



Full wwPDB NMR Structure Validation Report ⓘ

Mar 8, 2026 – 03:39 PM UTC

PDB ID : 9NS0 / pdb_00009ns0
BMRB ID : 31233
Title : Ground state of Src kinase domain
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Deposited on : 2025-03-14

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
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) : 2.49

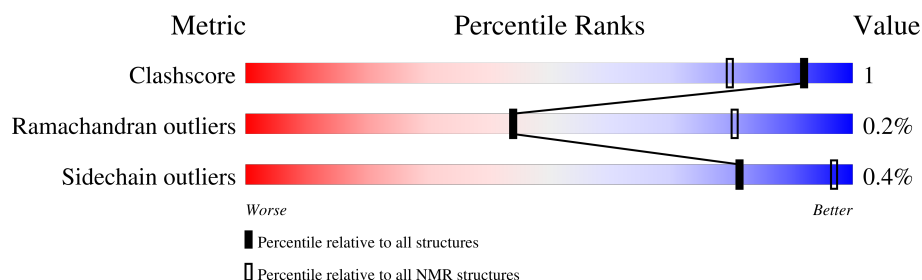
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 44%.

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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	286	

2 Ensemble composition and analysis

This entry contains 20 models. Model 4 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:263-A:414, A:427-A:531 (257)	0.75	4

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

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

The models can be grouped into 3 clusters and 9 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 4584 atoms, of which 2285 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Proto-oncogene tyrosine-protein kinase Src.

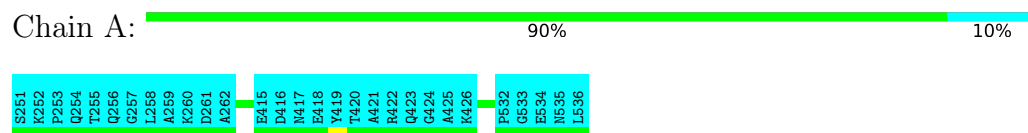
Mol	Chain	Residues	Atoms							Trace
1	A	286	Total	C	H	N	O	P	S	0
			4584	1467	2285	387	428	1	16	

4 Residue-property plots

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: Proto-oncogene tyrosine-protein kinase Src

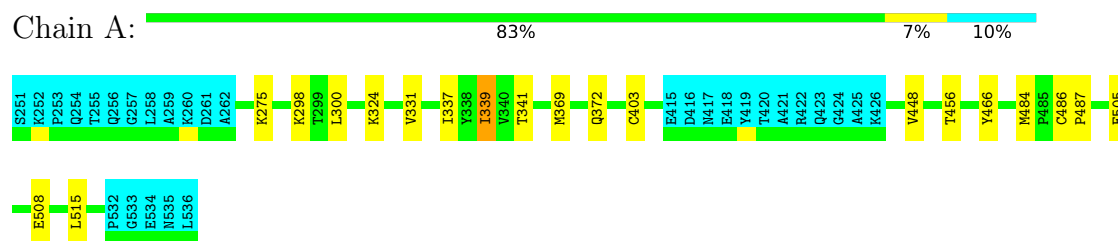


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

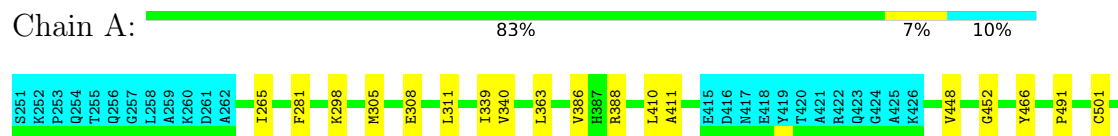
4.2.1 Score per residue for model 1

- Molecule 1: Proto-oncogene tyrosine-protein kinase Src



4.2.2 Score per residue for model 2

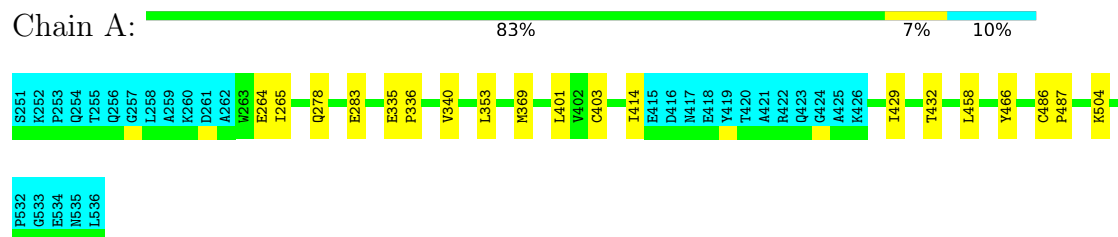
- Molecule 1: Proto-oncogene tyrosine-protein kinase Src





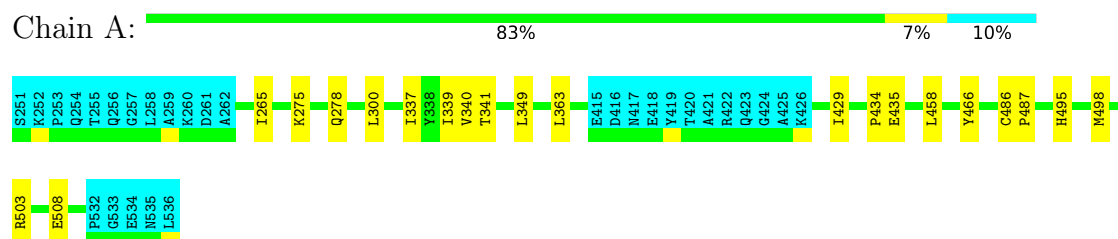
4.2.3 Score per residue for model 3

- Molecule 1: Proto-oncogene tyrosine-protein kinase Src



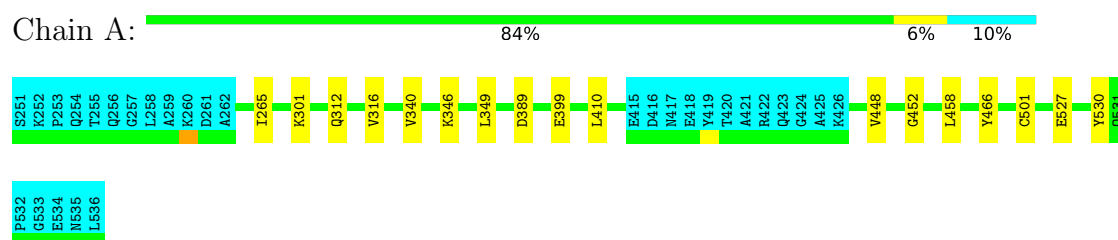
4.2.4 Score per residue for model 4 (medoid)

- Molecule 1: Proto-oncogene tyrosine-protein kinase Src



4.2.5 Score per residue for model 5

- Molecule 1: Proto-oncogene tyrosine-protein kinase Src



4.2.6 Score per residue for model 6

- Molecule 1: Proto-oncogene tyrosine-protein kinase Src

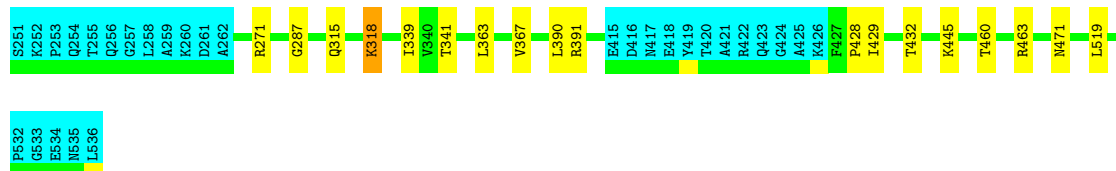




4.2.7 Score per residue for model 7

- Molecule 1: Proto-oncogene tyrosine-protein kinase Src

Chain A: 84% 6% 10%



4.2.8 Score per residue for model 8

- Molecule 1: Proto-oncogene tyrosine-protein kinase Src

Chain A: 84% 6% 10%



4.2.9 Score per residue for model 9

- Molecule 1: Proto-oncogene tyrosine-protein kinase Src

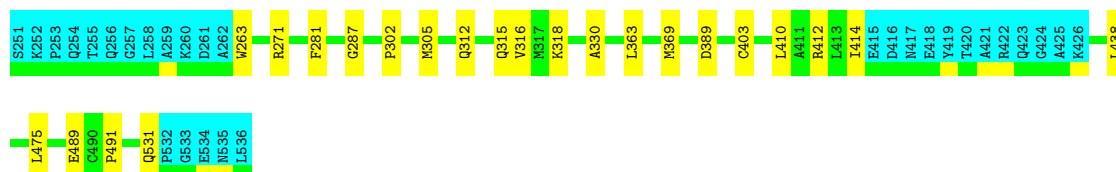
Chain A: 86% 6% 10%



4.2.10 Score per residue for model 10

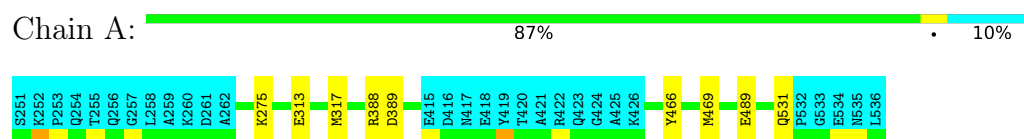
- Molecule 1: Proto-oncogene tyrosine-protein kinase Src

Chain A: 82% 8% 10%



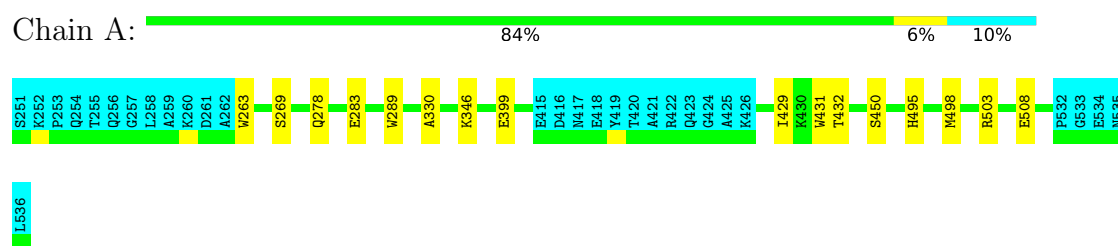
4.2.11 Score per residue for model 11

- Molecule 1: Proto-oncogene tyrosine-protein kinase Src



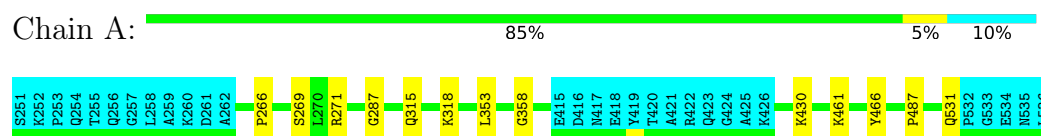
4.2.12 Score per residue for model 12

- Molecule 1: Proto-oncogene tyrosine-protein kinase Src



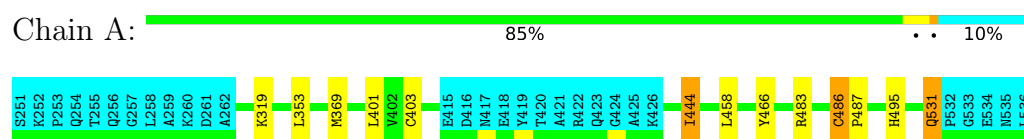
4.2.13 Score per residue for model 13

- Molecule 1: Proto-oncogene tyrosine-protein kinase Src



4.2.14 Score per residue for model 14

- Molecule 1: Proto-oncogene tyrosine-protein kinase Src



4.2.15 Score per residue for model 15

- Molecule 1: Proto-oncogene tyrosine-protein kinase Src





4.2.16 Score per residue for model 16

- Molecule 1: Proto-oncogene tyrosine-protein kinase Src

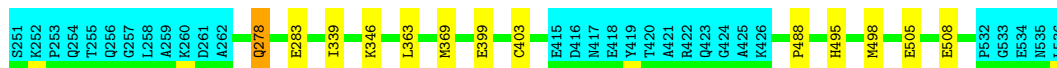
Chain A: 86% 10%



4.2.17 Score per residue for model 17

- Molecule 1: Proto-oncogene tyrosine-protein kinase Src

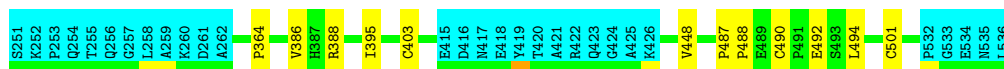
Chain A: 85% 10%



4.2.18 Score per residue for model 18

- Molecule 1: Proto-oncogene tyrosine-protein kinase Src

Chain A: 86% 10%



4.2.19 Score per residue for model 19

- Molecule 1: Proto-oncogene tyrosine-protein kinase Src

Chain A: 87% 10%



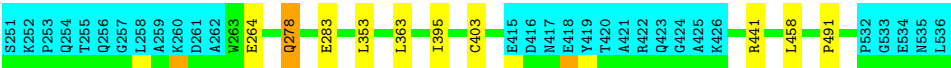
4.2.20 Score per residue for model 20

- Molecule 1: Proto-oncogene tyrosine-protein kinase Src

Chain A:

86%

10%



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	
CYANA	structure calculation	
PSVS	geometry optimization	

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	2
Total number of shifts	2128
Number of shifts mapped to atoms	2128
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	44%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	1.19±0.02	1±1/2129 (0.1± 0.1%)	0.97±0.01	0±0/2888 (0.0± 0.0%)
All	All	1.19	22/42580 (0.1%)	0.97	0/57760 (0.0%)

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	487	PRO	CA-C	8.55	1.56	1.51	14	6
1	A	486	CYS	C-N	6.38	1.39	1.33	3	5
1	A	466	TYR	CA-CB	6.12	1.56	1.52	4	7
1	A	389	ASP	CA-CB	5.64	1.57	1.53	11	1
1	A	339	ILE	CA-CB	5.26	1.59	1.53	1	2
1	A	444	ILE	CA-CB	5.07	1.61	1.54	14	1

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	2076	2077	2076	6±2
All	All	41520	41540	41520	124

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 1.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:461:LYS:HZ2	1:A:461:LYS:HB3	0.58	1.57	9	1
1:A:527:GLU:HB3	1:A:530:TYR:HB2	0.56	1.78	5	3
1:A:315:GLN:HA	1:A:318:LYS:HE2	0.56	1.77	10	3
1:A:363:LEU:HD11	1:A:491:PRO:HG2	0.53	1.80	20	3
1:A:429:ILE:HD11	1:A:434:PRO:HA	0.53	1.81	4	1
1:A:278:GLN:HG3	1:A:283:GLU:HG2	0.53	1.81	12	2
1:A:490:CYS:SG	1:A:494:LEU:HD12	0.52	2.45	18	1
1:A:369:MET:HB3	1:A:403:CYS:SG	0.51	2.46	10	7
1:A:429:ILE:HA	1:A:432:THR:HB	0.50	1.83	12	3
1:A:315:GLN:HA	1:A:318:LYS:HE3	0.50	1.83	7	1
1:A:353:LEU:HA	1:A:358:GLY:HA3	0.49	1.82	13	1
1:A:308:GLU:HA	1:A:311:LEU:HB2	0.49	1.84	2	1
1:A:448:VAL:O	1:A:501:CYS:SG	0.49	2.71	2	3
1:A:431:TRP:O	1:A:450:SER:HB3	0.48	2.09	12	1
1:A:452:GLY:HA3	1:A:501:CYS:SG	0.48	2.48	5	2
1:A:433:ALA:HB1	1:A:509:ARG:NH1	0.48	2.23	9	1
1:A:430:LYS:HD2	1:A:466:TYR:HB2	0.48	1.85	13	1
1:A:265:ILE:HD11	1:A:340:VAL:HG21	0.47	1.84	8	7
1:A:438:LEU:HG	1:A:475:LEU:HD11	0.47	1.86	10	1
1:A:363:LEU:HD11	1:A:491:PRO:HG3	0.47	1.85	16	1
1:A:346:LYS:HE2	1:A:399:GLU:HA	0.46	1.86	5	4
1:A:313:GLU:HG2	1:A:317:MET:SD	0.46	2.50	16	3
1:A:281:PHE:HB3	1:A:305:MET:SD	0.46	2.50	10	1
1:A:275:LYS:HD3	1:A:278:GLN:HB2	0.46	1.86	4	2
1:A:505:GLU:HB2	1:A:508:GLU:HG3	0.45	1.88	1	2
1:A:353:LEU:HD21	1:A:458:LEU:HA	0.45	1.87	20	3
1:A:271:ARG:O	1:A:287:GLY:HA3	0.45	2.11	10	4
1:A:503:ARG:HD3	1:A:508:GLU:HB3	0.45	1.88	12	2
1:A:369:MET:SD	1:A:401:LEU:HD23	0.45	2.51	14	2
1:A:263:TRP:HB3	1:A:330:ALA:HA	0.45	1.87	10	2
1:A:395:ILE:HG21	1:A:403:CYS:SG	0.45	2.52	16	3
1:A:300:LEU:HB3	1:A:337:ILE:HB	0.45	1.87	1	2
1:A:353:LEU:HD23	1:A:461:LYS:HA	0.45	1.87	13	1
1:A:495:HIS:HA	1:A:498:MET:SD	0.45	2.52	4	4
1:A:389:ASP:HB2	1:A:410:LEU:HD12	0.44	1.89	10	2
1:A:388:ARG:HH21	1:A:410:LEU:HD22	0.44	1.72	2	1
1:A:312:GLN:O	1:A:316:VAL:HG23	0.44	2.12	5	2
1:A:460:THR:HB	1:A:463:ARG:HB2	0.44	1.90	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:298:LYS:HB2	1:A:339:ILE:HB	0.43	1.90	2	2
1:A:335:GLU:HB2	1:A:336:PRO:HD3	0.43	1.91	3	1
1:A:386:VAL:HG12	1:A:388:ARG:HG3	0.43	1.89	18	1
1:A:486:CYS:HG	1:A:495:HIS:CG	0.43	2.32	14	1
1:A:278:GLN:HB3	1:A:283:GLU:HA	0.43	1.90	20	2
1:A:324:LYS:HD2	1:A:372:GLN:HB3	0.42	1.91	8	1
1:A:331:VAL:HG12	1:A:339:ILE:HA	0.42	1.91	1	1
1:A:456:THR:HG21	1:A:484:MET:SD	0.42	2.54	1	1
1:A:281:PHE:HD2	1:A:305:MET:SD	0.42	2.37	2	1
1:A:274:VAL:HB	1:A:286:MET:HB3	0.42	1.89	9	1
1:A:315:GLN:HA	1:A:318:LYS:HD3	0.42	1.90	13	1
1:A:324:LYS:HE2	1:A:372:GLN:HB3	0.42	1.91	1	1
1:A:487:PRO:HB2	1:A:490:CYS:HB3	0.42	1.91	18	1
1:A:339:ILE:HG22	1:A:341:THR:HG23	0.42	1.92	7	4
1:A:266:PRO:HG2	1:A:269:SER:HB2	0.42	1.92	13	1
1:A:531:GLN:HE21	1:A:531:GLN:HA	0.42	1.74	14	1
1:A:391:ARG:NH2	1:A:428:PRO:HG3	0.41	2.31	7	1
1:A:323:GLU:HG3	1:A:324:LYS:HG2	0.41	1.93	8	1
1:A:353:LEU:HD21	1:A:458:LEU:HD23	0.41	1.92	6	2
1:A:386:VAL:O	1:A:411:ALA:HA	0.41	2.14	2	1
1:A:503:ARG:NE	1:A:508:GLU:HB3	0.41	2.31	4	1
1:A:367:VAL:HG13	1:A:519:LEU:HD22	0.41	1.92	7	1
1:A:323:GLU:O	1:A:404:LYS:HE2	0.41	2.15	19	1
1:A:429:ILE:HG21	1:A:471:ASN:O	0.41	2.15	7	1
1:A:346:LYS:HD3	1:A:352:PHE:CE1	0.40	2.51	15	1
1:A:448:VAL:HG13	1:A:515:LEU:HD11	0.40	1.92	1	1
1:A:388:ARG:NH2	1:A:410:LEU:HD22	0.40	2.31	2	1
1:A:349:LEU:HD21	1:A:458:LEU:HD21	0.40	1.94	5	2
1:A:466:TYR:HB3	1:A:469:MET:SD	0.40	2.57	11	1
1:A:269:SER:HG	1:A:289:TRP:CD1	0.40	2.35	12	1
1:A:324:LYS:HA	1:A:404:LYS:HG2	0.40	1.93	19	1
1:A:487:PRO:HG3	1:A:492:GLU:HA	0.40	1.94	18	1

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	257/286 (90%)	240±3 (93±1%)	17±3 (7±1%)	1±1 (0±0%)	44	80
All	All	5140/5720 (90%)	4791 (93%)	337 (7%)	12 (0%)	44	80

All 7 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	414	ILE	3
1	A	278	GLN	3
1	A	488	PRO	2
1	A	390	LEU	1
1	A	302	PRO	1
1	A	444	ILE	1
1	A	334	GLU	1

6.3.2 Protein sidechains ⓘ

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	224/245 (91%)	223±1 (100±0%)	1±1 (0±0%)	81	97
All	All	4480/4900 (91%)	4460 (100%)	20 (0%)	81	97

All 12 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	275	LYS	4
1	A	531	GLN	3
1	A	504	LYS	2
1	A	435	GLU	2
1	A	483	ARG	2
1	A	301	LYS	1
1	A	318	LYS	1
1	A	445	LYS	1
1	A	268	GLU	1
1	A	412	ARG	1
1	A	319	LYS	1

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Mol	Chain	Res	Type	Models (Total)
1	A	354	LYS	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
1	PTR	A	419	1	15,16,17	1.01±0.06	0±0 (2±3%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
1	PTR	A	419	1	17,22,24	0.99±0.05	1±0 (6±1%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PTR	A	419	1	-	0±0,10,11,13	0±0,1,1,1

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	419	PTR	P-O2P	2.37	1.46	1.54	18	5
1	A	419	PTR	CB-CA	2.29	1.58	1.53	8	2

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	419	PTR	O2P-P-OH	3.45	115.53	105.32	10	20
1	A	419	PTR	OH-P-O1P	2.09	116.45	109.48	19	1

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 44% for the well-defined parts and 43% 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

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	1172
Number of shifts mapped to atoms	1172
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

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	0	—	None (insufficient data)
$^{13}\text{C}_\beta$	20	—	None (insufficient data)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	203	0.88 ± 0.23	Should be applied

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 30%, i.e. 1093 atoms were assigned a chemical shift out of a possible 3617. 0 out of 47 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	413/1270 (33%)	224/515 (43%)	0/514 (0%)	189/241 (78%)
Sidechain	580/2045 (28%)	435/1333 (33%)	145/634 (23%)	0/78 (0%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	100/302 (33%)	50/146 (34%)	44/146 (30%)	6/10 (60%)
Overall	1093/3617 (30%)	709/1994 (36%)	189/1294 (15%)	195/329 (59%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 29%, i.e. 1167 atoms were assigned a chemical shift out of a possible 3961. 0 out of 49 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	447/1409 (32%)	244/572 (43%)	0/570 (0%)	203/267 (76%)
Sidechain	620/2250 (28%)	465/1462 (32%)	155/699 (22%)	0/89 (0%)
Aromatic	100/302 (33%)	50/146 (34%)	44/146 (30%)	6/10 (60%)
Overall	1167/3961 (29%)	759/2180 (35%)	199/1415 (14%)	209/366 (57%)

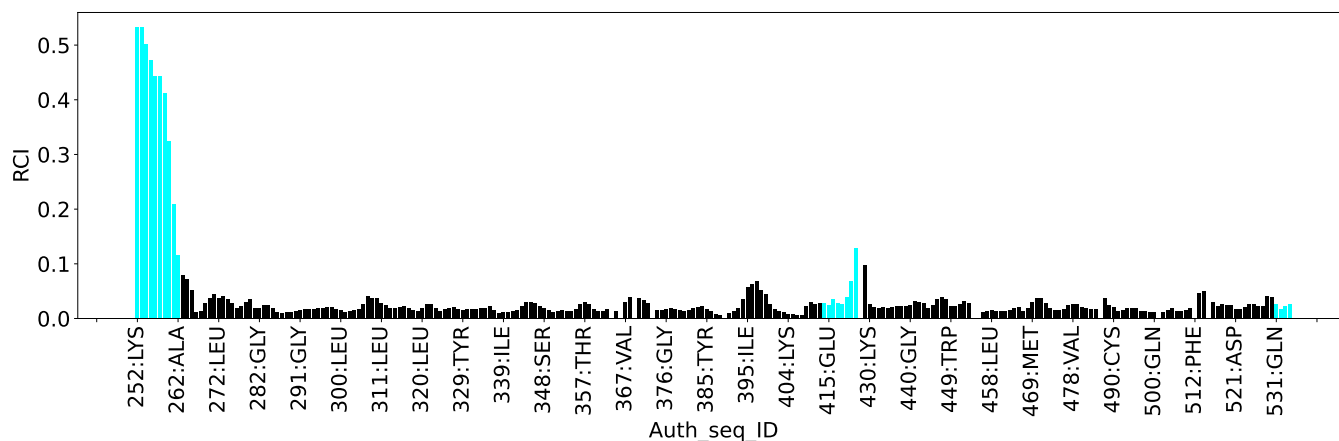
7.1.4 Statistically unusual chemical shifts [i](#)

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:



7.2 Chemical shift list 2

File name: working_cs.cif

Chemical shift list name: *chem_shift_list_2*

7.2.1 Bookkeeping

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

Total number of shifts	956
Number of shifts mapped to atoms	956
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

7.2.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	209	-0.85 ± 0.11	Should be checked
$^{13}\text{C}_\beta$	153	0.43 ± 0.10	None needed (< 0.5 ppm)
$^{13}\text{C}'$	182	-0.23 ± 0.12	None needed (< 0.5 ppm)
^{15}N	199	0.70 ± 0.28	Should be applied

7.2.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 24%, i.e. 885 atoms were assigned a chemical shift out of a possible 3617. 0 out of 47 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	736/1270 (58%)	189/515 (37%)	362/514 (70%)	185/241 (77%)
Sidechain	139/2045 (7%)	0/1333 (0%)	139/634 (22%)	0/78 (0%)
Aromatic	10/302 (3%)	5/146 (3%)	0/146 (0%)	5/10 (50%)
Overall	885/3617 (24%)	194/1994 (10%)	501/1294 (39%)	190/329 (58%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 24%, i.e. 956 atoms were assigned a chemical shift out of a possible 3961. 0 out of 49 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	793/1409 (56%)	203/572 (35%)	391/570 (69%)	199/267 (75%)
Sidechain	153/2250 (7%)	0/1462 (0%)	153/699 (22%)	0/89 (0%)
Aromatic	10/302 (3%)	5/146 (3%)	0/146 (0%)	5/10 (50%)
Overall	956/3961 (24%)	208/2180 (10%)	544/1415 (38%)	204/366 (56%)

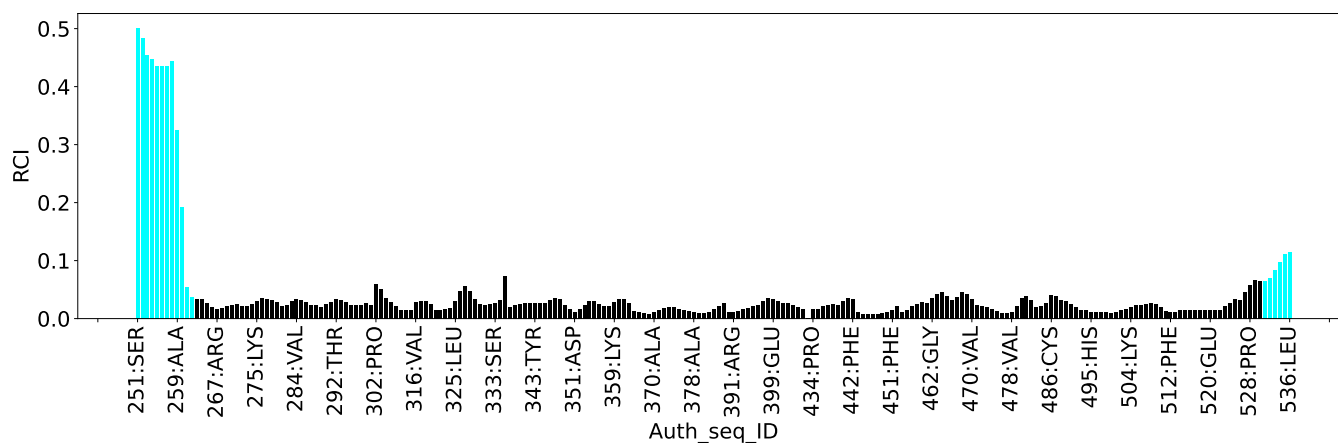
7.2.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

7.2.5 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	1603
Intra-residue ($ i-j =0$)	121
Sequential ($ i-j =1$)	329
Medium range ($ i-j >1$ and $ i-j <5$)	305
Long range ($ i-j \geq 5$)	641
Inter-chain	0
Hydrogen bond restraints	207
Disulfide bond restraints	0
Total dihedral-angle restraints	778
Number of unmapped restraints	0
Number of restraints per residue	8.3
Number of long range restraints per residue ¹	2.5

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

8.2 Residual restraint violations

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

8.2.1 Average number of distance violations per model

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

Bins (Å)	Average number of violations per model	Max (Å)
0.1-0.2 (Small)	19.6	0.2
0.2-0.5 (Medium)	6.0	0.49
>0.5 (Large)	None	None

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

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

Bins (°)	Average number of violations per model	Max (°)
1.0-10.0 (Small)	31.9	8.16
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis ⓘ

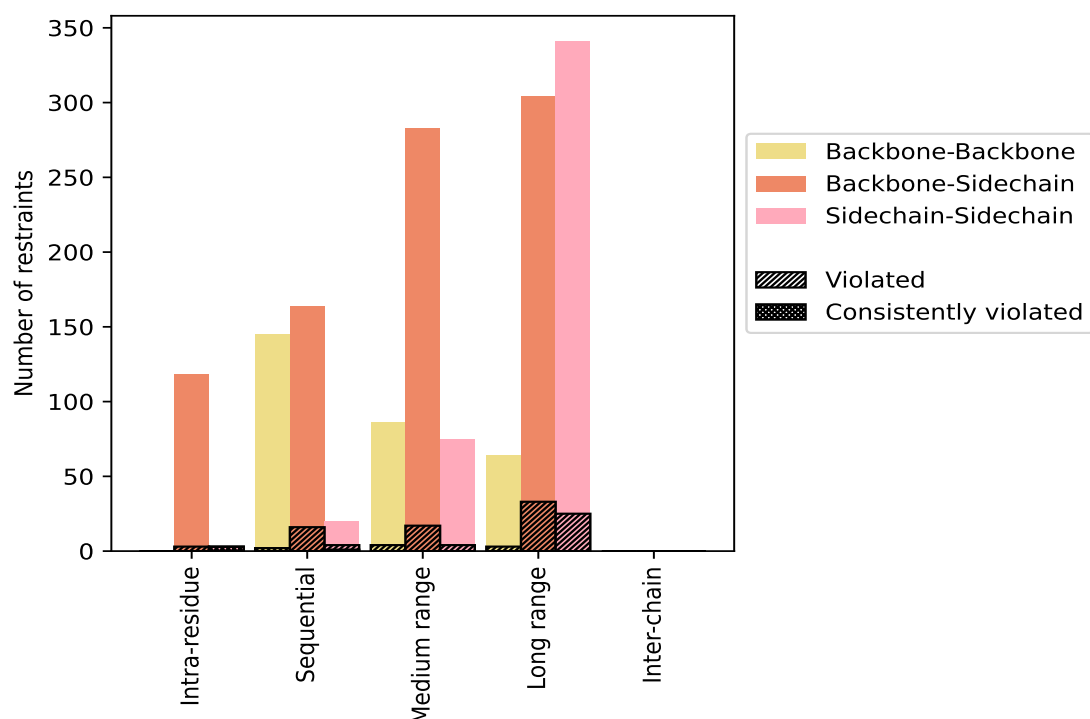
9.1 Summary of distance violations ⓘ

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)	121	7.5	6	5.0	0.4	3	2.5	0.2
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	118	7.4	3	2.5	0.2	0	0.0	0.0
Sidechain-Sidechain	3	0.2	3	100.0	0.2	3	100.0	0.2
Sequential (i-j =1)	329	20.5	22	6.7	1.4	1	0.3	0.1
Backbone-Backbone	145	9.0	2	1.4	0.1	0	0.0	0.0
Backbone-Sidechain	164	10.2	16	9.8	1.0	0	0.0	0.0
Sidechain-Sidechain	20	1.2	4	20.0	0.2	1	5.0	0.1
Medium range (i-j >1 & i-j <5)	305	19.0	18	5.9	1.1	0	0.0	0.0
Backbone-Backbone	86	5.4	4	4.7	0.2	0	0.0	0.0
Backbone-Sidechain	144	9.0	10	6.9	0.6	0	0.0	0.0
Sidechain-Sidechain	75	4.7	4	5.3	0.2	0	0.0	0.0
Long range (i-j ≥5)	641	40.0	57	8.9	3.6	0	0.0	0.0
Backbone-Backbone	64	4.0	3	4.7	0.2	0	0.0	0.0
Backbone-Sidechain	242	15.1	31	12.8	1.9	0	0.0	0.0
Sidechain-Sidechain	335	20.9	23	6.9	1.4	0	0.0	0.0
Inter-chain	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Hydrogen bond	207	12.9	11	5.3	0.7	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	1603	100.0	114	7.1	7.1	4	0.2	0.2
Backbone-Backbone	295	18.4	9	3.1	0.6	0	0.0	0.0
Backbone-Sidechain	869	54.2	69	7.9	4.3	0	0.0	0.0
Sidechain-Sidechain	439	27.4	36	8.2	2.2	4	0.9	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 disulfied bonds are counted in their appropriate category on the x-axis

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

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

Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
1	3	6	5	11	0	25	0.2	0.49	0.12	0.15
2	3	3	8	14	0	28	0.2	0.49	0.13	0.15
3	3	7	6	16	0	32	0.18	0.49	0.11	0.13
4	4	8	7	12	0	31	0.18	0.49	0.11	0.14
5	3	4	5	9	0	21	0.2	0.49	0.12	0.15
6	3	6	5	18	0	32	0.19	0.49	0.1	0.16
7	3	4	4	10	0	21	0.21	0.49	0.12	0.17
8	3	5	6	15	0	29	0.18	0.49	0.11	0.13
9	4	3	4	12	0	23	0.2	0.49	0.12	0.13
10	3	6	6	18	0	33	0.18	0.49	0.11	0.14

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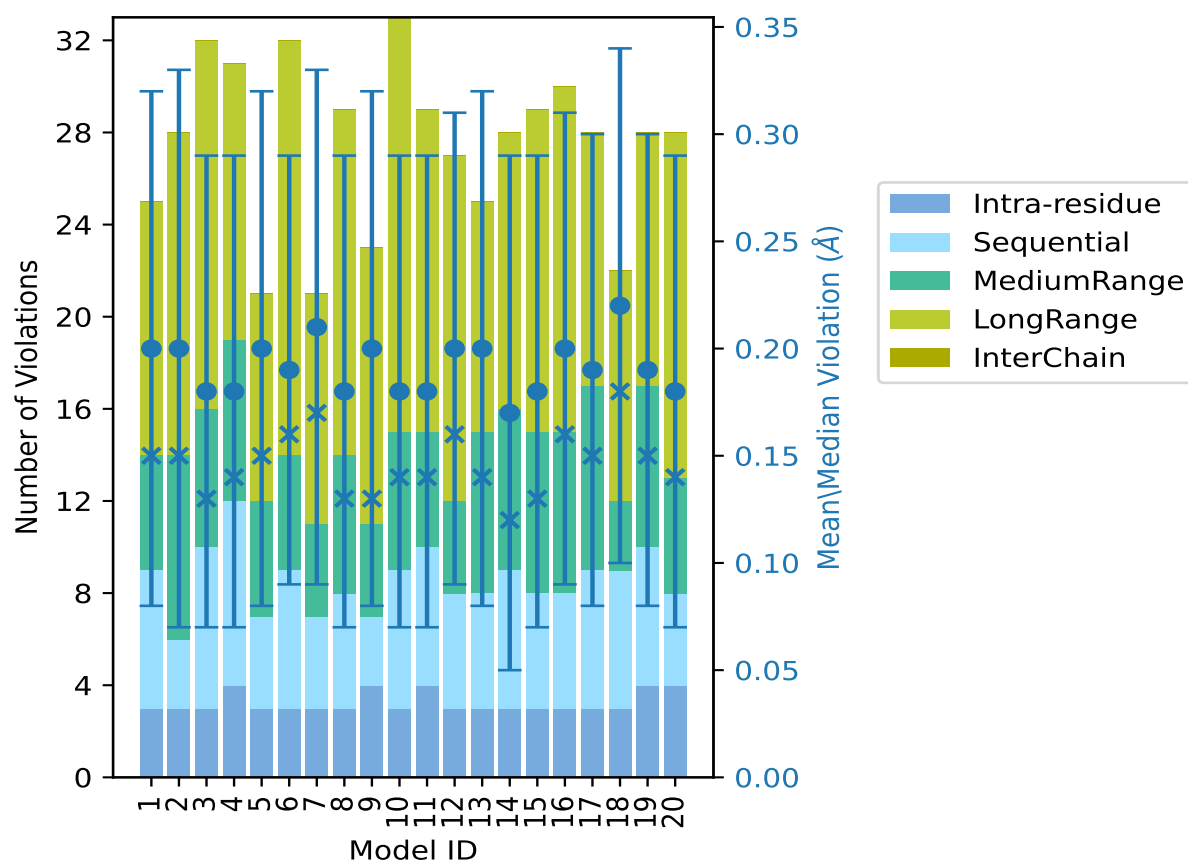
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	4	6	5	14	0	29	0.18	0.49	0.11	0.14
12	3	5	4	15	0	27	0.2	0.49	0.11	0.16
13	3	5	7	10	0	25	0.2	0.49	0.12	0.14
14	3	6	7	12	0	28	0.17	0.49	0.12	0.12
15	3	5	7	14	0	29	0.18	0.49	0.11	0.13
16	3	5	7	15	0	30	0.2	0.49	0.11	0.16
17	3	6	8	11	0	28	0.19	0.49	0.11	0.15
18	3	6	3	10	0	22	0.22	0.49	0.12	0.18
19	4	6	7	11	0	28	0.19	0.49	0.11	0.15
20	4	4	5	15	0	28	0.18	0.49	0.11	0.14

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

⁵Inter-chain restraints, ⁶Standard deviation

9.2.1 Bar graph : Distance Violation statistics for each model ⓘ



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

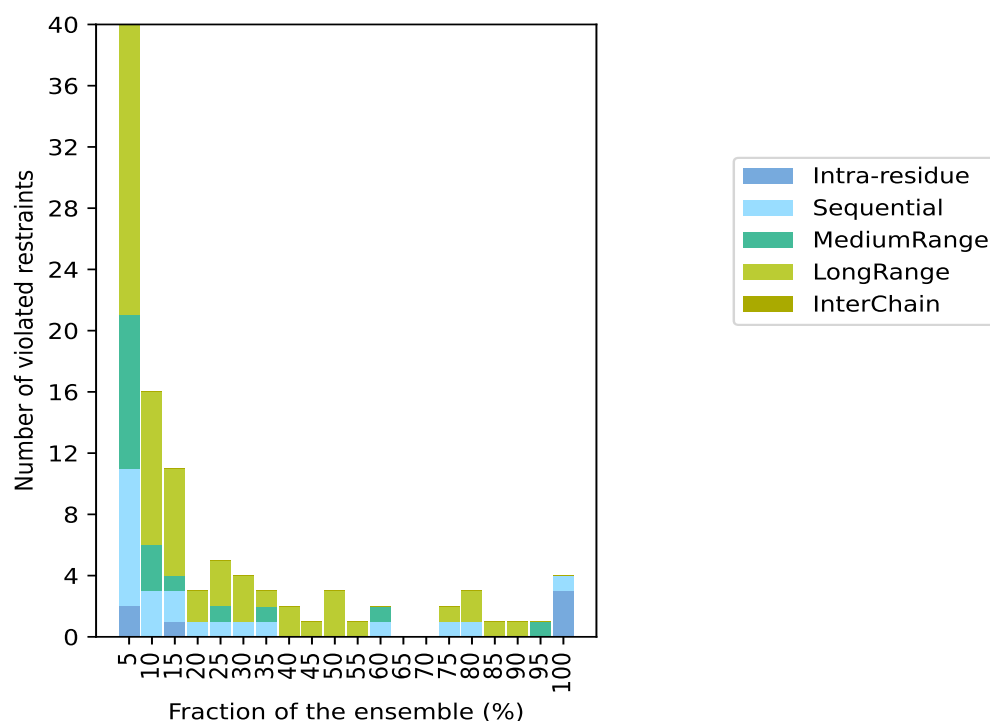
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 1293(IR:115, SQ:307, MR:287, LR:584, IC:0) restraints are 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	%
2	9	10	19	0	40	1	5.0
0	3	3	10	0	16	2	10.0
1	2	1	7	0	11	3	15.0
0	1	0	2	0	3	4	20.0
0	1	1	3	0	5	5	25.0
0	1	0	3	0	4	6	30.0
0	1	1	1	0	3	7	35.0
0	0	0	2	0	2	8	40.0
0	0	0	1	0	1	9	45.0
0	0	0	3	0	3	10	50.0
0	0	0	1	0	1	11	55.0
0	1	1	0	0	2	12	60.0
0	0	0	0	0	0	13	65.0
0	0	0	0	0	0	14	70.0
0	1	0	1	0	2	15	75.0
0	1	0	2	0	3	16	80.0
0	0	0	1	0	1	17	85.0
0	0	0	1	0	1	18	90.0
0	0	1	0	0	1	19	95.0
3	1	0	0	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

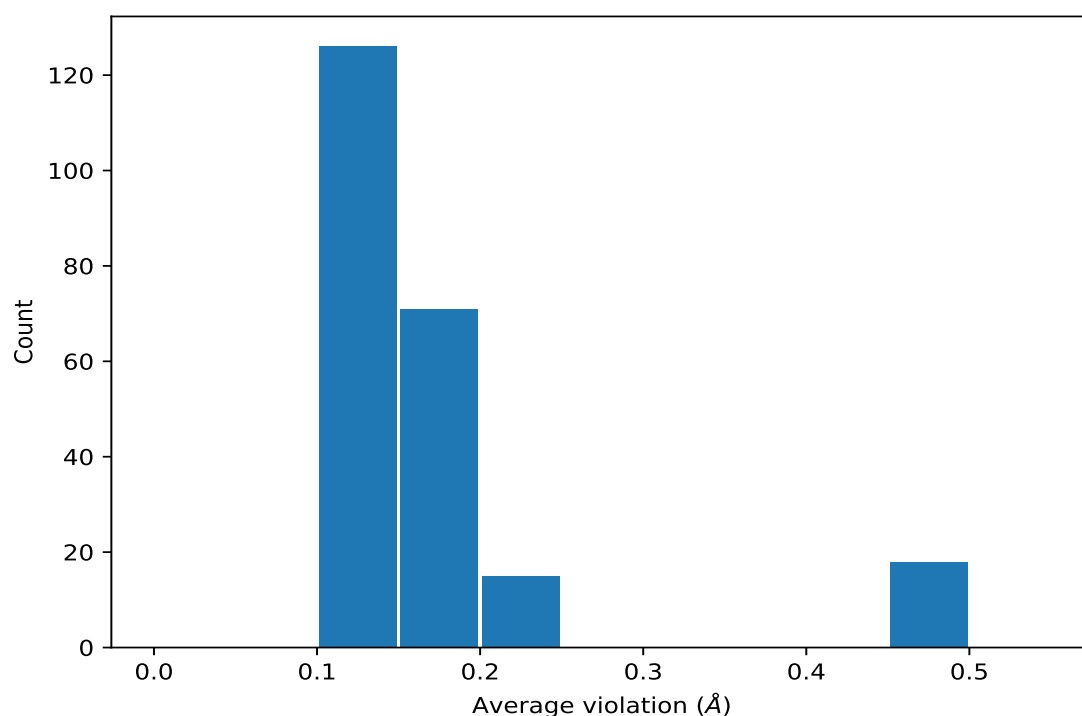
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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)
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB2	20	0.49	0.0	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB3	20	0.49	0.0	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB1	20	0.49	0.0	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB3	20	0.49	0.0	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB1	20	0.49	0.0	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB2	20	0.49	0.0	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB2	20	0.49	0.0	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB3	20	0.49	0.0	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB1	20	0.49	0.0	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB3	20	0.49	0.0	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB1	20	0.49	0.0	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB2	20	0.49	0.0	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD22	20	0.49	0.0	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD23	20	0.49	0.0	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD21	20	0.49	0.0	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD23	20	0.49	0.0	0.49

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD21	20	0.49	0.0	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD22	20	0.49	0.0	0.49
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD11	20	0.24	0.06	0.25
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD12	20	0.24	0.06	0.25
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD13	20	0.24	0.06	0.25
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD11	19	0.16	0.04	0.16
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD12	19	0.16	0.04	0.16
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD13	19	0.16	0.04	0.16
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD11	19	0.16	0.04	0.16
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD12	19	0.16	0.04	0.16
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD13	19	0.16	0.04	0.16
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD11	19	0.16	0.04	0.16
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD12	19	0.16	0.04	0.16
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD13	19	0.16	0.04	0.16
(1,1363)	1:295:A:VAL:HG21	1:340:A:VAL:H	18	0.14	0.02	0.14
(1,1363)	1:295:A:VAL:HG22	1:340:A:VAL:H	18	0.14	0.02	0.14
(1,1363)	1:295:A:VAL:HG23	1:340:A:VAL:H	18	0.14	0.02	0.14
(2,122)	1:518:A:PHE:O	1:522:A:TYR:H	18	0.14	0.02	0.15
(1,405)	1:286:A:MET:HE1	1:295:A:VAL:H	17	0.16	0.04	0.16
(1,405)	1:286:A:MET:HE2	1:295:A:VAL:H	17	0.16	0.04	0.16
(1,405)	1:286:A:MET:HE3	1:295:A:VAL:H	17	0.16	0.04	0.16
(1,949)	1:410:A:LEU:HD21	1:419:A:PTR:HE1	16	0.22	0.08	0.22
(1,949)	1:410:A:LEU:HD22	1:419:A:PTR:HE1	16	0.22	0.08	0.22
(1,949)	1:410:A:LEU:HD23	1:419:A:PTR:HE1	16	0.22	0.08	0.22
(1,965)	1:455:A:LEU:HD11	1:518:A:PHE:HE1	16	0.16	0.04	0.16
(1,965)	1:455:A:LEU:HD12	1:518:A:PHE:HE1	16	0.16	0.04	0.16
(1,965)	1:455:A:LEU:HD13	1:518:A:PHE:HE1	16	0.16	0.04	0.16
(1,642)	1:438:A:LEU:HD21	1:439:A:TYR:HE1	16	0.15	0.03	0.14
(1,642)	1:438:A:LEU:HD22	1:439:A:TYR:HE1	16	0.15	0.03	0.14
(1,642)	1:438:A:LEU:HD23	1:439:A:TYR:HE1	16	0.15	0.03	0.14
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD11	15	0.17	0.04	0.17
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD12	15	0.17	0.04	0.17
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD13	15	0.17	0.04	0.17
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD11	15	0.15	0.04	0.15
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD12	15	0.15	0.04	0.15
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD13	15	0.15	0.04	0.15
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD11	15	0.15	0.04	0.15
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD12	15	0.15	0.04	0.15
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD13	15	0.15	0.04	0.15
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD11	15	0.15	0.04	0.15
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD12	15	0.15	0.04	0.15
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD13	15	0.15	0.04	0.15

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(2,21)	1:364:A:PRO:O	1:368:A:ASP:N	15	0.11	0.01	0.11
(2,201)	1:389:A:ASP:N	1:387:A:HIS:ND1	13	0.13	0.02	0.13
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD11	12	0.16	0.06	0.15
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD12	12	0.16	0.06	0.15
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD13	12	0.16	0.06	0.15
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG11	12	0.13	0.03	0.13
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG12	12	0.13	0.03	0.13
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG13	12	0.13	0.03	0.13
(1,864)	1:297:A:ILE:HD11	1:338:A:TYR:HE2	11	0.14	0.03	0.14
(1,864)	1:297:A:ILE:HD12	1:338:A:TYR:HE2	11	0.14	0.03	0.14
(1,864)	1:297:A:ILE:HD13	1:338:A:TYR:HE2	11	0.14	0.03	0.14
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD21	10	0.17	0.05	0.16
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD22	10	0.17	0.05	0.16
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD23	10	0.17	0.05	0.16
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD11	10	0.16	0.03	0.16
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD12	10	0.16	0.03	0.16
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD13	10	0.16	0.03	0.16
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD11	10	0.16	0.03	0.16
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD12	10	0.16	0.03	0.16
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD13	10	0.16	0.03	0.16
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD11	10	0.16	0.03	0.16
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD12	10	0.16	0.03	0.16
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD13	10	0.16	0.03	0.16
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD11	10	0.14	0.03	0.14
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD12	10	0.14	0.03	0.14
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD13	10	0.14	0.03	0.14
(1,543)	1:363:A:LEU:HD21	1:523:A:PHE:HE1	9	0.18	0.06	0.18
(1,543)	1:363:A:LEU:HD22	1:523:A:PHE:HE1	9	0.18	0.06	0.18
(1,543)	1:363:A:LEU:HD23	1:523:A:PHE:HE1	9	0.18	0.06	0.18
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE1	8	0.16	0.06	0.12
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE2	8	0.16	0.06	0.12
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE3	8	0.16	0.06	0.12
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE1	8	0.16	0.06	0.12
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE2	8	0.16	0.06	0.12
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE3	8	0.16	0.06	0.12
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE1	8	0.16	0.06	0.12
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE2	8	0.16	0.06	0.12
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE3	8	0.16	0.06	0.12
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD21	8	0.14	0.02	0.14
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD22	8	0.14	0.02	0.14
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD23	8	0.14	0.02	0.14
(1,544)	1:363:A:LEU:HD21	1:530:A:TYR:HE1	7	0.22	0.06	0.23

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,544)	1:363:A:LEU:HD22	1:530:A:TYR:HE1	7	0.22	0.06	0.23
(1,544)	1:363:A:LEU:HD23	1:530:A:TYR:HE1	7	0.22	0.06	0.23
(1,699)	1:478:A:VAL:HG11	1:482:A:TYR:H	7	0.14	0.02	0.14
(1,699)	1:478:A:VAL:HG12	1:482:A:TYR:H	7	0.14	0.02	0.14
(1,699)	1:478:A:VAL:HG13	1:482:A:TYR:H	7	0.14	0.02	0.14
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD21	7	0.14	0.02	0.14
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD22	7	0.14	0.02	0.14
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD23	7	0.14	0.02	0.14
(1,708)	1:466:A:TYR:HE2	1:484:A:MET:HE1	6	0.16	0.04	0.16
(1,708)	1:466:A:TYR:HE2	1:484:A:MET:HE2	6	0.16	0.04	0.16
(1,708)	1:466:A:TYR:HE2	1:484:A:MET:HE3	6	0.16	0.04	0.16
(1,390)	1:272:A:LEU:HD11	1:285:A:TRP:HE1	6	0.15	0.03	0.15
(1,390)	1:272:A:LEU:HD12	1:285:A:TRP:HE1	6	0.15	0.03	0.15
(1,390)	1:272:A:LEU:HD13	1:285:A:TRP:HE1	6	0.15	0.03	0.15
(1,1054)	1:361:A:LEU:HD21	1:362:A:ARG:H	6	0.12	0.02	0.12
(1,1054)	1:361:A:LEU:HD22	1:362:A:ARG:H	6	0.12	0.02	0.12
(1,1054)	1:361:A:LEU:HD23	1:362:A:ARG:H	6	0.12	0.02	0.12
(1,577)	1:344:A:MET:H	1:396:A:LEU:HD21	6	0.11	0.01	0.12
(1,577)	1:344:A:MET:H	1:396:A:LEU:HD22	6	0.11	0.01	0.12
(1,577)	1:344:A:MET:H	1:396:A:LEU:HD23	6	0.11	0.01	0.12
(1,606)	1:410:A:LEU:HD11	1:411:A:ALA:H	5	0.15	0.05	0.13
(1,606)	1:410:A:LEU:HD12	1:411:A:ALA:H	5	0.15	0.05	0.13
(1,606)	1:410:A:LEU:HD13	1:411:A:ALA:H	5	0.15	0.05	0.13
(1,592)	1:398:A:GLY:H	1:402:A:VAL:HG21	5	0.14	0.02	0.14
(1,592)	1:398:A:GLY:H	1:402:A:VAL:HG22	5	0.14	0.02	0.14
(1,592)	1:398:A:GLY:H	1:402:A:VAL:HG23	5	0.14	0.02	0.14
(1,512)	1:298:A:LYS:H	1:340:A:VAL:HG21	5	0.13	0.02	0.13
(1,512)	1:298:A:LYS:H	1:340:A:VAL:HG22	5	0.13	0.02	0.13
(1,512)	1:298:A:LYS:H	1:340:A:VAL:HG23	5	0.13	0.02	0.13
(1,1282)	1:431:A:TRP:HE1	1:454:A:LEU:HD11	5	0.13	0.02	0.12
(1,1282)	1:431:A:TRP:HE1	1:454:A:LEU:HD12	5	0.13	0.02	0.12
(1,1282)	1:431:A:TRP:HE1	1:454:A:LEU:HD13	5	0.13	0.02	0.12
(2,94)	1:476:A:ASP:O	1:480:A:ARG:H	5	0.11	0.01	0.11
(1,1071)	1:270:A:LEU:HD11	1:339:A:ILE:H	5	0.11	0.01	0.11
(1,1071)	1:270:A:LEU:HD12	1:339:A:ILE:H	5	0.11	0.01	0.11
(1,1071)	1:270:A:LEU:HD13	1:339:A:ILE:H	5	0.11	0.01	0.11
(1,254)	1:386:A:VAL:HG11	1:414:A:ILE:HD11	4	0.18	0.06	0.17
(1,254)	1:386:A:VAL:HG11	1:414:A:ILE:HD12	4	0.18	0.06	0.17
(1,254)	1:386:A:VAL:HG11	1:414:A:ILE:HD13	4	0.18	0.06	0.17
(1,254)	1:386:A:VAL:HG12	1:414:A:ILE:HD11	4	0.18	0.06	0.17
(1,254)	1:386:A:VAL:HG12	1:414:A:ILE:HD12	4	0.18	0.06	0.17
(1,254)	1:386:A:VAL:HG12	1:414:A:ILE:HD13	4	0.18	0.06	0.17

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,254)	1:386:A:VAL:HG13	1:414:A:ILE:HD11	4	0.18	0.06	0.17
(1,254)	1:386:A:VAL:HG13	1:414:A:ILE:HD12	4	0.18	0.06	0.17
(1,254)	1:386:A:VAL:HG13	1:414:A:ILE:HD13	4	0.18	0.06	0.17
(1,617)	1:414:A:ILE:HD11	1:444:A:ILE:HD11	4	0.15	0.03	0.14
(1,617)	1:414:A:ILE:HD11	1:444:A:ILE:HD12	4	0.15	0.03	0.14
(1,617)	1:414:A:ILE:HD11	1:444:A:ILE:HD13	4	0.15	0.03	0.14
(1,617)	1:414:A:ILE:HD12	1:444:A:ILE:HD11	4	0.15	0.03	0.14
(1,617)	1:414:A:ILE:HD12	1:444:A:ILE:HD12	4	0.15	0.03	0.14
(1,617)	1:414:A:ILE:HD12	1:444:A:ILE:HD13	4	0.15	0.03	0.14
(1,617)	1:414:A:ILE:HD13	1:444:A:ILE:HD11	4	0.15	0.03	0.14
(1,617)	1:414:A:ILE:HD13	1:444:A:ILE:HD12	4	0.15	0.03	0.14
(1,617)	1:414:A:ILE:HD13	1:444:A:ILE:HD13	4	0.15	0.03	0.14
(1,782)	1:469:A:MET:HE1	1:470:A:VAL:H	4	0.11	0.01	0.11
(1,782)	1:469:A:MET:HE2	1:470:A:VAL:H	4	0.11	0.01	0.11
(1,782)	1:469:A:MET:HE3	1:470:A:VAL:H	4	0.11	0.01	0.11
(1,29)	1:284:A:VAL:H	1:285:A:TRP:HE1	3	0.16	0.04	0.14
(1,803)	1:421:A:ALA:HB1	1:427:A:PHE:HE1	3	0.15	0.02	0.17
(1,803)	1:421:A:ALA:HB2	1:427:A:PHE:HE1	3	0.15	0.02	0.17
(1,803)	1:421:A:ALA:HB3	1:427:A:PHE:HE1	3	0.15	0.02	0.17
(1,950)	1:419:A:PTR:HE1	1:420:A:THR:H	3	0.15	0.04	0.13
(1,614)	1:386:A:VAL:H	1:414:A:ILE:HD11	3	0.14	0.02	0.14
(1,614)	1:386:A:VAL:H	1:414:A:ILE:HD12	3	0.14	0.02	0.14
(1,614)	1:386:A:VAL:H	1:414:A:ILE:HD13	3	0.14	0.02	0.14
(1,956)	1:419:A:PTR:H	1:419:A:PTR:HE2	3	0.13	0.02	0.13
(1,1210)	1:410:A:LEU:HD21	1:425:A:ALA:H	3	0.13	0.01	0.13
(1,1210)	1:410:A:LEU:HD22	1:425:A:ALA:H	3	0.13	0.01	0.13
(1,1210)	1:410:A:LEU:HD23	1:425:A:ALA:H	3	0.13	0.01	0.13
(1,1288)	1:271:A:ARG:H	1:290:A:ASN:H	3	0.12	0.01	0.13
(1,1403)	1:366:A:LEU:HD11	1:461:A:LYS:H	3	0.12	0.01	0.12
(1,1403)	1:366:A:LEU:HD12	1:461:A:LYS:H	3	0.12	0.01	0.12
(1,1403)	1:366:A:LEU:HD13	1:461:A:LYS:H	3	0.12	0.01	0.12
(1,959)	1:289:A:TRP:H	1:329:A:TYR:HE2	3	0.12	0.01	0.13
(1,1408)	1:466:A:TYR:H	1:469:A:MET:HE1	3	0.12	0.01	0.12
(1,1408)	1:466:A:TYR:H	1:469:A:MET:HE2	3	0.12	0.01	0.12
(1,1408)	1:466:A:TYR:H	1:469:A:MET:HE3	3	0.12	0.01	0.12
(1,524)	1:344:A:MET:HE1	1:397:A:VAL:H	3	0.11	0.01	0.12
(1,524)	1:344:A:MET:HE2	1:397:A:VAL:H	3	0.11	0.01	0.12
(1,524)	1:344:A:MET:HE3	1:397:A:VAL:H	3	0.11	0.01	0.12
(1,1372)	1:349:A:LEU:H	1:369:A:MET:HE1	2	0.22	0.01	0.22
(1,1372)	1:349:A:LEU:H	1:369:A:MET:HE2	2	0.22	0.01	0.22
(1,1372)	1:349:A:LEU:H	1:369:A:MET:HE3	2	0.22	0.01	0.22
(1,749)	1:469:A:MET:HE1	1:477:A:GLN:H	2	0.21	0.06	0.21

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,749)	1:469:A:MET:HE2	1:477:A:GLN:H	2	0.21	0.06	0.21
(1,749)	1:469:A:MET:HE3	1:477:A:GLN:H	2	0.21	0.06	0.21
(1,754)	1:259:A:ALA:HB1	1:261:A:ASP:H	2	0.18	0.07	0.18
(1,754)	1:259:A:ALA:HB2	1:261:A:ASP:H	2	0.18	0.07	0.18
(1,754)	1:259:A:ALA:HB3	1:261:A:ASP:H	2	0.18	0.07	0.18
(1,548)	1:371:A:ALA:HB1	1:521:A:ASP:H	2	0.16	0.04	0.16
(1,548)	1:371:A:ALA:HB2	1:521:A:ASP:H	2	0.16	0.04	0.16
(1,548)	1:371:A:ALA:HB3	1:521:A:ASP:H	2	0.16	0.04	0.16
(1,780)	1:436:A:ALA:HB1	1:442:A:PHE:HE1	2	0.16	0.05	0.16
(1,780)	1:436:A:ALA:HB2	1:442:A:PHE:HE1	2	0.16	0.05	0.16
(1,780)	1:436:A:ALA:HB3	1:442:A:PHE:HE1	2	0.16	0.05	0.16
(1,1268)	1:262:A:ALA:H	1:264:A:GLU:H	2	0.16	0.04	0.16
(1,1302)	1:283:A:GLU:H	1:299:A:THR:HG21	2	0.16	0.04	0.16
(1,1302)	1:283:A:GLU:H	1:299:A:THR:HG22	2	0.16	0.04	0.16
(1,1302)	1:283:A:GLU:H	1:299:A:THR:HG23	2	0.16	0.04	0.16
(1,973)	1:259:A:ALA:HB1	1:260:A:LYS:H	2	0.15	0.03	0.15
(1,973)	1:259:A:ALA:HB2	1:260:A:LYS:H	2	0.15	0.03	0.15
(1,973)	1:259:A:ALA:HB3	1:260:A:LYS:H	2	0.15	0.03	0.15
(1,940)	1:426:A:LYS:H	1:427:A:PHE:HE1	2	0.14	0.03	0.14
(1,893)	1:367:A:VAL:HG21	1:523:A:PHE:HE2	2	0.14	0.01	0.14
(1,893)	1:367:A:VAL:HG22	1:523:A:PHE:HE2	2	0.14	0.01	0.14
(1,893)	1:367:A:VAL:HG23	1:523:A:PHE:HE2	2	0.14	0.01	0.14
(1,1393)	1:369:A:MET:HE1	1:403:A:CYS:H	2	0.14	0.0	0.14
(1,1393)	1:369:A:MET:HE2	1:403:A:CYS:H	2	0.14	0.0	0.14
(1,1393)	1:369:A:MET:HE3	1:403:A:CYS:H	2	0.14	0.0	0.14
(1,393)	1:273:A:GLU:H	1:274:A:VAL:HG21	2	0.12	0.02	0.12
(1,393)	1:273:A:GLU:H	1:274:A:VAL:HG22	2	0.12	0.02	0.12
(1,393)	1:273:A:GLU:H	1:274:A:VAL:HG23	2	0.12	0.02	0.12
(1,580)	1:347:A:GLY:H	1:396:A:LEU:HD21	2	0.12	0.02	0.12
(1,580)	1:347:A:GLY:H	1:396:A:LEU:HD22	2	0.12	0.02	0.12
(1,580)	1:347:A:GLY:H	1:396:A:LEU:HD23	2	0.12	0.02	0.12
(1,1355)	1:497:A:LEU:H	1:522:A:TYR:HE1	2	0.12	0.02	0.12
(1,728)	1:512:A:PHE:HE1	1:515:A:LEU:HD21	2	0.12	0.0	0.12
(1,728)	1:512:A:PHE:HE1	1:515:A:LEU:HD22	2	0.12	0.0	0.12
(1,728)	1:512:A:PHE:HE1	1:515:A:LEU:HD23	2	0.12	0.0	0.12
(1,111)	1:265:A:ILE:HD11	1:340:A:VAL:HG21	2	0.11	0.0	0.11
(1,111)	1:265:A:ILE:HD11	1:340:A:VAL:HG22	2	0.11	0.0	0.11
(1,111)	1:265:A:ILE:HD11	1:340:A:VAL:HG23	2	0.11	0.0	0.11
(1,111)	1:265:A:ILE:HD12	1:340:A:VAL:HG21	2	0.11	0.0	0.11
(1,111)	1:265:A:ILE:HD12	1:340:A:VAL:HG22	2	0.11	0.0	0.11
(1,111)	1:265:A:ILE:HD12	1:340:A:VAL:HG23	2	0.11	0.0	0.11
(1,111)	1:265:A:ILE:HD13	1:340:A:VAL:HG21	2	0.11	0.0	0.11

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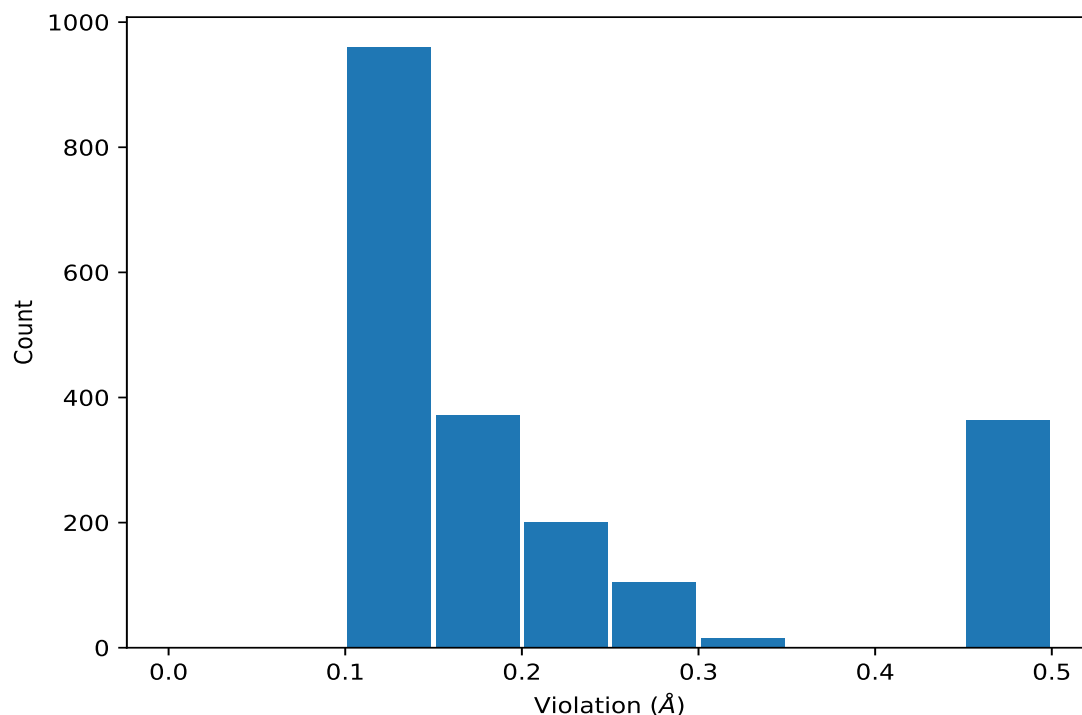
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,111)	1:265:A:ILE:HD13	1:340:A:VAL:HG22	2	0.11	0.0	0.11
(1,111)	1:265:A:ILE:HD13	1:340:A:VAL:HG23	2	0.11	0.0	0.11
(2,203)	1:394:A:ASN:OD1	1:407:A:ASP:OD2	2	0.11	0.0	0.11
(2,207)	1:264:A:GLU:OE1	1:333:A:SER:OG	2	0.11	0.0	0.11

¹Number of violated models, ²Standard deviation

9.5 All violated distance restraints [i](#)

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

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



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

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

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD22	1	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD23	1	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD21	1	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD23	1	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD21	1	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD22	1	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD22	2	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD23	2	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD21	2	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD23	2	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD21	2	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD22	2	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD22	3	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD23	3	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD21	3	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD23	3	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD21	3	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD22	3	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD22	4	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD23	4	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD21	4	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD23	4	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD21	4	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD22	4	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD22	5	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD23	5	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD21	5	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD23	5	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD21	5	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD22	5	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD22	6	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD23	6	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD21	6	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD23	6	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD21	6	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD22	6	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD22	7	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD23	7	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD21	7	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD23	7	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD21	7	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD22	7	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD22	8	0.49

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD23	8	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD21	8	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD23	8	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD21	8	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD22	8	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD22	9	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD23	9	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD21	9	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD23	9	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD21	9	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD22	9	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD22	10	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD23	10	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD21	10	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD23	10	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD21	10	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD22	10	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD22	11	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD23	11	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD21	11	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD23	11	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD21	11	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD22	11	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD22	12	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD23	12	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD21	12	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD23	12	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD21	12	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD22	12	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD22	13	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD23	13	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD21	13	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD23	13	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD21	13	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD22	13	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD22	14	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD23	14	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD21	14	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD23	14	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD21	14	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD22	14	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD22	15	0.49

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD23	15	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD21	15	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD23	15	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD21	15	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD22	15	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD22	16	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD23	16	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD21	16	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD23	16	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD21	16	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD22	16	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD22	17	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD23	17	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD21	17	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD23	17	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD21	17	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD22	17	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD22	18	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD23	18	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD21	18	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD23	18	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD21	18	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD22	18	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD22	19	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD23	19	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD21	19	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD23	19	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD21	19	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD22	19	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD22	20	0.49
(1,320)	1:497:A:LEU:HD21	1:497:A:LEU:HD23	20	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD21	20	0.49
(1,320)	1:497:A:LEU:HD22	1:497:A:LEU:HD23	20	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD21	20	0.49
(1,320)	1:497:A:LEU:HD23	1:497:A:LEU:HD22	20	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB2	1	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB3	1	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB1	1	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB3	1	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB1	1	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB2	1	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB2	2	0.49

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB3	2	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB1	2	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB3	2	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB1	2	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB2	2	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB2	3	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB3	3	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB1	3	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB3	3	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB1	3	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB2	3	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB2	4	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB3	4	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB1	4	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB3	4	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB1	4	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB2	4	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB2	5	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB3	5	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB1	5	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB3	5	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB1	5	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB2	5	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB2	6	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB3	6	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB1	6	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB3	6	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB1	6	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB2	6	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB2	7	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB3	7	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB1	7	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB3	7	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB1	7	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB2	7	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB2	8	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB3	8	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB1	8	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB3	8	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB1	8	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB2	8	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB2	9	0.49

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB3	9	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB1	9	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB3	9	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB1	9	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB2	9	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB2	10	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB3	10	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB1	10	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB3	10	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB1	10	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB2	10	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB2	11	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB3	11	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB1	11	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB3	11	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB1	11	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB2	11	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB2	12	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB3	12	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB1	12	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB3	12	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB1	12	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB2	12	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB2	13	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB3	13	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB1	13	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB3	13	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB1	13	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB2	13	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB2	14	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB3	14	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB1	14	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB3	14	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB1	14	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB2	14	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB2	15	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB3	15	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB1	15	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB3	15	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB1	15	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB2	15	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB2	16	0.49

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB3	16	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB1	16	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB3	16	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB1	16	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB2	16	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB2	17	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB3	17	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB1	17	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB3	17	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB1	17	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB2	17	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB2	18	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB3	18	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB1	18	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB3	18	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB1	18	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB2	18	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB2	19	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB3	19	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB1	19	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB3	19	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB1	19	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB2	19	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB2	20	0.49
(1,263)	1:436:A:ALA:HB1	1:436:A:ALA:HB3	20	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB1	20	0.49
(1,263)	1:436:A:ALA:HB2	1:436:A:ALA:HB3	20	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB1	20	0.49
(1,263)	1:436:A:ALA:HB3	1:436:A:ALA:HB2	20	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB2	1	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB3	1	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB1	1	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB3	1	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB1	1	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB2	1	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB2	2	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB3	2	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB1	2	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB3	2	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB1	2	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB2	2	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB2	3	0.49

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB3	3	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB1	3	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB3	3	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB1	3	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB2	3	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB2	4	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB3	4	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB1	4	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB3	4	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB1	4	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB2	4	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB2	5	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB3	5	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB1	5	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB3	5	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB1	5	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB2	5	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB2	6	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB3	6	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB1	6	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB3	6	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB1	6	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB2	6	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB2	7	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB3	7	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB1	7	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB3	7	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB1	7	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB2	7	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB2	8	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB3	8	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB1	8	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB3	8	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB1	8	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB2	8	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB2	9	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB3	9	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB1	9	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB3	9	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB1	9	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB2	9	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB2	10	0.49

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB3	10	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB1	10	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB3	10	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB1	10	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB2	10	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB2	11	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB3	11	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB1	11	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB3	11	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB1	11	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB2	11	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB2	12	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB3	12	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB1	12	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB3	12	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB1	12	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB2	12	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB2	13	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB3	13	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB1	13	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB3	13	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB1	13	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB2	13	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB2	14	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB3	14	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB1	14	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB3	14	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB1	14	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB2	14	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB2	15	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB3	15	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB1	15	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB3	15	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB1	15	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB2	15	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB2	16	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB3	16	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB1	16	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB3	16	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB1	16	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB2	16	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB2	17	0.49

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB3	17	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB1	17	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB3	17	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB1	17	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB2	17	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB2	18	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB3	18	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB1	18	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB3	18	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB1	18	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB2	18	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB2	19	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB3	19	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB1	19	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB3	19	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB1	19	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB2	19	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB2	20	0.49
(1,210)	1:374:A:ALA:HB1	1:374:A:ALA:HB3	20	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB1	20	0.49
(1,210)	1:374:A:ALA:HB2	1:374:A:ALA:HB3	20	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB1	20	0.49
(1,210)	1:374:A:ALA:HB3	1:374:A:ALA:HB2	20	0.49
(1,949)	1:410:A:LEU:HD21	1:419:A:PTR:HE1	2	0.45
(1,949)	1:410:A:LEU:HD22	1:419:A:PTR:HE1	2	0.45
(1,949)	1:410:A:LEU:HD23	1:419:A:PTR:HE1	2	0.45
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD11	17	0.34
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD12	17	0.34
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD13	17	0.34
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD11	9	0.32
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD12	9	0.32
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD13	9	0.32
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD11	13	0.32
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD12	13	0.32
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD13	13	0.32
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD11	18	0.31
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD12	18	0.31
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD13	18	0.31
(1,949)	1:410:A:LEU:HD21	1:419:A:PTR:HE1	19	0.31
(1,949)	1:410:A:LEU:HD22	1:419:A:PTR:HE1	19	0.31
(1,949)	1:410:A:LEU:HD23	1:419:A:PTR:HE1	19	0.31
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD11	12	0.3

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD12	12	0.3
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD13	12	0.3
(1,544)	1:363:A:LEU:HD21	1:530:A:TYR:HE1	19	0.3
(1,544)	1:363:A:LEU:HD22	1:530:A:TYR:HE1	19	0.3
(1,544)	1:363:A:LEU:HD23	1:530:A:TYR:HE1	19	0.3
(1,543)	1:363:A:LEU:HD21	1:523:A:PHE:HE1	1	0.29
(1,543)	1:363:A:LEU:HD22	1:523:A:PHE:HE1	1	0.29
(1,543)	1:363:A:LEU:HD23	1:523:A:PHE:HE1	1	0.29
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD11	2	0.28
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD12	2	0.28
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD13	2	0.28
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD11	13	0.28
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD12	13	0.28
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD13	13	0.28
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE1	2	0.28
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE2	2	0.28
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE3	2	0.28
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE1	2	0.28
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE2	2	0.28
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE3	2	0.28
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE1	2	0.28
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE2	2	0.28
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE3	2	0.28
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD11	14	0.27
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD12	14	0.27
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD13	14	0.27
(1,749)	1:469:A:MET:HE1	1:477:A:GLN:H	3	0.27
(1,749)	1:469:A:MET:HE2	1:477:A:GLN:H	3	0.27
(1,749)	1:469:A:MET:HE3	1:477:A:GLN:H	3	0.27
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD21	15	0.27
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD22	15	0.27
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD23	15	0.27
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD11	16	0.26
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD12	16	0.26
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD13	16	0.26
(1,949)	1:410:A:LEU:HD21	1:419:A:PTR:HE1	7	0.26
(1,949)	1:410:A:LEU:HD22	1:419:A:PTR:HE1	7	0.26
(1,949)	1:410:A:LEU:HD23	1:419:A:PTR:HE1	7	0.26
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD21	9	0.26
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD22	9	0.26
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD23	9	0.26
(1,544)	1:363:A:LEU:HD21	1:530:A:TYR:HE1	2	0.26

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,544)	1:363:A:LEU:HD22	1:530:A:TYR:HE1	2	0.26
(1,544)	1:363:A:LEU:HD23	1:530:A:TYR:HE1	2	0.26
(1,544)	1:363:A:LEU:HD21	1:530:A:TYR:HE1	16	0.26
(1,544)	1:363:A:LEU:HD22	1:530:A:TYR:HE1	16	0.26
(1,544)	1:363:A:LEU:HD23	1:530:A:TYR:HE1	16	0.26
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD11	16	0.26
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD12	16	0.26
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD13	16	0.26
(1,254)	1:386:A:VAL:HG11	1:414:A:ILE:HD11	5	0.26
(1,254)	1:386:A:VAL:HG11	1:414:A:ILE:HD12	5	0.26
(1,254)	1:386:A:VAL:HG11	1:414:A:ILE:HD13	5	0.26
(1,254)	1:386:A:VAL:HG12	1:414:A:ILE:HD11	5	0.26
(1,254)	1:386:A:VAL:HG12	1:414:A:ILE:HD12	5	0.26
(1,254)	1:386:A:VAL:HG12	1:414:A:ILE:HD13	5	0.26
(1,254)	1:386:A:VAL:HG13	1:414:A:ILE:HD11	5	0.26
(1,254)	1:386:A:VAL:HG13	1:414:A:ILE:HD12	5	0.26
(1,254)	1:386:A:VAL:HG13	1:414:A:ILE:HD13	5	0.26
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD11	3	0.25
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD12	3	0.25
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD13	3	0.25
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD11	7	0.25
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD12	7	0.25
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD13	7	0.25
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD11	10	0.25
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD12	10	0.25
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD13	10	0.25
(1,949)	1:410:A:LEU:HD21	1:419:A:PTR:HE1	16	0.25
(1,949)	1:410:A:LEU:HD22	1:419:A:PTR:HE1	16	0.25
(1,949)	1:410:A:LEU:HD23	1:419:A:PTR:HE1	16	0.25
(1,779)	1:421:A:ALA:H	1:425:A:ALA:HB1	6	0.25
(1,779)	1:421:A:ALA:H	1:425:A:ALA:HB2	6	0.25
(1,779)	1:421:A:ALA:H	1:425:A:ALA:HB3	6	0.25
(1,754)	1:259:A:ALA:HB1	1:261:A:ASP:H	17	0.25
(1,754)	1:259:A:ALA:HB2	1:261:A:ASP:H	17	0.25
(1,754)	1:259:A:ALA:HB3	1:261:A:ASP:H	17	0.25
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE1	18	0.25
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE2	18	0.25
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE3	18	0.25
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE1	18	0.25
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE2	18	0.25
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE3	18	0.25
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE1	18	0.25

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE2	18	0.25
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE3	18	0.25
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD11	11	0.25
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD12	11	0.25
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD13	11	0.25
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD11	11	0.25
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD12	11	0.25
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD13	11	0.25
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD11	11	0.25
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD12	11	0.25
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD13	11	0.25
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD11	18	0.25
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD12	18	0.25
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD13	18	0.25
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD11	18	0.25
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD12	18	0.25
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD13	18	0.25
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD11	18	0.25
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD12	18	0.25
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD13	18	0.25
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD11	20	0.24
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD12	20	0.24
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD13	20	0.24
(1,949)	1:410:A:LEU:HD21	1:419:A:PTR:HE1	12	0.24
(1,949)	1:410:A:LEU:HD22	1:419:A:PTR:HE1	12	0.24
(1,949)	1:410:A:LEU:HD23	1:419:A:PTR:HE1	12	0.24
(1,606)	1:410:A:LEU:HD11	1:411:A:ALA:H	18	0.24
(1,606)	1:410:A:LEU:HD12	1:411:A:ALA:H	18	0.24
(1,606)	1:410:A:LEU:HD13	1:411:A:ALA:H	18	0.24
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD11	10	0.24
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD12	10	0.24
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD13	10	0.24
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD11	5	0.23
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD12	5	0.23
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD13	5	0.23
(1,949)	1:410:A:LEU:HD21	1:419:A:PTR:HE1	3	0.23
(1,949)	1:410:A:LEU:HD22	1:419:A:PTR:HE1	3	0.23
(1,949)	1:410:A:LEU:HD23	1:419:A:PTR:HE1	3	0.23
(1,544)	1:363:A:LEU:HD21	1:530:A:TYR:HE1	6	0.23
(1,544)	1:363:A:LEU:HD22	1:530:A:TYR:HE1	6	0.23
(1,544)	1:363:A:LEU:HD23	1:530:A:TYR:HE1	6	0.23
(1,543)	1:363:A:LEU:HD21	1:523:A:PHE:HE1	7	0.23

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,543)	1:363:A:LEU:HD22	1:523:A:PHE:HE1	7	0.23
(1,543)	1:363:A:LEU:HD23	1:523:A:PHE:HE1	7	0.23
(1,405)	1:286:A:MET:HE1	1:295:A:VAL:H	17	0.23
(1,405)	1:286:A:MET:HE2	1:295:A:VAL:H	17	0.23
(1,405)	1:286:A:MET:HE3	1:295:A:VAL:H	17	0.23
(1,1372)	1:349:A:LEU:H	1:369:A:MET:HE1	20	0.22
(1,1372)	1:349:A:LEU:H	1:369:A:MET:HE2	20	0.22
(1,1372)	1:349:A:LEU:H	1:369:A:MET:HE3	20	0.22
(1,1231)	1:354:A:LYS:H	1:361:A:LEU:HD11	13	0.22
(1,1231)	1:354:A:LYS:H	1:361:A:LEU:HD12	13	0.22
(1,1231)	1:354:A:LYS:H	1:361:A:LEU:HD13	13	0.22
(1,949)	1:410:A:LEU:HD21	1:419:A:PTR:HE1	1	0.22
(1,949)	1:410:A:LEU:HD22	1:419:A:PTR:HE1	1	0.22
(1,949)	1:410:A:LEU:HD23	1:419:A:PTR:HE1	1	0.22
(1,949)	1:410:A:LEU:HD21	1:419:A:PTR:HE1	18	0.22
(1,949)	1:410:A:LEU:HD22	1:419:A:PTR:HE1	18	0.22
(1,949)	1:410:A:LEU:HD23	1:419:A:PTR:HE1	18	0.22
(1,642)	1:438:A:LEU:HD21	1:439:A:TYR:HE1	18	0.22
(1,642)	1:438:A:LEU:HD22	1:439:A:TYR:HE1	18	0.22
(1,642)	1:438:A:LEU:HD23	1:439:A:TYR:HE1	18	0.22
(1,543)	1:363:A:LEU:HD21	1:523:A:PHE:HE1	11	0.22
(1,543)	1:363:A:LEU:HD22	1:523:A:PHE:HE1	11	0.22
(1,543)	1:363:A:LEU:HD23	1:523:A:PHE:HE1	11	0.22
(1,405)	1:286:A:MET:HE1	1:295:A:VAL:H	14	0.22
(1,405)	1:286:A:MET:HE2	1:295:A:VAL:H	14	0.22
(1,405)	1:286:A:MET:HE3	1:295:A:VAL:H	14	0.22
(1,29)	1:284:A:VAL:H	1:285:A:TRP:HE1	17	0.22
(1,1372)	1:349:A:LEU:H	1:369:A:MET:HE1	4	0.21
(1,1372)	1:349:A:LEU:H	1:369:A:MET:HE2	4	0.21
(1,1372)	1:349:A:LEU:H	1:369:A:MET:HE3	4	0.21
(1,965)	1:455:A:LEU:HD11	1:518:A:PHE:HE1	8	0.21
(1,965)	1:455:A:LEU:HD12	1:518:A:PHE:HE1	8	0.21
(1,965)	1:455:A:LEU:HD13	1:518:A:PHE:HE1	8	0.21
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD11	6	0.21
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD12	6	0.21
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD13	6	0.21
(1,950)	1:419:A:PTR:HE1	1:420:A:THR:H	1	0.21
(1,949)	1:410:A:LEU:HD21	1:419:A:PTR:HE1	10	0.21
(1,949)	1:410:A:LEU:HD22	1:419:A:PTR:HE1	10	0.21
(1,949)	1:410:A:LEU:HD23	1:419:A:PTR:HE1	10	0.21
(1,864)	1:297:A:ILE:HD11	1:338:A:TYR:HE2	7	0.21
(1,864)	1:297:A:ILE:HD12	1:338:A:TYR:HE2	7	0.21

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,864)	1:297:A:ILE:HD13	1:338:A:TYR:HE2	7	0.21
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD11	18	0.21
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD12	18	0.21
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD13	18	0.21
(1,543)	1:363:A:LEU:HD21	1:523:A:PHE:HE1	5	0.21
(1,543)	1:363:A:LEU:HD22	1:523:A:PHE:HE1	5	0.21
(1,543)	1:363:A:LEU:HD23	1:523:A:PHE:HE1	5	0.21
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD11	3	0.21
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD12	3	0.21
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD13	3	0.21
(1,405)	1:286:A:MET:HE1	1:295:A:VAL:H	11	0.21
(1,405)	1:286:A:MET:HE2	1:295:A:VAL:H	11	0.21
(1,405)	1:286:A:MET:HE3	1:295:A:VAL:H	11	0.21
(1,405)	1:286:A:MET:HE1	1:295:A:VAL:H	16	0.21
(1,405)	1:286:A:MET:HE2	1:295:A:VAL:H	16	0.21
(1,405)	1:286:A:MET:HE3	1:295:A:VAL:H	16	0.21
(1,254)	1:386:A:VAL:HG11	1:414:A:ILE:HD11	15	0.21
(1,254)	1:386:A:VAL:HG11	1:414:A:ILE:HD12	15	0.21
(1,254)	1:386:A:VAL:HG11	1:414:A:ILE:HD13	15	0.21
(1,254)	1:386:A:VAL:HG12	1:414:A:ILE:HD11	15	0.21
(1,254)	1:386:A:VAL:HG12	1:414:A:ILE:HD12	15	0.21
(1,254)	1:386:A:VAL:HG12	1:414:A:ILE:HD13	15	0.21
(1,254)	1:386:A:VAL:HG13	1:414:A:ILE:HD11	15	0.21
(1,254)	1:386:A:VAL:HG13	1:414:A:ILE:HD12	15	0.21
(1,254)	1:386:A:VAL:HG13	1:414:A:ILE:HD13	15	0.21
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD11	2	0.21
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD12	2	0.21
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD13	2	0.21
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD11	2	0.21
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD12	2	0.21
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD13	2	0.21
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD11	2	0.21
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD12	2	0.21
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD13	2	0.21
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD11	6	0.2
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD12	6	0.2
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD13	6	0.2
(1,972)	1:260:A:LYS:H	1:261:A:ASP:H	17	0.2
(1,965)	1:455:A:LEU:HD11	1:518:A:PHE:HE1	9	0.2
(1,965)	1:455:A:LEU:HD12	1:518:A:PHE:HE1	9	0.2
(1,965)	1:455:A:LEU:HD13	1:518:A:PHE:HE1	9	0.2
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD11	4	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD12	4	0.2
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD13	4	0.2
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD11	11	0.2
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD12	11	0.2
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD13	11	0.2
(1,949)	1:410:A:LEU:HD21	1:419:A:PTR:HE1	13	0.2
(1,949)	1:410:A:LEU:HD22	1:419:A:PTR:HE1	13	0.2
(1,949)	1:410:A:LEU:HD23	1:419:A:PTR:HE1	13	0.2
(1,858)	1:419:A:PTR:HE1	1:421:A:ALA:HB1	8	0.2
(1,858)	1:419:A:PTR:HE1	1:421:A:ALA:HB2	8	0.2
(1,858)	1:419:A:PTR:HE1	1:421:A:ALA:HB3	8	0.2
(1,780)	1:436:A:ALA:HB1	1:442:A:PHE:HE1	6	0.2
(1,780)	1:436:A:ALA:HB2	1:442:A:PHE:HE1	6	0.2
(1,780)	1:436:A:ALA:HB3	1:442:A:PHE:HE1	6	0.2
(1,708)	1:466:A:TYR:HE2	1:484:A:MET:HE1	2	0.2
(1,708)	1:466:A:TYR:HE2	1:484:A:MET:HE2	2	0.2
(1,708)	1:466:A:TYR:HE2	1:484:A:MET:HE3	2	0.2
(1,708)	1:466:A:TYR:HE2	1:484:A:MET:HE1	6	0.2
(1,708)	1:466:A:TYR:HE2	1:484:A:MET:HE2	6	0.2
(1,708)	1:466:A:TYR:HE2	1:484:A:MET:HE3	6	0.2
(1,642)	1:438:A:LEU:HD21	1:439:A:TYR:HE1	7	0.2
(1,642)	1:438:A:LEU:HD22	1:439:A:TYR:HE1	7	0.2
(1,642)	1:438:A:LEU:HD23	1:439:A:TYR:HE1	7	0.2
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG11	8	0.2
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG12	8	0.2
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG13	8	0.2
(1,544)	1:363:A:LEU:HD21	1:530:A:TYR:HE1	20	0.2
(1,544)	1:363:A:LEU:HD22	1:530:A:TYR:HE1	20	0.2
(1,544)	1:363:A:LEU:HD23	1:530:A:TYR:HE1	20	0.2
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD11	9	0.2
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD12	9	0.2
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD13	9	0.2
(1,405)	1:286:A:MET:HE1	1:295:A:VAL:H	1	0.2
(1,405)	1:286:A:MET:HE2	1:295:A:VAL:H	1	0.2
(1,405)	1:286:A:MET:HE3	1:295:A:VAL:H	1	0.2
(1,405)	1:286:A:MET:HE1	1:295:A:VAL:H	18	0.2
(1,405)	1:286:A:MET:HE2	1:295:A:VAL:H	18	0.2
(1,405)	1:286:A:MET:HE3	1:295:A:VAL:H	18	0.2
(1,390)	1:272:A:LEU:HD11	1:285:A:TRP:HE1	12	0.2
(1,390)	1:272:A:LEU:HD12	1:285:A:TRP:HE1	12	0.2
(1,390)	1:272:A:LEU:HD13	1:285:A:TRP:HE1	12	0.2
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD11	3	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD12	3	0.2
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD13	3	0.2
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD11	3	0.2
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD12	3	0.2
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD13	3	0.2
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD11	3	0.2
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD12	3	0.2
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD13	3	0.2
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD11	12	0.2
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD12	12	0.2
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD13	12	0.2
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD11	12	0.2
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD12	12	0.2
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD13	12	0.2
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD11	12	0.2
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD12	12	0.2
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD13	12	0.2
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD11	13	0.2
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD12	13	0.2
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD13	13	0.2
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD11	13	0.2
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD12	13	0.2
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD13	13	0.2
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD11	13	0.2
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD12	13	0.2
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD13	13	0.2
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD11	9	0.2
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD12	9	0.2
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD13	9	0.2
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD11	9	0.2
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD12	9	0.2
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD13	9	0.2
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD11	9	0.2
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD12	9	0.2
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD13	9	0.2
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD11	12	0.2
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD12	12	0.2
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD13	12	0.2
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD11	12	0.2
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD12	12	0.2
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD13	12	0.2
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD11	12	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD12	12	0.2
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD13	12	0.2
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD11	3	0.2
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD12	3	0.2
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD13	3	0.2
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD11	3	0.2
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD12	3	0.2
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD13	3	0.2
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD11	3	0.2
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD12	3	0.2
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD13	3	0.2
(1,1302)	1:283:A:GLU:H	1:299:A:THR:HG21	10	0.19
(1,1302)	1:283:A:GLU:H	1:299:A:THR:HG22	10	0.19
(1,1302)	1:283:A:GLU:H	1:299:A:THR:HG23	10	0.19
(1,1268)	1:262:A:ALA:H	1:264:A:GLU:H	19	0.19
(1,965)	1:455:A:LEU:HD11	1:518:A:PHE:HE1	4	0.19
(1,965)	1:455:A:LEU:HD12	1:518:A:PHE:HE1	4	0.19
(1,965)	1:455:A:LEU:HD13	1:518:A:PHE:HE1	4	0.19
(1,965)	1:455:A:LEU:HD11	1:518:A:PHE:HE1	10	0.19
(1,965)	1:455:A:LEU:HD12	1:518:A:PHE:HE1	10	0.19
(1,965)	1:455:A:LEU:HD13	1:518:A:PHE:HE1	10	0.19
(1,965)	1:455:A:LEU:HD11	1:518:A:PHE:HE1	12	0.19
(1,965)	1:455:A:LEU:HD12	1:518:A:PHE:HE1	12	0.19
(1,965)	1:455:A:LEU:HD13	1:518:A:PHE:HE1	12	0.19
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD11	19	0.19
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD12	19	0.19
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD13	19	0.19
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD11	16	0.19
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD12	16	0.19
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD13	16	0.19
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD21	11	0.19
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD22	11	0.19
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD23	11	0.19
(1,617)	1:414:A:ILE:HD11	1:444:A:ILE:HD11	19	0.19
(1,617)	1:414:A:ILE:HD11	1:444:A:ILE:HD12	19	0.19
(1,617)	1:414:A:ILE:HD11	1:444:A:ILE:HD13	19	0.19
(1,617)	1:414:A:ILE:HD12	1:444:A:ILE:HD11	19	0.19
(1,617)	1:414:A:ILE:HD12	1:444:A:ILE:HD12	19	0.19
(1,617)	1:414:A:ILE:HD12	1:444:A:ILE:HD13	19	0.19
(1,617)	1:414:A:ILE:HD13	1:444:A:ILE:HD11	19	0.19
(1,617)	1:414:A:ILE:HD13	1:444:A:ILE:HD12	19	0.19
(1,617)	1:414:A:ILE:HD13	1:444:A:ILE:HD13	19	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,548)	1:371:A:ALA:HB1	1:521:A:ASP:H	16	0.19
(1,548)	1:371:A:ALA:HB2	1:521:A:ASP:H	16	0.19
(1,548)	1:371:A:ALA:HB3	1:521:A:ASP:H	16	0.19
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD11	20	0.19
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD12	20	0.19
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD13	20	0.19
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD11	11	0.19
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD12	11	0.19
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD13	11	0.19
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD11	11	0.19
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD12	11	0.19
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD13	11	0.19
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD11	11	0.19
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD12	11	0.19
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD13	11	0.19
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD11	2	0.19
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD12	2	0.19
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD13	2	0.19
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD11	2	0.19
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD12	2	0.19
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD13	2	0.19
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD11	2	0.19
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD12	2	0.19
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD13	2	0.19
(2,122)	1:518:A:PHE:O	1:522:A:TYR:H	8	0.18
(1,1363)	1:295:A:VAL:HG21	1:340:A:VAL:H	7	0.18
(1,1363)	1:295:A:VAL:HG22	1:340:A:VAL:H	7	0.18
(1,1363)	1:295:A:VAL:HG23	1:340:A:VAL:H	7	0.18
(1,1363)	1:295:A:VAL:HG21	1:340:A:VAL:H	16	0.18
(1,1363)	1:295:A:VAL:HG22	1:340:A:VAL:H	16	0.18
(1,1363)	1:295:A:VAL:HG23	1:340:A:VAL:H	16	0.18
(1,1009)	1:536:A:LEU:H	1:536:A:LEU:HD11	4	0.18
(1,1009)	1:536:A:LEU:H	1:536:A:LEU:HD12	4	0.18
(1,1009)	1:536:A:LEU:H	1:536:A:LEU:HD13	4	0.18
(1,973)	1:259:A:ALA:HB1	1:260:A:LYS:H	4	0.18
(1,973)	1:259:A:ALA:HB2	1:260:A:LYS:H	4	0.18
(1,973)	1:259:A:ALA:HB3	1:260:A:LYS:H	4	0.18
(1,965)	1:455:A:LEU:HD11	1:518:A:PHE:HE1	5	0.18
(1,965)	1:455:A:LEU:HD12	1:518:A:PHE:HE1	5	0.18
(1,965)	1:455:A:LEU:HD13	1:518:A:PHE:HE1	5	0.18
(1,965)	1:455:A:LEU:HD11	1:518:A:PHE:HE1	15	0.18
(1,965)	1:455:A:LEU:HD12	1:518:A:PHE:HE1	15	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,965)	1:455:A:LEU:HD13	1:518:A:PHE:HE1	15	0.18
(1,949)	1:410:A:LEU:HD21	1:419:A:PTR:HE1	15	0.18
(1,949)	1:410:A:LEU:HD22	1:419:A:PTR:HE1	15	0.18
(1,949)	1:410:A:LEU:HD23	1:419:A:PTR:HE1	15	0.18
(1,940)	1:426:A:LYS:H	1:427:A:PHE:HE1	6	0.18
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD11	12	0.18
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD12	12	0.18
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD13	12	0.18
(1,642)	1:438:A:LEU:HD21	1:439:A:TYR:HE1	6	0.18
(1,642)	1:438:A:LEU:HD22	1:439:A:TYR:HE1	6	0.18
(1,642)	1:438:A:LEU:HD23	1:439:A:TYR:HE1	6	0.18
(1,642)	1:438:A:LEU:HD21	1:439:A:TYR:HE1	14	0.18
(1,642)	1:438:A:LEU:HD22	1:439:A:TYR:HE1	14	0.18
(1,642)	1:438:A:LEU:HD23	1:439:A:TYR:HE1	14	0.18
(1,543)	1:363:A:LEU:HD21	1:523:A:PHE:HE1	9	0.18
(1,543)	1:363:A:LEU:HD22	1:523:A:PHE:HE1	9	0.18
(1,543)	1:363:A:LEU:HD23	1:523:A:PHE:HE1	9	0.18
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD21	6	0.18
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD22	6	0.18
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD23	6	0.18
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD11	12	0.18
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD12	12	0.18
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD13	12	0.18
(1,405)	1:286:A:MET:HE1	1:295:A:VAL:H	20	0.18
(1,405)	1:286:A:MET:HE2	1:295:A:VAL:H	20	0.18
(1,405)	1:286:A:MET:HE3	1:295:A:VAL:H	20	0.18
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD11	5	0.18
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD12	5	0.18
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD13	5	0.18
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD11	5	0.18
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD12	5	0.18
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD13	5	0.18
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD11	5	0.18
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD12	5	0.18
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD13	5	0.18
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD11	6	0.18
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD12	6	0.18
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD13	6	0.18
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD11	6	0.18
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD12	6	0.18
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD13	6	0.18
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD11	6	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD12	6	0.18
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD13	6	0.18
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD11	1	0.18
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD12	1	0.18
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD13	1	0.18
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD11	1	0.18
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD12	1	0.18
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD13	1	0.18
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD11	1	0.18
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD12	1	0.18
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD13	1	0.18
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD11	19	0.18
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD12	19	0.18
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD13	19	0.18
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD11	19	0.18
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD12	19	0.18
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD13	19	0.18
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD11	19	0.18
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD12	19	0.18
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD13	19	0.18
(2,201)	1:389:A:ASP:N	1:387:A:HIS:ND1	11	0.17
(2,122)	1:518:A:PHE:O	1:522:A:TYR:H	4	0.17
(2,122)	1:518:A:PHE:O	1:522:A:TYR:H	7	0.17
(2,122)	1:518:A:PHE:O	1:522:A:TYR:H	10	0.17
(1,1363)	1:295:A:VAL:HG21	1:340:A:VAL:H	10	0.17
(1,1363)	1:295:A:VAL:HG22	1:340:A:VAL:H	10	0.17
(1,1363)	1:295:A:VAL:HG23	1:340:A:VAL:H	10	0.17
(1,1282)	1:431:A:TRP:HE1	1:454:A:LEU:HD11	3	0.17
(1,1282)	1:431:A:TRP:HE1	1:454:A:LEU:HD12	3	0.17
(1,1282)	1:431:A:TRP:HE1	1:454:A:LEU:HD13	3	0.17
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD11	8	0.17
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD12	8	0.17
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD13	8	0.17
(1,949)	1:410:A:LEU:HD21	1:419:A:PTR:HE1	4	0.17
(1,949)	1:410:A:LEU:HD22	1:419:A:PTR:HE1	4	0.17
(1,949)	1:410:A:LEU:HD23	1:419:A:PTR:HE1	4	0.17
(1,949)	1:410:A:LEU:HD21	1:419:A:PTR:HE1	17	0.17
(1,949)	1:410:A:LEU:HD22	1:419:A:PTR:HE1	17	0.17
(1,949)	1:410:A:LEU:HD23	1:419:A:PTR:HE1	17	0.17
(1,928)	1:363:A:LEU:HD11	1:530:A:TYR:HE2	12	0.17
(1,928)	1:363:A:LEU:HD12	1:530:A:TYR:HE2	12	0.17
(1,928)	1:363:A:LEU:HD13	1:530:A:TYR:HE2	12	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,864)	1:297:A:ILE:HD11	1:338:A:TYR:HE2	18	0.17
(1,864)	1:297:A:ILE:HD12	1:338:A:TYR:HE2	18	0.17
(1,864)	1:297:A:ILE:HD13	1:338:A:TYR:HE2	18	0.17
(1,803)	1:421:A:ALA:HB1	1:427:A:PHE:HE1	1	0.17
(1,803)	1:421:A:ALA:HB2	1:427:A:PHE:HE1	1	0.17
(1,803)	1:421:A:ALA:HB3	1:427:A:PHE:HE1	1	0.17
(1,803)	1:421:A:ALA:HB1	1:427:A:PHE:HE1	10	0.17
(1,803)	1:421:A:ALA:HB2	1:427:A:PHE:HE1	10	0.17
(1,803)	1:421:A:ALA:HB3	1:427:A:PHE:HE1	10	0.17
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD11	7	0.17
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD12	7	0.17
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD13	7	0.17
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD21	6	0.17
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD22	6	0.17
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD23	6	0.17
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD21	18	0.17
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD22	18	0.17
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD23	18	0.17
(1,708)	1:466:A:TYR:HE2	1:484:A:MET:HE1	16	0.17
(1,708)	1:466:A:TYR:HE2	1:484:A:MET:HE2	16	0.17
(1,708)	1:466:A:TYR:HE2	1:484:A:MET:HE3	16	0.17
(1,699)	1:478:A:VAL:HG11	1:482:A:TYR:H	15	0.17
(1,699)	1:478:A:VAL:HG12	1:482:A:TYR:H	15	0.17
(1,699)	1:478:A:VAL:HG13	1:482:A:TYR:H	15	0.17
(1,699)	1:478:A:VAL:HG11	1:482:A:TYR:H	16	0.17
(1,699)	1:478:A:VAL:HG12	1:482:A:TYR:H	16	0.17
(1,699)	1:478:A:VAL:HG13	1:482:A:TYR:H	16	0.17
(1,605)	1:410:A:LEU:HD11	1:426:A:LYS:H	20	0.17
(1,605)	1:410:A:LEU:HD12	1:426:A:LYS:H	20	0.17
(1,605)	1:410:A:LEU:HD13	1:426:A:LYS:H	20	0.17
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD11	5	0.17
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD12	5	0.17
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD13	5	0.17
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD11	15	0.17
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD12	15	0.17
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD13	15	0.17
(1,407)	1:286:A:MET:HE1	1:288:A:THR:H	11	0.17
(1,407)	1:286:A:MET:HE2	1:288:A:THR:H	11	0.17
(1,407)	1:286:A:MET:HE3	1:288:A:THR:H	11	0.17
(1,390)	1:272:A:LEU:HD11	1:285:A:TRP:HE1	8	0.17
(1,390)	1:272:A:LEU:HD12	1:285:A:TRP:HE1	8	0.17
(1,390)	1:272:A:LEU:HD13	1:285:A:TRP:HE1	8	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,390)	1:272:A:LEU:HD11	1:285:A:TRP:HE1	11	0.17
(1,390)	1:272:A:LEU:HD12	1:285:A:TRP:HE1	11	0.17
(1,390)	1:272:A:LEU:HD13	1:285:A:TRP:HE1	11	0.17
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD11	16	0.17
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD12	16	0.17
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD13	16	0.17
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD11	16	0.17
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD12	16	0.17
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD13	16	0.17
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD11	16	0.17
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD12	16	0.17
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD13	16	0.17
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD11	12	0.17
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD12	12	0.17
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD13	12	0.17
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD11	12	0.17
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD12	12	0.17
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD13	12	0.17
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD11	12	0.17
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD12	12	0.17
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD13	12	0.17
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD11	14	0.17
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD12	14	0.17
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD13	14	0.17
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD11	14	0.17
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD12	14	0.17
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD13	14	0.17
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD11	14	0.17
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD12	14	0.17
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD13	14	0.17
(2,201)	1:389:A:ASP:N	1:387:A:HIS:ND1	19	0.16
(1,1367)	1:346:A:LYS:H	1:396:A:LEU:HD21	3	0.16
(1,1367)	1:346:A:LYS:H	1:396:A:LEU:HD22	3	0.16
(1,1367)	1:346:A:LYS:H	1:396:A:LEU:HD23	3	0.16
(1,1363)	1:295:A:VAL:HG21	1:340:A:VAL:H	2	0.16
(1,1363)	1:295:A:VAL:HG22	1:340:A:VAL:H	2	0.16
(1,1363)	1:295:A:VAL:HG23	1:340:A:VAL:H	2	0.16
(1,1363)	1:295:A:VAL:HG21	1:340:A:VAL:H	17	0.16
(1,1363)	1:295:A:VAL:HG22	1:340:A:VAL:H	17	0.16
(1,1363)	1:295:A:VAL:HG23	1:340:A:VAL:H	17	0.16
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD21	19	0.16
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD22	19	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD23	19	0.16
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD11	9	0.16
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD12	9	0.16
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD13	9	0.16
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD11	12	0.16
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD12	12	0.16
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD13	12	0.16
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD11	13	0.16
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD12	13	0.16
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD13	13	0.16
(1,965)	1:455:A:LEU:HD11	1:518:A:PHE:HE1	17	0.16
(1,965)	1:455:A:LEU:HD12	1:518:A:PHE:HE1	17	0.16
(1,965)	1:455:A:LEU:HD13	1:518:A:PHE:HE1	17	0.16
(1,965)	1:455:A:LEU:HD11	1:518:A:PHE:HE1	20	0.16
(1,965)	1:455:A:LEU:HD12	1:518:A:PHE:HE1	20	0.16
(1,965)	1:455:A:LEU:HD13	1:518:A:PHE:HE1	20	0.16
(1,864)	1:297:A:ILE:HD11	1:338:A:TYR:HE2	17	0.16
(1,864)	1:297:A:ILE:HD12	1:338:A:TYR:HE2	17	0.16
(1,864)	1:297:A:ILE:HD13	1:338:A:TYR:HE2	17	0.16
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD11	1	0.16
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD12	1	0.16
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD13	1	0.16
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD21	10	0.16
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD22	10	0.16
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD23	10	0.16
(1,708)	1:466:A:TYR:HE2	1:484:A:MET:HE1	11	0.16
(1,708)	1:466:A:TYR:HE2	1:484:A:MET:HE2	11	0.16
(1,708)	1:466:A:TYR:HE2	1:484:A:MET:HE3	11	0.16
(1,706)	1:484:A:MET:HE1	1:502:A:TRP:HE1	8	0.16
(1,706)	1:484:A:MET:HE2	1:502:A:TRP:HE1	8	0.16
(1,706)	1:484:A:MET:HE3	1:502:A:TRP:HE1	8	0.16
(1,699)	1:478:A:VAL:HG11	1:482:A:TYR:H	8	0.16
(1,699)	1:478:A:VAL:HG12	1:482:A:TYR:H	8	0.16
(1,699)	1:478:A:VAL:HG13	1:482:A:TYR:H	8	0.16
(1,642)	1:438:A:LEU:HD21	1:439:A:TYR:HE1	1	0.16
(1,642)	1:438:A:LEU:HD22	1:439:A:TYR:HE1	1	0.16
(1,642)	1:438:A:LEU:HD23	1:439:A:TYR:HE1	1	0.16
(1,642)	1:438:A:LEU:HD21	1:439:A:TYR:HE1	20	0.16
(1,642)	1:438:A:LEU:HD22	1:439:A:TYR:HE1	20	0.16
(1,642)	1:438:A:LEU:HD23	1:439:A:TYR:HE1	20	0.16
(1,614)	1:386:A:VAL:H	1:414:A:ILE:HD11	5	0.16
(1,614)	1:386:A:VAL:H	1:414:A:ILE:HD12	5	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,614)	1:386:A:VAL:H	1:414:A:ILE:HD13	5	0.16
(1,592)	1:398:A:GLY:H	1:402:A:VAL:HG21	6	0.16
(1,592)	1:398:A:GLY:H	1:402:A:VAL:HG22	6	0.16
(1,592)	1:398:A:GLY:H	1:402:A:VAL:HG23	6	0.16
(1,544)	1:363:A:LEU:HD21	1:530:A:TYR:HE1	15	0.16
(1,544)	1:363:A:LEU:HD22	1:530:A:TYR:HE1	15	0.16
(1,544)	1:363:A:LEU:HD23	1:530:A:TYR:HE1	15	0.16
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD11	1	0.16
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD12	1	0.16
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD13	1	0.16
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD11	17	0.16
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD12	17	0.16
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD13	17	0.16
(1,405)	1:286:A:MET:HE1	1:295:A:VAL:H	2	0.16
(1,405)	1:286:A:MET:HE2	1:295:A:VAL:H	2	0.16
(1,405)	1:286:A:MET:HE3	1:295:A:VAL:H	2	0.16
(1,405)	1:286:A:MET:HE1	1:295:A:VAL:H	6	0.16
(1,405)	1:286:A:MET:HE2	1:295:A:VAL:H	6	0.16
(1,405)	1:286:A:MET:HE3	1:295:A:VAL:H	6	0.16
(1,405)	1:286:A:MET:HE1	1:295:A:VAL:H	7	0.16
(1,405)	1:286:A:MET:HE2	1:295:A:VAL:H	7	0.16
(1,405)	1:286:A:MET:HE3	1:295:A:VAL:H	7	0.16
(1,405)	1:286:A:MET:HE1	1:295:A:VAL:H	19	0.16
(1,405)	1:286:A:MET:HE2	1:295:A:VAL:H	19	0.16
(1,405)	1:286:A:MET:HE3	1:295:A:VAL:H	19	0.16
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE1	16	0.16
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE2	16	0.16
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE3	16	0.16
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE1	16	0.16
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE2	16	0.16
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE3	16	0.16
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE1	16	0.16
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE2	16	0.16
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE3	16	0.16
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD11	16	0.16
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD12	16	0.16
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD13	16	0.16
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD11	16	0.16
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD12	16	0.16
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD13	16	0.16
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD11	16	0.16
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD12	16	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD13	16	0.16
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD11	4	0.16
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD12	4	0.16
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD13	4	0.16
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD11	4	0.16
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD12	4	0.16
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD13	4	0.16
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD11	4	0.16
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD12	4	0.16
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD13	4	0.16
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD11	20	0.16
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD12	20	0.16
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD13	20	0.16
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD11	20	0.16
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD12	20	0.16
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD13	20	0.16
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD11	20	0.16
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD12	20	0.16
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD13	20	0.16
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD11	4	0.16
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD12	4	0.16
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD13	4	0.16
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD11	4	0.16
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD12	4	0.16
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD13	4	0.16
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD11	4	0.16
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD12	4	0.16
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD13	4	0.16
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD11	7	0.16
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD12	7	0.16
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD13	7	0.16
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD11	7	0.16
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD12	7	0.16
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD13	7	0.16
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD11	7	0.16
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD12	7	0.16
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD13	7	0.16
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD11	8	0.16
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD12	8	0.16
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD13	8	0.16
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD11	8	0.16
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD12	8	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD13	8	0.16
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD11	8	0.16
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD12	8	0.16
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD13	8	0.16
(2,201)	1:389:A:ASP:N	1:387:A:HIS:ND1	5	0.15
(2,201)	1:389:A:ASP:N	1:387:A:HIS:ND1	10	0.15
(2,122)	1:518:A:PHE:O	1:522:A:TYR:H	1	0.15
(2,122)	1:518:A:PHE:O	1:522:A:TYR:H	3	0.15
(2,122)	1:518:A:PHE:O	1:522:A:TYR:H	6	0.15
(2,122)	1:518:A:PHE:O	1:522:A:TYR:H	15	0.15
(2,122)	1:518:A:PHE:O	1:522:A:TYR:H	17	0.15
(1,1363)	1:295:A:VAL:HG21	1:340:A:VAL:H	12	0.15
(1,1363)	1:295:A:VAL:HG22	1:340:A:VAL:H	12	0.15
(1,1363)	1:295:A:VAL:HG23	1:340:A:VAL:H	12	0.15
(1,1363)	1:295:A:VAL:HG21	1:340:A:VAL:H	15	0.15
(1,1363)	1:295:A:VAL:HG22	1:340:A:VAL:H	15	0.15
(1,1363)	1:295:A:VAL:HG23	1:340:A:VAL:H	15	0.15
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD21	3	0.15
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD22	3	0.15
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD23	3	0.15
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD11	8	0.15
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD12	8	0.15
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD13	8	0.15
(1,1054)	1:361:A:LEU:HD21	1:362:A:ARG:H	9	0.15
(1,1054)	1:361:A:LEU:HD22	1:362:A:ARG:H	9	0.15
(1,1054)	1:361:A:LEU:HD23	1:362:A:ARG:H	9	0.15
(1,985)	1:276:A:LEU:H	1:284:A:VAL:HG11	20	0.15
(1,985)	1:276:A:LEU:H	1:284:A:VAL:HG12	20	0.15
(1,985)	1:276:A:LEU:H	1:284:A:VAL:HG13	20	0.15
(1,965)	1:455:A:LEU:HD11	1:518:A:PHE:HE1	13	0.15
(1,965)	1:455:A:LEU:HD12	1:518:A:PHE:HE1	13	0.15
(1,965)	1:455:A:LEU:HD13	1:518:A:PHE:HE1	13	0.15
(1,965)	1:455:A:LEU:HD11	1:518:A:PHE:HE1	19	0.15
(1,965)	1:455:A:LEU:HD12	1:518:A:PHE:HE1	19	0.15
(1,965)	1:455:A:LEU:HD13	1:518:A:PHE:HE1	19	0.15
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD11	1	0.15
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD12	1	0.15
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD13	1	0.15
(1,956)	1:419:A:PTR:H	1:419:A:PTR:HE2	19	0.15
(1,893)	1:367:A:VAL:HG21	1:523:A:PHE:HE2	16	0.15
(1,893)	1:367:A:VAL:HG22	1:523:A:PHE:HE2	16	0.15
(1,893)	1:367:A:VAL:HG23	1:523:A:PHE:HE2	16	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,864)	1:297:A:ILE:HD11	1:338:A:TYR:HE2	2	0.15
(1,864)	1:297:A:ILE:HD12	1:338:A:TYR:HE2	2	0.15
(1,864)	1:297:A:ILE:HD13	1:338:A:TYR:HE2	2	0.15
(1,864)	1:297:A:ILE:HD11	1:338:A:TYR:HE2	14	0.15
(1,864)	1:297:A:ILE:HD12	1:338:A:TYR:HE2	14	0.15
(1,864)	1:297:A:ILE:HD13	1:338:A:TYR:HE2	14	0.15
(1,749)	1:469:A:MET:HE1	1:477:A:GLN:H	12	0.15
(1,749)	1:469:A:MET:HE2	1:477:A:GLN:H	12	0.15
(1,749)	1:469:A:MET:HE3	1:477:A:GLN:H	12	0.15
(1,642)	1:438:A:LEU:HD21	1:439:A:TYR:HE1	17	0.15
(1,642)	1:438:A:LEU:HD22	1:439:A:TYR:HE1	17	0.15
(1,642)	1:438:A:LEU:HD23	1:439:A:TYR:HE1	17	0.15
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG11	17	0.15
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG12	17	0.15
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG13	17	0.15
(1,592)	1:398:A:GLY:H	1:402:A:VAL:HG21	2	0.15
(1,592)	1:398:A:GLY:H	1:402:A:VAL:HG22	2	0.15
(1,592)	1:398:A:GLY:H	1:402:A:VAL:HG23	2	0.15
(1,543)	1:363:A:LEU:HD21	1:523:A:PHE:HE1	10	0.15
(1,543)	1:363:A:LEU:HD22	1:523:A:PHE:HE1	10	0.15
(1,543)	1:363:A:LEU:HD23	1:523:A:PHE:HE1	10	0.15
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD21	10	0.15
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD22	10	0.15
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD23	10	0.15
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD21	13	0.15
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD22	13	0.15
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD23	13	0.15
(1,512)	1:298:A:LYS:H	1:340:A:VAL:HG21	2	0.15
(1,512)	1:298:A:LYS:H	1:340:A:VAL:HG22	2	0.15
(1,512)	1:298:A:LYS:H	1:340:A:VAL:HG23	2	0.15
(1,512)	1:298:A:LYS:H	1:340:A:VAL:HG21	6	0.15
(1,512)	1:298:A:LYS:H	1:340:A:VAL:HG22	6	0.15
(1,512)	1:298:A:LYS:H	1:340:A:VAL:HG23	6	0.15
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD11	4	0.15
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD12	4	0.15
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD13	4	0.15
(1,393)	1:273:A:GLU:H	1:274:A:VAL:HG21	16	0.15
(1,393)	1:273:A:GLU:H	1:274:A:VAL:HG22	16	0.15
(1,393)	1:273:A:GLU:H	1:274:A:VAL:HG23	16	0.15
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD11	1	0.15
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD12	1	0.15
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD13	1	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD11	1	0.15
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD12	1	0.15
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD13	1	0.15
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD11	1	0.15
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD12	1	0.15
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD13	1	0.15
(2,201)	1:389:A:ASP:N	1:387:A:HIS:ND1	13	0.14
(2,122)	1:518:A:PHE:O	1:522:A:TYR:H	13	0.14
(1,1433)	1:521:A:ASP:H	1:523:A:PHE:H	17	0.14
(1,1405)	1:457:A:GLU:H	1:463:A:ARG:H	7	0.14
(1,1403)	1:366:A:LEU:HD11	1:461:A:LYS:H	6	0.14
(1,1403)	1:366:A:LEU:HD12	1:461:A:LYS:H	6	0.14
(1,1403)	1:366:A:LEU:HD13	1:461:A:LYS:H	6	0.14
(1,1400)	1:457:A:GLU:H	1:484:A:MET:HE1	19	0.14
(1,1400)	1:457:A:GLU:H	1:484:A:MET:HE2	19	0.14
(1,1400)	1:457:A:GLU:H	1:484:A:MET:HE3	19	0.14
(1,1393)	1:369:A:MET:HE1	1:403:A:CYS:H	4	0.14
(1,1393)	1:369:A:MET:HE2	1:403:A:CYS:H	4	0.14
(1,1393)	1:369:A:MET:HE3	1:403:A:CYS:H	4	0.14
(1,1393)	1:369:A:MET:HE1	1:403:A:CYS:H	20	0.14
(1,1393)	1:369:A:MET:HE2	1:403:A:CYS:H	20	0.14
(1,1393)	1:369:A:MET:HE3	1:403:A:CYS:H	20	0.14
(1,1363)	1:295:A:VAL:HG21	1:340:A:VAL:H	4	0.14
(1,1363)	1:295:A:VAL:HG22	1:340:A:VAL:H	4	0.14
(1,1363)	1:295:A:VAL:HG23	1:340:A:VAL:H	4	0.14
(1,1363)	1:295:A:VAL:HG21	1:340:A:VAL:H	6	0.14
(1,1363)	1:295:A:VAL:HG22	1:340:A:VAL:H	6	0.14
(1,1363)	1:295:A:VAL:HG23	1:340:A:VAL:H	6	0.14
(1,1363)	1:295:A:VAL:HG21	1:340:A:VAL:H	11	0.14
(1,1363)	1:295:A:VAL:HG22	1:340:A:VAL:H	11	0.14
(1,1363)	1:295:A:VAL:HG23	1:340:A:VAL:H	11	0.14
(1,1355)	1:497:A:LEU:H	1:522:A:TYR:HE1	12	0.14
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD21	13	0.14
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD22	13	0.14
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD23	13	0.14
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD21	17	0.14
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD22	17	0.14
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD23	17	0.14
(1,1210)	1:410:A:LEU:HD21	1:425:A:ALA:H	13	0.14
(1,1210)	1:410:A:LEU:HD22	1:425:A:ALA:H	13	0.14
(1,1210)	1:410:A:LEU:HD23	1:425:A:ALA:H	13	0.14
(1,967)	1:386:A:VAL:HG11	1:442:A:PHE:HE2	1	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,967)	1:386:A:VAL:HG12	1:442:A:PHE:HE2	1	0.14
(1,967)	1:386:A:VAL:HG13	1:442:A:PHE:HE2	1	0.14
(1,951)	1:410:A:LEU:HD11	1:427:A:PHE:HE2	4	0.14
(1,951)	1:410:A:LEU:HD12	1:427:A:PHE:HE2	4	0.14
(1,951)	1:410:A:LEU:HD13	1:427:A:PHE:HE2	4	0.14
(1,949)	1:410:A:LEU:HD21	1:419:A:PTR:HE1	5	0.14
(1,949)	1:410:A:LEU:HD22	1:419:A:PTR:HE1	5	0.14
(1,949)	1:410:A:LEU:HD23	1:419:A:PTR:HE1	5	0.14
(1,939)	1:439:A:TYR:H	1:439:A:TYR:HE1	11	0.14
(1,924)	1:329:A:TYR:HE1	1:342:A:GLU:H	12	0.14
(1,871)	1:425:A:ALA:H	1:427:A:PHE:HE1	14	0.14
(1,864)	1:297:A:ILE:HD11	1:338:A:TYR:HE2	1	0.14
(1,864)	1:297:A:ILE:HD12	1:338:A:TYR:HE2	1	0.14
(1,864)	1:297:A:ILE:HD13	1:338:A:TYR:HE2	1	0.14
(1,864)	1:297:A:ILE:HD11	1:338:A:TYR:HE2	10	0.14
(1,864)	1:297:A:ILE:HD12	1:338:A:TYR:HE2	10	0.14
(1,864)	1:297:A:ILE:HD13	1:338:A:TYR:HE2	10	0.14
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD21	12	0.14
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD22	12	0.14
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD23	12	0.14
(1,699)	1:478:A:VAL:HG11	1:482:A:TYR:H	11	0.14
(1,699)	1:478:A:VAL:HG12	1:482:A:TYR:H	11	0.14
(1,699)	1:478:A:VAL:HG13	1:482:A:TYR:H	11	0.14
(1,642)	1:438:A:LEU:HD21	1:439:A:TYR:HE1	4	0.14
(1,642)	1:438:A:LEU:HD22	1:439:A:TYR:HE1	4	0.14
(1,642)	1:438:A:LEU:HD23	1:439:A:TYR:HE1	4	0.14
(1,642)	1:438:A:LEU:HD21	1:439:A:TYR:HE1	19	0.14
(1,642)	1:438:A:LEU:HD22	1:439:A:TYR:HE1	19	0.14
(1,642)	1:438:A:LEU:HD23	1:439:A:TYR:HE1	19	0.14
(1,617)	1:414:A:ILE:HD11	1:444:A:ILE:HD11	10	0.14
(1,617)	1:414:A:ILE:HD11	1:444:A:ILE:HD12	10	0.14
(1,617)	1:414:A:ILE:HD11	1:444:A:ILE:HD13	10	0.14
(1,617)	1:414:A:ILE:HD12	1:444:A:ILE:HD11	10	0.14
(1,617)	1:414:A:ILE:HD12	1:444:A:ILE:HD12	10	0.14
(1,617)	1:414:A:ILE:HD12	1:444:A:ILE:HD13	10	0.14
(1,617)	1:414:A:ILE:HD13	1:444:A:ILE:HD11	10	0.14
(1,617)	1:414:A:ILE:HD13	1:444:A:ILE:HD12	10	0.14
(1,617)	1:414:A:ILE:HD13	1:444:A:ILE:HD13	10	0.14
(1,614)	1:386:A:VAL:H	1:414:A:ILE:HD11	15	0.14
(1,614)	1:386:A:VAL:H	1:414:A:ILE:HD12	15	0.14
(1,614)	1:386:A:VAL:H	1:414:A:ILE:HD13	15	0.14
(1,606)	1:410:A:LEU:HD11	1:411:A:ALA:H	1	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,606)	1:410:A:LEU:HD12	1:411:A:ALA:H	1	0.14
(1,606)	1:410:A:LEU:HD13	1:411:A:ALA:H	1	0.14
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG11	12	0.14
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG12	12	0.14
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG13	12	0.14
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG11	19	0.14
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG12	19	0.14
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG13	19	0.14
(1,592)	1:398:A:GLY:H	1:402:A:VAL:HG21	10	0.14
(1,592)	1:398:A:GLY:H	1:402:A:VAL:HG22	10	0.14
(1,592)	1:398:A:GLY:H	1:402:A:VAL:HG23	10	0.14
(1,592)	1:398:A:GLY:H	1:402:A:VAL:HG21	18	0.14
(1,592)	1:398:A:GLY:H	1:402:A:VAL:HG22	18	0.14
(1,592)	1:398:A:GLY:H	1:402:A:VAL:HG23	18	0.14
(1,580)	1:347:A:GLY:H	1:396:A:LEU:HD21	14	0.14
(1,580)	1:347:A:GLY:H	1:396:A:LEU:HD22	14	0.14
(1,580)	1:347:A:GLY:H	1:396:A:LEU:HD23	14	0.14
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD21	4	0.14
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD22	4	0.14
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD23	4	0.14
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD11	6	0.14
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD12	6	0.14
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD13	6	0.14
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD11	17	0.14
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD12	17	0.14
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD13	17	0.14
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD11	17	0.14
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD12	17	0.14
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD13	17	0.14
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD11	17	0.14
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD12	17	0.14
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD13	17	0.14
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD11	13	0.14
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD12	13	0.14
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD13	13	0.14
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD11	13	0.14
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD12	13	0.14
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD13	13	0.14
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD11	13	0.14
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD12	13	0.14
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD13	13	0.14
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD11	15	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD12	15	0.14
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD13	15	0.14
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD11	15	0.14
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD12	15	0.14
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD13	15	0.14
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD11	15	0.14
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD12	15	0.14
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD13	15	0.14
(1,29)	1:284:A:VAL:H	1:285:A:TRP:HE1	20	0.14
(2,201)	1:389:A:ASP:N	1:387:A:HIS:ND1	2	0.13
(2,201)	1:389:A:ASP:N	1:387:A:HIS:ND1	17	0.13
(2,122)	1:518:A:PHE:O	1:522:A:TYR:H	11	0.13
(2,122)	1:518:A:PHE:O	1:522:A:TYR:H	12	0.13
(2,122)	1:518:A:PHE:O	1:522:A:TYR:H	16	0.13
(2,122)	1:518:A:PHE:O	1:522:A:TYR:H	20	0.13
(2,94)	1:476:A:ASP:O	1:480:A:ARG:H	13	0.13
(2,21)	1:364:A:PRO:O	1:368:A:ASP:N	15	0.13
(1,1408)	1:466:A:TYR:H	1:469:A:MET:HE1	16	0.13
(1,1408)	1:466:A:TYR:H	1:469:A:MET:HE2	16	0.13
(1,1408)	1:466:A:TYR:H	1:469:A:MET:HE3	16	0.13
(1,1363)	1:295:A:VAL:HG21	1:340:A:VAL:H	1	0.13
(1,1363)	1:295:A:VAL:HG22	1:340:A:VAL:H	1	0.13
(1,1363)	1:295:A:VAL:HG23	1:340:A:VAL:H	1	0.13
(1,1363)	1:295:A:VAL:HG21	1:340:A:VAL:H	3	0.13
(1,1363)	1:295:A:VAL:HG22	1:340:A:VAL:H	3	0.13
(1,1363)	1:295:A:VAL:HG23	1:340:A:VAL:H	3	0.13
(1,1363)	1:295:A:VAL:HG21	1:340:A:VAL:H	5	0.13
(1,1363)	1:295:A:VAL:HG22	1:340:A:VAL:H	5	0.13
(1,1363)	1:295:A:VAL:HG23	1:340:A:VAL:H	5	0.13
(1,1363)	1:295:A:VAL:HG21	1:340:A:VAL:H	8	0.13
(1,1363)	1:295:A:VAL:HG22	1:340:A:VAL:H	8	0.13
(1,1363)	1:295:A:VAL:HG23	1:340:A:VAL:H	8	0.13
(1,1363)	1:295:A:VAL:HG21	1:340:A:VAL:H	9	0.13
(1,1363)	1:295:A:VAL:HG22	1:340:A:VAL:H	9	0.13
(1,1363)	1:295:A:VAL:HG23	1:340:A:VAL:H	9	0.13
(1,1363)	1:295:A:VAL:HG21	1:340:A:VAL:H	14	0.13
(1,1363)	1:295:A:VAL:HG22	1:340:A:VAL:H	14	0.13
(1,1363)	1:295:A:VAL:HG23	1:340:A:VAL:H	14	0.13
(1,1311)	1:289:A:TRP:HE1	1:290:A:ASN:H	4	0.13
(1,1288)	1:271:A:ARG:H	1:290:A:ASN:H	6	0.13
(1,1288)	1:271:A:ARG:H	1:290:A:ASN:H	16	0.13
(1,1282)	1:431:A:TRP:HE1	1:454:A:LEU:HD11	5	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1282)	1:431:A:TRP:HE1	1:454:A:LEU:HD12	5	0.13
(1,1282)	1:431:A:TRP:HE1	1:454:A:LEU:HD13	5	0.13
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD21	8	0.13
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD22	8	0.13
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD23	8	0.13
(1,1210)	1:410:A:LEU:HD21	1:425:A:ALA:H	8	0.13
(1,1210)	1:410:A:LEU:HD22	1:425:A:ALA:H	8	0.13
(1,1210)	1:410:A:LEU:HD23	1:425:A:ALA:H	8	0.13
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD11	3	0.13
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD12	3	0.13
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD13	3	0.13
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD11	15	0.13
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD12	15	0.13
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD13	15	0.13
(1,1071)	1:270:A:LEU:HD11	1:339:A:ILE:H	19	0.13
(1,1071)	1:270:A:LEU:HD12	1:339:A:ILE:H	19	0.13
(1,1071)	1:270:A:LEU:HD13	1:339:A:ILE:H	19	0.13
(1,1054)	1:361:A:LEU:HD21	1:362:A:ARG:H	4	0.13
(1,1054)	1:361:A:LEU:HD22	1:362:A:ARG:H	4	0.13
(1,1054)	1:361:A:LEU:HD23	1:362:A:ARG:H	4	0.13
(1,1054)	1:361:A:LEU:HD21	1:362:A:ARG:H	8	0.13
(1,1054)	1:361:A:LEU:HD22	1:362:A:ARG:H	8	0.13
(1,1054)	1:361:A:LEU:HD23	1:362:A:ARG:H	8	0.13
(1,959)	1:289:A:TRP:H	1:329:A:TYR:HE2	13	0.13
(1,959)	1:289:A:TRP:H	1:329:A:TYR:HE2	20	0.13
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD11	15	0.13
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD12	15	0.13
(1,958)	1:310:A:PHE:HE2	1:311:A:LEU:HD13	15	0.13
(1,956)	1:419:A:PTR:H	1:419:A:PTR:HE2	9	0.13
(1,950)	1:419:A:PTR:HE1	1:420:A:THR:H	17	0.13
(1,893)	1:367:A:VAL:HG21	1:523:A:PHE:HE2	2	0.13
(1,893)	1:367:A:VAL:HG22	1:523:A:PHE:HE2	2	0.13
(1,893)	1:367:A:VAL:HG23	1:523:A:PHE:HE2	2	0.13
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD11	4	0.13
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD12	4	0.13
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD13	4	0.13
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD11	5	0.13
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD12	5	0.13
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD13	5	0.13
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD11	19	0.13
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD12	19	0.13
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD13	19	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,782)	1:469:A:MET:HE1	1:470:A:VAL:H	3	0.13
(1,782)	1:469:A:MET:HE2	1:470:A:VAL:H	3	0.13
(1,782)	1:469:A:MET:HE3	1:470:A:VAL:H	3	0.13
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD21	14	0.13
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD22	14	0.13
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD23	14	0.13
(1,741)	1:459:A:THR:H	1:536:A:LEU:HD11	7	0.13
(1,741)	1:459:A:THR:H	1:536:A:LEU:HD12	7	0.13
(1,741)	1:459:A:THR:H	1:536:A:LEU:HD13	7	0.13
(1,699)	1:478:A:VAL:HG11	1:482:A:TYR:H	6	0.13
(1,699)	1:478:A:VAL:HG12	1:482:A:TYR:H	6	0.13
(1,699)	1:478:A:VAL:HG13	1:482:A:TYR:H	6	0.13
(1,699)	1:478:A:VAL:HG11	1:482:A:TYR:H	14	0.13
(1,699)	1:478:A:VAL:HG12	1:482:A:TYR:H	14	0.13
(1,699)	1:478:A:VAL:HG13	1:482:A:TYR:H	14	0.13
(1,642)	1:438:A:LEU:HD21	1:439:A:TYR:HE1	16	0.13
(1,642)	1:438:A:LEU:HD22	1:439:A:TYR:HE1	16	0.13
(1,642)	1:438:A:LEU:HD23	1:439:A:TYR:HE1	16	0.13
(1,617)	1:414:A:ILE:HD11	1:444:A:ILE:HD11	7	0.13
(1,617)	1:414:A:ILE:HD11	1:444:A:ILE:HD12	7	0.13
(1,617)	1:414:A:ILE:HD11	1:444:A:ILE:HD13	7	0.13
(1,617)	1:414:A:ILE:HD12	1:444:A:ILE:HD11	7	0.13
(1,617)	1:414:A:ILE:HD12	1:444:A:ILE:HD12	7	0.13
(1,617)	1:414:A:ILE:HD12	1:444:A:ILE:HD13	7	0.13
(1,617)	1:414:A:ILE:HD13	1:444:A:ILE:HD11	7	0.13
(1,617)	1:414:A:ILE:HD13	1:444:A:ILE:HD12	7	0.13
(1,617)	1:414:A:ILE:HD13	1:444:A:ILE:HD13	7	0.13
(1,606)	1:410:A:LEU:HD11	1:411:A:ALA:H	10	0.13
(1,606)	1:410:A:LEU:HD12	1:411:A:ALA:H	10	0.13
(1,606)	1:410:A:LEU:HD13	1:411:A:ALA:H	10	0.13
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG11	4	0.13
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG12	4	0.13
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG13	4	0.13
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG11	5	0.13
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG12	5	0.13
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG13	5	0.13
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG11	20	0.13
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG12	20	0.13
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG13	20	0.13
(1,544)	1:363:A:LEU:HD21	1:530:A:TYR:HE1	10	0.13
(1,544)	1:363:A:LEU:HD22	1:530:A:TYR:HE1	10	0.13
(1,544)	1:363:A:LEU:HD23	1:530:A:TYR:HE1	10	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,543)	1:363:A:LEU:HD21	1:523:A:PHE:HE1	13	0.13
(1,543)	1:363:A:LEU:HD22	1:523:A:PHE:HE1	13	0.13
(1,543)	1:363:A:LEU:HD23	1:523:A:PHE:HE1	13	0.13
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD21	1	0.13
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD22	1	0.13
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD23	1	0.13
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD21	18	0.13
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD22	18	0.13
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD23	18	0.13
(1,522)	1:344:A:MET:HE1	1:399:A:GLU:H	11	0.13
(1,522)	1:344:A:MET:HE2	1:399:A:GLU:H	11	0.13
(1,522)	1:344:A:MET:HE3	1:399:A:GLU:H	11	0.13
(1,512)	1:298:A:LYS:H	1:340:A:VAL:HG21	11	0.13
(1,512)	1:298:A:LYS:H	1:340:A:VAL:HG22	11	0.13
(1,512)	1:298:A:LYS:H	1:340:A:VAL:HG23	11	0.13
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD11	7	0.13
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD12	7	0.13
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD13	7	0.13
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD11	8	0.13
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD12	8	0.13
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD13	8	0.13
(1,405)	1:286:A:MET:HE1	1:295:A:VAL:H	4	0.13
(1,405)	1:286:A:MET:HE2	1:295:A:VAL:H	4	0.13
(1,405)	1:286:A:MET:HE3	1:295:A:VAL:H	4	0.13
(1,405)	1:286:A:MET:HE1	1:295:A:VAL:H	15	0.13
(1,405)	1:286:A:MET:HE2	1:295:A:VAL:H	15	0.13
(1,405)	1:286:A:MET:HE3	1:295:A:VAL:H	15	0.13
(1,390)	1:272:A:LEU:HD11	1:285:A:TRP:HE1	3	0.13
(1,390)	1:272:A:LEU:HD12	1:285:A:TRP:HE1	3	0.13
(1,390)	1:272:A:LEU:HD13	1:285:A:TRP:HE1	3	0.13
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE1	3	0.13
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE2	3	0.13
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE3	3	0.13
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE1	3	0.13
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE2	3	0.13
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE3	3	0.13
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE1	3	0.13
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE2	3	0.13
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE3	3	0.13
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD11	8	0.13
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD12	8	0.13
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD13	8	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD11	8	0.13
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD12	8	0.13
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD13	8	0.13
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD11	8	0.13
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD12	8	0.13
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD13	8	0.13
(1,254)	1:386:A:VAL:HG11	1:414:A:ILE:HD11	3	0.13
(1,254)	1:386:A:VAL:HG11	1:414:A:ILE:HD12	3	0.13
(1,254)	1:386:A:VAL:HG11	1:414:A:ILE:HD13	3	0.13
(1,254)	1:386:A:VAL:HG12	1:414:A:ILE:HD11	3	0.13
(1,254)	1:386:A:VAL:HG12	1:414:A:ILE:HD12	3	0.13
(1,254)	1:386:A:VAL:HG12	1:414:A:ILE:HD13	3	0.13
(1,254)	1:386:A:VAL:HG13	1:414:A:ILE:HD11	3	0.13
(1,254)	1:386:A:VAL:HG13	1:414:A:ILE:HD12	3	0.13
(1,254)	1:386:A:VAL:HG13	1:414:A:ILE:HD13	3	0.13
(1,254)	1:386:A:VAL:HG11	1:414:A:ILE:HD11	6	0.13
(1,254)	1:386:A:VAL:HG11	1:414:A:ILE:HD12	6	0.13
(1,254)	1:386:A:VAL:HG11	1:414:A:ILE:HD13	6	0.13
(1,254)	1:386:A:VAL:HG12	1:414:A:ILE:HD11	6	0.13
(1,254)	1:386:A:VAL:HG12	1:414:A:ILE:HD12	6	0.13
(1,254)	1:386:A:VAL:HG12	1:414:A:ILE:HD13	6	0.13
(1,254)	1:386:A:VAL:HG13	1:414:A:ILE:HD11	6	0.13
(1,254)	1:386:A:VAL:HG13	1:414:A:ILE:HD12	6	0.13
(1,254)	1:386:A:VAL:HG13	1:414:A:ILE:HD13	6	0.13
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD11	3	0.13
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD12	3	0.13
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD13	3	0.13
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD11	3	0.13
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD12	3	0.13
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD13	3	0.13
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD11	3	0.13
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD12	3	0.13
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD13	3	0.13
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD11	6	0.13
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD12	6	0.13
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD13	6	0.13
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD11	6	0.13
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD12	6	0.13
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD13	6	0.13
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD11	6	0.13
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD12	6	0.13
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD13	6	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD11	15	0.13
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD12	15	0.13
(1,205)	1:369:A:MET:HE1	1:401:A:LEU:HD13	15	0.13
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD11	15	0.13
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD12	15	0.13
(1,205)	1:369:A:MET:HE2	1:401:A:LEU:HD13	15	0.13
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD11	15	0.13
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD12	15	0.13
(1,205)	1:369:A:MET:HE3	1:401:A:LEU:HD13	15	0.13
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD11	9	0.13
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD12	9	0.13
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD13	9	0.13
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD11	9	0.13
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD12	9	0.13
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD13	9	0.13
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD11	9	0.13
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD12	9	0.13
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD13	9	0.13
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD11	16	0.13
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD12	16	0.13
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD13	16	0.13
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD11	16	0.13
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD12	16	0.13
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD13	16	0.13
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD11	16	0.13
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD12	16	0.13
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD13	16	0.13
(1,29)	1:284:A:VAL:H	1:285:A:TRP:HE1	15	0.13
(2,201)	1:389:A:ASP:N	1:387:A:HIS:ND1	9	0.12
(2,201)	1:389:A:ASP:N	1:387:A:HIS:ND1	15	0.12
(2,201)	1:389:A:ASP:N	1:387:A:HIS:ND1	16	0.12
(2,122)	1:518:A:PHE:O	1:522:A:TYR:H	5	0.12
(2,122)	1:518:A:PHE:O	1:522:A:TYR:H	19	0.12
(2,92)	1:475:A:LEU:O	1:479:A:GLU:H	1	0.12
(2,21)	1:364:A:PRO:O	1:368:A:ASP:N	2	0.12
(2,21)	1:364:A:PRO:O	1:368:A:ASP:N	3	0.12
(2,21)	1:364:A:PRO:O	1:368:A:ASP:N	10	0.12
(2,21)	1:364:A:PRO:O	1:368:A:ASP:N	12	0.12
(2,21)	1:364:A:PRO:O	1:368:A:ASP:N	14	0.12
(2,21)	1:364:A:PRO:O	1:368:A:ASP:N	16	0.12
(2,6)	1:312:A:GLN:O	1:316:A:VAL:H	2	0.12
(1,1408)	1:466:A:TYR:H	1:469:A:MET:HE1	19	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1408)	1:466:A:TYR:H	1:469:A:MET:HE2	19	0.12
(1,1408)	1:466:A:TYR:H	1:469:A:MET:HE3	19	0.12
(1,1403)	1:366:A:LEU:HD11	1:461:A:LYS:H	10	0.12
(1,1403)	1:366:A:LEU:HD12	1:461:A:LYS:H	10	0.12
(1,1403)	1:366:A:LEU:HD13	1:461:A:LYS:H	10	0.12
(1,1363)	1:295:A:VAL:HG21	1:340:A:VAL:H	19	0.12
(1,1363)	1:295:A:VAL:HG22	1:340:A:VAL:H	19	0.12
(1,1363)	1:295:A:VAL:HG23	1:340:A:VAL:H	19	0.12
(1,1302)	1:283:A:GLU:H	1:299:A:THR:HG21	18	0.12
(1,1302)	1:283:A:GLU:H	1:299:A:THR:HG22	18	0.12
(1,1302)	1:283:A:GLU:H	1:299:A:THR:HG23	18	0.12
(1,1282)	1:431:A:TRP:HE1	1:454:A:LEU:HD11	9	0.12
(1,1282)	1:431:A:TRP:HE1	1:454:A:LEU:HD12	9	0.12
(1,1282)	1:431:A:TRP:HE1	1:454:A:LEU:HD13	9	0.12
(1,1268)	1:262:A:ALA:H	1:264:A:GLU:H	17	0.12
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD21	5	0.12
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD22	5	0.12
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD23	5	0.12
(1,1199)	1:261:A:ASP:H	1:262:A:ALA:H	14	0.12
(1,1152)	1:523:A:PHE:H	1:525:A:SER:H	16	0.12
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD11	20	0.12
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD12	20	0.12
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD13	20	0.12
(1,1054)	1:361:A:LEU:HD21	1:362:A:ARG:H	2	0.12
(1,1054)	1:361:A:LEU:HD22	1:362:A:ARG:H	2	0.12
(1,1054)	1:361:A:LEU:HD23	1:362:A:ARG:H	2	0.12
(1,973)	1:259:A:ALA:HB1	1:260:A:LYS:H	19	0.12
(1,973)	1:259:A:ALA:HB2	1:260:A:LYS:H	19	0.12
(1,973)	1:259:A:ALA:HB3	1:260:A:LYS:H	19	0.12
(1,949)	1:410:A:LEU:HD21	1:419:A:PTR:HE1	9	0.12
(1,949)	1:410:A:LEU:HD22	1:419:A:PTR:HE1	9	0.12
(1,949)	1:410:A:LEU:HD23	1:419:A:PTR:HE1	9	0.12
(1,857)	1:419:A:PTR:HE1	1:421:A:ALA:H	20	0.12
(1,803)	1:421:A:ALA:HB1	1:427:A:PHE:HE1	4	0.12
(1,803)	1:421:A:ALA:HB2	1:427:A:PHE:HE1	4	0.12
(1,803)	1:421:A:ALA:HB3	1:427:A:PHE:HE1	4	0.12
(1,790)	1:525:A:SER:H	1:526:A:THR:HG21	20	0.12
(1,790)	1:525:A:SER:H	1:526:A:THR:HG22	20	0.12
(1,790)	1:525:A:SER:H	1:526:A:THR:HG23	20	0.12
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD11	3	0.12
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD12	3	0.12
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD13	3	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD11	11	0.12
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD12	11	0.12
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD13	11	0.12
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD21	8	0.12
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD22	8	0.12
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD23	8	0.12
(1,728)	1:512:A:PHE:HE1	1:515:A:LEU:HD21	18	0.12
(1,728)	1:512:A:PHE:HE1	1:515:A:LEU:HD22	18	0.12
(1,728)	1:512:A:PHE:HE1	1:515:A:LEU:HD23	18	0.12
(1,647)	1:284:A:VAL:H	1:299:A:THR:HG21	20	0.12
(1,647)	1:284:A:VAL:H	1:299:A:THR:HG22	20	0.12
(1,647)	1:284:A:VAL:H	1:299:A:THR:HG23	20	0.12
(1,642)	1:438:A:LEU:HD21	1:439:A:TYR:HE1	3	0.12
(1,642)	1:438:A:LEU:HD22	1:439:A:TYR:HE1	3	0.12
(1,642)	1:438:A:LEU:HD23	1:439:A:TYR:HE1	3	0.12
(1,642)	1:438:A:LEU:HD21	1:439:A:TYR:HE1	8	0.12
(1,642)	1:438:A:LEU:HD22	1:439:A:TYR:HE1	8	0.12
(1,642)	1:438:A:LEU:HD23	1:439:A:TYR:HE1	8	0.12
(1,642)	1:438:A:LEU:HD21	1:439:A:TYR:HE1	13	0.12
(1,642)	1:438:A:LEU:HD22	1:439:A:TYR:HE1	13	0.12
(1,642)	1:438:A:LEU:HD23	1:439:A:TYR:HE1	13	0.12
(1,617)	1:414:A:ILE:HD11	1:444:A:ILE:HD11	8	0.12
(1,617)	1:414:A:ILE:HD11	1:444:A:ILE:HD12	8	0.12
(1,617)	1:414:A:ILE:HD11	1:444:A:ILE:HD13	8	0.12
(1,617)	1:414:A:ILE:HD12	1:444:A:ILE:HD11	8	0.12
(1,617)	1:414:A:ILE:HD12	1:444:A:ILE:HD12	8	0.12
(1,617)	1:414:A:ILE:HD12	1:444:A:ILE:HD13	8	0.12
(1,617)	1:414:A:ILE:HD13	1:444:A:ILE:HD11	8	0.12
(1,617)	1:414:A:ILE:HD13	1:444:A:ILE:HD12	8	0.12
(1,617)	1:414:A:ILE:HD13	1:444:A:ILE:HD13	8	0.12
(1,614)	1:386:A:VAL:H	1:414:A:ILE:HD11	16	0.12
(1,614)	1:386:A:VAL:H	1:414:A:ILE:HD12	16	0.12
(1,614)	1:386:A:VAL:H	1:414:A:ILE:HD13	16	0.12
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG11	15	0.12
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG12	15	0.12
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG13	15	0.12
(1,577)	1:344:A:MET:H	1:396:A:LEU:HD21	7	0.12
(1,577)	1:344:A:MET:H	1:396:A:LEU:HD22	7	0.12
(1,577)	1:344:A:MET:H	1:396:A:LEU:HD23	7	0.12
(1,577)	1:344:A:MET:H	1:396:A:LEU:HD21	9	0.12
(1,577)	1:344:A:MET:H	1:396:A:LEU:HD22	9	0.12
(1,577)	1:344:A:MET:H	1:396:A:LEU:HD23	9	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,577)	1:344:A:MET:H	1:396:A:LEU:HD21	11	0.12
(1,577)	1:344:A:MET:H	1:396:A:LEU:HD22	11	0.12
(1,577)	1:344:A:MET:H	1:396:A:LEU:HD23	11	0.12
(1,577)	1:344:A:MET:H	1:396:A:LEU:HD21	14	0.12
(1,577)	1:344:A:MET:H	1:396:A:LEU:HD22	14	0.12
(1,577)	1:344:A:MET:H	1:396:A:LEU:HD23	14	0.12
(1,548)	1:371:A:ALA:HB1	1:521:A:ASP:H	12	0.12
(1,548)	1:371:A:ALA:HB2	1:521:A:ASP:H	12	0.12
(1,548)	1:371:A:ALA:HB3	1:521:A:ASP:H	12	0.12
(1,524)	1:344:A:MET:HE1	1:397:A:VAL:H	8	0.12
(1,524)	1:344:A:MET:HE2	1:397:A:VAL:H	8	0.12
(1,524)	1:344:A:MET:HE3	1:397:A:VAL:H	8	0.12
(1,524)	1:344:A:MET:HE1	1:397:A:VAL:H	10	0.12
(1,524)	1:344:A:MET:HE2	1:397:A:VAL:H	10	0.12
(1,524)	1:344:A:MET:HE3	1:397:A:VAL:H	10	0.12
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD11	19	0.12
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD12	19	0.12
(1,505)	1:332:A:VAL:H	1:337:A:ILE:HD13	19	0.12
(1,405)	1:286:A:MET:HE1	1:295:A:VAL:H	3	0.12
(1,405)	1:286:A:MET:HE2	1:295:A:VAL:H	3	0.12
(1,405)	1:286:A:MET:HE3	1:295:A:VAL:H	3	0.12
(1,378)	1:261:A:ASP:H	1:262:A:ALA:HB1	10	0.12
(1,378)	1:261:A:ASP:H	1:262:A:ALA:HB2	10	0.12
(1,378)	1:261:A:ASP:H	1:262:A:ALA:HB3	10	0.12
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE1	6	0.12
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE2	6	0.12
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE3	6	0.12
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE1	6	0.12
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE2	6	0.12
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE3	6	0.12
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE1	6	0.12
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE2	6	0.12
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE3	6	0.12
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE1	17	0.12
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE2	17	0.12
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE3	17	0.12
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE1	17	0.12
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE2	17	0.12
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE3	17	0.12
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE1	17	0.12
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE2	17	0.12
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE3	17	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD11	18	0.12
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD12	18	0.12
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD13	18	0.12
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD11	18	0.12
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD12	18	0.12
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD13	18	0.12
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD11	18	0.12
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD12	18	0.12
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD13	18	0.12
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD11	6	0.12
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD12	6	0.12
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD13	6	0.12
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD11	6	0.12
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD12	6	0.12
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD13	6	0.12
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD11	6	0.12
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD12	6	0.12
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD13	6	0.12
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD11	10	0.12
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD12	10	0.12
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD13	10	0.12
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD11	10	0.12
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD12	10	0.12
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD13	10	0.12
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD11	10	0.12
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD12	10	0.12
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD13	10	0.12
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD11	17	0.12
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD12	17	0.12
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD13	17	0.12
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD11	17	0.12
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD12	17	0.12
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD13	17	0.12
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD11	17	0.12
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD12	17	0.12
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD13	17	0.12
(2,207)	1:264:A:GLU:OE1	1:333:A:SER:OG	9	0.11
(2,203)	1:394:A:ASN:OD1	1:407:A:ASP:OD2	6	0.11
(2,203)	1:394:A:ASN:OD1	1:407:A:ASP:OD2	10	0.11
(2,201)	1:389:A:ASP:N	1:387:A:HIS:ND1	1	0.11
(2,201)	1:389:A:ASP:N	1:387:A:HIS:ND1	3	0.11
(2,201)	1:389:A:ASP:N	1:387:A:HIS:ND1	4	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,134)	1:277:A:GLY:O	1:284:A:VAL:H	15	0.11
(2,122)	1:518:A:PHE:O	1:522:A:TYR:H	2	0.11
(2,122)	1:518:A:PHE:O	1:522:A:TYR:H	14	0.11
(2,118)	1:516:A:GLN:O	1:520:A:GLU:H	9	0.11
(2,94)	1:476:A:ASP:O	1:480:A:ARG:H	3	0.11
(2,94)	1:476:A:ASP:O	1:480:A:ARG:H	7	0.11
(2,94)	1:476:A:ASP:O	1:480:A:ARG:H	14	0.11
(2,21)	1:364:A:PRO:O	1:368:A:ASP:N	1	0.11
(2,21)	1:364:A:PRO:O	1:368:A:ASP:N	5	0.11
(2,21)	1:364:A:PRO:O	1:368:A:ASP:N	8	0.11
(2,21)	1:364:A:PRO:O	1:368:A:ASP:N	13	0.11
(2,21)	1:364:A:PRO:O	1:368:A:ASP:N	17	0.11
(2,21)	1:364:A:PRO:O	1:368:A:ASP:N	19	0.11
(2,21)	1:364:A:PRO:O	1:368:A:ASP:N	20	0.11
(1,1408)	1:466:A:TYR:H	1:469:A:MET:HE1	13	0.11
(1,1408)	1:466:A:TYR:H	1:469:A:MET:HE2	13	0.11
(1,1408)	1:466:A:TYR:H	1:469:A:MET:HE3	13	0.11
(1,1403)	1:366:A:LEU:HD11	1:461:A:LYS:H	16	0.11
(1,1403)	1:366:A:LEU:HD12	1:461:A:LYS:H	16	0.11
(1,1403)	1:366:A:LEU:HD13	1:461:A:LYS:H	16	0.11
(1,1363)	1:295:A:VAL:HG21	1:340:A:VAL:H	18	0.11
(1,1363)	1:295:A:VAL:HG22	1:340:A:VAL:H	18	0.11
(1,1363)	1:295:A:VAL:HG23	1:340:A:VAL:H	18	0.11
(1,1322)	1:297:A:ILE:HD11	1:298:A:LYS:H	14	0.11
(1,1322)	1:297:A:ILE:HD12	1:298:A:LYS:H	14	0.11
(1,1322)	1:297:A:ILE:HD13	1:298:A:LYS:H	14	0.11
(1,1288)	1:271:A:ARG:H	1:290:A:ASN:H	18	0.11
(1,1282)	1:431:A:TRP:HE1	1:454:A:LEU:HD11	16	0.11
(1,1282)	1:431:A:TRP:HE1	1:454:A:LEU:HD12	16	0.11
(1,1282)	1:431:A:TRP:HE1	1:454:A:LEU:HD13	16	0.11
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD21	12	0.11
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD22	12	0.11
(1,1212)	1:324:A:LYS:H	1:325:A:LEU:HD23	12	0.11
(1,1210)	1:410:A:LEU:HD21	1:425:A:ALA:H	11	0.11
(1,1210)	1:410:A:LEU:HD22	1:425:A:ALA:H	11	0.11
(1,1210)	1:410:A:LEU:HD23	1:425:A:ALA:H	11	0.11
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD11	17	0.11
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD12	17	0.11
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD13	17	0.11
(1,1071)	1:270:A:LEU:HD11	1:339:A:ILE:H	11	0.11
(1,1071)	1:270:A:LEU:HD12	1:339:A:ILE:H	11	0.11
(1,1071)	1:270:A:LEU:HD13	1:339:A:ILE:H	11	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1071)	1:270:A:LEU:HD11	1:339:A:ILE:H	18	0.11
(1,1071)	1:270:A:LEU:HD12	1:339:A:ILE:H	18	0.11
(1,1071)	1:270:A:LEU:HD13	1:339:A:ILE:H	18	0.11
(1,1062)	1:367:A:VAL:HG11	1:368:A:ASP:H	6	0.11
(1,1062)	1:367:A:VAL:HG12	1:368:A:ASP:H	6	0.11
(1,1062)	1:367:A:VAL:HG13	1:368:A:ASP:H	6	0.11
(1,1055)	1:362:A:ARG:H	1:366:A:LEU:HD11	7	0.11
(1,1055)	1:362:A:ARG:H	1:366:A:LEU:HD12	7	0.11
(1,1055)	1:362:A:ARG:H	1:366:A:LEU:HD13	7	0.11
(1,1054)	1:361:A:LEU:HD21	1:362:A:ARG:H	7	0.11
(1,1054)	1:361:A:LEU:HD22	1:362:A:ARG:H	7	0.11
(1,1054)	1:361:A:LEU:HD23	1:362:A:ARG:H	7	0.11
(1,965)	1:455:A:LEU:HD11	1:518:A:PHE:HE1	2	0.11
(1,965)	1:455:A:LEU:HD12	1:518:A:PHE:HE1	2	0.11
(1,965)	1:455:A:LEU:HD13	1:518:A:PHE:HE1	2	0.11
(1,965)	1:455:A:LEU:HD11	1:518:A:PHE:HE1	11	0.11
(1,965)	1:455:A:LEU:HD12	1:518:A:PHE:HE1	11	0.11
(1,965)	1:455:A:LEU:HD13	1:518:A:PHE:HE1	11	0.11
(1,965)	1:455:A:LEU:HD11	1:518:A:PHE:HE1	14	0.11
(1,965)	1:455:A:LEU:HD12	1:518:A:PHE:HE1	14	0.11
(1,965)	1:455:A:LEU:HD13	1:518:A:PHE:HE1	14	0.11
(1,950)	1:419:A:PTR:HE1	1:420:A:THR:H	11	0.11
(1,949)	1:410:A:LEU:HD21	1:419:A:PTR:HE1	11	0.11
(1,949)	1:410:A:LEU:HD22	1:419:A:PTR:HE1	11	0.11
(1,949)	1:410:A:LEU:HD23	1:419:A:PTR:HE1	11	0.11
(1,940)	1:426:A:LYS:H	1:427:A:PHE:HE1	14	0.11
(1,865)	1:359:A:LYS:H	1:360:A:TYR:HE1	11	0.11
(1,864)	1:297:A:ILE:HD11	1:338:A:TYR:HE2	13	0.11
(1,864)	1:297:A:ILE:HD12	1:338:A:TYR:HE2	13	0.11
(1,864)	1:297:A:ILE:HD13	1:338:A:TYR:HE2	13	0.11
(1,864)	1:297:A:ILE:HD11	1:338:A:TYR:HE2	19	0.11
(1,864)	1:297:A:ILE:HD12	1:338:A:TYR:HE2	19	0.11
(1,864)	1:297:A:ILE:HD13	1:338:A:TYR:HE2	19	0.11
(1,864)	1:297:A:ILE:HD11	1:338:A:TYR:HE2	20	0.11
(1,864)	1:297:A:ILE:HD12	1:338:A:TYR:HE2	20	0.11
(1,864)	1:297:A:ILE:HD13	1:338:A:TYR:HE2	20	0.11
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD11	15	0.11
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD12	15	0.11
(1,788)	1:514:A:TYR:HE2	1:515:A:LEU:HD13	15	0.11
(1,782)	1:469:A:MET:HE1	1:470:A:VAL:H	9	0.11
(1,782)	1:469:A:MET:HE2	1:470:A:VAL:H	9	0.11
(1,782)	1:469:A:MET:HE3	1:470:A:VAL:H	9	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,782)	1:469:A:MET:HE1	1:470:A:VAL:H	10	0.11
(1,782)	1:469:A:MET:HE2	1:470:A:VAL:H	10	0.11
(1,782)	1:469:A:MET:HE3	1:470:A:VAL:H	10	0.11
(1,780)	1:436:A:ALA:HB1	1:442:A:PHE:HE1	13	0.11
(1,780)	1:436:A:ALA:HB2	1:442:A:PHE:HE1	13	0.11
(1,780)	1:436:A:ALA:HB3	1:442:A:PHE:HE1	13	0.11
(1,754)	1:259:A:ALA:HB1	1:261:A:ASP:H	4	0.11
(1,754)	1:259:A:ALA:HB2	1:261:A:ASP:H	4	0.11
(1,754)	1:259:A:ALA:HB3	1:261:A:ASP:H	4	0.11
(1,728)	1:512:A:PHE:HE1	1:515:A:LEU:HD21	20	0.11
(1,728)	1:512:A:PHE:HE1	1:515:A:LEU:HD22	20	0.11
(1,728)	1:512:A:PHE:HE1	1:515:A:LEU:HD23	20	0.11
(1,708)	1:466:A:TYR:HE2	1:484:A:MET:HE1	8	0.11
(1,708)	1:466:A:TYR:HE2	1:484:A:MET:HE2	8	0.11
(1,708)	1:466:A:TYR:HE2	1:484:A:MET:HE3	8	0.11
(1,708)	1:466:A:TYR:HE2	1:484:A:MET:HE1	20	0.11
(1,708)	1:466:A:TYR:HE2	1:484:A:MET:HE2	20	0.11
(1,708)	1:466:A:TYR:HE2	1:484:A:MET:HE3	20	0.11
(1,694)	1:438:A:LEU:H	1:475:A:LEU:HD11	2	0.11
(1,694)	1:438:A:LEU:H	1:475:A:LEU:HD12	2	0.11
(1,694)	1:438:A:LEU:H	1:475:A:LEU:HD13	2	0.11
(1,642)	1:438:A:LEU:HD21	1:439:A:TYR:HE1	10	0.11
(1,642)	1:438:A:LEU:HD22	1:439:A:TYR:HE1	10	0.11
(1,642)	1:438:A:LEU:HD23	1:439:A:TYR:HE1	10	0.11
(1,642)	1:438:A:LEU:HD21	1:439:A:TYR:HE1	11	0.11
(1,642)	1:438:A:LEU:HD22	1:439:A:TYR:HE1	11	0.11
(1,642)	1:438:A:LEU:HD23	1:439:A:TYR:HE1	11	0.11
(1,642)	1:438:A:LEU:HD21	1:439:A:TYR:HE1	12	0.11
(1,642)	1:438:A:LEU:HD22	1:439:A:TYR:HE1	12	0.11
(1,642)	1:438:A:LEU:HD23	1:439:A:TYR:HE1	12	0.11
(1,606)	1:410:A:LEU:HD11	1:411:A:ALA:H	2	0.11
(1,606)	1:410:A:LEU:HD12	1:411:A:ALA:H	2	0.11
(1,606)	1:410:A:LEU:HD13	1:411:A:ALA:H	2	0.11
(1,606)	1:410:A:LEU:HD11	1:411:A:ALA:H	6	0.11
(1,606)	1:410:A:LEU:HD12	1:411:A:ALA:H	6	0.11
(1,606)	1:410:A:LEU:HD13	1:411:A:ALA:H	6	0.11
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG11	3	0.11
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG12	3	0.11
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG13	3	0.11
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG11	13	0.11
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG12	13	0.11
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG13	13	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,580)	1:347:A:GLY:H	1:396:A:LEU:HD21	10	0.11
(1,580)	1:347:A:GLY:H	1:396:A:LEU:HD22	10	0.11
(1,580)	1:347:A:GLY:H	1:396:A:LEU:HD23	10	0.11
(1,543)	1:363:A:LEU:HD21	1:523:A:PHE:HE1	14	0.11
(1,543)	1:363:A:LEU:HD22	1:523:A:PHE:HE1	14	0.11
(1,543)	1:363:A:LEU:HD23	1:523:A:PHE:HE1	14	0.11
(1,543)	1:363:A:LEU:HD21	1:523:A:PHE:HE1	17	0.11
(1,543)	1:363:A:LEU:HD22	1:523:A:PHE:HE1	17	0.11
(1,543)	1:363:A:LEU:HD23	1:523:A:PHE:HE1	17	0.11
(1,512)	1:298:A:LYS:H	1:340:A:VAL:HG21	10	0.11
(1,512)	1:298:A:LYS:H	1:340:A:VAL:HG22	10	0.11
(1,512)	1:298:A:LYS:H	1:340:A:VAL:HG23	10	0.11
(1,512)	1:298:A:LYS:H	1:340:A:VAL:HG21	16	0.11
(1,512)	1:298:A:LYS:H	1:340:A:VAL:HG22	16	0.11
(1,512)	1:298:A:LYS:H	1:340:A:VAL:HG23	16	0.11
(1,405)	1:286:A:MET:HE1	1:295:A:VAL:H	5	0.11
(1,405)	1:286:A:MET:HE2	1:295:A:VAL:H	5	0.11
(1,405)	1:286:A:MET:HE3	1:295:A:VAL:H	5	0.11
(1,390)	1:272:A:LEU:HD11	1:285:A:TRP:HE1	15	0.11
(1,390)	1:272:A:LEU:HD12	1:285:A:TRP:HE1	15	0.11
(1,390)	1:272:A:LEU:HD13	1:285:A:TRP:HE1	15	0.11
(1,390)	1:272:A:LEU:HD11	1:285:A:TRP:HE1	20	0.11
(1,390)	1:272:A:LEU:HD12	1:285:A:TRP:HE1	20	0.11
(1,390)	1:272:A:LEU:HD13	1:285:A:TRP:HE1	20	0.11
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE1	10	0.11
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE2	10	0.11
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE3	10	0.11
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE1	10	0.11
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE2	10	0.11
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE3	10	0.11
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE1	10	0.11
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE2	10	0.11
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE3	10	0.11
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD11	10	0.11
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD12	10	0.11
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD13	10	0.11
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD11	10	0.11
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD12	10	0.11
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD13	10	0.11
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD11	10	0.11
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD12	10	0.11
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD13	10	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD11	14	0.11
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD12	14	0.11
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD13	14	0.11
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD11	14	0.11
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD12	14	0.11
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD13	14	0.11
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD11	14	0.11
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD12	14	0.11
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD13	14	0.11
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD11	15	0.11
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD12	15	0.11
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD13	15	0.11
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD11	15	0.11
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD12	15	0.11
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD13	15	0.11
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD11	15	0.11
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD12	15	0.11
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD13	15	0.11
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD11	19	0.11
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD12	19	0.11
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD13	19	0.11
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD11	19	0.11
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD12	19	0.11
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD13	19	0.11
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD11	19	0.11
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD12	19	0.11
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD13	19	0.11
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD11	5	0.11
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD12	5	0.11
(1,120)	1:274:A:VAL:HG11	1:276:A:LEU:HD13	5	0.11
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD11	5	0.11
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD12	5	0.11
(1,120)	1:274:A:VAL:HG12	1:276:A:LEU:HD13	5	0.11
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD11	5	0.11
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD12	5	0.11
(1,120)	1:274:A:VAL:HG13	1:276:A:LEU:HD13	5	0.11
(1,111)	1:265:A:ILE:HD11	1:340:A:VAL:HG21	3	0.11
(1,111)	1:265:A:ILE:HD11	1:340:A:VAL:HG22	3	0.11
(1,111)	1:265:A:ILE:HD11	1:340:A:VAL:HG23	3	0.11
(1,111)	1:265:A:ILE:HD12	1:340:A:VAL:HG21	3	0.11
(1,111)	1:265:A:ILE:HD12	1:340:A:VAL:HG22	3	0.11
(1,111)	1:265:A:ILE:HD12	1:340:A:VAL:HG23	3	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,111)	1:265:A:ILE:HD13	1:340:A:VAL:HG21	3	0.11
(1,111)	1:265:A:ILE:HD13	1:340:A:VAL:HG22	3	0.11
(1,111)	1:265:A:ILE:HD13	1:340:A:VAL:HG23	3	0.11
(1,111)	1:265:A:ILE:HD11	1:340:A:VAL:HG21	8	0.11
(1,111)	1:265:A:ILE:HD11	1:340:A:VAL:HG22	8	0.11
(1,111)	1:265:A:ILE:HD11	1:340:A:VAL:HG23	8	0.11
(1,111)	1:265:A:ILE:HD12	1:340:A:VAL:HG21	8	0.11
(1,111)	1:265:A:ILE:HD12	1:340:A:VAL:HG22	8	0.11
(1,111)	1:265:A:ILE:HD12	1:340:A:VAL:HG23	8	0.11
(1,111)	1:265:A:ILE:HD13	1:340:A:VAL:HG21	8	0.11
(1,111)	1:265:A:ILE:HD13	1:340:A:VAL:HG22	8	0.11
(1,111)	1:265:A:ILE:HD13	1:340:A:VAL:HG23	8	0.11
(1,98)	1:534:A:GLU:H	1:536:A:LEU:H	4	0.11
(2,207)	1:264:A:GLU:OE1	1:333:A:SER:OG	19	0.1
(2,130)	1:271:A:ARG:O	1:288:A:THR:H	9	0.1
(2,94)	1:476:A:ASP:O	1:480:A:ARG:H	15	0.1
(2,21)	1:364:A:PRO:O	1:368:A:ASP:N	4	0.1
(1,1407)	1:466:A:TYR:H	1:482:A:TYR:HE2	8	0.1
(1,1355)	1:497:A:LEU:H	1:522:A:TYR:HE1	6	0.1
(1,1310)	1:289:A:TRP:HE1	1:340:A:VAL:HG21	4	0.1
(1,1310)	1:289:A:TRP:HE1	1:340:A:VAL:HG22	4	0.1
(1,1310)	1:289:A:TRP:HE1	1:340:A:VAL:HG23	4	0.1
(1,1282)	1:431:A:TRP:HE1	1:454:A:LEU:HD11	14	0.1
(1,1282)	1:431:A:TRP:HE1	1:454:A:LEU:HD12	14	0.1
(1,1282)	1:431:A:TRP:HE1	1:454:A:LEU:HD13	14	0.1
(1,1279)	1:386:A:VAL:H	1:414:A:ILE:H	11	0.1
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD11	14	0.1
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD12	14	0.1
(1,1144)	1:489:A:GLU:H	1:536:A:LEU:HD13	14	0.1
(1,1071)	1:270:A:LEU:HD11	1:339:A:ILE:H	8	0.1
(1,1071)	1:270:A:LEU:HD12	1:339:A:ILE:H	8	0.1
(1,1071)	1:270:A:LEU:HD13	1:339:A:ILE:H	8	0.1
(1,1071)	1:270:A:LEU:HD11	1:339:A:ILE:H	17	0.1
(1,1071)	1:270:A:LEU:HD12	1:339:A:ILE:H	17	0.1
(1,1071)	1:270:A:LEU:HD13	1:339:A:ILE:H	17	0.1
(1,1054)	1:361:A:LEU:HD21	1:362:A:ARG:H	15	0.1
(1,1054)	1:361:A:LEU:HD22	1:362:A:ARG:H	15	0.1
(1,1054)	1:361:A:LEU:HD23	1:362:A:ARG:H	15	0.1
(1,965)	1:455:A:LEU:HD11	1:518:A:PHE:HE1	1	0.1
(1,965)	1:455:A:LEU:HD12	1:518:A:PHE:HE1	1	0.1
(1,965)	1:455:A:LEU:HD13	1:518:A:PHE:HE1	1	0.1
(1,965)	1:455:A:LEU:HD11	1:518:A:PHE:HE1	3	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,965)	1:455:A:LEU:HD12	1:518:A:PHE:HE1	3	0.1
(1,965)	1:455:A:LEU:HD13	1:518:A:PHE:HE1	3	0.1
(1,959)	1:289:A:TRP:H	1:329:A:TYR:HE2	12	0.1
(1,956)	1:419:A:PTR:H	1:419:A:PTR:HE2	20	0.1
(1,864)	1:297:A:ILE:HD11	1:338:A:TYR:HE2	15	0.1
(1,864)	1:297:A:ILE:HD12	1:338:A:TYR:HE2	15	0.1
(1,864)	1:297:A:ILE:HD13	1:338:A:TYR:HE2	15	0.1
(1,782)	1:469:A:MET:HE1	1:470:A:VAL:H	4	0.1
(1,782)	1:469:A:MET:HE2	1:470:A:VAL:H	4	0.1
(1,782)	1:469:A:MET:HE3	1:470:A:VAL:H	4	0.1
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD21	2	0.1
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD22	2	0.1
(1,744)	1:459:A:THR:H	1:536:A:LEU:HD23	2	0.1
(1,699)	1:478:A:VAL:HG11	1:482:A:TYR:H	2	0.1
(1,699)	1:478:A:VAL:HG12	1:482:A:TYR:H	2	0.1
(1,699)	1:478:A:VAL:HG13	1:482:A:TYR:H	2	0.1
(1,618)	1:420:A:THR:HG21	1:421:A:ALA:H	3	0.1
(1,618)	1:420:A:THR:HG22	1:421:A:ALA:H	3	0.1
(1,618)	1:420:A:THR:HG23	1:421:A:ALA:H	3	0.1
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG11	2	0.1
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG12	2	0.1
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG13	2	0.1
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG11	9	0.1
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG12	9	0.1
(1,594)	1:399:A:GLU:H	1:402:A:VAL:HG13	9	0.1
(1,592)	1:398:A:GLY:H	1:402:A:VAL:HG21	14	0.1
(1,592)	1:398:A:GLY:H	1:402:A:VAL:HG22	14	0.1
(1,592)	1:398:A:GLY:H	1:402:A:VAL:HG23	14	0.1
(1,577)	1:344:A:MET:H	1:396:A:LEU:HD21	1	0.1
(1,577)	1:344:A:MET:H	1:396:A:LEU:HD22	1	0.1
(1,577)	1:344:A:MET:H	1:396:A:LEU:HD23	1	0.1
(1,577)	1:344:A:MET:H	1:396:A:LEU:HD21	6	0.1
(1,577)	1:344:A:MET:H	1:396:A:LEU:HD22	6	0.1
(1,577)	1:344:A:MET:H	1:396:A:LEU:HD23	6	0.1
(1,559)	1:379:A:TYR:HE1	1:383:A:MET:HE1	10	0.1
(1,559)	1:379:A:TYR:HE1	1:383:A:MET:HE2	10	0.1
(1,559)	1:379:A:TYR:HE1	1:383:A:MET:HE3	10	0.1
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD21	2	0.1
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD22	2	0.1
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD23	2	0.1
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD21	14	0.1
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD22	14	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,528)	1:352:A:PHE:HE2	1:458:A:LEU:HD23	14	0.1
(1,524)	1:344:A:MET:HE1	1:397:A:VAL:H	3	0.1
(1,524)	1:344:A:MET:HE2	1:397:A:VAL:H	3	0.1
(1,524)	1:344:A:MET:HE3	1:397:A:VAL:H	3	0.1
(1,405)	1:286:A:MET:HE1	1:295:A:VAL:H	8	0.1
(1,405)	1:286:A:MET:HE2	1:295:A:VAL:H	8	0.1
(1,405)	1:286:A:MET:HE3	1:295:A:VAL:H	8	0.1
(1,405)	1:286:A:MET:HE1	1:295:A:VAL:H	12	0.1
(1,405)	1:286:A:MET:HE2	1:295:A:VAL:H	12	0.1
(1,405)	1:286:A:MET:HE3	1:295:A:VAL:H	12	0.1
(1,393)	1:273:A:GLU:H	1:274:A:VAL:HG21	18	0.1
(1,393)	1:273:A:GLU:H	1:274:A:VAL:HG22	18	0.1
(1,393)	1:273:A:GLU:H	1:274:A:VAL:HG23	18	0.1
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE1	14	0.1
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE2	14	0.1
(1,369)	1:353:A:LEU:HD21	1:369:A:MET:HE3	14	0.1
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE1	14	0.1
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE2	14	0.1
(1,369)	1:353:A:LEU:HD22	1:369:A:MET:HE3	14	0.1
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE1	14	0.1
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE2	14	0.1
(1,369)	1:353:A:LEU:HD23	1:369:A:MET:HE3	14	0.1
(1,300)	1:438:A:LEU:HD11	1:475:A:LEU:HD21	3	0.1
(1,300)	1:438:A:LEU:HD11	1:475:A:LEU:HD22	3	0.1
(1,300)	1:438:A:LEU:HD11	1:475:A:LEU:HD23	3	0.1
(1,300)	1:438:A:LEU:HD12	1:475:A:LEU:HD21	3	0.1
(1,300)	1:438:A:LEU:HD12	1:475:A:LEU:HD22	3	0.1
(1,300)	1:438:A:LEU:HD12	1:475:A:LEU:HD23	3	0.1
(1,300)	1:438:A:LEU:HD13	1:475:A:LEU:HD21	3	0.1
(1,300)	1:438:A:LEU:HD13	1:475:A:LEU:HD22	3	0.1
(1,300)	1:438:A:LEU:HD13	1:475:A:LEU:HD23	3	0.1
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD11	4	0.1
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD12	4	0.1
(1,294)	1:474:A:VAL:HG21	1:475:A:LEU:HD13	4	0.1
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD11	4	0.1
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD12	4	0.1
(1,294)	1:474:A:VAL:HG22	1:475:A:LEU:HD13	4	0.1
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD11	4	0.1
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD12	4	0.1
(1,294)	1:474:A:VAL:HG23	1:475:A:LEU:HD13	4	0.1

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

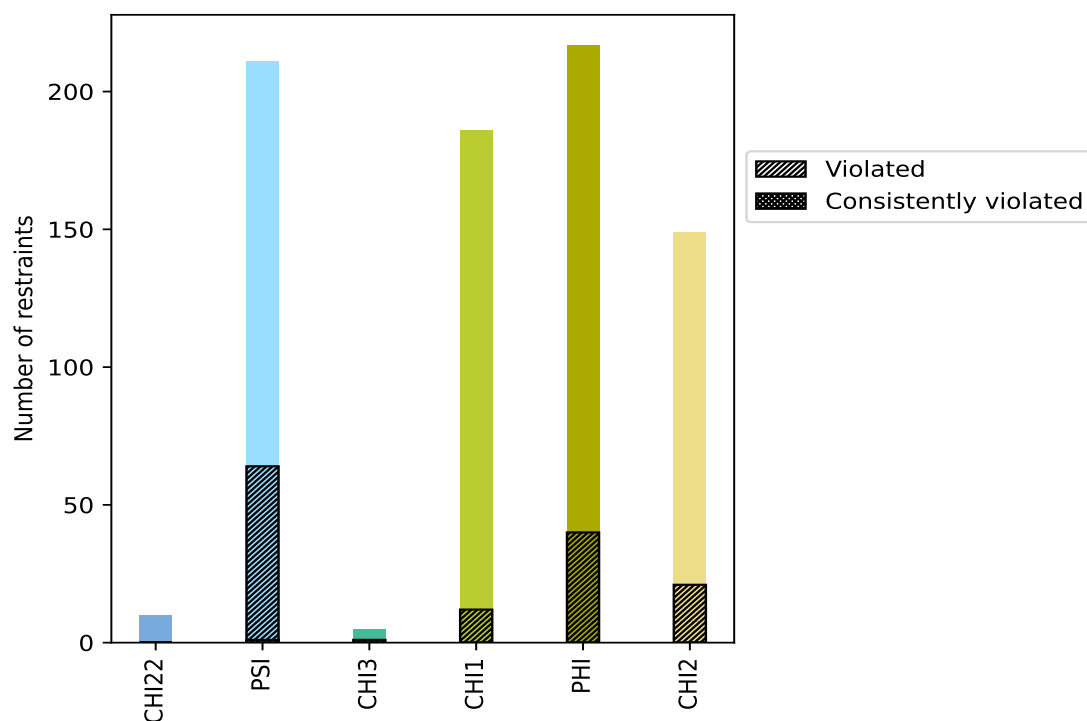
10.1 Summary of dihedral-angle violations [i](#)

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
CHI22	10	1.3	0	0.0	0.0	0	0.0	0.0
PSI	211	27.1	64	30.3	8.2	1	0.5	0.1
CHI3	5	0.6	1	20.0	0.1	0	0.0	0.0
CHI1	186	23.9	12	6.5	1.5	0	0.0	0.0
PHI	217	27.9	40	18.4	5.1	0	0.0	0.0
CHI2	149	19.2	21	14.1	2.7	0	0.0	0.0
Total	778	100.0	138	17.7	17.7	1	0.1	0.1

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

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



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

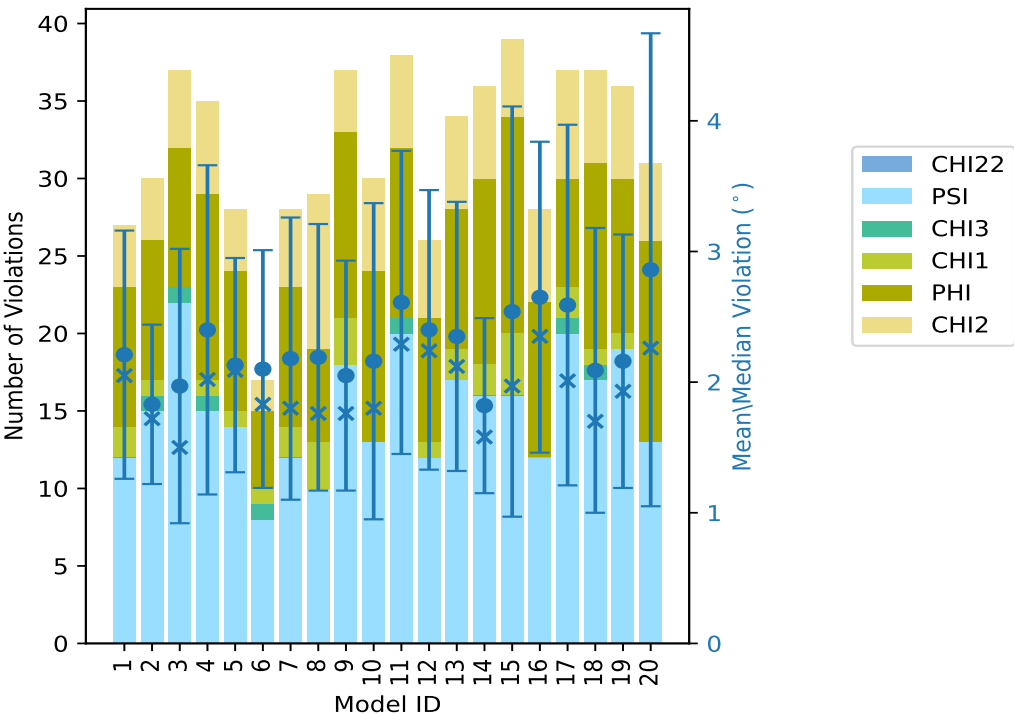
respective categories

10.2 Dihedral-angle violation statistics for each model ⓘ

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

Model ID	Number of violations							Mean (°)	Max (°)	SD (°)	Median
	CHI22	PSI	CHI3	CHI1	PHI	CHI2	Total				
1	0	12	0	2	9	4	27	2.21	4.19	0.95	2.03
2	0	15	1	1	9	4	30	1.83	3.28	0.61	1.72
3	0	22	1	0	9	5	37	1.97	5.75	1.05	1.53
4	0	15	1	1	12	6	35	2.4	6.75	1.26	2.02
5	0	14	0	1	9	4	28	2.13	4.96	0.82	2.09
6	0	8	1	1	5	2	17	2.1	4.17	0.91	1.83
7	0	12	0	2	9	5	28	2.18	5.99	1.08	1.83
8	0	10	0	3	6	10	29	2.19	4.5	1.02	1.76
9	0	18	0	3	12	4	37	2.05	4.5	0.88	1.76
10	0	13	0	0	11	6	30	2.16	6.48	1.21	1.83
11	0	20	1	0	11	6	38	2.61	5.58	1.16	2.23
12	0	12	0	1	8	5	26	2.4	5.94	1.07	2.23
13	0	17	0	2	9	6	34	2.35	4.76	1.03	2.12
14	0	16	0	2	12	6	36	1.82	4.16	0.67	1.53
15	0	16	0	4	14	5	39	2.54	7.1	1.57	1.97
16	0	12	0	0	10	6	28	2.65	6.13	1.19	2.33
17	0	20	1	2	7	7	37	2.59	5.95	1.38	2.02
18	0	17	1	1	12	6	37	2.09	5.21	1.09	1.72
19	0	19	0	1	10	6	36	2.16	4.33	0.97	1.93
20	0	13	0	0	13	5	31	2.86	8.16	1.81	2.23

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	
CHI22	PSI	CHI3	CHI1	PHI	CHI2	Total	Count ¹	%
0	19	0	7	8	6	40	1	5.0
0	7	0	0	7	3	17	2	10.0
0	12	0	3	6	3	24	3	15.0
0	5	0	1	5	1	12	4	20.0
0	3	0	0	3	0	6	5	25.0
0	2	0	0	2	1	5	6	30.0
0	2	1	1	0	3	7	7	35.0
0	2	0	0	0	0	2	8	40.0
0	1	0	0	0	0	1	9	45.0
0	0	0	0	3	0	3	10	50.0
0	3	0	0	3	1	7	11	55.0

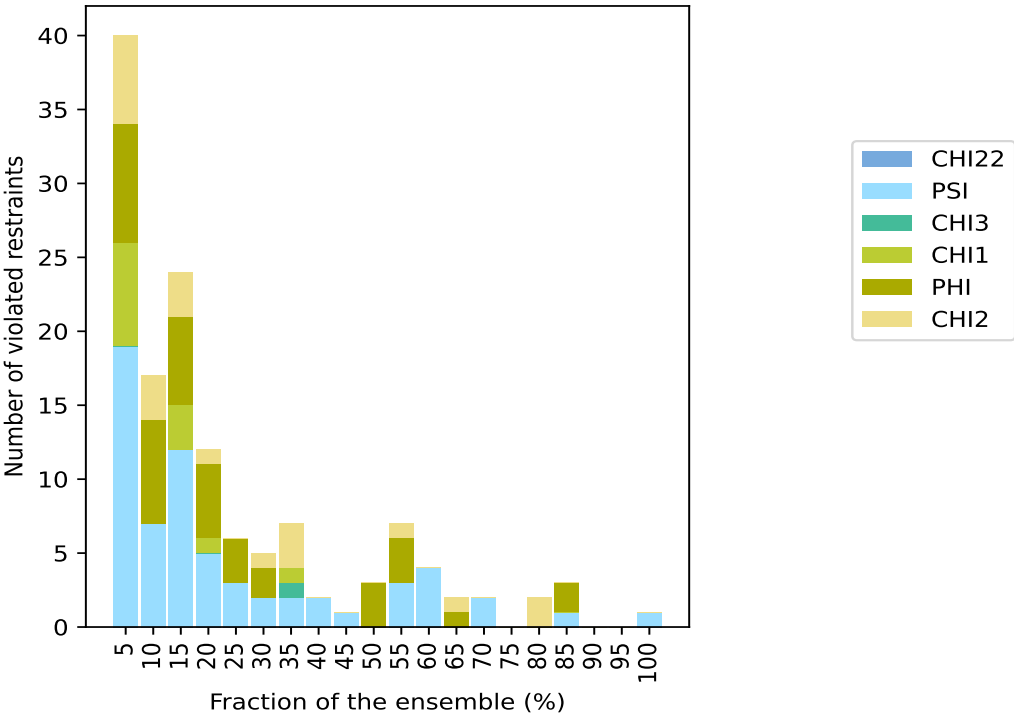
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Number of violated restraints							Fraction of the ensemble	
CHI22	PSI	CHI3	CHI1	PHI	CHI2	Total	Count ¹	%
0	4	0	0	0	0	4	12	60.0
0	0	0	0	1	1	2	13	65.0
0	2	0	0	0	0	2	14	70.0
0	0	0	0	0	0	0	15	75.0
0	0	0	0	0	2	2	16	80.0
0	1	0	0	2	0	3	17	85.0
0	0	0	0	0	0	0	18	90.0
0	0	0	0	0	0	0	19	95.0
0	1	0	0	0	0	1	20	100.0

¹ Number of models with violations

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

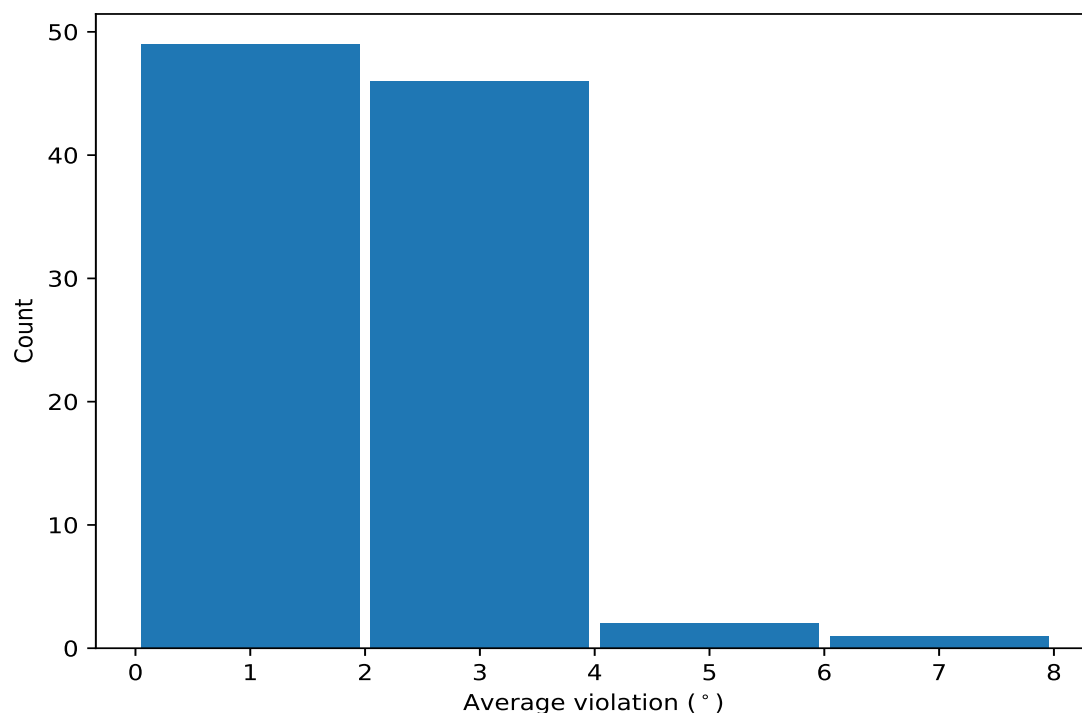


10.4 Most violated dihedral-angle restraints in the ensemble ⓘ

10.4.1 Histogram : Distribution of mean dihedral-angle violations ⓘ

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 ⓘ

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	Med
(1,205)	1:333:A:SER:N	1:333:A:SER:CA	1:333:A:SER:C	1:334:A:GLU:N	20	4.14	1.29	4.1
(1,419)	1:402:A:VAL:N	1:402:A:VAL:CA	1:402:A:VAL:C	1:403:A:CYS:N	17	3.27	1.19	3.0
(1,75)	1:285:A:TRP:C	1:286:A:MET:N	1:286:A:MET:CA	1:286:A:MET:C	17	1.89	0.59	1.8
(1,226)	1:340:A:VAL:C	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:C	17	1.86	0.41	1.8
(1,61)	1:281:A:PHE:CA	1:281:A:PHE:CB	1:281:A:PHE:CG	1:281:A:PHE:CD1	16	2.98	1.27	2.4
(1,361)	1:384:A:ASN:CA	1:384:A:ASN:CB	1:384:A:ASN:CG	1:384:A:ASN:OD1	16	1.88	0.78	1.6
(1,15)	1:266:A:PRO:N	1:266:A:PRO:CA	1:266:A:PRO:C	1:267:A:ARG:N	14	3.53	1.42	3.3
(1,363)	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	1:386:A:VAL:N	14	2.2	0.99	2.0
(1,735)	1:521:A:ASP:CA	1:521:A:ASP:CB	1:521:A:ASP:CG	1:521:A:ASP:OD1	13	2.02	0.45	2.0
(1,748)	1:525:A:SER:C	1:526:A:THR:N	1:526:A:THR:CA	1:526:A:THR:C	13	1.9	0.73	1.9
(1,303)	1:365:A:GLN:N	1:365:A:GLN:CA	1:365:A:GLN:C	1:366:A:LEU:N	12	2.98	1.32	3.1
(1,625)	1:485:A:PRO:N	1:485:A:PRO:CA	1:485:A:PRO:C	1:486:A:CYS:N	12	2.54	0.98	2.3
(1,123)	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	1:305:A:MET:N	12	2.51	0.8	2.5
(1,467)	1:429:A:ILE:N	1:429:A:ILE:CA	1:429:A:ILE:C	1:430:A:LYS:N	12	2.46	0.81	2.2
(1,362)	1:384:A:ASN:C	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	11	2.73	0.92	2.8
(1,617)	1:482:A:TYR:C	1:483:A:ARG:N	1:483:A:ARG:CA	1:483:A:ARG:C	11	2.68	1.02	2.7
(1,263)	1:351:A:ASP:CA	1:351:A:ASP:CB	1:351:A:ASP:CG	1:351:A:ASP:OD1	11	2.51	0.78	2.4
(1,567)	1:467:A:PRO:N	1:467:A:PRO:CA	1:467:A:PRO:C	1:468:A:GLY:N	11	2.34	0.78	2.0
(1,46)	1:275:A:LYS:N	1:275:A:LYS:CA	1:275:A:LYS:C	1:276:A:LEU:N	11	2.18	1.25	1.6
(1,442)	1:411:A:ALA:N	1:411:A:ALA:CA	1:411:A:ALA:C	1:412:A:ARG:N	11	2.07	0.83	1.7

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Med
(1,104)	1:296:A:ALA:C	1:297:A:ILE:N	1:297:A:ILE:CA	1:297:A:ILE:C	11	1.51	0.42	1.5
(1,122)	1:303:A:GLY:C	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	10	2.82	0.93	2.8
(1,114)	1:299:A:THR:C	1:300:A:LEU:N	1:300:A:LEU:CA	1:300:A:LEU:C	10	2.56	0.8	2.6
(1,188)	1:326:A:VAL:C	1:327:A:GLN:N	1:327:A:GLN:CA	1:327:A:GLN:C	10	1.5	0.31	1.4
(1,382)	1:390:A:LEU:N	1:390:A:LEU:CA	1:390:A:LEU:C	1:391:A:ARG:N	9	2.63	1.26	2.5
(1,774)	1:535:A:ASN:N	1:535:A:ASN:CA	1:535:A:ASN:C	1:536:A:LEU:N	8	2.57	0.92	2.5
(1,72)	1:285:A:TRP:N	1:285:A:TRP:CA	1:285:A:TRP:C	1:286:A:MET:N	8	1.71	0.68	1.5
(1,776)	1:535:A:ASN:CA	1:535:A:ASN:CB	1:535:A:ASN:CG	1:535:A:ASN:OD1	7	2.22	0.83	1.9
(1,380)	1:389:A:ASP:CA	1:389:A:ASP:CB	1:389:A:ASP:CG	1:389:A:ASP:OD1	7	1.98	0.79	1.7
(1,79)	1:286:A:MET:CB	1:286:A:MET:CG	1:286:A:MET:SD	1:286:A:MET:CE	7	1.7	0.53	1.4
(1,228)	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:CB	1:341:A:THR:OG1	7	1.61	0.28	1.6
(1,630)	1:489:A:GLU:N	1:489:A:GLU:CA	1:489:A:GLU:C	1:490:A:CYS:N	7	1.56	0.42	1.3
(1,515)	1:447:A:ASP:CA	1:447:A:ASP:CB	1:447:A:ASP:CG	1:447:A:ASP:OD1	7	1.46	0.32	1.4
(1,422)	1:403:A:CYS:N	1:403:A:CYS:CA	1:403:A:CYS:C	1:404:A:LYS:N	7	1.43	0.38	1.2
(1,19)	1:267:A:ARG:CA	1:267:A:ARG:CB	1:267:A:ARG:CG	1:267:A:ARG:CD	6	2.68	1.16	2.9
(1,473)	1:431:A:TRP:N	1:431:A:TRP:CA	1:431:A:TRP:C	1:432:A:THR:N	6	2.39	0.96	2.3
(1,42)	1:273:A:GLU:C	1:274:A:VAL:N	1:274:A:VAL:CA	1:274:A:VAL:C	6	2.34	0.74	2.1
(1,62)	1:281:A:PHE:C	1:282:A:GLY:N	1:282:A:GLY:CA	1:282:A:GLY:C	6	1.41	0.4	1.3
(1,91)	1:291:A:GLY:N	1:291:A:GLY:CA	1:291:A:GLY:C	1:292:A:THR:N	6	1.39	0.28	1.2
(1,3)	1:262:A:ALA:C	1:263:A:TRP:N	1:263:A:TRP:CA	1:263:A:TRP:C	5	2.51	1.08	2.5
(1,43)	1:274:A:VAL:N	1:274:A:VAL:CA	1:274:A:VAL:C	1:275:A:LYS:N	5	2.26	0.93	2.2
(1,294)	1:361:A:LEU:N	1:361:A:LEU:CA	1:361:A:LEU:C	1:362:A:ARG:N	5	2.11	0.54	2.0
(1,2)	1:262:A:ALA:N	1:262:A:ALA:CA	1:262:A:ALA:C	1:263:A:TRP:N	5	1.71	0.39	1.8
(1,493)	1:438:A:LEU:C	1:439:A:TYR:N	1:439:A:TYR:CA	1:439:A:TYR:C	5	1.54	0.26	1.5
(1,82)	1:288:A:THR:C	1:289:A:TRP:N	1:289:A:TRP:CA	1:289:A:TRP:C	5	1.54	0.33	1.5
(1,773)	1:534:A:GLU:C	1:535:A:ASN:N	1:535:A:ASN:CA	1:535:A:ASN:C	4	3.68	2.0	3.6
(1,768)	1:532:A:PRO:N	1:532:A:PRO:CA	1:532:A:PRO:C	1:533:A:GLY:N	4	2.99	1.84	2.9
(1,197)	1:329:A:TYR:CA	1:329:A:TYR:CB	1:329:A:TYR:CG	1:329:A:TYR:CD1	4	2.34	0.58	2.4
(1,480)	1:434:A:PRO:N	1:434:A:PRO:CA	1:434:A:PRO:C	1:435:A:GLU:N	4	2.23	0.4	2.2
(1,207)	1:334:A:GLU:N	1:334:A:GLU:CA	1:334:A:GLU:C	1:335:A:GLU:N	4	2.13	0.28	2.1
(1,487)	1:436:A:ALA:C	1:437:A:ALA:N	1:437:A:ALA:CA	1:437:A:ALA:C	4	2.06	0.78	1.9
(1,557)	1:462:A:GLY:C	1:463:A:ARG:N	1:463:A:ARG:CA	1:463:A:ARG:C	4	1.99	0.67	1.9
(1,31)	1:271:A:ARG:N	1:271:A:ARG:CA	1:271:A:ARG:C	1:272:A:LEU:N	4	1.67	0.61	1.3
(1,374)	1:388:A:ARG:N	1:388:A:ARG:CA	1:388:A:ARG:C	1:389:A:ASP:N	4	1.56	0.56	1.3
(1,606)	1:478:A:VAL:N	1:478:A:VAL:CA	1:478:A:VAL:CB	1:478:A:VAL:CG1	4	1.54	0.49	1.3
(1,30)	1:270:A:LEU:C	1:271:A:ARG:N	1:271:A:ARG:CA	1:271:A:ARG:C	4	1.5	0.18	1.4
(1,71)	1:284:A:VAL:C	1:285:A:TRP:N	1:285:A:TRP:CA	1:285:A:TRP:C	4	1.29	0.23	1.1
(1,53)	1:276:A:LEU:C	1:277:A:GLY:N	1:277:A:GLY:CA	1:277:A:GLY:C	3	7.02	0.97	7.0
(1,50)	1:276:A:LEU:N	1:276:A:LEU:CA	1:276:A:LEU:C	1:277:A:GLY:N	3	5.56	1.98	5.8
(1,407)	1:398:A:GLY:N	1:398:A:GLY:CA	1:398:A:GLY:C	1:399:A:GLU:N	3	3.32	0.23	3.3
(1,55)	1:277:A:GLY:C	1:278:A:GLN:N	1:278:A:GLN:CA	1:278:A:GLN:C	3	3.2	0.26	3.0
(1,277)	1:356:A:GLU:N	1:356:A:GLU:CA	1:356:A:GLU:C	1:357:A:THR:N	3	2.74	1.23	2.9
(1,679)	1:505:A:GLU:N	1:505:A:GLU:CA	1:505:A:GLU:C	1:506:A:PRO:N	3	2.68	0.7	2.9
(1,444)	1:412:A:ARG:C	1:413:A:LEU:N	1:413:A:LEU:CA	1:413:A:LEU:C	3	2.53	0.89	2.2
(1,458)	1:421:A:ALA:C	1:422:A:ARG:N	1:422:A:ARG:CA	1:422:A:ARG:C	3	2.26	0.91	2.2
(1,671)	1:503:A:ARG:N	1:503:A:ARG:CA	1:503:A:ARG:C	1:504:A:LYS:N	3	2.26	1.41	1.3
(1,618)	1:483:A:ARG:N	1:483:A:ARG:CA	1:483:A:ARG:C	1:484:A:MET:N	3	2.22	0.93	1.6
(1,756)	1:528:A:PRO:C	1:529:A:GLN:N	1:529:A:GLN:CA	1:529:A:GLN:C	3	2.1	0.77	1.8
(1,421)	1:402:A:VAL:C	1:403:A:CYS:N	1:403:A:CYS:CA	1:403:A:CYS:C	3	1.93	0.27	1.7
(1,27)	1:270:A:LEU:N	1:270:A:LEU:CA	1:270:A:LEU:C	1:271:A:ARG:N	3	1.89	0.38	1.7
(1,490)	1:438:A:LEU:N	1:438:A:LEU:CA	1:438:A:LEU:C	1:439:A:TYR:N	3	1.82	0.73	1.3

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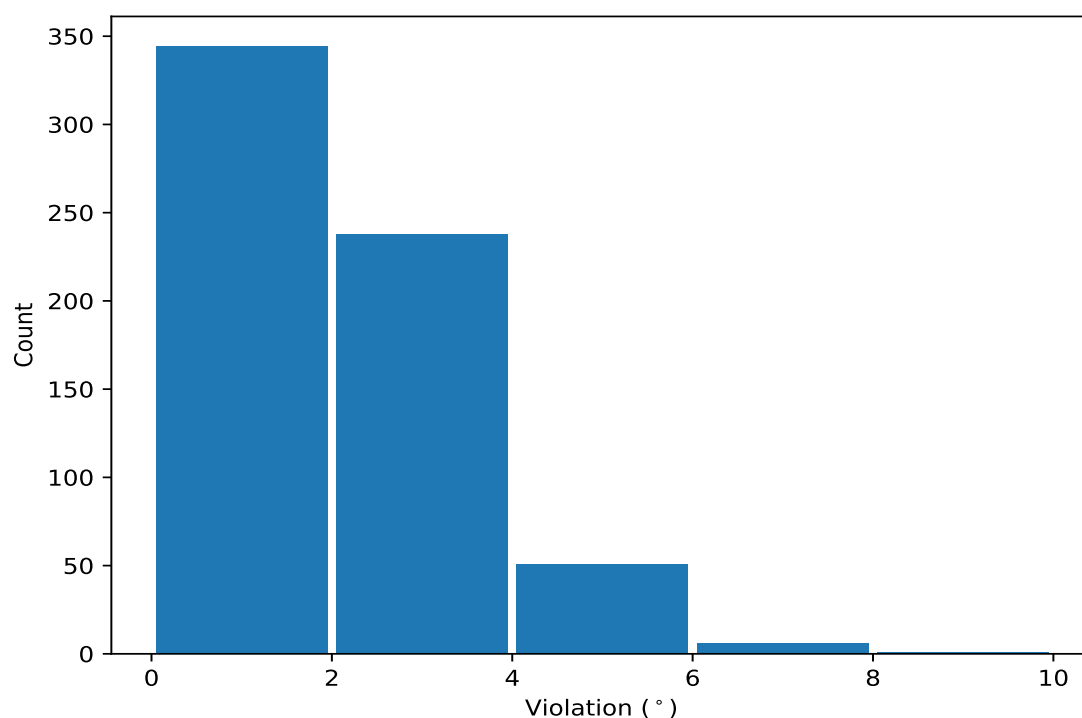
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Med
(1,505)	1:443:A:THR:N	1:443:A:THR:CA	1:443:A:THR:CB	1:443:A:THR:OG1	3	1.77	0.45	2.0
(1,614)	1:481:A:GLY:N	1:481:A:GLY:CA	1:481:A:GLY:C	1:482:A:TYR:N	3	1.56	0.19	1.4
(1,484)	1:435:A:GLU:CA	1:435:A:GLU:CB	1:435:A:GLU:CG	1:435:A:GLU:CD	3	1.56	0.15	1.5
(1,119)	1:301:A:LYS:N	1:301:A:LYS:CA	1:301:A:LYS:C	1:302:A:PRO:N	3	1.43	0.13	1.3
(1,365)	1:385:A:TYR:CA	1:385:A:TYR:CB	1:385:A:TYR:CG	1:385:A:TYR:CD1	3	1.4	0.4	1.1
(1,368)	1:386:A:VAL:N	1:386:A:VAL:CA	1:386:A:VAL:CB	1:386:A:VAL:CG1	3	1.39	0.28	1.3
(1,430)	1:407:A:ASP:N	1:407:A:ASP:CA	1:407:A:ASP:C	1:408:A:PHE:N	3	1.39	0.34	1.2
(1,537)	1:456:A:THR:N	1:456:A:THR:CA	1:456:A:THR:CB	1:456:A:THR:OG1	3	1.39	0.1	1.3
(1,653)	1:496:A:ASP:CA	1:496:A:ASP:CB	1:496:A:ASP:CG	1:496:A:ASP:OD1	3	1.31	0.2	1.3
(1,400)	1:396:A:LEU:N	1:396:A:LEU:CA	1:396:A:LEU:C	1:397:A:VAL:N	3	1.29	0.25	1.1
(1,451)	1:414:A:ILE:C	1:415:A:GLU:N	1:415:A:GLU:CA	1:415:A:GLU:C	2	3.38	2.11	3.3
(1,757)	1:529:A:GLN:N	1:529:A:GLN:CA	1:529:A:GLN:C	1:530:A:TYR:N	2	2.52	0.3	2.5
(1,353)	1:382:A:ARG:N	1:382:A:ARG:CA	1:382:A:ARG:C	1:383:A:MET:N	2	2.08	0.29	2.0
(1,575)	1:470:A:VAL:N	1:470:A:VAL:CA	1:470:A:VAL:C	1:471:A:ASN:N	2	2.08	0.75	2.0
(1,496)	1:439:A:TYR:CA	1:439:A:TYR:CB	1:439:A:TYR:CG	1:439:A:TYR:CD1	2	2.06	0.4	2.0
(1,1)	1:261:A:ASP:C	1:262:A:ALA:N	1:262:A:ALA:CA	1:262:A:ALA:C	2	1.62	0.51	1.6
(1,92)	1:292:A:THR:C	1:293:A:THR:N	1:293:A:THR:CA	1:293:A:THR:C	2	1.51	0.25	1.5
(1,522)	1:449:A:TRP:CA	1:449:A:TRP:CB	1:449:A:TRP:CG	1:449:A:TRP:CD1	2	1.5	0.38	1.5
(1,377)	1:388:A:ARG:C	1:389:A:ASP:N	1:389:A:ASP:CA	1:389:A:ASP:C	2	1.44	0.19	1.4
(1,770)	1:534:A:GLU:N	1:534:A:GLU:CA	1:534:A:GLU:C	1:535:A:ASN:N	2	1.44	0.09	1.4
(1,452)	1:415:A:GLU:C	1:416:A:ASP:N	1:416:A:ASP:CA	1:416:A:ASP:C	2	1.43	0.25	1.4
(1,613)	1:480:A:ARG:C	1:481:A:GLY:N	1:481:A:GLY:CA	1:481:A:GLY:C	2	1.42	0.08	1.4
(1,4)	1:263:A:TRP:N	1:263:A:TRP:CA	1:263:A:TRP:C	1:264:A:GLU:N	2	1.42	0.05	1.4
(1,63)	1:282:A:GLY:N	1:282:A:GLY:CA	1:282:A:GLY:C	1:283:A:GLU:N	2	1.42	0.29	1.4
(1,488)	1:437:A:ALA:N	1:437:A:ALA:CA	1:437:A:ALA:C	1:438:A:LEU:N	2	1.36	0.3	1.3
(1,687)	1:507:A:GLU:C	1:508:A:GLU:N	1:508:A:GLU:CA	1:508:A:GLU:C	2	1.22	0.15	1.2
(1,153)	1:317:A:MET:CA	1:317:A:MET:CB	1:317:A:MET:CG	1:317:A:MET:SD	2	1.2	0.16	1.2

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

10.5 All violated dihedral-angle restraints ⓘ

10.5.1 Histogram : Distribution of violations ⓘ

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



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

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

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,53)	1:276:A:LEU:C	1:277:A:GLY:N	1:277:A:GLY:CA	1:277:A:GLY:C	20	8.16
(1,50)	1:276:A:LEU:N	1:276:A:LEU:CA	1:276:A:LEU:C	1:277:A:GLY:N	20	7.82
(1,53)	1:276:A:LEU:C	1:277:A:GLY:N	1:277:A:GLY:CA	1:277:A:GLY:C	15	7.1
(1,419)	1:402:A:VAL:N	1:402:A:VAL:CA	1:402:A:VAL:C	1:403:A:CYS:N	4	6.75
(1,205)	1:333:A:SER:N	1:333:A:SER:CA	1:333:A:SER:C	1:334:A:GLU:N	10	6.48
(1,61)	1:281:A:PHE:CA	1:281:A:PHE:CB	1:281:A:PHE:CG	1:281:A:PHE:CD1	15	6.32
(1,205)	1:333:A:SER:N	1:333:A:SER:CA	1:333:A:SER:C	1:334:A:GLU:N	16	6.13
(1,773)	1:534:A:GLU:C	1:535:A:ASN:N	1:535:A:ASN:CA	1:535:A:ASN:C	7	5.99
(1,15)	1:266:A:PRO:N	1:266:A:PRO:CA	1:266:A:PRO:C	1:267:A:ARG:N	17	5.95
(1,15)	1:266:A:PRO:N	1:266:A:PRO:CA	1:266:A:PRO:C	1:267:A:ARG:N	12	5.94
(1,50)	1:276:A:LEU:N	1:276:A:LEU:CA	1:276:A:LEU:C	1:277:A:GLY:N	15	5.87
(1,682)	1:506:A:PRO:N	1:506:A:PRO:CA	1:506:A:PRO:C	1:507:A:GLU:N	16	5.82
(1,53)	1:276:A:LEU:C	1:277:A:GLY:N	1:277:A:GLY:CA	1:277:A:GLY:C	17	5.8
(1,768)	1:532:A:PRO:N	1:532:A:PRO:CA	1:532:A:PRO:C	1:533:A:GLY:N	3	5.75
(1,46)	1:275:A:LYS:N	1:275:A:LYS:CA	1:275:A:LYS:C	1:276:A:LEU:N	20	5.71
(1,205)	1:333:A:SER:N	1:333:A:SER:CA	1:333:A:SER:C	1:334:A:GLU:N	15	5.63
(1,382)	1:390:A:LEU:N	1:390:A:LEU:CA	1:390:A:LEU:C	1:391:A:ARG:N	11	5.58
(1,451)	1:414:A:ILE:C	1:415:A:GLU:N	1:415:A:GLU:CA	1:415:A:GLU:C	11	5.49
(1,773)	1:534:A:GLU:C	1:535:A:ASN:N	1:535:A:ASN:CA	1:535:A:ASN:C	4	5.32
(1,303)	1:365:A:GLN:N	1:365:A:GLN:CA	1:365:A:GLN:C	1:366:A:LEU:N	10	5.29
(1,625)	1:485:A:PRO:N	1:485:A:PRO:CA	1:485:A:PRO:C	1:486:A:CYS:N	18	5.21

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,205)	1:333:A:SER:N	1:333:A:SER:CA	1:333:A:SER:C	1:334:A:GLU:N	7	5.05
(1,205)	1:333:A:SER:N	1:333:A:SER:CA	1:333:A:SER:C	1:334:A:GLU:N	18	4.97
(1,205)	1:333:A:SER:N	1:333:A:SER:CA	1:333:A:SER:C	1:334:A:GLU:N	5	4.96
(1,15)	1:266:A:PRO:N	1:266:A:PRO:CA	1:266:A:PRO:C	1:267:A:ARG:N	11	4.95
(1,769)	1:533:A:GLY:C	1:534:A:GLU:N	1:534:A:GLU:CA	1:534:A:GLU:C	4	4.93
(1,122)	1:303:A:GLY:C	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	15	4.89
(1,205)	1:333:A:SER:N	1:333:A:SER:CA	1:333:A:SER:C	1:334:A:GLU:N	13	4.76
(1,205)	1:333:A:SER:N	1:333:A:SER:CA	1:333:A:SER:C	1:334:A:GLU:N	20	4.6
(1,467)	1:429:A:ILE:N	1:429:A:ILE:CA	1:429:A:ILE:C	1:430:A:LYS:N	17	4.58
(1,205)	1:333:A:SER:N	1:333:A:SER:CA	1:333:A:SER:C	1:334:A:GLU:N	3	4.58
(1,465)	1:427:A:PHE:CA	1:427:A:PHE:CB	1:427:A:PHE:CG	1:427:A:PHE:CD1	17	4.54
(1,617)	1:482:A:TYR:C	1:483:A:ARG:N	1:483:A:ARG:CA	1:483:A:ARG:C	8	4.5
(1,419)	1:402:A:VAL:N	1:402:A:VAL:CA	1:402:A:VAL:C	1:403:A:CYS:N	9	4.5
(1,61)	1:281:A:PHE:CA	1:281:A:PHE:CB	1:281:A:PHE:CG	1:281:A:PHE:CD1	20	4.5
(1,15)	1:266:A:PRO:N	1:266:A:PRO:CA	1:266:A:PRO:C	1:267:A:ARG:N	18	4.48
(1,61)	1:281:A:PHE:CA	1:281:A:PHE:CB	1:281:A:PHE:CG	1:281:A:PHE:CD1	17	4.43
(1,419)	1:402:A:VAL:N	1:402:A:VAL:CA	1:402:A:VAL:C	1:403:A:CYS:N	11	4.38
(1,3)	1:262:A:ALA:C	1:263:A:TRP:N	1:263:A:TRP:CA	1:263:A:TRP:C	11	4.38
(1,363)	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	1:386:A:VAL:N	19	4.33
(1,303)	1:365:A:GLN:N	1:365:A:GLN:CA	1:365:A:GLN:C	1:366:A:LEU:N	12	4.31
(1,473)	1:431:A:TRP:N	1:431:A:TRP:CA	1:431:A:TRP:C	1:432:A:THR:N	19	4.28
(1,774)	1:535:A:ASN:N	1:535:A:ASN:CA	1:535:A:ASN:C	1:536:A:LEU:N	17	4.26
(1,671)	1:503:A:ARG:N	1:503:A:ARG:CA	1:503:A:ARG:C	1:504:A:LYS:N	9	4.25
(1,303)	1:365:A:GLN:N	1:365:A:GLN:CA	1:365:A:GLN:C	1:366:A:LEU:N	15	4.25
(1,114)	1:299:A:THR:C	1:300:A:LEU:N	1:300:A:LEU:CA	1:300:A:LEU:C	20	4.23
(1,263)	1:351:A:ASP:CA	1:351:A:ASP:CB	1:351:A:ASP:CG	1:351:A:ASP:OD1	17	4.2
(1,205)	1:333:A:SER:N	1:333:A:SER:CA	1:333:A:SER:C	1:334:A:GLU:N	1	4.19
(1,205)	1:333:A:SER:N	1:333:A:SER:CA	1:333:A:SER:C	1:334:A:GLU:N	6	4.17
(1,464)	1:427:A:PHE:N	1:427:A:PHE:CA	1:427:A:PHE:CB	1:427:A:PHE:CG	17	4.16
(1,362)	1:384:A:ASN:C	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	14	4.16
(1,15)	1:266:A:PRO:N	1:266:A:PRO:CA	1:266:A:PRO:C	1:267:A:ARG:N	15	4.15
(1,362)	1:384:A:ASN:C	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	8	4.14
(1,277)	1:356:A:GLU:N	1:356:A:GLU:CA	1:356:A:GLU:C	1:357:A:THR:N	13	4.11
(1,617)	1:482:A:TYR:C	1:483:A:ARG:N	1:483:A:ARG:CA	1:483:A:ARG:C	19	4.07
(1,205)	1:333:A:SER:N	1:333:A:SER:CA	1:333:A:SER:C	1:334:A:GLU:N	8	4.07
(1,205)	1:333:A:SER:N	1:333:A:SER:CA	1:333:A:SER:C	1:334:A:GLU:N	17	4.07
(1,19)	1:267:A:ARG:CA	1:267:A:ARG:CB	1:267:A:ARG:CG	1:267:A:ARG:CD	10	4.01
(1,442)	1:411:A:ALA:N	1:411:A:ALA:CA	1:411:A:ALA:C	1:412:A:ARG:N	1	3.98
(1,123)	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	1:305:A:MET:N	6	3.98
(1,43)	1:274:A:VAL:N	1:274:A:VAL:CA	1:274:A:VAL:C	1:275:A:LYS:N	20	3.98
(1,15)	1:266:A:PRO:N	1:266:A:PRO:CA	1:266:A:PRO:C	1:267:A:ARG:N	3	3.98
(1,419)	1:402:A:VAL:N	1:402:A:VAL:CA	1:402:A:VAL:C	1:403:A:CYS:N	1	3.91
(1,303)	1:365:A:GLN:N	1:365:A:GLN:CA	1:365:A:GLN:C	1:366:A:LEU:N	8	3.91
(1,22)	1:268:A:GLU:N	1:268:A:GLU:CA	1:268:A:GLU:CB	1:268:A:GLU:CG	8	3.88
(1,303)	1:365:A:GLN:N	1:365:A:GLN:CA	1:365:A:GLN:C	1:366:A:LEU:N	13	3.87
(1,61)	1:281:A:PHE:CA	1:281:A:PHE:CB	1:281:A:PHE:CG	1:281:A:PHE:CD1	16	3.86
(1,61)	1:281:A:PHE:CA	1:281:A:PHE:CB	1:281:A:PHE:CG	1:281:A:PHE:CD1	13	3.85
(1,419)	1:402:A:VAL:N	1:402:A:VAL:CA	1:402:A:VAL:C	1:403:A:CYS:N	20	3.81
(1,205)	1:333:A:SER:N	1:333:A:SER:CA	1:333:A:SER:C	1:334:A:GLU:N	11	3.8
(1,19)	1:267:A:ARG:CA	1:267:A:ARG:CB	1:267:A:ARG:CG	1:267:A:ARG:CD	1	3.79
(1,444)	1:412:A:ARG:C	1:413:A:LEU:N	1:413:A:LEU:CA	1:413:A:LEU:C	15	3.75

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,567)	1:467:A:PRO:N	1:467:A:PRO:CA	1:467:A:PRO:C	1:468:A:GLY:N	18	3.72
(1,776)	1:535:A:ASN:CA	1:535:A:ASN:CB	1:535:A:ASN:CG	1:535:A:ASN:OD1	4	3.71
(1,363)	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	1:386:A:VAL:N	17	3.7
(1,42)	1:273:A:GLU:C	1:274:A:VAL:N	1:274:A:VAL:CA	1:274:A:VAL:C	13	3.69
(1,419)	1:402:A:VAL:N	1:402:A:VAL:CA	1:402:A:VAL:C	1:403:A:CYS:N	18	3.66
(1,123)	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	1:305:A:MET:N	13	3.63
(1,380)	1:389:A:ASP:CA	1:389:A:ASP:CB	1:389:A:ASP:CG	1:389:A:ASP:OD1	17	3.62
(1,407)	1:398:A:GLY:N	1:398:A:GLY:CA	1:398:A:GLY:C	1:399:A:GLU:N	4	3.59
(1,362)	1:384:A:ASN:C	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	9	3.59
(1,61)	1:281:A:PHE:CA	1:281:A:PHE:CB	1:281:A:PHE:CG	1:281:A:PHE:CD1	11	3.59
(1,55)	1:277:A:GLY:C	1:278:A:GLN:N	1:278:A:GLN:CA	1:278:A:GLN:C	20	3.57
(1,15)	1:266:A:PRO:N	1:266:A:PRO:CA	1:266:A:PRO:C	1:267:A:ARG:N	4	3.57
(1,618)	1:483:A:ARG:N	1:483:A:ARG:CA	1:483:A:ARG:C	1:484:A:MET:N	19	3.53
(1,768)	1:532:A:PRO:N	1:532:A:PRO:CA	1:532:A:PRO:C	1:533:A:GLY:N	11	3.51
(1,205)	1:333:A:SER:N	1:333:A:SER:CA	1:333:A:SER:C	1:334:A:GLU:N	19	3.51
(1,361)	1:384:A:ASN:CA	1:384:A:ASN:CB	1:384:A:ASN:CG	1:384:A:ASN:OD1	12	3.5
(1,303)	1:365:A:GLN:N	1:365:A:GLN:CA	1:365:A:GLN:C	1:366:A:LEU:N	3	3.46
(1,617)	1:482:A:TYR:C	1:483:A:ARG:N	1:483:A:ARG:CA	1:483:A:ARG:C	11	3.43
(1,19)	1:267:A:ARG:CA	1:267:A:ARG:CB	1:267:A:ARG:CG	1:267:A:ARG:CD	16	3.43
(1,679)	1:505:A:GLU:N	1:505:A:GLU:CA	1:505:A:GLU:C	1:506:A:PRO:N	15	3.4
(1,458)	1:421:A:ALA:C	1:422:A:ARG:N	1:422:A:ARG:CA	1:422:A:ARG:C	10	3.4
(1,122)	1:303:A:GLY:C	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	16	3.4
(1,114)	1:299:A:THR:C	1:300:A:LEU:N	1:300:A:LEU:CA	1:300:A:LEU:C	6	3.4
(1,72)	1:285:A:TRP:N	1:285:A:TRP:CA	1:285:A:TRP:C	1:286:A:MET:N	16	3.38
(1,407)	1:398:A:GLY:N	1:398:A:GLY:CA	1:398:A:GLY:C	1:399:A:GLU:N	19	3.36
(1,361)	1:384:A:ASN:CA	1:384:A:ASN:CB	1:384:A:ASN:CG	1:384:A:ASN:OD1	16	3.36
(1,122)	1:303:A:GLY:C	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	20	3.36
(1,567)	1:467:A:PRO:N	1:467:A:PRO:CA	1:467:A:PRO:C	1:468:A:GLY:N	20	3.34
(1,419)	1:402:A:VAL:N	1:402:A:VAL:CA	1:402:A:VAL:C	1:403:A:CYS:N	13	3.33
(1,263)	1:351:A:ASP:CA	1:351:A:ASP:CB	1:351:A:ASP:CG	1:351:A:ASP:OD1	16	3.32
(1,363)	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	1:386:A:VAL:N	11	3.31
(1,617)	1:482:A:TYR:C	1:483:A:ARG:N	1:483:A:ARG:CA	1:483:A:ARG:C	9	3.29
(1,382)	1:390:A:LEU:N	1:390:A:LEU:CA	1:390:A:LEU:C	1:391:A:ARG:N	2	3.28
(1,205)	1:333:A:SER:N	1:333:A:SER:CA	1:333:A:SER:C	1:334:A:GLU:N	12	3.28
(1,748)	1:525:A:SER:C	1:526:A:THR:N	1:526:A:THR:CA	1:526:A:THR:C	13	3.27
(1,442)	1:411:A:ALA:N	1:411:A:ALA:CA	1:411:A:ALA:C	1:412:A:ARG:N	13	3.24
(1,297)	1:362:A:ARG:N	1:362:A:ARG:CA	1:362:A:ARG:CB	1:362:A:ARG:CG	9	3.23
(1,625)	1:485:A:PRO:N	1:485:A:PRO:CA	1:485:A:PRO:C	1:486:A:CYS:N	11	3.22
(1,382)	1:390:A:LEU:N	1:390:A:LEU:CA	1:390:A:LEU:C	1:391:A:ARG:N	17	3.19
(1,419)	1:402:A:VAL:N	1:402:A:VAL:CA	1:402:A:VAL:C	1:403:A:CYS:N	7	3.17
(1,625)	1:485:A:PRO:N	1:485:A:PRO:CA	1:485:A:PRO:C	1:486:A:CYS:N	1	3.15
(1,756)	1:528:A:PRO:C	1:529:A:GLN:N	1:529:A:GLN:CA	1:529:A:GLN:C	9	3.13
(1,774)	1:535:A:ASN:N	1:535:A:ASN:CA	1:535:A:ASN:C	1:536:A:LEU:N	4	3.12
(1,46)	1:275:A:LYS:N	1:275:A:LYS:CA	1:275:A:LYS:C	1:276:A:LEU:N	19	3.12
(1,776)	1:535:A:ASN:CA	1:535:A:ASN:CB	1:535:A:ASN:CG	1:535:A:ASN:OD1	5	3.11
(1,748)	1:525:A:SER:C	1:526:A:THR:N	1:526:A:THR:CA	1:526:A:THR:C	5	3.11
(1,567)	1:467:A:PRO:N	1:467:A:PRO:CA	1:467:A:PRO:C	1:468:A:GLY:N	11	3.1
(1,205)	1:333:A:SER:N	1:333:A:SER:CA	1:333:A:SER:C	1:334:A:GLU:N	4	3.1
(1,774)	1:535:A:ASN:N	1:535:A:ASN:CA	1:535:A:ASN:C	1:536:A:LEU:N	20	3.08
(1,75)	1:285:A:TRP:C	1:286:A:MET:N	1:286:A:MET:CA	1:286:A:MET:C	13	3.08
(1,419)	1:402:A:VAL:N	1:402:A:VAL:CA	1:402:A:VAL:C	1:403:A:CYS:N	15	3.06

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,55)	1:277:A:GLY:C	1:278:A:GLN:N	1:278:A:GLN:CA	1:278:A:GLN:C	17	3.06
(1,123)	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	1:305:A:MET:N	16	3.05
(1,15)	1:266:A:PRO:N	1:266:A:PRO:CA	1:266:A:PRO:C	1:267:A:ARG:N	19	3.05
(1,487)	1:436:A:ALA:C	1:437:A:ALA:N	1:437:A:ALA:CA	1:437:A:ALA:C	1	3.04
(1,567)	1:467:A:PRO:N	1:467:A:PRO:CA	1:467:A:PRO:C	1:468:A:GLY:N	4	3.03
(1,263)	1:351:A:ASP:CA	1:351:A:ASP:CB	1:351:A:ASP:CG	1:351:A:ASP:OD1	12	3.03
(1,407)	1:398:A:GLY:N	1:398:A:GLY:CA	1:398:A:GLY:C	1:399:A:GLU:N	3	3.02
(1,361)	1:384:A:ASN:CA	1:384:A:ASN:CB	1:384:A:ASN:CG	1:384:A:ASN:OD1	13	3.02
(1,122)	1:303:A:GLY:C	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	18	3.0
(1,50)	1:276:A:LEU:N	1:276:A:LEU:CA	1:276:A:LEU:C	1:277:A:GLY:N	17	2.99
(1,277)	1:356:A:GLU:N	1:356:A:GLU:CA	1:356:A:GLU:C	1:357:A:THR:N	12	2.98
(1,122)	1:303:A:GLY:C	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	9	2.98
(1,55)	1:277:A:GLY:C	1:278:A:GLN:N	1:278:A:GLN:CA	1:278:A:GLN:C	15	2.98
(1,774)	1:535:A:ASN:N	1:535:A:ASN:CA	1:535:A:ASN:C	1:536:A:LEU:N	12	2.97
(1,362)	1:384:A:ASN:C	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	16	2.97
(1,15)	1:266:A:PRO:N	1:266:A:PRO:CA	1:266:A:PRO:C	1:267:A:ARG:N	7	2.97
(1,197)	1:329:A:TYR:CA	1:329:A:TYR:CB	1:329:A:TYR:CG	1:329:A:TYR:CD1	10	2.96
(1,557)	1:462:A:GLY:C	1:463:A:ARG:N	1:463:A:ARG:CA	1:463:A:ARG:C	8	2.95
(1,467)	1:429:A:ILE:N	1:429:A:ILE:CA	1:429:A:ILE:C	1:430:A:LYS:N	16	2.95
(1,748)	1:525:A:SER:C	1:526:A:THR:N	1:526:A:THR:CA	1:526:A:THR:C	15	2.94
(1,467)	1:429:A:ILE:N	1:429:A:ILE:CA	1:429:A:ILE:C	1:430:A:LYS:N	4	2.94
(1,362)	1:384:A:ASN:C	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	20	2.92
(1,679)	1:505:A:GLU:N	1:505:A:GLU:CA	1:505:A:GLU:C	1:506:A:PRO:N	1	2.91
(1,123)	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	1:305:A:MET:N	8	2.91
(1,362)	1:384:A:ASN:C	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	19	2.89
(1,467)	1:429:A:ILE:N	1:429:A:ILE:CA	1:429:A:ILE:C	1:430:A:LYS:N	2	2.88
(1,419)	1:402:A:VAL:N	1:402:A:VAL:CA	1:402:A:VAL:C	1:403:A:CYS:N	5	2.88
(1,419)	1:402:A:VAL:N	1:402:A:VAL:CA	1:402:A:VAL:C	1:403:A:CYS:N	16	2.86
(1,123)	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	1:305:A:MET:N	19	2.86
(1,625)	1:485:A:PRO:N	1:485:A:PRO:CA	1:485:A:PRO:C	1:486:A:CYS:N	2	2.85
(1,490)	1:438:A:LEU:N	1:438:A:LEU:CA	1:438:A:LEU:C	1:439:A:TYR:N	5	2.85
(1,575)	1:470:A:VAL:N	1:470:A:VAL:CA	1:470:A:VAL:C	1:471:A:ASN:N	12	2.83
(1,757)	1:529:A:GLN:N	1:529:A:GLN:CA	1:529:A:GLN:C	1:530:A:TYR:N	18	2.82
(1,684)	1:507:A:GLU:N	1:507:A:GLU:CA	1:507:A:GLU:C	1:508:A:GLU:N	9	2.82
(1,42)	1:273:A:GLU:C	1:274:A:VAL:N	1:274:A:VAL:CA	1:274:A:VAL:C	10	2.82
(1,15)	1:266:A:PRO:N	1:266:A:PRO:CA	1:266:A:PRO:C	1:267:A:ARG:N	8	2.81
(1,617)	1:482:A:TYR:C	1:483:A:ARG:N	1:483:A:ARG:CA	1:483:A:ARG:C	14	2.8
(1,480)	1:434:A:PRO:N	1:434:A:PRO:CA	1:434:A:PRO:C	1:435:A:GLU:N	4	2.8
(1,75)	1:285:A:TRP:C	1:286:A:MET:N	1:286:A:MET:CA	1:286:A:MET:C	14	2.8
(1,363)	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	1:386:A:VAL:N	9	2.79
(1,303)	1:365:A:GLN:N	1:365:A:GLN:CA	1:365:A:GLN:C	1:366:A:LEU:N	14	2.76
(1,122)	1:303:A:GLY:C	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	14	2.76
(1,79)	1:286:A:MET:CB	1:286:A:MET:CG	1:286:A:MET:SD	1:286:A:MET:CE	18	2.75
(1,226)	1:340:A:VAL:C	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:C	9	2.74
(1,617)	1:482:A:TYR:C	1:483:A:ARG:N	1:483:A:ARG:CA	1:483:A:ARG:C	1	2.73
(1,419)	1:402:A:VAL:N	1:402:A:VAL:CA	1:402:A:VAL:C	1:403:A:CYS:N	3	2.73
(1,75)	1:285:A:TRP:C	1:286:A:MET:N	1:286:A:MET:CA	1:286:A:MET:C	7	2.73
(1,3)	1:262:A:ALA:C	1:263:A:TRP:N	1:263:A:TRP:CA	1:263:A:TRP:C	13	2.73
(1,123)	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	1:305:A:MET:N	12	2.72
(1,31)	1:271:A:ARG:N	1:271:A:ARG:CA	1:271:A:ARG:C	1:272:A:LEU:N	11	2.72
(1,15)	1:266:A:PRO:N	1:266:A:PRO:CA	1:266:A:PRO:C	1:267:A:ARG:N	5	2.72

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,442)	1:411:A:ALA:N	1:411:A:ALA:CA	1:411:A:ALA:C	1:412:A:ARG:N	18	2.71
(1,735)	1:521:A:ASP:CA	1:521:A:ASP:CB	1:521:A:ASP:CG	1:521:A:ASP:OD1	3	2.7
(1,467)	1:429:A:ILE:N	1:429:A:ILE:CA	1:429:A:ILE:C	1:430:A:LYS:N	13	2.7
(1,361)	1:384:A:ASN:CA	1:384:A:ASN:CB	1:384:A:ASN:CG	1:384:A:ASN:OD1	19	2.7
(1,382)	1:390:A:LEU:N	1:390:A:LEU:CA	1:390:A:LEU:C	1:391:A:ARG:N	3	2.69
(1,294)	1:361:A:LEU:N	1:361:A:LEU:CA	1:361:A:LEU:C	1:362:A:ARG:N	7	2.69
(1,114)	1:299:A:THR:C	1:300:A:LEU:N	1:300:A:LEU:CA	1:300:A:LEU:C	8	2.69
(1,114)	1:299:A:THR:C	1:300:A:LEU:N	1:300:A:LEU:CA	1:300:A:LEU:C	2	2.68
(1,552)	1:461:A:LYS:N	1:461:A:LYS:CA	1:461:A:LYS:C	1:462:A:GLY:N	5	2.66
(1,114)	1:299:A:THR:C	1:300:A:LEU:N	1:300:A:LEU:CA	1:300:A:LEU:C	16	2.65
(1,294)	1:361:A:LEU:N	1:361:A:LEU:CA	1:361:A:LEU:C	1:362:A:ARG:N	14	2.63
(1,735)	1:521:A:ASP:CA	1:521:A:ASP:CB	1:521:A:ASP:CG	1:521:A:ASP:OD1	11	2.62
(1,114)	1:299:A:THR:C	1:300:A:LEU:N	1:300:A:LEU:CA	1:300:A:LEU:C	7	2.62
(1,487)	1:436:A:ALA:C	1:437:A:ALA:N	1:437:A:ALA:CA	1:437:A:ALA:C	11	2.61
(1,263)	1:351:A:ASP:CA	1:351:A:ASP:CB	1:351:A:ASP:CG	1:351:A:ASP:OD1	7	2.61
(1,362)	1:384:A:ASN:C	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	12	2.6
(1,473)	1:431:A:TRP:N	1:431:A:TRP:CA	1:431:A:TRP:C	1:432:A:THR:N	6	2.59
(1,263)	1:351:A:ASP:CA	1:351:A:ASP:CB	1:351:A:ASP:CG	1:351:A:ASP:OD1	3	2.58
(1,197)	1:329:A:TYR:CA	1:329:A:TYR:CB	1:329:A:TYR:CG	1:329:A:TYR:CD1	12	2.57
(1,419)	1:402:A:VAL:N	1:402:A:VAL:CA	1:402:A:VAL:C	1:403:A:CYS:N	2	2.56
(1,625)	1:485:A:PRO:N	1:485:A:PRO:CA	1:485:A:PRO:C	1:486:A:CYS:N	17	2.54
(1,3)	1:262:A:ALA:C	1:263:A:TRP:N	1:263:A:TRP:CA	1:263:A:TRP:C	1	2.54
(1,61)	1:281:A:PHE:CA	1:281:A:PHE:CB	1:281:A:PHE:CG	1:281:A:PHE:CD1	4	2.53
(1,419)	1:402:A:VAL:N	1:402:A:VAL:CA	1:402:A:VAL:C	1:403:A:CYS:N	14	2.51
(1,19)	1:267:A:ARG:CA	1:267:A:ARG:CB	1:267:A:ARG:CG	1:267:A:ARG:CD	18	2.51
(1,735)	1:521:A:ASP:CA	1:521:A:ASP:CB	1:521:A:ASP:CG	1:521:A:ASP:OD1	15	2.5
(1,374)	1:388:A:ARG:N	1:388:A:ARG:CA	1:388:A:ARG:C	1:389:A:ASP:N	11	2.49
(1,467)	1:429:A:ILE:N	1:429:A:ILE:CA	1:429:A:ILE:C	1:430:A:LYS:N	1	2.48
(1,617)	1:482:A:TYR:C	1:483:A:ARG:N	1:483:A:ARG:CA	1:483:A:ARG:C	12	2.46
(1,363)	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	1:386:A:VAL:N	5	2.46
(1,226)	1:340:A:VAL:C	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:C	10	2.46
(1,496)	1:439:A:TYR:CA	1:439:A:TYR:CB	1:439:A:TYR:CG	1:439:A:TYR:CD1	16	2.45
(1,46)	1:275:A:LYS:N	1:275:A:LYS:CA	1:275:A:LYS:C	1:276:A:LEU:N	13	2.45
(1,207)	1:334:A:GLU:N	1:334:A:GLU:CA	1:334:A:GLU:C	1:335:A:GLU:N	3	2.44
(1,263)	1:351:A:ASP:CA	1:351:A:ASP:CB	1:351:A:ASP:CG	1:351:A:ASP:OD1	13	2.43
(1,205)	1:333:A:SER:N	1:333:A:SER:CA	1:333:A:SER:C	1:334:A:GLU:N	2	2.42
(1,61)	1:281:A:PHE:CA	1:281:A:PHE:CB	1:281:A:PHE:CG	1:281:A:PHE:CD1	19	2.42
(1,27)	1:270:A:LEU:N	1:270:A:LEU:CA	1:270:A:LEU:C	1:271:A:ARG:N	6	2.42
(1,197)	1:329:A:TYR:CA	1:329:A:TYR:CB	1:329:A:TYR:CG	1:329:A:TYR:CD1	2	2.41
(1,42)	1:273:A:GLU:C	1:274:A:VAL:N	1:274:A:VAL:CA	1:274:A:VAL:C	4	2.41
(1,625)	1:485:A:PRO:N	1:485:A:PRO:CA	1:485:A:PRO:C	1:486:A:CYS:N	8	2.4
(1,382)	1:390:A:LEU:N	1:390:A:LEU:CA	1:390:A:LEU:C	1:391:A:ARG:N	5	2.4
(1,61)	1:281:A:PHE:CA	1:281:A:PHE:CB	1:281:A:PHE:CG	1:281:A:PHE:CD1	3	2.4
(1,380)	1:389:A:ASP:CA	1:389:A:ASP:CB	1:389:A:ASP:CG	1:389:A:ASP:OD1	11	2.39
(1,263)	1:351:A:ASP:CA	1:351:A:ASP:CB	1:351:A:ASP:CG	1:351:A:ASP:OD1	4	2.39
(1,207)	1:334:A:GLU:N	1:334:A:GLU:CA	1:334:A:GLU:C	1:335:A:GLU:N	5	2.38
(1,353)	1:382:A:ARG:N	1:382:A:ARG:CA	1:382:A:ARG:C	1:383:A:MET:N	11	2.37
(1,75)	1:285:A:TRP:C	1:286:A:MET:N	1:286:A:MET:CA	1:286:A:MET:C	20	2.36
(1,735)	1:521:A:ASP:CA	1:521:A:ASP:CB	1:521:A:ASP:CG	1:521:A:ASP:OD1	13	2.35
(1,606)	1:478:A:VAL:N	1:478:A:VAL:CA	1:478:A:VAL:CB	1:478:A:VAL:CG1	19	2.35
(1,104)	1:296:A:ALA:C	1:297:A:ILE:N	1:297:A:ILE:CA	1:297:A:ILE:C	7	2.34

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,122)	1:303:A:GLY:C	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	2	2.33
(1,630)	1:489:A:GLU:N	1:489:A:GLU:CA	1:489:A:GLU:C	1:490:A:CYS:N	5	2.32
(1,480)	1:434:A:PRO:N	1:434:A:PRO:CA	1:434:A:PRO:C	1:435:A:GLU:N	14	2.32
(1,421)	1:402:A:VAL:C	1:403:A:CYS:N	1:403:A:CYS:CA	1:403:A:CYS:C	14	2.32
(1,419)	1:402:A:VAL:N	1:402:A:VAL:CA	1:402:A:VAL:C	1:403:A:CYS:N	12	2.32
(1,363)	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	1:386:A:VAL:N	15	2.32
(1,123)	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	1:305:A:MET:N	18	2.32
(1,382)	1:390:A:LEU:N	1:390:A:LEU:CA	1:390:A:LEU:C	1:391:A:ARG:N	7	2.3
(1,122)	1:303:A:GLY:C	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	11	2.3
(1,68)	1:283:A:GLU:C	1:284:A:VAL:N	1:284:A:VAL:CA	1:284:A:VAL:C	20	2.29
(1,776)	1:535:A:ASN:CA	1:535:A:ASN:CB	1:535:A:ASN:CG	1:535:A:ASN:OD1	11	2.28
(1,625)	1:485:A:PRO:N	1:485:A:PRO:CA	1:485:A:PRO:C	1:486:A:CYS:N	19	2.28
(1,263)	1:351:A:ASP:CA	1:351:A:ASP:CB	1:351:A:ASP:CG	1:351:A:ASP:OD1	15	2.27
(1,123)	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	1:305:A:MET:N	20	2.26
(1,473)	1:431:A:TRP:N	1:431:A:TRP:CA	1:431:A:TRP:C	1:432:A:THR:N	11	2.25
(1,422)	1:403:A:CYS:N	1:403:A:CYS:CA	1:403:A:CYS:C	1:404:A:LYS:N	16	2.24
(1,188)	1:326:A:VAL:C	1:327:A:GLN:N	1:327:A:GLN:CA	1:327:A:GLN:C	18	2.24
(1,114)	1:299:A:THR:C	1:300:A:LEU:N	1:300:A:LEU:CA	1:300:A:LEU:C	10	2.24
(1,104)	1:296:A:ALA:C	1:297:A:ILE:N	1:297:A:ILE:CA	1:297:A:ILE:C	1	2.23
(1,62)	1:281:A:PHE:C	1:282:A:GLY:N	1:282:A:GLY:CA	1:282:A:GLY:C	1	2.23
(1,757)	1:529:A:GLN:N	1:529:A:GLN:CA	1:529:A:GLN:C	1:530:A:TYR:N	15	2.22
(1,444)	1:412:A:ARG:C	1:413:A:LEU:N	1:413:A:LEU:CA	1:413:A:LEU:C	18	2.22
(1,226)	1:340:A:VAL:C	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:C	16	2.22
(1,226)	1:340:A:VAL:C	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:C	5	2.21
(1,755)	1:528:A:PRO:N	1:528:A:PRO:CA	1:528:A:PRO:C	1:529:A:GLN:N	15	2.2
(1,735)	1:521:A:ASP:CA	1:521:A:ASP:CB	1:521:A:ASP:CG	1:521:A:ASP:OD1	2	2.2
(1,637)	1:492:A:GLU:N	1:492:A:GLU:CA	1:492:A:GLU:C	1:493:A:SER:N	17	2.2
(1,458)	1:421:A:ALA:C	1:422:A:ARG:N	1:422:A:ARG:CA	1:422:A:ARG:C	5	2.2
(1,75)	1:285:A:TRP:C	1:286:A:MET:N	1:286:A:MET:CA	1:286:A:MET:C	9	2.2
(1,226)	1:340:A:VAL:C	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:C	15	2.19
(1,735)	1:521:A:ASP:CA	1:521:A:ASP:CB	1:521:A:ASP:CG	1:521:A:ASP:OD1	10	2.17
(1,555)	1:461:A:LYS:C	1:462:A:GLY:N	1:462:A:GLY:CA	1:462:A:GLY:C	12	2.17
(1,473)	1:431:A:TRP:N	1:431:A:TRP:CA	1:431:A:TRP:C	1:432:A:THR:N	13	2.16
(1,61)	1:281:A:PHE:CA	1:281:A:PHE:CB	1:281:A:PHE:CG	1:281:A:PHE:CD1	6	2.15
(1,43)	1:274:A:VAL:N	1:274:A:VAL:CA	1:274:A:VAL:C	1:275:A:LYS:N	16	2.15
(1,505)	1:443:A:THR:N	1:443:A:THR:CA	1:443:A:THR:CB	1:443:A:THR:OG1	17	2.14
(1,46)	1:275:A:LYS:N	1:275:A:LYS:CA	1:275:A:LYS:C	1:276:A:LEU:N	4	2.14
(1,567)	1:467:A:PRO:N	1:467:A:PRO:CA	1:467:A:PRO:C	1:468:A:GLY:N	9	2.13
(1,1)	1:261:A:ASP:C	1:262:A:ALA:N	1:262:A:ALA:CA	1:262:A:ALA:C	19	2.13
(1,774)	1:535:A:ASN:N	1:535:A:ASN:CA	1:535:A:ASN:C	1:536:A:LEU:N	7	2.12
(1,46)	1:275:A:LYS:N	1:275:A:LYS:CA	1:275:A:LYS:C	1:276:A:LEU:N	1	2.11
(1,480)	1:434:A:PRO:N	1:434:A:PRO:CA	1:434:A:PRO:C	1:435:A:GLU:N	11	2.1
(1,43)	1:274:A:VAL:N	1:274:A:VAL:CA	1:274:A:VAL:C	1:275:A:LYS:N	5	2.1
(1,625)	1:485:A:PRO:N	1:485:A:PRO:CA	1:485:A:PRO:C	1:486:A:CYS:N	5	2.09
(1,118)	1:300:A:LEU:C	1:301:A:LYS:N	1:301:A:LYS:CA	1:301:A:LYS:C	4	2.09
(1,2)	1:262:A:ALA:N	1:262:A:ALA:CA	1:262:A:ALA:C	1:263:A:TRP:N	13	2.09
(1,380)	1:389:A:ASP:CA	1:389:A:ASP:CB	1:389:A:ASP:CG	1:389:A:ASP:OD1	19	2.07
(1,61)	1:281:A:PHE:CA	1:281:A:PHE:CB	1:281:A:PHE:CG	1:281:A:PHE:CD1	5	2.07
(1,735)	1:521:A:ASP:CA	1:521:A:ASP:CB	1:521:A:ASP:CG	1:521:A:ASP:OD1	18	2.06
(1,515)	1:447:A:ASP:CA	1:447:A:ASP:CB	1:447:A:ASP:CG	1:447:A:ASP:OD1	10	2.06
(1,467)	1:429:A:ILE:N	1:429:A:ILE:CA	1:429:A:ILE:C	1:430:A:LYS:N	19	2.06

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,263)	1:351:A:ASP:CA	1:351:A:ASP:CB	1:351:A:ASP:CG	1:351:A:ASP:OD1	8	2.06
(1,82)	1:288:A:THR:C	1:289:A:TRP:N	1:289:A:TRP:CA	1:289:A:TRP:C	11	2.06
(1,765)	1:531:A:GLN:N	1:531:A:GLN:CA	1:531:A:GLN:C	1:532:A:PRO:N	4	2.05
(1,467)	1:429:A:ILE:N	1:429:A:ILE:CA	1:429:A:ILE:C	1:430:A:LYS:N	10	2.05
(1,226)	1:340:A:VAL:C	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:C	12	2.05
(1,61)	1:281:A:PHE:CA	1:281:A:PHE:CB	1:281:A:PHE:CG	1:281:A:PHE:CD1	1	2.05
(1,774)	1:535:A:ASN:N	1:535:A:ASN:CA	1:535:A:ASN:C	1:536:A:LEU:N	10	2.04
(1,505)	1:443:A:THR:N	1:443:A:THR:CA	1:443:A:THR:CB	1:443:A:THR:OG1	14	2.04
(1,567)	1:467:A:PRO:N	1:467:A:PRO:CA	1:467:A:PRO:C	1:468:A:GLY:N	13	2.03
(1,61)	1:281:A:PHE:CA	1:281:A:PHE:CB	1:281:A:PHE:CG	1:281:A:PHE:CD1	8	2.03
(1,15)	1:266:A:PRO:N	1:266:A:PRO:CA	1:266:A:PRO:C	1:267:A:ARG:N	14	2.03
(1,567)	1:467:A:PRO:N	1:467:A:PRO:CA	1:467:A:PRO:C	1:468:A:GLY:N	17	2.02
(1,363)	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	1:386:A:VAL:N	16	2.02
(1,294)	1:361:A:LEU:N	1:361:A:LEU:CA	1:361:A:LEU:C	1:362:A:ARG:N	4	2.02
(1,748)	1:525:A:SER:C	1:526:A:THR:N	1:526:A:THR:CA	1:526:A:THR:C	9	2.01
(1,557)	1:462:A:GLY:C	1:463:A:ARG:N	1:463:A:ARG:CA	1:463:A:ARG:C	17	2.01
(1,442)	1:411:A:ALA:N	1:411:A:ALA:CA	1:411:A:ALA:C	1:412:A:ARG:N	11	2.01
(1,363)	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	1:386:A:VAL:N	8	2.0
(1,294)	1:361:A:LEU:N	1:361:A:LEU:CA	1:361:A:LEU:C	1:362:A:ARG:N	2	2.0
(1,79)	1:286:A:MET:CB	1:286:A:MET:CG	1:286:A:MET:SD	1:286:A:MET:CE	2	2.0
(1,567)	1:467:A:PRO:N	1:467:A:PRO:CA	1:467:A:PRO:C	1:468:A:GLY:N	19	1.99
(1,303)	1:365:A:GLN:N	1:365:A:GLN:CA	1:365:A:GLN:C	1:366:A:LEU:N	6	1.99
(1,114)	1:299:A:THR:C	1:300:A:LEU:N	1:300:A:LEU:CA	1:300:A:LEU:C	15	1.99
(1,79)	1:286:A:MET:CB	1:286:A:MET:CG	1:286:A:MET:SD	1:286:A:MET:CE	11	1.99
(1,75)	1:285:A:TRP:C	1:286:A:MET:N	1:286:A:MET:CA	1:286:A:MET:C	2	1.99
(1,2)	1:262:A:ALA:N	1:262:A:ALA:CA	1:262:A:ALA:C	1:263:A:TRP:N	11	1.99
(1,467)	1:429:A:ILE:N	1:429:A:ILE:CA	1:429:A:ILE:C	1:430:A:LYS:N	14	1.98
(1,114)	1:299:A:THR:C	1:300:A:LEU:N	1:300:A:LEU:CA	1:300:A:LEU:C	18	1.98
(1,735)	1:521:A:ASP:CA	1:521:A:ASP:CB	1:521:A:ASP:CG	1:521:A:ASP:OD1	20	1.97
(1,625)	1:485:A:PRO:N	1:485:A:PRO:CA	1:485:A:PRO:C	1:486:A:CYS:N	15	1.97
(1,598)	1:476:A:ASP:N	1:476:A:ASP:CA	1:476:A:ASP:CB	1:476:A:ASP:CG	7	1.97
(1,467)	1:429:A:ILE:N	1:429:A:ILE:CA	1:429:A:ILE:C	1:430:A:LYS:N	3	1.97
(1,226)	1:340:A:VAL:C	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:C	7	1.97
(1,226)	1:340:A:VAL:C	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:C	14	1.97
(1,365)	1:385:A:TYR:CA	1:385:A:TYR:CB	1:385:A:TYR:CG	1:385:A:TYR:CD1	18	1.96
(1,91)	1:291:A:GLY:N	1:291:A:GLY:CA	1:291:A:GLY:C	1:292:A:THR:N	9	1.96
(1,75)	1:285:A:TRP:C	1:286:A:MET:N	1:286:A:MET:CA	1:286:A:MET:C	12	1.96
(1,776)	1:535:A:ASN:CA	1:535:A:ASN:CB	1:535:A:ASN:CG	1:535:A:ASN:OD1	20	1.95
(1,774)	1:535:A:ASN:N	1:535:A:ASN:CA	1:535:A:ASN:C	1:536:A:LEU:N	8	1.95
(1,228)	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:CB	1:341:A:THR:OG1	15	1.95
(1,773)	1:534:A:GLU:C	1:535:A:ASN:N	1:535:A:ASN:CA	1:535:A:ASN:C	20	1.94
(1,557)	1:462:A:GLY:C	1:463:A:ARG:N	1:463:A:ARG:CA	1:463:A:ARG:C	12	1.93
(1,228)	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:CB	1:341:A:THR:OG1	14	1.93
(1,123)	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	1:305:A:MET:N	9	1.93
(1,625)	1:485:A:PRO:N	1:485:A:PRO:CA	1:485:A:PRO:C	1:486:A:CYS:N	13	1.92
(1,473)	1:431:A:TRP:N	1:431:A:TRP:CA	1:431:A:TRP:C	1:432:A:THR:N	4	1.92
(1,43)	1:274:A:VAL:N	1:274:A:VAL:CA	1:274:A:VAL:C	1:275:A:LYS:N	13	1.91
(1,226)	1:340:A:VAL:C	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:C	3	1.9
(1,75)	1:285:A:TRP:C	1:286:A:MET:N	1:286:A:MET:CA	1:286:A:MET:C	4	1.9
(1,756)	1:528:A:PRO:C	1:529:A:GLN:N	1:529:A:GLN:CA	1:529:A:GLN:C	18	1.89
(1,522)	1:449:A:TRP:CA	1:449:A:TRP:CB	1:449:A:TRP:CG	1:449:A:TRP:CD1	1	1.89

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,75)	1:285:A:TRP:C	1:286:A:MET:N	1:286:A:MET:CA	1:286:A:MET:C	16	1.88
(1,61)	1:281:A:PHE:CA	1:281:A:PHE:CB	1:281:A:PHE:CG	1:281:A:PHE:CD1	14	1.88
(1,419)	1:402:A:VAL:N	1:402:A:VAL:CA	1:402:A:VAL:C	1:403:A:CYS:N	19	1.87
(1,394)	1:394:A:ASN:N	1:394:A:ASN:CA	1:394:A:ASN:C	1:395:A:ILE:N	3	1.87
(1,207)	1:334:A:GLU:N	1:334:A:GLU:CA	1:334:A:GLU:C	1:335:A:GLU:N	20	1.87
(1,2)	1:262:A:ALA:N	1:262:A:ALA:CA	1:262:A:ALA:C	1:263:A:TRP:N	2	1.87
(1,630)	1:489:A:GLU:N	1:489:A:GLU:CA	1:489:A:GLU:C	1:490:A:CYS:N	11	1.86
(1,493)	1:438:A:LEU:C	1:439:A:TYR:N	1:439:A:TYR:CA	1:439:A:TYR:C	15	1.86
(1,75)	1:285:A:TRP:C	1:286:A:MET:N	1:286:A:MET:CA	1:286:A:MET:C	17	1.86
(1,430)	1:407:A:ASP:N	1:407:A:ASP:CA	1:407:A:ASP:C	1:408:A:PHE:N	18	1.85
(1,61)	1:281:A:PHE:CA	1:281:A:PHE:CB	1:281:A:PHE:CG	1:281:A:PHE:CD1	7	1.85
(1,42)	1:273:A:GLU:C	1:274:A:VAL:N	1:274:A:VAL:CA	1:274:A:VAL:C	20	1.85
(1,630)	1:489:A:GLU:N	1:489:A:GLU:CA	1:489:A:GLU:C	1:490:A:CYS:N	6	1.84
(1,362)	1:384:A:ASN:C	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	10	1.84
(1,26)	1:269:A:SER:C	1:270:A:LEU:N	1:270:A:LEU:CA	1:270:A:LEU:C	9	1.84
(1,614)	1:481:A:GLY:N	1:481:A:GLY:CA	1:481:A:GLY:C	1:482:A:TYR:N	9	1.83
(1,361)	1:384:A:ASN:CA	1:384:A:ASN:CB	1:384:A:ASN:CG	1:384:A:ASN:OD1	6	1.83
(1,207)	1:334:A:GLU:N	1:334:A:GLU:CA	1:334:A:GLU:C	1:335:A:GLU:N	16	1.83
(1,72)	1:285:A:TRP:N	1:285:A:TRP:CA	1:285:A:TRP:C	1:286:A:MET:N	3	1.83
(1,362)	1:384:A:ASN:C	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	5	1.82
(1,228)	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:CB	1:341:A:THR:OG1	4	1.82
(1,748)	1:525:A:SER:C	1:526:A:THR:N	1:526:A:THR:CA	1:526:A:THR:C	16	1.81
(1,226)	1:340:A:VAL:C	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:C	13	1.81
(1,30)	1:270:A:LEU:C	1:271:A:ARG:N	1:271:A:ARG:CA	1:271:A:ARG:C	4	1.81
(1,493)	1:438:A:LEU:C	1:439:A:TYR:N	1:439:A:TYR:CA	1:439:A:TYR:C	16	1.8
(1,363)	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	1:386:A:VAL:N	10	1.8
(1,353)	1:382:A:ARG:N	1:382:A:ARG:CA	1:382:A:ARG:C	1:383:A:MET:N	3	1.8
(1,104)	1:296:A:ALA:C	1:297:A:ILE:N	1:297:A:ILE:CA	1:297:A:ILE:C	2	1.8
(1,72)	1:285:A:TRP:N	1:285:A:TRP:CA	1:285:A:TRP:C	1:286:A:MET:N	10	1.8
(1,748)	1:525:A:SER:C	1:526:A:THR:N	1:526:A:THR:CA	1:526:A:THR:C	1	1.79
(1,158)	1:318:A:LYS:CA	1:318:A:LYS:CB	1:318:A:LYS:CG	1:318:A:LYS:CD	17	1.79
(1,122)	1:303:A:GLY:C	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	10	1.79
(1,442)	1:411:A:ALA:N	1:411:A:ALA:CA	1:411:A:ALA:C	1:412:A:ARG:N	20	1.78
(1,735)	1:521:A:ASP:CA	1:521:A:ASP:CB	1:521:A:ASP:CG	1:521:A:ASP:OD1	12	1.77
(1,502)	1:441:A:ARG:CA	1:441:A:ARG:CB	1:441:A:ARG:CG	1:441:A:ARG:CD	8	1.76
(1,421)	1:402:A:VAL:C	1:403:A:CYS:N	1:403:A:CYS:CA	1:403:A:CYS:C	1	1.76
(1,382)	1:390:A:LEU:N	1:390:A:LEU:CA	1:390:A:LEU:C	1:391:A:ARG:N	19	1.76
(1,380)	1:389:A:ASP:CA	1:389:A:ASP:CB	1:389:A:ASP:CG	1:389:A:ASP:OD1	9	1.76
(1,361)	1:384:A:ASN:CA	1:384:A:ASN:CB	1:384:A:ASN:CG	1:384:A:ASN:OD1	9	1.76
(1,303)	1:365:A:GLN:N	1:365:A:GLN:CA	1:365:A:GLN:C	1:366:A:LEU:N	11	1.76
(1,92)	1:292:A:THR:C	1:293:A:THR:N	1:293:A:THR:CA	1:293:A:THR:C	12	1.76
(1,75)	1:285:A:TRP:C	1:286:A:MET:N	1:286:A:MET:CA	1:286:A:MET:C	1	1.76
(1,442)	1:411:A:ALA:N	1:411:A:ALA:CA	1:411:A:ALA:C	1:412:A:ARG:N	19	1.75
(1,362)	1:384:A:ASN:C	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	17	1.75
(1,42)	1:273:A:GLU:C	1:274:A:VAL:N	1:274:A:VAL:CA	1:274:A:VAL:C	19	1.75
(1,735)	1:521:A:ASP:CA	1:521:A:ASP:CB	1:521:A:ASP:CG	1:521:A:ASP:OD1	8	1.74
(1,679)	1:505:A:GLU:N	1:505:A:GLU:CA	1:505:A:GLU:C	1:506:A:PRO:N	7	1.74
(1,367)	1:386:A:VAL:N	1:386:A:VAL:CA	1:386:A:VAL:C	1:387:A:HIS:N	2	1.74
(1,617)	1:482:A:TYR:C	1:483:A:ARG:N	1:483:A:ARG:CA	1:483:A:ARG:C	15	1.73
(1,484)	1:435:A:GLU:CA	1:435:A:GLU:CB	1:435:A:GLU:CG	1:435:A:GLU:CD	8	1.73
(1,75)	1:285:A:TRP:C	1:286:A:MET:N	1:286:A:MET:CA	1:286:A:MET:C	5	1.73

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,776)	1:535:A:ASN:CA	1:535:A:ASN:CB	1:535:A:ASN:CG	1:535:A:ASN:OD1	10	1.72
(1,421)	1:402:A:VAL:C	1:403:A:CYS:N	1:403:A:CYS:CA	1:403:A:CYS:C	19	1.72
(1,380)	1:389:A:ASP:CA	1:389:A:ASP:CB	1:389:A:ASP:CG	1:389:A:ASP:OD1	12	1.72
(1,515)	1:447:A:ASP:CA	1:447:A:ASP:CB	1:447:A:ASP:CG	1:447:A:ASP:OD1	7	1.71
(1,422)	1:403:A:CYS:N	1:403:A:CYS:CA	1:403:A:CYS:C	1:404:A:LYS:N	17	1.71
(1,361)	1:384:A:ASN:CA	1:384:A:ASN:CB	1:384:A:ASN:CG	1:384:A:ASN:OD1	8	1.71
(1,27)	1:270:A:LEU:N	1:270:A:LEU:CA	1:270:A:LEU:C	1:271:A:ARG:N	8	1.71
(1,768)	1:532:A:PRO:N	1:532:A:PRO:CA	1:532:A:PRO:C	1:533:A:GLY:N	18	1.7
(1,748)	1:525:A:SER:C	1:526:A:THR:N	1:526:A:THR:CA	1:526:A:THR:C	11	1.7
(1,480)	1:434:A:PRO:N	1:434:A:PRO:CA	1:434:A:PRO:C	1:435:A:GLU:N	2	1.7
(1,63)	1:282:A:GLY:N	1:282:A:GLY:CA	1:282:A:GLY:C	1:283:A:GLU:N	3	1.7
(1,748)	1:525:A:SER:C	1:526:A:THR:N	1:526:A:THR:CA	1:526:A:THR:C	3	1.69
(1,228)	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:CB	1:341:A:THR:OG1	9	1.69
(1,452)	1:415:A:GLU:C	1:416:A:ASP:N	1:416:A:ASP:CA	1:416:A:ASP:C	13	1.68
(1,361)	1:384:A:ASN:CA	1:384:A:ASN:CB	1:384:A:ASN:CG	1:384:A:ASN:OD1	11	1.68
(1,188)	1:326:A:VAL:C	1:327:A:GLN:N	1:327:A:GLN:CA	1:327:A:GLN:C	9	1.68
(1,104)	1:296:A:ALA:C	1:297:A:ILE:N	1:297:A:ILE:CA	1:297:A:ILE:C	16	1.68
(1,72)	1:285:A:TRP:N	1:285:A:TRP:CA	1:285:A:TRP:C	1:286:A:MET:N	7	1.68
(1,71)	1:284:A:VAL:C	1:285:A:TRP:N	1:285:A:TRP:CA	1:285:A:TRP:C	11	1.68
(1,61)	1:281:A:PHE:CA	1:281:A:PHE:CB	1:281:A:PHE:CG	1:281:A:PHE:CD1	9	1.68
(1,776)	1:535:A:ASN:CA	1:535:A:ASN:CB	1:535:A:ASN:CG	1:535:A:ASN:OD1	18	1.67
(1,618)	1:483:A:ARG:N	1:483:A:ARG:CA	1:483:A:ARG:C	1:484:A:MET:N	9	1.67
(1,617)	1:482:A:TYR:C	1:483:A:ARG:N	1:483:A:ARG:CA	1:483:A:ARG:C	17	1.67
(1,488)	1:437:A:ALA:N	1:437:A:ALA:CA	1:437:A:ALA:C	1:438:A:LEU:N	17	1.67
(1,368)	1:386:A:VAL:N	1:386:A:VAL:CA	1:386:A:VAL:CB	1:386:A:VAL:CG1	15	1.67
(1,123)	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	1:305:A:MET:N	17	1.67
(1,496)	1:439:A:TYR:CA	1:439:A:TYR:CB	1:439:A:TYR:CG	1:439:A:TYR:CD1	7	1.66
(1,205)	1:333:A:SER:N	1:333:A:SER:CA	1:333:A:SER:C	1:334:A:GLU:N	14	1.66
(1,46)	1:275:A:LYS:N	1:275:A:LYS:CA	1:275:A:LYS:C	1:276:A:LEU:N	5	1.65
(1,748)	1:525:A:SER:C	1:526:A:THR:N	1:526:A:THR:CA	1:526:A:THR:C	10	1.64
(1,377)	1:388:A:ARG:C	1:389:A:ASP:N	1:389:A:ASP:CA	1:389:A:ASP:C	4	1.64
(1,3)	1:262:A:ALA:C	1:263:A:TRP:N	1:263:A:TRP:CA	1:263:A:TRP:C	6	1.64
(1,569)	1:468:A:GLY:N	1:468:A:GLY:CA	1:468:A:GLY:C	1:469:A:MET:N	2	1.63
(1,444)	1:412:A:ARG:C	1:413:A:LEU:N	1:413:A:LEU:CA	1:413:A:LEU:C	5	1.63
(1,400)	1:396:A:LEU:N	1:396:A:LEU:CA	1:396:A:LEU:C	1:397:A:VAL:N	17	1.63
(1,226)	1:340:A:VAL:C	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:C	11	1.63
(1,226)	1:340:A:VAL:C	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:C	18	1.63
(1,188)	1:326:A:VAL:C	1:327:A:GLN:N	1:327:A:GLN:CA	1:327:A:GLN:C	4	1.63
(1,567)	1:467:A:PRO:N	1:467:A:PRO:CA	1:467:A:PRO:C	1:468:A:GLY:N	14	1.61
(1,119)	1:301:A:LYS:N	1:301:A:LYS:CA	1:301:A:LYS:C	1:302:A:PRO:N	4	1.61
(1,442)	1:411:A:ALA:N	1:411:A:ALA:CA	1:411:A:ALA:C	1:412:A:ARG:N	7	1.59
(1,361)	1:384:A:ASN:CA	1:384:A:ASN:CB	1:384:A:ASN:CG	1:384:A:ASN:OD1	14	1.59
(1,484)	1:435:A:GLU:CA	1:435:A:GLU:CB	1:435:A:GLU:CG	1:435:A:GLU:CD	17	1.58
(1,2)	1:262:A:ALA:N	1:262:A:ALA:CA	1:262:A:ALA:C	1:263:A:TRP:N	15	1.58
(1,303)	1:365:A:GLN:N	1:365:A:GLN:CA	1:365:A:GLN:C	1:366:A:LEU:N	9	1.57
(1,188)	1:326:A:VAL:C	1:327:A:GLN:N	1:327:A:GLN:CA	1:327:A:GLN:C	6	1.57
(1,82)	1:288:A:THR:C	1:289:A:TRP:N	1:289:A:TRP:CA	1:289:A:TRP:C	9	1.57
(1,653)	1:496:A:ASP:CA	1:496:A:ASP:CB	1:496:A:ASP:CG	1:496:A:ASP:OD1	14	1.56
(1,625)	1:485:A:PRO:N	1:485:A:PRO:CA	1:485:A:PRO:C	1:486:A:CYS:N	6	1.56
(1,361)	1:384:A:ASN:CA	1:384:A:ASN:CB	1:384:A:ASN:CG	1:384:A:ASN:OD1	4	1.56
(1,748)	1:525:A:SER:C	1:526:A:THR:N	1:526:A:THR:CA	1:526:A:THR:C	4	1.55

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,236)	1:343:A:TYR:CA	1:343:A:TYR:CB	1:343:A:TYR:CG	1:343:A:TYR:CD1	19	1.55
(1,46)	1:275:A:LYS:N	1:275:A:LYS:CA	1:275:A:LYS:C	1:276:A:LEU:N	18	1.55
(1,493)	1:438:A:LEU:C	1:439:A:TYR:N	1:439:A:TYR:CA	1:439:A:TYR:C	7	1.54
(1,442)	1:411:A:ALA:N	1:411:A:ALA:CA	1:411:A:ALA:C	1:412:A:ARG:N	10	1.54
(1,188)	1:326:A:VAL:C	1:327:A:GLN:N	1:327:A:GLN:CA	1:327:A:GLN:C	2	1.54
(1,82)	1:288:A:THR:C	1:289:A:TRP:N	1:289:A:TRP:CA	1:289:A:TRP:C	15	1.54
(1,27)	1:270:A:LEU:N	1:270:A:LEU:CA	1:270:A:LEU:C	1:271:A:ARG:N	9	1.54
(1,770)	1:534:A:GLU:N	1:534:A:GLU:CA	1:534:A:GLU:C	1:535:A:ASN:N	13	1.53
(1,514)	1:447:A:ASP:N	1:447:A:ASP:CA	1:447:A:ASP:CB	1:447:A:ASP:CG	8	1.53
(1,42)	1:273:A:GLU:C	1:274:A:VAL:N	1:274:A:VAL:CA	1:274:A:VAL:C	9	1.53
(1,442)	1:411:A:ALA:N	1:411:A:ALA:CA	1:411:A:ALA:C	1:412:A:ARG:N	16	1.52
(1,606)	1:478:A:VAL:N	1:478:A:VAL:CA	1:478:A:VAL:CB	1:478:A:VAL:CG1	13	1.51
(1,567)	1:467:A:PRO:N	1:467:A:PRO:CA	1:467:A:PRO:C	1:468:A:GLY:N	16	1.51
(1,537)	1:456:A:THR:N	1:456:A:THR:CA	1:456:A:THR:CB	1:456:A:THR:OG1	12	1.51
(1,735)	1:521:A:ASP:CA	1:521:A:ASP:CB	1:521:A:ASP:CG	1:521:A:ASP:OD1	4	1.5
(1,613)	1:480:A:ARG:C	1:481:A:GLY:N	1:481:A:GLY:CA	1:481:A:GLY:C	14	1.5
(1,467)	1:429:A:ILE:N	1:429:A:ILE:CA	1:429:A:ILE:C	1:430:A:LYS:N	11	1.5
(1,442)	1:411:A:ALA:N	1:411:A:ALA:CA	1:411:A:ALA:C	1:412:A:ARG:N	15	1.5
(1,374)	1:388:A:ARG:N	1:388:A:ARG:CA	1:388:A:ARG:C	1:389:A:ASP:N	3	1.5
(1,368)	1:386:A:VAL:N	1:386:A:VAL:CA	1:386:A:VAL:CB	1:386:A:VAL:CG1	18	1.5
(1,82)	1:288:A:THR:C	1:289:A:TRP:N	1:289:A:TRP:CA	1:289:A:TRP:C	4	1.5
(1,78)	1:286:A:MET:CA	1:286:A:MET:CB	1:286:A:MET:CG	1:286:A:MET:SD	2	1.5
(1,46)	1:275:A:LYS:N	1:275:A:LYS:CA	1:275:A:LYS:C	1:276:A:LEU:N	2	1.5
(1,515)	1:447:A:ASP:CA	1:447:A:ASP:CB	1:447:A:ASP:CG	1:447:A:ASP:OD1	15	1.49
(1,467)	1:429:A:ILE:N	1:429:A:ILE:CA	1:429:A:ILE:C	1:430:A:LYS:N	5	1.49
(1,303)	1:365:A:GLN:N	1:365:A:GLN:CA	1:365:A:GLN:C	1:366:A:LEU:N	17	1.49
(1,91)	1:291:A:GLY:N	1:291:A:GLY:CA	1:291:A:GLY:C	1:292:A:THR:N	14	1.49
(1,617)	1:482:A:TYR:C	1:483:A:ARG:N	1:483:A:ARG:CA	1:483:A:ARG:C	10	1.47
(1,226)	1:340:A:VAL:C	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:C	2	1.47
(1,62)	1:281:A:PHE:C	1:282:A:GLY:N	1:282:A:GLY:CA	1:282:A:GLY:C	3	1.47
(1,4)	1:263:A:TRP:N	1:263:A:TRP:CA	1:263:A:TRP:C	1:264:A:GLU:N	3	1.47
(1,618)	1:483:A:ARG:N	1:483:A:ARG:CA	1:483:A:ARG:C	1:484:A:MET:N	10	1.46
(1,773)	1:534:A:GLU:C	1:535:A:ASN:N	1:535:A:ASN:CA	1:535:A:ASN:C	5	1.45
(1,614)	1:481:A:GLY:N	1:481:A:GLY:CA	1:481:A:GLY:C	1:482:A:TYR:N	10	1.45
(1,224)	1:340:A:VAL:N	1:340:A:VAL:CA	1:340:A:VAL:C	1:341:A:THR:N	18	1.45
(1,79)	1:286:A:MET:CB	1:286:A:MET:CG	1:286:A:MET:SD	1:286:A:MET:CE	6	1.45
(1,46)	1:275:A:LYS:N	1:275:A:LYS:CA	1:275:A:LYS:C	1:276:A:LEU:N	7	1.45
(1,30)	1:270:A:LEU:C	1:271:A:ARG:N	1:271:A:ARG:CA	1:271:A:ARG:C	18	1.44
(1,361)	1:384:A:ASN:CA	1:384:A:ASN:CB	1:384:A:ASN:CG	1:384:A:ASN:OD1	7	1.43
(1,226)	1:340:A:VAL:C	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:C	6	1.43
(1,75)	1:285:A:TRP:C	1:286:A:MET:N	1:286:A:MET:CA	1:286:A:MET:C	3	1.43
(1,363)	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	1:386:A:VAL:N	20	1.42
(1,205)	1:333:A:SER:N	1:333:A:SER:CA	1:333:A:SER:C	1:334:A:GLU:N	9	1.42
(1,30)	1:270:A:LEU:C	1:271:A:ARG:N	1:271:A:ARG:CA	1:271:A:ARG:C	14	1.42
(1,15)	1:266:A:PRO:N	1:266:A:PRO:CA	1:266:A:PRO:C	1:267:A:ARG:N	9	1.42
(1,614)	1:481:A:GLY:N	1:481:A:GLY:CA	1:481:A:GLY:C	1:482:A:TYR:N	3	1.41
(1,104)	1:296:A:ALA:C	1:297:A:ILE:N	1:297:A:ILE:CA	1:297:A:ILE:C	14	1.41
(1,515)	1:447:A:ASP:CA	1:447:A:ASP:CB	1:447:A:ASP:CG	1:447:A:ASP:OD1	8	1.4
(1,228)	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:CB	1:341:A:THR:OG1	7	1.4
(1,197)	1:329:A:TYR:CA	1:329:A:TYR:CB	1:329:A:TYR:CG	1:329:A:TYR:CD1	11	1.4
(1,188)	1:326:A:VAL:C	1:327:A:GLN:N	1:327:A:GLN:CA	1:327:A:GLN:C	10	1.4

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,188)	1:326:A:VAL:C	1:327:A:GLN:N	1:327:A:GLN:CA	1:327:A:GLN:C	14	1.4
(1,123)	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	1:305:A:MET:N	10	1.4
(1,15)	1:266:A:PRO:N	1:266:A:PRO:CA	1:266:A:PRO:C	1:267:A:ARG:N	1	1.4
(1,362)	1:384:A:ASN:C	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	7	1.39
(1,361)	1:384:A:ASN:CA	1:384:A:ASN:CB	1:384:A:ASN:CG	1:384:A:ASN:OD1	10	1.39
(1,31)	1:271:A:ARG:N	1:271:A:ARG:CA	1:271:A:ARG:C	1:272:A:LEU:N	20	1.39
(1,537)	1:456:A:THR:N	1:456:A:THR:CA	1:456:A:THR:CB	1:456:A:THR:OG1	13	1.38
(1,72)	1:285:A:TRP:N	1:285:A:TRP:CA	1:285:A:TRP:C	1:286:A:MET:N	11	1.38
(1,62)	1:281:A:PHE:C	1:282:A:GLY:N	1:282:A:GLY:CA	1:282:A:GLY:C	18	1.38
(1,735)	1:521:A:ASP:CA	1:521:A:ASP:CB	1:521:A:ASP:CG	1:521:A:ASP:OD1	19	1.37
(1,687)	1:507:A:GLU:C	1:508:A:GLU:N	1:508:A:GLU:CA	1:508:A:GLU:C	19	1.37
(1,630)	1:489:A:GLU:N	1:489:A:GLU:CA	1:489:A:GLU:C	1:490:A:CYS:N	9	1.37
(1,484)	1:435:A:GLU:CA	1:435:A:GLU:CB	1:435:A:GLU:CG	1:435:A:GLU:CD	14	1.37
(1,263)	1:351:A:ASP:CA	1:351:A:ASP:CB	1:351:A:ASP:CG	1:351:A:ASP:OD1	14	1.37
(1,263)	1:351:A:ASP:CA	1:351:A:ASP:CB	1:351:A:ASP:CG	1:351:A:ASP:OD1	20	1.37
(1,226)	1:340:A:VAL:C	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:C	20	1.37
(1,123)	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	1:305:A:MET:N	7	1.37
(1,31)	1:271:A:ARG:N	1:271:A:ARG:CA	1:271:A:ARG:C	1:272:A:LEU:N	17	1.37
(1,153)	1:317:A:MET:CA	1:317:A:MET:CB	1:317:A:MET:CG	1:317:A:MET:SD	8	1.36
(1,79)	1:286:A:MET:CB	1:286:A:MET:CG	1:286:A:MET:SD	1:286:A:MET:CE	17	1.36
(1,4)	1:263:A:TRP:N	1:263:A:TRP:CA	1:263:A:TRP:C	1:264:A:GLU:N	9	1.36
(1,382)	1:390:A:LEU:N	1:390:A:LEU:CA	1:390:A:LEU:C	1:391:A:ARG:N	15	1.35
(1,119)	1:301:A:LYS:N	1:301:A:LYS:CA	1:301:A:LYS:C	1:302:A:PRO:N	14	1.35
(1,770)	1:534:A:GLU:N	1:534:A:GLU:CA	1:534:A:GLU:C	1:535:A:ASN:N	3	1.34
(1,671)	1:503:A:ARG:N	1:503:A:ARG:CA	1:503:A:ARG:C	1:504:A:LYS:N	13	1.34
(1,613)	1:480:A:ARG:C	1:481:A:GLY:N	1:481:A:GLY:CA	1:481:A:GLY:C	7	1.34
(1,575)	1:470:A:VAL:N	1:470:A:VAL:CA	1:470:A:VAL:C	1:471:A:ASN:N	5	1.34
(1,122)	1:303:A:GLY:C	1:304:A:THR:N	1:304:A:THR:CA	1:304:A:THR:C	19	1.34
(1,62)	1:281:A:PHE:C	1:282:A:GLY:N	1:282:A:GLY:CA	1:282:A:GLY:C	5	1.34
(1,30)	1:270:A:LEU:C	1:271:A:ARG:N	1:271:A:ARG:CA	1:271:A:ARG:C	16	1.34
(1,422)	1:403:A:CYS:N	1:403:A:CYS:CA	1:403:A:CYS:C	1:404:A:LYS:N	19	1.33
(1,617)	1:482:A:TYR:C	1:483:A:ARG:N	1:483:A:ARG:CA	1:483:A:ARG:C	7	1.32
(1,490)	1:438:A:LEU:N	1:438:A:LEU:CA	1:438:A:LEU:C	1:439:A:TYR:N	10	1.32
(1,119)	1:301:A:LYS:N	1:301:A:LYS:CA	1:301:A:LYS:C	1:302:A:PRO:N	15	1.32
(1,515)	1:447:A:ASP:CA	1:447:A:ASP:CB	1:447:A:ASP:CG	1:447:A:ASP:OD1	2	1.31
(1,493)	1:438:A:LEU:C	1:439:A:TYR:N	1:439:A:TYR:CA	1:439:A:TYR:C	3	1.31
(1,419)	1:402:A:VAL:N	1:402:A:VAL:CA	1:402:A:VAL:C	1:403:A:CYS:N	17	1.31
(1,91)	1:291:A:GLY:N	1:291:A:GLY:CA	1:291:A:GLY:C	1:292:A:THR:N	12	1.31
(1,653)	1:496:A:ASP:CA	1:496:A:ASP:CB	1:496:A:ASP:CG	1:496:A:ASP:OD1	8	1.3
(1,487)	1:436:A:ALA:C	1:437:A:ALA:N	1:437:A:ALA:CA	1:437:A:ALA:C	3	1.3
(1,487)	1:436:A:ALA:C	1:437:A:ALA:N	1:437:A:ALA:CA	1:437:A:ALA:C	10	1.3
(1,166)	1:321:A:ARG:N	1:321:A:ARG:CA	1:321:A:ARG:C	1:322:A:HIS:N	10	1.3
(1,104)	1:296:A:ALA:C	1:297:A:ILE:N	1:297:A:ILE:CA	1:297:A:ILE:C	15	1.3
(1,756)	1:528:A:PRO:C	1:529:A:GLN:N	1:529:A:GLN:CA	1:529:A:GLN:C	15	1.29
(1,490)	1:438:A:LEU:N	1:438:A:LEU:CA	1:438:A:LEU:C	1:439:A:TYR:N	15	1.29
(1,381)	1:389:A:ASP:C	1:390:A:LEU:N	1:390:A:LEU:CA	1:390:A:LEU:C	8	1.29
(1,226)	1:340:A:VAL:C	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:C	1	1.29
(1,771)	1:534:A:GLU:N	1:534:A:GLU:CA	1:534:A:GLU:CB	1:534:A:GLU:CG	1	1.28
(1,630)	1:489:A:GLU:N	1:489:A:GLU:CA	1:489:A:GLU:C	1:490:A:CYS:N	18	1.28
(1,625)	1:485:A:PRO:N	1:485:A:PRO:CA	1:485:A:PRO:C	1:486:A:CYS:N	3	1.28
(1,550)	1:460:A:THR:N	1:460:A:THR:CA	1:460:A:THR:CB	1:460:A:THR:OG1	15	1.28

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,349)	1:381:A:GLU:N	1:381:A:GLU:CA	1:381:A:GLU:C	1:382:A:ARG:N	3	1.28
(1,305)	1:365:A:GLN:CA	1:365:A:GLN:CB	1:365:A:GLN:CG	1:365:A:GLN:CD	15	1.28
(1,735)	1:521:A:ASP:CA	1:521:A:ASP:CB	1:521:A:ASP:CG	1:521:A:ASP:OD1	9	1.27
(1,537)	1:456:A:THR:N	1:456:A:THR:CA	1:456:A:THR:CB	1:456:A:THR:OG1	2	1.27
(1,451)	1:414:A:ILE:C	1:415:A:GLU:N	1:415:A:GLU:CA	1:415:A:GLU:C	20	1.27
(1,430)	1:407:A:ASP:N	1:407:A:ASP:CA	1:407:A:ASP:C	1:408:A:PHE:N	4	1.27
(1,422)	1:403:A:CYS:N	1:403:A:CYS:CA	1:403:A:CYS:C	1:404:A:LYS:N	11	1.27
(1,361)	1:384:A:ASN:CA	1:384:A:ASN:CB	1:384:A:ASN:CG	1:384:A:ASN:OD1	20	1.27
(1,228)	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:CB	1:341:A:THR:OG1	6	1.27
(1,188)	1:326:A:VAL:C	1:327:A:GLN:N	1:327:A:GLN:CA	1:327:A:GLN:C	3	1.27
(1,105)	1:297:A:ILE:N	1:297:A:ILE:CA	1:297:A:ILE:C	1:298:A:LYS:N	14	1.27
(1,72)	1:285:A:TRP:N	1:285:A:TRP:CA	1:285:A:TRP:C	1:286:A:MET:N	4	1.27
(1,3)	1:262:A:ALA:C	1:263:A:TRP:N	1:263:A:TRP:CA	1:263:A:TRP:C	2	1.27
(1,226)	1:340:A:VAL:C	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:C	8	1.26
(1,188)	1:326:A:VAL:C	1:327:A:GLN:N	1:327:A:GLN:CA	1:327:A:GLN:C	5	1.26
(1,104)	1:296:A:ALA:C	1:297:A:ILE:N	1:297:A:ILE:CA	1:297:A:ILE:C	3	1.26
(1,92)	1:292:A:THR:C	1:293:A:THR:N	1:293:A:THR:CA	1:293:A:THR:C	14	1.26
(1,71)	1:284:A:VAL:C	1:285:A:TRP:N	1:285:A:TRP:CA	1:285:A:TRP:C	16	1.26
(1,515)	1:447:A:ASP:CA	1:447:A:ASP:CB	1:447:A:ASP:CG	1:447:A:ASP:OD1	18	1.25
(1,422)	1:403:A:CYS:N	1:403:A:CYS:CA	1:403:A:CYS:C	1:404:A:LYS:N	14	1.25
(1,377)	1:388:A:ARG:C	1:389:A:ASP:N	1:389:A:ASP:CA	1:389:A:ASP:C	14	1.25
(1,732)	1:520:A:GLU:C	1:521:A:ASP:N	1:521:A:ASP:CA	1:521:A:ASP:C	18	1.24
(1,245)	1:346:A:LYS:N	1:346:A:LYS:CA	1:346:A:LYS:C	1:347:A:GLY:N	2	1.24
(1,228)	1:341:A:THR:N	1:341:A:THR:CA	1:341:A:THR:CB	1:341:A:THR:OG1	1	1.24
(1,91)	1:291:A:GLY:N	1:291:A:GLY:CA	1:291:A:GLY:C	1:292:A:THR:N	19	1.24
(1,567)	1:467:A:PRO:N	1:467:A:PRO:CA	1:467:A:PRO:C	1:468:A:GLY:N	1	1.23
(1,363)	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	1:386:A:VAL:N	13	1.23
(1,606)	1:478:A:VAL:N	1:478:A:VAL:CA	1:478:A:VAL:CB	1:478:A:VAL:CG1	9	1.22
(1,380)	1:389:A:ASP:CA	1:389:A:ASP:CB	1:389:A:ASP:CG	1:389:A:ASP:OD1	16	1.22
(1,79)	1:286:A:MET:CB	1:286:A:MET:CG	1:286:A:MET:SD	1:286:A:MET:CE	3	1.22
(1,75)	1:285:A:TRP:C	1:286:A:MET:N	1:286:A:MET:CA	1:286:A:MET:C	15	1.22
(1,31)	1:271:A:ARG:N	1:271:A:ARG:CA	1:271:A:ARG:C	1:272:A:LEU:N	19	1.22
(1,294)	1:361:A:LEU:N	1:361:A:LEU:CA	1:361:A:LEU:C	1:362:A:ARG:N	8	1.21
(1,46)	1:275:A:LYS:N	1:275:A:LYS:CA	1:275:A:LYS:C	1:276:A:LEU:N	17	1.21
(1,448)	1:413:A:LEU:C	1:414:A:ILE:N	1:414:A:ILE:CA	1:414:A:ILE:C	18	1.2
(1,104)	1:296:A:ALA:C	1:297:A:ILE:N	1:297:A:ILE:CA	1:297:A:ILE:C	11	1.2
(1,72)	1:285:A:TRP:N	1:285:A:TRP:CA	1:285:A:TRP:C	1:286:A:MET:N	12	1.2
(1,493)	1:438:A:LEU:C	1:439:A:TYR:N	1:439:A:TYR:CA	1:439:A:TYR:C	4	1.19
(1,400)	1:396:A:LEU:N	1:396:A:LEU:CA	1:396:A:LEU:C	1:397:A:VAL:N	1	1.19
(1,19)	1:267:A:ARG:CA	1:267:A:ARG:CB	1:267:A:ARG:CG	1:267:A:ARG:CD	4	1.19
(1,671)	1:503:A:ARG:N	1:503:A:ARG:CA	1:503:A:ARG:C	1:504:A:LYS:N	14	1.18
(1,452)	1:415:A:GLU:C	1:416:A:ASP:N	1:416:A:ASP:CA	1:416:A:ASP:C	12	1.18
(1,442)	1:411:A:ALA:N	1:411:A:ALA:CA	1:411:A:ALA:C	1:412:A:ARG:N	14	1.18
(1,363)	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	1:386:A:VAL:N	12	1.18
(1,104)	1:296:A:ALA:C	1:297:A:ILE:N	1:297:A:ILE:CA	1:297:A:ILE:C	6	1.18
(1,104)	1:296:A:ALA:C	1:297:A:ILE:N	1:297:A:ILE:CA	1:297:A:ILE:C	20	1.18
(1,91)	1:291:A:GLY:N	1:291:A:GLY:CA	1:291:A:GLY:C	1:292:A:THR:N	15	1.18
(1,19)	1:267:A:ARG:CA	1:267:A:ARG:CB	1:267:A:ARG:CG	1:267:A:ARG:CD	13	1.18
(1,458)	1:421:A:ALA:C	1:422:A:ARG:N	1:422:A:ARG:CA	1:422:A:ARG:C	9	1.17
(1,422)	1:403:A:CYS:N	1:403:A:CYS:CA	1:403:A:CYS:C	1:404:A:LYS:N	18	1.17
(1,374)	1:388:A:ARG:N	1:388:A:ARG:CA	1:388:A:ARG:C	1:389:A:ASP:N	6	1.17

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,91)	1:291:A:GLY:N	1:291:A:GLY:CA	1:291:A:GLY:C	1:292:A:THR:N	17	1.17
(1,43)	1:274:A:VAL:N	1:274:A:VAL:CA	1:274:A:VAL:C	1:275:A:LYS:N	7	1.17
(1,363)	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	1:386:A:VAL:N	14	1.16
(1,630)	1:489:A:GLU:N	1:489:A:GLU:CA	1:489:A:GLU:C	1:490:A:CYS:N	1	1.15
(1,361)	1:384:A:ASN:CA	1:384:A:ASN:CB	1:384:A:ASN:CG	1:384:A:ASN:OD1	5	1.15
(1,505)	1:443:A:THR:N	1:443:A:THR:CA	1:443:A:THR:CB	1:443:A:THR:OG1	8	1.14
(1,79)	1:286:A:MET:CB	1:286:A:MET:CG	1:286:A:MET:SD	1:286:A:MET:CE	4	1.14
(1,365)	1:385:A:TYR:CA	1:385:A:TYR:CB	1:385:A:TYR:CG	1:385:A:TYR:CD1	8	1.13
(1,277)	1:356:A:GLU:N	1:356:A:GLU:CA	1:356:A:GLU:C	1:357:A:THR:N	2	1.13
(1,72)	1:285:A:TRP:N	1:285:A:TRP:CA	1:285:A:TRP:C	1:286:A:MET:N	13	1.13
(1,71)	1:284:A:VAL:C	1:285:A:TRP:N	1:285:A:TRP:CA	1:285:A:TRP:C	17	1.13
(1,63)	1:282:A:GLY:N	1:282:A:GLY:CA	1:282:A:GLY:C	1:283:A:GLU:N	1	1.13
(1,776)	1:535:A:ASN:CA	1:535:A:ASN:CB	1:535:A:ASN:CG	1:535:A:ASN:OD1	1	1.12
(1,556)	1:462:A:GLY:N	1:462:A:GLY:CA	1:462:A:GLY:C	1:463:A:ARG:N	2	1.12
(1,522)	1:449:A:TRP:CA	1:449:A:TRP:CB	1:449:A:TRP:CG	1:449:A:TRP:CD1	5	1.12
(1,361)	1:384:A:ASN:CA	1:384:A:ASN:CB	1:384:A:ASN:CG	1:384:A:ASN:OD1	18	1.12
(1,75)	1:285:A:TRP:C	1:286:A:MET:N	1:286:A:MET:CA	1:286:A:MET:C	10	1.12
(1,748)	1:525:A:SER:C	1:526:A:THR:N	1:526:A:THR:CA	1:526:A:THR:C	19	1.11
(1,627)	1:486:A:CYS:N	1:486:A:CYS:CA	1:486:A:CYS:C	1:487:A:PRO:N	18	1.11
(1,473)	1:431:A:TRP:N	1:431:A:TRP:CA	1:431:A:TRP:C	1:432:A:THR:N	2	1.11
(1,1)	1:261:A:ASP:C	1:262:A:ALA:N	1:262:A:ALA:CA	1:262:A:ALA:C	3	1.11
(1,606)	1:478:A:VAL:N	1:478:A:VAL:CA	1:478:A:VAL:CB	1:478:A:VAL:CG1	15	1.1
(1,365)	1:385:A:TYR:CA	1:385:A:TYR:CB	1:385:A:TYR:CG	1:385:A:TYR:CD1	14	1.1
(1,114)	1:299:A:THR:C	1:300:A:LEU:N	1:300:A:LEU:CA	1:300:A:LEU:C	13	1.1
(1,46)	1:275:A:LYS:N	1:275:A:LYS:CA	1:275:A:LYS:C	1:276:A:LEU:N	3	1.1
(1,630)	1:489:A:GLU:N	1:489:A:GLU:CA	1:489:A:GLU:C	1:490:A:CYS:N	19	1.09
(1,524)	1:450:A:SER:N	1:450:A:SER:CA	1:450:A:SER:C	1:451:A:PHE:N	20	1.09
(1,303)	1:365:A:GLN:N	1:365:A:GLN:CA	1:365:A:GLN:C	1:366:A:LEU:N	19	1.09
(1,71)	1:284:A:VAL:C	1:285:A:TRP:N	1:285:A:TRP:CA	1:285:A:TRP:C	13	1.09
(1,382)	1:390:A:LEU:N	1:390:A:LEU:CA	1:390:A:LEU:C	1:391:A:ARG:N	14	1.08
(1,374)	1:388:A:ARG:N	1:388:A:ARG:CA	1:388:A:ARG:C	1:389:A:ASP:N	18	1.08
(1,687)	1:507:A:GLU:C	1:508:A:GLU:N	1:508:A:GLU:CA	1:508:A:GLU:C	18	1.07
(1,653)	1:496:A:ASP:CA	1:496:A:ASP:CB	1:496:A:ASP:CG	1:496:A:ASP:OD1	13	1.07
(1,634)	1:490:A:CYS:N	1:490:A:CYS:CA	1:490:A:CYS:C	1:491:A:PRO:N	18	1.07
(1,557)	1:462:A:GLY:C	1:463:A:ARG:N	1:463:A:ARG:CA	1:463:A:ARG:C	13	1.07
(1,380)	1:389:A:ASP:CA	1:389:A:ASP:CB	1:389:A:ASP:CG	1:389:A:ASP:OD1	3	1.07
(1,75)	1:285:A:TRP:C	1:286:A:MET:N	1:286:A:MET:CA	1:286:A:MET:C	18	1.07
(1,75)	1:285:A:TRP:C	1:286:A:MET:N	1:286:A:MET:CA	1:286:A:MET:C	19	1.07
(1,488)	1:437:A:ALA:N	1:437:A:ALA:CA	1:437:A:ALA:C	1:438:A:LEU:N	9	1.06
(1,748)	1:525:A:SER:C	1:526:A:THR:N	1:526:A:THR:CA	1:526:A:THR:C	20	1.05
(1,430)	1:407:A:ASP:N	1:407:A:ASP:CA	1:407:A:ASP:C	1:408:A:PHE:N	8	1.05
(1,115)	1:300:A:LEU:N	1:300:A:LEU:CA	1:300:A:LEU:C	1:301:A:LYS:N	10	1.05
(1,62)	1:281:A:PHE:C	1:282:A:GLY:N	1:282:A:GLY:CA	1:282:A:GLY:C	19	1.05
(1,400)	1:396:A:LEU:N	1:396:A:LEU:CA	1:396:A:LEU:C	1:397:A:VAL:N	3	1.04
(1,361)	1:384:A:ASN:CA	1:384:A:ASN:CB	1:384:A:ASN:CG	1:384:A:ASN:OD1	3	1.04
(1,153)	1:317:A:MET:CA	1:317:A:MET:CB	1:317:A:MET:CG	1:317:A:MET:SD	19	1.04
(1,104)	1:296:A:ALA:C	1:297:A:ILE:N	1:297:A:ILE:CA	1:297:A:ILE:C	4	1.04
(1,774)	1:535:A:ASN:N	1:535:A:ASN:CA	1:535:A:ASN:C	1:536:A:LEU:N	9	1.03
(1,422)	1:403:A:CYS:N	1:403:A:CYS:CA	1:403:A:CYS:C	1:404:A:LYS:N	12	1.03
(1,188)	1:326:A:VAL:C	1:327:A:GLN:N	1:327:A:GLN:CA	1:327:A:GLN:C	15	1.02
(1,82)	1:288:A:THR:C	1:289:A:TRP:N	1:289:A:TRP:CA	1:289:A:TRP:C	2	1.02

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,2)	1:262:A:ALA:N	1:262:A:ALA:CA	1:262:A:ALA:C	1:263:A:TRP:N	9	1.02
(1,768)	1:532:A:PRO:N	1:532:A:PRO:CA	1:532:A:PRO:C	1:533:A:GLY:N	17	1.01
(1,748)	1:525:A:SER:C	1:526:A:THR:N	1:526:A:THR:CA	1:526:A:THR:C	2	1.01
(1,368)	1:386:A:VAL:N	1:386:A:VAL:CA	1:386:A:VAL:CB	1:386:A:VAL:CG1	5	1.01
(1,363)	1:385:A:TYR:N	1:385:A:TYR:CA	1:385:A:TYR:C	1:386:A:VAL:N	3	1.01
(1,62)	1:281:A:PHE:C	1:282:A:GLY:N	1:282:A:GLY:CA	1:282:A:GLY:C	11	1.01
(1,515)	1:447:A:ASP:CA	1:447:A:ASP:CB	1:447:A:ASP:CG	1:447:A:ASP:OD1	17	1.0