



Full wwPDB NMR Structure Validation Report ⓘ

Oct 21, 2023 – 01:56 PM EDT

PDB ID : 8FTW
BMRB ID : 31069
Title : FliT-FliJ fusion complex
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Deposited on : 2023-01-13

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

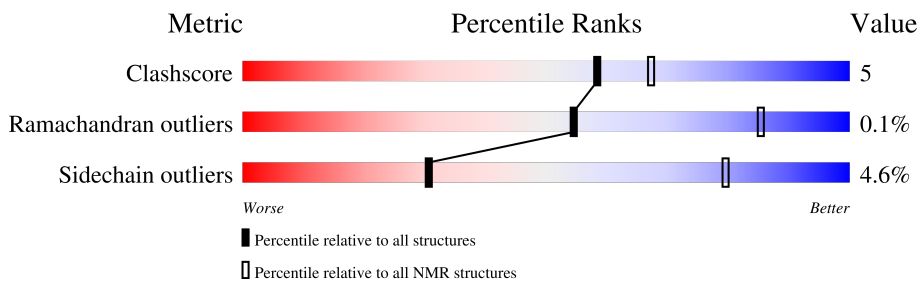
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 52%.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	166	

2 Ensemble composition and analysis

This entry contains 20 models. Model 11 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:2-A:91, A:132-A:156 (115)	0.50	11

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. No single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2663 atoms, of which 1339 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Flagellar FliT protein, Flagellar FliJ protein fusion.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	166	2663	834	1339	231	255	4	0

There are 20 discrepancies between the modelled and reference sequences:

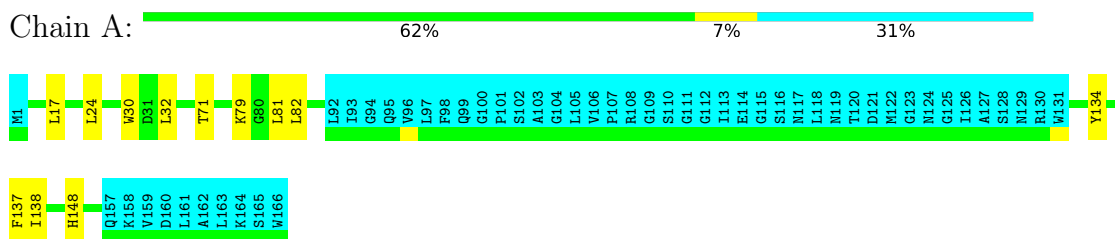
Chain	Residue	Modelled	Actual	Comment	Reference
A	96	VAL	-	linker	UNP A0A0F7J9R1
A	97	LEU	-	linker	UNP A0A0F7J9R1
A	98	PHE	-	linker	UNP A0A0F7J9R1
A	99	GLN	-	linker	UNP A0A0F7J9R1
A	100	GLY	-	linker	UNP A0A0F7J9R1
A	101	PRO	-	linker	UNP A0A0F7J9R1
A	102	SER	-	linker	UNP A0A0F7J9R1
A	103	ALA	-	linker	UNP A0A0F7J9R1
A	104	GLY	-	linker	UNP A0A0F7J9R1
A	105	LEU	-	linker	UNP A0A0F7J9R1
A	106	VAL	-	linker	UNP A0A0F7J9R1
A	107	PRO	-	linker	UNP A0A0F7J9R1
A	108	ARG	-	linker	UNP A0A0F7J9R1
A	109	GLY	-	linker	UNP A0A0F7J9R1
A	110	SER	-	linker	UNP A0A0F7J9R1
A	111	GLY	-	linker	UNP A0A0F7J9R1
A	112	GLY	-	linker	UNP A0A0F7J9R1
A	113	ILE	-	linker	UNP A0A0F7J9R1
A	114	GLU	-	linker	UNP A0A0F7J9R1
A	115	GLY	-	linker	UNP A0A0F7J9R1

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: Flagellar FliT protein, Flagellar FliJ protein fusion

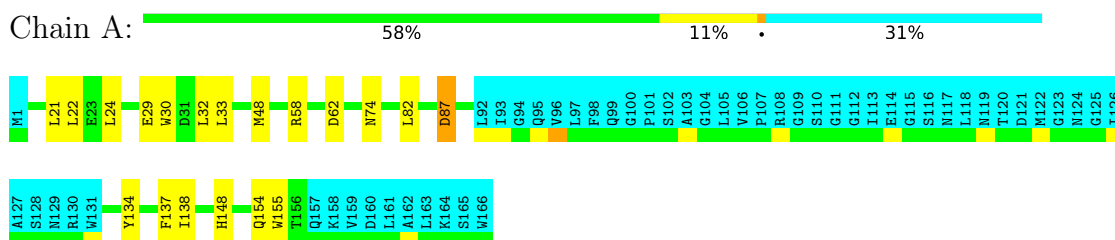


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

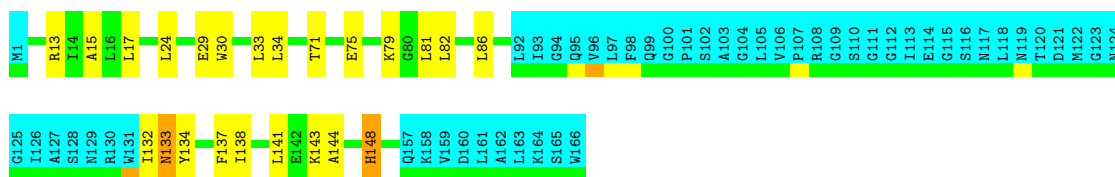
- Molecule 1: Flagellar FliT protein, Flagellar FliJ protein fusion



4.2.2 Score per residue for model 2

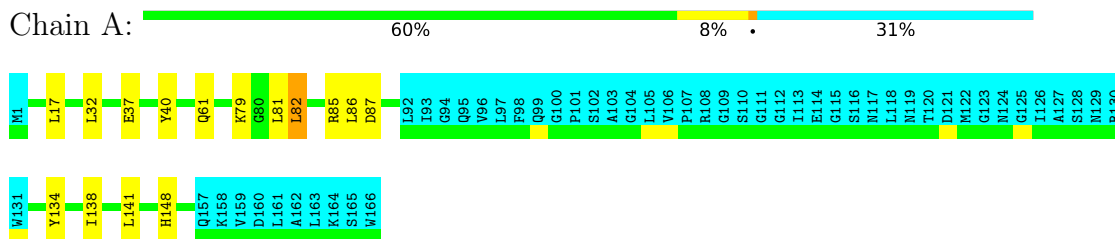
- Molecule 1: Flagellar FliT protein, Flagellar FliJ protein fusion





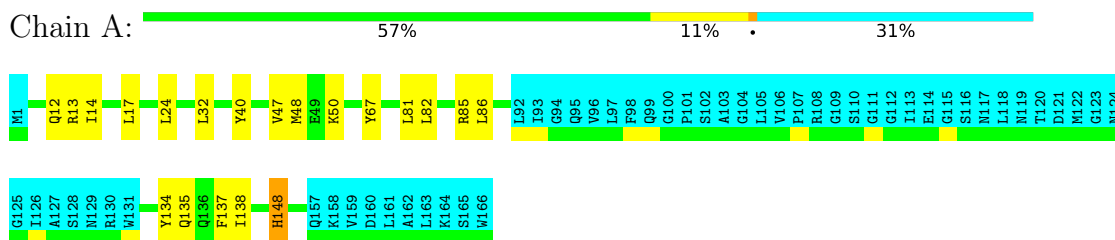
4.2.3 Score per residue for model 3

- Molecule 1: Flagellar FliT protein, Flagellar FliJ protein fusion



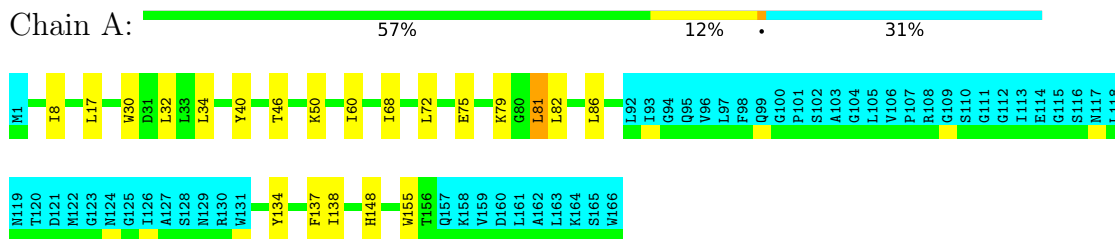
4.2.4 Score per residue for model 4

- Molecule 1: Flagellar FliT protein, Flagellar FliJ protein fusion



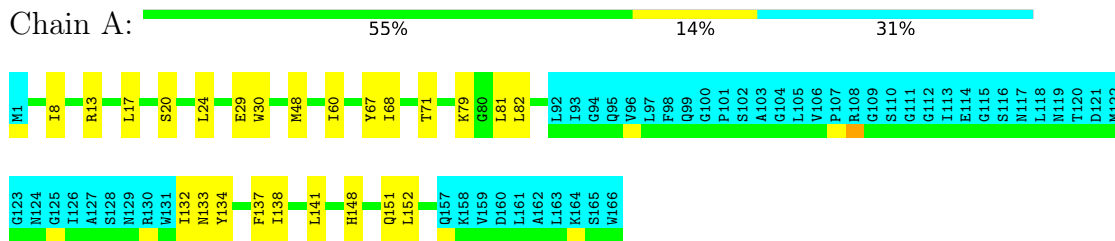
4.2.5 Score per residue for model 5

- Molecule 1: Flagellar FliT protein, Flagellar FliJ protein fusion



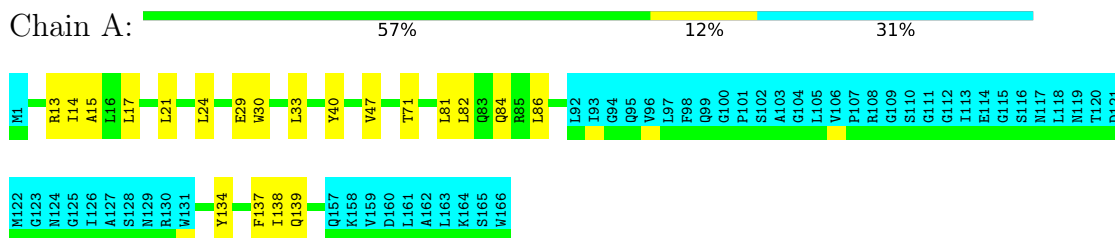
4.2.6 Score per residue for model 6

- Molecule 1: Flagellar FliT protein, Flagellar FliJ protein fusion



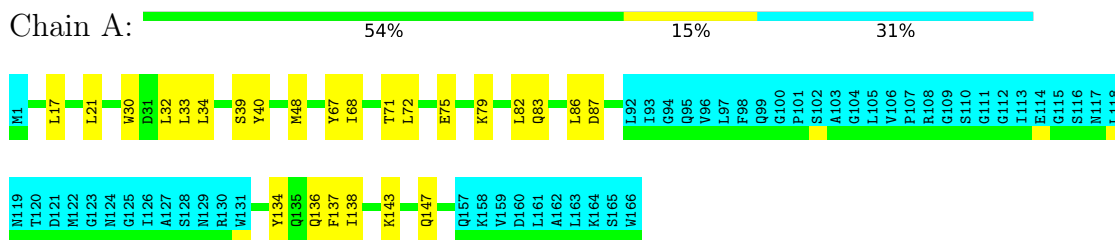
4.2.7 Score per residue for model 7

- Molecule 1: Flagellar FliT protein, Flagellar FliJ protein fusion



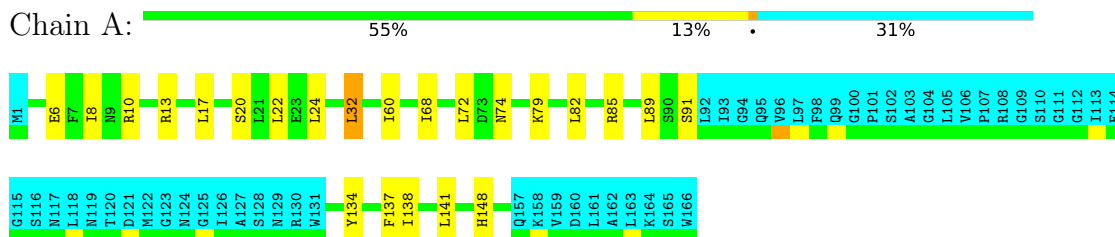
4.2.8 Score per residue for model 8

- Molecule 1: Flagellar FliT protein, Flagellar FliJ protein fusion



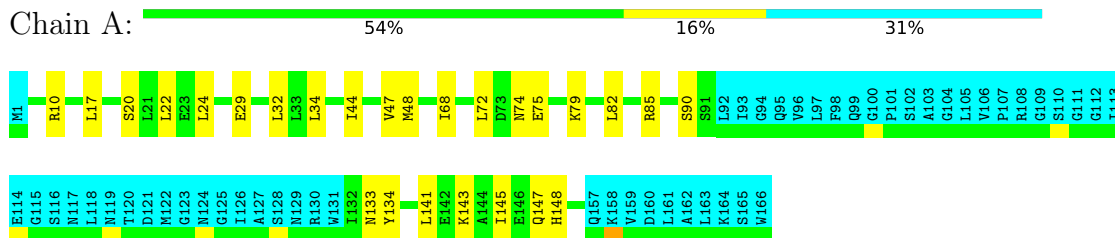
4.2.9 Score per residue for model 9

- Molecule 1: Flagellar FliT protein, Flagellar FliJ protein fusion



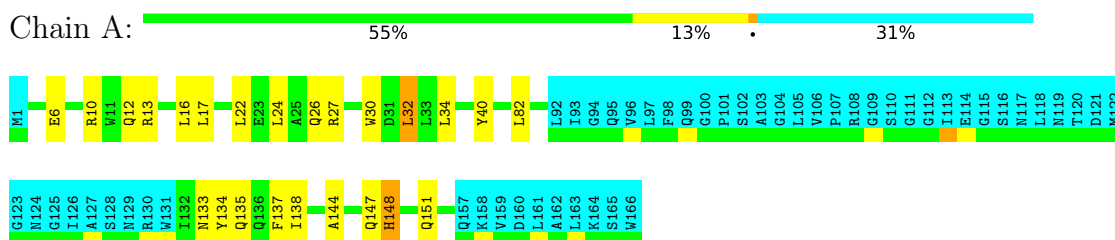
4.2.10 Score per residue for model 10

- Molecule 1: Flagellar FliT protein, Flagellar FliJ protein fusion



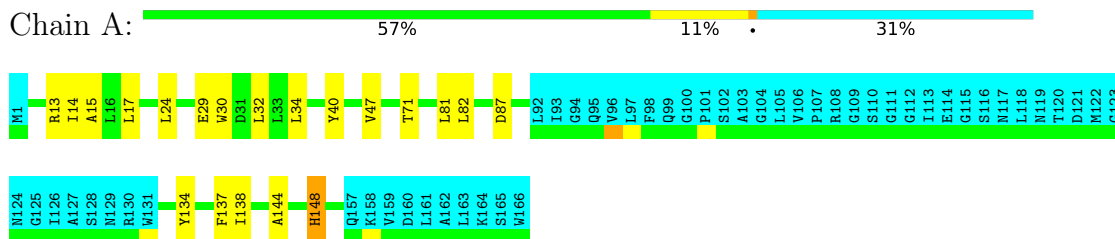
4.2.11 Score per residue for model 11 (medoid)

- Molecule 1: Flagellar FliT protein, Flagellar FliJ protein fusion



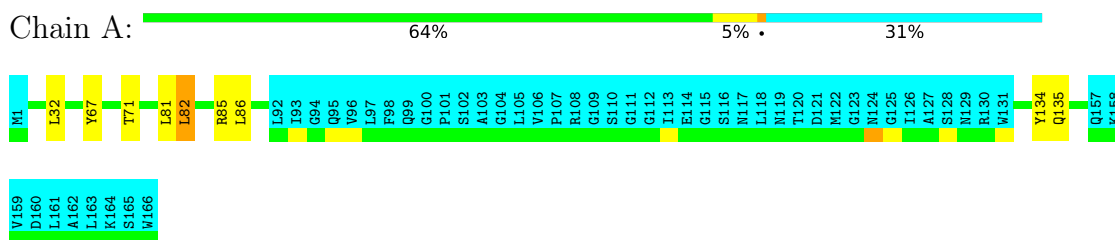
4.2.12 Score per residue for model 12

- Molecule 1: Flagellar FliT protein, Flagellar FliJ protein fusion



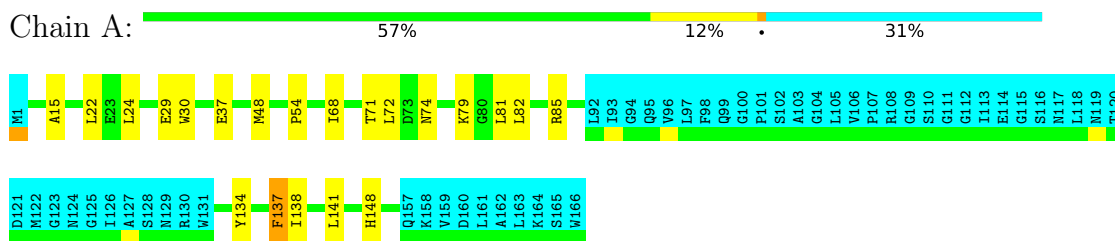
4.2.13 Score per residue for model 13

- Molecule 1: Flagellar FliT protein, Flagellar FliJ protein fusion



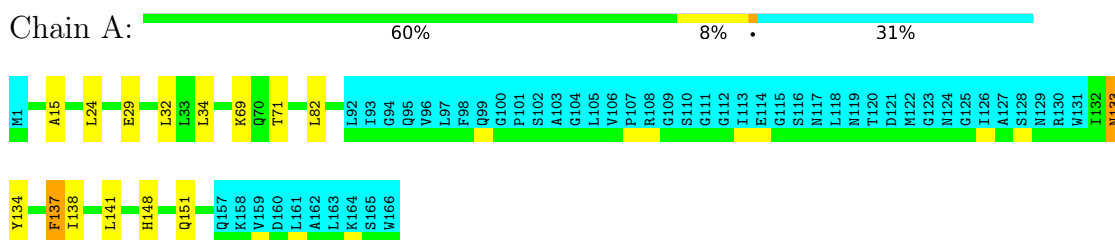
4.2.14 Score per residue for model 14

- Molecule 1: Flagellar FliT protein, Flagellar FliJ protein fusion



4.2.15 Score per residue for model 15

- Molecule 1: Flagellar FliT protein, Flagellar FliJ protein fusion



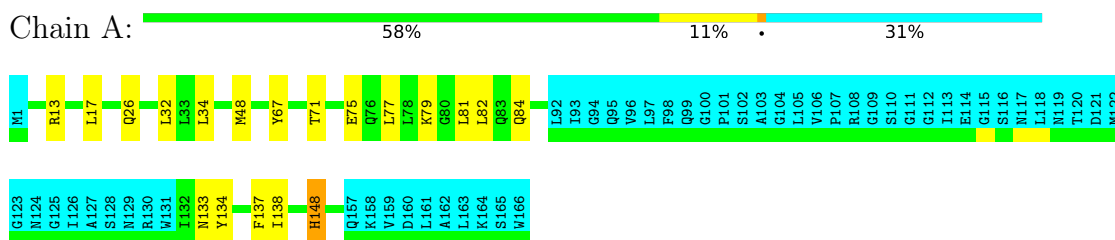
4.2.16 Score per residue for model 16

- Molecule 1: Flagellar FliT protein, Flagellar FliJ protein fusion



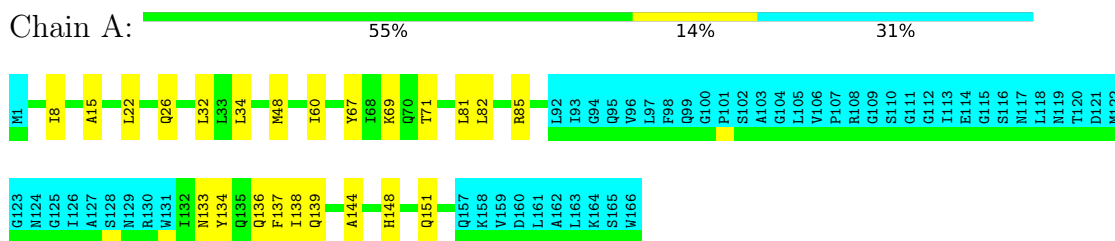
4.2.17 Score per residue for model 17

- Molecule 1: Flagellar FliT protein, Flagellar FliJ protein fusion



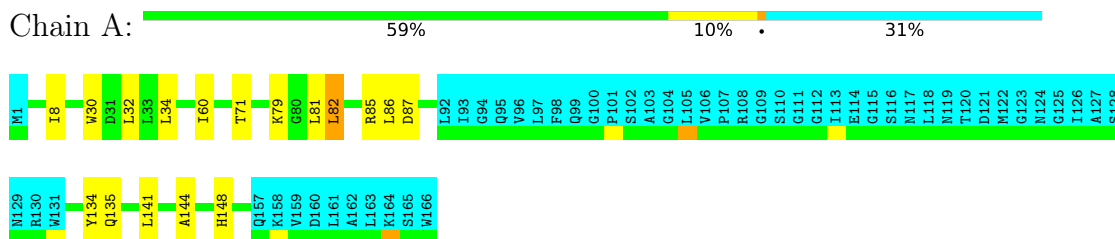
4.2.18 Score per residue for model 18

- Molecule 1: Flagellar FliT protein, Flagellar FliJ protein fusion



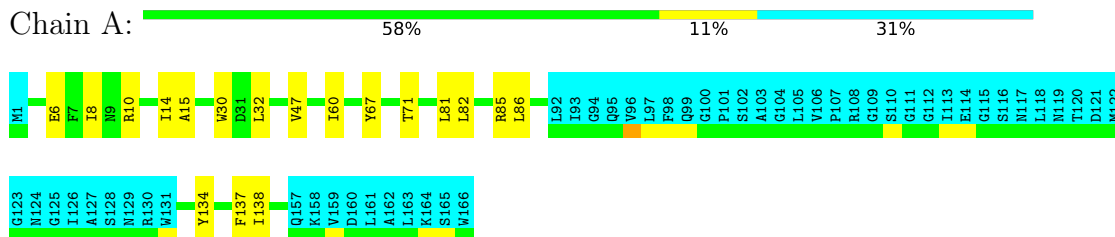
4.2.19 Score per residue for model 19

- Molecule 1: Flagellar FliT protein, Flagellar FliJ protein fusion



4.2.20 Score per residue for model 20

- Molecule 1: Flagellar FliT protein, Flagellar FliJ protein fusion



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 20 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
CNS	refinement	
TALOS	geometry optimization	
CYANA	structure calculation	3.98

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	1170
Number of shifts mapped to atoms	1170
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	52%

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	949	962	961	9±3
All	All	18980	19240	19220	186

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 5.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:82:LEU:HD22	1:A:138:ILE:HD11	0.73	1.61	11	17
1:A:8:ILE:HD11	1:A:60:ILE:HG23	0.65	1.66	6	1
1:A:79:LYS:HE2	1:A:141:LEU:HB3	0.64	1.69	10	4
1:A:24:LEU:HG	1:A:29:GLU:HB2	0.59	1.74	12	6
1:A:82:LEU:HD21	1:A:134:TYR:CD1	0.57	2.35	19	20
1:A:17:LEU:HD21	1:A:40:TYR:HA	0.56	1.78	8	7
1:A:13:ARG:NH1	1:A:17:LEU:HD22	0.56	2.14	11	5
1:A:14:ILE:HD11	1:A:47:VAL:HB	0.54	1.79	20	4
1:A:15:ALA:HA	1:A:71:THR:HB	0.54	1.79	14	8
1:A:34:LEU:HD22	1:A:133:ASN:HD22	0.54	1.62	18	1
1:A:30:TRP:HB3	1:A:134:TYR:OH	0.51	2.05	5	11
1:A:24:LEU:HD23	1:A:29:GLU:HB2	0.51	1.82	10	2
1:A:34:LEU:HD21	1:A:134:TYR:CD1	0.50	2.41	15	8
1:A:86:LEU:HD21	1:A:134:TYR:HB3	0.50	1.82	5	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:48:MET:SD	1:A:148:HIS:CD2	0.49	3.05	14	2
1:A:48:MET:HB3	1:A:151:GLN:HE22	0.49	1.67	18	2
1:A:6:GLU:HB3	1:A:10:ARG:NH1	0.49	2.22	20	1
1:A:72:LEU:HD21	1:A:148:HIS:HB3	0.49	1.84	14	1
1:A:34:LEU:HD22	1:A:133:ASN:HB3	0.48	1.86	15	2
1:A:79:LYS:HE2	1:A:141:LEU:HD22	0.48	1.85	14	1
1:A:8:ILE:HD11	1:A:60:ILE:HD12	0.48	1.86	19	6
1:A:48:MET:SD	1:A:147:GLN:HB2	0.48	2.49	8	1
1:A:24:LEU:HD21	1:A:32:LEU:HB3	0.47	1.84	9	2
1:A:79:LYS:NZ	1:A:141:LEU:HB3	0.47	2.25	19	1
1:A:22:LEU:HD22	1:A:74:ASN:HA	0.46	1.86	9	4
1:A:48:MET:SD	1:A:148:HIS:ND1	0.46	2.88	4	3
1:A:68:ILE:HB	1:A:152:LEU:HD23	0.46	1.87	6	1
1:A:22:LEU:HG	1:A:26:GLN:HE21	0.45	1.72	18	2
1:A:6:GLU:HB3	1:A:10:ARG:HH12	0.45	1.72	20	1
1:A:67:TYR:O	1:A:71:THR:HG22	0.45	2.12	13	5
1:A:75:GLU:HB2	1:A:145:ILE:HD11	0.45	1.89	10	1
1:A:34:LEU:HD22	1:A:133:ASN:ND2	0.44	2.26	2	1
1:A:12:GLN:HG2	1:A:67:TYR:HE2	0.44	1.71	4	1
1:A:13:ARG:O	1:A:17:LEU:HB3	0.44	2.13	17	3
1:A:67:TYR:O	1:A:71:THR:HG23	0.44	2.13	8	1
1:A:20:SER:O	1:A:24:LEU:HB2	0.44	2.11	6	3
1:A:44:ILE:HD11	1:A:148:HIS:CE1	0.44	2.48	10	1
1:A:75:GLU:O	1:A:79:LYS:HG2	0.44	2.13	2	4
1:A:48:MET:SD	1:A:148:HIS:HD2	0.43	2.36	14	1
1:A:68:ILE:O	1:A:72:LEU:HG	0.43	2.12	8	5
1:A:79:LYS:HD2	1:A:141:LEU:HB3	0.43	1.89	14	1
1:A:30:TRP:O	1:A:33:LEU:HB3	0.43	2.13	2	1
1:A:144:ALA:O	1:A:148:HIS:HB2	0.43	2.13	12	5
1:A:134:TYR:O	1:A:138:ILE:HG12	0.43	2.13	6	4
1:A:6:GLU:O	1:A:10:ARG:HG2	0.43	2.13	9	2
1:A:86:LEU:HD21	1:A:134:TYR:CB	0.43	2.44	4	1
1:A:10:ARG:HB3	1:A:47:VAL:HG13	0.42	1.91	10	1
1:A:21:LEU:HD22	1:A:33:LEU:HD12	0.42	1.92	7	3
1:A:12:GLN:O	1:A:16:LEU:HG	0.42	2.14	11	1
1:A:79:LYS:HE3	1:A:141:LEU:HB3	0.41	1.92	2	1
1:A:75:GLU:HB3	1:A:79:LYS:HE2	0.41	1.91	16	1
1:A:147:GLN:O	1:A:151:GLN:HG2	0.41	2.16	11	1
1:A:137:PHE:O	1:A:141:LEU:HG	0.41	2.15	14	2
1:A:85:ARG:O	1:A:89:LEU:HG	0.41	2.15	9	1
1:A:143:LYS:O	1:A:147:GLN:HG2	0.41	2.16	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:138:ILE:HD13	1:A:141:LEU:HD12	0.41	1.92	14	1
1:A:46:THR:O	1:A:50:LYS:HD3	0.40	2.17	5	1
1:A:24:LEU:HD11	1:A:32:LEU:HD12	0.40	1.93	11	1

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	115/166 (69%)	112±2 (97±1%)	3±1 (2±1%)	0±0 (0±0%)	54	85
All	All	2300/3320 (69%)	2241 (97%)	57 (2%)	2 (0%)	54	85

All 2 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	1
1	A	54	PRO	1

6.3.2 Protein sidechains [i](#)

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	107/146 (73%)	102±1 (95±1%)	5±1 (5±1%)	31	79
All	All	2140/2920 (73%)	2041 (95%)	99 (5%)	31	79

All 24 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	137	PHE	16
1	A	32	LEU	15
1	A	81	LEU	13
1	A	148	HIS	10
1	A	85	ARG	7
1	A	133	ASN	5
1	A	87	ASP	4
1	A	135	GLN	4
1	A	82	LEU	3
1	A	155	TRP	2
1	A	143	LYS	2
1	A	37	GLU	2
1	A	84	GLN	2
1	A	139	GLN	2
1	A	136	GLN	2
1	A	69	LYS	2
1	A	58	ARG	1
1	A	62	ASP	1
1	A	154	GLN	1
1	A	61	GLN	1
1	A	17	LEU	1
1	A	13	ARG	1
1	A	151	GLN	1
1	A	71	THR	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation i

The completeness of assignment taking into account all chemical shift lists is 52% for the well-defined parts and 50% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *chem_shift_list_1*

7.1.1 Bookkeeping i

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

Total number of shifts	1170
Number of shifts mapped to atoms	1170
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing i

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	156	-0.88 ± 0.05	Should be checked
$^{13}\text{C}_\beta$	143	0.41 ± 0.03	None needed (< 0.5 ppm)
$^{13}\text{C}'$	152	-0.54 ± 0.05	Should be applied
^{15}N	149	0.17 ± 0.19	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments i

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 52%, i.e. 865 atoms were assigned a chemical shift out of a possible 1676. 0 out of 23 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	437/575 (76%)	108/232 (47%)	221/230 (96%)	108/113 (96%)
Sidechain	378/1010 (37%)	207/654 (32%)	171/313 (55%)	0/43 (0%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	50/91 (55%)	25/44 (57%)	22/42 (52%)	3/5 (60%)
Overall	865/1676 (52%)	340/930 (37%)	414/585 (71%)	111/161 (69%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 50%, i.e. 1170 atoms were assigned a chemical shift out of a possible 2332. 0 out of 32 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	606/835 (73%)	149/341 (44%)	308/332 (93%)	149/162 (92%)
Sidechain	500/1372 (36%)	273/891 (31%)	227/423 (54%)	0/58 (0%)
Aromatic	64/125 (51%)	32/61 (52%)	27/57 (47%)	5/7 (71%)
Overall	1170/2332 (50%)	454/1293 (35%)	562/812 (69%)	154/227 (68%)

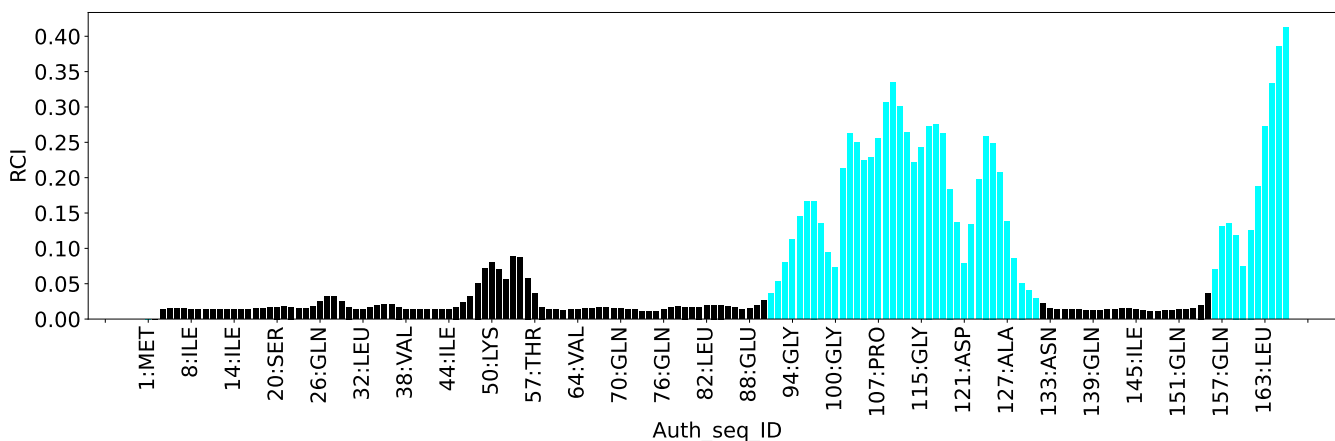
7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

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

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

Random coil index (RCI) for chain A:



8 NMR restraints analysis

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	1838
Intra-residue ($ i-j =0$)	98
Sequential ($ i-j =1$)	375
Medium range ($ i-j >1$ and $ i-j <5$)	542
Long range ($ i-j \geq 5$)	600
Inter-chain	0
Hydrogen bond restraints	223
Disulfide bond restraints	0
Total dihedral-angle restraints	227
Number of unmapped restraints	0
Number of restraints per residue	12.4
Number of long range restraints per residue ¹	3.6

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)	25.9	0.2
0.2-0.5 (Medium)	8.2	0.49
>0.5 (Large)	0.3	0.82

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)	5.6	7.47
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis [i](#)

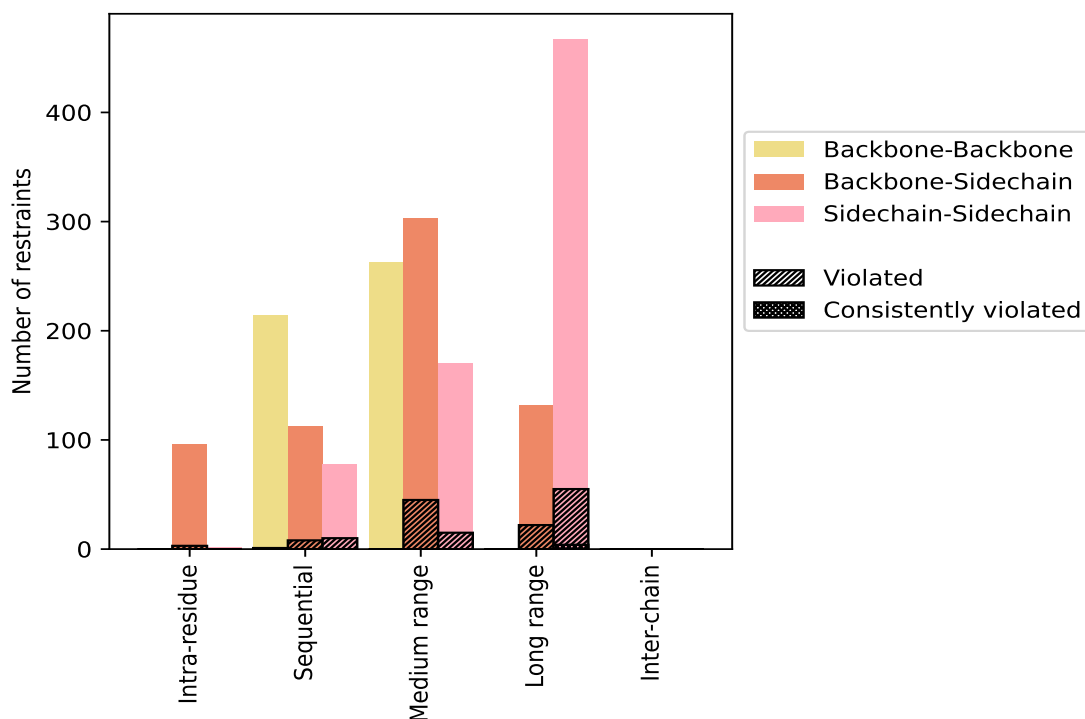
9.1 Summary of distance violations [i](#)

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 ($i-j =0$)	98	5.3	3	3.1	0.2	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	96	5.2	3	3.1	0.2	0	0.0	0.0
Sidechain-Sidechain	2	0.1	0	0.0	0.0	0	0.0	0.0
Sequential ($i-j =1$)	375	20.4	19	5.1	1.0	0	0.0	0.0
Backbone-Backbone	185	10.1	1	0.5	0.1	0	0.0	0.0
Backbone-Sidechain	112	6.1	8	7.1	0.4	0	0.0	0.0
Sidechain-Sidechain	78	4.2	10	12.8	0.5	0	0.0	0.0
Medium range ($i-j >1$ & $i-j <5$)	542	29.5	31	5.7	1.7	0	0.0	0.0
Backbone-Backbone	263	14.3	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	109	5.9	16	14.7	0.9	0	0.0	0.0
Sidechain-Sidechain	170	9.2	15	8.8	0.8	0	0.0	0.0
Long range ($i-j \geq 5$)	600	32.6	77	12.8	4.2	4	0.7	0.2
Backbone-Backbone	1	0.1	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	132	7.2	22	16.7	1.2	0	0.0	0.0
Sidechain-Sidechain	467	25.4	55	11.8	3.0	4	0.9	0.2
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	223	12.1	29	13.0	1.6	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	1838	100.0	159	8.7	8.7	4	0.2	0.2
Backbone-Backbone	478	26.0	1	0.2	0.1	0	0.0	0.0
Backbone-Sidechain	643	35.0	78	12.1	4.2	0	0.0	0.0
Sidechain-Sidechain	717	39.0	80	11.2	4.4	4	0.6	0.2

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

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



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

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

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

Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
1	2	4	8	21	0	35	0.18	0.55	0.09	0.16
2	0	3	9	18	0	30	0.17	0.43	0.08	0.14
3	0	3	8	20	0	31	0.17	0.51	0.09	0.13
4	1	0	11	25	0	37	0.17	0.69	0.1	0.13
5	1	4	9	23	0	37	0.17	0.48	0.09	0.15
6	1	1	10	22	0	34	0.19	0.44	0.09	0.16
7	1	1	6	24	0	32	0.16	0.51	0.08	0.14
8	2	6	12	24	0	44	0.16	0.48	0.07	0.13
9	2	4	10	21	0	37	0.16	0.49	0.07	0.13
10	0	4	11	18	0	33	0.17	0.52	0.08	0.15
11	1	2	11	23	0	37	0.18	0.41	0.07	0.17

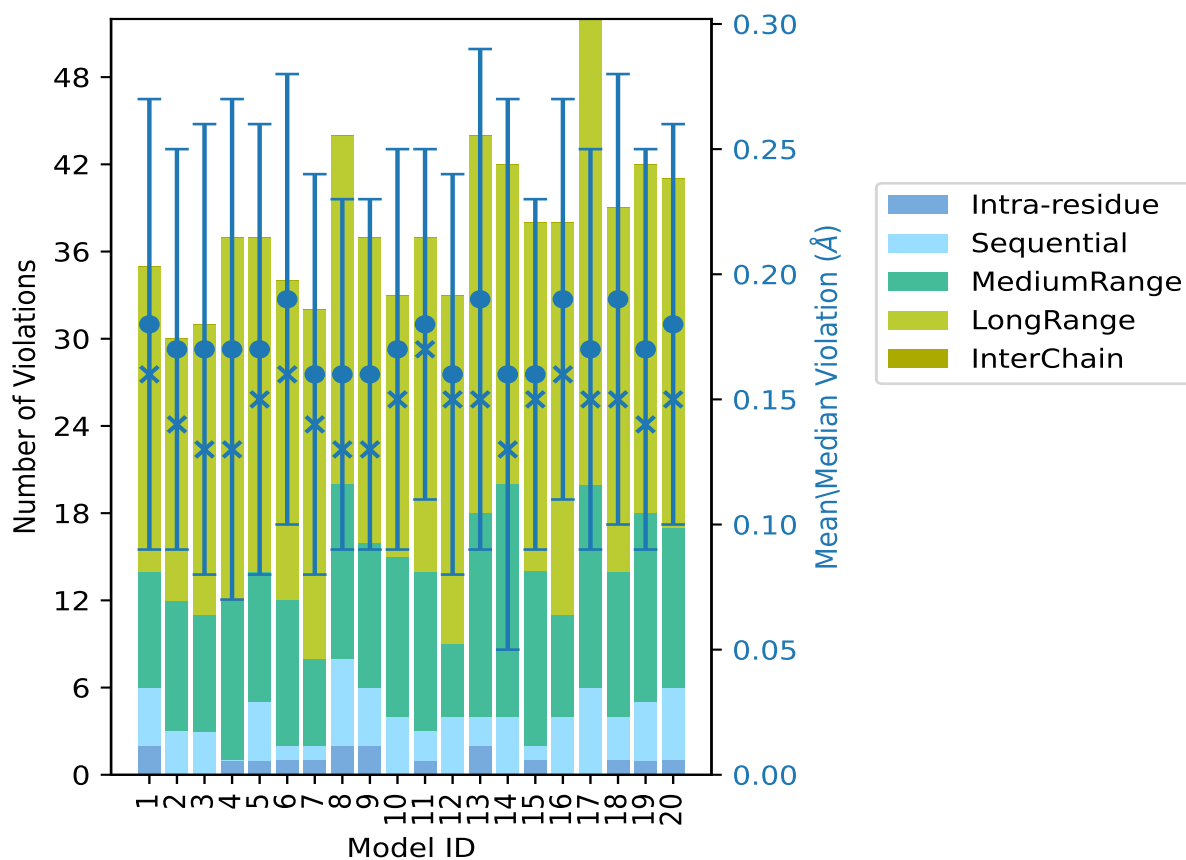
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Model ID	Number of violations					Total	Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵					
12	0	4	5	24	0	33	0.16	0.55	0.08	0.15
13	2	2	14	26	0	44	0.19	0.46	0.1	0.15
14	0	4	16	22	0	42	0.16	0.82	0.11	0.13
15	1	1	12	24	0	38	0.16	0.41	0.07	0.15
16	0	4	7	27	0	38	0.19	0.42	0.08	0.16
17	0	6	14	32	0	52	0.17	0.42	0.08	0.15
18	1	3	10	25	0	39	0.19	0.44	0.09	0.15
19	1	4	13	24	0	42	0.17	0.41	0.08	0.14
20	1	5	11	24	0	41	0.18	0.46	0.08	0.15

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

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



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

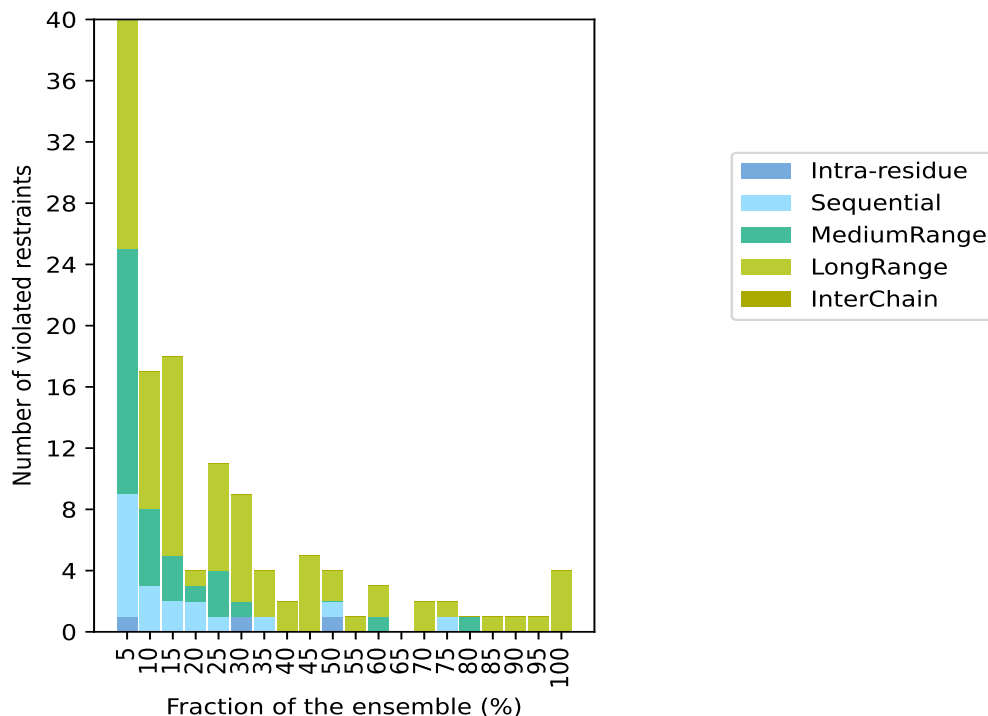
9.3 Distance violation statistics for the ensemble

Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 1485(IR:95, SQ:356, MR:511, LR:523, 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	8	16	15	0	40	1	5.0
0	3	5	9	0	17	2	10.0
0	2	3	13	0	18	3	15.0
0	2	1	1	0	4	4	20.0
0	1	3	7	0	11	5	25.0
1	0	1	7	0	9	6	30.0
0	1	0	3	0	4	7	35.0
0	0	0	2	0	2	8	40.0
0	0	0	5	0	5	9	45.0
1	1	0	2	0	4	10	50.0
0	0	0	1	0	1	11	55.0
0	0	1	2	0	3	12	60.0
0	0	0	0	0	0	13	65.0
0	0	0	2	0	2	14	70.0
0	1	0	1	0	2	15	75.0
0	0	1	0	0	1	16	80.0
0	0	0	1	0	1	17	85.0
0	0	0	1	0	1	18	90.0
0	0	0	1	0	1	19	95.0
0	0	0	4	0	4	20	100.0

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

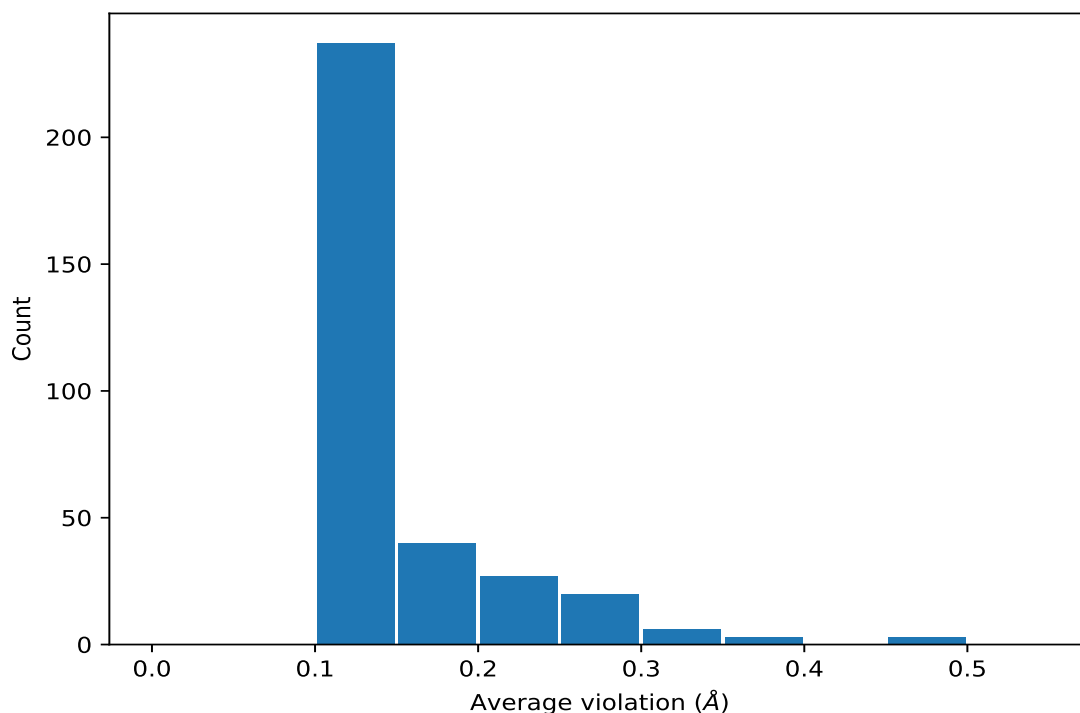
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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

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

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



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

The following table provides the mean and the standard deviation of the violation for each restraint sorted by number of violated models and the mean value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint. Rows with same key represent combinatorial or ambiguous restraints and are counted as a single restraint.

Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,1071)	1:82:A:LEU:HD21	1:137:A:PHE:CD1	20	0.48	0.12	0.46
(4,1071)	1:82:A:LEU:HD22	1:137:A:PHE:CD1	20	0.48	0.12	0.46
(4,1071)	1:82:A:LEU:HD23	1:137:A:PHE:CD1	20	0.48	0.12	0.46
(4,1073)	1:82:A:LEU:HD21	1:134:A:TYR:CE2	20	0.24	0.09	0.22
(4,1073)	1:82:A:LEU:HD22	1:134:A:TYR:CE2	20	0.24	0.09	0.22
(4,1073)	1:82:A:LEU:HD23	1:134:A:TYR:CE2	20	0.24	0.09	0.22
(4,458)	1:33:A:LEU:HD21	1:78:A:LEU:CD2	20	0.23	0.05	0.23
(4,458)	1:33:A:LEU:HD22	1:78:A:LEU:CD2	20	0.23	0.05	0.23
(4,458)	1:33:A:LEU:HD23	1:78:A:LEU:CD2	20	0.23	0.05	0.23
(4,1092)	1:33:A:LEU:HD21	1:137:A:PHE:CD1	20	0.23	0.05	0.22
(4,1092)	1:33:A:LEU:HD22	1:137:A:PHE:CD1	20	0.23	0.05	0.22
(4,1092)	1:33:A:LEU:HD23	1:137:A:PHE:CD1	20	0.23	0.05	0.22
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD11	19	0.21	0.04	0.19
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD12	19	0.21	0.04	0.19
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD13	19	0.21	0.04	0.19
(4,1091)	1:33:A:LEU:HD21	1:134:A:TYR:CD2	18	0.22	0.07	0.2

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,1091)	1:33:A:LEU:HD22	1:134:A:TYR:CD2	18	0.22	0.07	0.2
(4,1091)	1:33:A:LEU:HD23	1:134:A:TYR:CD2	18	0.22	0.07	0.2
(4,313)	1:11:A:TRP:HE1	1:155:A:TRP:HE1	17	0.15	0.03	0.16
(1,63)	1:41:A:LEU:O	1:45:A:GLU:H	17	0.12	0.02	0.12
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD21	16	0.15	0.03	0.15
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD22	16	0.15	0.03	0.15
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD23	16	0.15	0.03	0.15
(4,1076)	1:82:A:LEU:HD11	1:134:A:TYR:CD2	15	0.18	0.05	0.18
(4,1076)	1:82:A:LEU:HD12	1:134:A:TYR:CD2	15	0.18	0.05	0.18
(4,1076)	1:82:A:LEU:HD13	1:134:A:TYR:CD2	15	0.18	0.05	0.18
(4,1058)	1:92:A:LEU:HD11	1:93:A:ILE:H	15	0.14	0.02	0.14
(4,1058)	1:92:A:LEU:HD12	1:93:A:ILE:H	15	0.14	0.02	0.14
(4,1058)	1:92:A:LEU:HD13	1:93:A:ILE:H	15	0.14	0.02	0.14
(4,1206)	1:89:A:LEU:HD11	1:134:A:TYR:CE1	14	0.2	0.04	0.2
(4,1206)	1:89:A:LEU:HD12	1:134:A:TYR:CE1	14	0.2	0.04	0.2
(4,1206)	1:89:A:LEU:HD13	1:134:A:TYR:CE1	14	0.2	0.04	0.2
(4,530)	1:17:A:LEU:HD21	1:71:A:THR:CG2	14	0.2	0.07	0.18
(4,530)	1:17:A:LEU:HD22	1:71:A:THR:CG2	14	0.2	0.07	0.18
(4,530)	1:17:A:LEU:HD23	1:71:A:THR:CG2	14	0.2	0.07	0.18
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD11	12	0.2	0.07	0.19
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD12	12	0.2	0.07	0.19
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD13	12	0.2	0.07	0.19
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD11	12	0.15	0.03	0.14
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD12	12	0.15	0.03	0.14
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD13	12	0.15	0.03	0.14
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD11	12	0.15	0.03	0.14
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD12	12	0.15	0.03	0.14
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD13	12	0.15	0.03	0.14
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD11	12	0.15	0.03	0.14
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD12	12	0.15	0.03	0.14
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD13	12	0.15	0.03	0.14
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD21	12	0.15	0.02	0.15
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD22	12	0.15	0.02	0.15
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD23	12	0.15	0.02	0.15
(1,193)	1:153:A:THR:O	1:157:A:GLN:H	12	0.13	0.01	0.12
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD21	11	0.16	0.04	0.16
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD22	11	0.16	0.04	0.16
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD23	11	0.16	0.04	0.16
(4,1280)	1:8:A:ILE:HG21	1:67:A:TYR:CE1	10	0.27	0.07	0.28
(4,1280)	1:8:A:ILE:HG22	1:67:A:TYR:CE1	10	0.27	0.07	0.28
(4,1280)	1:8:A:ILE:HG23	1:67:A:TYR:CE1	10	0.27	0.07	0.28
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD11	10	0.15	0.03	0.15

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD12	10	0.15	0.03	0.15
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD13	10	0.15	0.03	0.15
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD11	10	0.14	0.02	0.15
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD12	10	0.14	0.02	0.15
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD13	10	0.14	0.02	0.15
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD11	10	0.13	0.02	0.13
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD12	10	0.13	0.02	0.13
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD13	10	0.13	0.02	0.13
(4,1279)	1:8:A:ILE:HG21	1:67:A:TYR:CD1	9	0.38	0.04	0.38
(4,1279)	1:8:A:ILE:HG22	1:67:A:TYR:CD1	9	0.38	0.04	0.38
(4,1279)	1:8:A:ILE:HG23	1:67:A:TYR:CD1	9	0.38	0.04	0.38
(4,1245)	1:15:A:ALA:HB1	1:67:A:TYR:CE2	9	0.32	0.1	0.37
(4,1245)	1:15:A:ALA:HB2	1:67:A:TYR:CE2	9	0.32	0.1	0.37
(4,1245)	1:15:A:ALA:HB3	1:67:A:TYR:CE2	9	0.32	0.1	0.37
(4,1117)	1:16:A:LEU:HD21	1:67:A:TYR:CD2	9	0.27	0.07	0.26
(4,1117)	1:16:A:LEU:HD22	1:67:A:TYR:CD2	9	0.27	0.07	0.26
(4,1117)	1:16:A:LEU:HD23	1:67:A:TYR:CD2	9	0.27	0.07	0.26
(4,875)	1:93:A:ILE:HD11	1:131:A:TRP:HE1	9	0.16	0.04	0.14
(4,875)	1:93:A:ILE:HD12	1:131:A:TRP:HE1	9	0.16	0.04	0.14
(4,875)	1:93:A:ILE:HD13	1:131:A:TRP:HE1	9	0.16	0.04	0.14
(4,794)	1:21:A:LEU:HD21	1:137:A:PHE:HE1	9	0.14	0.04	0.12
(4,794)	1:21:A:LEU:HD21	1:137:A:PHE:HE2	9	0.14	0.04	0.12
(4,794)	1:21:A:LEU:HD22	1:137:A:PHE:HE1	9	0.14	0.04	0.12
(4,794)	1:21:A:LEU:HD22	1:137:A:PHE:HE2	9	0.14	0.04	0.12
(4,794)	1:21:A:LEU:HD23	1:137:A:PHE:HE1	9	0.14	0.04	0.12
(4,794)	1:21:A:LEU:HD23	1:137:A:PHE:HE2	9	0.14	0.04	0.12
(1,13)	1:7:A:PHE:O	1:11:A:TRP:H	9	0.11	0.01	0.11
(4,859)	1:78:A:LEU:HD11	1:137:A:PHE:HE1	8	0.13	0.02	0.12
(4,859)	1:78:A:LEU:HD11	1:137:A:PHE:HE2	8	0.13	0.02	0.12
(4,859)	1:78:A:LEU:HD12	1:137:A:PHE:HE1	8	0.13	0.02	0.12
(4,859)	1:78:A:LEU:HD12	1:137:A:PHE:HE2	8	0.13	0.02	0.12
(4,859)	1:78:A:LEU:HD13	1:137:A:PHE:HE1	8	0.13	0.02	0.12
(4,859)	1:78:A:LEU:HD13	1:137:A:PHE:HE2	8	0.13	0.02	0.12
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG21	8	0.12	0.02	0.12
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG22	8	0.12	0.02	0.12
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG23	8	0.12	0.02	0.12
(4,757)	1:72:A:LEU:HD11	1:149:A:ARG:H	7	0.17	0.05	0.16
(4,757)	1:72:A:LEU:HD12	1:149:A:ARG:H	7	0.17	0.05	0.16
(4,757)	1:72:A:LEU:HD13	1:149:A:ARG:H	7	0.17	0.05	0.16
(4,882)	1:24:A:LEU:HD21	1:32:A:LEU:H	7	0.16	0.07	0.12
(4,882)	1:24:A:LEU:HD22	1:32:A:LEU:H	7	0.16	0.07	0.12
(4,882)	1:24:A:LEU:HD23	1:32:A:LEU:H	7	0.16	0.07	0.12

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,47)	1:30:A:TRP:O	1:34:A:LEU:H	7	0.12	0.01	0.13
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD11	7	0.12	0.02	0.12
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD12	7	0.12	0.02	0.12
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD13	7	0.12	0.02	0.12
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD11	7	0.12	0.02	0.12
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD12	7	0.12	0.02	0.12
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD13	7	0.12	0.02	0.12
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD21	7	0.12	0.01	0.11
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD22	7	0.12	0.01	0.11
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD23	7	0.12	0.01	0.11
(4,1244)	1:15:A:ALA:HB1	1:67:A:TYR:CD2	6	0.28	0.02	0.28
(4,1244)	1:15:A:ALA:HB2	1:67:A:TYR:CD2	6	0.28	0.02	0.28
(4,1244)	1:15:A:ALA:HB3	1:67:A:TYR:CD2	6	0.28	0.02	0.28
(4,49)	1:96:A:VAL:HG11	1:126:A:ILE:HD11	6	0.26	0.06	0.24
(4,49)	1:96:A:VAL:HG11	1:126:A:ILE:HD12	6	0.26	0.06	0.24
(4,49)	1:96:A:VAL:HG11	1:126:A:ILE:HD13	6	0.26	0.06	0.24
(4,49)	1:96:A:VAL:HG12	1:126:A:ILE:HD11	6	0.26	0.06	0.24
(4,49)	1:96:A:VAL:HG12	1:126:A:ILE:HD12	6	0.26	0.06	0.24
(4,49)	1:96:A:VAL:HG12	1:126:A:ILE:HD13	6	0.26	0.06	0.24
(4,49)	1:96:A:VAL:HG13	1:126:A:ILE:HD11	6	0.26	0.06	0.24
(4,49)	1:96:A:VAL:HG13	1:126:A:ILE:HD12	6	0.26	0.06	0.24
(4,49)	1:96:A:VAL:HG13	1:126:A:ILE:HD13	6	0.26	0.06	0.24
(1,143)	1:128:A:SER:O	1:132:A:ILE:H	6	0.16	0.02	0.17
(4,1317)	1:41:A:LEU:HD11	1:137:A:PHE:HD1	6	0.16	0.03	0.15
(4,1317)	1:41:A:LEU:HD11	1:137:A:PHE:HD2	6	0.16	0.03	0.15
(4,1317)	1:41:A:LEU:HD12	1:137:A:PHE:HD1	6	0.16	0.03	0.15
(4,1317)	1:41:A:LEU:HD12	1:137:A:PHE:HD2	6	0.16	0.03	0.15
(4,1317)	1:41:A:LEU:HD13	1:137:A:PHE:HD1	6	0.16	0.03	0.15
(4,1317)	1:41:A:LEU:HD13	1:137:A:PHE:HD2	6	0.16	0.03	0.15
(4,661)	1:86:A:LEU:HD11	1:135:A:GLN:H	6	0.15	0.03	0.15
(4,661)	1:86:A:LEU:HD12	1:135:A:GLN:H	6	0.15	0.03	0.15
(4,661)	1:86:A:LEU:HD13	1:135:A:GLN:H	6	0.15	0.03	0.15
(4,844)	1:22:A:LEU:HD11	1:26:A:GLN:H	6	0.14	0.03	0.14
(4,844)	1:22:A:LEU:HD12	1:26:A:GLN:H	6	0.14	0.03	0.14
(4,844)	1:22:A:LEU:HD13	1:26:A:GLN:H	6	0.14	0.03	0.14
(4,796)	1:21:A:LEU:HD21	1:137:A:PHE:HZ	6	0.12	0.02	0.12
(4,796)	1:21:A:LEU:HD22	1:137:A:PHE:HZ	6	0.12	0.02	0.12
(4,796)	1:21:A:LEU:HD23	1:137:A:PHE:HZ	6	0.12	0.02	0.12
(1,51)	1:33:A:LEU:O	1:37:A:GLU:H	6	0.12	0.01	0.12
(4,307)	1:155:A:TRP:H	1:155:A:TRP:HE1	6	0.12	0.02	0.11
(4,1014)	1:41:A:LEU:H	1:141:A:LEU:HD21	6	0.12	0.02	0.11
(4,1014)	1:41:A:LEU:H	1:141:A:LEU:HD22	6	0.12	0.02	0.11

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,1014)	1:41:A:LEU:H	1:141:A:LEU:HD23	6	0.12	0.02	0.11
(1,139)	1:90:A:SER:O	1:94:A:GLY:H	6	0.12	0.0	0.12
(4,43)	1:34:A:LEU:HD21	1:138:A:ILE:HD11	6	0.11	0.01	0.11
(4,43)	1:34:A:LEU:HD21	1:138:A:ILE:HD12	6	0.11	0.01	0.11
(4,43)	1:34:A:LEU:HD21	1:138:A:ILE:HD13	6	0.11	0.01	0.11
(4,43)	1:34:A:LEU:HD22	1:138:A:ILE:HD11	6	0.11	0.01	0.11
(4,43)	1:34:A:LEU:HD22	1:138:A:ILE:HD12	6	0.11	0.01	0.11
(4,43)	1:34:A:LEU:HD22	1:138:A:ILE:HD13	6	0.11	0.01	0.11
(4,43)	1:34:A:LEU:HD23	1:138:A:ILE:HD11	6	0.11	0.01	0.11
(4,43)	1:34:A:LEU:HD23	1:138:A:ILE:HD12	6	0.11	0.01	0.11
(4,43)	1:34:A:LEU:HD23	1:138:A:ILE:HD13	6	0.11	0.01	0.11
(1,29)	1:15:A:ALA:O	1:19:A:GLN:H	6	0.11	0.01	0.11
(1,133)	1:87:A:ASP:O	1:91:A:SER:H	6	0.11	0.01	0.11
(1,69)	1:44:A:ILE:O	1:48:A:MET:H	6	0.11	0.01	0.11
(4,1271)	1:67:A:TYR:CD2	1:71:A:THR:HG21	5	0.16	0.04	0.17
(4,1271)	1:67:A:TYR:CD2	1:71:A:THR:HG22	5	0.16	0.04	0.17
(4,1271)	1:67:A:TYR:CD2	1:71:A:THR:HG23	5	0.16	0.04	0.17
(4,966)	1:16:A:LEU:H	1:71:A:THR:HG21	5	0.15	0.03	0.15
(4,966)	1:16:A:LEU:H	1:71:A:THR:HG22	5	0.15	0.03	0.15
(4,966)	1:16:A:LEU:H	1:71:A:THR:HG23	5	0.15	0.03	0.15
(4,1230)	1:97:A:LEU:HD11	1:98:A:PHE:HE1	5	0.14	0.05	0.12
(4,1230)	1:97:A:LEU:HD11	1:98:A:PHE:HE2	5	0.14	0.05	0.12
(4,1230)	1:97:A:LEU:HD12	1:98:A:PHE:HE1	5	0.14	0.05	0.12
(4,1230)	1:97:A:LEU:HD12	1:98:A:PHE:HE2	5	0.14	0.05	0.12
(4,1230)	1:97:A:LEU:HD13	1:98:A:PHE:HE1	5	0.14	0.05	0.12
(4,1230)	1:97:A:LEU:HD13	1:98:A:PHE:HE2	5	0.14	0.05	0.12
(4,972)	1:70:A:GLN:H	1:72:A:LEU:HD21	5	0.14	0.03	0.14
(4,972)	1:70:A:GLN:H	1:72:A:LEU:HD22	5	0.14	0.03	0.14
(4,972)	1:70:A:GLN:H	1:72:A:LEU:HD23	5	0.14	0.03	0.14
(4,550)	1:21:A:LEU:HD21	1:33:A:LEU:CD2	5	0.14	0.03	0.14
(4,550)	1:21:A:LEU:HD22	1:33:A:LEU:CD2	5	0.14	0.03	0.14
(4,550)	1:21:A:LEU:HD23	1:33:A:LEU:CD2	5	0.14	0.03	0.14
(4,1063)	1:89:A:LEU:HD11	1:134:A:TYR:CD1	5	0.14	0.02	0.14
(4,1063)	1:89:A:LEU:HD12	1:134:A:TYR:CD1	5	0.14	0.02	0.14
(4,1063)	1:89:A:LEU:HD13	1:134:A:TYR:CD1	5	0.14	0.02	0.14
(4,1201)	1:44:A:ILE:HG21	1:148:A:HIS:CE1	5	0.13	0.03	0.12
(4,1201)	1:44:A:ILE:HG22	1:148:A:HIS:CE1	5	0.13	0.03	0.12
(4,1201)	1:44:A:ILE:HG23	1:148:A:HIS:CE1	5	0.13	0.03	0.12
(4,1250)	1:86:A:LEU:HD11	1:134:A:TYR:CD1	5	0.13	0.02	0.13
(4,1250)	1:86:A:LEU:HD12	1:134:A:TYR:CD1	5	0.13	0.02	0.13
(4,1250)	1:86:A:LEU:HD13	1:134:A:TYR:CD1	5	0.13	0.02	0.13
(4,961)	1:135:A:GLN:H	1:138:A:ILE:HD11	5	0.12	0.01	0.12

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,961)	1:135:A:GLN:H	1:138:A:ILE:HD12	5	0.12	0.01	0.12
(4,961)	1:135:A:GLN:H	1:138:A:ILE:HD13	5	0.12	0.01	0.12
(4,1107)	1:17:A:LEU:HD11	1:40:A:TYR:CE1	5	0.12	0.02	0.11
(4,1107)	1:17:A:LEU:HD12	1:40:A:TYR:CE1	5	0.12	0.02	0.11
(4,1107)	1:17:A:LEU:HD13	1:40:A:TYR:CE1	5	0.12	0.02	0.11
(4,1226)	1:33:A:LEU:HD21	1:137:A:PHE:CE1	5	0.12	0.01	0.12
(4,1226)	1:33:A:LEU:HD22	1:137:A:PHE:CE1	5	0.12	0.01	0.12
(4,1226)	1:33:A:LEU:HD23	1:137:A:PHE:CE1	5	0.12	0.01	0.12
(1,16)	1:8:A:ILE:O	1:12:A:GLN:N	5	0.11	0.01	0.11
(4,1077)	1:82:A:LEU:HD11	1:137:A:PHE:CD1	4	0.18	0.02	0.18
(4,1077)	1:82:A:LEU:HD12	1:137:A:PHE:CD1	4	0.18	0.02	0.18
(4,1077)	1:82:A:LEU:HD13	1:137:A:PHE:CD1	4	0.18	0.02	0.18
(4,563)	1:92:A:LEU:HD11	1:93:A:ILE:CD1	4	0.15	0.04	0.14
(4,563)	1:92:A:LEU:HD12	1:93:A:ILE:CD1	4	0.15	0.04	0.14
(4,563)	1:92:A:LEU:HD13	1:93:A:ILE:CD1	4	0.15	0.04	0.14
(4,1101)	1:96:A:VAL:HG21	1:98:A:PHE:CE1	4	0.14	0.06	0.11
(4,1101)	1:96:A:VAL:HG22	1:98:A:PHE:CE1	4	0.14	0.06	0.11
(4,1101)	1:96:A:VAL:HG23	1:98:A:PHE:CE1	4	0.14	0.06	0.11
(4,781)	1:81:A:LEU:HD11	1:82:A:LEU:H	4	0.11	0.01	0.11
(4,781)	1:81:A:LEU:HD12	1:82:A:LEU:H	4	0.11	0.01	0.11
(4,781)	1:81:A:LEU:HD13	1:82:A:LEU:H	4	0.11	0.01	0.11
(1,187)	1:150:A:LEU:O	1:154:A:GLN:H	4	0.11	0.0	0.11
(4,407)	1:16:A:LEU:H	1:67:A:TYR:HD1	3	0.28	0.07	0.28
(4,407)	1:16:A:LEU:H	1:67:A:TYR:HD2	3	0.28	0.07	0.28
(4,539)	1:71:A:THR:HG21	1:72:A:LEU:CD1	3	0.18	0.03	0.18
(4,539)	1:71:A:THR:HG22	1:72:A:LEU:CD1	3	0.18	0.03	0.18
(4,539)	1:71:A:THR:HG23	1:72:A:LEU:CD1	3	0.18	0.03	0.18
(4,568)	1:97:A:LEU:HD11	1:126:A:ILE:CD1	3	0.17	0.06	0.14
(4,568)	1:97:A:LEU:HD12	1:126:A:ILE:CD1	3	0.17	0.06	0.14
(4,568)	1:97:A:LEU:HD13	1:126:A:ILE:CD1	3	0.17	0.06	0.14
(4,1113)	1:96:A:VAL:HG11	1:98:A:PHE:CD1	3	0.16	0.01	0.16
(4,1113)	1:96:A:VAL:HG12	1:98:A:PHE:CD1	3	0.16	0.01	0.16
(4,1113)	1:96:A:VAL:HG13	1:98:A:PHE:CD1	3	0.16	0.01	0.16
(4,821)	1:24:A:LEU:HD21	1:30:A:TRP:H	3	0.15	0.03	0.15
(4,821)	1:24:A:LEU:HD22	1:30:A:TRP:H	3	0.15	0.03	0.15
(4,821)	1:24:A:LEU:HD23	1:30:A:TRP:H	3	0.15	0.03	0.15
(4,915)	1:25:A:ALA:H	1:81:A:LEU:HD11	3	0.15	0.04	0.13
(4,915)	1:25:A:ALA:H	1:81:A:LEU:HD12	3	0.15	0.04	0.13
(4,915)	1:25:A:ALA:H	1:81:A:LEU:HD13	3	0.15	0.04	0.13
(4,1070)	1:82:A:LEU:HD21	1:134:A:TYR:CD2	3	0.15	0.04	0.14
(4,1070)	1:82:A:LEU:HD22	1:134:A:TYR:CD2	3	0.15	0.04	0.14
(4,1070)	1:82:A:LEU:HD23	1:134:A:TYR:CD2	3	0.15	0.04	0.14

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,369)	1:21:A:LEU:H	1:40:A:TYR:HD1	3	0.14	0.02	0.15
(4,369)	1:21:A:LEU:H	1:40:A:TYR:HD2	3	0.14	0.02	0.15
(4,965)	1:96:A:VAL:HG21	1:98:A:PHE:H	3	0.14	0.03	0.12
(4,965)	1:96:A:VAL:HG22	1:98:A:PHE:H	3	0.14	0.03	0.12
(4,965)	1:96:A:VAL:HG23	1:98:A:PHE:H	3	0.14	0.03	0.12
(4,577)	1:97:A:LEU:HD21	1:126:A:ILE:CD1	3	0.14	0.02	0.13
(4,577)	1:97:A:LEU:HD22	1:126:A:ILE:CD1	3	0.14	0.02	0.13
(4,577)	1:97:A:LEU:HD23	1:126:A:ILE:CD1	3	0.14	0.02	0.13
(4,1106)	1:34:A:LEU:HD21	1:134:A:TYR:CE2	3	0.14	0.02	0.14
(4,1106)	1:34:A:LEU:HD22	1:134:A:TYR:CE2	3	0.14	0.02	0.14
(4,1106)	1:34:A:LEU:HD23	1:134:A:TYR:CE2	3	0.14	0.02	0.14
(4,914)	1:27:A:ARG:H	1:81:A:LEU:HD11	3	0.13	0.03	0.11
(4,914)	1:27:A:ARG:H	1:81:A:LEU:HD12	3	0.13	0.03	0.11
(4,914)	1:27:A:ARG:H	1:81:A:LEU:HD13	3	0.13	0.03	0.11
(1,145)	1:129:A:ASN:O	1:133:A:ASN:H	3	0.13	0.02	0.13
(4,489)	1:52:A:THR:HG21	1:56:A:ILE:CD1	3	0.13	0.02	0.13
(4,489)	1:52:A:THR:HG22	1:56:A:ILE:CD1	3	0.13	0.02	0.13
(4,489)	1:52:A:THR:HG23	1:56:A:ILE:CD1	3	0.13	0.02	0.13
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD11	3	0.13	0.02	0.13
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD12	3	0.13	0.02	0.13
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD13	3	0.13	0.02	0.13
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD21	3	0.13	0.02	0.13
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD22	3	0.13	0.02	0.13
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD23	3	0.13	0.02	0.13
(4,942)	1:24:A:LEU:HD21	1:29:A:GLU:H	3	0.13	0.01	0.13
(4,942)	1:24:A:LEU:HD22	1:29:A:GLU:H	3	0.13	0.01	0.13
(4,942)	1:24:A:LEU:HD23	1:29:A:GLU:H	3	0.13	0.01	0.13
(4,44)	1:34:A:LEU:HD21	1:86:A:LEU:HD21	3	0.12	0.02	0.11
(4,44)	1:34:A:LEU:HD21	1:86:A:LEU:HD22	3	0.12	0.02	0.11
(4,44)	1:34:A:LEU:HD21	1:86:A:LEU:HD23	3	0.12	0.02	0.11
(4,44)	1:34:A:LEU:HD22	1:86:A:LEU:HD21	3	0.12	0.02	0.11
(4,44)	1:34:A:LEU:HD22	1:86:A:LEU:HD22	3	0.12	0.02	0.11
(4,44)	1:34:A:LEU:HD22	1:86:A:LEU:HD23	3	0.12	0.02	0.11
(4,44)	1:34:A:LEU:HD23	1:86:A:LEU:HD21	3	0.12	0.02	0.11
(4,44)	1:34:A:LEU:HD23	1:86:A:LEU:HD22	3	0.12	0.02	0.11
(4,44)	1:34:A:LEU:HD23	1:86:A:LEU:HD23	3	0.12	0.02	0.11
(4,685)	1:26:A:GLN:H	1:78:A:LEU:HD11	3	0.12	0.02	0.11
(4,685)	1:26:A:GLN:H	1:78:A:LEU:HD12	3	0.12	0.02	0.11
(4,685)	1:26:A:GLN:H	1:78:A:LEU:HD13	3	0.12	0.02	0.11
(4,1046)	1:11:A:TRP:H	1:47:A:VAL:HG21	3	0.11	0.01	0.12
(4,1046)	1:11:A:TRP:H	1:47:A:VAL:HG22	3	0.11	0.01	0.12
(4,1046)	1:11:A:TRP:H	1:47:A:VAL:HG23	3	0.11	0.01	0.12

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,59)	1:39:A:SER:O	1:43:A:SER:H	3	0.1	0.0	0.1
(4,1022)	1:81:A:LEU:HD21	1:83:A:GLN:H	2	0.34	0.02	0.34
(4,1022)	1:81:A:LEU:HD22	1:83:A:GLN:H	2	0.34	0.02	0.34
(4,1022)	1:81:A:LEU:HD23	1:83:A:GLN:H	2	0.34	0.02	0.34
(4,1082)	1:82:A:LEU:HD11	1:134:A:TYR:CE2	2	0.2	0.08	0.2
(4,1082)	1:82:A:LEU:HD12	1:134:A:TYR:CE2	2	0.2	0.08	0.2
(4,1082)	1:82:A:LEU:HD13	1:134:A:TYR:CE2	2	0.2	0.08	0.2
(4,999)	1:96:A:VAL:HG11	1:97:A:LEU:H	2	0.18	0.06	0.18
(4,999)	1:96:A:VAL:HG12	1:97:A:LEU:H	2	0.18	0.06	0.18
(4,999)	1:96:A:VAL:HG13	1:97:A:LEU:H	2	0.18	0.06	0.18
(4,293)	1:96:A:VAL:H	1:97:A:LEU:H	2	0.15	0.01	0.15
(4,236)	1:137:A:PHE:HD1	1:141:A:LEU:H	2	0.15	0.02	0.15
(4,236)	1:137:A:PHE:HD2	1:141:A:LEU:H	2	0.15	0.02	0.15
(4,561)	1:24:A:LEU:CD2	1:33:A:LEU:HD11	2	0.15	0.0	0.15
(4,561)	1:24:A:LEU:CD2	1:33:A:LEU:HD12	2	0.15	0.0	0.15
(4,561)	1:24:A:LEU:CD2	1:33:A:LEU:HD13	2	0.15	0.0	0.15
(4,674)	1:159:A:VAL:HG11	1:161:A:LEU:H	2	0.15	0.0	0.15
(4,674)	1:159:A:VAL:HG12	1:161:A:LEU:H	2	0.15	0.0	0.15
(4,674)	1:159:A:VAL:HG13	1:161:A:LEU:H	2	0.15	0.0	0.15
(4,555)	1:21:A:LEU:CD1	1:141:A:LEU:HD21	2	0.14	0.02	0.14
(4,555)	1:21:A:LEU:CD1	1:141:A:LEU:HD22	2	0.14	0.02	0.14
(4,555)	1:21:A:LEU:CD1	1:141:A:LEU:HD23	2	0.14	0.02	0.14
(4,744)	1:69:A:LYS:H	1:72:A:LEU:HD21	2	0.13	0.0	0.13
(4,744)	1:69:A:LYS:H	1:72:A:LEU:HD22	2	0.13	0.0	0.13
(4,744)	1:69:A:LYS:H	1:72:A:LEU:HD23	2	0.13	0.0	0.13
(4,1125)	1:16:A:LEU:HD11	1:67:A:TYR:CE2	2	0.13	0.01	0.13
(4,1125)	1:16:A:LEU:HD12	1:67:A:TYR:CE2	2	0.13	0.01	0.13
(4,1125)	1:16:A:LEU:HD13	1:67:A:TYR:CE2	2	0.13	0.01	0.13
(1,75)	1:58:A:ARG:O	1:62:A:ASP:H	2	0.12	0.01	0.12
(4,243)	1:41:A:LEU:H	1:137:A:PHE:HE1	2	0.12	0.02	0.12
(4,243)	1:41:A:LEU:H	1:137:A:PHE:HE2	2	0.12	0.02	0.12
(4,1268)	1:64:A:VAL:HG21	1:67:A:TYR:CE1	2	0.12	0.01	0.12
(4,1268)	1:64:A:VAL:HG22	1:67:A:TYR:CE1	2	0.12	0.01	0.12
(4,1268)	1:64:A:VAL:HG23	1:67:A:TYR:CE1	2	0.12	0.01	0.12
(1,49)	1:31:A:ASP:O	1:35:A:GLN:H	2	0.12	0.0	0.12
(4,462)	1:96:A:VAL:HG21	1:97:A:LEU:CD1	2	0.12	0.0	0.12
(4,462)	1:96:A:VAL:HG22	1:97:A:LEU:CD1	2	0.12	0.0	0.12
(4,462)	1:96:A:VAL:HG23	1:97:A:LEU:CD1	2	0.12	0.0	0.12
(4,672)	1:16:A:LEU:HD21	1:67:A:TYR:HE1	2	0.12	0.01	0.12
(4,672)	1:16:A:LEU:HD21	1:67:A:TYR:HE2	2	0.12	0.01	0.12
(4,672)	1:16:A:LEU:HD22	1:67:A:TYR:HE1	2	0.12	0.01	0.12
(4,672)	1:16:A:LEU:HD22	1:67:A:TYR:HE2	2	0.12	0.01	0.12

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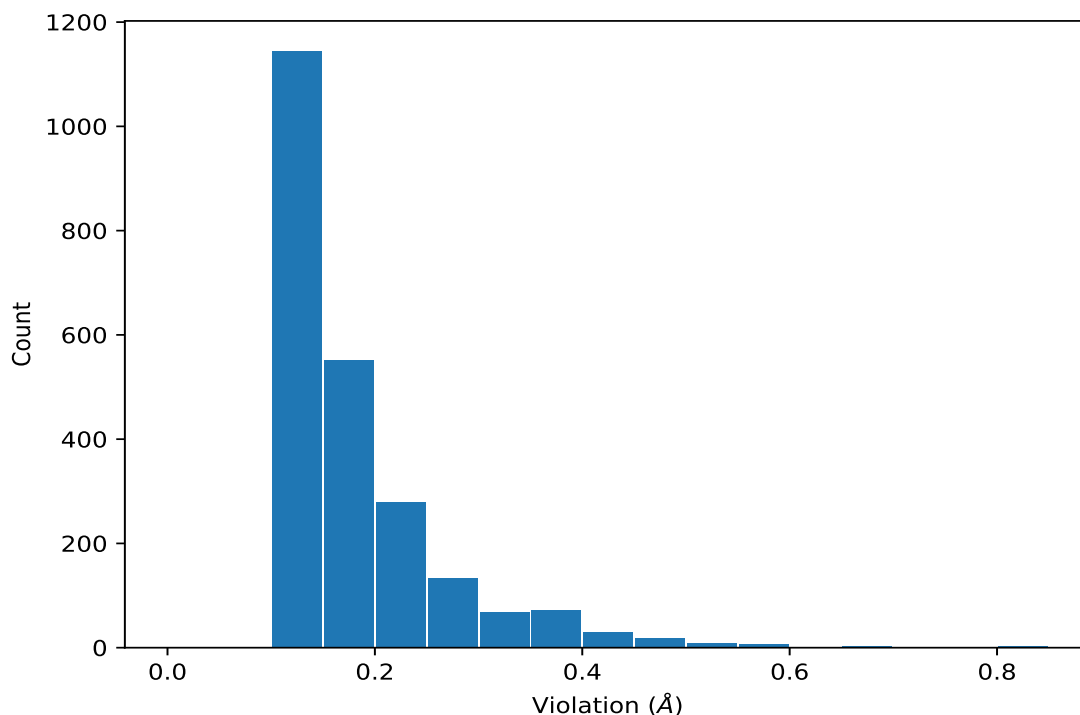
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,672)	1:16:A:LEU:HD23	1:67:A:TYR:HE1	2	0.12	0.01	0.12
(4,672)	1:16:A:LEU:HD23	1:67:A:TYR:HE2	2	0.12	0.01	0.12
(1,37)	1:19:A:GLN:O	1:23:A:GLU:H	2	0.12	0.0	0.12
(1,141)	1:127:A:ALA:O	1:131:A:TRP:H	2	0.12	0.0	0.12
(4,1247)	1:11:A:TRP:CZ2	1:48:A:MET:HE1	2	0.12	0.0	0.12
(4,1247)	1:11:A:TRP:CZ2	1:48:A:MET:HE2	2	0.12	0.0	0.12
(4,1247)	1:11:A:TRP:CZ2	1:48:A:MET:HE3	2	0.12	0.0	0.12
(4,1289)	1:17:A:LEU:HD21	1:40:A:TYR:HE1	2	0.12	0.0	0.12
(4,1289)	1:17:A:LEU:HD21	1:40:A:TYR:HE2	2	0.12	0.0	0.12
(4,1289)	1:17:A:LEU:HD22	1:40:A:TYR:HE1	2	0.12	0.0	0.12
(4,1289)	1:17:A:LEU:HD22	1:40:A:TYR:HE2	2	0.12	0.0	0.12
(4,1289)	1:17:A:LEU:HD23	1:40:A:TYR:HE1	2	0.12	0.0	0.12
(4,1289)	1:17:A:LEU:HD23	1:40:A:TYR:HE2	2	0.12	0.0	0.12
(1,159)	1:136:A:GLN:O	1:140:A:THR:H	2	0.11	0.0	0.11
(1,153)	1:133:A:ASN:O	1:137:A:PHE:H	2	0.11	0.0	0.11
(1,165)	1:139:A:GLN:O	1:143:A:LYS:H	2	0.11	0.0	0.11
(4,129)	1:24:A:LEU:HD21	1:33:A:LEU:HD11	2	0.11	0.0	0.11
(4,129)	1:24:A:LEU:HD21	1:33:A:LEU:HD12	2	0.11	0.0	0.11
(4,129)	1:24:A:LEU:HD21	1:33:A:LEU:HD13	2	0.11	0.0	0.11
(4,129)	1:24:A:LEU:HD22	1:33:A:LEU:HD11	2	0.11	0.0	0.11
(4,129)	1:24:A:LEU:HD22	1:33:A:LEU:HD12	2	0.11	0.0	0.11
(4,129)	1:24:A:LEU:HD22	1:33:A:LEU:HD13	2	0.11	0.0	0.11
(4,129)	1:24:A:LEU:HD23	1:33:A:LEU:HD11	2	0.11	0.0	0.11
(4,129)	1:24:A:LEU:HD23	1:33:A:LEU:HD12	2	0.11	0.0	0.11
(4,129)	1:24:A:LEU:HD23	1:33:A:LEU:HD13	2	0.11	0.0	0.11
(1,19)	1:10:A:ARG:O	1:14:A:ILE:H	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)
(4,1071)	1:82:A:LEU:HD21	1:137:A:PHE:CD1	14	0.82
(4,1071)	1:82:A:LEU:HD22	1:137:A:PHE:CD1	14	0.82
(4,1071)	1:82:A:LEU:HD23	1:137:A:PHE:CD1	14	0.82
(4,1071)	1:82:A:LEU:HD21	1:137:A:PHE:CD1	4	0.69
(4,1071)	1:82:A:LEU:HD22	1:137:A:PHE:CD1	4	0.69
(4,1071)	1:82:A:LEU:HD23	1:137:A:PHE:CD1	4	0.69
(4,1071)	1:82:A:LEU:HD21	1:137:A:PHE:CD1	1	0.55
(4,1071)	1:82:A:LEU:HD22	1:137:A:PHE:CD1	1	0.55
(4,1071)	1:82:A:LEU:HD23	1:137:A:PHE:CD1	1	0.55
(4,1071)	1:82:A:LEU:HD21	1:137:A:PHE:CD1	12	0.55
(4,1071)	1:82:A:LEU:HD22	1:137:A:PHE:CD1	12	0.55
(4,1071)	1:82:A:LEU:HD23	1:137:A:PHE:CD1	12	0.55
(4,1071)	1:82:A:LEU:HD21	1:137:A:PHE:CD1	10	0.52
(4,1071)	1:82:A:LEU:HD22	1:137:A:PHE:CD1	10	0.52
(4,1071)	1:82:A:LEU:HD23	1:137:A:PHE:CD1	10	0.52
(4,1071)	1:82:A:LEU:HD21	1:137:A:PHE:CD1	3	0.51

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1071)	1:82:A:LEU:HD22	1:137:A:PHE:CD1	3	0.51
(4,1071)	1:82:A:LEU:HD23	1:137:A:PHE:CD1	3	0.51
(4,1071)	1:82:A:LEU:HD21	1:137:A:PHE:CD1	7	0.51
(4,1071)	1:82:A:LEU:HD22	1:137:A:PHE:CD1	7	0.51
(4,1071)	1:82:A:LEU:HD23	1:137:A:PHE:CD1	7	0.51
(4,1071)	1:82:A:LEU:HD21	1:137:A:PHE:CD1	9	0.49
(4,1071)	1:82:A:LEU:HD22	1:137:A:PHE:CD1	9	0.49
(4,1071)	1:82:A:LEU:HD23	1:137:A:PHE:CD1	9	0.49
(4,1279)	1:8:A:ILE:HG21	1:67:A:TYR:CD1	5	0.48
(4,1279)	1:8:A:ILE:HG22	1:67:A:TYR:CD1	5	0.48
(4,1279)	1:8:A:ILE:HG23	1:67:A:TYR:CD1	5	0.48
(4,1071)	1:82:A:LEU:HD21	1:137:A:PHE:CD1	8	0.48
(4,1071)	1:82:A:LEU:HD22	1:137:A:PHE:CD1	8	0.48
(4,1071)	1:82:A:LEU:HD23	1:137:A:PHE:CD1	8	0.48
(4,1073)	1:82:A:LEU:HD21	1:134:A:TYR:CE2	13	0.46
(4,1073)	1:82:A:LEU:HD22	1:134:A:TYR:CE2	13	0.46
(4,1073)	1:82:A:LEU:HD23	1:134:A:TYR:CE2	13	0.46
(4,1071)	1:82:A:LEU:HD21	1:137:A:PHE:CD1	5	0.46
(4,1071)	1:82:A:LEU:HD22	1:137:A:PHE:CD1	5	0.46
(4,1071)	1:82:A:LEU:HD23	1:137:A:PHE:CD1	5	0.46
(4,1071)	1:82:A:LEU:HD21	1:137:A:PHE:CD1	20	0.46
(4,1071)	1:82:A:LEU:HD22	1:137:A:PHE:CD1	20	0.46
(4,1071)	1:82:A:LEU:HD23	1:137:A:PHE:CD1	20	0.46
(4,1071)	1:82:A:LEU:HD21	1:137:A:PHE:CD1	6	0.44
(4,1071)	1:82:A:LEU:HD22	1:137:A:PHE:CD1	6	0.44
(4,1071)	1:82:A:LEU:HD23	1:137:A:PHE:CD1	6	0.44
(4,1071)	1:82:A:LEU:HD21	1:137:A:PHE:CD1	18	0.44
(4,1071)	1:82:A:LEU:HD22	1:137:A:PHE:CD1	18	0.44
(4,1071)	1:82:A:LEU:HD23	1:137:A:PHE:CD1	18	0.44
(4,1071)	1:82:A:LEU:HD21	1:137:A:PHE:CD1	2	0.43
(4,1071)	1:82:A:LEU:HD22	1:137:A:PHE:CD1	2	0.43
(4,1071)	1:82:A:LEU:HD23	1:137:A:PHE:CD1	2	0.43
(4,1071)	1:82:A:LEU:HD21	1:137:A:PHE:CD1	16	0.42
(4,1071)	1:82:A:LEU:HD22	1:137:A:PHE:CD1	16	0.42
(4,1071)	1:82:A:LEU:HD23	1:137:A:PHE:CD1	16	0.42
(4,1071)	1:82:A:LEU:HD21	1:137:A:PHE:CD1	17	0.42
(4,1071)	1:82:A:LEU:HD22	1:137:A:PHE:CD1	17	0.42
(4,1071)	1:82:A:LEU:HD23	1:137:A:PHE:CD1	17	0.42
(4,1279)	1:8:A:ILE:HG21	1:67:A:TYR:CD1	11	0.41
(4,1279)	1:8:A:ILE:HG22	1:67:A:TYR:CD1	11	0.41
(4,1279)	1:8:A:ILE:HG23	1:67:A:TYR:CD1	11	0.41
(4,1245)	1:15:A:ALA:HB1	1:67:A:TYR:CE2	19	0.41

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1245)	1:15:A:ALA:HB2	1:67:A:TYR:CE2	19	0.41
(4,1245)	1:15:A:ALA:HB3	1:67:A:TYR:CE2	19	0.41
(4,1073)	1:82:A:LEU:HD21	1:134:A:TYR:CE2	3	0.41
(4,1073)	1:82:A:LEU:HD22	1:134:A:TYR:CE2	3	0.41
(4,1073)	1:82:A:LEU:HD23	1:134:A:TYR:CE2	3	0.41
(4,1071)	1:82:A:LEU:HD21	1:137:A:PHE:CD1	15	0.41
(4,1071)	1:82:A:LEU:HD22	1:137:A:PHE:CD1	15	0.41
(4,1071)	1:82:A:LEU:HD23	1:137:A:PHE:CD1	15	0.41
(4,1279)	1:8:A:ILE:HG21	1:67:A:TYR:CD1	18	0.4
(4,1279)	1:8:A:ILE:HG22	1:67:A:TYR:CD1	18	0.4
(4,1279)	1:8:A:ILE:HG23	1:67:A:TYR:CD1	18	0.4
(4,1279)	1:8:A:ILE:HG21	1:67:A:TYR:CD1	17	0.39
(4,1279)	1:8:A:ILE:HG22	1:67:A:TYR:CD1	17	0.39
(4,1279)	1:8:A:ILE:HG23	1:67:A:TYR:CD1	17	0.39
(4,1245)	1:15:A:ALA:HB1	1:67:A:TYR:CE2	20	0.39
(4,1245)	1:15:A:ALA:HB2	1:67:A:TYR:CE2	20	0.39
(4,1245)	1:15:A:ALA:HB3	1:67:A:TYR:CE2	20	0.39
(4,1091)	1:33:A:LEU:HD21	1:134:A:TYR:CD2	13	0.39
(4,1091)	1:33:A:LEU:HD22	1:134:A:TYR:CD2	13	0.39
(4,1091)	1:33:A:LEU:HD23	1:134:A:TYR:CD2	13	0.39
(4,1071)	1:82:A:LEU:HD21	1:137:A:PHE:CD1	13	0.39
(4,1071)	1:82:A:LEU:HD22	1:137:A:PHE:CD1	13	0.39
(4,1071)	1:82:A:LEU:HD23	1:137:A:PHE:CD1	13	0.39
(4,750)	1:152:A:LEU:H	1:153:A:THR:HG21	1	0.39
(4,750)	1:152:A:LEU:H	1:153:A:THR:HG22	1	0.39
(4,750)	1:152:A:LEU:H	1:153:A:THR:HG23	1	0.39
(4,1280)	1:8:A:ILE:HG21	1:67:A:TYR:CE1	13	0.38
(4,1280)	1:8:A:ILE:HG22	1:67:A:TYR:CE1	13	0.38
(4,1280)	1:8:A:ILE:HG23	1:67:A:TYR:CE1	13	0.38
(4,1279)	1:8:A:ILE:HG21	1:67:A:TYR:CD1	6	0.38
(4,1279)	1:8:A:ILE:HG22	1:67:A:TYR:CD1	6	0.38
(4,1279)	1:8:A:ILE:HG23	1:67:A:TYR:CD1	6	0.38
(4,1245)	1:15:A:ALA:HB1	1:67:A:TYR:CE2	6	0.38
(4,1245)	1:15:A:ALA:HB2	1:67:A:TYR:CE2	6	0.38
(4,1245)	1:15:A:ALA:HB3	1:67:A:TYR:CE2	6	0.38
(4,1245)	1:15:A:ALA:HB1	1:67:A:TYR:CE2	18	0.38
(4,1245)	1:15:A:ALA:HB2	1:67:A:TYR:CE2	18	0.38
(4,1245)	1:15:A:ALA:HB3	1:67:A:TYR:CE2	18	0.38
(4,1279)	1:8:A:ILE:HG21	1:67:A:TYR:CD1	13	0.37
(4,1279)	1:8:A:ILE:HG22	1:67:A:TYR:CD1	13	0.37
(4,1279)	1:8:A:ILE:HG23	1:67:A:TYR:CD1	13	0.37
(4,1245)	1:15:A:ALA:HB1	1:67:A:TYR:CE2	13	0.37

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1245)	1:15:A:ALA:HB2	1:67:A:TYR:CE2	13	0.37
(4,1245)	1:15:A:ALA:HB3	1:67:A:TYR:CE2	13	0.37
(4,1245)	1:15:A:ALA:HB1	1:67:A:TYR:CE2	17	0.37
(4,1245)	1:15:A:ALA:HB2	1:67:A:TYR:CE2	17	0.37
(4,1245)	1:15:A:ALA:HB3	1:67:A:TYR:CE2	17	0.37
(4,1117)	1:16:A:LEU:HD21	1:67:A:TYR:CD2	6	0.37
(4,1117)	1:16:A:LEU:HD22	1:67:A:TYR:CD2	6	0.37
(4,1117)	1:16:A:LEU:HD23	1:67:A:TYR:CD2	6	0.37
(4,1280)	1:8:A:ILE:HG21	1:67:A:TYR:CE1	17	0.36
(4,1280)	1:8:A:ILE:HG22	1:67:A:TYR:CE1	17	0.36
(4,1280)	1:8:A:ILE:HG23	1:67:A:TYR:CE1	17	0.36
(4,1279)	1:8:A:ILE:HG21	1:67:A:TYR:CD1	19	0.36
(4,1279)	1:8:A:ILE:HG22	1:67:A:TYR:CD1	19	0.36
(4,1279)	1:8:A:ILE:HG23	1:67:A:TYR:CD1	19	0.36
(4,1091)	1:33:A:LEU:HD21	1:134:A:TYR:CD2	2	0.36
(4,1091)	1:33:A:LEU:HD22	1:134:A:TYR:CD2	2	0.36
(4,1091)	1:33:A:LEU:HD23	1:134:A:TYR:CD2	2	0.36
(4,1022)	1:81:A:LEU:HD21	1:83:A:GLN:H	8	0.36
(4,1022)	1:81:A:LEU:HD22	1:83:A:GLN:H	8	0.36
(4,1022)	1:81:A:LEU:HD23	1:83:A:GLN:H	8	0.36
(4,407)	1:16:A:LEU:H	1:67:A:TYR:HD1	16	0.36
(4,407)	1:16:A:LEU:H	1:67:A:TYR:HD2	16	0.36
(4,49)	1:96:A:VAL:HG11	1:126:A:ILE:HD11	15	0.36
(4,49)	1:96:A:VAL:HG11	1:126:A:ILE:HD12	15	0.36
(4,49)	1:96:A:VAL:HG11	1:126:A:ILE:HD13	15	0.36
(4,49)	1:96:A:VAL:HG12	1:126:A:ILE:HD11	15	0.36
(4,49)	1:96:A:VAL:HG12	1:126:A:ILE:HD12	15	0.36
(4,49)	1:96:A:VAL:HG12	1:126:A:ILE:HD13	15	0.36
(4,49)	1:96:A:VAL:HG13	1:126:A:ILE:HD11	15	0.36
(4,49)	1:96:A:VAL:HG13	1:126:A:ILE:HD12	15	0.36
(4,49)	1:96:A:VAL:HG13	1:126:A:ILE:HD13	15	0.36
(4,1071)	1:82:A:LEU:HD21	1:137:A:PHE:CD1	11	0.35
(4,1071)	1:82:A:LEU:HD22	1:137:A:PHE:CD1	11	0.35
(4,1071)	1:82:A:LEU:HD23	1:137:A:PHE:CD1	11	0.35
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD11	19	0.35
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD12	19	0.35
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD13	19	0.35
(4,530)	1:17:A:LEU:HD21	1:71:A:THR:CG2	17	0.35
(4,530)	1:17:A:LEU:HD22	1:71:A:THR:CG2	17	0.35
(4,530)	1:17:A:LEU:HD23	1:71:A:THR:CG2	17	0.35
(4,1279)	1:8:A:ILE:HG21	1:67:A:TYR:CD1	16	0.34
(4,1279)	1:8:A:ILE:HG22	1:67:A:TYR:CD1	16	0.34

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1279)	1:8:A:ILE:HG23	1:67:A:TYR:CD1	16	0.34
(4,1073)	1:82:A:LEU:HD21	1:134:A:TYR:CE2	2	0.34
(4,1073)	1:82:A:LEU:HD22	1:134:A:TYR:CE2	2	0.34
(4,1073)	1:82:A:LEU:HD23	1:134:A:TYR:CE2	2	0.34
(4,1279)	1:8:A:ILE:HG21	1:67:A:TYR:CD1	20	0.33
(4,1279)	1:8:A:ILE:HG22	1:67:A:TYR:CD1	20	0.33
(4,1279)	1:8:A:ILE:HG23	1:67:A:TYR:CD1	20	0.33
(4,1117)	1:16:A:LEU:HD21	1:67:A:TYR:CD2	18	0.33
(4,1117)	1:16:A:LEU:HD22	1:67:A:TYR:CD2	18	0.33
(4,1117)	1:16:A:LEU:HD23	1:67:A:TYR:CD2	18	0.33
(4,1117)	1:16:A:LEU:HD21	1:67:A:TYR:CD2	20	0.33
(4,1117)	1:16:A:LEU:HD22	1:67:A:TYR:CD2	20	0.33
(4,1117)	1:16:A:LEU:HD23	1:67:A:TYR:CD2	20	0.33
(4,1092)	1:33:A:LEU:HD21	1:137:A:PHE:CD1	12	0.33
(4,1092)	1:33:A:LEU:HD22	1:137:A:PHE:CD1	12	0.33
(4,1092)	1:33:A:LEU:HD23	1:137:A:PHE:CD1	12	0.33
(4,1073)	1:82:A:LEU:HD21	1:134:A:TYR:CE2	19	0.33
(4,1073)	1:82:A:LEU:HD22	1:134:A:TYR:CE2	19	0.33
(4,1073)	1:82:A:LEU:HD23	1:134:A:TYR:CE2	19	0.33
(4,458)	1:33:A:LEU:HD21	1:78:A:LEU:CD2	3	0.33
(4,458)	1:33:A:LEU:HD22	1:78:A:LEU:CD2	3	0.33
(4,458)	1:33:A:LEU:HD23	1:78:A:LEU:CD2	3	0.33
(4,49)	1:96:A:VAL:HG11	1:126:A:ILE:HD11	18	0.33
(4,49)	1:96:A:VAL:HG11	1:126:A:ILE:HD12	18	0.33
(4,49)	1:96:A:VAL:HG11	1:126:A:ILE:HD13	18	0.33
(4,49)	1:96:A:VAL:HG12	1:126:A:ILE:HD11	18	0.33
(4,49)	1:96:A:VAL:HG12	1:126:A:ILE:HD12	18	0.33
(4,49)	1:96:A:VAL:HG12	1:126:A:ILE:HD13	18	0.33
(4,49)	1:96:A:VAL:HG13	1:126:A:ILE:HD11	18	0.33
(4,49)	1:96:A:VAL:HG13	1:126:A:ILE:HD12	18	0.33
(4,49)	1:96:A:VAL:HG13	1:126:A:ILE:HD13	18	0.33
(4,1117)	1:16:A:LEU:HD21	1:67:A:TYR:CD2	19	0.32
(4,1117)	1:16:A:LEU:HD22	1:67:A:TYR:CD2	19	0.32
(4,1117)	1:16:A:LEU:HD23	1:67:A:TYR:CD2	19	0.32
(4,1073)	1:82:A:LEU:HD21	1:134:A:TYR:CE2	4	0.32
(4,1073)	1:82:A:LEU:HD22	1:134:A:TYR:CE2	4	0.32
(4,1073)	1:82:A:LEU:HD23	1:134:A:TYR:CE2	4	0.32
(4,1280)	1:8:A:ILE:HG21	1:67:A:TYR:CE1	18	0.31
(4,1280)	1:8:A:ILE:HG22	1:67:A:TYR:CE1	18	0.31
(4,1280)	1:8:A:ILE:HG23	1:67:A:TYR:CE1	18	0.31
(4,1092)	1:33:A:LEU:HD21	1:137:A:PHE:CD1	9	0.31
(4,1092)	1:33:A:LEU:HD22	1:137:A:PHE:CD1	9	0.31

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1092)	1:33:A:LEU:HD23	1:137:A:PHE:CD1	9	0.31
(4,1092)	1:33:A:LEU:HD21	1:137:A:PHE:CD1	14	0.31
(4,1092)	1:33:A:LEU:HD22	1:137:A:PHE:CD1	14	0.31
(4,1092)	1:33:A:LEU:HD23	1:137:A:PHE:CD1	14	0.31
(4,1091)	1:33:A:LEU:HD21	1:134:A:TYR:CD2	6	0.31
(4,1091)	1:33:A:LEU:HD22	1:134:A:TYR:CD2	6	0.31
(4,1091)	1:33:A:LEU:HD23	1:134:A:TYR:CD2	6	0.31
(4,1022)	1:81:A:LEU:HD21	1:83:A:GLN:H	15	0.31
(4,1022)	1:81:A:LEU:HD22	1:83:A:GLN:H	15	0.31
(4,1022)	1:81:A:LEU:HD23	1:83:A:GLN:H	15	0.31
(4,458)	1:33:A:LEU:HD21	1:78:A:LEU:CD2	8	0.31
(4,458)	1:33:A:LEU:HD22	1:78:A:LEU:CD2	8	0.31
(4,458)	1:33:A:LEU:HD23	1:78:A:LEU:CD2	8	0.31
(4,1280)	1:8:A:ILE:HG21	1:67:A:TYR:CE1	11	0.3
(4,1280)	1:8:A:ILE:HG22	1:67:A:TYR:CE1	11	0.3
(4,1280)	1:8:A:ILE:HG23	1:67:A:TYR:CE1	11	0.3
(4,1280)	1:8:A:ILE:HG21	1:67:A:TYR:CE1	20	0.3
(4,1280)	1:8:A:ILE:HG22	1:67:A:TYR:CE1	20	0.3
(4,1280)	1:8:A:ILE:HG23	1:67:A:TYR:CE1	20	0.3
(4,1244)	1:15:A:ALA:HB1	1:67:A:TYR:CD2	19	0.3
(4,1244)	1:15:A:ALA:HB2	1:67:A:TYR:CD2	19	0.3
(4,1244)	1:15:A:ALA:HB3	1:67:A:TYR:CD2	19	0.3
(4,1244)	1:15:A:ALA:HB1	1:67:A:TYR:CD2	20	0.3
(4,1244)	1:15:A:ALA:HB2	1:67:A:TYR:CD2	20	0.3
(4,1244)	1:15:A:ALA:HB3	1:67:A:TYR:CD2	20	0.3
(4,1244)	1:15:A:ALA:HB1	1:67:A:TYR:CD2	13	0.29
(4,1244)	1:15:A:ALA:HB2	1:67:A:TYR:CD2	13	0.29
(4,1244)	1:15:A:ALA:HB3	1:67:A:TYR:CD2	13	0.29
(4,1206)	1:89:A:LEU:HD11	1:134:A:TYR:CE1	5	0.29
(4,1206)	1:89:A:LEU:HD12	1:134:A:TYR:CE1	5	0.29
(4,1206)	1:89:A:LEU:HD13	1:134:A:TYR:CE1	5	0.29
(4,1092)	1:33:A:LEU:HD21	1:137:A:PHE:CD1	6	0.29
(4,1092)	1:33:A:LEU:HD22	1:137:A:PHE:CD1	6	0.29
(4,1092)	1:33:A:LEU:HD23	1:137:A:PHE:CD1	6	0.29
(4,1092)	1:33:A:LEU:HD21	1:137:A:PHE:CD1	16	0.29
(4,1092)	1:33:A:LEU:HD22	1:137:A:PHE:CD1	16	0.29
(4,1092)	1:33:A:LEU:HD23	1:137:A:PHE:CD1	16	0.29
(4,1092)	1:33:A:LEU:HD21	1:137:A:PHE:CD1	17	0.29
(4,1092)	1:33:A:LEU:HD22	1:137:A:PHE:CD1	17	0.29
(4,1092)	1:33:A:LEU:HD23	1:137:A:PHE:CD1	17	0.29
(4,458)	1:33:A:LEU:HD21	1:78:A:LEU:CD2	13	0.29
(4,458)	1:33:A:LEU:HD22	1:78:A:LEU:CD2	13	0.29

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,458)	1:33:A:LEU:HD23	1:78:A:LEU:CD2	13	0.29
(4,458)	1:33:A:LEU:HD21	1:78:A:LEU:CD2	19	0.29
(4,458)	1:33:A:LEU:HD22	1:78:A:LEU:CD2	19	0.29
(4,458)	1:33:A:LEU:HD23	1:78:A:LEU:CD2	19	0.29
(4,1091)	1:33:A:LEU:HD21	1:134:A:TYR:CD2	4	0.28
(4,1091)	1:33:A:LEU:HD22	1:134:A:TYR:CD2	4	0.28
(4,1091)	1:33:A:LEU:HD23	1:134:A:TYR:CD2	4	0.28
(4,1082)	1:82:A:LEU:HD11	1:134:A:TYR:CE2	4	0.28
(4,1082)	1:82:A:LEU:HD12	1:134:A:TYR:CE2	4	0.28
(4,1082)	1:82:A:LEU:HD13	1:134:A:TYR:CE2	4	0.28
(4,530)	1:17:A:LEU:HD21	1:71:A:THR:CG2	15	0.28
(4,530)	1:17:A:LEU:HD22	1:71:A:THR:CG2	15	0.28
(4,530)	1:17:A:LEU:HD23	1:71:A:THR:CG2	15	0.28
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD11	11	0.28
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD12	11	0.28
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD13	11	0.28
(4,407)	1:16:A:LEU:H	1:67:A:TYR:HD1	11	0.28
(4,407)	1:16:A:LEU:H	1:67:A:TYR:HD2	11	0.28
(4,1244)	1:15:A:ALA:HB1	1:67:A:TYR:CD2	17	0.27
(4,1244)	1:15:A:ALA:HB2	1:67:A:TYR:CD2	17	0.27
(4,1244)	1:15:A:ALA:HB3	1:67:A:TYR:CD2	17	0.27
(4,1244)	1:15:A:ALA:HB1	1:67:A:TYR:CD2	18	0.27
(4,1244)	1:15:A:ALA:HB2	1:67:A:TYR:CD2	18	0.27
(4,1244)	1:15:A:ALA:HB3	1:67:A:TYR:CD2	18	0.27
(4,1091)	1:33:A:LEU:HD21	1:134:A:TYR:CD2	16	0.27
(4,1091)	1:33:A:LEU:HD22	1:134:A:TYR:CD2	16	0.27
(4,1091)	1:33:A:LEU:HD23	1:134:A:TYR:CD2	16	0.27
(4,1073)	1:82:A:LEU:HD21	1:134:A:TYR:CE2	1	0.27
(4,1073)	1:82:A:LEU:HD22	1:134:A:TYR:CE2	1	0.27
(4,1073)	1:82:A:LEU:HD23	1:134:A:TYR:CE2	1	0.27
(4,1073)	1:82:A:LEU:HD21	1:134:A:TYR:CE2	16	0.27
(4,1073)	1:82:A:LEU:HD22	1:134:A:TYR:CE2	16	0.27
(4,1073)	1:82:A:LEU:HD23	1:134:A:TYR:CE2	16	0.27
(4,882)	1:24:A:LEU:HD21	1:32:A:LEU:H	2	0.27
(4,882)	1:24:A:LEU:HD22	1:32:A:LEU:H	2	0.27
(4,882)	1:24:A:LEU:HD23	1:32:A:LEU:H	2	0.27
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD11	13	0.27
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD12	13	0.27
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD13	13	0.27
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD11	7	0.27
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD12	7	0.27
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD13	7	0.27

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,458)	1:33:A:LEU:HD21	1:78:A:LEU:CD2	9	0.27
(4,458)	1:33:A:LEU:HD22	1:78:A:LEU:CD2	9	0.27
(4,458)	1:33:A:LEU:HD23	1:78:A:LEU:CD2	9	0.27
(4,458)	1:33:A:LEU:HD21	1:78:A:LEU:CD2	14	0.27
(4,458)	1:33:A:LEU:HD22	1:78:A:LEU:CD2	14	0.27
(4,458)	1:33:A:LEU:HD23	1:78:A:LEU:CD2	14	0.27
(4,458)	1:33:A:LEU:HD21	1:78:A:LEU:CD2	16	0.27
(4,458)	1:33:A:LEU:HD22	1:78:A:LEU:CD2	16	0.27
(4,458)	1:33:A:LEU:HD23	1:78:A:LEU:CD2	16	0.27
(4,1280)	1:8:A:ILE:HG21	1:67:A:TYR:CE1	16	0.26
(4,1280)	1:8:A:ILE:HG22	1:67:A:TYR:CE1	16	0.26
(4,1280)	1:8:A:ILE:HG23	1:67:A:TYR:CE1	16	0.26
(4,1280)	1:8:A:ILE:HG21	1:67:A:TYR:CE1	19	0.26
(4,1280)	1:8:A:ILE:HG22	1:67:A:TYR:CE1	19	0.26
(4,1280)	1:8:A:ILE:HG23	1:67:A:TYR:CE1	19	0.26
(4,1244)	1:15:A:ALA:HB1	1:67:A:TYR:CD2	6	0.26
(4,1244)	1:15:A:ALA:HB2	1:67:A:TYR:CD2	6	0.26
(4,1244)	1:15:A:ALA:HB3	1:67:A:TYR:CD2	6	0.26
(4,1206)	1:89:A:LEU:HD11	1:134:A:TYR:CE1	20	0.26
(4,1206)	1:89:A:LEU:HD12	1:134:A:TYR:CE1	20	0.26
(4,1206)	1:89:A:LEU:HD13	1:134:A:TYR:CE1	20	0.26
(4,1117)	1:16:A:LEU:HD21	1:67:A:TYR:CD2	5	0.26
(4,1117)	1:16:A:LEU:HD22	1:67:A:TYR:CD2	5	0.26
(4,1117)	1:16:A:LEU:HD23	1:67:A:TYR:CD2	5	0.26
(4,1076)	1:82:A:LEU:HD11	1:134:A:TYR:CD2	20	0.26
(4,1076)	1:82:A:LEU:HD12	1:134:A:TYR:CD2	20	0.26
(4,1076)	1:82:A:LEU:HD13	1:134:A:TYR:CD2	20	0.26
(4,568)	1:97:A:LEU:HD11	1:126:A:ILE:CD1	11	0.26
(4,568)	1:97:A:LEU:HD12	1:126:A:ILE:CD1	11	0.26
(4,568)	1:97:A:LEU:HD13	1:126:A:ILE:CD1	11	0.26
(4,530)	1:17:A:LEU:HD21	1:71:A:THR:CG2	1	0.26
(4,530)	1:17:A:LEU:HD22	1:71:A:THR:CG2	1	0.26
(4,530)	1:17:A:LEU:HD23	1:71:A:THR:CG2	1	0.26
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD11	15	0.26
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD12	15	0.26
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD13	15	0.26
(4,458)	1:33:A:LEU:HD21	1:78:A:LEU:CD2	4	0.26
(4,458)	1:33:A:LEU:HD22	1:78:A:LEU:CD2	4	0.26
(4,458)	1:33:A:LEU:HD23	1:78:A:LEU:CD2	4	0.26
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD21	11	0.25
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD22	11	0.25
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD23	11	0.25

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1245)	1:15:A:ALA:HB1	1:67:A:TYR:CE2	5	0.25
(4,1245)	1:15:A:ALA:HB2	1:67:A:TYR:CE2	5	0.25
(4,1245)	1:15:A:ALA:HB3	1:67:A:TYR:CE2	5	0.25
(4,1092)	1:33:A:LEU:HD21	1:137:A:PHE:CD1	2	0.25
(4,1092)	1:33:A:LEU:HD22	1:137:A:PHE:CD1	2	0.25
(4,1092)	1:33:A:LEU:HD23	1:137:A:PHE:CD1	2	0.25
(4,1076)	1:82:A:LEU:HD11	1:134:A:TYR:CD2	7	0.25
(4,1076)	1:82:A:LEU:HD12	1:134:A:TYR:CD2	7	0.25
(4,1076)	1:82:A:LEU:HD13	1:134:A:TYR:CD2	7	0.25
(4,1071)	1:82:A:LEU:HD21	1:137:A:PHE:CD1	19	0.25
(4,1071)	1:82:A:LEU:HD22	1:137:A:PHE:CD1	19	0.25
(4,1071)	1:82:A:LEU:HD23	1:137:A:PHE:CD1	19	0.25
(4,757)	1:72:A:LEU:HD11	1:149:A:ARG:H	1	0.25
(4,757)	1:72:A:LEU:HD12	1:149:A:ARG:H	1	0.25
(4,757)	1:72:A:LEU:HD13	1:149:A:ARG:H	1	0.25
(4,757)	1:72:A:LEU:HD11	1:149:A:ARG:H	17	0.25
(4,757)	1:72:A:LEU:HD12	1:149:A:ARG:H	17	0.25
(4,757)	1:72:A:LEU:HD13	1:149:A:ARG:H	17	0.25
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD11	6	0.25
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD12	6	0.25
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD13	6	0.25
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD11	10	0.25
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD12	10	0.25
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD13	10	0.25
(4,49)	1:96:A:VAL:HG11	1:126:A:ILE:HD11	16	0.25
(4,49)	1:96:A:VAL:HG11	1:126:A:ILE:HD12	16	0.25
(4,49)	1:96:A:VAL:HG11	1:126:A:ILE:HD13	16	0.25
(4,49)	1:96:A:VAL:HG12	1:126:A:ILE:HD11	16	0.25
(4,49)	1:96:A:VAL:HG12	1:126:A:ILE:HD12	16	0.25
(4,49)	1:96:A:VAL:HG12	1:126:A:ILE:HD13	16	0.25
(4,49)	1:96:A:VAL:HG13	1:126:A:ILE:HD11	16	0.25
(4,49)	1:96:A:VAL:HG13	1:126:A:ILE:HD12	16	0.25
(4,49)	1:96:A:VAL:HG13	1:126:A:ILE:HD13	16	0.25
(4,1101)	1:96:A:VAL:HG21	1:98:A:PHE:CE1	13	0.24
(4,1101)	1:96:A:VAL:HG22	1:98:A:PHE:CE1	13	0.24
(4,1101)	1:96:A:VAL:HG23	1:98:A:PHE:CE1	13	0.24
(4,1076)	1:82:A:LEU:HD11	1:134:A:TYR:CD2	1	0.24
(4,1076)	1:82:A:LEU:HD12	1:134:A:TYR:CD2	1	0.24
(4,1076)	1:82:A:LEU:HD13	1:134:A:TYR:CD2	1	0.24
(4,875)	1:93:A:ILE:HD11	1:131:A:TRP:HE1	2	0.24
(4,875)	1:93:A:ILE:HD12	1:131:A:TRP:HE1	2	0.24
(4,875)	1:93:A:ILE:HD13	1:131:A:TRP:HE1	2	0.24

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD11	5	0.24
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD12	5	0.24
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD13	5	0.24
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD11	8	0.24
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD12	8	0.24
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD13	8	0.24
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD11	9	0.24
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD12	9	0.24
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD13	9	0.24
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD21	6	0.24
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD22	6	0.24
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD23	6	0.24
(4,458)	1:33:A:LEU:HD21	1:78:A:LEU:CD2	7	0.24
(4,458)	1:33:A:LEU:HD22	1:78:A:LEU:CD2	7	0.24
(4,458)	1:33:A:LEU:HD23	1:78:A:LEU:CD2	7	0.24
(4,458)	1:33:A:LEU:HD21	1:78:A:LEU:CD2	17	0.24
(4,458)	1:33:A:LEU:HD22	1:78:A:LEU:CD2	17	0.24
(4,458)	1:33:A:LEU:HD23	1:78:A:LEU:CD2	17	0.24
(4,313)	1:11:A:TRP:HE1	1:155:A:TRP:HE1	13	0.24
(4,49)	1:96:A:VAL:HG11	1:126:A:ILE:HD11	17	0.24
(4,49)	1:96:A:VAL:HG11	1:126:A:ILE:HD12	17	0.24
(4,49)	1:96:A:VAL:HG11	1:126:A:ILE:HD13	17	0.24
(4,49)	1:96:A:VAL:HG12	1:126:A:ILE:HD11	17	0.24
(4,49)	1:96:A:VAL:HG12	1:126:A:ILE:HD12	17	0.24
(4,49)	1:96:A:VAL:HG12	1:126:A:ILE:HD13	17	0.24
(4,49)	1:96:A:VAL:HG13	1:126:A:ILE:HD11	17	0.24
(4,49)	1:96:A:VAL:HG13	1:126:A:ILE:HD12	17	0.24
(4,49)	1:96:A:VAL:HG13	1:126:A:ILE:HD13	17	0.24
(4,1230)	1:97:A:LEU:HD11	1:98:A:PHE:HE1	11	0.23
(4,1230)	1:97:A:LEU:HD11	1:98:A:PHE:HE2	11	0.23
(4,1230)	1:97:A:LEU:HD12	1:98:A:PHE:HE1	11	0.23
(4,1230)	1:97:A:LEU:HD12	1:98:A:PHE:HE2	11	0.23
(4,1230)	1:97:A:LEU:HD13	1:98:A:PHE:HE1	11	0.23
(4,1230)	1:97:A:LEU:HD13	1:98:A:PHE:HE2	11	0.23
(4,1117)	1:16:A:LEU:HD21	1:67:A:TYR:CD2	16	0.23
(4,1117)	1:16:A:LEU:HD22	1:67:A:TYR:CD2	16	0.23
(4,1117)	1:16:A:LEU:HD23	1:67:A:TYR:CD2	16	0.23
(4,1092)	1:33:A:LEU:HD21	1:137:A:PHE:CD1	3	0.23
(4,1092)	1:33:A:LEU:HD22	1:137:A:PHE:CD1	3	0.23
(4,1092)	1:33:A:LEU:HD23	1:137:A:PHE:CD1	3	0.23
(4,1092)	1:33:A:LEU:HD21	1:137:A:PHE:CD1	10	0.23
(4,1092)	1:33:A:LEU:HD22	1:137:A:PHE:CD1	10	0.23

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1092)	1:33:A:LEU:HD23	1:137:A:PHE:CD1	10	0.23
(4,1092)	1:33:A:LEU:HD21	1:137:A:PHE:CD1	18	0.23
(4,1092)	1:33:A:LEU:HD22	1:137:A:PHE:CD1	18	0.23
(4,1092)	1:33:A:LEU:HD23	1:137:A:PHE:CD1	18	0.23
(4,1091)	1:33:A:LEU:HD21	1:134:A:TYR:CD2	3	0.23
(4,1091)	1:33:A:LEU:HD22	1:134:A:TYR:CD2	3	0.23
(4,1091)	1:33:A:LEU:HD23	1:134:A:TYR:CD2	3	0.23
(4,1076)	1:82:A:LEU:HD11	1:134:A:TYR:CD2	11	0.23
(4,1076)	1:82:A:LEU:HD12	1:134:A:TYR:CD2	11	0.23
(4,1076)	1:82:A:LEU:HD13	1:134:A:TYR:CD2	11	0.23
(4,1073)	1:82:A:LEU:HD21	1:134:A:TYR:CE2	18	0.23
(4,1073)	1:82:A:LEU:HD22	1:134:A:TYR:CE2	18	0.23
(4,1073)	1:82:A:LEU:HD23	1:134:A:TYR:CE2	18	0.23
(4,999)	1:96:A:VAL:HG11	1:97:A:LEU:H	5	0.23
(4,999)	1:96:A:VAL:HG12	1:97:A:LEU:H	5	0.23
(4,999)	1:96:A:VAL:HG13	1:97:A:LEU:H	5	0.23
(4,882)	1:24:A:LEU:HD21	1:32:A:LEU:H	15	0.23
(4,882)	1:24:A:LEU:HD22	1:32:A:LEU:H	15	0.23
(4,882)	1:24:A:LEU:HD23	1:32:A:LEU:H	15	0.23
(4,530)	1:17:A:LEU:HD21	1:71:A:THR:CG2	14	0.23
(4,530)	1:17:A:LEU:HD22	1:71:A:THR:CG2	14	0.23
(4,530)	1:17:A:LEU:HD23	1:71:A:THR:CG2	14	0.23
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD11	16	0.23
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD12	16	0.23
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD13	16	0.23
(4,1317)	1:41:A:LEU:HD11	1:137:A:PHE:HD1	5	0.22
(4,1317)	1:41:A:LEU:HD11	1:137:A:PHE:HD2	5	0.22
(4,1317)	1:41:A:LEU:HD12	1:137:A:PHE:HD1	5	0.22
(4,1317)	1:41:A:LEU:HD12	1:137:A:PHE:HD2	5	0.22
(4,1317)	1:41:A:LEU:HD13	1:137:A:PHE:HD1	5	0.22
(4,1317)	1:41:A:LEU:HD13	1:137:A:PHE:HD2	5	0.22
(4,1311)	1:8:A:ILE:HG21	1:67:A:TYR:HE1	4	0.22
(4,1311)	1:8:A:ILE:HG21	1:67:A:TYR:HE2	4	0.22
(4,1311)	1:8:A:ILE:HG22	1:67:A:TYR:HE1	4	0.22
(4,1311)	1:8:A:ILE:HG22	1:67:A:TYR:HE2	4	0.22
(4,1311)	1:8:A:ILE:HG23	1:67:A:TYR:HE1	4	0.22
(4,1311)	1:8:A:ILE:HG23	1:67:A:TYR:HE2	4	0.22
(4,1206)	1:89:A:LEU:HD11	1:134:A:TYR:CE1	8	0.22
(4,1206)	1:89:A:LEU:HD12	1:134:A:TYR:CE1	8	0.22
(4,1206)	1:89:A:LEU:HD13	1:134:A:TYR:CE1	8	0.22
(4,1206)	1:89:A:LEU:HD11	1:134:A:TYR:CE1	10	0.22
(4,1206)	1:89:A:LEU:HD12	1:134:A:TYR:CE1	10	0.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1206)	1:89:A:LEU:HD13	1:134:A:TYR:CE1	10	0.22
(4,1092)	1:33:A:LEU:HD21	1:137:A:PHE:CD1	11	0.22
(4,1092)	1:33:A:LEU:HD22	1:137:A:PHE:CD1	11	0.22
(4,1092)	1:33:A:LEU:HD23	1:137:A:PHE:CD1	11	0.22
(4,1091)	1:33:A:LEU:HD21	1:134:A:TYR:CD2	1	0.22
(4,1091)	1:33:A:LEU:HD22	1:134:A:TYR:CD2	1	0.22
(4,1091)	1:33:A:LEU:HD23	1:134:A:TYR:CD2	1	0.22
(4,1076)	1:82:A:LEU:HD11	1:134:A:TYR:CD2	18	0.22
(4,1076)	1:82:A:LEU:HD12	1:134:A:TYR:CD2	18	0.22
(4,1076)	1:82:A:LEU:HD13	1:134:A:TYR:CD2	18	0.22
(4,1073)	1:82:A:LEU:HD21	1:134:A:TYR:CE2	10	0.22
(4,1073)	1:82:A:LEU:HD22	1:134:A:TYR:CE2	10	0.22
(4,1073)	1:82:A:LEU:HD23	1:134:A:TYR:CE2	10	0.22
(4,1073)	1:82:A:LEU:HD21	1:134:A:TYR:CE2	17	0.22
(4,1073)	1:82:A:LEU:HD22	1:134:A:TYR:CE2	17	0.22
(4,1073)	1:82:A:LEU:HD23	1:134:A:TYR:CE2	17	0.22
(4,878)	1:150:A:LEU:H	1:153:A:THR:HG21	1	0.22
(4,878)	1:150:A:LEU:H	1:153:A:THR:HG22	1	0.22
(4,878)	1:150:A:LEU:H	1:153:A:THR:HG23	1	0.22
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD11	16	0.22
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD12	16	0.22
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD13	16	0.22
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD11	20	0.22
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD12	20	0.22
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD13	20	0.22
(4,539)	1:71:A:THR:HG21	1:72:A:LEU:CD1	9	0.22
(4,539)	1:71:A:THR:HG22	1:72:A:LEU:CD1	9	0.22
(4,539)	1:71:A:THR:HG23	1:72:A:LEU:CD1	9	0.22
(4,530)	1:17:A:LEU:HD21	1:71:A:THR:CG2	16	0.22
(4,530)	1:17:A:LEU:HD22	1:71:A:THR:CG2	16	0.22
(4,530)	1:17:A:LEU:HD23	1:71:A:THR:CG2	16	0.22
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD21	14	0.22
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD22	14	0.22
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD23	14	0.22
(4,458)	1:33:A:LEU:HD21	1:78:A:LEU:CD2	18	0.22
(4,458)	1:33:A:LEU:HD22	1:78:A:LEU:CD2	18	0.22
(4,458)	1:33:A:LEU:HD23	1:78:A:LEU:CD2	18	0.22
(4,458)	1:33:A:LEU:HD21	1:78:A:LEU:CD2	20	0.22
(4,458)	1:33:A:LEU:HD22	1:78:A:LEU:CD2	20	0.22
(4,458)	1:33:A:LEU:HD23	1:78:A:LEU:CD2	20	0.22
(4,309)	1:91:A:SER:H	1:131:A:TRP:HE1	10	0.22
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD11	16	0.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD12	16	0.22
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD13	16	0.22
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD11	16	0.22
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD12	16	0.22
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD13	16	0.22
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD11	16	0.22
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD12	16	0.22
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD13	16	0.22
(4,1280)	1:8:A:ILE:HG21	1:67:A:TYR:CE1	6	0.21
(4,1280)	1:8:A:ILE:HG22	1:67:A:TYR:CE1	6	0.21
(4,1280)	1:8:A:ILE:HG23	1:67:A:TYR:CE1	6	0.21
(4,1271)	1:67:A:TYR:CD2	1:71:A:THR:HG21	20	0.21
(4,1271)	1:67:A:TYR:CD2	1:71:A:THR:HG22	20	0.21
(4,1271)	1:67:A:TYR:CD2	1:71:A:THR:HG23	20	0.21
(4,1206)	1:89:A:LEU:HD11	1:134:A:TYR:CE1	4	0.21
(4,1206)	1:89:A:LEU:HD12	1:134:A:TYR:CE1	4	0.21
(4,1206)	1:89:A:LEU:HD13	1:134:A:TYR:CE1	4	0.21
(4,1206)	1:89:A:LEU:HD11	1:134:A:TYR:CE1	7	0.21
(4,1206)	1:89:A:LEU:HD12	1:134:A:TYR:CE1	7	0.21
(4,1206)	1:89:A:LEU:HD13	1:134:A:TYR:CE1	7	0.21
(4,1117)	1:16:A:LEU:HD21	1:67:A:TYR:CD2	13	0.21
(4,1117)	1:16:A:LEU:HD22	1:67:A:TYR:CD2	13	0.21
(4,1117)	1:16:A:LEU:HD23	1:67:A:TYR:CD2	13	0.21
(4,1092)	1:33:A:LEU:HD21	1:137:A:PHE:CD1	5	0.21
(4,1092)	1:33:A:LEU:HD22	1:137:A:PHE:CD1	5	0.21
(4,1092)	1:33:A:LEU:HD23	1:137:A:PHE:CD1	5	0.21
(4,1091)	1:33:A:LEU:HD21	1:134:A:TYR:CD2	17	0.21
(4,1091)	1:33:A:LEU:HD22	1:134:A:TYR:CD2	17	0.21
(4,1091)	1:33:A:LEU:HD23	1:134:A:TYR:CD2	17	0.21
(4,1091)	1:33:A:LEU:HD21	1:134:A:TYR:CD2	18	0.21
(4,1091)	1:33:A:LEU:HD22	1:134:A:TYR:CD2	18	0.21
(4,1091)	1:33:A:LEU:HD23	1:134:A:TYR:CD2	18	0.21
(4,1076)	1:82:A:LEU:HD11	1:134:A:TYR:CD2	4	0.21
(4,1076)	1:82:A:LEU:HD12	1:134:A:TYR:CD2	4	0.21
(4,1076)	1:82:A:LEU:HD13	1:134:A:TYR:CD2	4	0.21
(4,1073)	1:82:A:LEU:HD21	1:134:A:TYR:CE2	6	0.21
(4,1073)	1:82:A:LEU:HD22	1:134:A:TYR:CE2	6	0.21
(4,1073)	1:82:A:LEU:HD23	1:134:A:TYR:CE2	6	0.21
(4,882)	1:24:A:LEU:HD21	1:32:A:LEU:H	1	0.21
(4,882)	1:24:A:LEU:HD22	1:32:A:LEU:H	1	0.21
(4,882)	1:24:A:LEU:HD23	1:32:A:LEU:H	1	0.21
(4,875)	1:93:A:ILE:HD11	1:131:A:TRP:HE1	11	0.21

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,875)	1:93:A:ILE:HD12	1:131:A:TRP:HE1	11	0.21
(4,875)	1:93:A:ILE:HD13	1:131:A:TRP:HE1	11	0.21
(4,844)	1:22:A:LEU:HD11	1:26:A:GLN:H	8	0.21
(4,844)	1:22:A:LEU:HD12	1:26:A:GLN:H	8	0.21
(4,844)	1:22:A:LEU:HD13	1:26:A:GLN:H	8	0.21
(4,794)	1:21:A:LEU:HD21	1:137:A:PHE:HE1	6	0.21
(4,794)	1:21:A:LEU:HD21	1:137:A:PHE:HE2	6	0.21
(4,794)	1:21:A:LEU:HD22	1:137:A:PHE:HE1	6	0.21
(4,794)	1:21:A:LEU:HD22	1:137:A:PHE:HE2	6	0.21
(4,794)	1:21:A:LEU:HD23	1:137:A:PHE:HE1	6	0.21
(4,794)	1:21:A:LEU:HD23	1:137:A:PHE:HE2	6	0.21
(4,530)	1:17:A:LEU:HD21	1:71:A:THR:CG2	3	0.21
(4,530)	1:17:A:LEU:HD22	1:71:A:THR:CG2	3	0.21
(4,530)	1:17:A:LEU:HD23	1:71:A:THR:CG2	3	0.21
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD21	9	0.21
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD22	9	0.21
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD23	9	0.21
(4,458)	1:33:A:LEU:HD21	1:78:A:LEU:CD2	6	0.21
(4,458)	1:33:A:LEU:HD22	1:78:A:LEU:CD2	6	0.21
(4,458)	1:33:A:LEU:HD23	1:78:A:LEU:CD2	6	0.21
(4,458)	1:33:A:LEU:HD21	1:78:A:LEU:CD2	10	0.21
(4,458)	1:33:A:LEU:HD22	1:78:A:LEU:CD2	10	0.21
(4,458)	1:33:A:LEU:HD23	1:78:A:LEU:CD2	10	0.21
(4,458)	1:33:A:LEU:HD21	1:78:A:LEU:CD2	11	0.21
(4,458)	1:33:A:LEU:HD22	1:78:A:LEU:CD2	11	0.21
(4,458)	1:33:A:LEU:HD23	1:78:A:LEU:CD2	11	0.21
(4,458)	1:33:A:LEU:HD21	1:78:A:LEU:CD2	15	0.21
(4,458)	1:33:A:LEU:HD22	1:78:A:LEU:CD2	15	0.21
(4,458)	1:33:A:LEU:HD23	1:78:A:LEU:CD2	15	0.21
(4,49)	1:96:A:VAL:HG11	1:126:A:ILE:HD11	11	0.21
(4,49)	1:96:A:VAL:HG11	1:126:A:ILE:HD12	11	0.21
(4,49)	1:96:A:VAL:HG11	1:126:A:ILE:HD13	11	0.21
(4,49)	1:96:A:VAL:HG12	1:126:A:ILE:HD11	11	0.21
(4,49)	1:96:A:VAL:HG12	1:126:A:ILE:HD12	11	0.21
(4,49)	1:96:A:VAL:HG12	1:126:A:ILE:HD13	11	0.21
(4,49)	1:96:A:VAL:HG13	1:126:A:ILE:HD11	11	0.21
(4,49)	1:96:A:VAL:HG13	1:126:A:ILE:HD12	11	0.21
(4,49)	1:96:A:VAL:HG13	1:126:A:ILE:HD13	11	0.21
(4,1280)	1:8:A:ILE:HG21	1:67:A:TYR:CE1	5	0.2
(4,1280)	1:8:A:ILE:HG22	1:67:A:TYR:CE1	5	0.2
(4,1280)	1:8:A:ILE:HG23	1:67:A:TYR:CE1	5	0.2
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD21	20	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD22	20	0.2
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD23	20	0.2
(4,1206)	1:89:A:LEU:HD11	1:134:A:TYR:CE1	12	0.2
(4,1206)	1:89:A:LEU:HD12	1:134:A:TYR:CE1	12	0.2
(4,1206)	1:89:A:LEU:HD13	1:134:A:TYR:CE1	12	0.2
(4,1117)	1:16:A:LEU:HD21	1:67:A:TYR:CD2	17	0.2
(4,1117)	1:16:A:LEU:HD22	1:67:A:TYR:CD2	17	0.2
(4,1117)	1:16:A:LEU:HD23	1:67:A:TYR:CD2	17	0.2
(4,1092)	1:33:A:LEU:HD21	1:137:A:PHE:CD1	1	0.2
(4,1092)	1:33:A:LEU:HD22	1:137:A:PHE:CD1	1	0.2
(4,1092)	1:33:A:LEU:HD23	1:137:A:PHE:CD1	1	0.2
(4,1092)	1:33:A:LEU:HD21	1:137:A:PHE:CD1	15	0.2
(4,1092)	1:33:A:LEU:HD22	1:137:A:PHE:CD1	15	0.2
(4,1092)	1:33:A:LEU:HD23	1:137:A:PHE:CD1	15	0.2
(4,1091)	1:33:A:LEU:HD21	1:134:A:TYR:CD2	10	0.2
(4,1091)	1:33:A:LEU:HD22	1:134:A:TYR:CD2	10	0.2
(4,1091)	1:33:A:LEU:HD23	1:134:A:TYR:CD2	10	0.2
(4,1091)	1:33:A:LEU:HD21	1:134:A:TYR:CD2	20	0.2
(4,1091)	1:33:A:LEU:HD22	1:134:A:TYR:CD2	20	0.2
(4,1091)	1:33:A:LEU:HD23	1:134:A:TYR:CD2	20	0.2
(4,1077)	1:82:A:LEU:HD11	1:137:A:PHE:CD1	13	0.2
(4,1077)	1:82:A:LEU:HD12	1:137:A:PHE:CD1	13	0.2
(4,1077)	1:82:A:LEU:HD13	1:137:A:PHE:CD1	13	0.2
(4,1076)	1:82:A:LEU:HD11	1:134:A:TYR:CD2	16	0.2
(4,1076)	1:82:A:LEU:HD12	1:134:A:TYR:CD2	16	0.2
(4,1076)	1:82:A:LEU:HD13	1:134:A:TYR:CD2	16	0.2
(4,1070)	1:82:A:LEU:HD21	1:134:A:TYR:CD2	13	0.2
(4,1070)	1:82:A:LEU:HD22	1:134:A:TYR:CD2	13	0.2
(4,1070)	1:82:A:LEU:HD23	1:134:A:TYR:CD2	13	0.2
(4,915)	1:25:A:ALA:H	1:81:A:LEU:HD11	8	0.2
(4,915)	1:25:A:ALA:H	1:81:A:LEU:HD12	8	0.2
(4,915)	1:25:A:ALA:H	1:81:A:LEU:HD13	8	0.2
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD11	13	0.2
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD12	13	0.2
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD13	13	0.2
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD11	10	0.2
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD12	10	0.2
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD13	10	0.2
(4,563)	1:92:A:LEU:HD11	1:93:A:ILE:CD1	9	0.2
(4,563)	1:92:A:LEU:HD12	1:93:A:ILE:CD1	9	0.2
(4,563)	1:92:A:LEU:HD13	1:93:A:ILE:CD1	9	0.2
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD11	17	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD12	17	0.2
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD13	17	0.2
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD11	17	0.2
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD12	17	0.2
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD13	17	0.2
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD11	17	0.2
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD12	17	0.2
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD13	17	0.2
(4,49)	1:96:A:VAL:HG11	1:126:A:ILE:HD11	10	0.2
(4,49)	1:96:A:VAL:HG11	1:126:A:ILE:HD12	10	0.2
(4,49)	1:96:A:VAL:HG11	1:126:A:ILE:HD13	10	0.2
(4,49)	1:96:A:VAL:HG12	1:126:A:ILE:HD11	10	0.2
(4,49)	1:96:A:VAL:HG12	1:126:A:ILE:HD12	10	0.2
(4,49)	1:96:A:VAL:HG12	1:126:A:ILE:HD13	10	0.2
(4,49)	1:96:A:VAL:HG13	1:126:A:ILE:HD11	10	0.2
(4,49)	1:96:A:VAL:HG13	1:126:A:ILE:HD12	10	0.2
(4,49)	1:96:A:VAL:HG13	1:126:A:ILE:HD13	10	0.2
(1,143)	1:128:A:SER:O	1:132:A:ILE:H	18	0.2
(4,1206)	1:89:A:LEU:HD11	1:134:A:TYR:CE1	15	0.19
(4,1206)	1:89:A:LEU:HD12	1:134:A:TYR:CE1	15	0.19
(4,1206)	1:89:A:LEU:HD13	1:134:A:TYR:CE1	15	0.19
(4,1206)	1:89:A:LEU:HD11	1:134:A:TYR:CE1	17	0.19
(4,1206)	1:89:A:LEU:HD12	1:134:A:TYR:CE1	17	0.19
(4,1206)	1:89:A:LEU:HD13	1:134:A:TYR:CE1	17	0.19
(4,1121)	1:97:A:LEU:HD21	1:98:A:PHE:CD1	8	0.19
(4,1121)	1:97:A:LEU:HD22	1:98:A:PHE:CD1	8	0.19
(4,1121)	1:97:A:LEU:HD23	1:98:A:PHE:CD1	8	0.19
(4,1092)	1:33:A:LEU:HD21	1:137:A:PHE:CD1	4	0.19
(4,1092)	1:33:A:LEU:HD22	1:137:A:PHE:CD1	4	0.19
(4,1092)	1:33:A:LEU:HD23	1:137:A:PHE:CD1	4	0.19
(4,1092)	1:33:A:LEU:HD21	1:137:A:PHE:CD1	7	0.19
(4,1092)	1:33:A:LEU:HD22	1:137:A:PHE:CD1	7	0.19
(4,1092)	1:33:A:LEU:HD23	1:137:A:PHE:CD1	7	0.19
(4,1091)	1:33:A:LEU:HD21	1:134:A:TYR:CD2	5	0.19
(4,1091)	1:33:A:LEU:HD22	1:134:A:TYR:CD2	5	0.19
(4,1091)	1:33:A:LEU:HD23	1:134:A:TYR:CD2	5	0.19
(4,1091)	1:33:A:LEU:HD21	1:134:A:TYR:CD2	19	0.19
(4,1091)	1:33:A:LEU:HD22	1:134:A:TYR:CD2	19	0.19
(4,1091)	1:33:A:LEU:HD23	1:134:A:TYR:CD2	19	0.19
(4,1077)	1:82:A:LEU:HD11	1:137:A:PHE:CD1	19	0.19
(4,1077)	1:82:A:LEU:HD12	1:137:A:PHE:CD1	19	0.19
(4,1077)	1:82:A:LEU:HD13	1:137:A:PHE:CD1	19	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1073)	1:82:A:LEU:HD21	1:134:A:TYR:CE2	7	0.19
(4,1073)	1:82:A:LEU:HD22	1:134:A:TYR:CE2	7	0.19
(4,1073)	1:82:A:LEU:HD23	1:134:A:TYR:CE2	7	0.19
(4,1073)	1:82:A:LEU:HD21	1:134:A:TYR:CE2	9	0.19
(4,1073)	1:82:A:LEU:HD22	1:134:A:TYR:CE2	9	0.19
(4,1073)	1:82:A:LEU:HD23	1:134:A:TYR:CE2	9	0.19
(4,1073)	1:82:A:LEU:HD21	1:134:A:TYR:CE2	11	0.19
(4,1073)	1:82:A:LEU:HD22	1:134:A:TYR:CE2	11	0.19
(4,1073)	1:82:A:LEU:HD23	1:134:A:TYR:CE2	11	0.19
(4,1073)	1:82:A:LEU:HD21	1:134:A:TYR:CE2	14	0.19
(4,1073)	1:82:A:LEU:HD22	1:134:A:TYR:CE2	14	0.19
(4,1073)	1:82:A:LEU:HD23	1:134:A:TYR:CE2	14	0.19
(4,1058)	1:92:A:LEU:HD11	1:93:A:ILE:H	6	0.19
(4,1058)	1:92:A:LEU:HD12	1:93:A:ILE:H	6	0.19
(4,1058)	1:92:A:LEU:HD13	1:93:A:ILE:H	6	0.19
(4,972)	1:70:A:GLN:H	1:72:A:LEU:HD21	9	0.19
(4,972)	1:70:A:GLN:H	1:72:A:LEU:HD22	9	0.19
(4,972)	1:70:A:GLN:H	1:72:A:LEU:HD23	9	0.19
(4,966)	1:16:A:LEU:H	1:71:A:THR:HG21	14	0.19
(4,966)	1:16:A:LEU:H	1:71:A:THR:HG22	14	0.19
(4,966)	1:16:A:LEU:H	1:71:A:THR:HG23	14	0.19
(4,965)	1:96:A:VAL:HG21	1:98:A:PHE:H	10	0.19
(4,965)	1:96:A:VAL:HG22	1:98:A:PHE:H	10	0.19
(4,965)	1:96:A:VAL:HG23	1:98:A:PHE:H	10	0.19
(4,875)	1:93:A:ILE:HD11	1:131:A:TRP:HE1	14	0.19
(4,875)	1:93:A:ILE:HD12	1:131:A:TRP:HE1	14	0.19
(4,875)	1:93:A:ILE:HD13	1:131:A:TRP:HE1	14	0.19
(4,821)	1:24:A:LEU:HD21	1:30:A:TRP:H	3	0.19
(4,821)	1:24:A:LEU:HD22	1:30:A:TRP:H	3	0.19
(4,821)	1:24:A:LEU:HD23	1:30:A:TRP:H	3	0.19
(4,661)	1:86:A:LEU:HD11	1:135:A:GLN:H	11	0.19
(4,661)	1:86:A:LEU:HD12	1:135:A:GLN:H	11	0.19
(4,661)	1:86:A:LEU:HD13	1:135:A:GLN:H	11	0.19
(4,530)	1:17:A:LEU:HD21	1:71:A:THR:CG2	20	0.19
(4,530)	1:17:A:LEU:HD22	1:71:A:THR:CG2	20	0.19
(4,530)	1:17:A:LEU:HD23	1:71:A:THR:CG2	20	0.19
(4,511)	1:162:A:ALA:HB1	1:163:A:LEU:CD1	1	0.19
(4,511)	1:162:A:ALA:HB2	1:163:A:LEU:CD1	1	0.19
(4,511)	1:162:A:ALA:HB3	1:163:A:LEU:CD1	1	0.19
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD11	4	0.19
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD12	4	0.19
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD13	4	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD11	6	0.19
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD12	6	0.19
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD13	6	0.19
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD11	14	0.19
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD12	14	0.19
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD13	14	0.19
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD11	17	0.19
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD12	17	0.19
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD13	17	0.19
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD11	18	0.19
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD12	18	0.19
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD13	18	0.19
(4,407)	1:16:A:LEU:H	1:67:A:TYR:HD1	5	0.19
(4,407)	1:16:A:LEU:H	1:67:A:TYR:HD2	5	0.19
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD11	15	0.19
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD12	15	0.19
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD13	15	0.19
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD11	15	0.19
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD12	15	0.19
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD13	15	0.19
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD11	15	0.19
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD12	15	0.19
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD13	15	0.19
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD21	8	0.18
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD22	8	0.18
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD23	8	0.18
(4,1206)	1:89:A:LEU:HD11	1:134:A:TYR:CE1	16	0.18
(4,1206)	1:89:A:LEU:HD12	1:134:A:TYR:CE1	16	0.18
(4,1206)	1:89:A:LEU:HD13	1:134:A:TYR:CE1	16	0.18
(4,1201)	1:44:A:ILE:HG21	1:148:A:HIS:CE1	18	0.18
(4,1201)	1:44:A:ILE:HG22	1:148:A:HIS:CE1	18	0.18
(4,1201)	1:44:A:ILE:HG23	1:148:A:HIS:CE1	18	0.18
(4,1113)	1:96:A:VAL:HG11	1:98:A:PHE:CD1	16	0.18
(4,1113)	1:96:A:VAL:HG12	1:98:A:PHE:CD1	16	0.18
(4,1113)	1:96:A:VAL:HG13	1:98:A:PHE:CD1	16	0.18
(4,1092)	1:33:A:LEU:HD21	1:137:A:PHE:CD1	20	0.18
(4,1092)	1:33:A:LEU:HD22	1:137:A:PHE:CD1	20	0.18
(4,1092)	1:33:A:LEU:HD23	1:137:A:PHE:CD1	20	0.18
(4,1076)	1:82:A:LEU:HD11	1:134:A:TYR:CD2	14	0.18
(4,1076)	1:82:A:LEU:HD12	1:134:A:TYR:CD2	14	0.18
(4,1076)	1:82:A:LEU:HD13	1:134:A:TYR:CD2	14	0.18
(4,1073)	1:82:A:LEU:HD21	1:134:A:TYR:CE2	8	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1073)	1:82:A:LEU:HD22	1:134:A:TYR:CE2	8	0.18
(4,1073)	1:82:A:LEU:HD23	1:134:A:TYR:CE2	8	0.18
(4,1058)	1:92:A:LEU:HD11	1:93:A:ILE:H	3	0.18
(4,1058)	1:92:A:LEU:HD12	1:93:A:ILE:H	3	0.18
(4,1058)	1:92:A:LEU:HD13	1:93:A:ILE:H	3	0.18
(4,914)	1:27:A:ARG:H	1:81:A:LEU:HD11	17	0.18
(4,914)	1:27:A:ARG:H	1:81:A:LEU:HD12	17	0.18
(4,914)	1:27:A:ARG:H	1:81:A:LEU:HD13	17	0.18
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD11	19	0.18
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD12	19	0.18
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD13	19	0.18
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD11	2	0.18
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD12	2	0.18
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD13	2	0.18
(4,794)	1:21:A:LEU:HD21	1:137:A:PHE:HE1	12	0.18
(4,794)	1:21:A:LEU:HD21	1:137:A:PHE:HE2	12	0.18
(4,794)	1:21:A:LEU:HD22	1:137:A:PHE:HE1	12	0.18
(4,794)	1:21:A:LEU:HD22	1:137:A:PHE:HE2	12	0.18
(4,794)	1:21:A:LEU:HD23	1:137:A:PHE:HE1	12	0.18
(4,794)	1:21:A:LEU:HD23	1:137:A:PHE:HE2	12	0.18
(4,794)	1:21:A:LEU:HD21	1:137:A:PHE:HE1	18	0.18
(4,794)	1:21:A:LEU:HD21	1:137:A:PHE:HE2	18	0.18
(4,794)	1:21:A:LEU:HD22	1:137:A:PHE:HE1	18	0.18
(4,794)	1:21:A:LEU:HD22	1:137:A:PHE:HE2	18	0.18
(4,794)	1:21:A:LEU:HD23	1:137:A:PHE:HE1	18	0.18
(4,794)	1:21:A:LEU:HD23	1:137:A:PHE:HE2	18	0.18
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD11	5	0.18
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD12	5	0.18
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD13	5	0.18
(4,550)	1:21:A:LEU:HD21	1:33:A:LEU:CD2	17	0.18
(4,550)	1:21:A:LEU:HD22	1:33:A:LEU:CD2	17	0.18
(4,550)	1:21:A:LEU:HD23	1:33:A:LEU:CD2	17	0.18
(4,539)	1:71:A:THR:HG21	1:72:A:LEU:CD1	8	0.18
(4,539)	1:71:A:THR:HG22	1:72:A:LEU:CD1	8	0.18
(4,539)	1:71:A:THR:HG23	1:72:A:LEU:CD1	8	0.18
(4,530)	1:17:A:LEU:HD21	1:71:A:THR:CG2	6	0.18
(4,530)	1:17:A:LEU:HD22	1:71:A:THR:CG2	6	0.18
(4,530)	1:17:A:LEU:HD23	1:71:A:THR:CG2	6	0.18
(4,530)	1:17:A:LEU:HD21	1:71:A:THR:CG2	18	0.18
(4,530)	1:17:A:LEU:HD22	1:71:A:THR:CG2	18	0.18
(4,530)	1:17:A:LEU:HD23	1:71:A:THR:CG2	18	0.18
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD11	1	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD12	1	0.18
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD13	1	0.18
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD11	12	0.18
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD12	12	0.18
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD13	12	0.18
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD11	19	0.18
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD12	19	0.18
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD13	19	0.18
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD21	11	0.18
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD22	11	0.18
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD23	11	0.18
(4,313)	1:11:A:TRP:HE1	1:155:A:TRP:HE1	1	0.18
(4,313)	1:11:A:TRP:HE1	1:155:A:TRP:HE1	3	0.18
(1,143)	1:128:A:SER:O	1:132:A:ILE:H	6	0.18
(1,143)	1:128:A:SER:O	1:132:A:ILE:H	15	0.18
(4,1317)	1:41:A:LEU:HD11	1:137:A:PHE:HD1	8	0.17
(4,1317)	1:41:A:LEU:HD11	1:137:A:PHE:HD2	8	0.17
(4,1317)	1:41:A:LEU:HD12	1:137:A:PHE:HD1	8	0.17
(4,1317)	1:41:A:LEU:HD12	1:137:A:PHE:HD2	8	0.17
(4,1317)	1:41:A:LEU:HD13	1:137:A:PHE:HD1	8	0.17
(4,1317)	1:41:A:LEU:HD13	1:137:A:PHE:HD2	8	0.17
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD21	1	0.17
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD22	1	0.17
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD23	1	0.17
(4,1271)	1:67:A:TYR:CD2	1:71:A:THR:HG21	13	0.17
(4,1271)	1:67:A:TYR:CD2	1:71:A:THR:HG22	13	0.17
(4,1271)	1:67:A:TYR:CD2	1:71:A:THR:HG23	13	0.17
(4,1271)	1:67:A:TYR:CD2	1:71:A:THR:HG21	17	0.17
(4,1271)	1:67:A:TYR:CD2	1:71:A:THR:HG22	17	0.17
(4,1271)	1:67:A:TYR:CD2	1:71:A:THR:HG23	17	0.17
(4,1245)	1:15:A:ALA:HB1	1:67:A:TYR:CE2	11	0.17
(4,1245)	1:15:A:ALA:HB2	1:67:A:TYR:CE2	11	0.17
(4,1245)	1:15:A:ALA:HB3	1:67:A:TYR:CE2	11	0.17
(4,1241)	1:93:A:ILE:HD11	1:131:A:TRP:CD1	9	0.17
(4,1241)	1:93:A:ILE:HD12	1:131:A:TRP:CD1	9	0.17
(4,1241)	1:93:A:ILE:HD13	1:131:A:TRP:CD1	9	0.17
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD21	5	0.17
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD22	5	0.17
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD23	5	0.17
(4,1206)	1:89:A:LEU:HD11	1:134:A:TYR:CE1	1	0.17
(4,1206)	1:89:A:LEU:HD12	1:134:A:TYR:CE1	1	0.17
(4,1206)	1:89:A:LEU:HD13	1:134:A:TYR:CE1	1	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1206)	1:89:A:LEU:HD11	1:134:A:TYR:CE1	11	0.17
(4,1206)	1:89:A:LEU:HD12	1:134:A:TYR:CE1	11	0.17
(4,1206)	1:89:A:LEU:HD13	1:134:A:TYR:CE1	11	0.17
(4,1162)	1:64:A:VAL:H	1:67:A:TYR:HE1	16	0.17
(4,1162)	1:64:A:VAL:H	1:67:A:TYR:HE2	16	0.17
(4,1117)	1:16:A:LEU:HD21	1:67:A:TYR:CD2	11	0.17
(4,1117)	1:16:A:LEU:HD22	1:67:A:TYR:CD2	11	0.17
(4,1117)	1:16:A:LEU:HD23	1:67:A:TYR:CD2	11	0.17
(4,1092)	1:33:A:LEU:HD21	1:137:A:PHE:CD1	8	0.17
(4,1092)	1:33:A:LEU:HD22	1:137:A:PHE:CD1	8	0.17
(4,1092)	1:33:A:LEU:HD23	1:137:A:PHE:CD1	8	0.17
(4,1091)	1:33:A:LEU:HD21	1:134:A:TYR:CD2	8	0.17
(4,1091)	1:33:A:LEU:HD22	1:134:A:TYR:CD2	8	0.17
(4,1091)	1:33:A:LEU:HD23	1:134:A:TYR:CD2	8	0.17
(4,1058)	1:92:A:LEU:HD11	1:93:A:ILE:H	9	0.17
(4,1058)	1:92:A:LEU:HD12	1:93:A:ILE:H	9	0.17
(4,1058)	1:92:A:LEU:HD13	1:93:A:ILE:H	9	0.17
(4,875)	1:93:A:ILE:HD11	1:131:A:TRP:HE1	20	0.17
(4,875)	1:93:A:ILE:HD12	1:131:A:TRP:HE1	20	0.17
(4,875)	1:93:A:ILE:HD13	1:131:A:TRP:HE1	20	0.17
(4,859)	1:78:A:LEU:HD11	1:137:A:PHE:HE1	7	0.17
(4,859)	1:78:A:LEU:HD11	1:137:A:PHE:HE2	7	0.17
(4,859)	1:78:A:LEU:HD12	1:137:A:PHE:HE1	7	0.17
(4,859)	1:78:A:LEU:HD12	1:137:A:PHE:HE2	7	0.17
(4,859)	1:78:A:LEU:HD13	1:137:A:PHE:HE1	7	0.17
(4,859)	1:78:A:LEU:HD13	1:137:A:PHE:HE2	7	0.17
(4,757)	1:72:A:LEU:HD11	1:149:A:ARG:H	9	0.17
(4,757)	1:72:A:LEU:HD12	1:149:A:ARG:H	9	0.17
(4,757)	1:72:A:LEU:HD13	1:149:A:ARG:H	9	0.17
(4,577)	1:97:A:LEU:HD21	1:126:A:ILE:CD1	20	0.17
(4,577)	1:97:A:LEU:HD22	1:126:A:ILE:CD1	20	0.17
(4,577)	1:97:A:LEU:HD23	1:126:A:ILE:CD1	20	0.17
(4,530)	1:17:A:LEU:HD21	1:71:A:THR:CG2	13	0.17
(4,530)	1:17:A:LEU:HD22	1:71:A:THR:CG2	13	0.17
(4,530)	1:17:A:LEU:HD23	1:71:A:THR:CG2	13	0.17
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD21	12	0.17
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD22	12	0.17
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD23	12	0.17
(4,458)	1:33:A:LEU:HD21	1:78:A:LEU:CD2	2	0.17
(4,458)	1:33:A:LEU:HD22	1:78:A:LEU:CD2	2	0.17
(4,458)	1:33:A:LEU:HD23	1:78:A:LEU:CD2	2	0.17
(4,458)	1:33:A:LEU:HD21	1:78:A:LEU:CD2	5	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,458)	1:33:A:LEU:HD22	1:78:A:LEU:CD2	5	0.17
(4,458)	1:33:A:LEU:HD23	1:78:A:LEU:CD2	5	0.17
(4,458)	1:33:A:LEU:HD21	1:78:A:LEU:CD2	12	0.17
(4,458)	1:33:A:LEU:HD22	1:78:A:LEU:CD2	12	0.17
(4,458)	1:33:A:LEU:HD23	1:78:A:LEU:CD2	12	0.17
(4,313)	1:11:A:TRP:HE1	1:155:A:TRP:HE1	8	0.17
(4,313)	1:11:A:TRP:HE1	1:155:A:TRP:HE1	10	0.17
(4,313)	1:11:A:TRP:HE1	1:155:A:TRP:HE1	17	0.17
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD11	11	0.17
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD12	11	0.17
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD13	11	0.17
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD11	11	0.17
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD12	11	0.17
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD13	11	0.17
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD11	11	0.17
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD12	11	0.17
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD13	11	0.17
(4,48)	1:14:A:ILE:HD11	1:17:A:LEU:HD11	17	0.17
(4,48)	1:14:A:ILE:HD11	1:17:A:LEU:HD12	17	0.17
(4,48)	1:14:A:ILE:HD11	1:17:A:LEU:HD13	17	0.17
(4,48)	1:14:A:ILE:HD12	1:17:A:LEU:HD11	17	0.17
(4,48)	1:14:A:ILE:HD12	1:17:A:LEU:HD12	17	0.17
(4,48)	1:14:A:ILE:HD12	1:17:A:LEU:HD13	17	0.17
(4,48)	1:14:A:ILE:HD13	1:17:A:LEU:HD11	17	0.17
(4,48)	1:14:A:ILE:HD13	1:17:A:LEU:HD12	17	0.17
(4,48)	1:14:A:ILE:HD13	1:17:A:LEU:HD13	17	0.17
(4,1317)	1:41:A:LEU:HD11	1:137:A:PHE:HD1	1	0.16
(4,1317)	1:41:A:LEU:HD11	1:137:A:PHE:HD2	1	0.16
(4,1317)	1:41:A:LEU:HD12	1:137:A:PHE:HD1	1	0.16
(4,1317)	1:41:A:LEU:HD12	1:137:A:PHE:HD2	1	0.16
(4,1317)	1:41:A:LEU:HD13	1:137:A:PHE:HD1	1	0.16
(4,1317)	1:41:A:LEU:HD13	1:137:A:PHE:HD2	1	0.16
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD21	7	0.16
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD22	7	0.16
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD23	7	0.16
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD21	12	0.16
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD22	12	0.16
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD23	12	0.16
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD21	14	0.16
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD22	14	0.16
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD23	14	0.16
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG21	12	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG22	12	0.16
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG23	12	0.16
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD21	4	0.16
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD22	4	0.16
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD23	4	0.16
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD21	7	0.16
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD22	7	0.16
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD23	7	0.16
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD21	18	0.16
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD22	18	0.16
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD23	18	0.16
(4,1128)	1:40:A:TYR:CD2	1:44:A:ILE:HD11	16	0.16
(4,1128)	1:40:A:TYR:CD2	1:44:A:ILE:HD12	16	0.16
(4,1128)	1:40:A:TYR:CD2	1:44:A:ILE:HD13	16	0.16
(4,1113)	1:96:A:VAL:HG11	1:98:A:PHE:CD1	17	0.16
(4,1113)	1:96:A:VAL:HG12	1:98:A:PHE:CD1	17	0.16
(4,1113)	1:96:A:VAL:HG13	1:98:A:PHE:CD1	17	0.16
(4,1106)	1:34:A:LEU:HD21	1:134:A:TYR:CE2	13	0.16
(4,1106)	1:34:A:LEU:HD22	1:134:A:TYR:CE2	13	0.16
(4,1106)	1:34:A:LEU:HD23	1:134:A:TYR:CE2	13	0.16
(4,1092)	1:33:A:LEU:HD21	1:137:A:PHE:CD1	19	0.16
(4,1092)	1:33:A:LEU:HD22	1:137:A:PHE:CD1	19	0.16
(4,1092)	1:33:A:LEU:HD23	1:137:A:PHE:CD1	19	0.16
(4,1091)	1:33:A:LEU:HD21	1:134:A:TYR:CD2	12	0.16
(4,1091)	1:33:A:LEU:HD22	1:134:A:TYR:CD2	12	0.16
(4,1091)	1:33:A:LEU:HD23	1:134:A:TYR:CD2	12	0.16
(4,1091)	1:33:A:LEU:HD21	1:134:A:TYR:CD2	14	0.16
(4,1091)	1:33:A:LEU:HD22	1:134:A:TYR:CD2	14	0.16
(4,1091)	1:33:A:LEU:HD23	1:134:A:TYR:CD2	14	0.16
(4,1077)	1:82:A:LEU:HD11	1:137:A:PHE:CD1	3	0.16
(4,1077)	1:82:A:LEU:HD12	1:137:A:PHE:CD1	3	0.16
(4,1077)	1:82:A:LEU:HD13	1:137:A:PHE:CD1	3	0.16
(4,1073)	1:82:A:LEU:HD21	1:134:A:TYR:CE2	20	0.16
(4,1073)	1:82:A:LEU:HD22	1:134:A:TYR:CE2	20	0.16
(4,1073)	1:82:A:LEU:HD23	1:134:A:TYR:CE2	20	0.16
(4,1063)	1:89:A:LEU:HD11	1:134:A:TYR:CD1	10	0.16
(4,1063)	1:89:A:LEU:HD12	1:134:A:TYR:CD1	10	0.16
(4,1063)	1:89:A:LEU:HD13	1:134:A:TYR:CD1	10	0.16
(4,1058)	1:92:A:LEU:HD11	1:93:A:ILE:H	14	0.16
(4,1058)	1:92:A:LEU:HD12	1:93:A:ILE:H	14	0.16
(4,1058)	1:92:A:LEU:HD13	1:93:A:ILE:H	14	0.16
(4,1027)	1:151:A:GLN:H	1:153:A:THR:HG21	1	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1027)	1:151:A:GLN:H	1:153:A:THR:HG22	1	0.16
(4,1027)	1:151:A:GLN:H	1:153:A:THR:HG23	1	0.16
(4,1014)	1:41:A:LEU:H	1:141:A:LEU:HD21	15	0.16
(4,1014)	1:41:A:LEU:H	1:141:A:LEU:HD22	15	0.16
(4,1014)	1:41:A:LEU:H	1:141:A:LEU:HD23	15	0.16
(4,966)	1:16:A:LEU:H	1:71:A:THR:HG21	12	0.16
(4,966)	1:16:A:LEU:H	1:71:A:THR:HG22	12	0.16
(4,966)	1:16:A:LEU:H	1:71:A:THR:HG23	12	0.16
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD11	13	0.16
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD12	13	0.16
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD13	13	0.16
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD11	19	0.16
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD12	19	0.16
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD13	19	0.16
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD11	1	0.16
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD12	1	0.16
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD13	1	0.16
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD11	14	0.16
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD12	14	0.16
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD13	14	0.16
(4,859)	1:78:A:LEU:HD11	1:137:A:PHE:HE1	18	0.16
(4,859)	1:78:A:LEU:HD11	1:137:A:PHE:HE2	18	0.16
(4,859)	1:78:A:LEU:HD12	1:137:A:PHE:HE1	18	0.16
(4,859)	1:78:A:LEU:HD12	1:137:A:PHE:HE2	18	0.16
(4,859)	1:78:A:LEU:HD13	1:137:A:PHE:HE1	18	0.16
(4,859)	1:78:A:LEU:HD13	1:137:A:PHE:HE2	18	0.16
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD11	13	0.16
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD12	13	0.16
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD13	13	0.16
(4,807)	1:31:A:ASP:H	1:34:A:LEU:HD11	14	0.16
(4,807)	1:31:A:ASP:H	1:34:A:LEU:HD12	14	0.16
(4,807)	1:31:A:ASP:H	1:34:A:LEU:HD13	14	0.16
(4,796)	1:21:A:LEU:HD21	1:137:A:PHE:HZ	13	0.16
(4,796)	1:21:A:LEU:HD22	1:137:A:PHE:HZ	13	0.16
(4,796)	1:21:A:LEU:HD23	1:137:A:PHE:HZ	13	0.16
(4,757)	1:72:A:LEU:HD11	1:149:A:ARG:H	15	0.16
(4,757)	1:72:A:LEU:HD12	1:149:A:ARG:H	15	0.16
(4,757)	1:72:A:LEU:HD13	1:149:A:ARG:H	15	0.16
(4,661)	1:86:A:LEU:HD11	1:135:A:GLN:H	12	0.16
(4,661)	1:86:A:LEU:HD12	1:135:A:GLN:H	12	0.16
(4,661)	1:86:A:LEU:HD13	1:135:A:GLN:H	12	0.16
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD11	12	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD12	12	0.16
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD13	12	0.16
(4,563)	1:92:A:LEU:HD11	1:93:A:ILE:CD1	3	0.16
(4,563)	1:92:A:LEU:HD12	1:93:A:ILE:CD1	3	0.16
(4,563)	1:92:A:LEU:HD13	1:93:A:ILE:CD1	3	0.16
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD21	16	0.16
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD22	16	0.16
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD23	16	0.16
(4,369)	1:21:A:LEU:H	1:40:A:TYR:HD1	2	0.16
(4,369)	1:21:A:LEU:H	1:40:A:TYR:HD2	2	0.16
(4,313)	1:11:A:TRP:HE1	1:155:A:TRP:HE1	9	0.16
(4,313)	1:11:A:TRP:HE1	1:155:A:TRP:HE1	11	0.16
(4,313)	1:11:A:TRP:HE1	1:155:A:TRP:HE1	12	0.16
(4,293)	1:96:A:VAL:H	1:97:A:LEU:H	5	0.16
(4,236)	1:137:A:PHE:HD1	1:141:A:LEU:H	10	0.16
(4,236)	1:137:A:PHE:HD2	1:141:A:LEU:H	10	0.16
(1,143)	1:128:A:SER:O	1:132:A:ILE:H	17	0.16
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD11	17	0.15
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD12	17	0.15
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD13	17	0.15
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD21	17	0.15
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD22	17	0.15
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD23	17	0.15
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD21	4	0.15
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD22	4	0.15
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD23	4	0.15
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD21	15	0.15
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD22	15	0.15
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD23	15	0.15
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD21	17	0.15
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD22	17	0.15
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD23	17	0.15
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD21	20	0.15
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD22	20	0.15
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD23	20	0.15
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG21	15	0.15
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG22	15	0.15
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG23	15	0.15
(4,1271)	1:67:A:TYR:CD2	1:71:A:THR:HG21	18	0.15
(4,1271)	1:67:A:TYR:CD2	1:71:A:THR:HG22	18	0.15
(4,1271)	1:67:A:TYR:CD2	1:71:A:THR:HG23	18	0.15
(4,1250)	1:86:A:LEU:HD11	1:134:A:TYR:CD1	5	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1250)	1:86:A:LEU:HD12	1:134:A:TYR:CD1	5	0.15
(4,1250)	1:86:A:LEU:HD13	1:134:A:TYR:CD1	5	0.15
(4,1230)	1:97:A:LEU:HD11	1:98:A:PHE:HE1	16	0.15
(4,1230)	1:97:A:LEU:HD11	1:98:A:PHE:HE2	16	0.15
(4,1230)	1:97:A:LEU:HD12	1:98:A:PHE:HE1	16	0.15
(4,1230)	1:97:A:LEU:HD12	1:98:A:PHE:HE2	16	0.15
(4,1230)	1:97:A:LEU:HD13	1:98:A:PHE:HE1	16	0.15
(4,1230)	1:97:A:LEU:HD13	1:98:A:PHE:HE2	16	0.15
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD21	2	0.15
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD22	2	0.15
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD23	2	0.15
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD21	8	0.15
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD22	8	0.15
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD23	8	0.15
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD21	11	0.15
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD22	11	0.15
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD23	11	0.15
(4,1201)	1:44:A:ILE:HG21	1:148:A:HIS:CE1	16	0.15
(4,1201)	1:44:A:ILE:HG22	1:148:A:HIS:CE1	16	0.15
(4,1201)	1:44:A:ILE:HG23	1:148:A:HIS:CE1	16	0.15
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD11	12	0.15
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD12	12	0.15
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD13	12	0.15
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD11	12	0.15
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD12	12	0.15
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD13	12	0.15
(4,1113)	1:96:A:VAL:HG11	1:98:A:PHE:CD1	15	0.15
(4,1113)	1:96:A:VAL:HG12	1:98:A:PHE:CD1	15	0.15
(4,1113)	1:96:A:VAL:HG13	1:98:A:PHE:CD1	15	0.15
(4,1107)	1:17:A:LEU:HD11	1:40:A:TYR:CE1	5	0.15
(4,1107)	1:17:A:LEU:HD12	1:40:A:TYR:CE1	5	0.15
(4,1107)	1:17:A:LEU:HD13	1:40:A:TYR:CE1	5	0.15
(4,1092)	1:33:A:LEU:HD21	1:137:A:PHE:CD1	13	0.15
(4,1092)	1:33:A:LEU:HD22	1:137:A:PHE:CD1	13	0.15
(4,1092)	1:33:A:LEU:HD23	1:137:A:PHE:CD1	13	0.15
(4,1077)	1:82:A:LEU:HD11	1:137:A:PHE:CD1	10	0.15
(4,1077)	1:82:A:LEU:HD12	1:137:A:PHE:CD1	10	0.15
(4,1077)	1:82:A:LEU:HD13	1:137:A:PHE:CD1	10	0.15
(4,1076)	1:82:A:LEU:HD11	1:134:A:TYR:CD2	8	0.15
(4,1076)	1:82:A:LEU:HD12	1:134:A:TYR:CD2	8	0.15
(4,1076)	1:82:A:LEU:HD13	1:134:A:TYR:CD2	8	0.15
(4,1076)	1:82:A:LEU:HD11	1:134:A:TYR:CD2	15	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1076)	1:82:A:LEU:HD12	1:134:A:TYR:CD2	15	0.15
(4,1076)	1:82:A:LEU:HD13	1:134:A:TYR:CD2	15	0.15
(4,1073)	1:82:A:LEU:HD21	1:134:A:TYR:CE2	15	0.15
(4,1073)	1:82:A:LEU:HD22	1:134:A:TYR:CE2	15	0.15
(4,1073)	1:82:A:LEU:HD23	1:134:A:TYR:CE2	15	0.15
(4,1063)	1:89:A:LEU:HD11	1:134:A:TYR:CD1	20	0.15
(4,1063)	1:89:A:LEU:HD12	1:134:A:TYR:CD1	20	0.15
(4,1063)	1:89:A:LEU:HD13	1:134:A:TYR:CD1	20	0.15
(4,1058)	1:92:A:LEU:HD11	1:93:A:ILE:H	1	0.15
(4,1058)	1:92:A:LEU:HD12	1:93:A:ILE:H	1	0.15
(4,1058)	1:92:A:LEU:HD13	1:93:A:ILE:H	1	0.15
(4,1058)	1:92:A:LEU:HD11	1:93:A:ILE:H	15	0.15
(4,1058)	1:92:A:LEU:HD12	1:93:A:ILE:H	15	0.15
(4,1058)	1:92:A:LEU:HD13	1:93:A:ILE:H	15	0.15
(4,1058)	1:92:A:LEU:HD11	1:93:A:ILE:H	19	0.15
(4,1058)	1:92:A:LEU:HD12	1:93:A:ILE:H	19	0.15
(4,1058)	1:92:A:LEU:HD13	1:93:A:ILE:H	19	0.15
(4,998)	1:96:A:VAL:HG21	1:97:A:LEU:H	1	0.15
(4,998)	1:96:A:VAL:HG22	1:97:A:LEU:H	1	0.15
(4,998)	1:96:A:VAL:HG23	1:97:A:LEU:H	1	0.15
(4,972)	1:70:A:GLN:H	1:72:A:LEU:HD21	10	0.15
(4,972)	1:70:A:GLN:H	1:72:A:LEU:HD22	10	0.15
(4,972)	1:70:A:GLN:H	1:72:A:LEU:HD23	10	0.15
(4,966)	1:16:A:LEU:H	1:71:A:THR:HG21	7	0.15
(4,966)	1:16:A:LEU:H	1:71:A:THR:HG22	7	0.15
(4,966)	1:16:A:LEU:H	1:71:A:THR:HG23	7	0.15
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD11	8	0.15
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD12	8	0.15
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD13	8	0.15
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD11	2	0.15
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD12	2	0.15
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD13	2	0.15
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD11	7	0.15
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD12	7	0.15
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD13	7	0.15
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD11	3	0.15
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD12	3	0.15
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD13	3	0.15
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD11	14	0.15
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD12	14	0.15
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD13	14	0.15
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD11	17	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD12	17	0.15
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD13	17	0.15
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD11	20	0.15
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD12	20	0.15
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD13	20	0.15
(4,821)	1:24:A:LEU:HD21	1:30:A:TRP:H	12	0.15
(4,821)	1:24:A:LEU:HD22	1:30:A:TRP:H	12	0.15
(4,821)	1:24:A:LEU:HD23	1:30:A:TRP:H	12	0.15
(4,740)	1:120:A:THR:HG21	1:121:A:ASP:H	14	0.15
(4,740)	1:120:A:THR:HG22	1:121:A:ASP:H	14	0.15
(4,740)	1:120:A:THR:HG23	1:121:A:ASP:H	14	0.15
(4,685)	1:26:A:GLN:H	1:78:A:LEU:HD11	2	0.15
(4,685)	1:26:A:GLN:H	1:78:A:LEU:HD12	2	0.15
(4,685)	1:26:A:GLN:H	1:78:A:LEU:HD13	2	0.15
(4,674)	1:159:A:VAL:HG11	1:161:A:LEU:H	5	0.15
(4,674)	1:159:A:VAL:HG12	1:161:A:LEU:H	5	0.15
(4,674)	1:159:A:VAL:HG13	1:161:A:LEU:H	5	0.15
(4,661)	1:86:A:LEU:HD11	1:135:A:GLN:H	1	0.15
(4,661)	1:86:A:LEU:HD12	1:135:A:GLN:H	1	0.15
(4,661)	1:86:A:LEU:HD13	1:135:A:GLN:H	1	0.15
(4,661)	1:86:A:LEU:HD11	1:135:A:GLN:H	6	0.15
(4,661)	1:86:A:LEU:HD12	1:135:A:GLN:H	6	0.15
(4,661)	1:86:A:LEU:HD13	1:135:A:GLN:H	6	0.15
(4,561)	1:24:A:LEU:CD2	1:33:A:LEU:HD11	16	0.15
(4,561)	1:24:A:LEU:CD2	1:33:A:LEU:HD12	16	0.15
(4,561)	1:24:A:LEU:CD2	1:33:A:LEU:HD13	16	0.15
(4,555)	1:21:A:LEU:CD1	1:141:A:LEU:HD21	2	0.15
(4,555)	1:21:A:LEU:CD1	1:141:A:LEU:HD22	2	0.15
(4,555)	1:21:A:LEU:CD1	1:141:A:LEU:HD23	2	0.15
(4,518)	1:8:A:ILE:HD11	1:63:A:MET:CE	6	0.15
(4,518)	1:8:A:ILE:HD12	1:63:A:MET:CE	6	0.15
(4,518)	1:8:A:ILE:HD13	1:63:A:MET:CE	6	0.15
(4,489)	1:52:A:THR:HG21	1:56:A:ILE:CD1	10	0.15
(4,489)	1:52:A:THR:HG22	1:56:A:ILE:CD1	10	0.15
(4,489)	1:52:A:THR:HG23	1:56:A:ILE:CD1	10	0.15
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD11	20	0.15
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD12	20	0.15
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD13	20	0.15
(4,369)	1:21:A:LEU:H	1:40:A:TYR:HD1	4	0.15
(4,369)	1:21:A:LEU:H	1:40:A:TYR:HD2	4	0.15
(4,307)	1:155:A:TRP:H	1:155:A:TRP:HE1	8	0.15
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD11	12	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD12	12	0.15
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD13	12	0.15
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD11	12	0.15
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD12	12	0.15
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD13	12	0.15
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD11	12	0.15
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD12	12	0.15
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD13	12	0.15
(4,44)	1:34:A:LEU:HD21	1:86:A:LEU:HD21	10	0.15
(4,44)	1:34:A:LEU:HD21	1:86:A:LEU:HD22	10	0.15
(4,44)	1:34:A:LEU:HD21	1:86:A:LEU:HD23	10	0.15
(4,44)	1:34:A:LEU:HD22	1:86:A:LEU:HD21	10	0.15
(4,44)	1:34:A:LEU:HD22	1:86:A:LEU:HD22	10	0.15
(4,44)	1:34:A:LEU:HD22	1:86:A:LEU:HD23	10	0.15
(4,44)	1:34:A:LEU:HD23	1:86:A:LEU:HD21	10	0.15
(4,44)	1:34:A:LEU:HD23	1:86:A:LEU:HD22	10	0.15
(4,44)	1:34:A:LEU:HD23	1:86:A:LEU:HD23	10	0.15
(1,193)	1:153:A:THR:O	1:157:A:GLN:H	13	0.15
(1,193)	1:153:A:THR:O	1:157:A:GLN:H	18	0.15
(1,145)	1:129:A:ASN:O	1:133:A:ASN:H	2	0.15
(1,63)	1:41:A:LEU:O	1:45:A:GLU:H	4	0.15
(1,63)	1:41:A:LEU:O	1:45:A:GLU:H	10	0.15
(1,63)	1:41:A:LEU:O	1:45:A:GLU:H	11	0.15
(4,1359)	1:32:A:LEU:HD11	1:35:A:GLN:H	6	0.14
(4,1359)	1:32:A:LEU:HD12	1:35:A:GLN:H	6	0.14
(4,1359)	1:32:A:LEU:HD13	1:35:A:GLN:H	6	0.14
(4,1359)	1:32:A:LEU:HD21	1:35:A:GLN:H	6	0.14
(4,1359)	1:32:A:LEU:HD22	1:35:A:GLN:H	6	0.14
(4,1359)	1:32:A:LEU:HD23	1:35:A:GLN:H	6	0.14
(4,1317)	1:41:A:LEU:HD11	1:137:A:PHE:HD1	16	0.14
(4,1317)	1:41:A:LEU:HD11	1:137:A:PHE:HD2	16	0.14
(4,1317)	1:41:A:LEU:HD12	1:137:A:PHE:HD1	16	0.14
(4,1317)	1:41:A:LEU:HD12	1:137:A:PHE:HD2	16	0.14
(4,1317)	1:41:A:LEU:HD13	1:137:A:PHE:HD1	16	0.14
(4,1317)	1:41:A:LEU:HD13	1:137:A:PHE:HD2	16	0.14
(4,1317)	1:41:A:LEU:HD11	1:137:A:PHE:HD1	17	0.14
(4,1317)	1:41:A:LEU:HD11	1:137:A:PHE:HD2	17	0.14
(4,1317)	1:41:A:LEU:HD12	1:137:A:PHE:HD1	17	0.14
(4,1317)	1:41:A:LEU:HD12	1:137:A:PHE:HD2	17	0.14
(4,1317)	1:41:A:LEU:HD13	1:137:A:PHE:HD1	17	0.14
(4,1317)	1:41:A:LEU:HD13	1:137:A:PHE:HD2	17	0.14
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD21	9	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD22	9	0.14
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD23	9	0.14
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD21	16	0.14
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD22	16	0.14
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD23	16	0.14
(4,1250)	1:86:A:LEU:HD11	1:134:A:TYR:CD1	4	0.14
(4,1250)	1:86:A:LEU:HD12	1:134:A:TYR:CD1	4	0.14
(4,1250)	1:86:A:LEU:HD13	1:134:A:TYR:CD1	4	0.14
(4,1245)	1:15:A:ALA:HB1	1:67:A:TYR:CE2	16	0.14
(4,1245)	1:15:A:ALA:HB2	1:67:A:TYR:CE2	16	0.14
(4,1245)	1:15:A:ALA:HB3	1:67:A:TYR:CE2	16	0.14
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD21	1	0.14
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD22	1	0.14
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD23	1	0.14
(4,1206)	1:89:A:LEU:HD11	1:134:A:TYR:CE1	19	0.14
(4,1206)	1:89:A:LEU:HD12	1:134:A:TYR:CE1	19	0.14
(4,1206)	1:89:A:LEU:HD13	1:134:A:TYR:CE1	19	0.14
(4,1125)	1:16:A:LEU:HD11	1:67:A:TYR:CE2	19	0.14
(4,1125)	1:16:A:LEU:HD12	1:67:A:TYR:CE2	19	0.14
(4,1125)	1:16:A:LEU:HD13	1:67:A:TYR:CE2	19	0.14
(4,1106)	1:34:A:LEU:HD21	1:134:A:TYR:CE2	19	0.14
(4,1106)	1:34:A:LEU:HD22	1:134:A:TYR:CE2	19	0.14
(4,1106)	1:34:A:LEU:HD23	1:134:A:TYR:CE2	19	0.14
(4,1091)	1:33:A:LEU:HD21	1:134:A:TYR:CD2	7	0.14
(4,1091)	1:33:A:LEU:HD22	1:134:A:TYR:CD2	7	0.14
(4,1091)	1:33:A:LEU:HD23	1:134:A:TYR:CD2	7	0.14
(4,1076)	1:82:A:LEU:HD11	1:134:A:TYR:CD2	2	0.14
(4,1076)	1:82:A:LEU:HD12	1:134:A:TYR:CD2	2	0.14
(4,1076)	1:82:A:LEU:HD13	1:134:A:TYR:CD2	2	0.14
(4,1076)	1:82:A:LEU:HD11	1:134:A:TYR:CD2	5	0.14
(4,1076)	1:82:A:LEU:HD12	1:134:A:TYR:CD2	5	0.14
(4,1076)	1:82:A:LEU:HD13	1:134:A:TYR:CD2	5	0.14
(4,1076)	1:82:A:LEU:HD11	1:134:A:TYR:CD2	9	0.14
(4,1076)	1:82:A:LEU:HD12	1:134:A:TYR:CD2	9	0.14
(4,1076)	1:82:A:LEU:HD13	1:134:A:TYR:CD2	9	0.14
(4,1070)	1:82:A:LEU:HD21	1:134:A:TYR:CD2	19	0.14
(4,1070)	1:82:A:LEU:HD22	1:134:A:TYR:CD2	19	0.14
(4,1070)	1:82:A:LEU:HD23	1:134:A:TYR:CD2	19	0.14
(4,1063)	1:89:A:LEU:HD11	1:134:A:TYR:CD1	1	0.14
(4,1063)	1:89:A:LEU:HD12	1:134:A:TYR:CD1	1	0.14
(4,1063)	1:89:A:LEU:HD13	1:134:A:TYR:CD1	1	0.14
(4,1058)	1:92:A:LEU:HD11	1:93:A:ILE:H	10	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1058)	1:92:A:LEU:HD12	1:93:A:ILE:H	10	0.14
(4,1058)	1:92:A:LEU:HD13	1:93:A:ILE:H	10	0.14
(4,1058)	1:92:A:LEU:HD11	1:93:A:ILE:H	16	0.14
(4,1058)	1:92:A:LEU:HD12	1:93:A:ILE:H	16	0.14
(4,1058)	1:92:A:LEU:HD13	1:93:A:ILE:H	16	0.14
(4,972)	1:70:A:GLN:H	1:72:A:LEU:HD21	17	0.14
(4,972)	1:70:A:GLN:H	1:72:A:LEU:HD22	17	0.14
(4,972)	1:70:A:GLN:H	1:72:A:LEU:HD23	17	0.14
(4,966)	1:16:A:LEU:H	1:71:A:THR:HG21	2	0.14
(4,966)	1:16:A:LEU:H	1:71:A:THR:HG22	2	0.14
(4,966)	1:16:A:LEU:H	1:71:A:THR:HG23	2	0.14
(4,961)	1:135:A:GLN:H	1:138:A:ILE:HD11	20	0.14
(4,961)	1:135:A:GLN:H	1:138:A:ILE:HD12	20	0.14
(4,961)	1:135:A:GLN:H	1:138:A:ILE:HD13	20	0.14
(4,942)	1:24:A:LEU:HD21	1:29:A:GLU:H	14	0.14
(4,942)	1:24:A:LEU:HD22	1:29:A:GLU:H	14	0.14
(4,942)	1:24:A:LEU:HD23	1:29:A:GLU:H	14	0.14
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD11	5	0.14
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD12	5	0.14
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD13	5	0.14
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD11	20	0.14
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD12	20	0.14
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD13	20	0.14
(4,875)	1:93:A:ILE:HD11	1:131:A:TRP:HE1	3	0.14
(4,875)	1:93:A:ILE:HD12	1:131:A:TRP:HE1	3	0.14
(4,875)	1:93:A:ILE:HD13	1:131:A:TRP:HE1	3	0.14
(4,875)	1:93:A:ILE:HD11	1:131:A:TRP:HE1	6	0.14
(4,875)	1:93:A:ILE:HD12	1:131:A:TRP:HE1	6	0.14
(4,875)	1:93:A:ILE:HD13	1:131:A:TRP:HE1	6	0.14
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD21	1	0.14
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD22	1	0.14
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD23	1	0.14
(4,844)	1:22:A:LEU:HD11	1:26:A:GLN:H	3	0.14
(4,844)	1:22:A:LEU:HD12	1:26:A:GLN:H	3	0.14
(4,844)	1:22:A:LEU:HD13	1:26:A:GLN:H	3	0.14
(4,844)	1:22:A:LEU:HD11	1:26:A:GLN:H	15	0.14
(4,844)	1:22:A:LEU:HD12	1:26:A:GLN:H	15	0.14
(4,844)	1:22:A:LEU:HD13	1:26:A:GLN:H	15	0.14
(4,674)	1:159:A:VAL:HG11	1:161:A:LEU:H	4	0.14
(4,674)	1:159:A:VAL:HG12	1:161:A:LEU:H	4	0.14
(4,674)	1:159:A:VAL:HG13	1:161:A:LEU:H	4	0.14
(4,661)	1:86:A:LEU:HD11	1:135:A:GLN:H	17	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,661)	1:86:A:LEU:HD12	1:135:A:GLN:H	17	0.14
(4,661)	1:86:A:LEU:HD13	1:135:A:GLN:H	17	0.14
(4,631)	1:17:A:LEU:CD1	1:21:A:LEU:HD11	17	0.14
(4,631)	1:17:A:LEU:CD1	1:21:A:LEU:HD12	17	0.14
(4,631)	1:17:A:LEU:CD1	1:21:A:LEU:HD13	17	0.14
(4,568)	1:97:A:LEU:HD11	1:126:A:ILE:CD1	18	0.14
(4,568)	1:97:A:LEU:HD12	1:126:A:ILE:CD1	18	0.14
(4,568)	1:97:A:LEU:HD13	1:126:A:ILE:CD1	18	0.14
(4,561)	1:24:A:LEU:CD2	1:33:A:LEU:HD11	17	0.14
(4,561)	1:24:A:LEU:CD2	1:33:A:LEU:HD12	17	0.14
(4,561)	1:24:A:LEU:CD2	1:33:A:LEU:HD13	17	0.14
(4,550)	1:21:A:LEU:HD21	1:33:A:LEU:CD2	4	0.14
(4,550)	1:21:A:LEU:HD22	1:33:A:LEU:CD2	4	0.14
(4,550)	1:21:A:LEU:HD23	1:33:A:LEU:CD2	4	0.14
(4,550)	1:21:A:LEU:HD21	1:33:A:LEU:CD2	16	0.14
(4,550)	1:21:A:LEU:HD22	1:33:A:LEU:CD2	16	0.14
(4,550)	1:21:A:LEU:HD23	1:33:A:LEU:CD2	16	0.14
(4,539)	1:71:A:THR:HG21	1:72:A:LEU:CD1	10	0.14
(4,539)	1:71:A:THR:HG22	1:72:A:LEU:CD1	10	0.14
(4,539)	1:71:A:THR:HG23	1:72:A:LEU:CD1	10	0.14
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD11	2	0.14
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD12	2	0.14
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD13	2	0.14
(4,313)	1:11:A:TRP:HE1	1:155:A:TRP:HE1	7	0.14
(4,307)	1:155:A:TRP:H	1:155:A:TRP:HE1	15	0.14
(4,293)	1:96:A:VAL:H	1:97:A:LEU:H	8	0.14
(4,243)	1:41:A:LEU:H	1:137:A:PHE:HE1	9	0.14
(4,243)	1:41:A:LEU:H	1:137:A:PHE:HE2	9	0.14
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD11	4	0.14
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD12	4	0.14
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD13	4	0.14
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD11	4	0.14
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD12	4	0.14
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD13	4	0.14
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD11	4	0.14
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD12	4	0.14
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD13	4	0.14
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD11	7	0.14
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD12	7	0.14
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD13	7	0.14
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD11	7	0.14
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD12	7	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD13	7	0.14
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD11	7	0.14
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD12	7	0.14
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD13	7	0.14
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD11	10	0.14
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD12	10	0.14
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD13	10	0.14
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD11	10	0.14
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD12	10	0.14
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD13	10	0.14
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD11	10	0.14
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD12	10	0.14
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD13	10	0.14
(1,143)	1:128:A:SER:O	1:132:A:ILE:H	11	0.14
(1,63)	1:41:A:LEU:O	1:45:A:GLU:H	19	0.14
(1,51)	1:33:A:LEU:O	1:37:A:GLU:H	7	0.14
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD11	19	0.13
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD12	19	0.13
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD13	19	0.13
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD21	19	0.13
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD22	19	0.13
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD23	19	0.13
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD21	5	0.13
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD22	5	0.13
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD23	5	0.13
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD21	6	0.13
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD22	6	0.13
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD23	6	0.13
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG21	20	0.13
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG22	20	0.13
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG23	20	0.13
(4,1280)	1:8:A:ILE:HG21	1:67:A:TYR:CE1	4	0.13
(4,1280)	1:8:A:ILE:HG22	1:67:A:TYR:CE1	4	0.13
(4,1280)	1:8:A:ILE:HG23	1:67:A:TYR:CE1	4	0.13
(4,1268)	1:64:A:VAL:HG21	1:67:A:TYR:CE1	20	0.13
(4,1268)	1:64:A:VAL:HG22	1:67:A:TYR:CE1	20	0.13
(4,1268)	1:64:A:VAL:HG23	1:67:A:TYR:CE1	20	0.13
(4,1250)	1:86:A:LEU:HD11	1:134:A:TYR:CD1	3	0.13
(4,1250)	1:86:A:LEU:HD12	1:134:A:TYR:CD1	3	0.13
(4,1250)	1:86:A:LEU:HD13	1:134:A:TYR:CD1	3	0.13
(4,1226)	1:33:A:LEU:HD21	1:137:A:PHE:CE1	12	0.13
(4,1226)	1:33:A:LEU:HD22	1:137:A:PHE:CE1	12	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1226)	1:33:A:LEU:HD23	1:137:A:PHE:CE1	12	0.13
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD21	6	0.13
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD22	6	0.13
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD23	6	0.13
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD11	17	0.13
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD12	17	0.13
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD13	17	0.13
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD11	17	0.13
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD12	17	0.13
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD13	17	0.13
(4,1160)	1:63:A:MET:HE1	1:67:A:TYR:HD1	16	0.13
(4,1160)	1:63:A:MET:HE1	1:67:A:TYR:HD2	16	0.13
(4,1160)	1:63:A:MET:HE2	1:67:A:TYR:HD1	16	0.13
(4,1160)	1:63:A:MET:HE2	1:67:A:TYR:HD2	16	0.13
(4,1160)	1:63:A:MET:HE3	1:67:A:TYR:HD1	16	0.13
(4,1160)	1:63:A:MET:HE3	1:67:A:TYR:HD2	16	0.13
(4,1107)	1:17:A:LEU:HD11	1:40:A:TYR:CE1	4	0.13
(4,1107)	1:17:A:LEU:HD12	1:40:A:TYR:CE1	4	0.13
(4,1107)	1:17:A:LEU:HD13	1:40:A:TYR:CE1	4	0.13
(4,1091)	1:33:A:LEU:HD21	1:134:A:TYR:CD2	9	0.13
(4,1091)	1:33:A:LEU:HD22	1:134:A:TYR:CD2	9	0.13
(4,1091)	1:33:A:LEU:HD23	1:134:A:TYR:CD2	9	0.13
(4,1082)	1:82:A:LEU:HD11	1:134:A:TYR:CE2	7	0.13
(4,1082)	1:82:A:LEU:HD12	1:134:A:TYR:CE2	7	0.13
(4,1082)	1:82:A:LEU:HD13	1:134:A:TYR:CE2	7	0.13
(4,1076)	1:82:A:LEU:HD11	1:134:A:TYR:CD2	12	0.13
(4,1076)	1:82:A:LEU:HD12	1:134:A:TYR:CD2	12	0.13
(4,1076)	1:82:A:LEU:HD13	1:134:A:TYR:CD2	12	0.13
(4,1058)	1:92:A:LEU:HD11	1:93:A:ILE:H	13	0.13
(4,1058)	1:92:A:LEU:HD12	1:93:A:ILE:H	13	0.13
(4,1058)	1:92:A:LEU:HD13	1:93:A:ILE:H	13	0.13
(4,1058)	1:92:A:LEU:HD11	1:93:A:ILE:H	20	0.13
(4,1058)	1:92:A:LEU:HD12	1:93:A:ILE:H	20	0.13
(4,1058)	1:92:A:LEU:HD13	1:93:A:ILE:H	20	0.13
(4,961)	1:135:A:GLN:H	1:138:A:ILE:HD11	5	0.13
(4,961)	1:135:A:GLN:H	1:138:A:ILE:HD12	5	0.13
(4,961)	1:135:A:GLN:H	1:138:A:ILE:HD13	5	0.13
(4,942)	1:24:A:LEU:HD21	1:29:A:GLU:H	7	0.13
(4,942)	1:24:A:LEU:HD22	1:29:A:GLU:H	7	0.13
(4,942)	1:24:A:LEU:HD23	1:29:A:GLU:H	7	0.13
(4,939)	1:89:A:LEU:H	1:92:A:LEU:HD21	19	0.13
(4,939)	1:89:A:LEU:H	1:92:A:LEU:HD22	19	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,939)	1:89:A:LEU:H	1:92:A:LEU:HD23	19	0.13
(4,915)	1:25:A:ALA:H	1:81:A:LEU:HD11	14	0.13
(4,915)	1:25:A:ALA:H	1:81:A:LEU:HD12	14	0.13
(4,915)	1:25:A:ALA:H	1:81:A:LEU:HD13	14	0.13
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD11	18	0.13
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD12	18	0.13
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD13	18	0.13
(4,875)	1:93:A:ILE:HD11	1:131:A:TRP:HE1	8	0.13
(4,875)	1:93:A:ILE:HD12	1:131:A:TRP:HE1	8	0.13
(4,875)	1:93:A:ILE:HD13	1:131:A:TRP:HE1	8	0.13
(4,859)	1:78:A:LEU:HD11	1:137:A:PHE:HE1	8	0.13
(4,859)	1:78:A:LEU:HD11	1:137:A:PHE:HE2	8	0.13
(4,859)	1:78:A:LEU:HD12	1:137:A:PHE:HE1	8	0.13
(4,859)	1:78:A:LEU:HD12	1:137:A:PHE:HE2	8	0.13
(4,859)	1:78:A:LEU:HD13	1:137:A:PHE:HE1	8	0.13
(4,859)	1:78:A:LEU:HD13	1:137:A:PHE:HE2	8	0.13
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD11	18	0.13
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD12	18	0.13
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD13	18	0.13
(4,844)	1:22:A:LEU:HD11	1:26:A:GLN:H	5	0.13
(4,844)	1:22:A:LEU:HD12	1:26:A:GLN:H	5	0.13
(4,844)	1:22:A:LEU:HD13	1:26:A:GLN:H	5	0.13
(4,796)	1:21:A:LEU:HD21	1:137:A:PHE:HZ	3	0.13
(4,796)	1:21:A:LEU:HD22	1:137:A:PHE:HZ	3	0.13
(4,796)	1:21:A:LEU:HD23	1:137:A:PHE:HZ	3	0.13
(4,794)	1:21:A:LEU:HD21	1:137:A:PHE:HE1	14	0.13
(4,794)	1:21:A:LEU:HD21	1:137:A:PHE:HE2	14	0.13
(4,794)	1:21:A:LEU:HD22	1:137:A:PHE:HE1	14	0.13
(4,794)	1:21:A:LEU:HD22	1:137:A:PHE:HE2	14	0.13
(4,794)	1:21:A:LEU:HD23	1:137:A:PHE:HE1	14	0.13
(4,794)	1:21:A:LEU:HD23	1:137:A:PHE:HE2	14	0.13
(4,781)	1:81:A:LEU:HD11	1:82:A:LEU:H	12	0.13
(4,781)	1:81:A:LEU:HD12	1:82:A:LEU:H	12	0.13
(4,781)	1:81:A:LEU:HD13	1:82:A:LEU:H	12	0.13
(4,757)	1:72:A:LEU:HD11	1:149:A:ARG:H	3	0.13
(4,757)	1:72:A:LEU:HD12	1:149:A:ARG:H	3	0.13
(4,757)	1:72:A:LEU:HD13	1:149:A:ARG:H	3	0.13
(4,757)	1:72:A:LEU:HD11	1:149:A:ARG:H	4	0.13
(4,757)	1:72:A:LEU:HD12	1:149:A:ARG:H	4	0.13
(4,757)	1:72:A:LEU:HD13	1:149:A:ARG:H	4	0.13
(4,752)	1:153:A:THR:H	1:153:A:THR:HG21	1	0.13
(4,752)	1:153:A:THR:H	1:153:A:THR:HG22	1	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,752)	1:153:A:THR:H	1:153:A:THR:HG23	1	0.13
(4,744)	1:69:A:LYS:H	1:72:A:LEU:HD21	9	0.13
(4,744)	1:69:A:LYS:H	1:72:A:LEU:HD22	9	0.13
(4,744)	1:69:A:LYS:H	1:72:A:LEU:HD23	9	0.13
(4,744)	1:69:A:LYS:H	1:72:A:LEU:HD21	14	0.13
(4,744)	1:69:A:LYS:H	1:72:A:LEU:HD22	14	0.13
(4,744)	1:69:A:LYS:H	1:72:A:LEU:HD23	14	0.13
(4,672)	1:16:A:LEU:HD21	1:67:A:TYR:HE1	4	0.13
(4,672)	1:16:A:LEU:HD21	1:67:A:TYR:HE2	4	0.13
(4,672)	1:16:A:LEU:HD22	1:67:A:TYR:HE1	4	0.13
(4,672)	1:16:A:LEU:HD22	1:67:A:TYR:HE2	4	0.13
(4,672)	1:16:A:LEU:HD23	1:67:A:TYR:HE1	4	0.13
(4,672)	1:16:A:LEU:HD23	1:67:A:TYR:HE2	4	0.13
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD11	4	0.13
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD12	4	0.13
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD13	4	0.13
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD11	8	0.13
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD12	8	0.13
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD13	8	0.13
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD11	9	0.13
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD12	9	0.13
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD13	9	0.13
(4,577)	1:97:A:LEU:HD21	1:126:A:ILE:CD1	12	0.13
(4,577)	1:97:A:LEU:HD22	1:126:A:ILE:CD1	12	0.13
(4,577)	1:97:A:LEU:HD23	1:126:A:ILE:CD1	12	0.13
(4,530)	1:17:A:LEU:HD21	1:71:A:THR:CG2	12	0.13
(4,530)	1:17:A:LEU:HD22	1:71:A:THR:CG2	12	0.13
(4,530)	1:17:A:LEU:HD23	1:71:A:THR:CG2	12	0.13
(4,530)	1:17:A:LEU:HD21	1:71:A:THR:CG2	19	0.13
(4,530)	1:17:A:LEU:HD22	1:71:A:THR:CG2	19	0.13
(4,530)	1:17:A:LEU:HD23	1:71:A:THR:CG2	19	0.13
(4,489)	1:52:A:THR:HG21	1:56:A:ILE:CD1	13	0.13
(4,489)	1:52:A:THR:HG22	1:56:A:ILE:CD1	13	0.13
(4,489)	1:52:A:THR:HG23	1:56:A:ILE:CD1	13	0.13
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD11	3	0.13
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD12	3	0.13
(4,473)	1:34:A:LEU:CD2	1:138:A:ILE:HD13	3	0.13
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD21	1	0.13
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD22	1	0.13
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD23	1	0.13
(4,313)	1:11:A:TRP:HE1	1:155:A:TRP:HE1	4	0.13
(4,313)	1:11:A:TRP:HE1	1:155:A:TRP:HE1	5	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,236)	1:137:A:PHE:HD1	1:141:A:LEU:H	13	0.13
(4,236)	1:137:A:PHE:HD2	1:141:A:LEU:H	13	0.13
(4,103)	1:1:A:MET:HE1	1:5:A:VAL:HG11	20	0.13
(4,103)	1:1:A:MET:HE1	1:5:A:VAL:HG12	20	0.13
(4,103)	1:1:A:MET:HE1	1:5:A:VAL:HG13	20	0.13
(4,103)	1:1:A:MET:HE2	1:5:A:VAL:HG11	20	0.13
(4,103)	1:1:A:MET:HE2	1:5:A:VAL:HG12	20	0.13
(4,103)	1:1:A:MET:HE2	1:5:A:VAL:HG13	20	0.13
(4,103)	1:1:A:MET:HE3	1:5:A:VAL:HG11	20	0.13
(4,103)	1:1:A:MET:HE3	1:5:A:VAL:HG12	20	0.13
(4,103)	1:1:A:MET:HE3	1:5:A:VAL:HG13	20	0.13
(4,43)	1:34:A:LEU:HD21	1:138:A:ILE:HD11	7	0.13
(4,43)	1:34:A:LEU:HD21	1:138:A:ILE:HD12	7	0.13
(4,43)	1:34:A:LEU:HD21	1:138:A:ILE:HD13	7	0.13
(4,43)	1:34:A:LEU:HD22	1:138:A:ILE:HD11	7	0.13
(4,43)	1:34:A:LEU:HD22	1:138:A:ILE:HD12	7	0.13
(4,43)	1:34:A:LEU:HD22	1:138:A:ILE:HD13	7	0.13
(4,43)	1:34:A:LEU:HD23	1:138:A:ILE:HD11	7	0.13
(4,43)	1:34:A:LEU:HD23	1:138:A:ILE:HD12	7	0.13
(4,43)	1:34:A:LEU:HD23	1:138:A:ILE:HD13	7	0.13
(4,43)	1:34:A:LEU:HD21	1:138:A:ILE:HD11	11	0.13
(4,43)	1:34:A:LEU:HD21	1:138:A:ILE:HD12	11	0.13
(4,43)	1:34:A:LEU:HD21	1:138:A:ILE:HD13	11	0.13
(4,43)	1:34:A:LEU:HD22	1:138:A:ILE:HD11	11	0.13
(4,43)	1:34:A:LEU:HD22	1:138:A:ILE:HD12	11	0.13
(4,43)	1:34:A:LEU:HD22	1:138:A:ILE:HD13	11	0.13
(4,43)	1:34:A:LEU:HD23	1:138:A:ILE:HD11	11	0.13
(4,43)	1:34:A:LEU:HD23	1:138:A:ILE:HD12	11	0.13
(4,43)	1:34:A:LEU:HD23	1:138:A:ILE:HD13	11	0.13
(1,193)	1:153:A:THR:O	1:157:A:GLN:H	6	0.13
(1,193)	1:153:A:THR:O	1:157:A:GLN:H	7	0.13
(1,193)	1:153:A:THR:O	1:157:A:GLN:H	16	0.13
(1,171)	1:142:A:GLU:O	1:146:A:GLU:H	11	0.13
(1,145)	1:129:A:ASN:O	1:133:A:ASN:H	17	0.13
(1,143)	1:128:A:SER:O	1:132:A:ILE:H	14	0.13
(1,111)	1:76:A:GLN:O	1:80:A:GLY:H	19	0.13
(1,75)	1:58:A:ARG:O	1:62:A:ASP:H	14	0.13
(1,69)	1:44:A:ILE:O	1:48:A:MET:H	4	0.13
(1,63)	1:41:A:LEU:O	1:45:A:GLU:H	13	0.13
(1,63)	1:41:A:LEU:O	1:45:A:GLU:H	17	0.13
(1,51)	1:33:A:LEU:O	1:37:A:GLU:H	1	0.13
(1,47)	1:30:A:TRP:O	1:34:A:LEU:H	4	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,47)	1:30:A:TRP:O	1:34:A:LEU:H	5	0.13
(1,47)	1:30:A:TRP:O	1:34:A:LEU:H	19	0.13
(1,47)	1:30:A:TRP:O	1:34:A:LEU:H	20	0.13
(1,13)	1:7:A:PHE:O	1:11:A:TRP:H	3	0.13
(4,1379)	1:152:A:LEU:HD11	1:155:A:TRP:HE1	6	0.12
(4,1379)	1:152:A:LEU:HD12	1:155:A:TRP:HE1	6	0.12
(4,1379)	1:152:A:LEU:HD13	1:155:A:TRP:HE1	6	0.12
(4,1379)	1:152:A:LEU:HD21	1:155:A:TRP:HE1	6	0.12
(4,1379)	1:152:A:LEU:HD22	1:155:A:TRP:HE1	6	0.12
(4,1379)	1:152:A:LEU:HD23	1:155:A:TRP:HE1	6	0.12
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG21	8	0.12
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG22	8	0.12
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG23	8	0.12
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG21	13	0.12
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG22	13	0.12
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG23	13	0.12
(4,1289)	1:17:A:LEU:HD21	1:40:A:TYR:HE1	8	0.12
(4,1289)	1:17:A:LEU:HD21	1:40:A:TYR:HE2	8	0.12
(4,1289)	1:17:A:LEU:HD22	1:40:A:TYR:HE1	8	0.12
(4,1289)	1:17:A:LEU:HD22	1:40:A:TYR:HE2	8	0.12
(4,1289)	1:17:A:LEU:HD23	1:40:A:TYR:HE1	8	0.12
(4,1289)	1:17:A:LEU:HD23	1:40:A:TYR:HE2	8	0.12
(4,1269)	1:11:A:TRP:CH2	1:71:A:THR:HG21	7	0.12
(4,1269)	1:11:A:TRP:CH2	1:71:A:THR:HG22	7	0.12
(4,1269)	1:11:A:TRP:CH2	1:71:A:THR:HG23	7	0.12
(4,1268)	1:64:A:VAL:HG21	1:67:A:TYR:CE1	13	0.12
(4,1268)	1:64:A:VAL:HG22	1:67:A:TYR:CE1	13	0.12
(4,1268)	1:64:A:VAL:HG23	1:67:A:TYR:CE1	13	0.12
(4,1260)	1:41:A:LEU:HD11	1:137:A:PHE:CE2	10	0.12
(4,1260)	1:41:A:LEU:HD12	1:137:A:PHE:CE2	10	0.12
(4,1260)	1:41:A:LEU:HD13	1:137:A:PHE:CE2	10	0.12
(4,1247)	1:11:A:TRP:CZ2	1:48:A:MET:HE1	14	0.12
(4,1247)	1:11:A:TRP:CZ2	1:48:A:MET:HE2	14	0.12
(4,1247)	1:11:A:TRP:CZ2	1:48:A:MET:HE3	14	0.12
(4,1230)	1:97:A:LEU:HD11	1:98:A:PHE:HE1	17	0.12
(4,1230)	1:97:A:LEU:HD11	1:98:A:PHE:HE2	17	0.12
(4,1230)	1:97:A:LEU:HD12	1:98:A:PHE:HE1	17	0.12
(4,1230)	1:97:A:LEU:HD12	1:98:A:PHE:HE2	17	0.12
(4,1230)	1:97:A:LEU:HD13	1:98:A:PHE:HE1	17	0.12
(4,1230)	1:97:A:LEU:HD13	1:98:A:PHE:HE2	17	0.12
(4,1226)	1:33:A:LEU:HD21	1:137:A:PHE:CE1	9	0.12
(4,1226)	1:33:A:LEU:HD22	1:137:A:PHE:CE1	9	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1226)	1:33:A:LEU:HD23	1:137:A:PHE:CE1	9	0.12
(4,1226)	1:33:A:LEU:HD21	1:137:A:PHE:CE1	14	0.12
(4,1226)	1:33:A:LEU:HD22	1:137:A:PHE:CE1	14	0.12
(4,1226)	1:33:A:LEU:HD23	1:137:A:PHE:CE1	14	0.12
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD21	9	0.12
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD22	9	0.12
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD23	9	0.12
(4,1201)	1:44:A:ILE:HG21	1:148:A:HIS:CE1	13	0.12
(4,1201)	1:44:A:ILE:HG22	1:148:A:HIS:CE1	13	0.12
(4,1201)	1:44:A:ILE:HG23	1:148:A:HIS:CE1	13	0.12
(4,1201)	1:44:A:ILE:HG21	1:148:A:HIS:CE1	20	0.12
(4,1201)	1:44:A:ILE:HG22	1:148:A:HIS:CE1	20	0.12
(4,1201)	1:44:A:ILE:HG23	1:148:A:HIS:CE1	20	0.12
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD11	18	0.12
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD12	18	0.12
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD13	18	0.12
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD11	18	0.12
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD12	18	0.12
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD13	18	0.12
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD11	20	0.12
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD12	20	0.12
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD13	20	0.12
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD11	20	0.12
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD12	20	0.12
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD13	20	0.12
(4,1170)	1:82:A:LEU:HD21	1:137:A:PHE:HE1	4	0.12
(4,1170)	1:82:A:LEU:HD21	1:137:A:PHE:HE2	4	0.12
(4,1170)	1:82:A:LEU:HD22	1:137:A:PHE:HE1	4	0.12
(4,1170)	1:82:A:LEU:HD22	1:137:A:PHE:HE2	4	0.12
(4,1170)	1:82:A:LEU:HD23	1:137:A:PHE:HE1	4	0.12
(4,1170)	1:82:A:LEU:HD23	1:137:A:PHE:HE2	4	0.12
(4,1161)	1:64:A:VAL:HG21	1:67:A:TYR:HD1	4	0.12
(4,1161)	1:64:A:VAL:HG21	1:67:A:TYR:HD2	4	0.12
(4,1161)	1:64:A:VAL:HG22	1:67:A:TYR:HD1	4	0.12
(4,1161)	1:64:A:VAL:HG22	1:67:A:TYR:HD2	4	0.12
(4,1161)	1:64:A:VAL:HG23	1:67:A:TYR:HD1	4	0.12
(4,1161)	1:64:A:VAL:HG23	1:67:A:TYR:HD2	4	0.12
(4,1125)	1:16:A:LEU:HD11	1:67:A:TYR:CE2	11	0.12
(4,1125)	1:16:A:LEU:HD12	1:67:A:TYR:CE2	11	0.12
(4,1125)	1:16:A:LEU:HD13	1:67:A:TYR:CE2	11	0.12
(4,1076)	1:82:A:LEU:HD11	1:134:A:TYR:CD2	17	0.12
(4,1076)	1:82:A:LEU:HD12	1:134:A:TYR:CD2	17	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1076)	1:82:A:LEU:HD13	1:134:A:TYR:CD2	17	0.12
(4,1073)	1:82:A:LEU:HD21	1:134:A:TYR:CE2	12	0.12
(4,1073)	1:82:A:LEU:HD22	1:134:A:TYR:CE2	12	0.12
(4,1073)	1:82:A:LEU:HD23	1:134:A:TYR:CE2	12	0.12
(4,1063)	1:89:A:LEU:HD11	1:134:A:TYR:CD1	5	0.12
(4,1063)	1:89:A:LEU:HD12	1:134:A:TYR:CD1	5	0.12
(4,1063)	1:89:A:LEU:HD13	1:134:A:TYR:CD1	5	0.12
(4,1058)	1:92:A:LEU:HD11	1:93:A:ILE:H	5	0.12
(4,1058)	1:92:A:LEU:HD12	1:93:A:ILE:H	5	0.12
(4,1058)	1:92:A:LEU:HD13	1:93:A:ILE:H	5	0.12
(4,1058)	1:92:A:LEU:HD11	1:93:A:ILE:H	12	0.12
(4,1058)	1:92:A:LEU:HD12	1:93:A:ILE:H	12	0.12
(4,1058)	1:92:A:LEU:HD13	1:93:A:ILE:H	12	0.12
(4,1046)	1:11:A:TRP:H	1:47:A:VAL:HG21	4	0.12
(4,1046)	1:11:A:TRP:H	1:47:A:VAL:HG22	4	0.12
(4,1046)	1:11:A:TRP:H	1:47:A:VAL:HG23	4	0.12
(4,1046)	1:11:A:TRP:H	1:47:A:VAL:HG21	8	0.12
(4,1046)	1:11:A:TRP:H	1:47:A:VAL:HG22	8	0.12
(4,1046)	1:11:A:TRP:H	1:47:A:VAL:HG23	8	0.12
(4,1004)	1:24:A:LEU:HD21	1:34:A:LEU:H	16	0.12
(4,1004)	1:24:A:LEU:HD22	1:34:A:LEU:H	16	0.12
(4,1004)	1:24:A:LEU:HD23	1:34:A:LEU:H	16	0.12
(4,999)	1:96:A:VAL:HG11	1:97:A:LEU:H	16	0.12
(4,999)	1:96:A:VAL:HG12	1:97:A:LEU:H	16	0.12
(4,999)	1:96:A:VAL:HG13	1:97:A:LEU:H	16	0.12
(4,972)	1:70:A:GLN:H	1:72:A:LEU:HD21	14	0.12
(4,972)	1:70:A:GLN:H	1:72:A:LEU:HD22	14	0.12
(4,972)	1:70:A:GLN:H	1:72:A:LEU:HD23	14	0.12
(4,965)	1:96:A:VAL:HG21	1:98:A:PHE:H	11	0.12
(4,965)	1:96:A:VAL:HG22	1:98:A:PHE:H	11	0.12
(4,965)	1:96:A:VAL:HG23	1:98:A:PHE:H	11	0.12
(4,965)	1:96:A:VAL:HG21	1:98:A:PHE:H	18	0.12
(4,965)	1:96:A:VAL:HG22	1:98:A:PHE:H	18	0.12
(4,965)	1:96:A:VAL:HG23	1:98:A:PHE:H	18	0.12
(4,961)	1:135:A:GLN:H	1:138:A:ILE:HD11	8	0.12
(4,961)	1:135:A:GLN:H	1:138:A:ILE:HD12	8	0.12
(4,961)	1:135:A:GLN:H	1:138:A:ILE:HD13	8	0.12
(4,961)	1:135:A:GLN:H	1:138:A:ILE:HD11	19	0.12
(4,961)	1:135:A:GLN:H	1:138:A:ILE:HD12	19	0.12
(4,961)	1:135:A:GLN:H	1:138:A:ILE:HD13	19	0.12
(4,915)	1:25:A:ALA:H	1:81:A:LEU:HD11	15	0.12
(4,915)	1:25:A:ALA:H	1:81:A:LEU:HD12	15	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,915)	1:25:A:ALA:H	1:81:A:LEU:HD13	15	0.12
(4,907)	1:44:A:ILE:H	1:48:A:MET:HE1	5	0.12
(4,907)	1:44:A:ILE:H	1:48:A:MET:HE2	5	0.12
(4,907)	1:44:A:ILE:H	1:48:A:MET:HE3	5	0.12
(4,882)	1:24:A:LEU:HD21	1:32:A:LEU:H	12	0.12
(4,882)	1:24:A:LEU:HD22	1:32:A:LEU:H	12	0.12
(4,882)	1:24:A:LEU:HD23	1:32:A:LEU:H	12	0.12
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD11	4	0.12
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD12	4	0.12
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD13	4	0.12
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD11	18	0.12
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD12	18	0.12
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD13	18	0.12
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD11	11	0.12
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD12	11	0.12
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD13	11	0.12
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD11	15	0.12
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD12	15	0.12
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD13	15	0.12
(4,859)	1:78:A:LEU:HD11	1:137:A:PHE:HE1	2	0.12
(4,859)	1:78:A:LEU:HD11	1:137:A:PHE:HE2	2	0.12
(4,859)	1:78:A:LEU:HD12	1:137:A:PHE:HE1	2	0.12
(4,859)	1:78:A:LEU:HD12	1:137:A:PHE:HE2	2	0.12
(4,859)	1:78:A:LEU:HD13	1:137:A:PHE:HE1	2	0.12
(4,859)	1:78:A:LEU:HD13	1:137:A:PHE:HE2	2	0.12
(4,859)	1:78:A:LEU:HD11	1:137:A:PHE:HE1	14	0.12
(4,859)	1:78:A:LEU:HD11	1:137:A:PHE:HE2	14	0.12
(4,859)	1:78:A:LEU:HD12	1:137:A:PHE:HE1	14	0.12
(4,859)	1:78:A:LEU:HD12	1:137:A:PHE:HE2	14	0.12
(4,859)	1:78:A:LEU:HD13	1:137:A:PHE:HE1	14	0.12
(4,859)	1:78:A:LEU:HD13	1:137:A:PHE:HE2	14	0.12
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD21	9	0.12
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD22	9	0.12
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD23	9	0.12
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD21	15	0.12
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD22	15	0.12
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD23	15	0.12
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD11	19	0.12
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD12	19	0.12
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD13	19	0.12
(4,844)	1:22:A:LEU:HD11	1:26:A:GLN:H	11	0.12
(4,844)	1:22:A:LEU:HD12	1:26:A:GLN:H	11	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,844)	1:22:A:LEU:HD13	1:26:A:GLN:H	11	0.12
(4,796)	1:21:A:LEU:HD21	1:137:A:PHE:HZ	15	0.12
(4,796)	1:21:A:LEU:HD22	1:137:A:PHE:HZ	15	0.12
(4,796)	1:21:A:LEU:HD23	1:137:A:PHE:HZ	15	0.12
(4,794)	1:21:A:LEU:HD21	1:137:A:PHE:HE1	2	0.12
(4,794)	1:21:A:LEU:HD21	1:137:A:PHE:HE2	2	0.12
(4,794)	1:21:A:LEU:HD22	1:137:A:PHE:HE1	2	0.12
(4,794)	1:21:A:LEU:HD22	1:137:A:PHE:HE2	2	0.12
(4,794)	1:21:A:LEU:HD23	1:137:A:PHE:HE1	2	0.12
(4,794)	1:21:A:LEU:HD23	1:137:A:PHE:HE2	2	0.12
(4,794)	1:21:A:LEU:HD21	1:137:A:PHE:HE1	9	0.12
(4,794)	1:21:A:LEU:HD21	1:137:A:PHE:HE2	9	0.12
(4,794)	1:21:A:LEU:HD22	1:137:A:PHE:HE1	9	0.12
(4,794)	1:21:A:LEU:HD22	1:137:A:PHE:HE2	9	0.12
(4,794)	1:21:A:LEU:HD23	1:137:A:PHE:HE1	9	0.12
(4,794)	1:21:A:LEU:HD23	1:137:A:PHE:HE2	9	0.12
(4,794)	1:21:A:LEU:HD21	1:137:A:PHE:HE1	19	0.12
(4,794)	1:21:A:LEU:HD21	1:137:A:PHE:HE2	19	0.12
(4,794)	1:21:A:LEU:HD22	1:137:A:PHE:HE1	19	0.12
(4,794)	1:21:A:LEU:HD22	1:137:A:PHE:HE2	19	0.12
(4,794)	1:21:A:LEU:HD23	1:137:A:PHE:HE1	19	0.12
(4,794)	1:21:A:LEU:HD23	1:137:A:PHE:HE2	19	0.12
(4,781)	1:81:A:LEU:HD11	1:82:A:LEU:H	19	0.12
(4,781)	1:81:A:LEU:HD12	1:82:A:LEU:H	19	0.12
(4,781)	1:81:A:LEU:HD13	1:82:A:LEU:H	19	0.12
(4,694)	1:56:A:ILE:HD11	1:61:A:GLN:H	13	0.12
(4,694)	1:56:A:ILE:HD12	1:61:A:GLN:H	13	0.12
(4,694)	1:56:A:ILE:HD13	1:61:A:GLN:H	13	0.12
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD11	18	0.12
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD12	18	0.12
(4,586)	1:17:A:LEU:CD2	1:44:A:ILE:HD13	18	0.12
(4,577)	1:97:A:LEU:HD21	1:126:A:ILE:CD1	9	0.12
(4,577)	1:97:A:LEU:HD22	1:126:A:ILE:CD1	9	0.12
(4,577)	1:97:A:LEU:HD23	1:126:A:ILE:CD1	9	0.12
(4,568)	1:97:A:LEU:HD11	1:126:A:ILE:CD1	17	0.12
(4,568)	1:97:A:LEU:HD12	1:126:A:ILE:CD1	17	0.12
(4,568)	1:97:A:LEU:HD13	1:126:A:ILE:CD1	17	0.12
(4,563)	1:92:A:LEU:HD11	1:93:A:ILE:CD1	20	0.12
(4,563)	1:92:A:LEU:HD12	1:93:A:ILE:CD1	20	0.12
(4,563)	1:92:A:LEU:HD13	1:93:A:ILE:CD1	20	0.12
(4,555)	1:21:A:LEU:CD1	1:141:A:LEU:HD21	13	0.12
(4,555)	1:21:A:LEU:CD1	1:141:A:LEU:HD22	13	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,555)	1:21:A:LEU:CD1	1:141:A:LEU:HD23	13	0.12
(4,543)	1:1:A:MET:CE	1:2:A:THR:HG21	8	0.12
(4,543)	1:1:A:MET:CE	1:2:A:THR:HG22	8	0.12
(4,543)	1:1:A:MET:CE	1:2:A:THR:HG23	8	0.12
(4,530)	1:17:A:LEU:HD21	1:71:A:THR:CG2	9	0.12
(4,530)	1:17:A:LEU:HD22	1:71:A:THR:CG2	9	0.12
(4,530)	1:17:A:LEU:HD23	1:71:A:THR:CG2	9	0.12
(4,510)	1:161:A:LEU:CD1	1:162:A:ALA:HB1	8	0.12
(4,510)	1:161:A:LEU:CD1	1:162:A:ALA:HB2	8	0.12
(4,510)	1:161:A:LEU:CD1	1:162:A:ALA:HB3	8	0.12
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD21	7	0.12
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD22	7	0.12
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD23	7	0.12
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD21	15	0.12
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD22	15	0.12
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD23	15	0.12
(4,462)	1:96:A:VAL:HG21	1:97:A:LEU:CD1	2	0.12
(4,462)	1:96:A:VAL:HG22	1:97:A:LEU:CD1	2	0.12
(4,462)	1:96:A:VAL:HG23	1:97:A:LEU:CD1	2	0.12
(4,462)	1:96:A:VAL:HG21	1:97:A:LEU:CD1	20	0.12
(4,462)	1:96:A:VAL:HG22	1:97:A:LEU:CD1	20	0.12
(4,462)	1:96:A:VAL:HG23	1:97:A:LEU:CD1	20	0.12
(4,458)	1:33:A:LEU:HD21	1:78:A:LEU:CD2	1	0.12
(4,458)	1:33:A:LEU:HD22	1:78:A:LEU:CD2	1	0.12
(4,458)	1:33:A:LEU:HD23	1:78:A:LEU:CD2	1	0.12
(4,369)	1:21:A:LEU:H	1:40:A:TYR:HD1	10	0.12
(4,369)	1:21:A:LEU:H	1:40:A:TYR:HD2	10	0.12
(4,313)	1:11:A:TRP:HE1	1:155:A:TRP:HE1	14	0.12
(4,313)	1:11:A:TRP:HE1	1:155:A:TRP:HE1	18	0.12
(4,307)	1:155:A:TRP:H	1:155:A:TRP:HE1	1	0.12
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD11	8	0.12
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD12	8	0.12
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD13	8	0.12
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD11	8	0.12
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD12	8	0.12
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD13	8	0.12
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD11	8	0.12
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD12	8	0.12
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD13	8	0.12
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD11	20	0.12
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD12	20	0.12
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD13	20	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD11	20	0.12
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD12	20	0.12
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD13	20	0.12
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD11	20	0.12
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD12	20	0.12
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD13	20	0.12
(4,43)	1:34:A:LEU:HD21	1:138:A:ILE:HD11	15	0.12
(4,43)	1:34:A:LEU:HD21	1:138:A:ILE:HD12	15	0.12
(4,43)	1:34:A:LEU:HD21	1:138:A:ILE:HD13	15	0.12
(4,43)	1:34:A:LEU:HD22	1:138:A:ILE:HD11	15	0.12
(4,43)	1:34:A:LEU:HD22	1:138:A:ILE:HD12	15	0.12
(4,43)	1:34:A:LEU:HD22	1:138:A:ILE:HD13	15	0.12
(4,43)	1:34:A:LEU:HD23	1:138:A:ILE:HD11	15	0.12
(4,43)	1:34:A:LEU:HD23	1:138:A:ILE:HD12	15	0.12
(4,43)	1:34:A:LEU:HD23	1:138:A:ILE:HD13	15	0.12
(1,193)	1:153:A:THR:O	1:157:A:GLN:H	4	0.12
(1,193)	1:153:A:THR:O	1:157:A:GLN:H	8	0.12
(1,193)	1:153:A:THR:O	1:157:A:GLN:H	9	0.12
(1,193)	1:153:A:THR:O	1:157:A:GLN:H	10	0.12
(1,193)	1:153:A:THR:O	1:157:A:GLN:H	20	0.12
(1,179)	1:146:A:GLU:O	1:150:A:LEU:H	18	0.12
(1,141)	1:127:A:ALA:O	1:131:A:TRP:H	17	0.12
(1,139)	1:90:A:SER:O	1:94:A:GLY:H	3	0.12
(1,139)	1:90:A:SER:O	1:94:A:GLY:H	8	0.12
(1,139)	1:90:A:SER:O	1:94:A:GLY:H	10	0.12
(1,133)	1:87:A:ASP:O	1:91:A:SER:H	6	0.12
(1,133)	1:87:A:ASP:O	1:91:A:SER:H	14	0.12
(1,75)	1:58:A:ARG:O	1:62:A:ASP:H	12	0.12
(1,63)	1:41:A:LEU:O	1:45:A:GLU:H	1	0.12
(1,63)	1:41:A:LEU:O	1:45:A:GLU:H	7	0.12
(1,63)	1:41:A:LEU:O	1:45:A:GLU:H	12	0.12
(1,63)	1:41:A:LEU:O	1:45:A:GLU:H	14	0.12
(1,63)	1:41:A:LEU:O	1:45:A:GLU:H	20	0.12
(1,51)	1:33:A:LEU:O	1:37:A:GLU:H	14	0.12
(1,49)	1:31:A:ASP:O	1:35:A:GLN:H	6	0.12
(1,49)	1:31:A:ASP:O	1:35:A:GLN:H	15	0.12
(1,47)	1:30:A:TRP:O	1:34:A:LEU:H	10	0.12
(1,37)	1:19:A:GLN:O	1:23:A:GLU:H	8	0.12
(1,29)	1:15:A:ALA:O	1:19:A:GLN:H	6	0.12
(1,29)	1:15:A:ALA:O	1:19:A:GLN:H	13	0.12
(1,16)	1:8:A:ILE:O	1:12:A:GLN:N	18	0.12
(1,16)	1:8:A:ILE:O	1:12:A:GLN:N	19	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,13)	1:7:A:PHE:O	1:11:A:TRP:H	8	0.12
(1,13)	1:7:A:PHE:O	1:11:A:TRP:H	12	0.12
(1,13)	1:7:A:PHE:O	1:11:A:TRP:H	13	0.12
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD11	8	0.11
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD12	8	0.11
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD13	8	0.11
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD21	8	0.11
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD22	8	0.11
(4,1394)	1:162:A:ALA:H	1:163:A:LEU:HD23	8	0.11
(4,1317)	1:41:A:LEU:HD11	1:137:A:PHE:HD1	9	0.11
(4,1317)	1:41:A:LEU:HD11	1:137:A:PHE:HD2	9	0.11
(4,1317)	1:41:A:LEU:HD12	1:137:A:PHE:HD1	9	0.11
(4,1317)	1:41:A:LEU:HD12	1:137:A:PHE:HD2	9	0.11
(4,1317)	1:41:A:LEU:HD13	1:137:A:PHE:HD1	9	0.11
(4,1317)	1:41:A:LEU:HD13	1:137:A:PHE:HD2	9	0.11
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD21	18	0.11
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD22	18	0.11
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD23	18	0.11
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG21	3	0.11
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG22	3	0.11
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG23	3	0.11
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG21	14	0.11
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG22	14	0.11
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG23	14	0.11
(4,1289)	1:17:A:LEU:HD21	1:40:A:TYR:HE1	16	0.11
(4,1289)	1:17:A:LEU:HD21	1:40:A:TYR:HE2	16	0.11
(4,1289)	1:17:A:LEU:HD22	1:40:A:TYR:HE1	16	0.11
(4,1289)	1:17:A:LEU:HD22	1:40:A:TYR:HE2	16	0.11
(4,1289)	1:17:A:LEU:HD23	1:40:A:TYR:HE1	16	0.11
(4,1289)	1:17:A:LEU:HD23	1:40:A:TYR:HE2	16	0.11
(4,1250)	1:86:A:LEU:HD11	1:134:A:TYR:CD1	7	0.11
(4,1250)	1:86:A:LEU:HD12	1:134:A:TYR:CD1	7	0.11
(4,1250)	1:86:A:LEU:HD13	1:134:A:TYR:CD1	7	0.11
(4,1250)	1:86:A:LEU:HD11	1:134:A:TYR:CD1	8	0.11
(4,1250)	1:86:A:LEU:HD12	1:134:A:TYR:CD1	8	0.11
(4,1250)	1:86:A:LEU:HD13	1:134:A:TYR:CD1	8	0.11
(4,1247)	1:11:A:TRP:CZ2	1:48:A:MET:HE1	7	0.11
(4,1247)	1:11:A:TRP:CZ2	1:48:A:MET:HE2	7	0.11
(4,1247)	1:11:A:TRP:CZ2	1:48:A:MET:HE3	7	0.11
(4,1230)	1:97:A:LEU:HD11	1:98:A:PHE:HE1	10	0.11
(4,1230)	1:97:A:LEU:HD11	1:98:A:PHE:HE2	10	0.11
(4,1230)	1:97:A:LEU:HD12	1:98:A:PHE:HE1	10	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1230)	1:97:A:LEU:HD12	1:98:A:PHE:HE2	10	0.11
(4,1230)	1:97:A:LEU:HD13	1:98:A:PHE:HE1	10	0.11
(4,1230)	1:97:A:LEU:HD13	1:98:A:PHE:HE2	10	0.11
(4,1230)	1:97:A:LEU:HD11	1:98:A:PHE:HE1	18	0.11
(4,1230)	1:97:A:LEU:HD11	1:98:A:PHE:HE2	18	0.11
(4,1230)	1:97:A:LEU:HD12	1:98:A:PHE:HE1	18	0.11
(4,1230)	1:97:A:LEU:HD12	1:98:A:PHE:HE2	18	0.11
(4,1230)	1:97:A:LEU:HD13	1:98:A:PHE:HE1	18	0.11
(4,1230)	1:97:A:LEU:HD13	1:98:A:PHE:HE2	18	0.11
(4,1226)	1:33:A:LEU:HD21	1:137:A:PHE:CE1	3	0.11
(4,1226)	1:33:A:LEU:HD22	1:137:A:PHE:CE1	3	0.11
(4,1226)	1:33:A:LEU:HD23	1:137:A:PHE:CE1	3	0.11
(4,1226)	1:33:A:LEU:HD21	1:137:A:PHE:CE1	17	0.11
(4,1226)	1:33:A:LEU:HD22	1:137:A:PHE:CE1	17	0.11
(4,1226)	1:33:A:LEU:HD23	1:137:A:PHE:CE1	17	0.11
(4,1206)	1:89:A:LEU:HD11	1:134:A:TYR:CE1	6	0.11
(4,1206)	1:89:A:LEU:HD12	1:134:A:TYR:CE1	6	0.11
(4,1206)	1:89:A:LEU:HD13	1:134:A:TYR:CE1	6	0.11
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD11	7	0.11
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD12	7	0.11
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD13	7	0.11
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD11	7	0.11
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD12	7	0.11
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD13	7	0.11
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD11	16	0.11
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD12	16	0.11
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD13	16	0.11
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD11	16	0.11
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD12	16	0.11
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD13	16	0.11
(4,1107)	1:17:A:LEU:HD11	1:40:A:TYR:CE1	7	0.11
(4,1107)	1:17:A:LEU:HD12	1:40:A:TYR:CE1	7	0.11
(4,1107)	1:17:A:LEU:HD13	1:40:A:TYR:CE1	7	0.11
(4,1106)	1:34:A:LEU:HD21	1:134:A:TYR:CE2	8	0.11
(4,1106)	1:34:A:LEU:HD22	1:134:A:TYR:CE2	8	0.11
(4,1106)	1:34:A:LEU:HD23	1:134:A:TYR:CE2	8	0.11
(4,1101)	1:96:A:VAL:HG21	1:98:A:PHE:CE1	9	0.11
(4,1101)	1:96:A:VAL:HG22	1:98:A:PHE:CE1	9	0.11
(4,1101)	1:96:A:VAL:HG23	1:98:A:PHE:CE1	9	0.11
(4,1101)	1:96:A:VAL:HG21	1:98:A:PHE:CE1	15	0.11
(4,1101)	1:96:A:VAL:HG22	1:98:A:PHE:CE1	15	0.11
(4,1101)	1:96:A:VAL:HG23	1:98:A:PHE:CE1	15	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1074)	1:64:A:VAL:HG11	1:67:A:TYR:CE1	19	0.11
(4,1074)	1:64:A:VAL:HG12	1:67:A:TYR:CE1	19	0.11
(4,1074)	1:64:A:VAL:HG13	1:67:A:TYR:CE1	19	0.11
(4,1073)	1:82:A:LEU:HD21	1:134:A:TYR:CE2	5	0.11
(4,1073)	1:82:A:LEU:HD22	1:134:A:TYR:CE2	5	0.11
(4,1073)	1:82:A:LEU:HD23	1:134:A:TYR:CE2	5	0.11
(4,1070)	1:82:A:LEU:HD21	1:134:A:TYR:CD2	3	0.11
(4,1070)	1:82:A:LEU:HD22	1:134:A:TYR:CD2	3	0.11
(4,1070)	1:82:A:LEU:HD23	1:134:A:TYR:CD2	3	0.11
(4,1063)	1:89:A:LEU:HD11	1:134:A:TYR:CD1	17	0.11
(4,1063)	1:89:A:LEU:HD12	1:134:A:TYR:CD1	17	0.11
(4,1063)	1:89:A:LEU:HD13	1:134:A:TYR:CD1	17	0.11
(4,1058)	1:92:A:LEU:HD11	1:93:A:ILE:H	2	0.11
(4,1058)	1:92:A:LEU:HD12	1:93:A:ILE:H	2	0.11
(4,1058)	1:92:A:LEU:HD13	1:93:A:ILE:H	2	0.11
(4,1051)	1:26:A:GLN:H	1:81:A:LEU:HD21	1	0.11
(4,1051)	1:26:A:GLN:H	1:81:A:LEU:HD22	1	0.11
(4,1051)	1:26:A:GLN:H	1:81:A:LEU:HD23	1	0.11
(4,1014)	1:41:A:LEU:H	1:141:A:LEU:HD21	3	0.11
(4,1014)	1:41:A:LEU:H	1:141:A:LEU:HD22	3	0.11
(4,1014)	1:41:A:LEU:H	1:141:A:LEU:HD23	3	0.11
(4,1014)	1:41:A:LEU:H	1:141:A:LEU:HD21	12	0.11
(4,1014)	1:41:A:LEU:H	1:141:A:LEU:HD22	12	0.11
(4,1014)	1:41:A:LEU:H	1:141:A:LEU:HD23	12	0.11
(4,1014)	1:41:A:LEU:H	1:141:A:LEU:HD21	13	0.11
(4,1014)	1:41:A:LEU:H	1:141:A:LEU:HD22	13	0.11
(4,1014)	1:41:A:LEU:H	1:141:A:LEU:HD23	13	0.11
(4,972)	1:70:A:GLN:H	1:72:A:LEU:HD21	3	0.11
(4,972)	1:70:A:GLN:H	1:72:A:LEU:HD22	3	0.11
(4,972)	1:70:A:GLN:H	1:72:A:LEU:HD23	3	0.11
(4,957)	1:38:A:VAL:H	1:41:A:LEU:HD11	15	0.11
(4,957)	1:38:A:VAL:H	1:41:A:LEU:HD12	15	0.11
(4,957)	1:38:A:VAL:H	1:41:A:LEU:HD13	15	0.11
(4,942)	1:24:A:LEU:HD21	1:29:A:GLU:H	2	0.11
(4,942)	1:24:A:LEU:HD22	1:29:A:GLU:H	2	0.11
(4,942)	1:24:A:LEU:HD23	1:29:A:GLU:H	2	0.11
(4,914)	1:27:A:ARG:H	1:81:A:LEU:HD11	2	0.11
(4,914)	1:27:A:ARG:H	1:81:A:LEU:HD12	2	0.11
(4,914)	1:27:A:ARG:H	1:81:A:LEU:HD13	2	0.11
(4,914)	1:27:A:ARG:H	1:81:A:LEU:HD11	18	0.11
(4,914)	1:27:A:ARG:H	1:81:A:LEU:HD12	18	0.11
(4,914)	1:27:A:ARG:H	1:81:A:LEU:HD13	18	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,882)	1:24:A:LEU:HD21	1:32:A:LEU:H	5	0.11
(4,882)	1:24:A:LEU:HD22	1:32:A:LEU:H	5	0.11
(4,882)	1:24:A:LEU:HD23	1:32:A:LEU:H	5	0.11
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD11	9	0.11
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD12	9	0.11
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD13	9	0.11
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD11	11	0.11
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD12	11	0.11
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD13	11	0.11
(4,875)	1:93:A:ILE:HD11	1:131:A:TRP:HE1	12	0.11
(4,875)	1:93:A:ILE:HD12	1:131:A:TRP:HE1	12	0.11
(4,875)	1:93:A:ILE:HD13	1:131:A:TRP:HE1	12	0.11
(4,875)	1:93:A:ILE:HD11	1:131:A:TRP:HE1	17	0.11
(4,875)	1:93:A:ILE:HD12	1:131:A:TRP:HE1	17	0.11
(4,875)	1:93:A:ILE:HD13	1:131:A:TRP:HE1	17	0.11
(4,859)	1:78:A:LEU:HD11	1:137:A:PHE:HE1	12	0.11
(4,859)	1:78:A:LEU:HD11	1:137:A:PHE:HE2	12	0.11
(4,859)	1:78:A:LEU:HD12	1:137:A:PHE:HE1	12	0.11
(4,859)	1:78:A:LEU:HD12	1:137:A:PHE:HE2	12	0.11
(4,859)	1:78:A:LEU:HD13	1:137:A:PHE:HE1	12	0.11
(4,859)	1:78:A:LEU:HD13	1:137:A:PHE:HE2	12	0.11
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD21	3	0.11
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD22	3	0.11
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD23	3	0.11
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD21	8	0.11
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD22	8	0.11
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD23	8	0.11
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD21	14	0.11
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD22	14	0.11
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD23	14	0.11
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD11	12	0.11
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD12	12	0.11
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD13	12	0.11
(4,821)	1:24:A:LEU:HD21	1:30:A:TRP:H	14	0.11
(4,821)	1:24:A:LEU:HD22	1:30:A:TRP:H	14	0.11
(4,821)	1:24:A:LEU:HD23	1:30:A:TRP:H	14	0.11
(4,796)	1:21:A:LEU:HD21	1:137:A:PHE:HZ	19	0.11
(4,796)	1:21:A:LEU:HD22	1:137:A:PHE:HZ	19	0.11
(4,796)	1:21:A:LEU:HD23	1:137:A:PHE:HZ	19	0.11
(4,796)	1:21:A:LEU:HD21	1:137:A:PHE:HZ	20	0.11
(4,796)	1:21:A:LEU:HD22	1:137:A:PHE:HZ	20	0.11
(4,796)	1:21:A:LEU:HD23	1:137:A:PHE:HZ	20	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,794)	1:21:A:LEU:HD21	1:137:A:PHE:HE1	15	0.11
(4,794)	1:21:A:LEU:HD21	1:137:A:PHE:HE2	15	0.11
(4,794)	1:21:A:LEU:HD22	1:137:A:PHE:HE1	15	0.11
(4,794)	1:21:A:LEU:HD22	1:137:A:PHE:HE2	15	0.11
(4,794)	1:21:A:LEU:HD23	1:137:A:PHE:HE1	15	0.11
(4,794)	1:21:A:LEU:HD23	1:137:A:PHE:HE2	15	0.11
(4,713)	1:8:A:ILE:HD11	1:64:A:VAL:H	10	0.11
(4,713)	1:8:A:ILE:HD12	1:64:A:VAL:H	10	0.11
(4,713)	1:8:A:ILE:HD13	1:64:A:VAL:H	10	0.11
(4,685)	1:26:A:GLN:H	1:78:A:LEU:HD11	18	0.11
(4,685)	1:26:A:GLN:H	1:78:A:LEU:HD12	18	0.11
(4,685)	1:26:A:GLN:H	1:78:A:LEU:HD13	18	0.11
(4,672)	1:16:A:LEU:HD21	1:67:A:TYR:HE1	7	0.11
(4,672)	1:16:A:LEU:HD21	1:67:A:TYR:HE2	7	0.11
(4,672)	1:16:A:LEU:HD22	1:67:A:TYR:HE1	7	0.11
(4,672)	1:16:A:LEU:HD22	1:67:A:TYR:HE2	7	0.11
(4,672)	1:16:A:LEU:HD23	1:67:A:TYR:HE1	7	0.11
(4,672)	1:16:A:LEU:HD23	1:67:A:TYR:HE2	7	0.11
(4,563)	1:92:A:LEU:HD11	1:93:A:ILE:CD1	17	0.11
(4,563)	1:92:A:LEU:HD12	1:93:A:ILE:CD1	17	0.11
(4,563)	1:92:A:LEU:HD13	1:93:A:ILE:CD1	17	0.11
(4,550)	1:21:A:LEU:HD21	1:33:A:LEU:CD2	1	0.11
(4,550)	1:21:A:LEU:HD22	1:33:A:LEU:CD2	1	0.11
(4,550)	1:21:A:LEU:HD23	1:33:A:LEU:CD2	1	0.11
(4,550)	1:21:A:LEU:HD21	1:33:A:LEU:CD2	20	0.11
(4,550)	1:21:A:LEU:HD22	1:33:A:LEU:CD2	20	0.11
(4,550)	1:21:A:LEU:HD23	1:33:A:LEU:CD2	20	0.11
(4,489)	1:52:A:THR:HG21	1:56:A:ILE:CD1	8	0.11
(4,489)	1:52:A:THR:HG22	1:56:A:ILE:CD1	8	0.11
(4,489)	1:52:A:THR:HG23	1:56:A:ILE:CD1	8	0.11
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD21	4	0.11
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD22	4	0.11
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD23	4	0.11
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD21	18	0.11
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD22	18	0.11
(4,465)	1:34:A:LEU:CD2	1:82:A:LEU:HD23	18	0.11
(4,313)	1:11:A:TRP:HE1	1:155:A:TRP:HE1	20	0.11
(4,243)	1:41:A:LEU:H	1:137:A:PHE:HE1	17	0.11
(4,243)	1:41:A:LEU:H	1:137:A:PHE:HE2	17	0.11
(4,129)	1:24:A:LEU:HD21	1:33:A:LEU:HD11	16	0.11
(4,129)	1:24:A:LEU:HD21	1:33:A:LEU:HD12	16	0.11
(4,129)	1:24:A:LEU:HD21	1:33:A:LEU:HD13	16	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,129)	1:24:A:LEU:HD22	1:33:A:LEU:HD11	16	0.11
(4,129)	1:24:A:LEU:HD22	1:33:A:LEU:HD12	16	0.11
(4,129)	1:24:A:LEU:HD22	1:33:A:LEU:HD13	16	0.11
(4,129)	1:24:A:LEU:HD23	1:33:A:LEU:HD11	16	0.11
(4,129)	1:24:A:LEU:HD23	1:33:A:LEU:HD12	16	0.11
(4,129)	1:24:A:LEU:HD23	1:33:A:LEU:HD13	16	0.11
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD11	5	0.11
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD12	5	0.11
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD13	5	0.11
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD11	5	0.11
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD12	5	0.11
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD13	5	0.11
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD11	5	0.11
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD12	5	0.11
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD13	5	0.11
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD11	6	0.11
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD12	6	0.11
(4,120)	1:86:A:LEU:HD21	1:138:A:ILE:HD13	6	0.11
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD11	6	0.11
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD12	6	0.11
(4,120)	1:86:A:LEU:HD22	1:138:A:ILE:HD13	6	0.11
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD11	6	0.11
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD12	6	0.11
(4,120)	1:86:A:LEU:HD23	1:138:A:ILE:HD13	6	0.11
(4,44)	1:34:A:LEU:HD21	1:86:A:LEU:HD21	16	0.11
(4,44)	1:34:A:LEU:HD21	1:86:A:LEU:HD22	16	0.11
(4,44)	1:34:A:LEU:HD21	1:86:A:LEU:HD23	16	0.11
(4,44)	1:34:A:LEU:HD22	1:86:A:LEU:HD21	16	0.11
(4,44)	1:34:A:LEU:HD22	1:86:A:LEU:HD22	16	0.11
(4,44)	1:34:A:LEU:HD22	1:86:A:LEU:HD23	16	0.11
(4,44)	1:34:A:LEU:HD23	1:86:A:LEU:HD21	16	0.11
(4,44)	1:34:A:LEU:HD23	1:86:A:LEU:HD22	16	0.11
(4,44)	1:34:A:LEU:HD23	1:86:A:LEU:HD23	16	0.11
(4,44)	1:34:A:LEU:HD21	1:86:A:LEU:HD21	19	0.11
(4,44)	1:34:A:LEU:HD21	1:86:A:LEU:HD22	19	0.11
(4,44)	1:34:A:LEU:HD21	1:86:A:LEU:HD23	19	0.11
(4,44)	1:34:A:LEU:HD22	1:86:A:LEU:HD21	19	0.11
(4,44)	1:34:A:LEU:HD22	1:86:A:LEU:HD22	19	0.11
(4,44)	1:34:A:LEU:HD22	1:86:A:LEU:HD23	19	0.11
(4,44)	1:34:A:LEU:HD23	1:86:A:LEU:HD21	19	0.11
(4,44)	1:34:A:LEU:HD23	1:86:A:LEU:HD22	19	0.11
(4,44)	1:34:A:LEU:HD23	1:86:A:LEU:HD23	19	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,33)	1:71:A:THR:HG21	1:72:A:LEU:HD11	9	0.11
(4,33)	1:71:A:THR:HG21	1:72:A:LEU:HD12	9	0.11
(4,33)	1:71:A:THR:HG21	1:72:A:LEU:HD13	9	0.11
(4,33)	1:71:A:THR:HG22	1:72:A:LEU:HD11	9	0.11
(4,33)	1:71:A:THR:HG22	1:72:A:LEU:HD12	9	0.11
(4,33)	1:71:A:THR:HG22	1:72:A:LEU:HD13	9	0.11
(4,33)	1:71:A:THR:HG23	1:72:A:LEU:HD11	9	0.11
(4,33)	1:71:A:THR:HG23	1:72:A:LEU:HD12	9	0.11
(4,33)	1:71:A:THR:HG23	1:72:A:LEU:HD13	9	0.11
(1,193)	1:153:A:THR:O	1:157:A:GLN:H	2	0.11
(1,193)	1:153:A:THR:O	1:157:A:GLN:H	3	0.11
(1,187)	1:150:A:LEU:O	1:154:A:GLN:H	9	0.11
(1,187)	1:150:A:LEU:O	1:154:A:GLN:H	13	0.11
(1,165)	1:139:A:GLN:O	1:143:A:LYS:H	17	0.11
(1,159)	1:136:A:GLN:O	1:140:A:THR:H	14	0.11
(1,159)	1:136:A:GLN:O	1:140:A:THR:H	17	0.11
(1,153)	1:133:A:ASN:O	1:137:A:PHE:H	17	0.11
(1,151)	1:132:A:ILE:O	1:136:A:GLN:H	15	0.11
(1,145)	1:129:A:ASN:O	1:133:A:ASN:H	14	0.11
(1,141)	1:127:A:ALA:O	1:131:A:TRP:H	2	0.11
(1,139)	1:90:A:SER:O	1:94:A:GLY:H	7	0.11
(1,139)	1:90:A:SER:O	1:94:A:GLY:H	11	0.11
(1,139)	1:90:A:SER:O	1:94:A:GLY:H	19	0.11
(1,133)	1:87:A:ASP:O	1:91:A:SER:H	1	0.11
(1,133)	1:87:A:ASP:O	1:91:A:SER:H	18	0.11
(1,115)	1:78:A:LEU:O	1:82:A:LEU:H	4	0.11
(1,69)	1:44:A:ILE:O	1:48:A:MET:H	12	0.11
(1,69)	1:44:A:ILE:O	1:48:A:MET:H	14	0.11
(1,63)	1:41:A:LEU:O	1:45:A:GLU:H	2	0.11
(1,63)	1:41:A:LEU:O	1:45:A:GLU:H	3	0.11
(1,63)	1:41:A:LEU:O	1:45:A:GLU:H	15	0.11
(1,63)	1:41:A:LEU:O	1:45:A:GLU:H	16	0.11
(1,63)	1:41:A:LEU:O	1:45:A:GLU:H	18	0.11
(1,59)	1:39:A:SER:O	1:43:A:SER:H	13	0.11
(1,51)	1:33:A:LEU:O	1:37:A:GLU:H	4	0.11
(1,51)	1:33:A:LEU:O	1:37:A:GLU:H	10	0.11
(1,47)	1:30:A:TRP:O	1:34:A:LEU:H	1	0.11
(1,47)	1:30:A:TRP:O	1:34:A:LEU:H	13	0.11
(1,37)	1:19:A:GLN:O	1:23:A:GLU:H	19	0.11
(1,29)	1:15:A:ALA:O	1:19:A:GLN:H	11	0.11
(1,29)	1:15:A:ALA:O	1:19:A:GLN:H	15	0.11
(1,29)	1:15:A:ALA:O	1:19:A:GLN:H	20	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,16)	1:8:A:ILE:O	1:12:A:GLN:N	13	0.11
(1,13)	1:7:A:PHE:O	1:11:A:TRP:H	2	0.11
(1,13)	1:7:A:PHE:O	1:11:A:TRP:H	9	0.11
(1,13)	1:7:A:PHE:O	1:11:A:TRP:H	11	0.11
(1,13)	1:7:A:PHE:O	1:11:A:TRP:H	14	0.11
(4,1354)	1:24:A:LEU:HD11	1:32:A:LEU:HD11	13	0.1
(4,1354)	1:24:A:LEU:HD11	1:32:A:LEU:HD12	13	0.1
(4,1354)	1:24:A:LEU:HD11	1:32:A:LEU:HD13	13	0.1
(4,1354)	1:24:A:LEU:HD11	1:32:A:LEU:HD21	13	0.1
(4,1354)	1:24:A:LEU:HD11	1:32:A:LEU:HD22	13	0.1
(4,1354)	1:24:A:LEU:HD11	1:32:A:LEU:HD23	13	0.1
(4,1354)	1:24:A:LEU:HD12	1:32:A:LEU:HD11	13	0.1
(4,1354)	1:24:A:LEU:HD12	1:32:A:LEU:HD12	13	0.1
(4,1354)	1:24:A:LEU:HD12	1:32:A:LEU:HD13	13	0.1
(4,1354)	1:24:A:LEU:HD12	1:32:A:LEU:HD21	13	0.1
(4,1354)	1:24:A:LEU:HD12	1:32:A:LEU:HD22	13	0.1
(4,1354)	1:24:A:LEU:HD12	1:32:A:LEU:HD23	13	0.1
(4,1354)	1:24:A:LEU:HD13	1:32:A:LEU:HD11	13	0.1
(4,1354)	1:24:A:LEU:HD13	1:32:A:LEU:HD12	13	0.1
(4,1354)	1:24:A:LEU:HD13	1:32:A:LEU:HD13	13	0.1
(4,1354)	1:24:A:LEU:HD13	1:32:A:LEU:HD21	13	0.1
(4,1354)	1:24:A:LEU:HD13	1:32:A:LEU:HD22	13	0.1
(4,1354)	1:24:A:LEU:HD13	1:32:A:LEU:HD23	13	0.1
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD21	2	0.1
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD22	2	0.1
(4,1313)	1:137:A:PHE:HZ	1:141:A:LEU:HD23	2	0.1
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG21	17	0.1
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG22	17	0.1
(4,1299)	1:7:A:PHE:HZ	1:64:A:VAL:HG23	17	0.1
(4,1271)	1:67:A:TYR:CD2	1:71:A:THR:HG21	19	0.1
(4,1271)	1:67:A:TYR:CD2	1:71:A:THR:HG22	19	0.1
(4,1271)	1:67:A:TYR:CD2	1:71:A:THR:HG23	19	0.1
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD21	15	0.1
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD22	15	0.1
(4,1225)	1:137:A:PHE:CD2	1:141:A:LEU:HD23	15	0.1
(4,1223)	1:17:A:LEU:HD11	1:40:A:TYR:CD1	4	0.1
(4,1223)	1:17:A:LEU:HD12	1:40:A:TYR:CD1	4	0.1
(4,1223)	1:17:A:LEU:HD13	1:40:A:TYR:CD1	4	0.1
(4,1201)	1:44:A:ILE:HG21	1:148:A:HIS:CE1	7	0.1
(4,1201)	1:44:A:ILE:HG22	1:148:A:HIS:CE1	7	0.1
(4,1201)	1:44:A:ILE:HG23	1:148:A:HIS:CE1	7	0.1
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD11	14	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD12	14	0.1
(4,1174)	1:137:A:PHE:HD1	1:138:A:ILE:HD13	14	0.1
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD11	14	0.1
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD12	14	0.1
(4,1174)	1:137:A:PHE:HD2	1:138:A:ILE:HD13	14	0.1
(4,1107)	1:17:A:LEU:HD11	1:40:A:TYR:CE1	8	0.1
(4,1107)	1:17:A:LEU:HD12	1:40:A:TYR:CE1	8	0.1
(4,1107)	1:17:A:LEU:HD13	1:40:A:TYR:CE1	8	0.1
(4,1107)	1:17:A:LEU:HD11	1:40:A:TYR:CE1	18	0.1
(4,1107)	1:17:A:LEU:HD12	1:40:A:TYR:CE1	18	0.1
(4,1107)	1:17:A:LEU:HD13	1:40:A:TYR:CE1	18	0.1
(4,1101)	1:96:A:VAL:HG21	1:98:A:PHE:CE1	3	0.1
(4,1101)	1:96:A:VAL:HG22	1:98:A:PHE:CE1	3	0.1
(4,1101)	1:96:A:VAL:HG23	1:98:A:PHE:CE1	3	0.1
(4,1058)	1:92:A:LEU:HD11	1:93:A:ILE:H	11	0.1
(4,1058)	1:92:A:LEU:HD12	1:93:A:ILE:H	11	0.1
(4,1058)	1:92:A:LEU:HD13	1:93:A:ILE:H	11	0.1
(4,1046)	1:11:A:TRP:H	1:47:A:VAL:HG21	7	0.1
(4,1046)	1:11:A:TRP:H	1:47:A:VAL:HG22	7	0.1
(4,1046)	1:11:A:TRP:H	1:47:A:VAL:HG23	7	0.1
(4,1014)	1:41:A:LEU:H	1:141:A:LEU:HD21	1	0.1
(4,1014)	1:41:A:LEU:H	1:141:A:LEU:HD22	1	0.1
(4,1014)	1:41:A:LEU:H	1:141:A:LEU:HD23	1	0.1
(4,1014)	1:41:A:LEU:H	1:141:A:LEU:HD21	6	0.1
(4,1014)	1:41:A:LEU:H	1:141:A:LEU:HD22	6	0.1
(4,1014)	1:41:A:LEU:H	1:141:A:LEU:HD23	6	0.1
(4,966)	1:16:A:LEU:H	1:71:A:THR:HG21	15	0.1
(4,966)	1:16:A:LEU:H	1:71:A:THR:HG22	15	0.1
(4,966)	1:16:A:LEU:H	1:71:A:THR:HG23	15	0.1
(4,961)	1:135:A:GLN:H	1:138:A:ILE:HD11	13	0.1
(4,961)	1:135:A:GLN:H	1:138:A:ILE:HD12	13	0.1
(4,961)	1:135:A:GLN:H	1:138:A:ILE:HD13	13	0.1
(4,882)	1:24:A:LEU:HD21	1:32:A:LEU:H	3	0.1
(4,882)	1:24:A:LEU:HD22	1:32:A:LEU:H	3	0.1
(4,882)	1:24:A:LEU:HD23	1:32:A:LEU:H	3	0.1
(4,882)	1:24:A:LEU:HD21	1:32:A:LEU:H	17	0.1
(4,882)	1:24:A:LEU:HD22	1:32:A:LEU:H	17	0.1
(4,882)	1:24:A:LEU:HD23	1:32:A:LEU:H	17	0.1
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD11	6	0.1
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD12	6	0.1
(4,881)	1:24:A:LEU:H	1:24:A:LEU:HD13	6	0.1
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD11	5	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD12	5	0.1
(4,880)	1:24:A:LEU:H	1:33:A:LEU:HD13	5	0.1
(4,859)	1:78:A:LEU:HD11	1:137:A:PHE:HE1	15	0.1
(4,859)	1:78:A:LEU:HD11	1:137:A:PHE:HE2	15	0.1
(4,859)	1:78:A:LEU:HD12	1:137:A:PHE:HE1	15	0.1
(4,859)	1:78:A:LEU:HD12	1:137:A:PHE:HE2	15	0.1
(4,859)	1:78:A:LEU:HD13	1:137:A:PHE:HE1	15	0.1
(4,859)	1:78:A:LEU:HD13	1:137:A:PHE:HE2	15	0.1
(4,859)	1:78:A:LEU:HD11	1:137:A:PHE:HE1	17	0.1
(4,859)	1:78:A:LEU:HD11	1:137:A:PHE:HE2	17	0.1
(4,859)	1:78:A:LEU:HD12	1:137:A:PHE:HE1	17	0.1
(4,859)	1:78:A:LEU:HD12	1:137:A:PHE:HE2	17	0.1
(4,859)	1:78:A:LEU:HD13	1:137:A:PHE:HE1	17	0.1
(4,859)	1:78:A:LEU:HD13	1:137:A:PHE:HE2	17	0.1
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD21	19	0.1
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD22	19	0.1
(4,858)	1:25:A:ALA:H	1:33:A:LEU:HD23	19	0.1
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD11	10	0.1
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD12	10	0.1
(4,845)	1:137:A:PHE:H	1:138:A:ILE:HD13	10	0.1
(4,844)	1:22:A:LEU:HD11	1:26:A:GLN:H	19	0.1
(4,844)	1:22:A:LEU:HD12	1:26:A:GLN:H	19	0.1
(4,844)	1:22:A:LEU:HD13	1:26:A:GLN:H	19	0.1
(4,809)	1:34:A:LEU:HD11	1:134:A:TYR:H	6	0.1
(4,809)	1:34:A:LEU:HD12	1:134:A:TYR:H	6	0.1
(4,809)	1:34:A:LEU:HD13	1:134:A:TYR:H	6	0.1
(4,796)	1:21:A:LEU:HD21	1:137:A:PHE:HZ	8	0.1
(4,796)	1:21:A:LEU:HD22	1:137:A:PHE:HZ	8	0.1
(4,796)	1:21:A:LEU:HD23	1:137:A:PHE:HZ	8	0.1
(4,794)	1:21:A:LEU:HD21	1:137:A:PHE:HE1	13	0.1
(4,794)	1:21:A:LEU:HD21	1:137:A:PHE:HE2	13	0.1
(4,794)	1:21:A:LEU:HD22	1:137:A:PHE:HE1	13	0.1
(4,794)	1:21:A:LEU:HD22	1:137:A:PHE:HE2	13	0.1
(4,794)	1:21:A:LEU:HD23	1:137:A:PHE:HE1	13	0.1
(4,794)	1:21:A:LEU:HD23	1:137:A:PHE:HE2	13	0.1
(4,781)	1:81:A:LEU:HD11	1:82:A:LEU:H	5	0.1
(4,781)	1:81:A:LEU:HD12	1:82:A:LEU:H	5	0.1
(4,781)	1:81:A:LEU:HD13	1:82:A:LEU:H	5	0.1
(4,781)	1:81:A:LEU:HD11	1:82:A:LEU:H	17	0.1
(4,781)	1:81:A:LEU:HD12	1:82:A:LEU:H	17	0.1
(4,781)	1:81:A:LEU:HD13	1:82:A:LEU:H	17	0.1
(4,757)	1:72:A:LEU:HD11	1:149:A:ARG:H	13	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,757)	1:72:A:LEU:HD12	1:149:A:ARG:H	13	0.1
(4,757)	1:72:A:LEU:HD13	1:149:A:ARG:H	13	0.1
(4,685)	1:26:A:GLN:H	1:78:A:LEU:HD11	11	0.1
(4,685)	1:26:A:GLN:H	1:78:A:LEU:HD12	11	0.1
(4,685)	1:26:A:GLN:H	1:78:A:LEU:HD13	11	0.1
(4,661)	1:86:A:LEU:HD11	1:135:A:GLN:H	15	0.1
(4,661)	1:86:A:LEU:HD12	1:135:A:GLN:H	15	0.1
(4,661)	1:86:A:LEU:HD13	1:135:A:GLN:H	15	0.1
(4,530)	1:17:A:LEU:HD21	1:71:A:THR:CG2	4	0.1
(4,530)	1:17:A:LEU:HD22	1:71:A:THR:CG2	4	0.1
(4,530)	1:17:A:LEU:HD23	1:71:A:THR:CG2	4	0.1
(4,498)	1:24:A:LEU:HD21	1:32:A:LEU:CD1	9	0.1
(4,498)	1:24:A:LEU:HD22	1:32:A:LEU:CD1	9	0.1
(4,498)	1:24:A:LEU:HD23	1:32:A:LEU:CD1	9	0.1
(4,313)	1:11:A:TRP:HE1	1:155:A:TRP:HE1	16	0.1
(4,313)	1:11:A:TRP:HE1	1:155:A:TRP:HE1	19	0.1
(4,307)	1:155:A:TRP:H	1:155:A:TRP:HE1	7	0.1
(4,307)	1:155:A:TRP:H	1:155:A:TRP:HE1	9	0.1
(4,307)	1:155:A:TRP:H	1:155:A:TRP:HE1	13	0.1
(4,129)	1:24:A:LEU:HD21	1:33:A:LEU:HD11	17	0.1
(4,129)	1:24:A:LEU:HD21	1:33:A:LEU:HD12	17	0.1
(4,129)	1:24:A:LEU:HD21	1:33:A:LEU:HD13	17	0.1
(4,129)	1:24:A:LEU:HD22	1:33:A:LEU:HD11	17	0.1
(4,129)	1:24:A:LEU:HD22	1:33:A:LEU:HD12	17	0.1
(4,129)	1:24:A:LEU:HD22	1:33:A:LEU:HD13	17	0.1
(4,129)	1:24:A:LEU:HD23	1:33:A:LEU:HD11	17	0.1
(4,129)	1:24:A:LEU:HD23	1:33:A:LEU:HD12	17	0.1
(4,129)	1:24:A:LEU:HD23	1:33:A:LEU:HD13	17	0.1
(4,43)	1:34:A:LEU:HD21	1:138:A:ILE:HD11	5	0.1
(4,43)	1:34:A:LEU:HD21	1:138:A:ILE:HD12	5	0.1
(4,43)	1:34:A:LEU:HD21	1:138:A:ILE:HD13	5	0.1
(4,43)	1:34:A:LEU:HD22	1:138:A:ILE:HD11	5	0.1
(4,43)	1:34:A:LEU:HD22	1:138:A:ILE:HD12	5	0.1
(4,43)	1:34:A:LEU:HD22	1:138:A:ILE:HD13	5	0.1
(4,43)	1:34:A:LEU:HD23	1:138:A:ILE:HD11	5	0.1
(4,43)	1:34:A:LEU:HD23	1:138:A:ILE:HD12	5	0.1
(4,43)	1:34:A:LEU:HD23	1:138:A:ILE:HD13	5	0.1
(4,43)	1:34:A:LEU:HD21	1:138:A:ILE:HD11	8	0.1
(4,43)	1:34:A:LEU:HD21	1:138:A:ILE:HD12	8	0.1
(4,43)	1:34:A:LEU:HD21	1:138:A:ILE:HD13	8	0.1
(4,43)	1:34:A:LEU:HD22	1:138:A:ILE:HD11	8	0.1
(4,43)	1:34:A:LEU:HD22	1:138:A:ILE:HD12	8	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,43)	1:34:A:LEU:HD22	1:138:A:ILE:HD13	8	0.1
(4,43)	1:34:A:LEU:HD23	1:138:A:ILE:HD11	8	0.1
(4,43)	1:34:A:LEU:HD23	1:138:A:ILE:HD12	8	0.1
(4,43)	1:34:A:LEU:HD23	1:138:A:ILE:HD13	8	0.1
(4,43)	1:34:A:LEU:HD21	1:138:A:ILE:HD11	9	0.1
(4,43)	1:34:A:LEU:HD21	1:138:A:ILE:HD12	9	0.1
(4,43)	1:34:A:LEU:HD21	1:138:A:ILE:HD13	9	0.1
(4,43)	1:34:A:LEU:HD22	1:138:A:ILE:HD11	9	0.1
(4,43)	1:34:A:LEU:HD22	1:138:A:ILE:HD12	9	0.1
(4,43)	1:34:A:LEU:HD22	1:138:A:ILE:HD13	9	0.1
(4,43)	1:34:A:LEU:HD23	1:138:A:ILE:HD11	9	0.1
(4,43)	1:34:A:LEU:HD23	1:138:A:ILE:HD12	9	0.1
(4,43)	1:34:A:LEU:HD23	1:138:A:ILE:HD13	9	0.1
(1,187)	1:150:A:LEU:O	1:154:A:GLN:H	8	0.1
(1,187)	1:150:A:LEU:O	1:154:A:GLN:H	14	0.1
(1,165)	1:139:A:GLN:O	1:143:A:LYS:H	5	0.1
(1,153)	1:133:A:ASN:O	1:137:A:PHE:H	2	0.1
(1,133)	1:87:A:ASP:O	1:91:A:SER:H	3	0.1
(1,133)	1:87:A:ASP:O	1:91:A:SER:H	10	0.1
(1,125)	1:83:A:GLN:O	1:87:A:ASP:H	14	0.1
(1,107)	1:74:A:ASN:O	1:78:A:LEU:H	14	0.1
(1,69)	1:44:A:ILE:O	1:48:A:MET:H	2	0.1
(1,69)	1:44:A:ILE:O	1:48:A:MET:H	8	0.1
(1,69)	1:44:A:ILE:O	1:48:A:MET:H	11	0.1
(1,63)	1:41:A:LEU:O	1:45:A:GLU:H	9	0.1
(1,59)	1:39:A:SER:O	1:43:A:SER:H	4	0.1
(1,59)	1:39:A:SER:O	1:43:A:SER:H	10	0.1
(1,51)	1:33:A:LEU:O	1:37:A:GLU:H	20	0.1
(1,29)	1:15:A:ALA:O	1:19:A:GLN:H	19	0.1
(1,19)	1:10:A:ARG:O	1:14:A:ILE:H	5	0.1
(1,19)	1:10:A:ARG:O	1:14:A:ILE:H	9	0.1
(1,16)	1:8:A:ILE:O	1:12:A:GLN:N	6	0.1
(1,16)	1:8:A:ILE:O	1:12:A:GLN:N	17	0.1
(1,13)	1:7:A:PHE:O	1:11:A:TRP:H	19	0.1

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

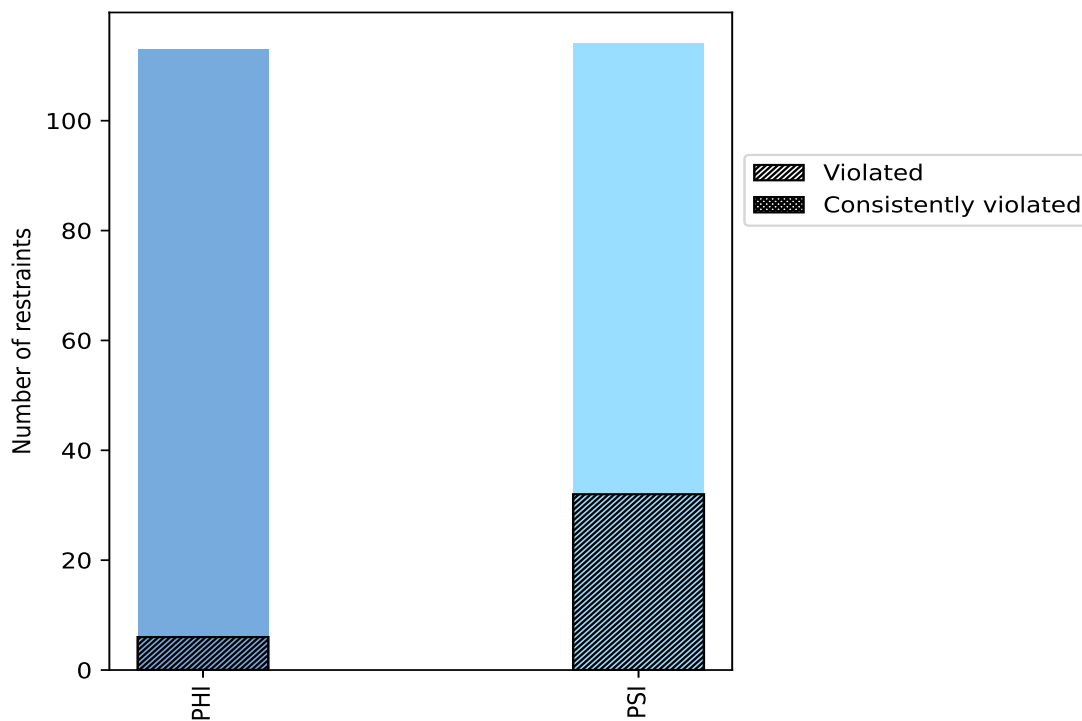
10.1 Summary of dihedral-angle violations [i](#)

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
PHI	113	49.8	6	5.3	2.6	0	0.0	0.0
PSI	114	50.2	32	28.1	14.1	0	0.0	0.0
Total	227	100.0	38	16.7	16.7	0	0.0	0.0

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

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



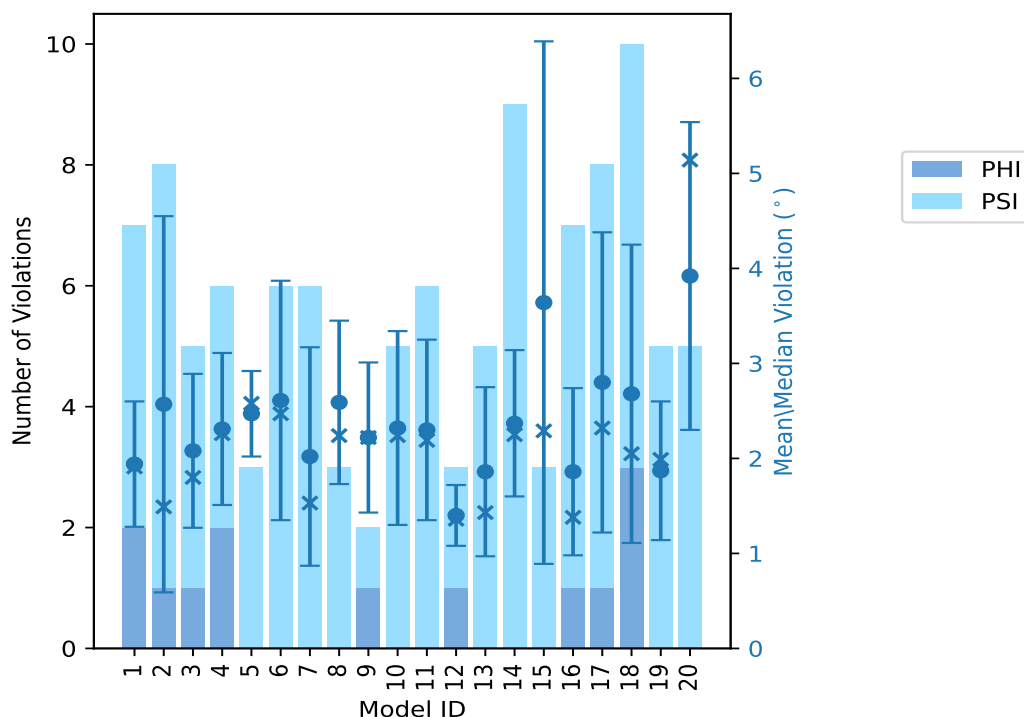
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

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

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

Model ID	Number of violations			Mean (°)	Max (°)	SD (°)	Median (°)
	PHI	PSI	Total				
1	2	5	7	1.94	3.23	0.66	1.91
2	1	7	8	2.57	6.96	1.98	1.49
3	1	4	5	2.08	3.48	0.81	1.8
4	2	4	6	2.31	3.3	0.8	2.26
5	0	3	3	2.47	2.95	0.45	2.58
6	0	6	6	2.61	4.99	1.26	2.47
7	0	6	6	2.02	4.54	1.15	1.53
8	0	3	3	2.59	3.78	0.86	2.24
9	1	1	2	2.22	3.01	0.79	2.22
10	0	5	5	2.32	4.19	1.02	2.24
11	0	6	6	2.3	3.76	0.95	2.19
12	1	2	3	1.4	1.82	0.32	1.36
13	0	5	5	1.86	3.62	0.89	1.43
14	0	9	9	2.37	3.91	0.77	2.25
15	0	3	3	3.64	7.47	2.75	2.29
16	1	6	7	1.86	3.44	0.88	1.38
17	1	7	8	2.8	5.12	1.58	2.32
18	3	7	10	2.68	6.08	1.57	2.05
19	0	5	5	1.87	2.93	0.73	1.99
20	0	5	5	3.92	5.27	1.62	5.14

10.2.1 Bar graph : Dihedral violation statistics for each model [i](#)



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

10.3 Dihedral-angle violation statistics for the ensemble [i](#)

Violation analysis may find that some restraints are violated in very few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of ensemble.

Number of violated restraints			Fraction of the ensemble	
PHI	PSI	Total	Count ¹	%
3	14	17	1	5.0
0	6	6	2	10.0
2	3	5	3	15.0
1	2	3	4	20.0
0	1	1	5	25.0
0	2	2	6	30.0
0	1	1	7	35.0
0	1	1	8	40.0
0	0	0	9	45.0
0	1	1	10	50.0
0	0	0	11	55.0

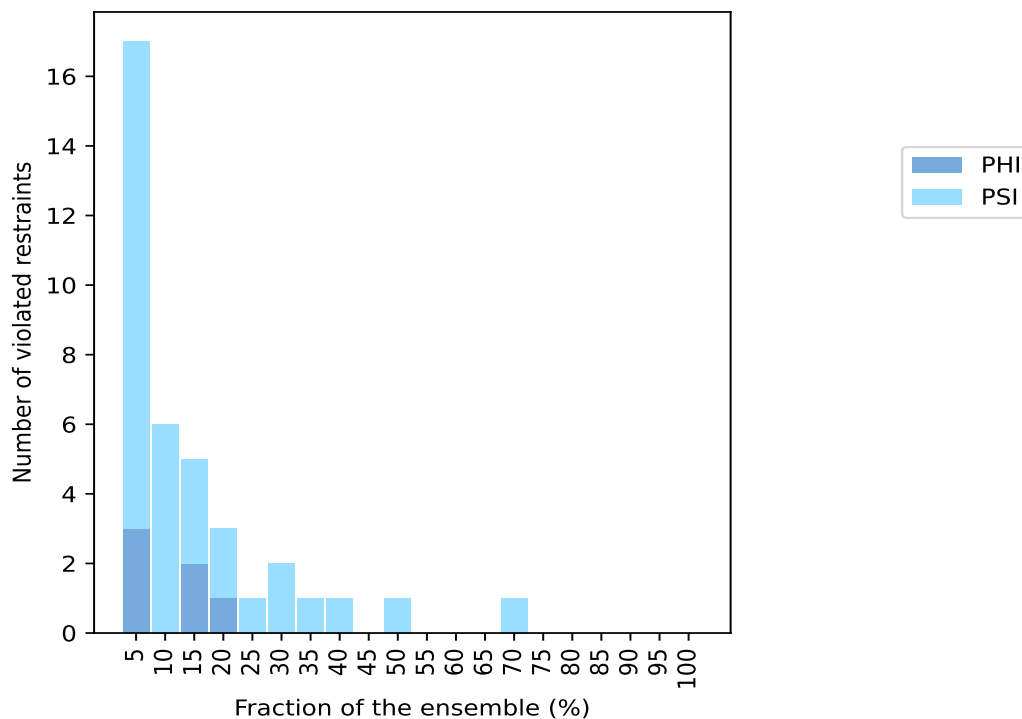
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Number of violated restraints			Fraction of the ensemble	
PHI	PSI	Total	Count ¹	%
0	0	0	12	60.0
0	0	0	13	65.0
0	1	1	14	70.0
0	0	0	15	75.0
0	0	0	16	80.0
0	0	0	17	85.0
0	0	0	18	90.0
0	0	0	19	95.0
0	0	0	20	100.0

¹ Number of models with violations

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

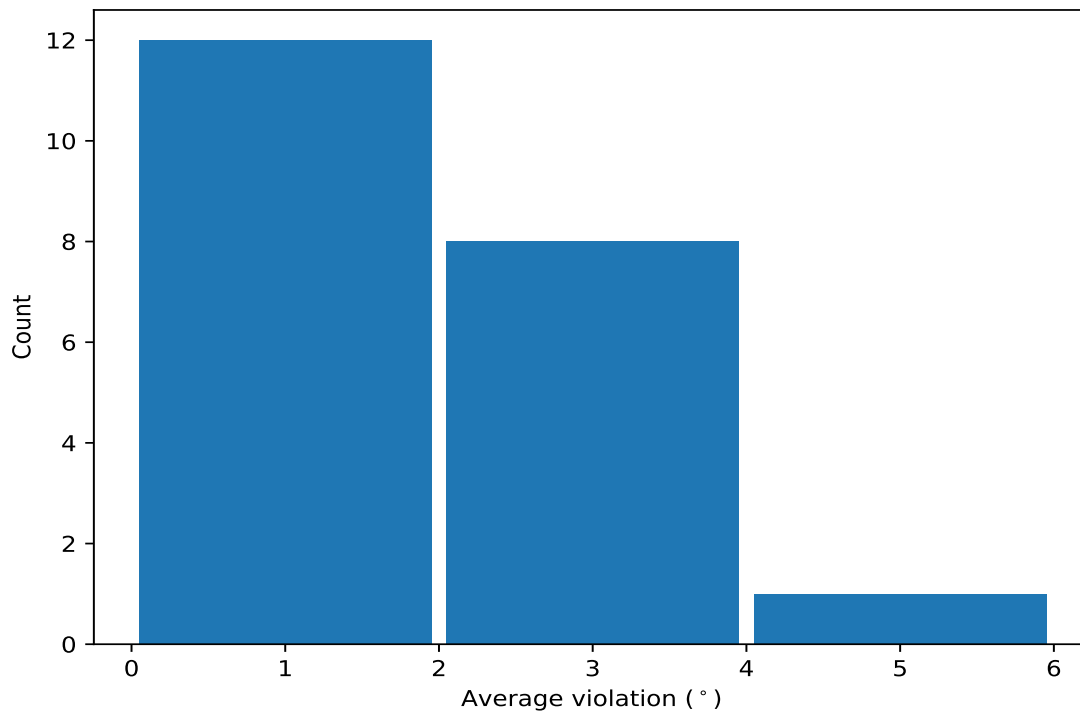


10.4 Most violated dihedral-angle restraints in the ensemble [i](#)

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

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

in the ensemble



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

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

Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,18)	1:13:A:ARG:N	1:13:A:ARG:CA	1:13:A:ARG:C	1:14:A:ILE:N	14	3.73	1.07	3.55
(1,123)	1:71:A:THR:N	1:71:A:THR:CA	1:71:A:THR:C	1:72:A:LEU:N	10	1.92	0.69	1.76
(1,227)	1:156:A:THR:N	1:156:A:THR:CA	1:156:A:THR:C	1:157:A:GLN:N	8	3.11	1.49	2.5
(1,95)	1:57:A:THR:N	1:57:A:THR:CA	1:57:A:THR:C	1:58:A:ARG:N	7	2.43	0.67	2.66
(1,171)	1:128:A:SER:N	1:128:A:SER:CA	1:128:A:SER:C	1:129:A:ASN:N	6	4.17	1.83	4.17
(1,131)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:GLN:N	6	1.62	0.22	1.69
(1,173)	1:129:A:ASN:N	1:129:A:ASN:CA	1:129:A:ASN:C	1:130:A:ARG:N	5	3.55	1.9	3.32
(1,168)	1:120:A:THR:C	1:121:A:ASP:N	1:121:A:ASP:CA	1:121:A:ASP:C	4	2.65	0.56	2.72
(1,169)	1:121:A:ASP:N	1:121:A:ASP:CA	1:121:A:ASP:C	1:122:A:MET:N	4	2.34	1.27	1.91
(1,207)	1:146:A:GLU:N	1:146:A:GLU:CA	1:146:A:GLU:C	1:147:A:GLN:N	4	1.84	0.3	1.84
(1,167)	1:93:A:ILE:N	1:93:A:ILE:CA	1:93:A:ILE:C	1:94:A:GLY:N	3	3.26	1.45	2.61
(1,157)	1:88:A:GLU:N	1:88:A:GLU:CA	1:88:A:GLU:C	1:89:A:LEU:N	3	2.46	1.47	1.51
(1,170)	1:127:A:ALA:C	1:128:A:SER:N	1:128:A:SER:CA	1:128:A:SER:C	3	1.88	0.7	1.88
(1,58)	1:34:A:LEU:N	1:34:A:LEU:CA	1:34:A:LEU:C	1:35:A:GLN:N	3	1.62	0.5	1.6
(1,47)	1:27:A:ARG:C	1:28:A:GLY:N	1:28:A:GLY:CA	1:28:A:GLY:C	3	1.19	0.13	1.12
(1,70)	1:40:A:TYR:N	1:40:A:TYR:CA	1:40:A:TYR:C	1:41:A:LEU:N	2	1.55	0.2	1.55
(1,141)	1:80:A:GLY:N	1:80:A:GLY:CA	1:80:A:GLY:C	1:81:A:LEU:N	2	1.48	0.17	1.48
(1,195)	1:140:A:THR:N	1:140:A:THR:CA	1:140:A:THR:C	1:141:A:LEU:N	2	1.44	0.09	1.44
(1,14)	1:11:A:TRP:N	1:11:A:TRP:CA	1:11:A:TRP:C	1:12:A:GLN:N	2	1.36	0.09	1.36
(1,74)	1:42:A:GLN:N	1:42:A:GLN:CA	1:42:A:GLN:C	1:43:A:SER:N	2	1.34	0.17	1.34

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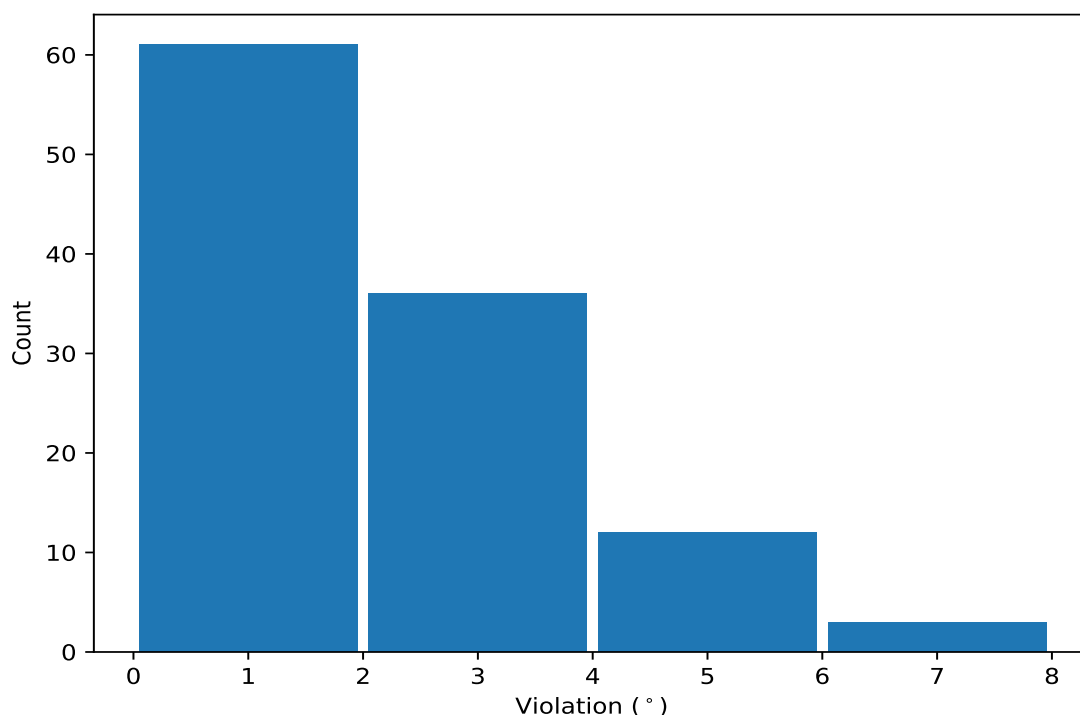
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,165)	1:92:A:LEU:N	1:92:A:LEU:CA	1:92:A:LEU:C	1:93:A:ILE:N	2	1.25	0.02	1.25

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

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

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

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



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

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

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,171)	1:128:A:SER:N	1:128:A:SER:CA	1:128:A:SER:C	1:129:A:ASN:N	15	7.47
(1,173)	1:129:A:ASN:N	1:129:A:ASN:CA	1:129:A:ASN:C	1:130:A:ARG:N	2	6.96
(1,18)	1:13:A:ARG:N	1:13:A:ARG:CA	1:13:A:ARG:C	1:14:A:ILE:N	18	6.08
(1,167)	1:93:A:ILE:N	1:93:A:ILE:CA	1:93:A:ILE:C	1:94:A:GLY:N	20	5.27
(1,18)	1:13:A:ARG:N	1:13:A:ARG:CA	1:13:A:ARG:C	1:14:A:ILE:N	20	5.19
(1,227)	1:156:A:THR:N	1:156:A:THR:CA	1:156:A:THR:C	1:157:A:GLN:N	20	5.14

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,227)	1:156:A:THR:N	1:156:A:THR:CA	1:156:A:THR:C	1:157:A:GLN:N	17	5.12
(1,18)	1:13:A:ARG:N	1:13:A:ARG:CA	1:13:A:ARG:C	1:14:A:ILE:N	6	4.99
(1,18)	1:13:A:ARG:N	1:13:A:ARG:CA	1:13:A:ARG:C	1:14:A:ILE:N	17	4.56
(1,227)	1:156:A:THR:N	1:156:A:THR:CA	1:156:A:THR:C	1:157:A:GLN:N	7	4.54
(1,157)	1:88:A:GLU:N	1:88:A:GLU:CA	1:88:A:GLU:C	1:89:A:LEU:N	2	4.53
(1,169)	1:121:A:ASP:N	1:121:A:ASP:CA	1:121:A:ASP:C	1:122:A:MET:N	18	4.37
(1,171)	1:128:A:SER:N	1:128:A:SER:CA	1:128:A:SER:C	1:129:A:ASN:N	17	4.29
(1,171)	1:128:A:SER:N	1:128:A:SER:CA	1:128:A:SER:C	1:129:A:ASN:N	10	4.19
(1,171)	1:128:A:SER:N	1:128:A:SER:CA	1:128:A:SER:C	1:129:A:ASN:N	18	4.15
(1,18)	1:13:A:ARG:N	1:13:A:ARG:CA	1:13:A:ARG:C	1:14:A:ILE:N	14	3.91
(1,18)	1:13:A:ARG:N	1:13:A:ARG:CA	1:13:A:ARG:C	1:14:A:ILE:N	8	3.78
(1,171)	1:128:A:SER:N	1:128:A:SER:CA	1:128:A:SER:C	1:129:A:ASN:N	11	3.76
(1,18)	1:13:A:ARG:N	1:13:A:ARG:CA	1:13:A:ARG:C	1:14:A:ILE:N	13	3.62
(1,18)	1:13:A:ARG:N	1:13:A:ARG:CA	1:13:A:ARG:C	1:14:A:ILE:N	3	3.48
(1,173)	1:129:A:ASN:N	1:129:A:ASN:CA	1:129:A:ASN:C	1:130:A:ARG:N	16	3.44
(1,173)	1:129:A:ASN:N	1:129:A:ASN:CA	1:129:A:ASN:C	1:130:A:ARG:N	14	3.32
(1,168)	1:120:A:THR:C	1:121:A:ASP:N	1:121:A:ASP:CA	1:121:A:ASP:C	4	3.3
(1,18)	1:13:A:ARG:N	1:13:A:ARG:CA	1:13:A:ARG:C	1:14:A:ILE:N	1	3.23
(1,123)	1:71:A:THR:N	1:71:A:THR:CA	1:71:A:THR:C	1:72:A:LEU:N	17	3.19
(1,95)	1:57:A:THR:N	1:57:A:THR:CA	1:57:A:THR:C	1:58:A:ARG:N	4	3.18
(1,95)	1:57:A:THR:N	1:57:A:THR:CA	1:57:A:THR:C	1:58:A:ARG:N	11	3.09
(1,168)	1:120:A:THR:C	1:121:A:ASP:N	1:121:A:ASP:CA	1:121:A:ASP:C	9	3.01
(1,95)	1:57:A:THR:N	1:57:A:THR:CA	1:57:A:THR:C	1:58:A:ARG:N	6	3.01
(1,123)	1:71:A:THR:N	1:71:A:THR:CA	1:71:A:THR:C	1:72:A:LEU:N	5	2.95
(1,173)	1:129:A:ASN:N	1:129:A:ASN:CA	1:129:A:ASN:C	1:130:A:ARG:N	6	2.94
(1,18)	1:13:A:ARG:N	1:13:A:ARG:CA	1:13:A:ARG:C	1:14:A:ILE:N	19	2.93
(1,18)	1:13:A:ARG:N	1:13:A:ARG:CA	1:13:A:ARG:C	1:14:A:ILE:N	16	2.9
(1,170)	1:127:A:ALA:C	1:128:A:SER:N	1:128:A:SER:CA	1:128:A:SER:C	18	2.74
(1,227)	1:156:A:THR:N	1:156:A:THR:CA	1:156:A:THR:C	1:157:A:GLN:N	11	2.67
(1,18)	1:13:A:ARG:N	1:13:A:ARG:CA	1:13:A:ARG:C	1:14:A:ILE:N	4	2.67
(1,95)	1:57:A:THR:N	1:57:A:THR:CA	1:57:A:THR:C	1:58:A:ARG:N	20	2.66
(1,167)	1:93:A:ILE:N	1:93:A:ILE:CA	1:93:A:ILE:C	1:94:A:GLY:N	14	2.61
(1,52)	1:31:A:ASP:N	1:31:A:ASP:CA	1:31:A:ASP:C	1:32:A:LEU:N	2	2.58
(1,18)	1:13:A:ARG:N	1:13:A:ARG:CA	1:13:A:ARG:C	1:14:A:ILE:N	5	2.58
(1,169)	1:121:A:ASP:N	1:121:A:ASP:CA	1:121:A:ASP:C	1:122:A:MET:N	14	2.46
(1,168)	1:120:A:THR:C	1:121:A:ASP:N	1:121:A:ASP:CA	1:121:A:ASP:C	3	2.44
(1,123)	1:71:A:THR:N	1:71:A:THR:CA	1:71:A:THR:C	1:72:A:LEU:N	1	2.42
(1,227)	1:156:A:THR:N	1:156:A:THR:CA	1:156:A:THR:C	1:157:A:GLN:N	19	2.32
(1,18)	1:13:A:ARG:N	1:13:A:ARG:CA	1:13:A:ARG:C	1:14:A:ILE:N	10	2.32
(1,175)	1:130:A:ARG:N	1:130:A:ARG:CA	1:130:A:ARG:C	1:131:A:TRP:N	15	2.29
(1,24)	1:16:A:LEU:N	1:16:A:LEU:CA	1:16:A:LEU:C	1:17:A:LEU:N	18	2.26
(1,227)	1:156:A:THR:N	1:156:A:THR:CA	1:156:A:THR:C	1:157:A:GLN:N	14	2.25
(1,207)	1:146:A:GLU:N	1:146:A:GLU:CA	1:146:A:GLU:C	1:147:A:GLN:N	8	2.24
(1,58)	1:34:A:LEU:N	1:34:A:LEU:CA	1:34:A:LEU:C	1:35:A:GLN:N	10	2.24
(1,123)	1:71:A:THR:N	1:71:A:THR:CA	1:71:A:THR:C	1:72:A:LEU:N	6	2.01
(1,207)	1:146:A:GLU:N	1:146:A:GLU:CA	1:146:A:GLU:C	1:147:A:GLN:N	19	1.99
(1,95)	1:57:A:THR:N	1:57:A:THR:CA	1:57:A:THR:C	1:58:A:ARG:N	14	1.93
(1,167)	1:93:A:ILE:N	1:93:A:ILE:CA	1:93:A:ILE:C	1:94:A:GLY:N	1	1.91
(1,163)	1:91:A:SER:N	1:91:A:SER:CA	1:91:A:SER:C	1:92:A:LEU:N	1	1.91
(1,209)	1:147:A:GLN:N	1:147:A:GLN:CA	1:147:A:GLN:C	1:148:A:HIS:N	7	1.88
(1,170)	1:127:A:ALA:C	1:128:A:SER:N	1:128:A:SER:CA	1:128:A:SER:C	16	1.88

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,219)	1:152:A:LEU:N	1:152:A:LEU:CA	1:152:A:LEU:C	1:153:A:THR:N	5	1.87
(1,168)	1:120:A:THR:C	1:121:A:ASP:N	1:121:A:ASP:CA	1:121:A:ASP:C	18	1.85
(1,90)	1:52:A:THR:N	1:52:A:THR:CA	1:52:A:THR:C	1:53:A:PRO:N	4	1.84
(1,131)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:GLN:N	12	1.82
(1,131)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:GLN:N	14	1.82
(1,123)	1:71:A:THR:N	1:71:A:THR:CA	1:71:A:THR:C	1:72:A:LEU:N	3	1.8
(1,131)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:GLN:N	4	1.76
(1,70)	1:40:A:TYR:N	1:40:A:TYR:CA	1:40:A:TYR:C	1:41:A:LEU:N	8	1.75
(1,95)	1:57:A:THR:N	1:57:A:THR:CA	1:57:A:THR:C	1:58:A:ARG:N	1	1.73
(1,123)	1:71:A:THR:N	1:71:A:THR:CA	1:71:A:THR:C	1:72:A:LEU:N	11	1.71
(1,207)	1:146:A:GLU:N	1:146:A:GLU:CA	1:146:A:GLU:C	1:147:A:GLN:N	14	1.7
(1,141)	1:80:A:GLY:N	1:80:A:GLY:CA	1:80:A:GLY:C	1:81:A:LEU:N	10	1.65
(1,227)	1:156:A:THR:N	1:156:A:THR:CA	1:156:A:THR:C	1:157:A:GLN:N	2	1.63
(1,131)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:GLN:N	7	1.62
(1,58)	1:34:A:LEU:N	1:34:A:LEU:CA	1:34:A:LEU:C	1:35:A:GLN:N	13	1.6
(1,195)	1:140:A:THR:N	1:140:A:THR:CA	1:140:A:THR:C	1:141:A:LEU:N	18	1.54
(1,157)	1:88:A:GLU:N	1:88:A:GLU:CA	1:88:A:GLU:C	1:89:A:LEU:N	6	1.51
(1,74)	1:42:A:GLN:N	1:42:A:GLN:CA	1:42:A:GLN:C	1:43:A:SER:N	3	1.51
(1,131)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:GLN:N	18	1.5
(1,14)	1:11:A:TRP:N	1:11:A:TRP:CA	1:11:A:TRP:C	1:12:A:GLN:N	17	1.45
(1,95)	1:57:A:THR:N	1:57:A:THR:CA	1:57:A:THR:C	1:58:A:ARG:N	7	1.44
(1,207)	1:146:A:GLU:N	1:146:A:GLU:CA	1:146:A:GLU:C	1:147:A:GLN:N	13	1.43
(1,88)	1:49:A:GLU:N	1:49:A:GLU:CA	1:49:A:GLU:C	1:50:A:LYS:N	9	1.43
(1,193)	1:139:A:GLN:N	1:139:A:GLN:CA	1:139:A:GLN:C	1:140:A:THR:N	16	1.38
(1,123)	1:71:A:THR:N	1:71:A:THR:CA	1:71:A:THR:C	1:72:A:LEU:N	13	1.38
(1,47)	1:27:A:ARG:C	1:28:A:GLY:N	1:28:A:GLY:CA	1:28:A:GLY:C	17	1.37
(1,169)	1:121:A:ASP:N	1:121:A:ASP:CA	1:121:A:ASP:C	1:122:A:MET:N	17	1.36
(1,123)	1:71:A:THR:N	1:71:A:THR:CA	1:71:A:THR:C	1:72:A:LEU:N	12	1.36
(1,195)	1:140:A:THR:N	1:140:A:THR:CA	1:140:A:THR:C	1:141:A:LEU:N	7	1.35
(1,70)	1:40:A:TYR:N	1:40:A:TYR:CA	1:40:A:TYR:C	1:41:A:LEU:N	16	1.35
(1,51)	1:30:A:TRP:C	1:31:A:ASP:N	1:31:A:ASP:CA	1:31:A:ASP:C	2	1.35
(1,157)	1:88:A:GLU:N	1:88:A:GLU:CA	1:88:A:GLU:C	1:89:A:LEU:N	20	1.34
(1,179)	1:132:A:ILE:N	1:132:A:ILE:CA	1:132:A:ILE:C	1:133:A:ASN:N	14	1.33
(1,49)	1:29:A:GLU:C	1:30:A:TRP:N	1:30:A:TRP:CA	1:30:A:TRP:C	1	1.31
(1,141)	1:80:A:GLY:N	1:80:A:GLY:CA	1:80:A:GLY:C	1:81:A:LEU:N	11	1.3
(1,165)	1:92:A:LEU:N	1:92:A:LEU:CA	1:92:A:LEU:C	1:93:A:ILE:N	7	1.27
(1,14)	1:11:A:TRP:N	1:11:A:TRP:CA	1:11:A:TRP:C	1:12:A:GLN:N	13	1.27
(1,123)	1:71:A:THR:N	1:71:A:THR:CA	1:71:A:THR:C	1:72:A:LEU:N	2	1.26
(1,226)	1:155:A:TRP:C	1:156:A:THR:N	1:156:A:THR:CA	1:156:A:THR:C	18	1.25
(1,165)	1:92:A:LEU:N	1:92:A:LEU:CA	1:92:A:LEU:C	1:93:A:ILE:N	11	1.24
(1,131)	1:75:A:GLU:N	1:75:A:GLU:CA	1:75:A:GLU:C	1:76:A:GLN:N	6	1.2
(1,227)	1:156:A:THR:N	1:156:A:THR:CA	1:156:A:THR:C	1:157:A:GLN:N	10	1.18
(1,74)	1:42:A:GLN:N	1:42:A:GLN:CA	1:42:A:GLN:C	1:43:A:SER:N	2	1.18
(1,171)	1:128:A:SER:N	1:128:A:SER:CA	1:128:A:SER:C	1:129:A:ASN:N	3	1.17
(1,169)	1:121:A:ASP:N	1:121:A:ASP:CA	1:121:A:ASP:C	1:122:A:MET:N	15	1.16
(1,47)	1:27:A:ARG:C	1:28:A:GLY:N	1:28:A:GLY:CA	1:28:A:GLY:C	4	1.12
(1,173)	1:129:A:ASN:N	1:129:A:ASN:CA	1:129:A:ASN:C	1:130:A:ARG:N	19	1.11
(1,42)	1:25:A:ALA:N	1:25:A:ALA:CA	1:25:A:ALA:C	1:26:A:GLN:N	18	1.11
(1,86)	1:48:A:MET:N	1:48:A:MET:CA	1:48:A:MET:C	1:49:A:GLU:N	2	1.09
(1,47)	1:27:A:ARG:C	1:28:A:GLY:N	1:28:A:GLY:CA	1:28:A:GLY:C	1	1.09
(1,123)	1:71:A:THR:N	1:71:A:THR:CA	1:71:A:THR:C	1:72:A:LEU:N	16	1.07

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,170)	1:127:A:ALA:C	1:128:A:SER:N	1:128:A:SER:CA	1:128:A:SER:C	12	1.03
(1,143)	1:81:A:LEU:N	1:81:A:LEU:CA	1:81:A:LEU:C	1:82:A:LEU:N	16	1.03
(1,91)	1:53:A:PRO:N	1:53:A:PRO:CA	1:53:A:PRO:C	1:54:A:PRO:N	17	1.02
(1,58)	1:34:A:LEU:N	1:34:A:LEU:CA	1:34:A:LEU:C	1:35:A:GLN:N	19	1.02