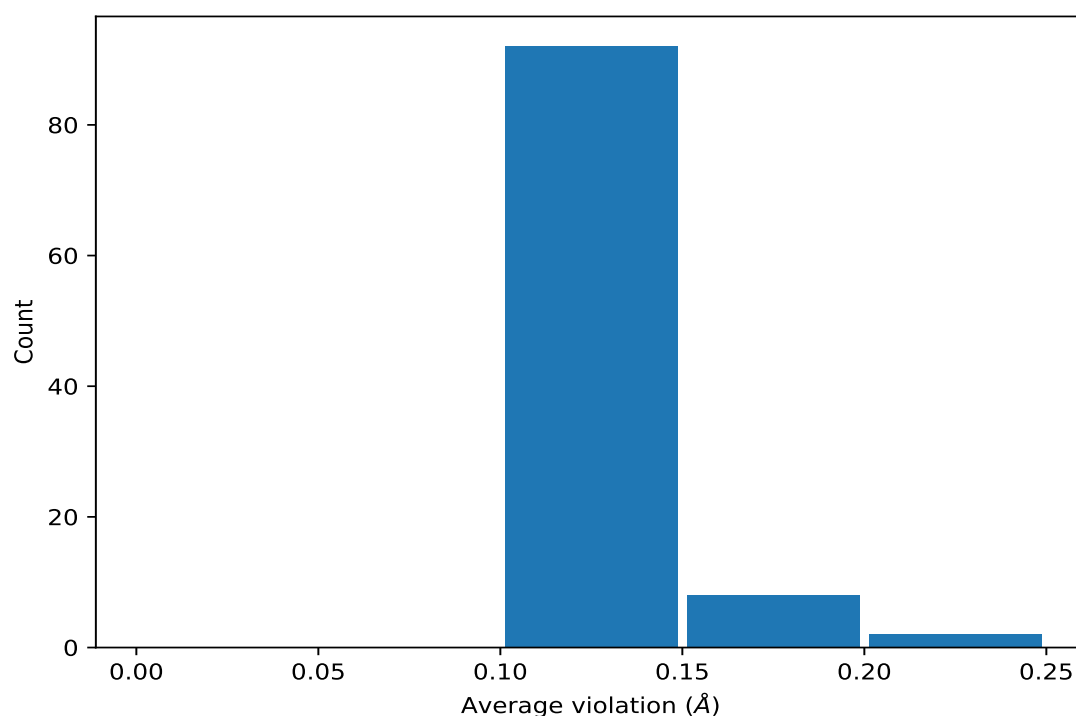
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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)
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	31	0.2	0.0	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	31	0.2	0.0	0.2
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	25	0.13	0.02	0.13
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	23	0.16	0.06	0.14
(2,139)	1:22:A:HIS:HE1	1:49:A:LYS:HB2	22	0.12	0.02	0.12
(1,33)	1:8:A:TRP:HA	1:68:A:LYS:HA	20	0.15	0.04	0.13
(2,7)	1:6:A:ILE:HD11	1:50:A:LYS:HA	20	0.12	0.02	0.12
(2,7)	1:6:A:ILE:HD12	1:50:A:LYS:HA	20	0.12	0.02	0.12
(2,7)	1:6:A:ILE:HD13	1:50:A:LYS:HA	20	0.12	0.02	0.12
(2,80)	1:10:A:PHE:HZ	1:30:A:TYR:HA	19	0.13	0.03	0.12
(1,15)	1:6:A:ILE:HG12	1:73:A:GLN:H	17	0.12	0.01	0.12
(1,418)	1:33:A:GLU:HA	1:41:A:HIS:H	13	0.15	0.05	0.13
(1,474)	1:40:A:ILE:H	1:40:A:ILE:HB	12	0.14	0.03	0.14
(1,716)	1:76:A:ALA:HA	1:77:A:ARG:H	11	0.1	0.01	0.1
(1,531)	1:49:A:LYS:H	1:50:A:LYS:H	10	0.13	0.02	0.14
(1,703)	1:72:A:THR:HA	1:73:A:GLN:H	9	0.15	0.03	0.14

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,690)	1:69:A:ARG:HA	1:70:A:ARG:H	9	0.14	0.01	0.15
(1,806)	1:94:A:GLY:H	1:95:A:GLU:H	9	0.11	0.01	0.12
(1,484)	1:40:A:ILE:HG21	1:42:A:PHE:HD1	8	0.14	0.03	0.13
(1,484)	1:40:A:ILE:HG21	1:42:A:PHE:HD2	8	0.14	0.03	0.13
(1,484)	1:40:A:ILE:HG22	1:42:A:PHE:HD1	8	0.14	0.03	0.13
(1,484)	1:40:A:ILE:HG22	1:42:A:PHE:HD2	8	0.14	0.03	0.13
(1,484)	1:40:A:ILE:HG23	1:42:A:PHE:HD1	8	0.14	0.03	0.13
(1,484)	1:40:A:ILE:HG23	1:42:A:PHE:HD2	8	0.14	0.03	0.13
(1,491)	1:41:A:HIS:HD2	1:87:A:LEU:HB2	8	0.14	0.03	0.13
(1,125)	1:11:A:THR:HA	1:44:A:GLY:H	8	0.14	0.02	0.14
(1,660)	1:62:A:PRO:HB3	1:63:A:GLY:H	8	0.13	0.03	0.13
(1,61)	1:8:A:TRP:HZ3	1:67:A:GLU:HA	8	0.12	0.02	0.12
(2,224)	1:41:A:HIS:HD2	1:87:A:LEU:HB3	7	0.14	0.03	0.12
(1,358)	1:30:A:TYR:H	1:92:A:GLU:HA	7	0.12	0.01	0.12
(1,655)	1:61:A:ILE:HD11	1:66:A:PHE:HD1	6	0.14	0.02	0.14
(1,655)	1:61:A:ILE:HD11	1:66:A:PHE:HD2	6	0.14	0.02	0.14
(1,655)	1:61:A:ILE:HD12	1:66:A:PHE:HD1	6	0.14	0.02	0.14
(1,655)	1:61:A:ILE:HD12	1:66:A:PHE:HD2	6	0.14	0.02	0.14
(1,655)	1:61:A:ILE:HD13	1:66:A:PHE:HD1	6	0.14	0.02	0.14
(1,655)	1:61:A:ILE:HD13	1:66:A:PHE:HD2	6	0.14	0.02	0.14
(2,6)	1:6:A:ILE:HA	1:8:A:TRP:HD1	6	0.13	0.05	0.12
(1,302)	1:27:A:TYR:H	1:46:A:ILE:HA	6	0.11	0.01	0.11
(2,140)	1:22:A:HIS:HE1	1:59:A:LYS:HA	6	0.1	0.0	0.1
(2,268)	1:67:A:GLU:HA	1:71:A:GLY:H	5	0.14	0.02	0.14
(1,482)	1:40:A:ILE:HG13	1:42:A:PHE:HZ	5	0.13	0.02	0.12
(1,307)	1:27:A:TYR:HA	1:27:A:TYR:HE1	5	0.12	0.02	0.11
(1,307)	1:27:A:TYR:HA	1:27:A:TYR:HE2	5	0.12	0.02	0.11
(2,133)	1:22:A:HIS:HD2	1:24:A:SER:HA	5	0.11	0.01	0.11
(1,463)	1:37:A:ALA:H	1:38:A:GLY:H	4	0.15	0.01	0.16
(1,374)	1:31:A:GLN:HA	1:90:A:PRO:HA	4	0.14	0.03	0.12
(1,694)	1:70:A:ARG:H	1:73:A:GLN:H	4	0.14	0.04	0.12
(1,382)	1:32:A:THR:H	1:81:A:MET:HE1	4	0.13	0.03	0.12
(1,382)	1:32:A:THR:H	1:81:A:MET:HE2	4	0.13	0.03	0.12
(1,382)	1:32:A:THR:H	1:81:A:MET:HE3	4	0.13	0.03	0.12
(1,335)	1:28:A:LEU:HD21	1:94:A:GLY:H	4	0.13	0.01	0.12
(1,335)	1:28:A:LEU:HD22	1:94:A:GLY:H	4	0.13	0.01	0.12
(1,335)	1:28:A:LEU:HD23	1:94:A:GLY:H	4	0.13	0.01	0.12
(1,251)	1:22:A:HIS:H	1:26:A:LYS:H	4	0.12	0.01	0.12
(2,69)	1:10:A:PHE:HE1	1:57:A:MET:HG3	4	0.12	0.01	0.12
(2,69)	1:10:A:PHE:HE2	1:57:A:MET:HG3	4	0.12	0.01	0.12
(1,265)	1:23:A:ASP:HA	1:25:A:MET:H	4	0.11	0.01	0.11
(2,193)	1:30:A:TYR:HA	1:80:A:SER:HB2	3	0.18	0.03	0.18

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(2,193)	1:30:A:TYR:HA	1:80:A:SER:HB3	3	0.18	0.03	0.18
(2,221)	1:36:A:GLU:HG2	1:42:A:PHE:HD1	3	0.17	0.09	0.11
(2,221)	1:36:A:GLU:HG2	1:42:A:PHE:HD2	3	0.17	0.09	0.11
(2,221)	1:36:A:GLU:HG3	1:42:A:PHE:HD1	3	0.17	0.09	0.11
(2,221)	1:36:A:GLU:HG3	1:42:A:PHE:HD2	3	0.17	0.09	0.11
(2,17)	1:8:A:TRP:HE3	1:54:A:LEU:HB3	3	0.13	0.01	0.13
(1,126)	1:11:A:THR:HB	1:12:A:LEU:H	3	0.13	0.02	0.12
(1,584)	1:55:A:ALA:HA	1:59:A:LYS:H	3	0.13	0.0	0.13
(1,72)	1:9:A:CYS:H	1:9:A:CYS:HB3	3	0.13	0.01	0.12
(1,171)	1:14:A:ASN:H	1:40:A:ILE:HA	3	0.12	0.02	0.12
(1,350)	1:29:A:VAL:HG21	1:81:A:MET:HE1	3	0.12	0.01	0.12
(1,350)	1:29:A:VAL:HG21	1:81:A:MET:HE2	3	0.12	0.01	0.12
(1,350)	1:29:A:VAL:HG21	1:81:A:MET:HE3	3	0.12	0.01	0.12
(1,350)	1:29:A:VAL:HG22	1:81:A:MET:HE1	3	0.12	0.01	0.12
(1,350)	1:29:A:VAL:HG22	1:81:A:MET:HE2	3	0.12	0.01	0.12
(1,350)	1:29:A:VAL:HG22	1:81:A:MET:HE3	3	0.12	0.01	0.12
(1,350)	1:29:A:VAL:HG23	1:81:A:MET:HE1	3	0.12	0.01	0.12
(1,350)	1:29:A:VAL:HG23	1:81:A:MET:HE2	3	0.12	0.01	0.12
(1,350)	1:29:A:VAL:HG23	1:81:A:MET:HE3	3	0.12	0.01	0.12
(1,393)	1:32:A:THR:HA	1:91:A:TRP:HH2	3	0.12	0.01	0.12
(2,220)	1:36:A:GLU:HG2	1:41:A:HIS:HD2	3	0.12	0.01	0.12
(2,220)	1:36:A:GLU:HG3	1:41:A:HIS:HD2	3	0.12	0.01	0.12
(1,37)	1:8:A:TRP:HD1	1:48:A:MET:HA	3	0.11	0.0	0.11
(1,658)	1:62:A:PRO:HA	1:63:A:GLY:H	2	0.16	0.01	0.16
(1,453)	1:35:A:GLY:H	1:40:A:ILE:HA	2	0.14	0.04	0.14
(1,131)	1:11:A:THR:HG21	1:41:A:HIS:HD2	2	0.13	0.01	0.13
(1,131)	1:11:A:THR:HG22	1:41:A:HIS:HD2	2	0.13	0.01	0.13
(1,131)	1:11:A:THR:HG23	1:41:A:HIS:HD2	2	0.13	0.01	0.13
(1,363)	1:30:A:TYR:HB3	1:43:A:GLN:H	2	0.12	0.02	0.12
(2,35)	1:9:A:CYS:HB3	1:45:A:TYR:HE1	2	0.12	0.01	0.12
(2,35)	1:9:A:CYS:HB3	1:45:A:TYR:HE2	2	0.12	0.01	0.12
(1,372)	1:31:A:GLN:H	1:91:A:TRP:H	2	0.12	0.02	0.12
(1,565)	1:54:A:LEU:HB3	1:58:A:LYS:HE2	2	0.12	0.02	0.12
(1,565)	1:54:A:LEU:HB3	1:58:A:LYS:HE3	2	0.12	0.02	0.12
(1,483)	1:40:A:ILE:HG21	1:41:A:HIS:H	2	0.12	0.0	0.12
(1,483)	1:40:A:ILE:HG22	1:41:A:HIS:H	2	0.12	0.0	0.12
(1,483)	1:40:A:ILE:HG23	1:41:A:HIS:H	2	0.12	0.0	0.12
(1,100)	1:10:A:PHE:HD1	1:64:A:ALA:H	2	0.11	0.01	0.11
(1,100)	1:10:A:PHE:HD2	1:64:A:ALA:H	2	0.11	0.01	0.11
(1,260)	1:22:A:HIS:HD2	1:60:A:LEU:HB3	2	0.11	0.0	0.11
(2,76)	1:10:A:PHE:HZ	1:12:A:LEU:HG	2	0.11	0.01	0.11
(1,414)	1:33:A:GLU:H	1:41:A:HIS:HA	2	0.11	0.0	0.11

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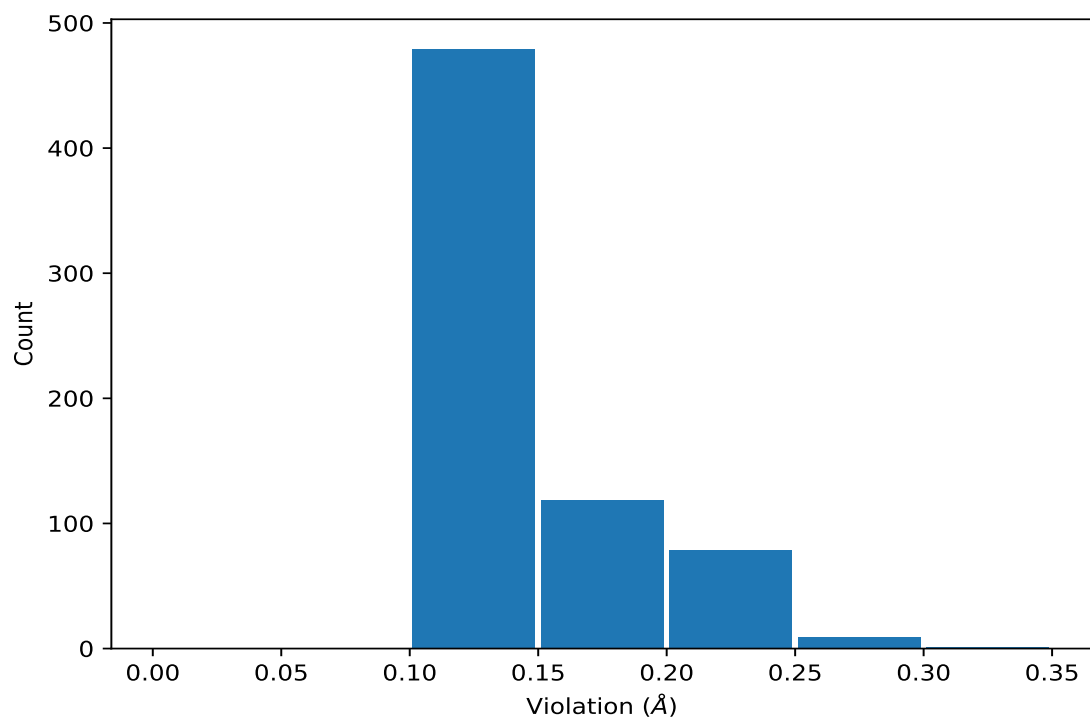
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,323)	1:28:A:LEU:H	1:94:A:GLY:HA2	2	0.1	0.0	0.1
(1,434)	1:34:A:GLN:H	1:87:A:LEU:HG	2	0.1	0.0	0.1

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)
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	25	0.34
(2,221)	1:36:A:GLU:HG2	1:42:A:PHE:HD1	26	0.29

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,221)	1:36:A:GLU:HG2	1:42:A:PHE:HD2	26	0.29
(2,221)	1:36:A:GLU:HG3	1:42:A:PHE:HD1	26	0.29
(2,221)	1:36:A:GLU:HG3	1:42:A:PHE:HD2	26	0.29
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	30	0.28
(1,695)	1:70:A:ARG:HA	1:71:A:GLY:H	27	0.26
(1,33)	1:8:A:TRP:HA	1:68:A:LYS:HA	12	0.26
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	31	0.25
(1,418)	1:33:A:GLU:HA	1:41:A:HIS:H	31	0.25
(2,6)	1:6:A:ILE:HA	1:8:A:TRP:HD1	25	0.24
(1,418)	1:33:A:GLU:HA	1:41:A:HIS:H	10	0.24
(2,193)	1:30:A:TYR:HA	1:80:A:SER:HB2	29	0.22
(2,193)	1:30:A:TYR:HA	1:80:A:SER:HB3	29	0.22
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	17	0.22
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	27	0.22
(1,418)	1:33:A:GLU:HA	1:41:A:HIS:H	26	0.22
(1,63)	1:8:A:TRP:HZ3	1:68:A:LYS:HA	25	0.22
(1,703)	1:72:A:THR:HA	1:73:A:GLN:H	13	0.21
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	1	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	1	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	2	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	2	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	3	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	3	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	4	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	4	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	5	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	5	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	6	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	6	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	7	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	7	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	8	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	8	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	9	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	9	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	10	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	10	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	11	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	11	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	12	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	12	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	13	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	13	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	14	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	14	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	15	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	15	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	16	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	16	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	17	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	17	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	18	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	18	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	19	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	19	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	20	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	20	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	21	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	21	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	22	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	22	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	23	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	23	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	24	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	24	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	25	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	25	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	26	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	26	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	27	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	27	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	28	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	28	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	29	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	29	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	30	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	30	0.2
(3,1)	1:89:A:GLY:HA3	1:90:A:PRO:CA	31	0.2
(3,1)	1:89:A:GLY:HA2	1:90:A:PRO:CA	31	0.2
(2,80)	1:10:A:PHE:HZ	1:30:A:TYR:HA	29	0.2
(1,694)	1:70:A:ARG:H	1:73:A:GLN:H	18	0.2
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	15	0.2
(1,491)	1:41:A:HIS:HD2	1:87:A:LEU:HB2	24	0.2
(1,418)	1:33:A:GLU:HA	1:41:A:HIS:H	7	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,275)	1:25:A:MET:H	1:46:A:ILE:HG21	21	0.2
(1,275)	1:25:A:MET:H	1:46:A:ILE:HG22	21	0.2
(1,275)	1:25:A:MET:H	1:46:A:ILE:HG23	21	0.2
(2,224)	1:41:A:HIS:HD2	1:87:A:LEU:HB3	25	0.19
(1,703)	1:72:A:THR:HA	1:73:A:GLN:H	31	0.19
(1,484)	1:40:A:ILE:HG21	1:42:A:PHE:HD1	26	0.19
(1,484)	1:40:A:ILE:HG21	1:42:A:PHE:HD2	26	0.19
(1,484)	1:40:A:ILE:HG22	1:42:A:PHE:HD1	26	0.19
(1,484)	1:40:A:ILE:HG22	1:42:A:PHE:HD2	26	0.19
(1,484)	1:40:A:ILE:HG23	1:42:A:PHE:HD1	26	0.19
(1,484)	1:40:A:ILE:HG23	1:42:A:PHE:HD2	26	0.19
(1,474)	1:40:A:ILE:H	1:40:A:ILE:HB	6	0.19
(1,474)	1:40:A:ILE:H	1:40:A:ILE:HB	18	0.19
(1,474)	1:40:A:ILE:H	1:40:A:ILE:HB	30	0.19
(1,374)	1:31:A:GLN:HA	1:90:A:PRO:HA	28	0.19
(1,33)	1:8:A:TRP:HA	1:68:A:LYS:HA	11	0.19
(2,193)	1:30:A:TYR:HA	1:80:A:SER:HB2	16	0.18
(2,193)	1:30:A:TYR:HA	1:80:A:SER:HB3	16	0.18
(1,655)	1:61:A:ILE:HD11	1:66:A:PHE:HD1	22	0.18
(1,655)	1:61:A:ILE:HD11	1:66:A:PHE:HD2	22	0.18
(1,655)	1:61:A:ILE:HD12	1:66:A:PHE:HD1	22	0.18
(1,655)	1:61:A:ILE:HD12	1:66:A:PHE:HD2	22	0.18
(1,655)	1:61:A:ILE:HD13	1:66:A:PHE:HD1	22	0.18
(1,655)	1:61:A:ILE:HD13	1:66:A:PHE:HD2	22	0.18
(1,484)	1:40:A:ILE:HG21	1:42:A:PHE:HD1	28	0.18
(1,484)	1:40:A:ILE:HG21	1:42:A:PHE:HD2	28	0.18
(1,484)	1:40:A:ILE:HG22	1:42:A:PHE:HD1	28	0.18
(1,484)	1:40:A:ILE:HG22	1:42:A:PHE:HD2	28	0.18
(1,484)	1:40:A:ILE:HG23	1:42:A:PHE:HD1	28	0.18
(1,484)	1:40:A:ILE:HG23	1:42:A:PHE:HD2	28	0.18
(1,449)	1:34:A:GLN:HG2	1:41:A:HIS:H	26	0.18
(1,449)	1:34:A:GLN:HG3	1:41:A:HIS:H	26	0.18
(1,382)	1:32:A:THR:H	1:81:A:MET:HE1	28	0.18
(1,382)	1:32:A:THR:H	1:81:A:MET:HE2	28	0.18
(1,382)	1:32:A:THR:H	1:81:A:MET:HE3	28	0.18
(1,33)	1:8:A:TRP:HA	1:68:A:LYS:HA	9	0.18
(1,33)	1:8:A:TRP:HA	1:68:A:LYS:HA	25	0.18
(1,33)	1:8:A:TRP:HA	1:68:A:LYS:HA	31	0.18
(2,268)	1:67:A:GLU:HA	1:71:A:GLY:H	12	0.17
(2,224)	1:41:A:HIS:HD2	1:87:A:LEU:HB3	19	0.17
(2,80)	1:10:A:PHE:HZ	1:30:A:TYR:HA	17	0.17
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	11	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,660)	1:62:A:PRO:HB3	1:63:A:GLY:H	12	0.17
(1,660)	1:62:A:PRO:HB3	1:63:A:GLY:H	28	0.17
(1,658)	1:62:A:PRO:HA	1:63:A:GLY:H	28	0.17
(1,453)	1:35:A:GLY:H	1:40:A:ILE:HA	24	0.17
(1,418)	1:33:A:GLU:HA	1:41:A:HIS:H	3	0.17
(1,149)	1:12:A:LEU:HG	1:42:A:PHE:H	31	0.17
(1,125)	1:11:A:THR:HA	1:44:A:GLY:H	25	0.17
(1,61)	1:8:A:TRP:HZ3	1:67:A:GLU:HA	17	0.17
(2,139)	1:22:A:HIS:HE1	1:49:A:LYS:HB2	20	0.16
(2,7)	1:6:A:ILE:HD11	1:50:A:LYS:HA	20	0.16
(2,7)	1:6:A:ILE:HD12	1:50:A:LYS:HA	20	0.16
(2,7)	1:6:A:ILE:HD13	1:50:A:LYS:HA	20	0.16
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	10	0.16
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	19	0.16
(1,658)	1:62:A:PRO:HA	1:63:A:GLY:H	12	0.16
(1,531)	1:49:A:LYS:H	1:50:A:LYS:H	29	0.16
(1,491)	1:41:A:HIS:HD2	1:87:A:LEU:HB2	15	0.16
(1,484)	1:40:A:ILE:HG21	1:42:A:PHE:HD1	19	0.16
(1,484)	1:40:A:ILE:HG21	1:42:A:PHE:HD2	19	0.16
(1,484)	1:40:A:ILE:HG22	1:42:A:PHE:HD1	19	0.16
(1,484)	1:40:A:ILE:HG22	1:42:A:PHE:HD2	19	0.16
(1,484)	1:40:A:ILE:HG23	1:42:A:PHE:HD1	19	0.16
(1,484)	1:40:A:ILE:HG23	1:42:A:PHE:HD2	19	0.16
(1,482)	1:40:A:ILE:HG13	1:42:A:PHE:HZ	24	0.16
(1,474)	1:40:A:ILE:H	1:40:A:ILE:HB	14	0.16
(1,463)	1:37:A:ALA:H	1:38:A:GLY:H	23	0.16
(1,463)	1:37:A:ALA:H	1:38:A:GLY:H	30	0.16
(1,126)	1:11:A:THR:HB	1:12:A:LEU:H	14	0.16
(1,33)	1:8:A:TRP:HA	1:68:A:LYS:HA	18	0.16
(1,33)	1:8:A:TRP:HA	1:68:A:LYS:HA	30	0.16
(2,268)	1:67:A:GLU:HA	1:71:A:GLY:H	16	0.15
(2,193)	1:30:A:TYR:HA	1:80:A:SER:HB2	15	0.15
(2,193)	1:30:A:TYR:HA	1:80:A:SER:HB3	15	0.15
(2,139)	1:22:A:HIS:HE1	1:49:A:LYS:HB2	8	0.15
(2,139)	1:22:A:HIS:HE1	1:49:A:LYS:HB2	22	0.15
(2,139)	1:22:A:HIS:HE1	1:49:A:LYS:HB2	23	0.15
(2,80)	1:10:A:PHE:HZ	1:30:A:TYR:HA	25	0.15
(2,80)	1:10:A:PHE:HZ	1:30:A:TYR:HA	26	0.15
(2,80)	1:10:A:PHE:HZ	1:30:A:TYR:HA	27	0.15
(2,17)	1:8:A:TRP:HE3	1:54:A:LEU:HB3	22	0.15
(2,7)	1:6:A:ILE:HD11	1:50:A:LYS:HA	17	0.15
(2,7)	1:6:A:ILE:HD12	1:50:A:LYS:HA	17	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,7)	1:6:A:ILE:HD13	1:50:A:LYS:HA	17	0.15
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	14	0.15
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	16	0.15
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	20	0.15
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	22	0.15
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	30	0.15
(1,703)	1:72:A:THR:HA	1:73:A:GLN:H	28	0.15
(1,690)	1:69:A:ARG:HA	1:70:A:ARG:H	14	0.15
(1,690)	1:69:A:ARG:HA	1:70:A:ARG:H	20	0.15
(1,690)	1:69:A:ARG:HA	1:70:A:ARG:H	22	0.15
(1,690)	1:69:A:ARG:HA	1:70:A:ARG:H	24	0.15
(1,690)	1:69:A:ARG:HA	1:70:A:ARG:H	25	0.15
(1,690)	1:69:A:ARG:HA	1:70:A:ARG:H	27	0.15
(1,690)	1:69:A:ARG:HA	1:70:A:ARG:H	30	0.15
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	13	0.15
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	26	0.15
(1,655)	1:61:A:ILE:HD11	1:66:A:PHE:HD1	29	0.15
(1,655)	1:61:A:ILE:HD11	1:66:A:PHE:HD2	29	0.15
(1,655)	1:61:A:ILE:HD12	1:66:A:PHE:HD1	29	0.15
(1,655)	1:61:A:ILE:HD12	1:66:A:PHE:HD2	29	0.15
(1,655)	1:61:A:ILE:HD13	1:66:A:PHE:HD1	29	0.15
(1,655)	1:61:A:ILE:HD13	1:66:A:PHE:HD2	29	0.15
(1,531)	1:49:A:LYS:H	1:50:A:LYS:H	8	0.15
(1,531)	1:49:A:LYS:H	1:50:A:LYS:H	20	0.15
(1,531)	1:49:A:LYS:H	1:50:A:LYS:H	22	0.15
(1,531)	1:49:A:LYS:H	1:50:A:LYS:H	23	0.15
(1,510)	1:45:A:TYR:HA	1:47:A:GLU:HG2	17	0.15
(1,510)	1:45:A:TYR:HA	1:47:A:GLU:HG3	17	0.15
(1,491)	1:41:A:HIS:HD2	1:87:A:LEU:HB2	17	0.15
(1,463)	1:37:A:ALA:H	1:38:A:GLY:H	22	0.15
(1,460)	1:36:A:GLU:HA	1:37:A:ALA:H	26	0.15
(1,418)	1:33:A:GLU:HA	1:41:A:HIS:H	11	0.15
(1,363)	1:30:A:TYR:HB3	1:43:A:GLN:H	26	0.15
(1,307)	1:27:A:TYR:HA	1:27:A:TYR:HE1	21	0.15
(1,307)	1:27:A:TYR:HA	1:27:A:TYR:HE2	21	0.15
(1,171)	1:14:A:ASN:H	1:40:A:ILE:HA	15	0.15
(1,125)	1:11:A:THR:HA	1:44:A:GLY:H	14	0.15
(1,33)	1:8:A:TRP:HA	1:68:A:LYS:HA	28	0.15
(2,272)	1:72:A:THR:HA	1:79:A:TYR:HE1	15	0.14
(2,272)	1:72:A:THR:HA	1:79:A:TYR:HE2	15	0.14
(2,268)	1:67:A:GLU:HA	1:71:A:GLY:H	11	0.14
(2,224)	1:41:A:HIS:HD2	1:87:A:LEU:HB3	21	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,139)	1:22:A:HIS:HE1	1:49:A:LYS:HB2	24	0.14
(2,139)	1:22:A:HIS:HE1	1:49:A:LYS:HB2	29	0.14
(2,139)	1:22:A:HIS:HE1	1:49:A:LYS:HB2	31	0.14
(2,133)	1:22:A:HIS:HD2	1:24:A:SER:HA	21	0.14
(2,7)	1:6:A:ILE:HD11	1:50:A:LYS:HA	2	0.14
(2,7)	1:6:A:ILE:HD12	1:50:A:LYS:HA	2	0.14
(2,7)	1:6:A:ILE:HD13	1:50:A:LYS:HA	2	0.14
(2,7)	1:6:A:ILE:HD11	1:50:A:LYS:HA	12	0.14
(2,7)	1:6:A:ILE:HD12	1:50:A:LYS:HA	12	0.14
(2,7)	1:6:A:ILE:HD13	1:50:A:LYS:HA	12	0.14
(2,7)	1:6:A:ILE:HD11	1:50:A:LYS:HA	22	0.14
(2,7)	1:6:A:ILE:HD12	1:50:A:LYS:HA	22	0.14
(2,7)	1:6:A:ILE:HD13	1:50:A:LYS:HA	22	0.14
(2,7)	1:6:A:ILE:HD11	1:50:A:LYS:HA	25	0.14
(2,7)	1:6:A:ILE:HD12	1:50:A:LYS:HA	25	0.14
(2,7)	1:6:A:ILE:HD13	1:50:A:LYS:HA	25	0.14
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	23	0.14
(1,716)	1:76:A:ALA:HA	1:77:A:ARG:H	28	0.14
(1,703)	1:72:A:THR:HA	1:73:A:GLN:H	4	0.14
(1,703)	1:72:A:THR:HA	1:73:A:GLN:H	17	0.14
(1,694)	1:70:A:ARG:H	1:73:A:GLN:H	23	0.14
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	1	0.14
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	6	0.14
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	12	0.14
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	29	0.14
(1,660)	1:62:A:PRO:HB3	1:63:A:GLY:H	20	0.14
(1,660)	1:62:A:PRO:HB3	1:63:A:GLY:H	23	0.14
(1,655)	1:61:A:ILE:HD11	1:66:A:PHE:HD1	8	0.14
(1,655)	1:61:A:ILE:HD11	1:66:A:PHE:HD2	8	0.14
(1,655)	1:61:A:ILE:HD12	1:66:A:PHE:HD1	8	0.14
(1,655)	1:61:A:ILE:HD12	1:66:A:PHE:HD2	8	0.14
(1,655)	1:61:A:ILE:HD13	1:66:A:PHE:HD1	8	0.14
(1,655)	1:61:A:ILE:HD13	1:66:A:PHE:HD2	8	0.14
(1,491)	1:41:A:HIS:HD2	1:87:A:LEU:HB2	30	0.14
(1,484)	1:40:A:ILE:HG21	1:42:A:PHE:HD1	25	0.14
(1,484)	1:40:A:ILE:HG21	1:42:A:PHE:HD2	25	0.14
(1,484)	1:40:A:ILE:HG22	1:42:A:PHE:HD1	25	0.14
(1,484)	1:40:A:ILE:HG22	1:42:A:PHE:HD2	25	0.14
(1,484)	1:40:A:ILE:HG23	1:42:A:PHE:HD1	25	0.14
(1,484)	1:40:A:ILE:HG23	1:42:A:PHE:HD2	25	0.14
(1,474)	1:40:A:ILE:H	1:40:A:ILE:HB	15	0.14
(1,474)	1:40:A:ILE:H	1:40:A:ILE:HB	24	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,463)	1:37:A:ALA:H	1:38:A:GLY:H	8	0.14
(1,374)	1:31:A:GLN:HA	1:90:A:PRO:HA	24	0.14
(1,372)	1:31:A:GLN:H	1:91:A:TRP:H	24	0.14
(1,358)	1:30:A:TYR:H	1:92:A:GLU:HA	16	0.14
(1,358)	1:30:A:TYR:H	1:92:A:GLU:HA	27	0.14
(1,350)	1:29:A:VAL:HG21	1:81:A:MET:HE1	15	0.14
(1,350)	1:29:A:VAL:HG21	1:81:A:MET:HE2	15	0.14
(1,350)	1:29:A:VAL:HG21	1:81:A:MET:HE3	15	0.14
(1,350)	1:29:A:VAL:HG22	1:81:A:MET:HE1	15	0.14
(1,350)	1:29:A:VAL:HG22	1:81:A:MET:HE2	15	0.14
(1,350)	1:29:A:VAL:HG22	1:81:A:MET:HE3	15	0.14
(1,350)	1:29:A:VAL:HG23	1:81:A:MET:HE1	15	0.14
(1,350)	1:29:A:VAL:HG23	1:81:A:MET:HE2	15	0.14
(1,350)	1:29:A:VAL:HG23	1:81:A:MET:HE3	15	0.14
(1,335)	1:28:A:LEU:HD21	1:94:A:GLY:H	16	0.14
(1,335)	1:28:A:LEU:HD22	1:94:A:GLY:H	16	0.14
(1,335)	1:28:A:LEU:HD23	1:94:A:GLY:H	16	0.14
(1,302)	1:27:A:TYR:H	1:46:A:ILE:HA	21	0.14
(1,131)	1:11:A:THR:HG21	1:41:A:HIS:HD2	24	0.14
(1,131)	1:11:A:THR:HG22	1:41:A:HIS:HD2	24	0.14
(1,131)	1:11:A:THR:HG23	1:41:A:HIS:HD2	24	0.14
(1,125)	1:11:A:THR:HA	1:44:A:GLY:H	22	0.14
(1,125)	1:11:A:THR:HA	1:44:A:GLY:H	24	0.14
(1,72)	1:9:A:CYS:H	1:9:A:CYS:HB3	23	0.14
(1,33)	1:8:A:TRP:HA	1:68:A:LYS:HA	7	0.14
(1,15)	1:6:A:ILE:HG12	1:73:A:GLN:H	12	0.14
(1,15)	1:6:A:ILE:HG12	1:73:A:GLN:H	16	0.14
(2,220)	1:36:A:GLU:HG2	1:41:A:HIS:HD2	6	0.13
(2,220)	1:36:A:GLU:HG3	1:41:A:HIS:HD2	6	0.13
(2,139)	1:22:A:HIS:HE1	1:49:A:LYS:HB2	17	0.13
(2,139)	1:22:A:HIS:HE1	1:49:A:LYS:HB2	25	0.13
(2,80)	1:10:A:PHE:HZ	1:30:A:TYR:HA	5	0.13
(2,80)	1:10:A:PHE:HZ	1:30:A:TYR:HA	23	0.13
(2,69)	1:10:A:PHE:HE1	1:57:A:MET:HG3	23	0.13
(2,69)	1:10:A:PHE:HE2	1:57:A:MET:HG3	23	0.13
(2,35)	1:9:A:CYS:HB3	1:45:A:TYR:HE1	17	0.13
(2,35)	1:9:A:CYS:HB3	1:45:A:TYR:HE2	17	0.13
(2,17)	1:8:A:TRP:HE3	1:54:A:LEU:HB3	29	0.13
(2,7)	1:6:A:ILE:HD11	1:50:A:LYS:HA	10	0.13
(2,7)	1:6:A:ILE:HD12	1:50:A:LYS:HA	10	0.13
(2,7)	1:6:A:ILE:HD13	1:50:A:LYS:HA	10	0.13
(2,7)	1:6:A:ILE:HD11	1:50:A:LYS:HA	23	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,7)	1:6:A:ILE:HD12	1:50:A:LYS:HA	23	0.13
(2,7)	1:6:A:ILE:HD13	1:50:A:LYS:HA	23	0.13
(2,7)	1:6:A:ILE:HD11	1:50:A:LYS:HA	29	0.13
(2,7)	1:6:A:ILE:HD12	1:50:A:LYS:HA	29	0.13
(2,7)	1:6:A:ILE:HD13	1:50:A:LYS:HA	29	0.13
(1,806)	1:94:A:GLY:H	1:95:A:GLU:H	16	0.13
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	9	0.13
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	11	0.13
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	15	0.13
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	21	0.13
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	29	0.13
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	31	0.13
(1,703)	1:72:A:THR:HA	1:73:A:GLN:H	2	0.13
(1,703)	1:72:A:THR:HA	1:73:A:GLN:H	25	0.13
(1,690)	1:69:A:ARG:HA	1:70:A:ARG:H	23	0.13
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	10	0.13
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	19	0.13
(1,655)	1:61:A:ILE:HD11	1:66:A:PHE:HD1	7	0.13
(1,655)	1:61:A:ILE:HD11	1:66:A:PHE:HD2	7	0.13
(1,655)	1:61:A:ILE:HD12	1:66:A:PHE:HD1	7	0.13
(1,655)	1:61:A:ILE:HD12	1:66:A:PHE:HD2	7	0.13
(1,655)	1:61:A:ILE:HD13	1:66:A:PHE:HD1	7	0.13
(1,655)	1:61:A:ILE:HD13	1:66:A:PHE:HD2	7	0.13
(1,655)	1:61:A:ILE:HD11	1:66:A:PHE:HD1	20	0.13
(1,655)	1:61:A:ILE:HD11	1:66:A:PHE:HD2	20	0.13
(1,655)	1:61:A:ILE:HD12	1:66:A:PHE:HD1	20	0.13
(1,655)	1:61:A:ILE:HD12	1:66:A:PHE:HD2	20	0.13
(1,655)	1:61:A:ILE:HD13	1:66:A:PHE:HD1	20	0.13
(1,655)	1:61:A:ILE:HD13	1:66:A:PHE:HD2	20	0.13
(1,584)	1:55:A:ALA:HA	1:59:A:LYS:H	8	0.13
(1,584)	1:55:A:ALA:HA	1:59:A:LYS:H	20	0.13
(1,584)	1:55:A:ALA:HA	1:59:A:LYS:H	23	0.13
(1,565)	1:54:A:LEU:HB3	1:58:A:LYS:HE2	21	0.13
(1,565)	1:54:A:LEU:HB3	1:58:A:LYS:HE3	21	0.13
(1,531)	1:49:A:LYS:H	1:50:A:LYS:H	18	0.13
(1,531)	1:49:A:LYS:H	1:50:A:LYS:H	31	0.13
(1,482)	1:40:A:ILE:HG13	1:42:A:PHE:HZ	31	0.13
(1,474)	1:40:A:ILE:H	1:40:A:ILE:HB	16	0.13
(1,474)	1:40:A:ILE:H	1:40:A:ILE:HB	22	0.13
(1,418)	1:33:A:GLU:HA	1:41:A:HIS:H	12	0.13
(1,393)	1:32:A:THR:HA	1:91:A:TRP:HH2	14	0.13
(1,358)	1:30:A:TYR:H	1:92:A:GLU:HA	14	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,335)	1:28:A:LEU:HD21	1:94:A:GLY:H	19	0.13
(1,335)	1:28:A:LEU:HD22	1:94:A:GLY:H	19	0.13
(1,335)	1:28:A:LEU:HD23	1:94:A:GLY:H	19	0.13
(1,251)	1:22:A:HIS:H	1:26:A:LYS:H	31	0.13
(1,125)	1:11:A:THR:HA	1:44:A:GLY:H	20	0.13
(1,125)	1:11:A:THR:HA	1:44:A:GLY:H	30	0.13
(1,61)	1:8:A:TRP:HZ3	1:67:A:GLU:HA	11	0.13
(1,61)	1:8:A:TRP:HZ3	1:67:A:GLU:HA	30	0.13
(1,33)	1:8:A:TRP:HA	1:68:A:LYS:HA	2	0.13
(1,33)	1:8:A:TRP:HA	1:68:A:LYS:HA	6	0.13
(1,33)	1:8:A:TRP:HA	1:68:A:LYS:HA	8	0.13
(1,33)	1:8:A:TRP:HA	1:68:A:LYS:HA	10	0.13
(1,33)	1:8:A:TRP:HA	1:68:A:LYS:HA	13	0.13
(1,15)	1:6:A:ILE:HG12	1:73:A:GLN:H	2	0.13
(1,15)	1:6:A:ILE:HG12	1:73:A:GLN:H	9	0.13
(1,15)	1:6:A:ILE:HG12	1:73:A:GLN:H	13	0.13
(1,15)	1:6:A:ILE:HG12	1:73:A:GLN:H	17	0.13
(2,236)	1:45:A:TYR:HE1	1:47:A:GLU:HA	15	0.12
(2,236)	1:45:A:TYR:HE2	1:47:A:GLU:HA	15	0.12
(2,224)	1:41:A:HIS:HD2	1:87:A:LEU:HB3	2	0.12
(2,224)	1:41:A:HIS:HD2	1:87:A:LEU:HB3	28	0.12
(2,220)	1:36:A:GLU:HG2	1:41:A:HIS:HD2	18	0.12
(2,220)	1:36:A:GLU:HG3	1:41:A:HIS:HD2	18	0.12
(2,139)	1:22:A:HIS:HE1	1:49:A:LYS:HB2	12	0.12
(2,139)	1:22:A:HIS:HE1	1:49:A:LYS:HB2	13	0.12
(2,139)	1:22:A:HIS:HE1	1:49:A:LYS:HB2	16	0.12
(2,139)	1:22:A:HIS:HE1	1:49:A:LYS:HB2	18	0.12
(2,139)	1:22:A:HIS:HE1	1:49:A:LYS:HB2	28	0.12
(2,80)	1:10:A:PHE:HZ	1:30:A:TYR:HA	7	0.12
(2,80)	1:10:A:PHE:HZ	1:30:A:TYR:HA	11	0.12
(2,80)	1:10:A:PHE:HZ	1:30:A:TYR:HA	30	0.12
(2,76)	1:10:A:PHE:HZ	1:12:A:LEU:HG	29	0.12
(2,69)	1:10:A:PHE:HE1	1:57:A:MET:HG3	20	0.12
(2,69)	1:10:A:PHE:HE2	1:57:A:MET:HG3	20	0.12
(2,35)	1:9:A:CYS:HB3	1:45:A:TYR:HE1	29	0.12
(2,35)	1:9:A:CYS:HB3	1:45:A:TYR:HE2	29	0.12
(2,17)	1:8:A:TRP:HE3	1:54:A:LEU:HB3	31	0.12
(2,7)	1:6:A:ILE:HD11	1:50:A:LYS:HA	4	0.12
(2,7)	1:6:A:ILE:HD12	1:50:A:LYS:HA	4	0.12
(2,7)	1:6:A:ILE:HD13	1:50:A:LYS:HA	4	0.12
(2,7)	1:6:A:ILE:HD11	1:50:A:LYS:HA	28	0.12
(2,7)	1:6:A:ILE:HD12	1:50:A:LYS:HA	28	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,7)	1:6:A:ILE:HD13	1:50:A:LYS:HA	28	0.12
(2,7)	1:6:A:ILE:HD11	1:50:A:LYS:HA	31	0.12
(2,7)	1:6:A:ILE:HD12	1:50:A:LYS:HA	31	0.12
(2,7)	1:6:A:ILE:HD13	1:50:A:LYS:HA	31	0.12
(2,6)	1:6:A:ILE:HA	1:8:A:TRP:HD1	13	0.12
(2,6)	1:6:A:ILE:HA	1:8:A:TRP:HD1	31	0.12
(1,806)	1:94:A:GLY:H	1:95:A:GLU:H	19	0.12
(1,806)	1:94:A:GLY:H	1:95:A:GLU:H	21	0.12
(1,806)	1:94:A:GLY:H	1:95:A:GLU:H	30	0.12
(1,806)	1:94:A:GLY:H	1:95:A:GLU:H	31	0.12
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	8	0.12
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	24	0.12
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	25	0.12
(1,704)	1:72:A:THR:HB	1:73:A:GLN:H	15	0.12
(1,703)	1:72:A:THR:HA	1:73:A:GLN:H	14	0.12
(1,703)	1:72:A:THR:HA	1:73:A:GLN:H	22	0.12
(1,690)	1:69:A:ARG:HA	1:70:A:ARG:H	18	0.12
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	8	0.12
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	28	0.12
(1,660)	1:62:A:PRO:HB3	1:63:A:GLY:H	8	0.12
(1,655)	1:61:A:ILE:HD11	1:66:A:PHE:HD1	23	0.12
(1,655)	1:61:A:ILE:HD11	1:66:A:PHE:HD2	23	0.12
(1,655)	1:61:A:ILE:HD12	1:66:A:PHE:HD1	23	0.12
(1,655)	1:61:A:ILE:HD12	1:66:A:PHE:HD2	23	0.12
(1,655)	1:61:A:ILE:HD13	1:66:A:PHE:HD1	23	0.12
(1,655)	1:61:A:ILE:HD13	1:66:A:PHE:HD2	23	0.12
(1,531)	1:49:A:LYS:H	1:50:A:LYS:H	25	0.12
(1,491)	1:41:A:HIS:HD2	1:87:A:LEU:HB2	16	0.12
(1,484)	1:40:A:ILE:HG21	1:42:A:PHE:HD1	8	0.12
(1,484)	1:40:A:ILE:HG21	1:42:A:PHE:HD2	8	0.12
(1,484)	1:40:A:ILE:HG22	1:42:A:PHE:HD1	8	0.12
(1,484)	1:40:A:ILE:HG22	1:42:A:PHE:HD2	8	0.12
(1,484)	1:40:A:ILE:HG23	1:42:A:PHE:HD1	8	0.12
(1,484)	1:40:A:ILE:HG23	1:42:A:PHE:HD2	8	0.12
(1,484)	1:40:A:ILE:HG21	1:42:A:PHE:HD1	23	0.12
(1,484)	1:40:A:ILE:HG21	1:42:A:PHE:HD2	23	0.12
(1,484)	1:40:A:ILE:HG22	1:42:A:PHE:HD1	23	0.12
(1,484)	1:40:A:ILE:HG22	1:42:A:PHE:HD2	23	0.12
(1,484)	1:40:A:ILE:HG23	1:42:A:PHE:HD1	23	0.12
(1,484)	1:40:A:ILE:HG23	1:42:A:PHE:HD2	23	0.12
(1,483)	1:40:A:ILE:HG21	1:41:A:HIS:H	24	0.12
(1,483)	1:40:A:ILE:HG22	1:41:A:HIS:H	24	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,483)	1:40:A:ILE:HG23	1:41:A:HIS:H	24	0.12
(1,482)	1:40:A:ILE:HG13	1:42:A:PHE:HZ	14	0.12
(1,482)	1:40:A:ILE:HG13	1:42:A:PHE:HZ	30	0.12
(1,474)	1:40:A:ILE:H	1:40:A:ILE:HB	21	0.12
(1,474)	1:40:A:ILE:H	1:40:A:ILE:HB	27	0.12
(1,418)	1:33:A:GLU:HA	1:41:A:HIS:H	6	0.12
(1,393)	1:32:A:THR:HA	1:91:A:TRP:HH2	24	0.12
(1,382)	1:32:A:THR:H	1:81:A:MET:HE1	4	0.12
(1,382)	1:32:A:THR:H	1:81:A:MET:HE2	4	0.12
(1,382)	1:32:A:THR:H	1:81:A:MET:HE3	4	0.12
(1,358)	1:30:A:TYR:H	1:92:A:GLU:HA	15	0.12
(1,358)	1:30:A:TYR:H	1:92:A:GLU:HA	18	0.12
(1,350)	1:29:A:VAL:HG21	1:81:A:MET:HE1	31	0.12
(1,350)	1:29:A:VAL:HG21	1:81:A:MET:HE2	31	0.12
(1,350)	1:29:A:VAL:HG21	1:81:A:MET:HE3	31	0.12
(1,350)	1:29:A:VAL:HG22	1:81:A:MET:HE1	31	0.12
(1,350)	1:29:A:VAL:HG22	1:81:A:MET:HE2	31	0.12
(1,350)	1:29:A:VAL:HG22	1:81:A:MET:HE3	31	0.12
(1,350)	1:29:A:VAL:HG23	1:81:A:MET:HE1	31	0.12
(1,350)	1:29:A:VAL:HG23	1:81:A:MET:HE2	31	0.12
(1,350)	1:29:A:VAL:HG23	1:81:A:MET:HE3	31	0.12
(1,335)	1:28:A:LEU:HD21	1:94:A:GLY:H	30	0.12
(1,335)	1:28:A:LEU:HD22	1:94:A:GLY:H	30	0.12
(1,335)	1:28:A:LEU:HD23	1:94:A:GLY:H	30	0.12
(1,335)	1:28:A:LEU:HD21	1:94:A:GLY:H	31	0.12
(1,335)	1:28:A:LEU:HD22	1:94:A:GLY:H	31	0.12
(1,335)	1:28:A:LEU:HD23	1:94:A:GLY:H	31	0.12
(1,307)	1:27:A:TYR:HA	1:27:A:TYR:HE1	30	0.12
(1,307)	1:27:A:TYR:HA	1:27:A:TYR:HE2	30	0.12
(1,265)	1:23:A:ASP:HA	1:25:A:MET:H	21	0.12
(1,251)	1:22:A:HIS:H	1:26:A:LYS:H	16	0.12
(1,171)	1:14:A:ASN:H	1:40:A:ILE:HA	14	0.12
(1,131)	1:11:A:THR:HG21	1:41:A:HIS:HD2	11	0.12
(1,131)	1:11:A:THR:HG22	1:41:A:HIS:HD2	11	0.12
(1,131)	1:11:A:THR:HG23	1:41:A:HIS:HD2	11	0.12
(1,126)	1:11:A:THR:HB	1:12:A:LEU:H	29	0.12
(1,125)	1:11:A:THR:HA	1:44:A:GLY:H	27	0.12
(1,100)	1:10:A:PHE:HD1	1:64:A:ALA:H	18	0.12
(1,100)	1:10:A:PHE:HD2	1:64:A:ALA:H	18	0.12
(1,72)	1:9:A:CYS:H	1:9:A:CYS:HB3	5	0.12
(1,72)	1:9:A:CYS:H	1:9:A:CYS:HB3	11	0.12
(1,61)	1:8:A:TRP:HZ3	1:67:A:GLU:HA	2	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,61)	1:8:A:TRP:HZ3	1:67:A:GLU:HA	3	0.12
(1,33)	1:8:A:TRP:HA	1:68:A:LYS:HA	1	0.12
(1,33)	1:8:A:TRP:HA	1:68:A:LYS:HA	21	0.12
(1,33)	1:8:A:TRP:HA	1:68:A:LYS:HA	29	0.12
(1,15)	1:6:A:ILE:HG12	1:73:A:GLN:H	10	0.12
(1,15)	1:6:A:ILE:HG12	1:73:A:GLN:H	15	0.12
(1,15)	1:6:A:ILE:HG12	1:73:A:GLN:H	28	0.12
(1,15)	1:6:A:ILE:HG12	1:73:A:GLN:H	29	0.12
(1,15)	1:6:A:ILE:HG12	1:73:A:GLN:H	30	0.12
(2,268)	1:67:A:GLU:HA	1:71:A:GLY:H	2	0.11
(2,268)	1:67:A:GLU:HA	1:71:A:GLY:H	31	0.11
(2,224)	1:41:A:HIS:HD2	1:87:A:LEU:HB3	26	0.11
(2,221)	1:36:A:GLU:HG2	1:42:A:PHE:HD1	21	0.11
(2,221)	1:36:A:GLU:HG2	1:42:A:PHE:HD2	21	0.11
(2,221)	1:36:A:GLU:HG3	1:42:A:PHE:HD1	21	0.11
(2,221)	1:36:A:GLU:HG3	1:42:A:PHE:HD2	21	0.11
(2,220)	1:36:A:GLU:HG2	1:41:A:HIS:HD2	12	0.11
(2,220)	1:36:A:GLU:HG3	1:41:A:HIS:HD2	12	0.11
(2,140)	1:22:A:HIS:HE1	1:59:A:LYS:HA	8	0.11
(2,140)	1:22:A:HIS:HE1	1:59:A:LYS:HA	17	0.11
(2,139)	1:22:A:HIS:HE1	1:49:A:LYS:HB2	2	0.11
(2,139)	1:22:A:HIS:HE1	1:49:A:LYS:HB2	19	0.11
(2,139)	1:22:A:HIS:HE1	1:49:A:LYS:HB2	26	0.11
(2,139)	1:22:A:HIS:HE1	1:49:A:LYS:HB2	27	0.11
(2,133)	1:22:A:HIS:HD2	1:24:A:SER:HA	8	0.11
(2,133)	1:22:A:HIS:HD2	1:24:A:SER:HA	14	0.11
(2,133)	1:22:A:HIS:HD2	1:24:A:SER:HA	19	0.11
(2,83)	1:11:A:THR:H	1:66:A:PHE:HZ	10	0.11
(2,80)	1:10:A:PHE:HZ	1:30:A:TYR:HA	2	0.11
(2,80)	1:10:A:PHE:HZ	1:30:A:TYR:HA	4	0.11
(2,80)	1:10:A:PHE:HZ	1:30:A:TYR:HA	14	0.11
(2,80)	1:10:A:PHE:HZ	1:30:A:TYR:HA	18	0.11
(2,80)	1:10:A:PHE:HZ	1:30:A:TYR:HA	19	0.11
(2,80)	1:10:A:PHE:HZ	1:30:A:TYR:HA	20	0.11
(2,80)	1:10:A:PHE:HZ	1:30:A:TYR:HA	28	0.11
(2,69)	1:10:A:PHE:HE1	1:57:A:MET:HG3	8	0.11
(2,69)	1:10:A:PHE:HE2	1:57:A:MET:HG3	8	0.11
(2,7)	1:6:A:ILE:HD11	1:50:A:LYS:HA	9	0.11
(2,7)	1:6:A:ILE:HD12	1:50:A:LYS:HA	9	0.11
(2,7)	1:6:A:ILE:HD13	1:50:A:LYS:HA	9	0.11
(2,7)	1:6:A:ILE:HD11	1:50:A:LYS:HA	15	0.11
(2,7)	1:6:A:ILE:HD12	1:50:A:LYS:HA	15	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,7)	1:6:A:ILE:HD13	1:50:A:LYS:HA	15	0.11
(2,7)	1:6:A:ILE:HD11	1:50:A:LYS:HA	18	0.11
(2,7)	1:6:A:ILE:HD12	1:50:A:LYS:HA	18	0.11
(2,7)	1:6:A:ILE:HD13	1:50:A:LYS:HA	18	0.11
(2,7)	1:6:A:ILE:HD11	1:50:A:LYS:HA	21	0.11
(2,7)	1:6:A:ILE:HD12	1:50:A:LYS:HA	21	0.11
(2,7)	1:6:A:ILE:HD13	1:50:A:LYS:HA	21	0.11
(2,7)	1:6:A:ILE:HD11	1:50:A:LYS:HA	30	0.11
(2,7)	1:6:A:ILE:HD12	1:50:A:LYS:HA	30	0.11
(2,7)	1:6:A:ILE:HD13	1:50:A:LYS:HA	30	0.11
(2,6)	1:6:A:ILE:HA	1:8:A:TRP:HD1	16	0.11
(2,6)	1:6:A:ILE:HA	1:8:A:TRP:HD1	19	0.11
(2,6)	1:6:A:ILE:HA	1:8:A:TRP:HD1	27	0.11
(1,806)	1:94:A:GLY:H	1:95:A:GLU:H	2	0.11
(1,806)	1:94:A:GLY:H	1:95:A:GLU:H	27	0.11
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	1	0.11
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	2	0.11
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	4	0.11
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	5	0.11
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	6	0.11
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	7	0.11
(1,716)	1:76:A:ALA:HA	1:77:A:ARG:H	24	0.11
(1,694)	1:70:A:ARG:H	1:73:A:GLN:H	24	0.11
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	2	0.11
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	3	0.11
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	5	0.11
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	18	0.11
(1,662)	1:63:A:GLY:HA2	1:64:A:ALA:H	16	0.11
(1,660)	1:62:A:PRO:HB3	1:63:A:GLY:H	7	0.11
(1,660)	1:62:A:PRO:HB3	1:63:A:GLY:H	29	0.11
(1,491)	1:41:A:HIS:HD2	1:87:A:LEU:HB2	11	0.11
(1,491)	1:41:A:HIS:HD2	1:87:A:LEU:HB2	27	0.11
(1,491)	1:41:A:HIS:HD2	1:87:A:LEU:HB2	29	0.11
(1,484)	1:40:A:ILE:HG21	1:42:A:PHE:HD1	3	0.11
(1,484)	1:40:A:ILE:HG21	1:42:A:PHE:HD2	3	0.11
(1,484)	1:40:A:ILE:HG22	1:42:A:PHE:HD1	3	0.11
(1,484)	1:40:A:ILE:HG22	1:42:A:PHE:HD2	3	0.11
(1,484)	1:40:A:ILE:HG23	1:42:A:PHE:HD1	3	0.11
(1,484)	1:40:A:ILE:HG23	1:42:A:PHE:HD2	3	0.11
(1,483)	1:40:A:ILE:HG21	1:41:A:HIS:H	14	0.11
(1,483)	1:40:A:ILE:HG22	1:41:A:HIS:H	14	0.11
(1,483)	1:40:A:ILE:HG23	1:41:A:HIS:H	14	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,474)	1:40:A:ILE:H	1:40:A:ILE:HB	26	0.11
(1,418)	1:33:A:GLU:HA	1:41:A:HIS:H	5	0.11
(1,418)	1:33:A:GLU:HA	1:41:A:HIS:H	18	0.11
(1,414)	1:33:A:GLU:H	1:41:A:HIS:HA	16	0.11
(1,393)	1:32:A:THR:HA	1:91:A:TRP:HH2	17	0.11
(1,382)	1:32:A:THR:H	1:81:A:MET:HE1	17	0.11
(1,382)	1:32:A:THR:H	1:81:A:MET:HE2	17	0.11
(1,382)	1:32:A:THR:H	1:81:A:MET:HE3	17	0.11
(1,382)	1:32:A:THR:H	1:81:A:MET:HE1	20	0.11
(1,382)	1:32:A:THR:H	1:81:A:MET:HE2	20	0.11
(1,382)	1:32:A:THR:H	1:81:A:MET:HE3	20	0.11
(1,374)	1:31:A:GLN:HA	1:90:A:PRO:HA	11	0.11
(1,374)	1:31:A:GLN:HA	1:90:A:PRO:HA	31	0.11
(1,371)	1:31:A:GLN:H	1:81:A:MET:HE1	9	0.11
(1,371)	1:31:A:GLN:H	1:81:A:MET:HE2	9	0.11
(1,371)	1:31:A:GLN:H	1:81:A:MET:HE3	9	0.11
(1,365)	1:31:A:GLN:H	1:31:A:GLN:HB3	17	0.11
(1,358)	1:30:A:TYR:H	1:92:A:GLU:HA	19	0.11
(1,350)	1:29:A:VAL:HG21	1:81:A:MET:HE1	19	0.11
(1,350)	1:29:A:VAL:HG21	1:81:A:MET:HE2	19	0.11
(1,350)	1:29:A:VAL:HG21	1:81:A:MET:HE3	19	0.11
(1,350)	1:29:A:VAL:HG22	1:81:A:MET:HE1	19	0.11
(1,350)	1:29:A:VAL:HG22	1:81:A:MET:HE2	19	0.11
(1,350)	1:29:A:VAL:HG22	1:81:A:MET:HE3	19	0.11
(1,350)	1:29:A:VAL:HG23	1:81:A:MET:HE1	19	0.11
(1,350)	1:29:A:VAL:HG23	1:81:A:MET:HE2	19	0.11
(1,350)	1:29:A:VAL:HG23	1:81:A:MET:HE3	19	0.11
(1,313)	1:27:A:TYR:HB3	1:28:A:LEU:H	21	0.11
(1,311)	1:27:A:TYR:HB2	1:28:A:LEU:H	24	0.11
(1,307)	1:27:A:TYR:HA	1:27:A:TYR:HE1	19	0.11
(1,307)	1:27:A:TYR:HA	1:27:A:TYR:HE2	19	0.11
(1,307)	1:27:A:TYR:HA	1:27:A:TYR:HE1	31	0.11
(1,307)	1:27:A:TYR:HA	1:27:A:TYR:HE2	31	0.11
(1,302)	1:27:A:TYR:H	1:46:A:ILE:HA	8	0.11
(1,302)	1:27:A:TYR:H	1:46:A:ILE:HA	18	0.11
(1,302)	1:27:A:TYR:H	1:46:A:ILE:HA	20	0.11
(1,279)	1:25:A:MET:HA	1:27:A:TYR:H	19	0.11
(1,265)	1:23:A:ASP:HA	1:25:A:MET:H	12	0.11
(1,265)	1:23:A:ASP:HA	1:25:A:MET:H	17	0.11
(1,260)	1:22:A:HIS:HD2	1:60:A:LEU:HB3	21	0.11
(1,260)	1:22:A:HIS:HD2	1:60:A:LEU:HB3	22	0.11
(1,251)	1:22:A:HIS:H	1:26:A:LYS:H	21	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,251)	1:22:A:HIS:H	1:26:A:LYS:H	30	0.11
(1,204)	1:18:A:PRO:HG3	1:42:A:PHE:HZ	12	0.11
(1,126)	1:11:A:THR:HB	1:12:A:LEU:H	25	0.11
(1,61)	1:8:A:TRP:HZ3	1:67:A:GLU:HA	10	0.11
(1,61)	1:8:A:TRP:HZ3	1:67:A:GLU:HA	12	0.11
(1,37)	1:8:A:TRP:HD1	1:48:A:MET:HA	16	0.11
(1,37)	1:8:A:TRP:HD1	1:48:A:MET:HA	31	0.11
(1,33)	1:8:A:TRP:HA	1:68:A:LYS:HA	3	0.11
(1,33)	1:8:A:TRP:HA	1:68:A:LYS:HA	17	0.11
(1,15)	1:6:A:ILE:HG12	1:73:A:GLN:H	5	0.11
(1,15)	1:6:A:ILE:HG12	1:73:A:GLN:H	8	0.11
(1,15)	1:6:A:ILE:HG12	1:73:A:GLN:H	18	0.11
(1,15)	1:6:A:ILE:HG12	1:73:A:GLN:H	24	0.11
(1,15)	1:6:A:ILE:HG12	1:73:A:GLN:H	31	0.11
(2,224)	1:41:A:HIS:HD2	1:87:A:LEU:HB3	13	0.1
(2,221)	1:36:A:GLU:HG2	1:42:A:PHE:HD1	24	0.1
(2,221)	1:36:A:GLU:HG2	1:42:A:PHE:HD2	24	0.1
(2,221)	1:36:A:GLU:HG3	1:42:A:PHE:HD1	24	0.1
(2,221)	1:36:A:GLU:HG3	1:42:A:PHE:HD2	24	0.1
(2,140)	1:22:A:HIS:HE1	1:59:A:LYS:HA	11	0.1
(2,140)	1:22:A:HIS:HE1	1:59:A:LYS:HA	19	0.1
(2,140)	1:22:A:HIS:HE1	1:59:A:LYS:HA	20	0.1
(2,140)	1:22:A:HIS:HE1	1:59:A:LYS:HA	23	0.1
(2,139)	1:22:A:HIS:HE1	1:49:A:LYS:HB2	5	0.1
(2,139)	1:22:A:HIS:HE1	1:49:A:LYS:HB2	6	0.1
(2,139)	1:22:A:HIS:HE1	1:49:A:LYS:HB2	7	0.1
(2,139)	1:22:A:HIS:HE1	1:49:A:LYS:HB2	11	0.1
(2,133)	1:22:A:HIS:HD2	1:24:A:SER:HA	7	0.1
(2,80)	1:10:A:PHE:HZ	1:30:A:TYR:HA	6	0.1
(2,80)	1:10:A:PHE:HZ	1:30:A:TYR:HA	15	0.1
(2,76)	1:10:A:PHE:HZ	1:12:A:LEU:HG	26	0.1
(2,69)	1:10:A:PHE:HE1	1:57:A:MET:HG3	29	0.1
(2,69)	1:10:A:PHE:HE2	1:57:A:MET:HG3	29	0.1
(2,7)	1:6:A:ILE:HD11	1:50:A:LYS:HA	13	0.1
(2,7)	1:6:A:ILE:HD12	1:50:A:LYS:HA	13	0.1
(2,7)	1:6:A:ILE:HD13	1:50:A:LYS:HA	13	0.1
(2,7)	1:6:A:ILE:HD11	1:50:A:LYS:HA	14	0.1
(2,7)	1:6:A:ILE:HD12	1:50:A:LYS:HA	14	0.1
(2,7)	1:6:A:ILE:HD13	1:50:A:LYS:HA	14	0.1
(2,7)	1:6:A:ILE:HD11	1:50:A:LYS:HA	16	0.1
(2,7)	1:6:A:ILE:HD12	1:50:A:LYS:HA	16	0.1
(2,7)	1:6:A:ILE:HD13	1:50:A:LYS:HA	16	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,806)	1:94:A:GLY:H	1:95:A:GLU:H	10	0.1
(1,806)	1:94:A:GLY:H	1:95:A:GLU:H	28	0.1
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	26	0.1
(1,728)	1:77:A:ARG:HA	1:78:A:ALA:H	27	0.1
(1,716)	1:76:A:ALA:HA	1:77:A:ARG:H	2	0.1
(1,716)	1:76:A:ALA:HA	1:77:A:ARG:H	14	0.1
(1,716)	1:76:A:ALA:HA	1:77:A:ARG:H	15	0.1
(1,716)	1:76:A:ALA:HA	1:77:A:ARG:H	18	0.1
(1,716)	1:76:A:ALA:HA	1:77:A:ARG:H	19	0.1
(1,716)	1:76:A:ALA:HA	1:77:A:ARG:H	20	0.1
(1,716)	1:76:A:ALA:HA	1:77:A:ARG:H	22	0.1
(1,716)	1:76:A:ALA:HA	1:77:A:ARG:H	23	0.1
(1,716)	1:76:A:ALA:HA	1:77:A:ARG:H	27	0.1
(1,694)	1:70:A:ARG:H	1:73:A:GLN:H	22	0.1
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	4	0.1
(1,685)	1:67:A:GLU:HA	1:70:A:ARG:H	7	0.1
(1,661)	1:63:A:GLY:H	1:64:A:ALA:H	12	0.1
(1,660)	1:62:A:PRO:HB3	1:63:A:GLY:H	30	0.1
(1,565)	1:54:A:LEU:HB3	1:58:A:LYS:HE2	14	0.1
(1,565)	1:54:A:LEU:HB3	1:58:A:LYS:HE3	14	0.1
(1,531)	1:49:A:LYS:H	1:50:A:LYS:H	19	0.1
(1,531)	1:49:A:LYS:H	1:50:A:LYS:H	21	0.1
(1,484)	1:40:A:ILE:HG21	1:42:A:PHE:HD1	4	0.1
(1,484)	1:40:A:ILE:HG21	1:42:A:PHE:HD2	4	0.1
(1,484)	1:40:A:ILE:HG22	1:42:A:PHE:HD1	4	0.1
(1,484)	1:40:A:ILE:HG22	1:42:A:PHE:HD2	4	0.1
(1,484)	1:40:A:ILE:HG23	1:42:A:PHE:HD1	4	0.1
(1,484)	1:40:A:ILE:HG23	1:42:A:PHE:HD2	4	0.1
(1,482)	1:40:A:ILE:HG13	1:42:A:PHE:HZ	16	0.1
(1,474)	1:40:A:ILE:H	1:40:A:ILE:HB	28	0.1
(1,453)	1:35:A:GLY:H	1:40:A:ILE:HA	11	0.1
(1,434)	1:34:A:GLN:H	1:87:A:LEU:HG	2	0.1
(1,434)	1:34:A:GLN:H	1:87:A:LEU:HG	15	0.1
(1,418)	1:33:A:GLU:HA	1:41:A:HIS:H	16	0.1
(1,418)	1:33:A:GLU:HA	1:41:A:HIS:H	19	0.1
(1,418)	1:33:A:GLU:HA	1:41:A:HIS:H	28	0.1
(1,414)	1:33:A:GLU:H	1:41:A:HIS:HA	26	0.1
(1,372)	1:31:A:GLN:H	1:91:A:TRP:H	28	0.1
(1,363)	1:30:A:TYR:HB3	1:43:A:GLN:H	24	0.1
(1,358)	1:30:A:TYR:H	1:92:A:GLU:HA	28	0.1
(1,323)	1:28:A:LEU:H	1:94:A:GLY:HA2	13	0.1
(1,323)	1:28:A:LEU:H	1:94:A:GLY:HA2	24	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,307)	1:27:A:TYR:HA	1:27:A:TYR:HE1	16	0.1
(1,307)	1:27:A:TYR:HA	1:27:A:TYR:HE2	16	0.1
(1,302)	1:27:A:TYR:H	1:46:A:ILE:HA	11	0.1
(1,302)	1:27:A:TYR:H	1:46:A:ILE:HA	12	0.1
(1,265)	1:23:A:ASP:HA	1:25:A:MET:H	25	0.1
(1,171)	1:14:A:ASN:H	1:40:A:ILE:HA	21	0.1
(1,125)	1:11:A:THR:HA	1:44:A:GLY:H	19	0.1
(1,100)	1:10:A:PHE:HD1	1:64:A:ALA:H	7	0.1
(1,100)	1:10:A:PHE:HD2	1:64:A:ALA:H	7	0.1
(1,61)	1:8:A:TRP:HZ3	1:67:A:GLU:HA	5	0.1
(1,37)	1:8:A:TRP:HD1	1:48:A:MET:HA	19	0.1
(1,33)	1:8:A:TRP:HA	1:68:A:LYS:HA	27	0.1
(1,15)	1:6:A:ILE:HG12	1:73:A:GLN:H	19	0.1

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

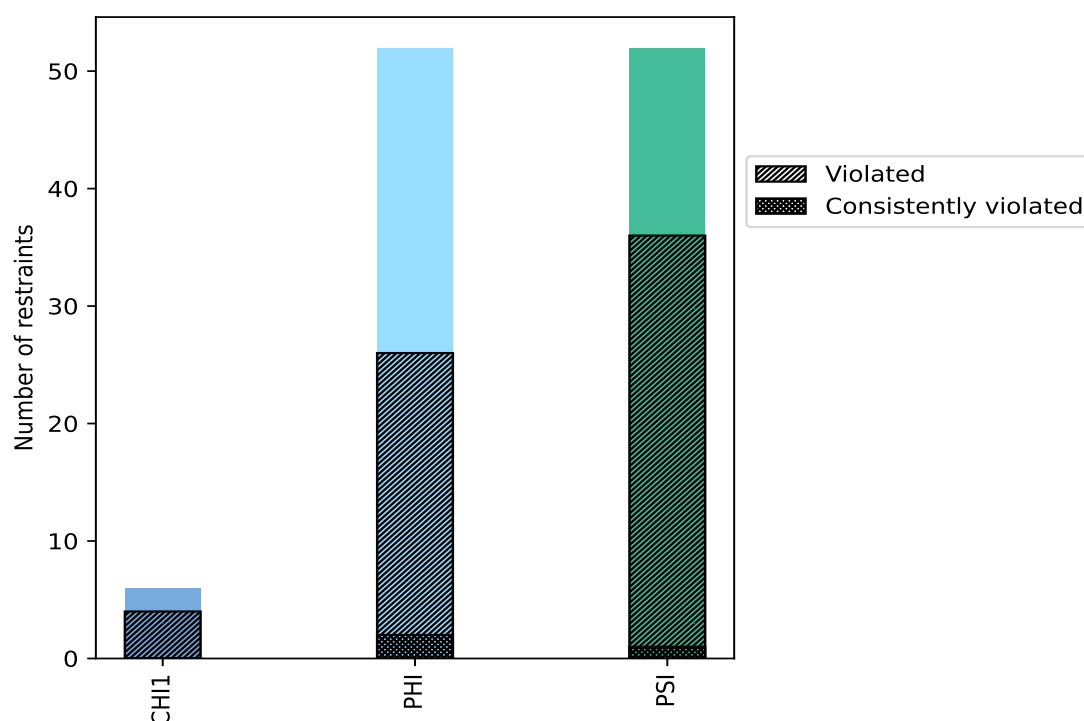
10.1 Summary of dihedral-angle violations [i](#)

The following table provides the summary of dihedral-angle violations in different dihedral-angle types. Violations less than 1° are not included in the calculation.

Angle type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
CHI1	6	5.5	4	66.7	3.6	0	0.0	0.0
PHI	52	47.3	26	50.0	23.6	2	3.8	1.8
PSI	52	47.3	36	69.2	32.7	1	1.9	0.9
Total	110	100.0	66	60.0	60.0	3	2.7	2.7

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](#)



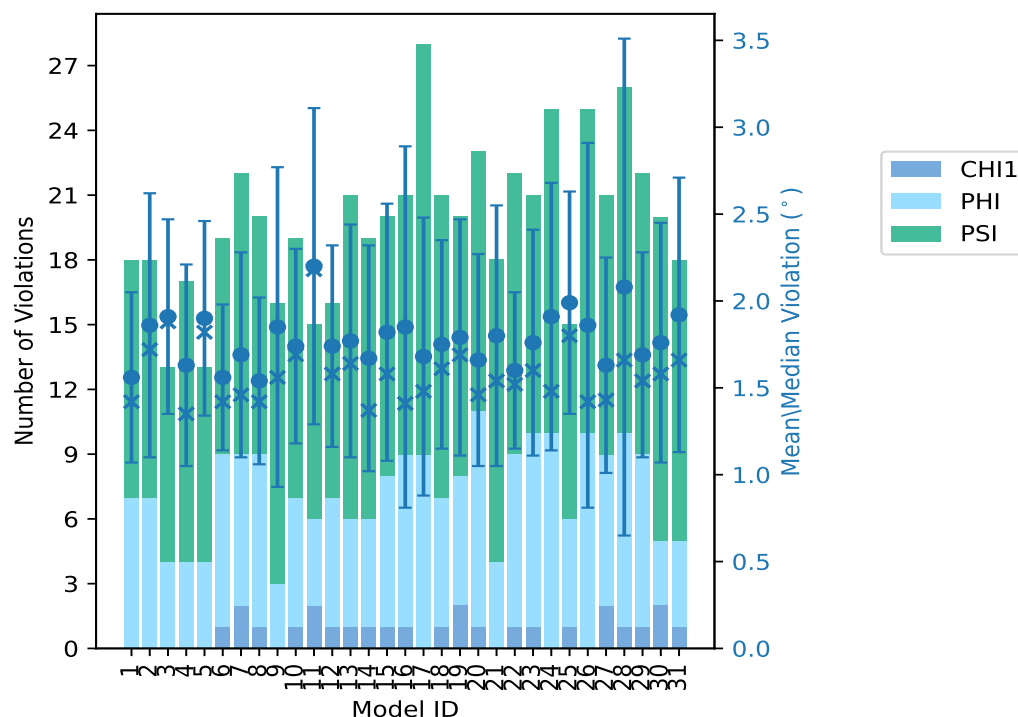
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

10.2 Dihedral-angle violation statistics for each model

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 (°)
	CHI1	PHI	PSI	Total				
1	0	7	11	18	1.56	2.66	0.49	1.42
2	0	7	11	18	1.86	4.43	0.76	1.72
3	0	4	9	13	1.91	3.01	0.56	1.88
4	0	4	13	17	1.63	2.9	0.58	1.35
5	0	4	9	13	1.9	2.96	0.56	1.82
6	1	8	10	19	1.56	2.7	0.42	1.42
7	2	7	13	22	1.69	3.29	0.59	1.46
8	1	8	11	20	1.54	2.74	0.48	1.42
9	0	3	13	16	1.85	4.52	0.92	1.56
10	1	6	12	19	1.74	3.05	0.56	1.69
11	2	4	9	15	2.2	3.79	0.91	2.18
12	1	6	9	16	1.74	3.19	0.58	1.58
13	1	5	15	21	1.77	3.11	0.67	1.64
14	1	5	13	19	1.67	3.11	0.65	1.37
15	1	7	12	20	1.82	3.51	0.74	1.58
16	1	8	12	21	1.85	5.48	1.04	1.41
17	0	9	19	28	1.68	5.03	0.8	1.48
18	1	6	14	21	1.75	3.93	0.6	1.61
19	2	6	12	20	1.79	3.35	0.68	1.69
20	1	10	12	23	1.66	3.75	0.61	1.46
21	0	4	14	18	1.8	3.78	0.75	1.54
22	1	8	13	22	1.6	2.67	0.45	1.52
23	1	9	11	21	1.76	3.72	0.65	1.6
24	0	10	15	25	1.91	3.69	0.77	1.48
25	1	5	9	15	1.99	3.3	0.64	1.8
26	0	10	15	25	1.86	5.24	1.05	1.42
27	2	7	12	21	1.63	3.55	0.62	1.43
28	1	9	16	26	2.08	8.11	1.43	1.66
29	1	8	13	22	1.69	3.71	0.59	1.54
30	2	3	15	20	1.76	3.38	0.69	1.58
31	1	4	13	18	1.92	3.84	0.79	1.66

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	
CHI1	PHI	PSI	Total	Count ¹	%
0	7	6	13	1	3.2
2	2	5	9	2	6.5
0	3	3	6	3	9.7
0	2	2	4	4	12.9
0	0	3	3	5	16.1
0	0	1	1	6	19.4
0	2	0	2	7	22.6
0	1	1	2	8	25.8
1	2	0	3	9	29.0
0	0	1	1	10	32.3
0	0	1	1	11	35.5

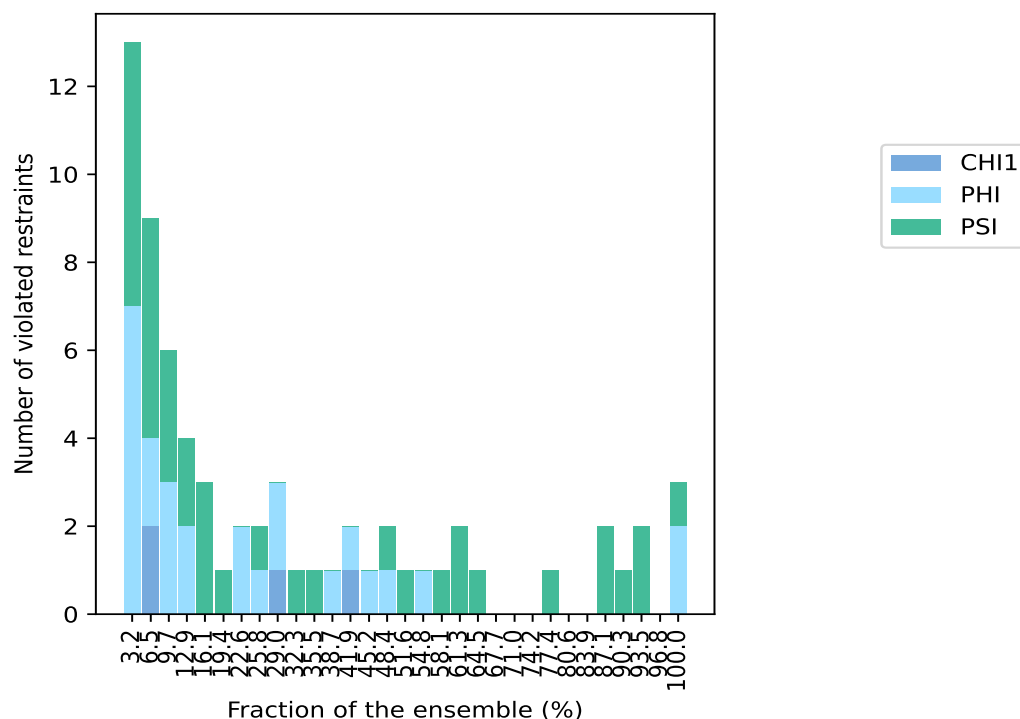
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Number of violated restraints				Fraction of the ensemble	
CHI1	PHI	PSI	Total	Count ¹	%
0	1	0	1	12	38.7
1	1	0	2	13	41.9
0	1	0	1	14	45.2
0	1	1	2	15	48.4
0	0	1	1	16	51.6
0	1	0	1	17	54.8
0	0	1	1	18	58.1
0	0	2	2	19	61.3
0	0	1	1	20	64.5
0	0	0	0	21	67.7
0	0	0	0	22	71.0
0	0	0	0	23	74.2
0	0	1	1	24	77.4
0	0	0	0	25	80.6
0	0	0	0	26	83.9
0	0	2	2	27	87.1
0	0	1	1	28	90.3
0	0	2	2	29	93.5
0	0	0	0	30	96.8
0	2	1	3	31	100.0

¹ Number of models with violations

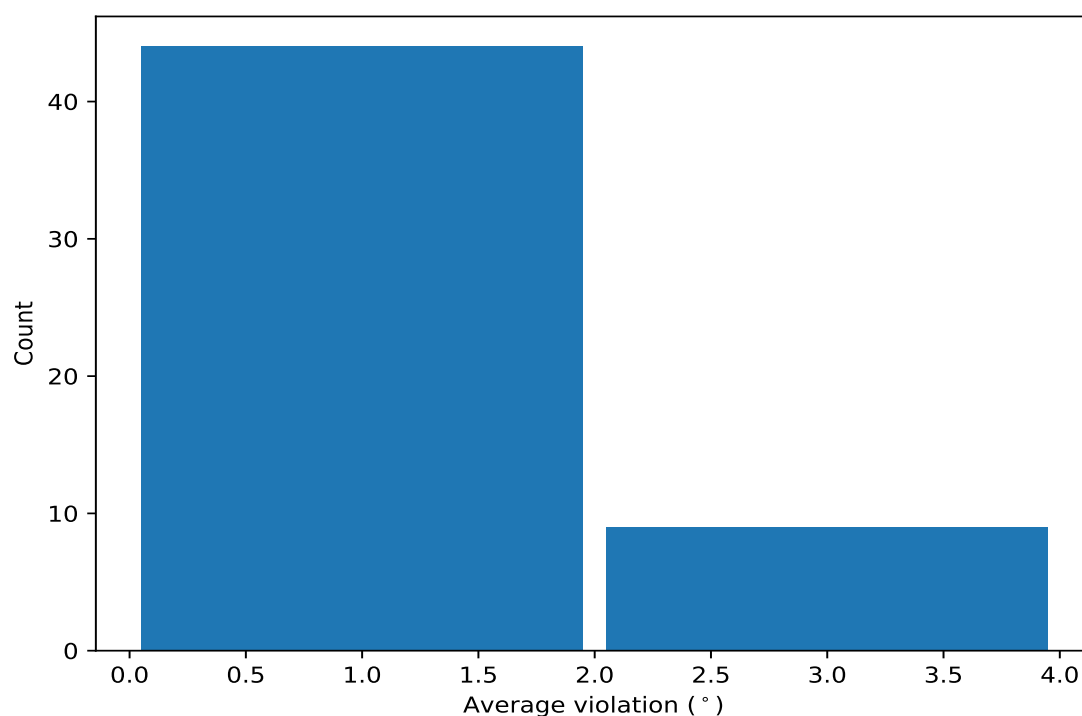
10.3.1 Bar graph : Dihedral-angle Violation statistics for the ensemble [i](#)



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
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	31	2.68	1.02	2.39
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	31	2.43	0.65	2.52
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	31	2.32	0.48	2.24
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	29	2.08	0.63	2.04
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	29	1.65	0.38	1.64
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	28	1.43	0.32	1.38
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	27	1.87	0.76	1.71
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	27	1.4	0.24	1.42
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	24	2.43	0.79	2.33
(1,10)	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	1:9:A:CYS:N	20	1.94	0.88	1.62
(1,94)	1:85:A:THR:N	1:85:A:THR:CA	1:85:A:THR:C	1:86:A:ARG:N	19	1.57	0.6	1.5
(1,6)	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	1:7:A:CYS:N	19	1.38	0.36	1.27
(1,84)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:ALA:N	18	2.05	0.61	2.02
(1,33)	1:29:A:VAL:C	1:30:A:TYR:N	1:30:A:TYR:CA	1:30:A:TYR:C	17	1.72	0.38	1.65
(1,64)	1:54:A:LEU:N	1:54:A:LEU:CA	1:54:A:LEU:C	1:55:A:ALA:N	16	1.29	0.17	1.21
(1,37)	1:31:A:GLN:C	1:32:A:THR:N	1:32:A:THR:CA	1:32:A:THR:C	15	1.99	0.69	2.01
(1,32)	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	1:30:A:TYR:N	15	1.53	0.42	1.47
(1,89)	1:82:A:LYS:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	14	1.58	0.68	1.23
(1,107)	1:42:A:PHE:N	1:42:A:PHE:CA	1:42:A:PHE:CB	1:42:A:PHE:CG	13	1.87	0.5	1.82
(1,5)	1:5:A:VAL:C	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	13	1.24	0.2	1.18
(1,85)	1:75:A:GLU:C	1:76:A:ALA:N	1:76:A:ALA:CA	1:76:A:ALA:C	12	1.78	0.46	1.68

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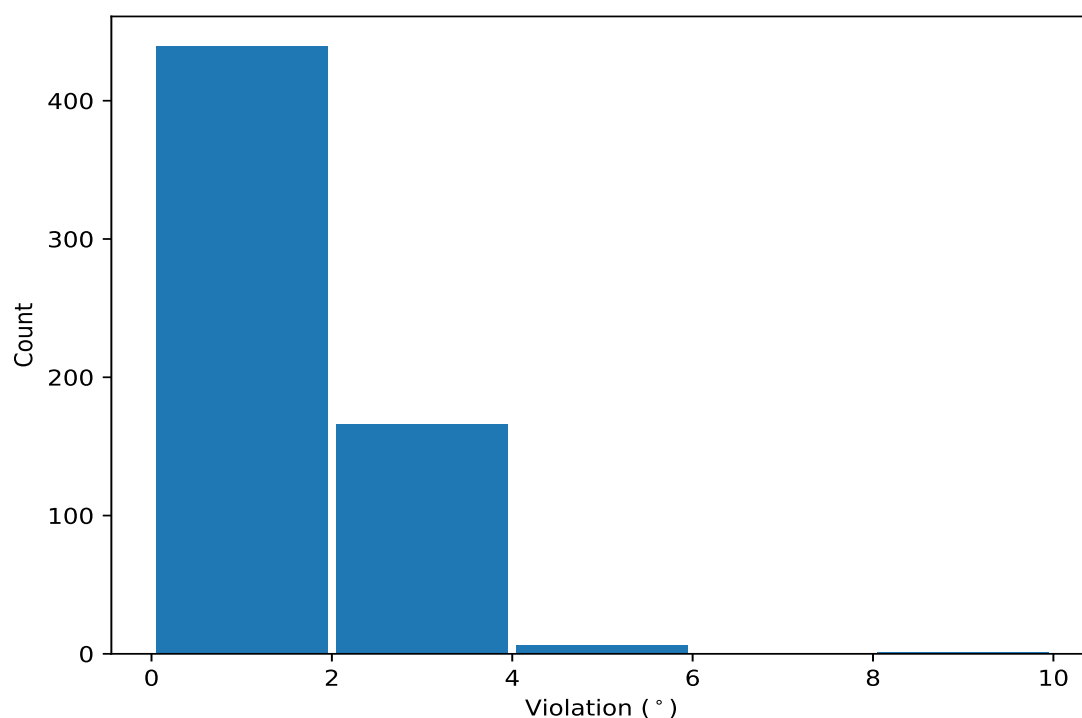
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,74)	1:59:A:LYS:N	1:59:A:LYS:CA	1:59:A:LYS:C	1:60:A:LEU:N	11	1.27	0.17	1.21
(1,76)	1:60:A:LEU:N	1:60:A:LEU:CA	1:60:A:LEU:C	1:61:A:ILE:N	10	1.24	0.24	1.15
(1,108)	1:66:A:PHE:N	1:66:A:PHE:CA	1:66:A:PHE:CB	1:66:A:PHE:CG	9	1.7	0.46	1.78
(1,73)	1:58:A:LYS:C	1:59:A:LYS:N	1:59:A:LYS:CA	1:59:A:LYS:C	9	1.35	0.18	1.4
(1,65)	1:54:A:LEU:C	1:55:A:ALA:N	1:55:A:ALA:CA	1:55:A:ALA:C	9	1.28	0.29	1.15
(1,70)	1:57:A:MET:N	1:57:A:MET:CA	1:57:A:MET:C	1:58:A:LYS:N	8	1.31	0.25	1.21
(1,103)	1:92:A:GLU:C	1:93:A:TYR:N	1:93:A:TYR:CA	1:93:A:TYR:C	8	1.2	0.17	1.14
(1,31)	1:28:A:LEU:C	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	7	1.84	0.73	1.56
(1,71)	1:57:A:MET:C	1:58:A:LYS:N	1:58:A:LYS:CA	1:58:A:LYS:C	7	1.43	0.3	1.46
(1,54)	1:46:A:ILE:N	1:46:A:ILE:CA	1:46:A:ILE:C	1:47:A:GLU:N	6	1.22	0.15	1.17
(1,30)	1:28:A:LEU:N	1:28:A:LEU:CA	1:28:A:LEU:C	1:29:A:VAL:N	5	2.15	0.49	2.15
(1,90)	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	1:84:A:ASP:N	5	1.38	0.32	1.34
(1,102)	1:92:A:GLU:N	1:92:A:GLU:CA	1:92:A:GLU:C	1:93:A:TYR:N	5	1.21	0.13	1.27
(1,104)	1:93:A:TYR:N	1:93:A:TYR:CA	1:93:A:TYR:C	1:94:A:GLY:N	4	1.69	0.18	1.76
(1,75)	1:59:A:LYS:C	1:60:A:LEU:N	1:60:A:LEU:CA	1:60:A:LEU:C	4	1.42	0.12	1.42
(1,67)	1:55:A:ALA:C	1:56:A:GLY:N	1:56:A:GLY:CA	1:56:A:GLY:C	4	1.42	0.13	1.41
(1,62)	1:53:A:SER:N	1:53:A:SER:CA	1:53:A:SER:C	1:54:A:LEU:N	4	1.18	0.13	1.18
(1,88)	1:79:A:TYR:N	1:79:A:TYR:CA	1:79:A:TYR:C	1:80:A:SER:N	3	3.47	3.28	1.21
(1,49)	1:42:A:PHE:C	1:43:A:GLN:N	1:43:A:GLN:CA	1:43:A:GLN:C	3	1.79	0.44	1.73
(1,98)	1:88:A:GLU:N	1:88:A:GLU:CA	1:88:A:GLU:C	1:89:A:GLY:N	3	1.38	0.37	1.18
(1,101)	1:91:A:TRP:C	1:92:A:GLU:N	1:92:A:GLU:CA	1:92:A:GLU:C	3	1.32	0.26	1.26
(1,92)	1:84:A:ASP:N	1:84:A:ASP:CA	1:84:A:ASP:C	1:85:A:THR:N	3	1.14	0.13	1.07
(1,57)	1:47:A:GLU:C	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	3	1.13	0.01	1.13
(1,40)	1:33:A:GLU:N	1:33:A:GLU:CA	1:33:A:GLU:C	1:34:A:GLN:N	2	2.76	1.66	2.76
(1,42)	1:34:A:GLN:N	1:34:A:GLN:CA	1:34:A:GLN:C	1:35:A:GLY:N	2	1.87	0.5	1.87
(1,68)	1:56:A:GLY:N	1:56:A:GLY:CA	1:56:A:GLY:C	1:57:A:MET:N	2	1.84	0.39	1.84
(1,105)	1:22:A:HIS:N	1:22:A:HIS:CA	1:22:A:HIS:CB	1:22:A:HIS:CG	2	1.6	0.02	1.6
(1,106)	1:65:A:HIS:N	1:65:A:HIS:CA	1:65:A:HIS:CB	1:65:A:HIS:CG	2	1.31	0.24	1.31
(1,83)	1:74:A:GLY:C	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	2	1.27	0.21	1.27
(1,82)	1:67:A:GLU:N	1:67:A:GLU:CA	1:67:A:GLU:C	1:68:A:LYS:N	2	1.21	0.02	1.21
(1,17)	1:11:A:THR:C	1:12:A:LEU:N	1:12:A:LEU:CA	1:12:A:LEU:C	2	1.17	0.17	1.17
(1,52)	1:45:A:TYR:N	1:45:A:TYR:CA	1:45:A:TYR:C	1:46:A:ILE:N	2	1.16	0.06	1.16

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

10.5 All violated dihedral-angle restraints ⓘ

10.5.1 Histogram : Distribution of violations ⓘ

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



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

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

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,88)	1:79:A:TYR:N	1:79:A:TYR:CA	1:79:A:TYR:C	1:80:A:SER:N	28	8.11
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	16	5.48
(1,41)	1:33:A:GLU:C	1:34:A:GLN:N	1:34:A:GLN:CA	1:34:A:GLN:C	26	5.24
(1,10)	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	1:9:A:CYS:N	17	5.03
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	9	4.52
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	2	4.43
(1,40)	1:33:A:GLU:N	1:33:A:GLU:CA	1:33:A:GLU:C	1:34:A:GLN:N	26	4.42
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	18	3.93
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	28	3.93
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	31	3.84
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	11	3.79
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	21	3.78
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	20	3.75
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	11	3.74
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	23	3.72
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	29	3.71
(1,94)	1:85:A:THR:N	1:85:A:THR:CA	1:85:A:THR:C	1:86:A:ARG:N	24	3.69
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	27	3.55
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	28	3.51
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	15	3.51
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	16	3.51

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	24	3.46
(1,37)	1:31:A:GLN:C	1:32:A:THR:N	1:32:A:THR:CA	1:32:A:THR:C	11	3.44
(1,89)	1:82:A:LYS:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	30	3.38
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	15	3.38
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	19	3.35
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	25	3.3
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	7	3.29
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	30	3.23
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	9	3.21
(1,10)	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	1:9:A:CYS:N	25	3.2
(1,37)	1:31:A:GLN:C	1:32:A:THR:N	1:32:A:THR:CA	1:32:A:THR:C	28	3.19
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	12	3.19
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	31	3.16
(1,84)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:ALA:N	24	3.15
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	13	3.11
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	14	3.11
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	19	3.09
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	13	3.07
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	26	3.06
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	23	3.06
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	10	3.05
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	3	3.01
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	19	2.99
(1,31)	1:28:A:LEU:C	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	28	2.97
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	5	2.96
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	17	2.95
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	31	2.95
(1,84)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:ALA:N	13	2.92
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	26	2.92
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	4	2.9
(1,85)	1:75:A:GLU:C	1:76:A:ALA:N	1:76:A:ALA:CA	1:76:A:ALA:C	24	2.87
(1,31)	1:28:A:LEU:C	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	24	2.84
(1,30)	1:28:A:LEU:N	1:28:A:LEU:CA	1:28:A:LEU:C	1:29:A:VAL:N	21	2.84
(1,84)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:ALA:N	15	2.82
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	5	2.82
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	14	2.82
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	21	2.81
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	11	2.8
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	12	2.79
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	21	2.77
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	8	2.74
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	6	2.7
(1,107)	1:42:A:PHE:N	1:42:A:PHE:CA	1:42:A:PHE:CB	1:42:A:PHE:CG	31	2.69
(1,84)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:ALA:N	14	2.67
(1,84)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:ALA:N	22	2.67
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	1	2.66
(1,107)	1:42:A:PHE:N	1:42:A:PHE:CA	1:42:A:PHE:CB	1:42:A:PHE:CG	11	2.65
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	30	2.65
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	10	2.63
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	8	2.61
(1,108)	1:66:A:PHE:N	1:66:A:PHE:CA	1:66:A:PHE:CB	1:66:A:PHE:CG	30	2.6

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,27)	1:26:A:LYS:C	1:27:A:TYR:N	1:27:A:TYR:CA	1:27:A:TYR:C	27	2.6
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	3	2.59
(1,89)	1:82:A:LYS:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	16	2.58
(1,10)	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	1:9:A:CYS:N	11	2.58
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	7	2.58
(1,84)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:ALA:N	20	2.57
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	25	2.56
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	17	2.54
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	2	2.54
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	1	2.54
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	24	2.54
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	25	2.53
(1,10)	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	1:9:A:CYS:N	29	2.52
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	20	2.52
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	24	2.52
(1,30)	1:28:A:LEU:N	1:28:A:LEU:CA	1:28:A:LEU:C	1:29:A:VAL:N	28	2.51
(1,37)	1:31:A:GLN:C	1:32:A:THR:N	1:32:A:THR:CA	1:32:A:THR:C	16	2.5
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	4	2.5
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	16	2.49
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	3	2.48
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	18	2.48
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	14	2.47
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	15	2.45
(1,32)	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	1:30:A:TYR:N	3	2.45
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	18	2.44
(1,33)	1:29:A:VAL:C	1:30:A:TYR:N	1:30:A:TYR:CA	1:30:A:TYR:C	5	2.43
(1,33)	1:29:A:VAL:C	1:30:A:TYR:N	1:30:A:TYR:CA	1:30:A:TYR:C	29	2.43
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1	2.42
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	22	2.41
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	13	2.41
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	19	2.39
(1,6)	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	1:7:A:CYS:N	9	2.39
(1,107)	1:42:A:PHE:N	1:42:A:PHE:CA	1:42:A:PHE:CB	1:42:A:PHE:CG	10	2.38
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	9	2.38
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	16	2.38
(1,42)	1:34:A:GLN:N	1:34:A:GLN:CA	1:34:A:GLN:C	1:35:A:GLY:N	26	2.37
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	23	2.37
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	4	2.37
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	17	2.37
(1,49)	1:42:A:PHE:C	1:43:A:GLN:N	1:43:A:GLN:CA	1:43:A:GLN:C	26	2.36
(1,37)	1:31:A:GLN:C	1:32:A:THR:N	1:32:A:THR:CA	1:32:A:THR:C	6	2.35
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	31	2.34
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	13	2.34
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	7	2.33
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	27	2.32
(1,37)	1:31:A:GLN:C	1:32:A:THR:N	1:32:A:THR:CA	1:32:A:THR:C	26	2.31
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	7	2.31
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	12	2.3
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	9	2.3
(1,107)	1:42:A:PHE:N	1:42:A:PHE:CA	1:42:A:PHE:CB	1:42:A:PHE:CG	25	2.29
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	15	2.27

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,33)	1:29:A:VAL:C	1:30:A:TYR:N	1:30:A:TYR:CA	1:30:A:TYR:C	2	2.27
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	12	2.25
(1,37)	1:31:A:GLN:C	1:32:A:THR:N	1:32:A:THR:CA	1:32:A:THR:C	7	2.25
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	2	2.25
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	2	2.25
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	10	2.24
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	4	2.24
(1,89)	1:82:A:LYS:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	15	2.23
(1,68)	1:56:A:GLY:N	1:56:A:GLY:CA	1:56:A:GLY:C	1:57:A:MET:N	28	2.23
(1,32)	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	1:30:A:TYR:N	5	2.23
(1,85)	1:75:A:GLU:C	1:76:A:ALA:N	1:76:A:ALA:CA	1:76:A:ALA:C	22	2.22
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	31	2.21
(1,85)	1:75:A:GLU:C	1:76:A:ALA:N	1:76:A:ALA:CA	1:76:A:ALA:C	14	2.2
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	31	2.19
(1,94)	1:85:A:THR:N	1:85:A:THR:CA	1:85:A:THR:C	1:86:A:ARG:N	15	2.18
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	11	2.18
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	11	2.18
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	13	2.16
(1,30)	1:28:A:LEU:N	1:28:A:LEU:CA	1:28:A:LEU:C	1:29:A:VAL:N	24	2.15
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	4	2.15
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	17	2.14
(1,37)	1:31:A:GLN:C	1:32:A:THR:N	1:32:A:THR:CA	1:32:A:THR:C	24	2.14
(1,10)	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	1:9:A:CYS:N	23	2.13
(1,107)	1:42:A:PHE:N	1:42:A:PHE:CA	1:42:A:PHE:CB	1:42:A:PHE:CG	7	2.12
(1,94)	1:85:A:THR:N	1:85:A:THR:CA	1:85:A:THR:C	1:86:A:ARG:N	13	2.12
(1,84)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:ALA:N	10	2.12
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	6	2.11
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	7	2.11
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	22	2.11
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	28	2.09
(1,84)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:ALA:N	27	2.08
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	27	2.07
(1,84)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:ALA:N	19	2.06
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	8	2.06
(1,10)	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	1:9:A:CYS:N	18	2.06
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	30	2.06
(1,108)	1:66:A:PHE:N	1:66:A:PHE:CA	1:66:A:PHE:CB	1:66:A:PHE:CG	20	2.05
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	20	2.05
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	5	2.04
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	27	2.03
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	7	2.03
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	5	2.03
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	28	2.02
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	17	2.02
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	23	2.01
(1,37)	1:31:A:GLN:C	1:32:A:THR:N	1:32:A:THR:CA	1:32:A:THR:C	19	2.01
(1,10)	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	1:9:A:CYS:N	30	2.01
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	8	2.0
(1,31)	1:28:A:LEU:C	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	13	2.0
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	22	2.0
(1,84)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:ALA:N	23	1.98

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	10	1.98
(1,84)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:ALA:N	29	1.97
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	29	1.97
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	29	1.97
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	4	1.96
(1,85)	1:75:A:GLU:C	1:76:A:ALA:N	1:76:A:ALA:CA	1:76:A:ALA:C	20	1.95
(1,33)	1:29:A:VAL:C	1:30:A:TYR:N	1:30:A:TYR:CA	1:30:A:TYR:C	3	1.95
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	6	1.95
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	23	1.95
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	2	1.94
(1,10)	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	1:9:A:CYS:N	21	1.94
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	17	1.94
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	2	1.93
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	3	1.93
(1,33)	1:29:A:VAL:C	1:30:A:TYR:N	1:30:A:TYR:CA	1:30:A:TYR:C	9	1.93
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	14	1.93
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	21	1.93
(1,108)	1:66:A:PHE:N	1:66:A:PHE:CA	1:66:A:PHE:CB	1:66:A:PHE:CG	23	1.92
(1,90)	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	1:84:A:ASP:N	13	1.92
(1,108)	1:66:A:PHE:N	1:66:A:PHE:CA	1:66:A:PHE:CB	1:66:A:PHE:CG	22	1.91
(1,10)	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	1:9:A:CYS:N	10	1.91
(1,98)	1:88:A:GLU:N	1:88:A:GLU:CA	1:88:A:GLU:C	1:89:A:GLY:N	24	1.9
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	26	1.9
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	20	1.89
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	21	1.89
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	10	1.88
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	18	1.88
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	3	1.88
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	29	1.88
(1,65)	1:54:A:LEU:C	1:55:A:ALA:N	1:55:A:ALA:CA	1:55:A:ALA:C	25	1.87
(1,32)	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	1:30:A:TYR:N	9	1.87
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	25	1.87
(1,104)	1:93:A:TYR:N	1:93:A:TYR:CA	1:93:A:TYR:C	1:94:A:GLY:N	19	1.86
(1,71)	1:57:A:MET:C	1:58:A:LYS:N	1:58:A:LYS:CA	1:58:A:LYS:C	22	1.86
(1,6)	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	1:7:A:CYS:N	16	1.86
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	10	1.85
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	18	1.85
(1,107)	1:42:A:PHE:N	1:42:A:PHE:CA	1:42:A:PHE:CB	1:42:A:PHE:CG	16	1.84
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	8	1.84
(1,89)	1:82:A:LYS:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	11	1.83
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	30	1.83
(1,33)	1:29:A:VAL:C	1:30:A:TYR:N	1:30:A:TYR:CA	1:30:A:TYR:C	1	1.83
(1,32)	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	1:30:A:TYR:N	2	1.83
(1,107)	1:42:A:PHE:N	1:42:A:PHE:CA	1:42:A:PHE:CB	1:42:A:PHE:CG	15	1.82
(1,85)	1:75:A:GLU:C	1:76:A:ALA:N	1:76:A:ALA:CA	1:76:A:ALA:C	15	1.82
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	5	1.82
(1,94)	1:85:A:THR:N	1:85:A:THR:CA	1:85:A:THR:C	1:86:A:ARG:N	28	1.81
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	12	1.81
(1,6)	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	1:7:A:CYS:N	18	1.81
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	25	1.8
(1,71)	1:57:A:MET:C	1:58:A:LYS:N	1:58:A:LYS:CA	1:58:A:LYS:C	29	1.79

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	7	1.79
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	20	1.79
(1,6)	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	1:7:A:CYS:N	19	1.79
(1,108)	1:66:A:PHE:N	1:66:A:PHE:CA	1:66:A:PHE:CB	1:66:A:PHE:CG	18	1.78
(1,76)	1:60:A:LEU:N	1:60:A:LEU:CA	1:60:A:LEU:C	1:61:A:ILE:N	31	1.78
(1,104)	1:93:A:TYR:N	1:93:A:TYR:CA	1:93:A:TYR:C	1:94:A:GLY:N	31	1.77
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	11	1.77
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	21	1.76
(1,104)	1:93:A:TYR:N	1:93:A:TYR:CA	1:93:A:TYR:C	1:94:A:GLY:N	30	1.75
(1,89)	1:82:A:LYS:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	27	1.75
(1,37)	1:31:A:GLN:C	1:32:A:THR:N	1:32:A:THR:CA	1:32:A:THR:C	25	1.75
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	2	1.75
(1,107)	1:42:A:PHE:N	1:42:A:PHE:CA	1:42:A:PHE:CB	1:42:A:PHE:CG	19	1.73
(1,49)	1:42:A:PHE:C	1:43:A:GLN:N	1:43:A:GLN:CA	1:43:A:GLN:C	18	1.73
(1,6)	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	1:7:A:CYS:N	21	1.73
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	3	1.72
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	25	1.72
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	6	1.72
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	19	1.72
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	23	1.72
(1,65)	1:54:A:LEU:C	1:55:A:ALA:N	1:55:A:ALA:CA	1:55:A:ALA:C	14	1.71
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	16	1.71
(1,32)	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	1:30:A:TYR:N	29	1.71
(1,5)	1:5:A:VAL:C	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	17	1.71
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	9	1.7
(1,37)	1:31:A:GLN:C	1:32:A:THR:N	1:32:A:THR:CA	1:32:A:THR:C	2	1.7
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	1	1.7
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	28	1.7
(1,85)	1:75:A:GLU:C	1:76:A:ALA:N	1:76:A:ALA:CA	1:76:A:ALA:C	10	1.69
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	1	1.69
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	26	1.69
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	28	1.69
(1,94)	1:85:A:THR:N	1:85:A:THR:CA	1:85:A:THR:C	1:86:A:ARG:N	8	1.68
(1,85)	1:75:A:GLU:C	1:76:A:ALA:N	1:76:A:ALA:CA	1:76:A:ALA:C	27	1.68
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	6	1.68
(1,33)	1:29:A:VAL:C	1:30:A:TYR:N	1:30:A:TYR:CA	1:30:A:TYR:C	22	1.68
(1,7)	1:6:A:ILE:C	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	12	1.68
(1,101)	1:91:A:TRP:C	1:92:A:GLU:N	1:92:A:GLU:CA	1:92:A:GLU:C	24	1.67
(1,85)	1:75:A:GLU:C	1:76:A:ALA:N	1:76:A:ALA:CA	1:76:A:ALA:C	19	1.67
(1,30)	1:28:A:LEU:N	1:28:A:LEU:CA	1:28:A:LEU:C	1:29:A:VAL:N	13	1.67
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	28	1.67
(1,33)	1:29:A:VAL:C	1:30:A:TYR:N	1:30:A:TYR:CA	1:30:A:TYR:C	17	1.66
(1,70)	1:57:A:MET:N	1:57:A:MET:CA	1:57:A:MET:C	1:58:A:LYS:N	18	1.65
(1,64)	1:54:A:LEU:N	1:54:A:LEU:CA	1:54:A:LEU:C	1:55:A:ALA:N	14	1.65
(1,33)	1:29:A:VAL:C	1:30:A:TYR:N	1:30:A:TYR:CA	1:30:A:TYR:C	28	1.65
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	15	1.65
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	26	1.65
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	22	1.64
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	23	1.64
(1,33)	1:29:A:VAL:C	1:30:A:TYR:N	1:30:A:TYR:CA	1:30:A:TYR:C	20	1.64
(1,10)	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	1:9:A:CYS:N	13	1.64

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,70)	1:57:A:MET:N	1:57:A:MET:CA	1:57:A:MET:C	1:58:A:LYS:N	12	1.63
(1,105)	1:22:A:HIS:N	1:22:A:HIS:CA	1:22:A:HIS:CB	1:22:A:HIS:CG	19	1.62
(1,32)	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	1:30:A:TYR:N	10	1.62
(1,94)	1:85:A:THR:N	1:85:A:THR:CA	1:85:A:THR:C	1:86:A:ARG:N	7	1.61
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	18	1.61
(1,75)	1:59:A:LYS:C	1:60:A:LEU:N	1:60:A:LEU:CA	1:60:A:LEU:C	23	1.6
(1,64)	1:54:A:LEU:N	1:54:A:LEU:CA	1:54:A:LEU:C	1:55:A:ALA:N	25	1.6
(1,94)	1:85:A:THR:N	1:85:A:THR:CA	1:85:A:THR:C	1:86:A:ARG:N	30	1.59
(1,84)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:ALA:N	4	1.59
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	3	1.59
(1,10)	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	1:9:A:CYS:N	12	1.59
(1,105)	1:22:A:HIS:N	1:22:A:HIS:CA	1:22:A:HIS:CB	1:22:A:HIS:CG	30	1.58
(1,70)	1:57:A:MET:N	1:57:A:MET:CA	1:57:A:MET:C	1:58:A:LYS:N	19	1.58
(1,67)	1:55:A:ALA:C	1:56:A:GLY:N	1:56:A:GLY:CA	1:56:A:GLY:C	23	1.58
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	8	1.58
(1,76)	1:60:A:LEU:N	1:60:A:LEU:CA	1:60:A:LEU:C	1:61:A:ILE:N	30	1.57
(1,69)	1:56:A:GLY:C	1:57:A:MET:N	1:57:A:MET:CA	1:57:A:MET:C	28	1.57
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	6	1.57
(1,84)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:ALA:N	18	1.56
(1,73)	1:58:A:LYS:C	1:59:A:LYS:N	1:59:A:LYS:CA	1:59:A:LYS:C	12	1.56
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	5	1.56
(1,31)	1:28:A:LEU:C	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	17	1.56
(1,30)	1:28:A:LEU:N	1:28:A:LEU:CA	1:28:A:LEU:C	1:29:A:VAL:N	17	1.56
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	8	1.56
(1,108)	1:66:A:PHE:N	1:66:A:PHE:CA	1:66:A:PHE:CB	1:66:A:PHE:CG	29	1.55
(1,107)	1:42:A:PHE:N	1:42:A:PHE:CA	1:42:A:PHE:CB	1:42:A:PHE:CG	28	1.55
(1,94)	1:85:A:THR:N	1:85:A:THR:CA	1:85:A:THR:C	1:86:A:ARG:N	26	1.55
(1,84)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:ALA:N	2	1.55
(1,84)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:ALA:N	25	1.55
(1,74)	1:59:A:LYS:N	1:59:A:LYS:CA	1:59:A:LYS:C	1:60:A:LEU:N	18	1.55
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	22	1.55
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	29	1.55
(1,106)	1:65:A:HIS:N	1:65:A:HIS:CA	1:65:A:HIS:CB	1:65:A:HIS:CG	12	1.54
(1,64)	1:54:A:LEU:N	1:54:A:LEU:CA	1:54:A:LEU:C	1:55:A:ALA:N	22	1.54
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	31	1.54
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	29	1.54
(1,33)	1:29:A:VAL:C	1:30:A:TYR:N	1:30:A:TYR:CA	1:30:A:TYR:C	4	1.54
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	5	1.54
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	6	1.54
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	25	1.54
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	26	1.53
(1,90)	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	1:84:A:ASP:N	17	1.52
(1,67)	1:55:A:ALA:C	1:56:A:GLY:N	1:56:A:GLY:CA	1:56:A:GLY:C	20	1.52
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	10	1.52
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	28	1.52
(1,103)	1:92:A:GLU:C	1:93:A:TYR:N	1:93:A:TYR:CA	1:93:A:TYR:C	24	1.51
(1,94)	1:85:A:THR:N	1:85:A:THR:CA	1:85:A:THR:C	1:86:A:ARG:N	27	1.51
(1,85)	1:75:A:GLU:C	1:76:A:ALA:N	1:76:A:ALA:CA	1:76:A:ALA:C	23	1.51
(1,33)	1:29:A:VAL:C	1:30:A:TYR:N	1:30:A:TYR:CA	1:30:A:TYR:C	7	1.51
(1,5)	1:5:A:VAL:C	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	2	1.51
(1,94)	1:85:A:THR:N	1:85:A:THR:CA	1:85:A:THR:C	1:86:A:ARG:N	17	1.5

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,73)	1:58:A:LYS:C	1:59:A:LYS:N	1:59:A:LYS:CA	1:59:A:LYS:C	8	1.5
(1,73)	1:58:A:LYS:C	1:59:A:LYS:N	1:59:A:LYS:CA	1:59:A:LYS:C	23	1.5
(1,54)	1:46:A:ILE:N	1:46:A:ILE:CA	1:46:A:ILE:C	1:47:A:GLU:N	15	1.5
(1,10)	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	1:9:A:CYS:N	31	1.5
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	20	1.5
(1,84)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:ALA:N	12	1.49
(1,74)	1:59:A:LYS:N	1:59:A:LYS:CA	1:59:A:LYS:C	1:60:A:LEU:N	31	1.49
(1,71)	1:57:A:MET:C	1:58:A:LYS:N	1:58:A:LYS:CA	1:58:A:LYS:C	23	1.49
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	27	1.49
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	17	1.49
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	22	1.49
(1,89)	1:82:A:LYS:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	24	1.48
(1,83)	1:74:A:GLY:C	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	29	1.48
(1,32)	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	1:30:A:TYR:N	1	1.48
(1,10)	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	1:9:A:CYS:N	24	1.48
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	13	1.47
(1,32)	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	1:30:A:TYR:N	17	1.47
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	3	1.47
(1,10)	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	1:9:A:CYS:N	2	1.47
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	5	1.47
(1,71)	1:57:A:MET:C	1:58:A:LYS:N	1:58:A:LYS:CA	1:58:A:LYS:C	20	1.46
(1,35)	1:30:A:TYR:C	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	24	1.46
(1,85)	1:75:A:GLU:C	1:76:A:ALA:N	1:76:A:ALA:CA	1:76:A:ALA:C	2	1.45
(1,68)	1:56:A:GLY:N	1:56:A:GLY:CA	1:56:A:GLY:C	1:57:A:MET:N	30	1.45
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	18	1.45
(1,75)	1:59:A:LYS:C	1:60:A:LEU:N	1:60:A:LEU:CA	1:60:A:LEU:C	20	1.44
(1,73)	1:58:A:LYS:C	1:59:A:LYS:N	1:59:A:LYS:CA	1:59:A:LYS:C	22	1.44
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	24	1.44
(1,33)	1:29:A:VAL:C	1:30:A:TYR:N	1:30:A:TYR:CA	1:30:A:TYR:C	8	1.44
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	6	1.44
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	1	1.43
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	19	1.43
(1,6)	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	1:7:A:CYS:N	27	1.43
(1,107)	1:42:A:PHE:N	1:42:A:PHE:CA	1:42:A:PHE:CB	1:42:A:PHE:CG	6	1.42
(1,107)	1:42:A:PHE:N	1:42:A:PHE:CA	1:42:A:PHE:CB	1:42:A:PHE:CG	13	1.42
(1,94)	1:85:A:THR:N	1:85:A:THR:CA	1:85:A:THR:C	1:86:A:ARG:N	16	1.42
(1,74)	1:59:A:LYS:N	1:59:A:LYS:CA	1:59:A:LYS:C	1:60:A:LEU:N	24	1.42
(1,64)	1:54:A:LEU:N	1:54:A:LEU:CA	1:54:A:LEU:C	1:55:A:ALA:N	26	1.42
(1,64)	1:54:A:LEU:N	1:54:A:LEU:CA	1:54:A:LEU:C	1:55:A:ALA:N	28	1.42
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	7	1.42
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	1	1.42
(1,33)	1:29:A:VAL:C	1:30:A:TYR:N	1:30:A:TYR:CA	1:30:A:TYR:C	23	1.42
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	1	1.42
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	9	1.42
(1,5)	1:5:A:VAL:C	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	26	1.42
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	10	1.42
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	24	1.41
(1,10)	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	1:9:A:CYS:N	5	1.41
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	16	1.41
(1,75)	1:59:A:LYS:C	1:60:A:LEU:N	1:60:A:LEU:CA	1:60:A:LEU:C	8	1.4
(1,73)	1:58:A:LYS:C	1:59:A:LYS:N	1:59:A:LYS:CA	1:59:A:LYS:C	16	1.4

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	18	1.4
(1,104)	1:93:A:TYR:N	1:93:A:TYR:CA	1:93:A:TYR:C	1:94:A:GLY:N	16	1.39
(1,74)	1:59:A:LYS:N	1:59:A:LYS:CA	1:59:A:LYS:C	1:60:A:LEU:N	14	1.39
(1,73)	1:58:A:LYS:C	1:59:A:LYS:N	1:59:A:LYS:CA	1:59:A:LYS:C	20	1.39
(1,33)	1:29:A:VAL:C	1:30:A:TYR:N	1:30:A:TYR:CA	1:30:A:TYR:C	15	1.39
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	11	1.39
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	1	1.39
(1,103)	1:92:A:GLU:C	1:93:A:TYR:N	1:93:A:TYR:CA	1:93:A:TYR:C	7	1.38
(1,33)	1:29:A:VAL:C	1:30:A:TYR:N	1:30:A:TYR:CA	1:30:A:TYR:C	6	1.38
(1,32)	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	1:30:A:TYR:N	28	1.38
(1,42)	1:34:A:GLN:N	1:34:A:GLN:CA	1:34:A:GLN:C	1:35:A:GLY:N	14	1.37
(1,32)	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	1:30:A:TYR:N	7	1.37
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	14	1.37
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	30	1.37
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	29	1.36
(1,10)	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	1:9:A:CYS:N	3	1.36
(1,10)	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	1:9:A:CYS:N	20	1.36
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	3	1.36
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	27	1.36
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	4	1.35
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	21	1.35
(1,102)	1:92:A:GLU:N	1:92:A:GLU:CA	1:92:A:GLU:C	1:93:A:TYR:N	24	1.34
(1,90)	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	1:84:A:ASP:N	24	1.34
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	26	1.34
(1,17)	1:11:A:THR:C	1:12:A:LEU:N	1:12:A:LEU:CA	1:12:A:LEU:C	17	1.34
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	8	1.34
(1,5)	1:5:A:VAL:C	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	21	1.34
(1,76)	1:60:A:LEU:N	1:60:A:LEU:CA	1:60:A:LEU:C	1:61:A:ILE:N	18	1.33
(1,74)	1:59:A:LYS:N	1:59:A:LYS:CA	1:59:A:LYS:C	1:60:A:LEU:N	22	1.33
(1,62)	1:53:A:SER:N	1:53:A:SER:CA	1:53:A:SER:C	1:54:A:LEU:N	17	1.33
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	20	1.33
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	17	1.33
(1,102)	1:92:A:GLU:N	1:92:A:GLU:CA	1:92:A:GLU:C	1:93:A:TYR:N	17	1.32
(1,92)	1:84:A:ASP:N	1:84:A:ASP:CA	1:84:A:ASP:C	1:85:A:THR:N	30	1.32
(1,54)	1:46:A:ILE:N	1:46:A:ILE:CA	1:46:A:ILE:C	1:47:A:GLU:N	18	1.32
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	2	1.32
(1,6)	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	1:7:A:CYS:N	1	1.32
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	4	1.32
(1,94)	1:85:A:THR:N	1:85:A:THR:CA	1:85:A:THR:C	1:86:A:ARG:N	21	1.31
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	29	1.31
(1,6)	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	1:7:A:CYS:N	26	1.31
(1,6)	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	1:7:A:CYS:N	30	1.31
(1,94)	1:85:A:THR:N	1:85:A:THR:CA	1:85:A:THR:C	1:86:A:ARG:N	6	1.3
(1,67)	1:55:A:ALA:C	1:56:A:GLY:N	1:56:A:GLY:CA	1:56:A:GLY:C	8	1.3
(1,62)	1:53:A:SER:N	1:53:A:SER:CA	1:53:A:SER:C	1:54:A:LEU:N	22	1.3
(1,37)	1:31:A:GLN:C	1:32:A:THR:N	1:32:A:THR:CA	1:32:A:THR:C	10	1.3
(1,32)	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	1:30:A:TYR:N	6	1.3
(1,5)	1:5:A:VAL:C	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	6	1.3
(1,89)	1:82:A:LYS:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	29	1.29
(1,77)	1:64:A:ALA:C	1:65:A:HIS:N	1:65:A:HIS:CA	1:65:A:HIS:C	18	1.29
(1,65)	1:54:A:LEU:C	1:55:A:ALA:N	1:55:A:ALA:CA	1:55:A:ALA:C	13	1.29

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,49)	1:42:A:PHE:C	1:43:A:GLN:N	1:43:A:GLN:CA	1:43:A:GLN:C	6	1.29
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	7	1.29
(1,65)	1:54:A:LEU:C	1:55:A:ALA:N	1:55:A:ALA:CA	1:55:A:ALA:C	24	1.28
(1,64)	1:54:A:LEU:N	1:54:A:LEU:CA	1:54:A:LEU:C	1:55:A:ALA:N	31	1.28
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	20	1.28
(1,37)	1:31:A:GLN:C	1:32:A:THR:N	1:32:A:THR:CA	1:32:A:THR:C	12	1.28
(1,12)	1:9:A:CYS:N	1:9:A:CYS:CA	1:9:A:CYS:C	1:10:A:PHE:N	17	1.28
(1,103)	1:92:A:GLU:C	1:93:A:TYR:N	1:93:A:TYR:CA	1:93:A:TYR:C	17	1.27
(1,102)	1:92:A:GLU:N	1:92:A:GLU:CA	1:92:A:GLU:C	1:93:A:TYR:N	7	1.27
(1,76)	1:60:A:LEU:N	1:60:A:LEU:CA	1:60:A:LEU:C	1:61:A:ILE:N	21	1.27
(1,67)	1:55:A:ALA:C	1:56:A:GLY:N	1:56:A:GLY:CA	1:56:A:GLY:C	22	1.27
(1,37)	1:31:A:GLN:C	1:32:A:THR:N	1:32:A:THR:CA	1:32:A:THR:C	29	1.27
(1,10)	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	1:9:A:CYS:N	9	1.27
(1,6)	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	1:7:A:CYS:N	6	1.27
(1,101)	1:91:A:TRP:C	1:92:A:GLU:N	1:92:A:GLU:CA	1:92:A:GLU:C	5	1.26
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	17	1.26
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	11	1.26
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	14	1.26
(1,85)	1:75:A:GLU:C	1:76:A:ALA:N	1:76:A:ALA:CA	1:76:A:ALA:C	18	1.25
(1,75)	1:59:A:LYS:C	1:60:A:LEU:N	1:60:A:LEU:CA	1:60:A:LEU:C	12	1.25
(1,70)	1:57:A:MET:N	1:57:A:MET:CA	1:57:A:MET:C	1:58:A:LYS:N	16	1.25
(1,64)	1:54:A:LEU:N	1:54:A:LEU:CA	1:54:A:LEU:C	1:55:A:ALA:N	27	1.25
(1,16)	1:11:A:THR:N	1:11:A:THR:CA	1:11:A:THR:C	1:12:A:LEU:N	29	1.25
(1,10)	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	1:9:A:CYS:N	4	1.25
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	22	1.24
(1,31)	1:28:A:LEU:C	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	26	1.24
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	20	1.24
(1,108)	1:66:A:PHE:N	1:66:A:PHE:CA	1:66:A:PHE:CB	1:66:A:PHE:CG	8	1.23
(1,94)	1:85:A:THR:N	1:85:A:THR:CA	1:85:A:THR:C	1:86:A:ARG:N	22	1.23
(1,82)	1:67:A:GLU:N	1:67:A:GLU:CA	1:67:A:GLU:C	1:68:A:LYS:N	28	1.23
(1,71)	1:57:A:MET:C	1:58:A:LYS:N	1:58:A:LYS:CA	1:58:A:LYS:C	8	1.23
(1,52)	1:45:A:TYR:N	1:45:A:TYR:CA	1:45:A:TYR:C	1:46:A:ILE:N	29	1.23
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	4	1.23
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	13	1.23
(1,6)	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	1:7:A:CYS:N	20	1.23
(1,76)	1:60:A:LEU:N	1:60:A:LEU:CA	1:60:A:LEU:C	1:61:A:ILE:N	26	1.22
(1,64)	1:54:A:LEU:N	1:54:A:LEU:CA	1:54:A:LEU:C	1:55:A:ALA:N	24	1.22
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	13	1.22
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	15	1.22
(1,6)	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	1:7:A:CYS:N	14	1.22
(1,5)	1:5:A:VAL:C	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	15	1.22
(1,88)	1:79:A:TYR:N	1:79:A:TYR:CA	1:79:A:TYR:C	1:80:A:SER:N	18	1.21
(1,74)	1:59:A:LYS:N	1:59:A:LYS:CA	1:59:A:LYS:C	1:60:A:LEU:N	30	1.21
(1,73)	1:58:A:LYS:C	1:59:A:LYS:N	1:59:A:LYS:CA	1:59:A:LYS:C	6	1.21
(1,64)	1:54:A:LEU:N	1:54:A:LEU:CA	1:54:A:LEU:C	1:55:A:ALA:N	12	1.21
(1,64)	1:54:A:LEU:N	1:54:A:LEU:CA	1:54:A:LEU:C	1:55:A:ALA:N	15	1.21
(1,37)	1:31:A:GLN:C	1:32:A:THR:N	1:32:A:THR:CA	1:32:A:THR:C	1	1.21
(1,8)	1:7:A:CYS:N	1:7:A:CYS:CA	1:7:A:CYS:C	1:8:A:TRP:N	26	1.21
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	19	1.21
(1,107)	1:42:A:PHE:N	1:42:A:PHE:CA	1:42:A:PHE:CB	1:42:A:PHE:CG	27	1.2
(1,74)	1:59:A:LYS:N	1:59:A:LYS:CA	1:59:A:LYS:C	1:60:A:LEU:N	19	1.2

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,64)	1:54:A:LEU:N	1:54:A:LEU:CA	1:54:A:LEU:C	1:55:A:ALA:N	21	1.2
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	15	1.2
(1,82)	1:67:A:GLU:N	1:67:A:GLU:CA	1:67:A:GLU:C	1:68:A:LYS:N	31	1.19
(1,64)	1:54:A:LEU:N	1:54:A:LEU:CA	1:54:A:LEU:C	1:55:A:ALA:N	1	1.19
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	6	1.19
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	15	1.19
(1,54)	1:46:A:ILE:N	1:46:A:ILE:CA	1:46:A:ILE:C	1:47:A:GLU:N	27	1.19
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	27	1.19
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	31	1.19
(1,107)	1:42:A:PHE:N	1:42:A:PHE:CA	1:42:A:PHE:CB	1:42:A:PHE:CG	14	1.18
(1,103)	1:92:A:GLU:C	1:93:A:TYR:N	1:93:A:TYR:CA	1:93:A:TYR:C	1	1.18
(1,98)	1:88:A:GLU:N	1:88:A:GLU:CA	1:88:A:GLU:C	1:89:A:GLY:N	25	1.18
(1,5)	1:5:A:VAL:C	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	8	1.18
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	22	1.18
(1,89)	1:82:A:LYS:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	14	1.17
(1,70)	1:57:A:MET:N	1:57:A:MET:CA	1:57:A:MET:C	1:58:A:LYS:N	10	1.17
(1,64)	1:54:A:LEU:N	1:54:A:LEU:CA	1:54:A:LEU:C	1:55:A:ALA:N	13	1.17
(1,63)	1:53:A:SER:C	1:54:A:LEU:N	1:54:A:LEU:CA	1:54:A:LEU:C	17	1.17
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	24	1.17
(1,37)	1:31:A:GLN:C	1:32:A:THR:N	1:32:A:THR:CA	1:32:A:THR:C	31	1.17
(1,89)	1:82:A:LYS:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	21	1.16
(1,74)	1:59:A:LYS:N	1:59:A:LYS:CA	1:59:A:LYS:C	1:60:A:LEU:N	26	1.16
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	11	1.16
(1,54)	1:46:A:ILE:N	1:46:A:ILE:CA	1:46:A:ILE:C	1:47:A:GLU:N	9	1.16
(1,54)	1:46:A:ILE:N	1:46:A:ILE:CA	1:46:A:ILE:C	1:47:A:GLU:N	16	1.16
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	21	1.16
(1,14)	1:10:A:PHE:N	1:10:A:PHE:CA	1:10:A:PHE:C	1:11:A:THR:N	9	1.16
(1,5)	1:5:A:VAL:C	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	28	1.16
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	29	1.16
(1,108)	1:66:A:PHE:N	1:66:A:PHE:CA	1:66:A:PHE:CB	1:66:A:PHE:CG	7	1.15
(1,65)	1:54:A:LEU:C	1:55:A:ALA:N	1:55:A:ALA:CA	1:55:A:ALA:C	15	1.15
(1,64)	1:54:A:LEU:N	1:54:A:LEU:CA	1:54:A:LEU:C	1:55:A:ALA:N	23	1.15
(1,6)	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	1:7:A:CYS:N	7	1.15
(1,5)	1:5:A:VAL:C	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	18	1.15
(1,57)	1:47:A:GLU:C	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	27	1.14
(1,6)	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	1:7:A:CYS:N	23	1.14
(1,94)	1:85:A:THR:N	1:85:A:THR:CA	1:85:A:THR:C	1:86:A:ARG:N	31	1.13
(1,57)	1:47:A:GLU:C	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	12	1.13
(1,32)	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	1:30:A:TYR:N	20	1.13
(1,31)	1:28:A:LEU:C	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	27	1.13
(1,74)	1:59:A:LYS:N	1:59:A:LYS:CA	1:59:A:LYS:C	1:60:A:LEU:N	10	1.12
(1,73)	1:58:A:LYS:C	1:59:A:LYS:N	1:59:A:LYS:CA	1:59:A:LYS:C	29	1.12
(1,57)	1:47:A:GLU:C	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	16	1.12
(1,5)	1:5:A:VAL:C	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	16	1.12
(1,103)	1:92:A:GLU:C	1:93:A:TYR:N	1:93:A:TYR:CA	1:93:A:TYR:C	4	1.11
(1,94)	1:85:A:THR:N	1:85:A:THR:CA	1:85:A:THR:C	1:86:A:ARG:N	11	1.11
(1,71)	1:57:A:MET:C	1:58:A:LYS:N	1:58:A:LYS:CA	1:58:A:LYS:C	7	1.11
(1,65)	1:54:A:LEU:C	1:55:A:ALA:N	1:55:A:ALA:CA	1:55:A:ALA:C	1	1.11
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	14	1.11
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	2	1.11
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	9	1.11

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,40)	1:33:A:GLU:N	1:33:A:GLU:CA	1:33:A:GLU:C	1:34:A:GLN:N	21	1.11
(1,31)	1:28:A:LEU:C	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	2	1.11
(1,10)	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	1:9:A:CYS:N	26	1.11
(1,6)	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	1:7:A:CYS:N	4	1.11
(1,108)	1:66:A:PHE:N	1:66:A:PHE:CA	1:66:A:PHE:CB	1:66:A:PHE:CG	27	1.1
(1,70)	1:57:A:MET:N	1:57:A:MET:CA	1:57:A:MET:C	1:58:A:LYS:N	9	1.1
(1,64)	1:54:A:LEU:N	1:54:A:LEU:CA	1:54:A:LEU:C	1:55:A:ALA:N	8	1.1
(1,58)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:LYS:N	30	1.1
(1,52)	1:45:A:TYR:N	1:45:A:TYR:CA	1:45:A:TYR:C	1:46:A:ILE:N	27	1.1
(1,36)	1:31:A:GLN:N	1:31:A:GLN:CA	1:31:A:GLN:C	1:32:A:THR:N	14	1.1
(1,32)	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	1:30:A:TYR:N	23	1.1
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	12	1.1
(1,6)	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	1:7:A:CYS:N	22	1.1
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	9	1.1
(1,102)	1:92:A:GLU:N	1:92:A:GLU:CA	1:92:A:GLU:C	1:93:A:TYR:N	1	1.09
(1,94)	1:85:A:THR:N	1:85:A:THR:CA	1:85:A:THR:C	1:86:A:ARG:N	5	1.09
(1,89)	1:82:A:LYS:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	28	1.09
(1,88)	1:79:A:TYR:N	1:79:A:TYR:CA	1:79:A:TYR:C	1:80:A:SER:N	24	1.09
(1,103)	1:92:A:GLU:C	1:93:A:TYR:N	1:93:A:TYR:CA	1:93:A:TYR:C	20	1.08
(1,90)	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	1:84:A:ASP:N	7	1.08
(1,89)	1:82:A:LYS:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	17	1.08
(1,84)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:ALA:N	17	1.08
(1,76)	1:60:A:LEU:N	1:60:A:LEU:CA	1:60:A:LEU:C	1:61:A:ILE:N	19	1.08
(1,65)	1:54:A:LEU:C	1:55:A:ALA:N	1:55:A:ALA:CA	1:55:A:ALA:C	31	1.08
(1,9)	1:7:A:CYS:C	1:8:A:TRP:N	1:8:A:TRP:CA	1:8:A:TRP:C	15	1.08
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	24	1.08
(1,106)	1:65:A:HIS:N	1:65:A:HIS:CA	1:65:A:HIS:CB	1:65:A:HIS:CG	11	1.07
(1,92)	1:84:A:ASP:N	1:84:A:ASP:CA	1:84:A:ASP:C	1:85:A:THR:N	16	1.07
(1,89)	1:82:A:LYS:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	26	1.07
(1,85)	1:75:A:GLU:C	1:76:A:ALA:N	1:76:A:ALA:CA	1:76:A:ALA:C	25	1.07
(1,84)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:ALA:N	30	1.07
(1,78)	1:65:A:HIS:N	1:65:A:HIS:CA	1:65:A:HIS:C	1:66:A:PHE:N	17	1.07
(1,76)	1:60:A:LEU:N	1:60:A:LEU:CA	1:60:A:LEU:C	1:61:A:ILE:N	14	1.07
(1,70)	1:57:A:MET:N	1:57:A:MET:CA	1:57:A:MET:C	1:58:A:LYS:N	4	1.07
(1,28)	1:27:A:TYR:N	1:27:A:TYR:CA	1:27:A:TYR:C	1:28:A:LEU:N	21	1.07
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	30	1.07
(1,98)	1:88:A:GLU:N	1:88:A:GLU:CA	1:88:A:GLU:C	1:89:A:GLY:N	28	1.06
(1,90)	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	1:84:A:ASP:N	16	1.06
(1,89)	1:82:A:LYS:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	10	1.06
(1,83)	1:74:A:GLY:C	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	20	1.06
(1,64)	1:54:A:LEU:N	1:54:A:LEU:CA	1:54:A:LEU:C	1:55:A:ALA:N	20	1.06
(1,76)	1:60:A:LEU:N	1:60:A:LEU:CA	1:60:A:LEU:C	1:61:A:ILE:N	16	1.05
(1,74)	1:59:A:LYS:N	1:59:A:LYS:CA	1:59:A:LYS:C	1:60:A:LEU:N	17	1.05
(1,62)	1:53:A:SER:N	1:53:A:SER:CA	1:53:A:SER:C	1:54:A:LEU:N	7	1.05
(1,62)	1:53:A:SER:N	1:53:A:SER:CA	1:53:A:SER:C	1:54:A:LEU:N	29	1.05
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	8	1.05
(1,6)	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	1:7:A:CYS:N	8	1.05
(1,6)	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	1:7:A:CYS:N	10	1.05
(1,101)	1:91:A:TRP:C	1:92:A:GLU:N	1:92:A:GLU:CA	1:92:A:GLU:C	13	1.04
(1,94)	1:85:A:THR:N	1:85:A:THR:CA	1:85:A:THR:C	1:86:A:ARG:N	19	1.04
(1,80)	1:66:A:PHE:N	1:66:A:PHE:CA	1:66:A:PHE:C	1:67:A:GLU:N	4	1.04

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,76)	1:60:A:LEU:N	1:60:A:LEU:CA	1:60:A:LEU:C	1:61:A:ILE:N	22	1.04
(1,71)	1:57:A:MET:C	1:58:A:LYS:N	1:58:A:LYS:CA	1:58:A:LYS:C	28	1.04
(1,70)	1:57:A:MET:N	1:57:A:MET:CA	1:57:A:MET:C	1:58:A:LYS:N	13	1.04
(1,15)	1:10:A:PHE:C	1:11:A:THR:N	1:11:A:THR:CA	1:11:A:THR:C	16	1.04
(1,103)	1:92:A:GLU:C	1:93:A:TYR:N	1:93:A:TYR:CA	1:93:A:TYR:C	23	1.03
(1,92)	1:84:A:ASP:N	1:84:A:ASP:CA	1:84:A:ASP:C	1:85:A:THR:N	17	1.03
(1,74)	1:59:A:LYS:N	1:59:A:LYS:CA	1:59:A:LYS:C	1:60:A:LEU:N	9	1.03
(1,65)	1:54:A:LEU:C	1:55:A:ALA:N	1:55:A:ALA:CA	1:55:A:ALA:C	10	1.03
(1,65)	1:54:A:LEU:C	1:55:A:ALA:N	1:55:A:ALA:CA	1:55:A:ALA:C	26	1.03
(1,44)	1:40:A:ILE:N	1:40:A:ILE:CA	1:40:A:ILE:C	1:41:A:HIS:N	28	1.03
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	23	1.03
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	27	1.03
(1,4)	1:5:A:VAL:N	1:5:A:VAL:CA	1:5:A:VAL:C	1:6:A:ILE:N	13	1.03
(1,89)	1:82:A:LYS:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	22	1.02
(1,6)	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	1:7:A:CYS:N	28	1.02
(1,5)	1:5:A:VAL:C	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	19	1.02
(1,102)	1:92:A:GLU:N	1:92:A:GLU:CA	1:92:A:GLU:C	1:93:A:TYR:N	4	1.01
(1,96)	1:86:A:ARG:N	1:86:A:ARG:CA	1:86:A:ARG:C	1:87:A:LEU:N	15	1.01
(1,94)	1:85:A:THR:N	1:85:A:THR:CA	1:85:A:THR:C	1:86:A:ARG:N	14	1.01
(1,73)	1:58:A:LYS:C	1:59:A:LYS:N	1:59:A:LYS:CA	1:59:A:LYS:C	19	1.01
(1,54)	1:46:A:ILE:N	1:46:A:ILE:CA	1:46:A:ILE:C	1:47:A:GLU:N	2	1.01
(1,33)	1:29:A:VAL:C	1:30:A:TYR:N	1:30:A:TYR:CA	1:30:A:TYR:C	26	1.01
(1,32)	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	1:30:A:TYR:N	8	1.01
(1,5)	1:5:A:VAL:C	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	1	1.01
(1,5)	1:5:A:VAL:C	1:6:A:ILE:N	1:6:A:ILE:CA	1:6:A:ILE:C	7	1.01
(1,103)	1:92:A:GLU:C	1:93:A:TYR:N	1:93:A:TYR:CA	1:93:A:TYR:C	6	1.0
(1,76)	1:60:A:LEU:N	1:60:A:LEU:CA	1:60:A:LEU:C	1:61:A:ILE:N	13	1.0
(1,32)	1:29:A:VAL:N	1:29:A:VAL:CA	1:29:A:VAL:C	1:30:A:TYR:N	26	1.0
(1,26)	1:23:A:ASP:N	1:23:A:ASP:CA	1:23:A:ASP:C	1:24:A:SER:N	30	1.0
(1,17)	1:11:A:THR:C	1:12:A:LEU:N	1:12:A:LEU:CA	1:12:A:LEU:C	3	1.0