Full wwPDB NMR Structure Validation Report (i)

Jun 3, 2023 – 07:49 PM EDT

PDB ID	:	2MY3
BMRB ID	:	25443
Title	:	Snu17p-Pml1p structure intermediate during RES complex assembly
Authors	:	Wysoczanski, P.; Becker, S.; Zweckstetter, M.
Deposited on	:	2015-01-19

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/NMRValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

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

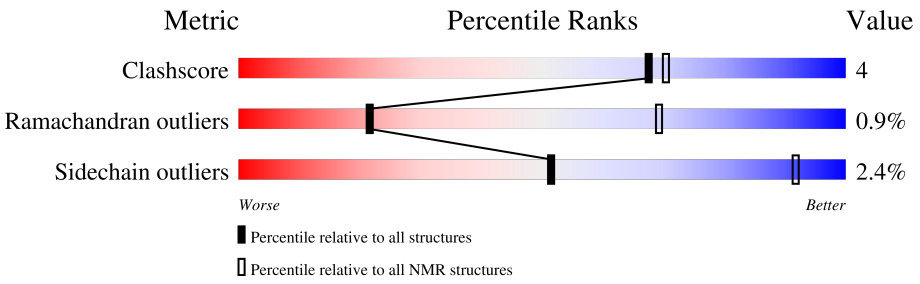
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal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

1 Overall quality at a glance (i)

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

The overall completeness of chemical shifts assignment is 87%.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	118	77% 5% 18%
2	B	23	57% 43%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 8 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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:11-A:107, B:207-B:219 (110)	0.90	8

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 4 clusters and 3 single-model clusters were found.

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

3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 2227 atoms, of which 1099 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called U2 snRNP component IST3.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	118	1881	598	929	162	191	1	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP P40565
A	2	ALA	-	expression tag	UNP P40565
A	3	MET	-	expression tag	UNP P40565
A	4	GLY	-	expression tag	UNP P40565

- Molecule 2 is a protein called Pre-mRNA leakage protein 1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
2	B	23	346	111	170	25	39	1	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	200	GLY	-	expression tag	UNP Q07930
B	201	SER	-	expression tag	UNP Q07930

4 Residue-property plots (i)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

• Molecule 1: U2 snRNP component IST3

Chain A: 77% 5% 18%

G1 A2 M3 G4 N5 E6 Y7 K8 D9 N10 A11 Y12 V38 K58 Y59 E60 D61 T65 R108 D109 I110 V111 S112 K113 N114 N115 A116 E117 K118

• Molecule 2: Pre-mRNA leakage protein 1

Chain B: 57% 43%

G200 S201 K202 S203 Q204 Y205 I206 L220 E221 S222

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: U2 snRNP component IST3

Chain A: 69% 11% • 18%

G1 A2 M3 G4 N5 E6 Y7 K8 D9 N10 A11 Y12 E21 V38 L57 K58 Y59 E60 D61 T65 V69 N73 Y89 R90 P91 K92 E100 K103 R108 D109 I110 V111 S112 K113 N114 N115 A116 E117 K118

• Molecule 2: Pre-mRNA leakage protein 1

Chain B: 48% 9% 43%

G200 S201 K202 S203 Q204 Y205 I206 P214 L217 L220 E221 S222

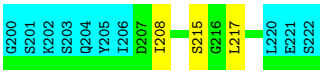
4.2.2 Score per residue for model 2

- Molecule 1: U2 snRNP component IST3

Chain A: 69% 12% • 18%

- Molecule 2: Pre-mRNA leakage protein 1

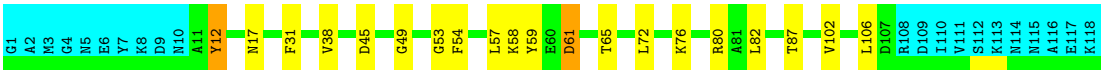
Chain B: 43% 13% 43%



4.2.3 Score per residue for model 3

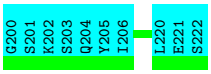
- Molecule 1: U2 snRNP component IST3

Chain A: 65% 15% • 18%



- Molecule 2: Pre-mRNA leakage protein 1

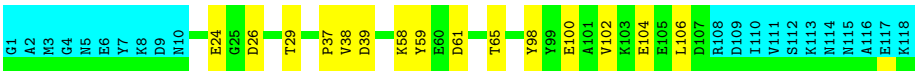
Chain B: 57% 43%



4.2.4 Score per residue for model 4

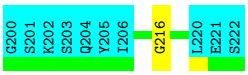
- Molecule 1: U2 snRNP component IST3

Chain A: 69% 13% 18%



- Molecule 2: Pre-mRNA leakage protein 1

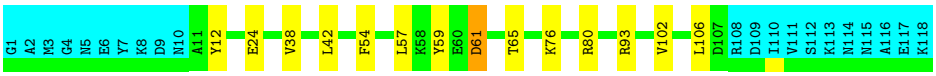
Chain B: 52% • 43%



4.2.5 Score per residue for model 5

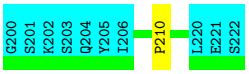
- Molecule 1: U2 snRNP component IST3

Chain A: 70% 11% • 18%



- Molecule 2: Pre-mRNA leakage protein 1

Chain B: 52% • 43%



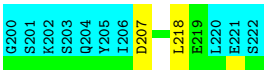
4.2.6 Score per residue for model 6

- Molecule 1: U2 snRNP component IST3

Chain A: 72% 10% 18%

- Molecule 2: Pre-mRNA leakage protein 1

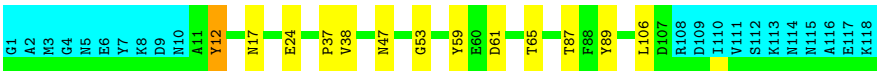
Chain B: 48% 9% 43%



4.2.7 Score per residue for model 7

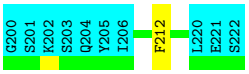
- Molecule 1: U2 snRNP component IST3

Chain A: 71% 10% • 18%



- Molecule 2: Pre-mRNA leakage protein 1

Chain B: 52% • 43%



4.2.8 Score per residue for model 8 (medoid)

- Molecule 1: U2 snRNP component IST3

Chain A: 71% 11% 18%

G1 A2 M3 G4 N5 E6 Y7 K8 D9 N10 A11 Y12 D26 Y34 V38 D39 K58 Y59 T65 V69 L72 L82 V102 L106 D107 R108 D109 I110 V111 S112 K113 N114 N115 A116 E117 K118

- Molecule 2: Pre-mRNA leakage protein 1

Chain B: 52% • 43%

G200 S201 K202 S203 Q204 Y205 I206 E219 L220 E221 S222

4.2.9 Score per residue for model 9

- Molecule 1: U2 snRNP component IST3

Chain A: 69% 12% • 18%

G1 A2 M3 G4 N5 E6 Y7 K8 D9 N10 A11 Y12 N17 V38 D45 G49 G53 K58 Y59 E60 D61 T65 V69 N73 L82 E100 E104 R108 D109 I110 V111 S112 K113 N114 N115 A116 E117 K118

- Molecule 2: Pre-mRNA leakage protein 1

Chain B: 57% 43%

G200 S201 K202 S203 Q204 Y205 I206 L220 E221 S222

4.2.10 Score per residue for model 10

- Molecule 1: U2 snRNP component IST3

Chain A: 72% 10% 18%

G1 A2 M3 G4 N5 E6 Y7 K8 D9 N10 D26 T29 Y34 V38 D45 E46 G49 Y59 T65 A68 A101 L106 D107 R108 D109 I110 V111 S112 K113 N114 N115 A116 E117 K118

- Molecule 2: Pre-mRNA leakage protein 1

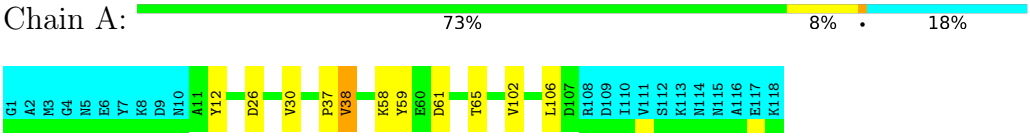
Chain B: 43% 13% 43%

G200 S201 K202 S203 Q204 Y205 I206 D207 I208 M209 L217 L220 E221 S222

4.2.11 Score per residue for model 11

- Molecule 1: U2 snRNP component IST3

Chain A:



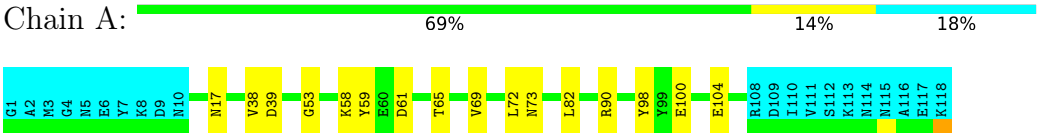
- Molecule 2: Pre-mRNA leakage protein 1

Chain B:

4.2.12 Score per residue for model 12

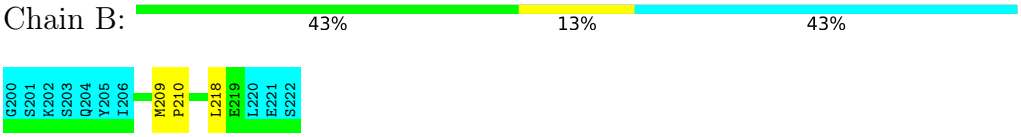
- Molecule 1: U2 snRNP component IST3

Chain A:



- Molecule 2: Pre-mRNA leakage protein 1

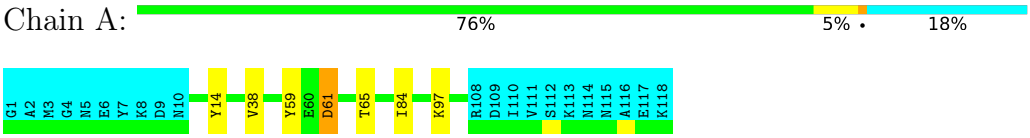
Chain B:



4.2.13 Score per residue for model 13

- Molecule 1: U2 snRNP component IST3

Chain A:



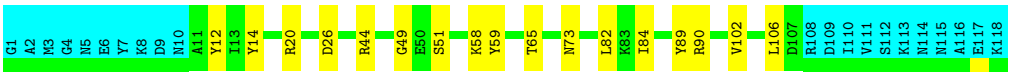
- Molecule 2: Pre-mRNA leakage protein 1

Chain B:

4.2.14 Score per residue for model 14

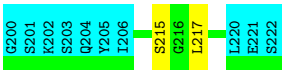
- Molecule 1: U2 snRNP component IST3

Chain A: 68% 14% 18%



- Molecule 2: Pre-mRNA leakage protein 1

Chain B: 48% 9% 43%



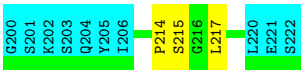
4.2.15 Score per residue for model 15

- Molecule 1: U2 snRNP component IST3

Chain A: 74% 8% • 18%

- Molecule 2: Pre-mRNA leakage protein 1

Chain B: 43% 13% 43%



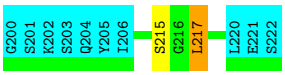
4.2.16 Score per residue for model 16

- Molecule 1: U2 snRNP component IST3

Chain A: 73% 8% • 18%

- Molecule 2: Pre-mRNA leakage protein 1

Chain B: 48% • • 43%



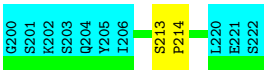
4.2.17 Score per residue for model 17

- Molecule 1: U2 snRNP component IST3

Chain A: 78% • 18%

- Molecule 2: Pre-mRNA leakage protein 1

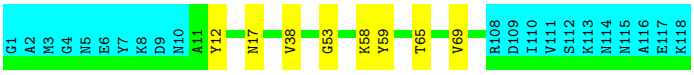
Chain B: 48% 9% 43%



4.2.18 Score per residue for model 18

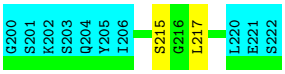
- Molecule 1: U2 snRNP component IST3

Chain A: 75% 7% 18%



- Molecule 2: Pre-mRNA leakage protein 1

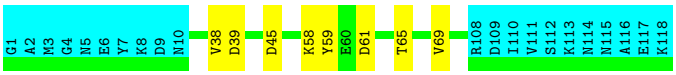
Chain B: 48% 9% 43%



4.2.19 Score per residue for model 19

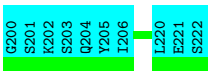
- Molecule 1: U2 snRNP component IST3

Chain A: 75% 7% 18%



- Molecule 2: Pre-mRNA leakage protein 1

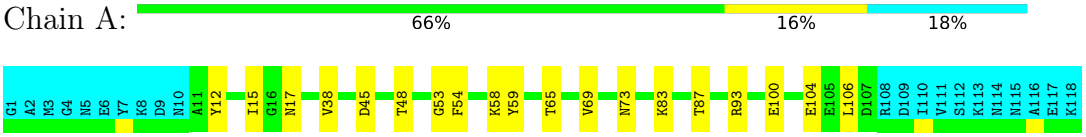
Chain B: 57% 43%



4.2.20 Score per residue for model 20

- Molecule 1: U2 snRNP component IST3

Chain A:



- Molecule 2: Pre-mRNA leakage protein 1

Chain B:

5 Refinement protocol and experimental data overview (i)

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

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
CYANA	structure solution	3.0
CYANA	refinement	3.0

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

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1637
Number of shifts mapped to atoms	1637
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	87%

6 Model quality (i)

6.1 Standard geometry (i)

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	788	772	771	6±2
2	B	98	92	92	1±1
All	All	17720	17280	17260	136

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:59:TYR:OH	1:A:65:THR:HA	0.66	1.89	8	20
1:A:12:TYR:CE1	1:A:89:TYR:HB2	0.59	2.31	7	1
1:A:14:TYR:O	1:A:84:ILE:HA	0.59	1.96	13	2
1:A:38:VAL:HG12	1:A:39:ASP:H	0.58	1.58	8	5
1:A:38:VAL:HB	1:A:58:LYS:O	0.57	1.99	19	9
1:A:61:ASP:O	1:A:65:THR:HG23	0.57	2.00	3	4
1:A:12:TYR:CE1	1:A:87:THR:HG23	0.55	2.36	7	2
1:A:69:VAL:O	1:A:73:ASN:HB2	0.54	2.03	16	5
1:A:100:GLU:O	1:A:104:GLU:HG3	0.54	2.03	12	1
1:A:12:TYR:HB2	1:A:57:LEU:O	0.54	2.03	1	2
1:A:100:GLU:O	1:A:104:GLU:HG2	0.54	2.03	4	3
1:A:12:TYR:CZ	1:A:89:TYR:HB2	0.54	2.38	7	1
1:A:34:TYR:OH	1:A:72:LEU:HG	0.53	2.03	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:17:ASN:HA	1:A:53:GLY:O	0.52	2.05	3	6
1:A:20:ARG:HA	1:A:51:SER:OG	0.52	2.04	14	1
1:A:102:VAL:O	1:A:106:LEU:HG	0.51	2.06	14	5
1:A:12:TYR:CE2	1:A:58:LYS:HB2	0.51	2.41	8	4
1:A:73:ASN:HA	1:A:82:LEU:O	0.50	2.06	14	3
1:A:12:TYR:CZ	1:A:58:LYS:HG3	0.50	2.42	20	1
1:A:26:ASP:O	1:A:29:THR:HB	0.49	2.07	2	3
1:A:12:TYR:CE1	1:A:58:LYS:HB2	0.49	2.41	16	1
1:A:45:ASP:O	1:A:49:GLY:HA2	0.49	2.07	3	3
2:B:215:SER:HB3	2:B:217:LEU:CD1	0.49	2.38	14	3
1:A:59:TYR:CZ	1:A:65:THR:HA	0.49	2.42	2	1
2:B:215:SER:O	2:B:217:LEU:HD12	0.49	2.07	18	1
1:A:38:VAL:HG11	1:A:59:TYR:HA	0.48	1.84	6	1
1:A:11:ALA:O	1:A:58:LYS:HG3	0.48	2.08	17	1
2:B:209:MET:SD	2:B:210:PRO:HD2	0.48	2.48	12	1
1:A:102:VAL:O	1:A:106:LEU:HB2	0.48	2.09	8	1
1:A:59:TYR:CE2	1:A:65:THR:HA	0.47	2.44	2	1
1:A:69:VAL:O	1:A:73:ASN:HB3	0.46	2.10	9	1
1:A:46:GLU:HA	2:B:208:ILE:HD11	0.46	1.87	10	2
1:A:30:VAL:HG22	2:B:218:LEU:HD13	0.46	1.88	11	1
1:A:102:VAL:O	1:A:106:LEU:HD13	0.45	2.11	4	1
1:A:76:LYS:HG3	1:A:80:ARG:C	0.45	2.31	2	1
1:A:97:LYS:HB3	2:B:209:MET:SD	0.45	2.51	13	1
1:A:12:TYR:HB2	1:A:87:THR:O	0.45	2.12	20	2
1:A:31:PHE:CG	1:A:57:LEU:HD22	0.45	2.47	3	1
1:A:15:ILE:HA	1:A:83:LYS:O	0.45	2.12	20	1
1:A:96:GLN:O	1:A:100:GLU:HG3	0.45	2.12	6	1
1:A:24:GLU:HB2	2:B:212:PHE:CD2	0.45	2.47	7	1
1:A:45:ASP:OD2	1:A:48:THR:HG22	0.44	2.11	20	1
1:A:44:ARG:HD2	1:A:49:GLY:O	0.44	2.13	14	1
1:A:34:TYR:OH	1:A:68:ALA:HA	0.43	2.12	10	1
1:A:24:GLU:HB2	2:B:212:PHE:CG	0.43	2.48	7	1
1:A:72:LEU:O	1:A:82:LEU:HB2	0.43	2.13	3	3
1:A:21:GLU:HB2	2:B:217:LEU:HD11	0.43	1.89	1	1
1:A:12:TYR:CG	1:A:89:TYR:HB3	0.43	2.49	2	1
1:A:42:LEU:HD12	1:A:54:PHE:O	0.43	2.13	5	1
1:A:76:LYS:HA	1:A:80:ARG:O	0.43	2.14	5	2
1:A:12:TYR:CZ	1:A:58:LYS:HB2	0.43	2.48	18	1
1:A:97:LYS:HG3	2:B:207:ASP:OD2	0.42	2.14	6	1
1:A:100:GLU:O	1:A:103:LYS:HG3	0.42	2.14	1	1
1:A:90:ARG:N	1:A:90:ARG:HD3	0.42	2.30	1	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:44:ARG:H	1:A:44:ARG:NE	0.42	2.12	2	1
1:A:12:TYR:HB3	1:A:58:LYS:HA	0.42	1.91	1	1
1:A:27:ILE:O	1:A:31:PHE:HD1	0.41	1.98	2	1
2:B:215:SER:OG	2:B:217:LEU:HB2	0.41	2.14	16	1
1:A:65:THR:O	1:A:69:VAL:HG23	0.41	2.15	18	5
1:A:12:TYR:CE2	1:A:89:TYR:HB3	0.41	2.51	1	1
1:A:12:TYR:CD2	1:A:89:TYR:HB3	0.41	2.50	14	1
1:A:101:ALA:HB2	2:B:209:MET:SD	0.40	2.56	10	1
1:A:98:TYR:O	1:A:102:VAL:HG23	0.40	2.15	16	1
1:A:24:GLU:OE2	2:B:210:PRO:HA	0.40	2.17	5	1

6.3 Torsion angles (i)

6.3.1 Protein backbone (i)

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	97/118 (82%)	91±1 (94±1%)	5±2 (5±2%)	1±1 (1±1%)	21	69
2	B	13/23 (57%)	12±0 (92±3%)	1±1 (7±4%)	0±0 (1±3%)	17	64
All	All	2200/2820 (78%)	2065 (94%)	115 (5%)	20 (1%)	21	69

All 5 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	61	ASP	12
2	B	214	PRO	3
1	A	37	PRO	3
1	A	17	ASN	1
1	A	60	GLU	1

6.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR

entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	84/101 (83%)	82±1 (98±1%)	2±1 (2±1%)	51	92
2	B	12/21 (57%)	12±0 (97±4%)	0±0 (3±4%)	45	89
All	All	1920/2440 (79%)	1873 (98%)	47 (2%)	51	92

All 21 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	38	VAL	12
1	A	90	ARG	4
1	A	26	ASP	4
1	A	12	TYR	3
2	B	218	LEU	3
1	A	54	PHE	2
1	A	98	TYR	2
1	A	93	ARG	2
1	A	45	ASP	2
2	B	219	GLU	2
1	A	60	GLU	1
1	A	92	LYS	1
1	A	103	LYS	1
1	A	44	ARG	1
1	A	59	TYR	1
1	A	24	GLU	1
1	A	99	TYR	1
1	A	47	ASN	1
1	A	58	LYS	1
2	B	217	LEU	1
2	B	213	SER	1

6.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates (i)

There are no monosaccharides in this entry.

6.6 Ligand geometry (i)

There are no ligands in this entry.

6.7 Other polymers (i)

There are no such molecules in this entry.

6.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

7 Chemical shift validation (i)

The completeness of assignment taking into account all chemical shift lists is 87% for the well-defined parts and 85% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *SHIFT_LIST*

7.1.1 Bookkeeping (i)

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

Total number of shifts	1637
Number of shifts mapped to atoms	1637
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	3

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	133	-0.21 ± 0.14	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	119	0.01 ± 0.09	None needed (< 0.5 ppm)
$^{13}C'$	111	-0.06 ± 0.16	None needed (< 0.5 ppm)
^{15}N	129	-0.10 ± 0.27	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments (i)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 87%, i.e. 1325 atoms were assigned a chemical shift out of a possible 1517. 0 out of 18 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	517/551 (94%)	216/225 (96%)	197/220 (90%)	104/106 (98%)
Sidechain	702/836 (84%)	481/540 (89%)	216/264 (82%)	5/32 (16%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	106/130 (82%)	53/61 (87%)	53/67 (79%)	0/2 (0%)
Overall	1325/1517 (87%)	750/826 (91%)	466/551 (85%)	109/140 (78%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 85%, i.e. 1635 atoms were assigned a chemical shift out of a possible 1915. 0 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	641/709 (90%)	268/290 (92%)	244/282 (87%)	129/137 (94%)
Sidechain	872/1058 (82%)	599/680 (88%)	267/334 (80%)	6/44 (14%)
Aromatic	122/148 (82%)	61/69 (88%)	61/77 (79%)	0/2 (0%)
Overall	1635/1915 (85%)	928/1039 (89%)	572/693 (83%)	135/183 (74%)

7.1.4 Statistically unusual chemical shifts (i)

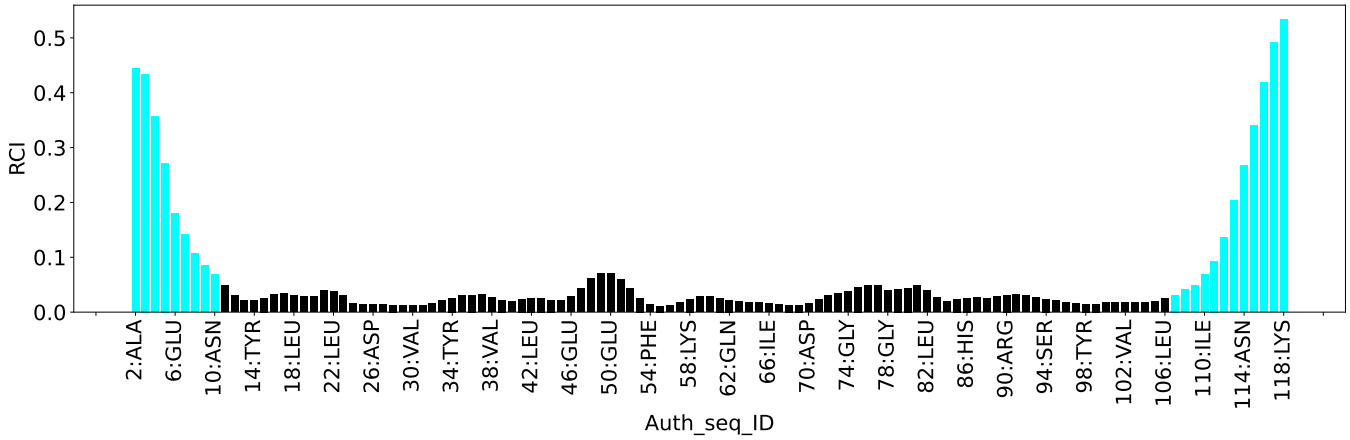
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	105	GLU	HG2	0.38	1.24 – 3.30	-9.2
1	A	58	LYS	HB3	-0.01	0.46 – 3.04	-6.8
1	A	64	SER	HB3	2.38	2.49 – 5.20	-5.4

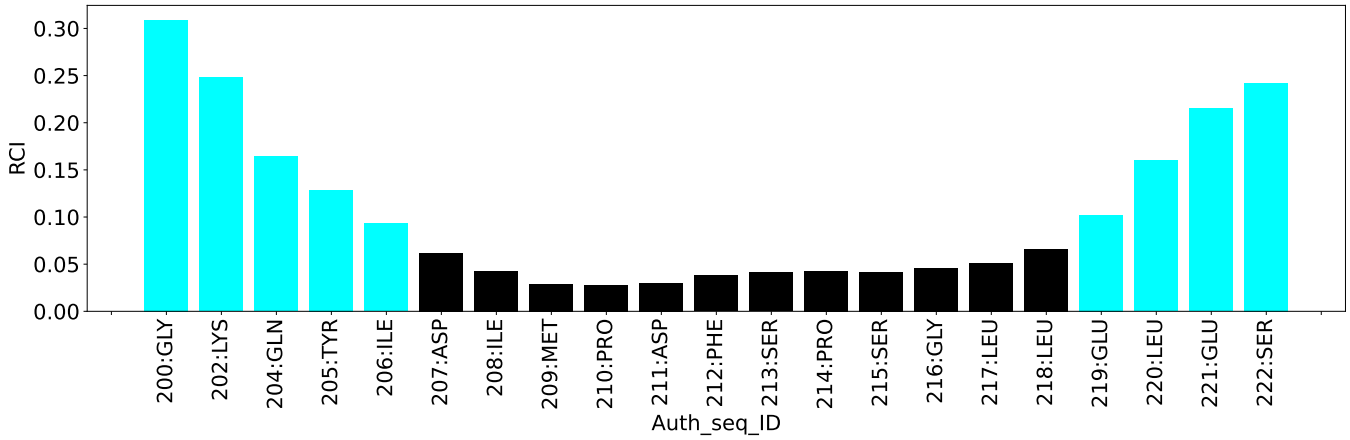
7.1.5 Random Coil Index (RCI) plots (i)

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:



Random coil index (RCI) for chain B:



8 NMR restraints analysis (i)

8.1 Conformationally restricting restraints (i)

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

Description	Value
Total distance restraints	2308
Intra-residue (|i-j|=0)	558
Sequential (|i-j|=1)	616
Medium range (|i-j|>1 and |i-j|<5)	379
Long range (|i-j|≥5)	477
Inter-chain	228
Hydrogen bond restraints	50
Disulfide bond restraints	0
Total dihedral-angle restraints	230
Number of unmapped restraints	0
Number of restraints per residue	18.0
Number of long range restraints per residue[1]	3.5

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

8.2 Residual restraint violations (i)

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

8.2.1 Average number of distance violations per model (i)

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

Bins (Å)	Average number of violations per model	Max (Å)
0.1-0.2 (Small)	15.2	0.2
0.2-0.5 (Medium)	6.2	0.49
>0.5 (Large)	0.1	0.7

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)	10.5	8.7
10.0-20.0 (Medium)	0.1	10.1
>20.0 (Large)	None	None

9 Distance violation analysis (i)

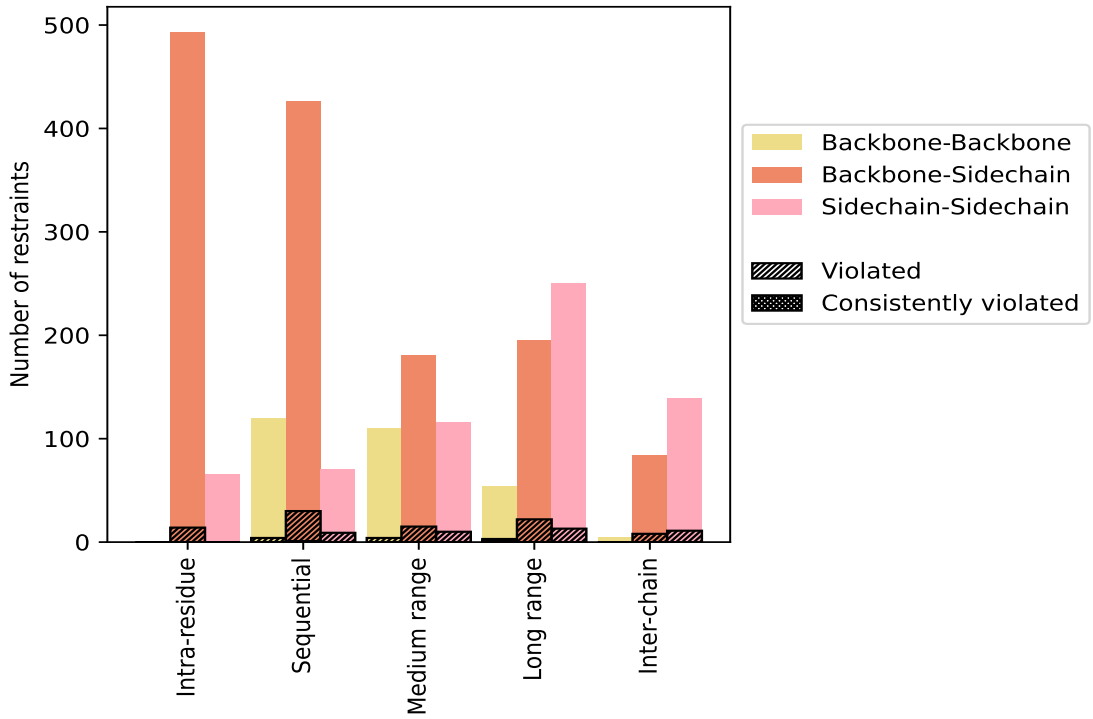
9.1 Summary of distance violations (i)

The following table shows the summary of distance violations in different restraint categories based on the sequence separation of the atoms involved. Each category is further sub-divided into three sub-categories based on the atoms involved. Violations less than 0.1 Å are not included in the statistics.

Restraints type	Count	%[1]	Violated[3]			Consistently Violated[4]		
			Count	%[2]	%[1]	Count	%[2]	%[1]
Intra-residue (|i-j|=0)	558	24.2	14	2.5	0.6	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	493	21.4	14	2.8	0.6	0	0.0	0.0
Sidechain-Sidechain	65	2.8	0	0.0	0.0	0	0.0	0.0
Sequential (|i-j|=1)	616	26.7	43	7.0	1.9	1	0.2	0.0
Backbone-Backbone	120	5.2	4	3.3	0.2	0	0.0	0.0
Backbone-Sidechain	426	18.5	30	7.0	1.3	1	0.2	0.0
Sidechain-Sidechain	70	3.0	9	12.9	0.4	0	0.0	0.0
Medium range (|i-j|>1 & |i-j|<5)	379	16.4	26	6.9	1.1	0	0.0	0.0
Backbone-Backbone	82	3.6	1	1.2	0.0	0	0.0	0.0
Backbone-Sidechain	181	7.8	15	8.3	0.6	0	0.0	0.0
Sidechain-Sidechain	116	5.0	10	8.6	0.4	0	0.0	0.0
Long range (|i-j|≥5)	477	20.7	35	7.3	1.5	0	0.0	0.0
Backbone-Backbone	32	1.4	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	195	8.4	22	11.3	1.0	0	0.0	0.0
Sidechain-Sidechain	250	10.8	13	5.2	0.6	0	0.0	0.0
Inter-chain	228	9.9	19	8.3	0.8	0	0.0	0.0
Backbone-Backbone	5	0.2	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	84	3.6	8	9.5	0.3	0	0.0	0.0
Sidechain-Sidechain	139	6.0	11	7.9	0.5	0	0.0	0.0
Hydrogen bond	50	2.2	6	12.0	0.3	1	2.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	2308	100.0	143	6.2	6.2	2	0.1	0.1
Backbone-Backbone	289	12.5	11	3.8	0.5	1	0.3	0.0
Backbone-Sidechain	1379	59.7	89	6.5	3.9	1	0.1	0.0
Sidechain-Sidechain	640	27.7	43	6.7	1.9	0	0.0	0.0

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

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



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

9.2 Distance violation statistics for each model (i)

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

Model ID	Number of violations						Mean (Å)	Max (Å)	SD[6] (Å)	Median (Å)
	IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total				
1	0	10	2	9	1	22	0.19	0.36	0.07	0.18
2	5	7	4	7	1	24	0.17	0.36	0.07	0.14
3	1	9	3	7	3	23	0.19	0.3	0.05	0.18
4	1	8	4	3	2	18	0.17	0.3	0.05	0.16
5	5	13	1	6	1	26	0.18	0.33	0.07	0.16
6	0	9	3	5	2	19	0.2	0.36	0.07	0.19
7	2	8	7	4	5	26	0.17	0.32	0.06	0.14
8	1	10	3	6	3	23	0.17	0.35	0.06	0.16
9	1	11	4	5	2	23	0.18	0.31	0.06	0.16
10	2	11	4	5	5	27	0.2	0.49	0.08	0.19
11	0	7	3	6	1	17	0.21	0.44	0.09	0.2

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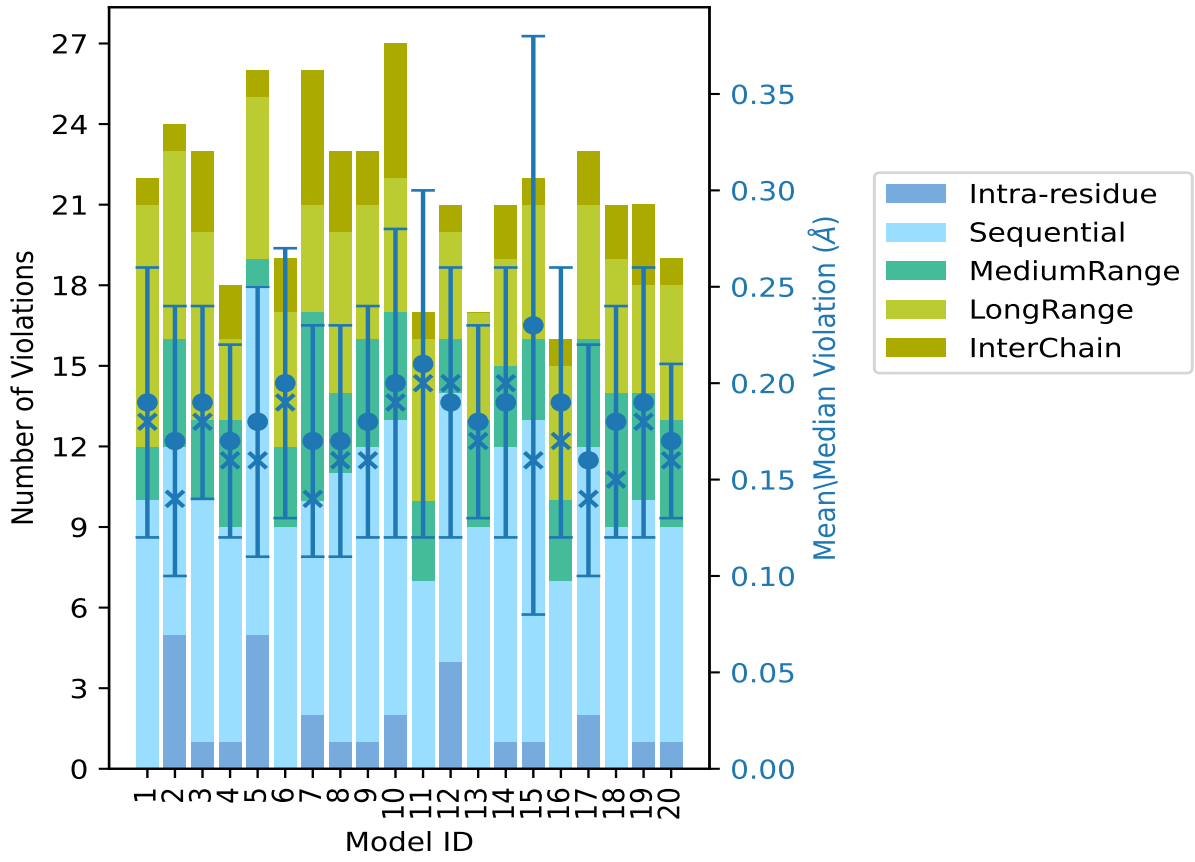
Model ID	Number of violations						Mean (Å)	Max (Å)	SD[6] (Å)	Median (Å)
	IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total				
12	4	10	2	4	1	21	0.19	0.34	0.07	0.2
13	0	9	4	4	0	17	0.18	0.28	0.05	0.17
14	1	11	3	4	2	21	0.19	0.39	0.07	0.2
15	1	12	3	5	1	22	0.23	0.7	0.15	0.16
16	0	7	3	5	1	16	0.19	0.38	0.07	0.17
17	2	10	4	5	2	23	0.16	0.33	0.06	0.14
18	0	9	5	5	2	21	0.18	0.3	0.06	0.15
19	1	9	4	4	3	21	0.19	0.36	0.07	0.18
20	1	8	4	5	1	19	0.17	0.29	0.04	0.16

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

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



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

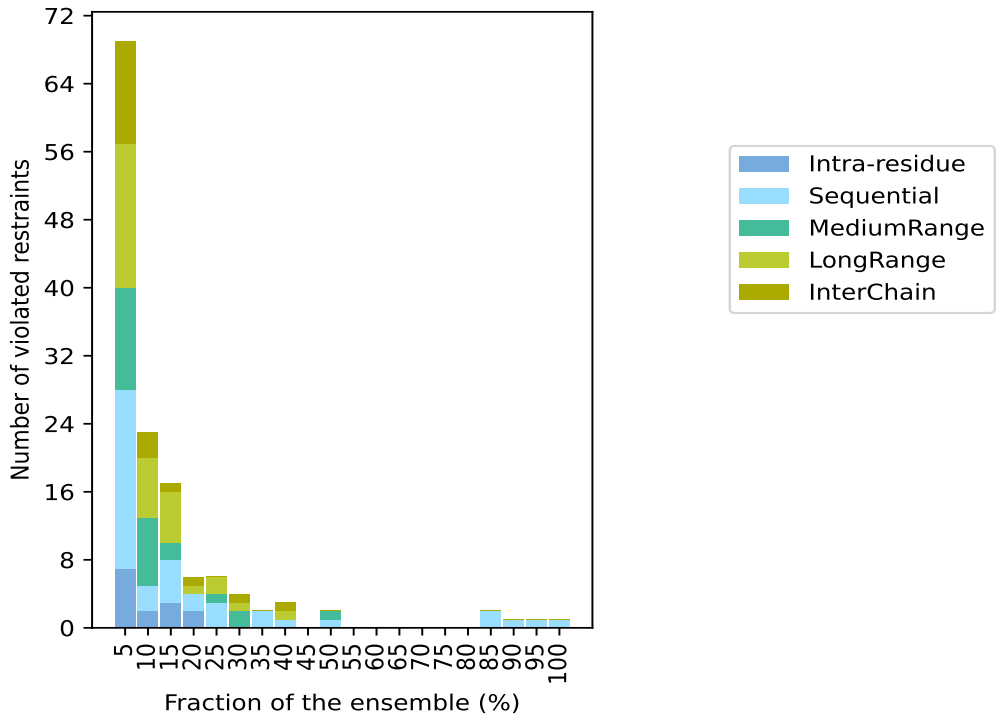
9.3 Distance violation statistics for the ensemble (i)

Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 2121(IR:544, SQ:573, MR:353, LR:442, IC:209) 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]	%
7	21	12	17	12	69	1	5.0
2	3	8	7	3	23	2	10.0
3	5	2	6	1	17	3	15.0
2	2	0	1	1	6	4	20.0
0	3	1	2	0	6	5	25.0
0	0	2	1	1	4	6	30.0
0	2	0	0	0	2	7	35.0
0	1	0	1	1	3	8	40.0
0	0	0	0	0	0	9	45.0
0	1	1	0	0	2	10	50.0
0	0	0	0	0	0	11	55.0
0	0	0	0	0	0	12	60.0
0	0	0	0	0	0	13	65.0
0	0	0	0	0	0	14	70.0
0	0	0	0	0	0	15	75.0
0	0	0	0	0	0	16	80.0
0	2	0	0	0	2	17	85.0
0	1	0	0	0	1	18	90.0
0	1	0	0	0	1	19	95.0
0	1	0	0	0	1	20	100.0

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

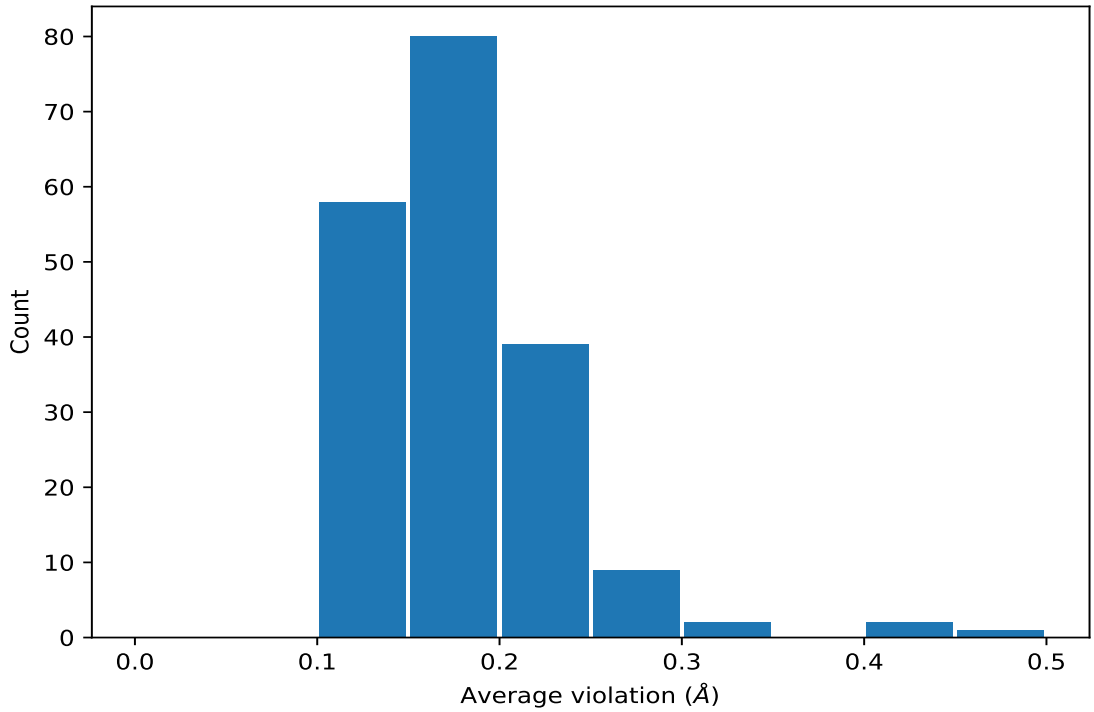
9.3.1 Bar graph : Distance violation statistics for the ensemble (i)



9.4 Most violated distance restraints in the ensemble (i)

9.4.1 Histogram : Distribution of mean distance violations (i)

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



9.4.2 Table: Most violated distance restraints (i)

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

Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(2,13)	1:A:39:ASP:H	1:A:58:LYS:O	20	0.27	0.04	0.27
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG21	20	0.18	0.02	0.18
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG22	20	0.18	0.02	0.18
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG23	20	0.18	0.02	0.18
(1,323)	1:A:29:THR:HG21	1:A:30:VAL:HB	19	0.18	0.03	0.18
(1,323)	1:A:29:THR:HG22	1:A:30:VAL:HB	19	0.18	0.03	0.18
(1,323)	1:A:29:THR:HG23	1:A:30:VAL:HB	19	0.18	0.03	0.18
(1,643)	1:A:59:TYR:HD1	1:A:60:GLU:HB3	18	0.27	0.05	0.28
(1,643)	1:A:59:TYR:HD2	1:A:60:GLU:HB3	18	0.27	0.05	0.28
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD11	17	0.19	0.03	0.19
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD12	17	0.19	0.03	0.19
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD13	17	0.19	0.03	0.19
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD11	17	0.19	0.03	0.19
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD12	17	0.19	0.03	0.19
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD13	17	0.19	0.03	0.19
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD11	17	0.19	0.03	0.19

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Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD12	17	0.19	0.03	0.19
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD13	17	0.19	0.03	0.19
(1,1086)	1:A:38:VAL:HG11	1:A:39:ASP:H	17	0.14	0.02	0.14
(1,1086)	1:A:38:VAL:HG12	1:A:39:ASP:H	17	0.14	0.02	0.14
(1,1086)	1:A:38:VAL:HG13	1:A:39:ASP:H	17	0.14	0.02	0.14
(1,1878)	1:A:60:GLU:HG2	1:A:61:ASP:H	10	0.18	0.05	0.18
(1,1878)	1:A:60:GLU:HG3	1:A:61:ASP:H	10	0.18	0.05	0.18
(1,127)	1:A:57:LEU:HD21	1:A:60:GLU:H	10	0.15	0.03	0.16
(1,127)	1:A:57:LEU:HD22	1:A:60:GLU:H	10	0.15	0.03	0.16
(1,127)	1:A:57:LEU:HD23	1:A:60:GLU:H	10	0.15	0.03	0.16
(1,1820)	1:A:43:SER:HB2	1:A:54:PHE:HZ	8	0.23	0.03	0.24
(1,1820)	1:A:43:SER:HB3	1:A:54:PHE:HZ	8	0.23	0.03	0.24
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE1	8	0.16	0.03	0.16
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE2	8	0.16	0.03	0.16
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE3	8	0.16	0.03	0.16
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE1	8	0.16	0.03	0.16
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE2	8	0.16	0.03	0.16
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE3	8	0.16	0.03	0.16
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG11	8	0.12	0.01	0.12
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG12	8	0.12	0.01	0.12
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG13	8	0.12	0.01	0.12
(1,1566)	1:A:6:GLU:HG2	1:A:7:TYR:HE1	7	0.29	0.18	0.21
(1,1566)	1:A:6:GLU:HG2	1:A:7:TYR:HE2	7	0.29	0.18	0.21
(1,1566)	1:A:6:GLU:HG3	1:A:7:TYR:HE1	7	0.29	0.18	0.21
(1,1566)	1:A:6:GLU:HG3	1:A:7:TYR:HE2	7	0.29	0.18	0.21
(1,1564)	1:A:6:GLU:HB2	1:A:7:TYR:HE1	7	0.23	0.04	0.24
(1,1564)	1:A:6:GLU:HB2	1:A:7:TYR:HE2	7	0.23	0.04	0.24
(1,1564)	1:A:6:GLU:HB3	1:A:7:TYR:HE1	7	0.23	0.04	0.24
(1,1564)	1:A:6:GLU:HB3	1:A:7:TYR:HE2	7	0.23	0.04	0.24
(1,709)	2:B:215:SER:HA	2:B:217:LEU:HG	6	0.18	0.07	0.15
(1,375)	1:A:38:VAL:HG11	1:A:58:LYS:HD2	6	0.17	0.03	0.16
(1,375)	1:A:38:VAL:HG12	1:A:58:LYS:HD2	6	0.17	0.03	0.16
(1,375)	1:A:38:VAL:HG13	1:A:58:LYS:HD2	6	0.17	0.03	0.16
(1,1441)	1:A:101:ALA:HB1	2:B:211:ASP:H	6	0.17	0.03	0.18
(1,1441)	1:A:101:ALA:HB2	2:B:211:ASP:H	6	0.17	0.03	0.18
(1,1441)	1:A:101:ALA:HB3	2:B:211:ASP:H	6	0.17	0.03	0.18
(1,334)	1:A:13:ILE:HB	1:A:15:ILE:HD11	6	0.14	0.03	0.14
(1,334)	1:A:13:ILE:HB	1:A:15:ILE:HD12	6	0.14	0.03	0.14
(1,334)	1:A:13:ILE:HB	1:A:15:ILE:HD13	6	0.14	0.03	0.14
(1,772)	2:B:206:ILE:HA	2:B:207:ASP:HB2	5	0.27	0.06	0.26
(1,1580)	1:A:10:ASN:HD21	1:A:11:ALA:HB1	5	0.24	0.09	0.21
(1,1580)	1:A:10:ASN:HD21	1:A:11:ALA:HB2	5	0.24	0.09	0.21

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Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(1,1580)	1:A:10:ASN:HD21	1:A:11:ALA:HB3	5	0.24	0.09	0.21
(1,1580)	1:A:10:ASN:HD22	1:A:11:ALA:HB1	5	0.24	0.09	0.21
(1,1580)	1:A:10:ASN:HD22	1:A:11:ALA:HB2	5	0.24	0.09	0.21
(1,1580)	1:A:10:ASN:HD22	1:A:11:ALA:HB3	5	0.24	0.09	0.21
(1,1388)	1:A:111:VAL:H	1:A:112:SER:H	5	0.19	0.05	0.19
(1,101)	1:A:11:ALA:HB1	1:A:58:LYS:HG3	5	0.18	0.07	0.15
(1,101)	1:A:11:ALA:HB2	1:A:58:LYS:HG3	5	0.18	0.07	0.15
(1,101)	1:A:11:ALA:HB3	1:A:58:LYS:HG3	5	0.18	0.07	0.15
(1,2180)	1:A:111:VAL:HG11	1:A:113:LYS:H	5	0.17	0.07	0.13
(1,2180)	1:A:111:VAL:HG12	1:A:113:LYS:H	5	0.17	0.07	0.13
(1,2180)	1:A:111:VAL:HG13	1:A:113:LYS:H	5	0.17	0.07	0.13
(1,2180)	1:A:111:VAL:HG21	1:A:113:LYS:H	5	0.17	0.07	0.13
(1,2180)	1:A:111:VAL:HG22	1:A:113:LYS:H	5	0.17	0.07	0.13
(1,2180)	1:A:111:VAL:HG23	1:A:113:LYS:H	5	0.17	0.07	0.13
(1,1166)	1:A:59:TYR:H	1:A:68:ALA:HB1	5	0.16	0.03	0.16
(1,1166)	1:A:59:TYR:H	1:A:68:ALA:HB2	5	0.16	0.03	0.16
(1,1166)	1:A:59:TYR:H	1:A:68:ALA:HB3	5	0.16	0.03	0.16
(2,35)	1:A:65:THR:O	1:A:69:VAL:H	5	0.16	0.03	0.17
(1,1494)	2:B:221:GLU:H	2:B:222:SER:H	4	0.22	0.04	0.24
(1,1896)	1:A:63:ARG:H	1:A:63:ARG:HG2	4	0.18	0.03	0.18
(1,1896)	1:A:63:ARG:H	1:A:63:ARG:HG3	4	0.18	0.03	0.18
(1,426)	1:A:34:TYR:HA	1:A:67:LEU:HD11	4	0.18	0.07	0.16
(1,426)	1:A:34:TYR:HA	1:A:67:LEU:HD12	4	0.18	0.07	0.16
(1,426)	1:A:34:TYR:HA	1:A:67:LEU:HD13	4	0.18	0.07	0.16
(1,2253)	2:B:221:GLU:H	2:B:221:GLU:HG2	4	0.16	0.03	0.18
(1,2253)	2:B:221:GLU:H	2:B:221:GLU:HG3	4	0.16	0.03	0.18
(1,721)	1:A:19:ASN:HB2	2:B:217:LEU:HD21	4	0.15	0.05	0.12
(1,721)	1:A:19:ASN:HB2	2:B:217:LEU:HD22	4	0.15	0.05	0.12
(1,721)	1:A:19:ASN:HB2	2:B:217:LEU:HD23	4	0.15	0.05	0.12
(1,242)	1:A:40:VAL:H	1:A:41:ILE:HD11	4	0.13	0.02	0.12
(1,242)	1:A:40:VAL:H	1:A:41:ILE:HD12	4	0.13	0.02	0.12
(1,242)	1:A:40:VAL:H	1:A:41:ILE:HD13	4	0.13	0.02	0.12
(2,11)	1:A:15:ILE:O	1:A:55:ALA:H	4	0.12	0.02	0.11
(1,1363)	1:A:60:GLU:HB3	1:A:61:ASP:H	3	0.45	0.12	0.44
(1,2000)	1:A:79:GLY:H	1:A:80:ARG:HG2	3	0.41	0.06	0.39
(1,2000)	1:A:79:GLY:H	1:A:80:ARG:HG3	3	0.41	0.06	0.39
(1,1503)	2:B:221:GLU:HA	2:B:222:SER:H	3	0.33	0.04	0.32
(1,1387)	1:A:111:VAL:HB	1:A:112:SER:H	3	0.26	0.08	0.26
(1,1570)	1:A:8:LYS:H	1:A:8:LYS:HG2	3	0.24	0.06	0.27
(1,1570)	1:A:8:LYS:H	1:A:8:LYS:HG3	3	0.24	0.06	0.27
(1,1581)	1:A:11:ALA:HB1	1:A:58:LYS:HE2	3	0.19	0.01	0.19
(1,1581)	1:A:11:ALA:HB1	1:A:58:LYS:HE3	3	0.19	0.01	0.19

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Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(1,1581)	1:A:11:ALA:HB2	1:A:58:LYS:HE2	3	0.19	0.01	0.19
(1,1581)	1:A:11:ALA:HB2	1:A:58:LYS:HE3	3	0.19	0.01	0.19
(1,1581)	1:A:11:ALA:HB3	1:A:58:LYS:HE2	3	0.19	0.01	0.19
(1,1581)	1:A:11:ALA:HB3	1:A:58:LYS:HE3	3	0.19	0.01	0.19
(1,520)	1:A:38:VAL:HG11	1:A:60:GLU:HA	3	0.18	0.08	0.13
(1,520)	1:A:38:VAL:HG12	1:A:60:GLU:HA	3	0.18	0.08	0.13
(1,520)	1:A:38:VAL:HG13	1:A:60:GLU:HA	3	0.18	0.08	0.13
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD11	3	0.17	0.08	0.13
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD12	3	0.17	0.08	0.13
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD13	3	0.17	0.08	0.13
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD21	3	0.17	0.08	0.13
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD22	3	0.17	0.08	0.13
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD23	3	0.17	0.08	0.13
(1,697)	2:B:206:ILE:HD11	2:B:207:ASP:H	3	0.16	0.02	0.17
(1,697)	2:B:206:ILE:HD12	2:B:207:ASP:H	3	0.16	0.02	0.17
(1,697)	2:B:206:ILE:HD13	2:B:207:ASP:H	3	0.16	0.02	0.17
(1,1828)	1:A:45:ASP:H	1:A:50:GLU:HG2	3	0.16	0.05	0.13
(1,1828)	1:A:45:ASP:H	1:A:50:GLU:HG3	3	0.16	0.05	0.13
(2,21)	1:A:43:SER:H	1:A:54:PHE:O	3	0.16	0.03	0.17
(1,2185)	1:A:113:LYS:H	1:A:113:LYS:HG2	3	0.15	0.04	0.12
(1,2185)	1:A:113:LYS:H	1:A:113:LYS:HG3	3	0.15	0.04	0.12
(1,1894)	1:A:62:GLN:HG2	1:A:86:HIS:HE1	3	0.14	0.02	0.14
(1,1894)	1:A:62:GLN:HG3	1:A:86:HIS:HE1	3	0.14	0.02	0.14
(1,135)	1:A:31:PHE:HA	1:A:57:LEU:HD11	3	0.14	0.02	0.13
(1,135)	1:A:31:PHE:HA	1:A:57:LEU:HD12	3	0.14	0.02	0.13
(1,135)	1:A:31:PHE:HA	1:A:57:LEU:HD13	3	0.14	0.02	0.13
(1,428)	1:A:67:LEU:HD11	1:A:71:ASN:HD22	3	0.14	0.0	0.14
(1,428)	1:A:67:LEU:HD12	1:A:71:ASN:HD22	3	0.14	0.0	0.14
(1,428)	1:A:67:LEU:HD13	1:A:71:ASN:HD22	3	0.14	0.0	0.14
(1,424)	1:A:67:LEU:HD21	1:A:71:ASN:HD22	3	0.13	0.02	0.12
(1,424)	1:A:67:LEU:HD22	1:A:71:ASN:HD22	3	0.13	0.02	0.12
(1,424)	1:A:67:LEU:HD23	1:A:71:ASN:HD22	3	0.13	0.02	0.12
(2,31)	1:A:63:ARG:O	1:A:67:LEU:H	3	0.13	0.02	0.12
(1,1279)	1:A:74:GLY:H	1:A:84:ILE:HD11	3	0.12	0.01	0.13
(1,1279)	1:A:74:GLY:H	1:A:84:ILE:HD12	3	0.12	0.01	0.13
(1,1279)	1:A:74:GLY:H	1:A:84:ILE:HD13	3	0.12	0.01	0.13
(1,2090)	1:A:100:GLU:H	1:A:100:GLU:HG2	3	0.12	0.01	0.12
(1,2090)	1:A:100:GLU:H	1:A:100:GLU:HG3	3	0.12	0.01	0.12
(1,1403)	1:A:6:GLU:H	1:A:6:GLU:HG3	2	0.32	0.04	0.32
(1,2182)	1:A:112:SER:H	1:A:113:LYS:HG2	2	0.22	0.11	0.22
(1,2182)	1:A:112:SER:H	1:A:113:LYS:HG3	2	0.22	0.11	0.22
(1,1536)	2:B:215:SER:HG	2:B:217:LEU:H	2	0.22	0.02	0.22

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Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(1,774)	2:B:206:ILE:HG21	2:B:208:ILE:HD11	2	0.22	0.07	0.22
(1,774)	2:B:206:ILE:HG21	2:B:208:ILE:HD12	2	0.22	0.07	0.22
(1,774)	2:B:206:ILE:HG21	2:B:208:ILE:HD13	2	0.22	0.07	0.22
(1,774)	2:B:206:ILE:HG22	2:B:208:ILE:HD11	2	0.22	0.07	0.22
(1,774)	2:B:206:ILE:HG22	2:B:208:ILE:HD12	2	0.22	0.07	0.22
(1,774)	2:B:206:ILE:HG22	2:B:208:ILE:HD13	2	0.22	0.07	0.22
(1,774)	2:B:206:ILE:HG23	2:B:208:ILE:HD11	2	0.22	0.07	0.22
(1,774)	2:B:206:ILE:HG23	2:B:208:ILE:HD12	2	0.22	0.07	0.22
(1,774)	2:B:206:ILE:HG23	2:B:208:ILE:HD13	2	0.22	0.07	0.22
(1,1189)	1:A:63:ARG:H	1:A:66:ILE:HD11	2	0.22	0.01	0.22
(1,1189)	1:A:63:ARG:H	1:A:66:ILE:HD12	2	0.22	0.01	0.22
(1,1189)	1:A:63:ARG:H	1:A:66:ILE:HD13	2	0.22	0.01	0.22
(1,1450)	1:A:22:LEU:HG	2:B:217:LEU:HD21	2	0.22	0.02	0.22
(1,1450)	1:A:22:LEU:HG	2:B:217:LEU:HD22	2	0.22	0.02	0.22
(1,1450)	1:A:22:LEU:HG	2:B:217:LEU:HD23	2	0.22	0.02	0.22
(1,2216)	2:B:215:SER:HA	2:B:217:LEU:HD11	2	0.21	0.0	0.21
(1,2216)	2:B:215:SER:HA	2:B:217:LEU:HD12	2	0.21	0.0	0.21
(1,2216)	2:B:215:SER:HA	2:B:217:LEU:HD13	2	0.21	0.0	0.21
(1,2216)	2:B:215:SER:HA	2:B:217:LEU:HD21	2	0.21	0.0	0.21
(1,2216)	2:B:215:SER:HA	2:B:217:LEU:HD22	2	0.21	0.0	0.21
(1,2216)	2:B:215:SER:HA	2:B:217:LEU:HD23	2	0.21	0.0	0.21
(1,756)	1:A:46:GLU:HB3	2:B:207:ASP:H	2	0.18	0.01	0.18
(1,1396)	1:A:115:ASN:H	1:A:116:ALA:H	2	0.18	0.04	0.18
(1,1397)	1:A:6:GLU:H	1:A:6:GLU:HG2	2	0.18	0.04	0.18
(1,664)	1:A:12:TYR:HE1	1:A:41:ILE:H	2	0.16	0.03	0.16
(1,664)	1:A:12:TYR:HE2	1:A:41:ILE:H	2	0.16	0.03	0.16
(1,1304)	1:A:76:LYS:HB3	1:A:80:ARG:H	2	0.16	0.02	0.16
(1,1981)	1:A:76:LYS:HD2	1:A:81:ALA:H	2	0.16	0.05	0.16
(1,1981)	1:A:76:LYS:HD3	1:A:81:ALA:H	2	0.16	0.05	0.16
(1,934)	1:A:41:ILE:H	1:A:57:LEU:HB2	2	0.14	0.03	0.14
(1,1829)	1:A:45:ASP:HA	1:A:46:GLU:HG2	2	0.14	0.03	0.14
(1,1829)	1:A:45:ASP:HA	1:A:46:GLU:HG3	2	0.14	0.03	0.14
(1,521)	1:A:38:VAL:HG21	1:A:60:GLU:HB2	2	0.14	0.02	0.14
(1,521)	1:A:38:VAL:HG22	1:A:60:GLU:HB2	2	0.14	0.02	0.14
(1,521)	1:A:38:VAL:HG23	1:A:60:GLU:HB2	2	0.14	0.02	0.14
(1,1181)	1:A:61:ASP:H	1:A:63:ARG:H	2	0.14	0.01	0.14
(1,794)	1:A:23:THR:HG21	2:B:215:SER:HA	2	0.13	0.02	0.13
(1,794)	1:A:23:THR:HG22	2:B:215:SER:HA	2	0.13	0.02	0.13
(1,794)	1:A:23:THR:HG23	2:B:215:SER:HA	2	0.13	0.02	0.13
(1,644)	1:A:59:TYR:HD1	1:A:65:THR:HA	2	0.12	0.02	0.12
(1,644)	1:A:59:TYR:HD2	1:A:65:THR:HA	2	0.12	0.02	0.12
(1,1860)	1:A:51:SER:HB2	1:A:54:PHE:H	2	0.12	0.02	0.12

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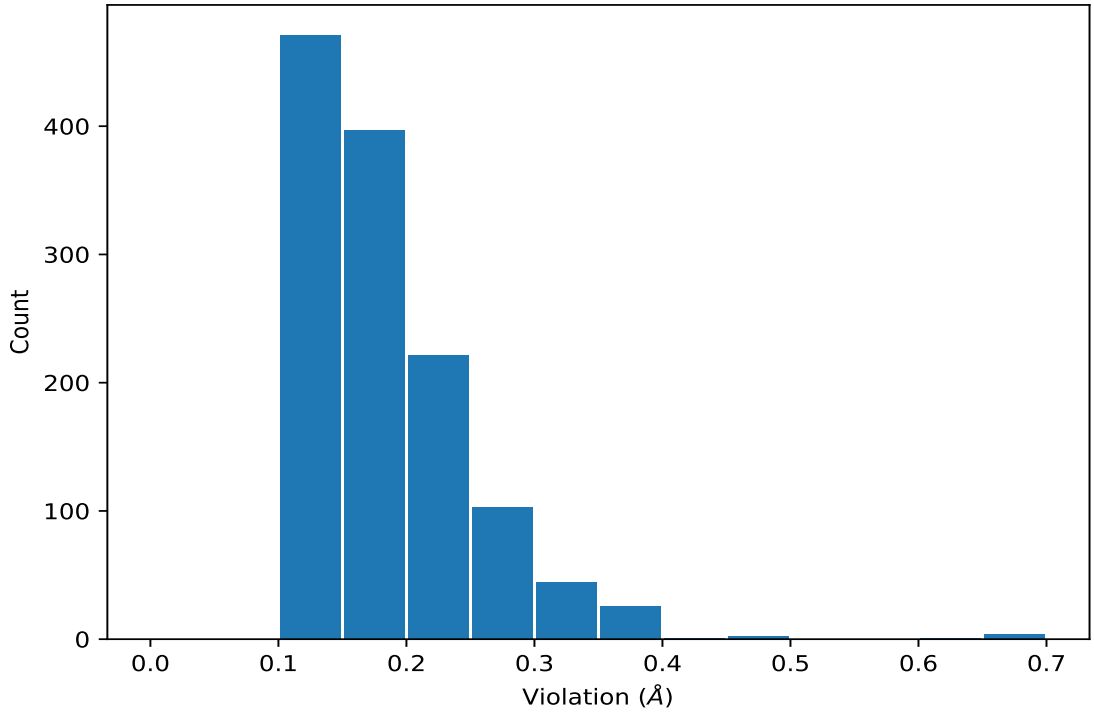
Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(1,1860)	1:A:51:SER:HB3	1:A:54:PHE:H	2	0.12	0.02	0.12
(1,553)	1:A:34:TYR:HE1	1:A:72:LEU:HG	2	0.12	0.01	0.12
(1,553)	1:A:34:TYR:HE2	1:A:72:LEU:HG	2	0.12	0.01	0.12
(1,1161)	1:A:11:ALA:HB1	1:A:59:TYR:H	2	0.12	0.0	0.12
(1,1161)	1:A:11:ALA:HB2	1:A:59:TYR:H	2	0.12	0.0	0.12
(1,1161)	1:A:11:ALA:HB3	1:A:59:TYR:H	2	0.12	0.0	0.12
(1,1219)	1:A:68:ALA:H	1:A:71:ASN:HB3	2	0.11	0.0	0.11

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

9.5 All violated distance restraints (i)

9.5.1 Histogram : Distribution of distance violations (i)

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



9.5.2 Table : All distance violations (i)

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

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1566)	1:A:6:GLU:HG2	1:A:7:TYR:HE1	15	0.7
(1,1566)	1:A:6:GLU:HG2	1:A:7:TYR:HE2	15	0.7
(1,1566)	1:A:6:GLU:HG3	1:A:7:TYR:HE1	15	0.7
(1,1566)	1:A:6:GLU:HG3	1:A:7:TYR:HE2	15	0.7
(1,1363)	1:A:60:GLU:HB3	1:A:61:ASP:H	15	0.6
(1,2000)	1:A:79:GLY:H	1:A:80:ARG:HG2	10	0.49
(1,2000)	1:A:79:GLY:H	1:A:80:ARG:HG3	10	0.49
(1,1363)	1:A:60:GLU:HB3	1:A:61:ASP:H	11	0.44
(1,2000)	1:A:79:GLY:H	1:A:80:ARG:HG2	15	0.39
(1,2000)	1:A:79:GLY:H	1:A:80:ARG:HG3	15	0.39
(1,1847)	1:A:48:THR:HG21	1:A:49:GLY:HA2	14	0.39
(1,1847)	1:A:48:THR:HG21	1:A:49:GLY:HA3	14	0.39
(1,1847)	1:A:48:THR:HG22	1:A:49:GLY:HA2	14	0.39
(1,1847)	1:A:48:THR:HG22	1:A:49:GLY:HA3	14	0.39
(1,1847)	1:A:48:THR:HG23	1:A:49:GLY:HA2	14	0.39
(1,1847)	1:A:48:THR:HG23	1:A:49:GLY:HA3	14	0.39
(1,1503)	2:B:221:GLU:HA	2:B:222:SER:H	15	0.39
(2,13)	1:A:39:ASP:H	1:A:58:LYS:O	16	0.38
(1,1460)	1:A:46:GLU:HG3	2:B:208:ILE:HD11	10	0.38
(1,1460)	1:A:46:GLU:HG3	2:B:208:ILE:HD12	10	0.38
(1,1460)	1:A:46:GLU:HG3	2:B:208:ILE:HD13	10	0.38
(1,772)	2:B:206:ILE:HA	2:B:207:ASP:HB2	1	0.36
(1,2000)	1:A:79:GLY:H	1:A:80:ARG:HG2	6	0.36
(1,2000)	1:A:79:GLY:H	1:A:80:ARG:HG3	6	0.36
(1,1403)	1:A:6:GLU:H	1:A:6:GLU:HG3	2	0.36
(1,1387)	1:A:111:VAL:HB	1:A:112:SER:H	19	0.36
(1,643)	1:A:59:TYR:HD1	1:A:60:GLU:HB3	8	0.35
(1,643)	1:A:59:TYR:HD2	1:A:60:GLU:HB3	8	0.35
(1,1580)	1:A:10:ASN:HD21	1:A:11:ALA:HB1	6	0.35
(1,1580)	1:A:10:ASN:HD21	1:A:11:ALA:HB2	6	0.35
(1,1580)	1:A:10:ASN:HD21	1:A:11:ALA:HB3	6	0.35
(1,1580)	1:A:10:ASN:HD22	1:A:11:ALA:HB1	6	0.35
(1,1580)	1:A:10:ASN:HD22	1:A:11:ALA:HB2	6	0.35
(1,1580)	1:A:10:ASN:HD22	1:A:11:ALA:HB3	6	0.35
(2,13)	1:A:39:ASP:H	1:A:58:LYS:O	11	0.34
(1,643)	1:A:59:TYR:HD1	1:A:60:GLU:HB3	12	0.34
(1,643)	1:A:59:TYR:HD2	1:A:60:GLU:HB3	12	0.34
(1,1580)	1:A:10:ASN:HD21	1:A:11:ALA:HB1	2	0.34
(1,1580)	1:A:10:ASN:HD21	1:A:11:ALA:HB2	2	0.34
(1,1580)	1:A:10:ASN:HD21	1:A:11:ALA:HB3	2	0.34
(1,1580)	1:A:10:ASN:HD22	1:A:11:ALA:HB1	2	0.34
(1,1580)	1:A:10:ASN:HD22	1:A:11:ALA:HB2	2	0.34
(1,1580)	1:A:10:ASN:HD22	1:A:11:ALA:HB3	2	0.34

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,13)	1:A:39:ASP:H	1:A:58:LYS:O	19	0.33
(1,643)	1:A:59:TYR:HD1	1:A:60:GLU:HB3	17	0.33
(1,643)	1:A:59:TYR:HD2	1:A:60:GLU:HB3	17	0.33
(1,2182)	1:A:112:SER:H	1:A:113:LYS:HG2	5	0.33
(1,2182)	1:A:112:SER:H	1:A:113:LYS:HG3	5	0.33
(1,772)	2:B:206:ILE:HA	2:B:207:ASP:HB2	7	0.32
(1,1774)	1:A:36:VAL:HG11	1:A:60:GLU:H	11	0.32
(1,1774)	1:A:36:VAL:HG12	1:A:60:GLU:H	11	0.32
(1,1774)	1:A:36:VAL:HG13	1:A:60:GLU:H	11	0.32
(1,1774)	1:A:36:VAL:HG21	1:A:60:GLU:H	11	0.32
(1,1774)	1:A:36:VAL:HG22	1:A:60:GLU:H	11	0.32
(1,1774)	1:A:36:VAL:HG23	1:A:60:GLU:H	11	0.32
(1,1503)	2:B:221:GLU:HA	2:B:222:SER:H	8	0.32
(1,643)	1:A:59:TYR:HD1	1:A:60:GLU:HB3	9	0.31
(1,643)	1:A:59:TYR:HD2	1:A:60:GLU:HB3	9	0.31
(2,13)	1:A:39:ASP:H	1:A:58:LYS:O	3	0.3
(2,13)	1:A:39:ASP:H	1:A:58:LYS:O	7	0.3
(1,709)	2:B:215:SER:HA	2:B:217:LEU:HG	16	0.3
(1,643)	1:A:59:TYR:HD1	1:A:60:GLU:HB3	4	0.3
(1,643)	1:A:59:TYR:HD2	1:A:60:GLU:HB3	4	0.3
(1,643)	1:A:59:TYR:HD1	1:A:60:GLU:HB3	18	0.3
(1,643)	1:A:59:TYR:HD2	1:A:60:GLU:HB3	18	0.3
(1,520)	1:A:38:VAL:HG11	1:A:60:GLU:HA	3	0.3
(1,520)	1:A:38:VAL:HG12	1:A:60:GLU:HA	3	0.3
(1,520)	1:A:38:VAL:HG13	1:A:60:GLU:HA	3	0.3
(1,1570)	1:A:8:LYS:H	1:A:8:LYS:HG2	12	0.3
(1,1570)	1:A:8:LYS:H	1:A:8:LYS:HG3	12	0.3
(1,1566)	1:A:6:GLU:HG2	1:A:7:TYR:HE1	9	0.3
(1,1566)	1:A:6:GLU:HG2	1:A:7:TYR:HE2	9	0.3
(1,1566)	1:A:6:GLU:HG3	1:A:7:TYR:HE1	9	0.3
(1,1566)	1:A:6:GLU:HG3	1:A:7:TYR:HE2	9	0.3
(1,1363)	1:A:60:GLU:HB3	1:A:61:ASP:H	1	0.3
(1,101)	1:A:11:ALA:HB1	1:A:58:LYS:HG3	1	0.3
(1,101)	1:A:11:ALA:HB2	1:A:58:LYS:HG3	1	0.3
(1,101)	1:A:11:ALA:HB3	1:A:58:LYS:HG3	1	0.3
(2,13)	1:A:39:ASP:H	1:A:58:LYS:O	6	0.29
(1,774)	2:B:206:ILE:HG21	2:B:208:ILE:HD11	7	0.29
(1,774)	2:B:206:ILE:HG21	2:B:208:ILE:HD12	7	0.29
(1,774)	2:B:206:ILE:HG21	2:B:208:ILE:HD13	7	0.29
(1,774)	2:B:206:ILE:HG22	2:B:208:ILE:HD11	7	0.29
(1,774)	2:B:206:ILE:HG22	2:B:208:ILE:HD12	7	0.29
(1,774)	2:B:206:ILE:HG22	2:B:208:ILE:HD13	7	0.29

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,774)	2:B:206:ILE:HG23	2:B:208:ILE:HD11	7	0.29
(1,774)	2:B:206:ILE:HG23	2:B:208:ILE:HD12	7	0.29
(1,774)	2:B:206:ILE:HG23	2:B:208:ILE:HD13	7	0.29
(1,643)	1:A:59:TYR:HD1	1:A:60:GLU:HB3	6	0.29
(1,643)	1:A:59:TYR:HD2	1:A:60:GLU:HB3	6	0.29
(1,643)	1:A:59:TYR:HD1	1:A:60:GLU:HB3	20	0.29
(1,643)	1:A:59:TYR:HD2	1:A:60:GLU:HB3	20	0.29
(1,2180)	1:A:111:VAL:HG11	1:A:113:LYS:H	10	0.29
(1,2180)	1:A:111:VAL:HG12	1:A:113:LYS:H	10	0.29
(1,2180)	1:A:111:VAL:HG13	1:A:113:LYS:H	10	0.29
(1,2180)	1:A:111:VAL:HG21	1:A:113:LYS:H	10	0.29
(1,2180)	1:A:111:VAL:HG22	1:A:113:LYS:H	10	0.29
(1,2180)	1:A:111:VAL:HG23	1:A:113:LYS:H	10	0.29
(1,1503)	2:B:221:GLU:HA	2:B:222:SER:H	10	0.29
(1,1403)	1:A:6:GLU:H	1:A:6:GLU:HG3	12	0.29
(2,13)	1:A:39:ASP:H	1:A:58:LYS:O	5	0.28
(1,643)	1:A:59:TYR:HD1	1:A:60:GLU:HB3	13	0.28
(1,643)	1:A:59:TYR:HD2	1:A:60:GLU:HB3	13	0.28
(1,643)	1:A:59:TYR:HD1	1:A:60:GLU:HB3	14	0.28
(1,643)	1:A:59:TYR:HD2	1:A:60:GLU:HB3	14	0.28
(1,426)	1:A:34:TYR:HA	1:A:67:LEU:HD11	19	0.28
(1,426)	1:A:34:TYR:HA	1:A:67:LEU:HD12	19	0.28
(1,426)	1:A:34:TYR:HA	1:A:67:LEU:HD13	19	0.28
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD11	6	0.28
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD12	6	0.28
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD13	6	0.28
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD21	6	0.28
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD22	6	0.28
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD23	6	0.28
(1,1564)	1:A:6:GLU:HB2	1:A:7:TYR:HE1	5	0.28
(1,1564)	1:A:6:GLU:HB2	1:A:7:TYR:HE2	5	0.28
(1,1564)	1:A:6:GLU:HB3	1:A:7:TYR:HE1	5	0.28
(1,1564)	1:A:6:GLU:HB3	1:A:7:TYR:HE2	5	0.28
(1,1564)	1:A:6:GLU:HB2	1:A:7:TYR:HE1	9	0.28
(1,1564)	1:A:6:GLU:HB2	1:A:7:TYR:HE2	9	0.28
(1,1564)	1:A:6:GLU:HB3	1:A:7:TYR:HE1	9	0.28
(1,1564)	1:A:6:GLU:HB3	1:A:7:TYR:HE2	9	0.28
(2,13)	1:A:39:ASP:H	1:A:58:LYS:O	4	0.27
(2,13)	1:A:39:ASP:H	1:A:58:LYS:O	8	0.27
(2,13)	1:A:39:ASP:H	1:A:58:LYS:O	9	0.27
(2,13)	1:A:39:ASP:H	1:A:58:LYS:O	14	0.27
(2,13)	1:A:39:ASP:H	1:A:58:LYS:O	15	0.27

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,13)	1:A:39:ASP:H	1:A:58:LYS:O	18	0.27
(1,643)	1:A:59:TYR:HD1	1:A:60:GLU:HB3	5	0.27
(1,643)	1:A:59:TYR:HD2	1:A:60:GLU:HB3	5	0.27
(1,643)	1:A:59:TYR:HD1	1:A:60:GLU:HB3	10	0.27
(1,643)	1:A:59:TYR:HD2	1:A:60:GLU:HB3	10	0.27
(1,1820)	1:A:43:SER:HB2	1:A:54:PHE:HZ	5	0.27
(1,1820)	1:A:43:SER:HB3	1:A:54:PHE:HZ	5	0.27
(1,1570)	1:A:8:LYS:H	1:A:8:LYS:HG2	17	0.27
(1,1570)	1:A:8:LYS:H	1:A:8:LYS:HG3	17	0.27
(1,1494)	2:B:221:GLU:H	2:B:222:SER:H	5	0.27
(1,772)	2:B:206:ILE:HA	2:B:207:ASP:HB2	10	0.26
(1,643)	1:A:59:TYR:HD1	1:A:60:GLU:HB3	3	0.26
(1,643)	1:A:59:TYR:HD2	1:A:60:GLU:HB3	3	0.26
(1,1566)	1:A:6:GLU:HG2	1:A:7:TYR:HE1	5	0.26
(1,1566)	1:A:6:GLU:HG2	1:A:7:TYR:HE2	5	0.26
(1,1566)	1:A:6:GLU:HG3	1:A:7:TYR:HE1	5	0.26
(1,1566)	1:A:6:GLU:HG3	1:A:7:TYR:HE2	5	0.26
(1,1564)	1:A:6:GLU:HB2	1:A:7:TYR:HE1	18	0.26
(1,1564)	1:A:6:GLU:HB2	1:A:7:TYR:HE2	18	0.26
(1,1564)	1:A:6:GLU:HB3	1:A:7:TYR:HE1	18	0.26
(1,1564)	1:A:6:GLU:HB3	1:A:7:TYR:HE2	18	0.26
(1,1387)	1:A:111:VAL:HB	1:A:112:SER:H	15	0.26
(2,13)	1:A:39:ASP:H	1:A:58:LYS:O	12	0.25
(2,13)	1:A:39:ASP:H	1:A:58:LYS:O	13	0.25
(2,13)	1:A:39:ASP:H	1:A:58:LYS:O	17	0.25
(1,643)	1:A:59:TYR:HD1	1:A:60:GLU:HB3	19	0.25
(1,643)	1:A:59:TYR:HD2	1:A:60:GLU:HB3	19	0.25
(1,538)	1:A:7:TYR:HA	1:A:7:TYR:HE1	15	0.25
(1,538)	1:A:7:TYR:HA	1:A:7:TYR:HE2	15	0.25
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD11	2	0.25
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD12	2	0.25
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD13	2	0.25
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD11	2	0.25
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD12	2	0.25
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD13	2	0.25
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD11	2	0.25
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD12	2	0.25
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD13	2	0.25
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD11	17	0.25
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD12	17	0.25
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD13	17	0.25
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD11	17	0.25

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD12	17	0.25
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD13	17	0.25
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD11	17	0.25
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD12	17	0.25
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD13	17	0.25
(1,323)	1:A:29:THR:HG21	1:A:30:VAL:HB	14	0.25
(1,323)	1:A:29:THR:HG22	1:A:30:VAL:HB	14	0.25
(1,323)	1:A:29:THR:HG23	1:A:30:VAL:HB	14	0.25
(1,2222)	2:B:215:SER:HB2	2:B:218:LEU:H	18	0.25
(1,2222)	2:B:215:SER:HB3	2:B:218:LEU:H	18	0.25
(1,1878)	1:A:60:GLU:HG2	1:A:61:ASP:H	13	0.25
(1,1878)	1:A:60:GLU:HG3	1:A:61:ASP:H	13	0.25
(2,13)	1:A:39:ASP:H	1:A:58:LYS:O	20	0.24
(1,772)	2:B:206:ILE:HA	2:B:207:ASP:HB2	12	0.24
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE1	14	0.24
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE2	14	0.24
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE3	14	0.24
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE1	14	0.24
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE2	14	0.24
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE3	14	0.24
(1,643)	1:A:59:TYR:HD1	1:A:60:GLU:HB3	16	0.24
(1,643)	1:A:59:TYR:HD2	1:A:60:GLU:HB3	16	0.24
(1,1980)	1:A:76:LYS:HD2	1:A:77:ILE:H	11	0.24
(1,1980)	1:A:76:LYS:HD3	1:A:77:ILE:H	11	0.24
(1,1878)	1:A:60:GLU:HG2	1:A:61:ASP:H	9	0.24
(1,1878)	1:A:60:GLU:HG3	1:A:61:ASP:H	9	0.24
(1,1820)	1:A:43:SER:HB2	1:A:54:PHE:HZ	1	0.24
(1,1820)	1:A:43:SER:HB3	1:A:54:PHE:HZ	1	0.24
(1,1820)	1:A:43:SER:HB2	1:A:54:PHE:HZ	14	0.24
(1,1820)	1:A:43:SER:HB3	1:A:54:PHE:HZ	14	0.24
(1,1820)	1:A:43:SER:HB2	1:A:54:PHE:HZ	16	0.24
(1,1820)	1:A:43:SER:HB3	1:A:54:PHE:HZ	16	0.24
(1,1820)	1:A:43:SER:HB2	1:A:54:PHE:HZ	18	0.24
(1,1820)	1:A:43:SER:HB3	1:A:54:PHE:HZ	18	0.24
(1,1564)	1:A:6:GLU:HB2	1:A:7:TYR:HE1	11	0.24
(1,1564)	1:A:6:GLU:HB2	1:A:7:TYR:HE2	11	0.24
(1,1564)	1:A:6:GLU:HB3	1:A:7:TYR:HE1	11	0.24
(1,1564)	1:A:6:GLU:HB3	1:A:7:TYR:HE2	11	0.24
(1,1494)	2:B:221:GLU:H	2:B:222:SER:H	14	0.24
(1,1450)	1:A:22:LEU:HG	2:B:217:LEU:HD21	19	0.24
(1,1450)	1:A:22:LEU:HG	2:B:217:LEU:HD22	19	0.24
(1,1450)	1:A:22:LEU:HG	2:B:217:LEU:HD23	19	0.24

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1388)	1:A:111:VAL:H	1:A:112:SER:H	11	0.24
(2,13)	1:A:39:ASP:H	1:A:58:LYS:O	2	0.23
(1,721)	1:A:19:ASN:HB2	2:B:217:LEU:HD21	16	0.23
(1,721)	1:A:19:ASN:HB2	2:B:217:LEU:HD22	16	0.23
(1,721)	1:A:19:ASN:HB2	2:B:217:LEU:HD23	16	0.23
(1,709)	2:B:215:SER:HA	2:B:217:LEU:HG	15	0.23
(1,398)	1:A:48:THR:HG21	1:A:49:GLY:HA2	14	0.23
(1,398)	1:A:48:THR:HG22	1:A:49:GLY:HA2	14	0.23
(1,398)	1:A:48:THR:HG23	1:A:49:GLY:HA2	14	0.23
(1,375)	1:A:38:VAL:HG11	1:A:58:LYS:HD2	3	0.23
(1,375)	1:A:38:VAL:HG12	1:A:58:LYS:HD2	3	0.23
(1,375)	1:A:38:VAL:HG13	1:A:58:LYS:HD2	3	0.23
(1,323)	1:A:29:THR:HG21	1:A:30:VAL:HB	11	0.23
(1,323)	1:A:29:THR:HG22	1:A:30:VAL:HB	11	0.23
(1,323)	1:A:29:THR:HG23	1:A:30:VAL:HB	11	0.23
(1,1896)	1:A:63:ARG:H	1:A:63:ARG:HG2	19	0.23
(1,1896)	1:A:63:ARG:H	1:A:63:ARG:HG3	19	0.23
(1,1828)	1:A:45:ASP:H	1:A:50:GLU:HG2	9	0.23
(1,1828)	1:A:45:ASP:H	1:A:50:GLU:HG3	9	0.23
(1,1536)	2:B:215:SER:HG	2:B:217:LEU:H	9	0.23
(1,1494)	2:B:221:GLU:H	2:B:222:SER:H	12	0.23
(1,1396)	1:A:115:ASN:H	1:A:116:ALA:H	3	0.23
(1,1388)	1:A:111:VAL:H	1:A:112:SER:H	19	0.23
(2,13)	1:A:39:ASP:H	1:A:58:LYS:O	1	0.22
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG21	7	0.22
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG22	7	0.22
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG23	7	0.22
(1,679)	2:B:206:ILE:HA	2:B:207:ASP:HB3	3	0.22
(1,643)	1:A:59:TYR:HD1	1:A:60:GLU:HB3	1	0.22
(1,643)	1:A:59:TYR:HD2	1:A:60:GLU:HB3	1	0.22
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD11	4	0.22
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD12	4	0.22
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD13	4	0.22
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD11	4	0.22
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD12	4	0.22
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD13	4	0.22
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD11	4	0.22
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD12	4	0.22
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD13	4	0.22
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD11	5	0.22
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD12	5	0.22
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD13	5	0.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD11	5	0.22
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD12	5	0.22
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD13	5	0.22
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD11	5	0.22
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD12	5	0.22
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD13	5	0.22
(1,323)	1:A:29:THR:HG21	1:A:30:VAL:HB	1	0.22
(1,323)	1:A:29:THR:HG22	1:A:30:VAL:HB	1	0.22
(1,323)	1:A:29:THR:HG23	1:A:30:VAL:HB	1	0.22
(1,323)	1:A:29:THR:HG21	1:A:30:VAL:HB	8	0.22
(1,323)	1:A:29:THR:HG22	1:A:30:VAL:HB	8	0.22
(1,323)	1:A:29:THR:HG23	1:A:30:VAL:HB	8	0.22
(1,1878)	1:A:60:GLU:HG2	1:A:61:ASP:H	12	0.22
(1,1878)	1:A:60:GLU:HG3	1:A:61:ASP:H	12	0.22
(1,1820)	1:A:43:SER:HB2	1:A:54:PHE:HZ	20	0.22
(1,1820)	1:A:43:SER:HB3	1:A:54:PHE:HZ	20	0.22
(1,1397)	1:A:6:GLU:H	1:A:6:GLU:HG2	12	0.22
(1,1189)	1:A:63:ARG:H	1:A:66:ILE:HD11	11	0.22
(1,1189)	1:A:63:ARG:H	1:A:66:ILE:HD12	11	0.22
(1,1189)	1:A:63:ARG:H	1:A:66:ILE:HD13	11	0.22
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG21	6	0.21
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG22	6	0.21
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG23	6	0.21
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG21	17	0.21
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG22	17	0.21
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG23	17	0.21
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD11	20	0.21
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD12	20	0.21
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD13	20	0.21
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD11	20	0.21
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD12	20	0.21
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD13	20	0.21
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD11	20	0.21
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD12	20	0.21
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD13	20	0.21
(1,323)	1:A:29:THR:HG21	1:A:30:VAL:HB	13	0.21
(1,323)	1:A:29:THR:HG22	1:A:30:VAL:HB	13	0.21
(1,323)	1:A:29:THR:HG23	1:A:30:VAL:HB	13	0.21
(1,323)	1:A:29:THR:HG21	1:A:30:VAL:HB	18	0.21
(1,323)	1:A:29:THR:HG22	1:A:30:VAL:HB	18	0.21
(1,323)	1:A:29:THR:HG23	1:A:30:VAL:HB	18	0.21
(1,2216)	2:B:215:SER:HA	2:B:217:LEU:HD11	3	0.21

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2216)	2:B:215:SER:HA	2:B:217:LEU:HD12	3	0.21
(1,2216)	2:B:215:SER:HA	2:B:217:LEU:HD13	3	0.21
(1,2216)	2:B:215:SER:HA	2:B:217:LEU:HD21	3	0.21
(1,2216)	2:B:215:SER:HA	2:B:217:LEU:HD22	3	0.21
(1,2216)	2:B:215:SER:HA	2:B:217:LEU:HD23	3	0.21
(1,2216)	2:B:215:SER:HA	2:B:217:LEU:HD11	17	0.21
(1,2216)	2:B:215:SER:HA	2:B:217:LEU:HD12	17	0.21
(1,2216)	2:B:215:SER:HA	2:B:217:LEU:HD13	17	0.21
(1,2216)	2:B:215:SER:HA	2:B:217:LEU:HD21	17	0.21
(1,2216)	2:B:215:SER:HA	2:B:217:LEU:HD22	17	0.21
(1,2216)	2:B:215:SER:HA	2:B:217:LEU:HD23	17	0.21
(1,2180)	1:A:111:VAL:HG11	1:A:113:LYS:H	13	0.21
(1,2180)	1:A:111:VAL:HG12	1:A:113:LYS:H	13	0.21
(1,2180)	1:A:111:VAL:HG13	1:A:113:LYS:H	13	0.21
(1,2180)	1:A:111:VAL:HG21	1:A:113:LYS:H	13	0.21
(1,2180)	1:A:111:VAL:HG22	1:A:113:LYS:H	13	0.21
(1,2180)	1:A:111:VAL:HG23	1:A:113:LYS:H	13	0.21
(1,1981)	1:A:76:LYS:HD2	1:A:81:ALA:H	1	0.21
(1,1981)	1:A:76:LYS:HD3	1:A:81:ALA:H	1	0.21
(1,1820)	1:A:43:SER:HB2	1:A:54:PHE:HZ	6	0.21
(1,1820)	1:A:43:SER:HB3	1:A:54:PHE:HZ	6	0.21
(1,1580)	1:A:10:ASN:HD21	1:A:11:ALA:HB1	13	0.21
(1,1580)	1:A:10:ASN:HD21	1:A:11:ALA:HB2	13	0.21
(1,1580)	1:A:10:ASN:HD21	1:A:11:ALA:HB3	13	0.21
(1,1580)	1:A:10:ASN:HD22	1:A:11:ALA:HB1	13	0.21
(1,1580)	1:A:10:ASN:HD22	1:A:11:ALA:HB2	13	0.21
(1,1580)	1:A:10:ASN:HD22	1:A:11:ALA:HB3	13	0.21
(1,1566)	1:A:6:GLU:HG2	1:A:7:TYR:HE1	10	0.21
(1,1566)	1:A:6:GLU:HG2	1:A:7:TYR:HE2	10	0.21
(1,1566)	1:A:6:GLU:HG3	1:A:7:TYR:HE1	10	0.21
(1,1566)	1:A:6:GLU:HG3	1:A:7:TYR:HE2	10	0.21
(1,1189)	1:A:63:ARG:H	1:A:66:ILE:HD11	12	0.21
(1,1189)	1:A:63:ARG:H	1:A:66:ILE:HD12	12	0.21
(1,1189)	1:A:63:ARG:H	1:A:66:ILE:HD13	12	0.21
(2,13)	1:A:39:ASP:H	1:A:58:LYS:O	10	0.2
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG21	12	0.2
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG22	12	0.2
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG23	12	0.2
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG21	13	0.2
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG22	13	0.2
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG23	13	0.2
(1,452)	1:A:48:THR:HG21	1:A:49:GLY:HA3	14	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,452)	1:A:48:THR:HG22	1:A:49:GLY:HA3	14	0.2
(1,452)	1:A:48:THR:HG23	1:A:49:GLY:HA3	14	0.2
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD11	1	0.2
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD12	1	0.2
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD13	1	0.2
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD11	1	0.2
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD12	1	0.2
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD13	1	0.2
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD11	1	0.2
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD12	1	0.2
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD13	1	0.2
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD11	3	0.2
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD12	3	0.2
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD13	3	0.2
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD11	3	0.2
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD12	3	0.2
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD13	3	0.2
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD11	3	0.2
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD12	3	0.2
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD13	3	0.2
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD11	14	0.2
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD12	14	0.2
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD13	14	0.2
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD11	14	0.2
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD12	14	0.2
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD13	14	0.2
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD11	14	0.2
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD12	14	0.2
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD13	14	0.2
(1,323)	1:A:29:THR:HG21	1:A:30:VAL:HB	20	0.2
(1,323)	1:A:29:THR:HG22	1:A:30:VAL:HB	20	0.2
(1,323)	1:A:29:THR:HG23	1:A:30:VAL:HB	20	0.2
(1,2185)	1:A:113:LYS:H	1:A:113:LYS:HG2	3	0.2
(1,2185)	1:A:113:LYS:H	1:A:113:LYS:HG3	3	0.2
(1,1896)	1:A:63:ARG:H	1:A:63:ARG:HG2	5	0.2
(1,1896)	1:A:63:ARG:H	1:A:63:ARG:HG3	5	0.2
(1,1878)	1:A:60:GLU:HG2	1:A:61:ASP:H	4	0.2
(1,1878)	1:A:60:GLU:HG3	1:A:61:ASP:H	4	0.2
(1,1878)	1:A:60:GLU:HG2	1:A:61:ASP:H	14	0.2
(1,1878)	1:A:60:GLU:HG3	1:A:61:ASP:H	14	0.2
(1,1581)	1:A:11:ALA:HB1	1:A:58:LYS:HE2	6	0.2
(1,1581)	1:A:11:ALA:HB1	1:A:58:LYS:HE3	6	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1581)	1:A:11:ALA:HB2	1:A:58:LYS:HE2	6	0.2
(1,1581)	1:A:11:ALA:HB2	1:A:58:LYS:HE3	6	0.2
(1,1581)	1:A:11:ALA:HB3	1:A:58:LYS:HE2	6	0.2
(1,1581)	1:A:11:ALA:HB3	1:A:58:LYS:HE3	6	0.2
(1,1566)	1:A:6:GLU:HG2	1:A:7:TYR:HE1	7	0.2
(1,1566)	1:A:6:GLU:HG2	1:A:7:TYR:HE2	7	0.2
(1,1566)	1:A:6:GLU:HG3	1:A:7:TYR:HE1	7	0.2
(1,1566)	1:A:6:GLU:HG3	1:A:7:TYR:HE2	7	0.2
(1,1566)	1:A:6:GLU:HG2	1:A:7:TYR:HE1	11	0.2
(1,1566)	1:A:6:GLU:HG2	1:A:7:TYR:HE2	11	0.2
(1,1566)	1:A:6:GLU:HG3	1:A:7:TYR:HE1	11	0.2
(1,1566)	1:A:6:GLU:HG3	1:A:7:TYR:HE2	11	0.2
(1,1564)	1:A:6:GLU:HB2	1:A:7:TYR:HE1	10	0.2
(1,1564)	1:A:6:GLU:HB2	1:A:7:TYR:HE2	10	0.2
(1,1564)	1:A:6:GLU:HB3	1:A:7:TYR:HE1	10	0.2
(1,1564)	1:A:6:GLU:HB3	1:A:7:TYR:HE2	10	0.2
(1,1536)	2:B:215:SER:HG	2:B:217:LEU:H	18	0.2
(1,1441)	1:A:101:ALA:HB1	2:B:211:ASP:H	10	0.2
(1,1441)	1:A:101:ALA:HB2	2:B:211:ASP:H	10	0.2
(1,1441)	1:A:101:ALA:HB3	2:B:211:ASP:H	10	0.2
(1,127)	1:A:57:LEU:HD21	1:A:60:GLU:H	12	0.2
(1,127)	1:A:57:LEU:HD22	1:A:60:GLU:H	12	0.2
(1,127)	1:A:57:LEU:HD23	1:A:60:GLU:H	12	0.2
(2,35)	1:A:65:THR:O	1:A:69:VAL:H	10	0.19
(2,35)	1:A:65:THR:O	1:A:69:VAL:H	18	0.19
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG21	2	0.19
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG22	2	0.19
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG23	2	0.19
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG21	5	0.19
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG22	5	0.19
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG23	5	0.19
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG21	16	0.19
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG22	16	0.19
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG23	16	0.19
(1,756)	1:A:46:GLU:HB3	2:B:207:ASP:H	8	0.19
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE1	4	0.19
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE2	4	0.19
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE3	4	0.19
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE1	4	0.19
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE2	4	0.19
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE3	4	0.19
(1,664)	1:A:12:TYR:HE1	1:A:41:ILE:H	1	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,664)	1:A:12:TYR:HE2	1:A:41:ILE:H	1	0.19
(1,643)	1:A:59:TYR:HD1	1:A:60:GLU:HB3	7	0.19
(1,643)	1:A:59:TYR:HD2	1:A:60:GLU:HB3	7	0.19
(1,517)	2:B:218:LEU:HG	2:B:219:GLU:HA	6	0.19
(1,426)	1:A:34:TYR:HA	1:A:67:LEU:HD11	3	0.19
(1,426)	1:A:34:TYR:HA	1:A:67:LEU:HD12	3	0.19
(1,426)	1:A:34:TYR:HA	1:A:67:LEU:HD13	3	0.19
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD11	6	0.19
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD12	6	0.19
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD13	6	0.19
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD11	6	0.19
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD12	6	0.19
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD13	6	0.19
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD11	6	0.19
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD12	6	0.19
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD13	6	0.19
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD11	10	0.19
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD12	10	0.19
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD13	10	0.19
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD11	10	0.19
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD12	10	0.19
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD13	10	0.19
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD11	10	0.19
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD12	10	0.19
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD13	10	0.19
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD11	13	0.19
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD12	13	0.19
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD13	13	0.19
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD11	13	0.19
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD12	13	0.19
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD13	13	0.19
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD11	13	0.19
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD12	13	0.19
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD13	13	0.19
(1,375)	1:A:38:VAL:HG11	1:A:58:LYS:HD2	6	0.19
(1,375)	1:A:38:VAL:HG12	1:A:58:LYS:HD2	6	0.19
(1,375)	1:A:38:VAL:HG13	1:A:58:LYS:HD2	6	0.19
(1,323)	1:A:29:THR:HG21	1:A:30:VAL:HB	10	0.19
(1,323)	1:A:29:THR:HG22	1:A:30:VAL:HB	10	0.19
(1,323)	1:A:29:THR:HG23	1:A:30:VAL:HB	10	0.19
(1,2253)	2:B:221:GLU:H	2:B:221:GLU:HG2	5	0.19
(1,2253)	2:B:221:GLU:H	2:B:221:GLU:HG3	5	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1581)	1:A:11:ALA:HB1	1:A:58:LYS:HE2	1	0.19
(1,1581)	1:A:11:ALA:HB1	1:A:58:LYS:HE3	1	0.19
(1,1581)	1:A:11:ALA:HB2	1:A:58:LYS:HE2	1	0.19
(1,1581)	1:A:11:ALA:HB2	1:A:58:LYS:HE3	1	0.19
(1,1581)	1:A:11:ALA:HB3	1:A:58:LYS:HE2	1	0.19
(1,1581)	1:A:11:ALA:HB3	1:A:58:LYS:HE3	1	0.19
(1,1564)	1:A:6:GLU:HB2	1:A:7:TYR:HE1	7	0.19
(1,1564)	1:A:6:GLU:HB2	1:A:7:TYR:HE2	7	0.19
(1,1564)	1:A:6:GLU:HB3	1:A:7:TYR:HE1	7	0.19
(1,1564)	1:A:6:GLU:HB3	1:A:7:TYR:HE2	7	0.19
(1,1564)	1:A:6:GLU:HB2	1:A:7:TYR:HE1	20	0.19
(1,1564)	1:A:6:GLU:HB2	1:A:7:TYR:HE2	20	0.19
(1,1564)	1:A:6:GLU:HB3	1:A:7:TYR:HE1	20	0.19
(1,1564)	1:A:6:GLU:HB3	1:A:7:TYR:HE2	20	0.19
(1,1450)	1:A:22:LEU:HG	2:B:217:LEU:HD21	10	0.19
(1,1450)	1:A:22:LEU:HG	2:B:217:LEU:HD22	10	0.19
(1,1450)	1:A:22:LEU:HG	2:B:217:LEU:HD23	10	0.19
(1,1388)	1:A:111:VAL:H	1:A:112:SER:H	15	0.19
(1,1166)	1:A:59:TYR:H	1:A:68:ALA:HB1	3	0.19
(1,1166)	1:A:59:TYR:H	1:A:68:ALA:HB2	3	0.19
(1,1166)	1:A:59:TYR:H	1:A:68:ALA:HB3	3	0.19
(1,1166)	1:A:59:TYR:H	1:A:68:ALA:HB1	4	0.19
(1,1166)	1:A:59:TYR:H	1:A:68:ALA:HB2	4	0.19
(1,1166)	1:A:59:TYR:H	1:A:68:ALA:HB3	4	0.19
(1,101)	1:A:11:ALA:HB1	1:A:58:LYS:HG3	7	0.19
(1,101)	1:A:11:ALA:HB2	1:A:58:LYS:HG3	7	0.19
(1,101)	1:A:11:ALA:HB3	1:A:58:LYS:HG3	7	0.19
(2,21)	1:A:43:SER:H	1:A:54:PHE:O	10	0.18
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG21	9	0.18
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG22	9	0.18
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG23	9	0.18
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG21	19	0.18
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG22	19	0.18
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG23	19	0.18
(1,791)	2:B:204:GLN:HA	2:B:205:TYR:HD1	1	0.18
(1,791)	2:B:204:GLN:HA	2:B:205:TYR:HD2	1	0.18
(1,772)	2:B:206:ILE:HA	2:B:207:ASP:HB2	8	0.18
(1,756)	1:A:46:GLU:HB3	2:B:207:ASP:H	3	0.18
(1,714)	2:B:215:SER:HG	2:B:217:LEU:HD21	15	0.18
(1,714)	2:B:215:SER:HG	2:B:217:LEU:HD22	15	0.18
(1,714)	2:B:215:SER:HG	2:B:217:LEU:HD23	15	0.18
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD11	16	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD12	16	0.18
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD13	16	0.18
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD11	16	0.18
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD12	16	0.18
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD13	16	0.18
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD11	16	0.18
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD12	16	0.18
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD13	16	0.18
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD11	18	0.18
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD12	18	0.18
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD13	18	0.18
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD11	18	0.18
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD12	18	0.18
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD13	18	0.18
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD11	18	0.18
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD12	18	0.18
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD13	18	0.18
(1,323)	1:A:29:THR:HG21	1:A:30:VAL:HB	3	0.18
(1,323)	1:A:29:THR:HG22	1:A:30:VAL:HB	3	0.18
(1,323)	1:A:29:THR:HG23	1:A:30:VAL:HB	3	0.18
(1,323)	1:A:29:THR:HG21	1:A:30:VAL:HB	5	0.18
(1,323)	1:A:29:THR:HG22	1:A:30:VAL:HB	5	0.18
(1,323)	1:A:29:THR:HG23	1:A:30:VAL:HB	5	0.18
(1,323)	1:A:29:THR:HG21	1:A:30:VAL:HB	17	0.18
(1,323)	1:A:29:THR:HG22	1:A:30:VAL:HB	17	0.18
(1,323)	1:A:29:THR:HG23	1:A:30:VAL:HB	17	0.18
(1,323)	1:A:29:THR:HG21	1:A:30:VAL:HB	19	0.18
(1,323)	1:A:29:THR:HG22	1:A:30:VAL:HB	19	0.18
(1,323)	1:A:29:THR:HG23	1:A:30:VAL:HB	19	0.18
(1,2253)	2:B:221:GLU:H	2:B:221:GLU:HG2	20	0.18
(1,2253)	2:B:221:GLU:H	2:B:221:GLU:HG3	20	0.18
(1,1820)	1:A:43:SER:HB2	1:A:54:PHE:HZ	3	0.18
(1,1820)	1:A:43:SER:HB3	1:A:54:PHE:HZ	3	0.18
(1,1777)	1:A:38:VAL:HG11	1:A:58:LYS:HE2	19	0.18
(1,1777)	1:A:38:VAL:HG11	1:A:58:LYS:HE3	19	0.18
(1,1777)	1:A:38:VAL:HG12	1:A:58:LYS:HE2	19	0.18
(1,1777)	1:A:38:VAL:HG12	1:A:58:LYS:HE3	19	0.18
(1,1777)	1:A:38:VAL:HG13	1:A:58:LYS:HE2	19	0.18
(1,1777)	1:A:38:VAL:HG13	1:A:58:LYS:HE3	19	0.18
(1,1661)	1:A:22:LEU:HD11	2:B:218:LEU:HB3	2	0.18
(1,1661)	1:A:22:LEU:HD12	2:B:218:LEU:HB3	2	0.18
(1,1661)	1:A:22:LEU:HD13	2:B:218:LEU:HB3	2	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1661)	1:A:22:LEU:HD21	2:B:218:LEU:HB3	2	0.18
(1,1661)	1:A:22:LEU:HD22	2:B:218:LEU:HB3	2	0.18
(1,1661)	1:A:22:LEU:HD23	2:B:218:LEU:HB3	2	0.18
(1,1441)	1:A:101:ALA:HB1	2:B:211:ASP:H	3	0.18
(1,1441)	1:A:101:ALA:HB2	2:B:211:ASP:H	3	0.18
(1,1441)	1:A:101:ALA:HB3	2:B:211:ASP:H	3	0.18
(1,1441)	1:A:101:ALA:HB1	2:B:211:ASP:H	9	0.18
(1,1441)	1:A:101:ALA:HB2	2:B:211:ASP:H	9	0.18
(1,1441)	1:A:101:ALA:HB3	2:B:211:ASP:H	9	0.18
(1,1304)	1:A:76:LYS:HB3	1:A:80:ARG:H	4	0.18
(1,1086)	1:A:38:VAL:HG11	1:A:39:ASP:H	19	0.18
(1,1086)	1:A:38:VAL:HG12	1:A:39:ASP:H	19	0.18
(1,1086)	1:A:38:VAL:HG13	1:A:39:ASP:H	19	0.18
(2,35)	1:A:65:THR:O	1:A:69:VAL:H	6	0.17
(2,21)	1:A:43:SER:H	1:A:54:PHE:O	11	0.17
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG21	11	0.17
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG22	11	0.17
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG23	11	0.17
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG21	20	0.17
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG22	20	0.17
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG23	20	0.17
(1,934)	1:A:41:ILE:H	1:A:57:LEU:HB2	6	0.17
(1,697)	2:B:206:ILE:HD11	2:B:207:ASP:H	2	0.17
(1,697)	2:B:206:ILE:HD12	2:B:207:ASP:H	2	0.17
(1,697)	2:B:206:ILE:HD13	2:B:207:ASP:H	2	0.17
(1,697)	2:B:206:ILE:HD11	2:B:207:ASP:H	5	0.17
(1,697)	2:B:206:ILE:HD12	2:B:207:ASP:H	5	0.17
(1,697)	2:B:206:ILE:HD13	2:B:207:ASP:H	5	0.17
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD11	8	0.17
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD12	8	0.17
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD13	8	0.17
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD11	8	0.17
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD12	8	0.17
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD13	8	0.17
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD11	8	0.17
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD12	8	0.17
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD13	8	0.17
(1,404)	1:A:62:GLN:HG2	1:A:65:THR:HG21	7	0.17
(1,404)	1:A:62:GLN:HG2	1:A:65:THR:HG22	7	0.17
(1,404)	1:A:62:GLN:HG2	1:A:65:THR:HG23	7	0.17
(1,334)	1:A:13:ILE:HB	1:A:15:ILE:HD11	9	0.17
(1,334)	1:A:13:ILE:HB	1:A:15:ILE:HD12	9	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,334)	1:A:13:ILE:HB	1:A:15:ILE:HD13	9	0.17
(1,2253)	2:B:221:GLU:H	2:B:221:GLU:HG2	2	0.17
(1,2253)	2:B:221:GLU:H	2:B:221:GLU:HG3	2	0.17
(1,1983)	1:A:76:LYS:HE2	1:A:81:ALA:H	2	0.17
(1,1983)	1:A:76:LYS:HE3	1:A:81:ALA:H	2	0.17
(1,1894)	1:A:62:GLN:HG2	1:A:86:HIS:HE1	8	0.17
(1,1894)	1:A:62:GLN:HG3	1:A:86:HIS:HE1	8	0.17
(1,1878)	1:A:60:GLU:HG2	1:A:61:ASP:H	17	0.17
(1,1878)	1:A:60:GLU:HG3	1:A:61:ASP:H	17	0.17
(1,1829)	1:A:45:ASP:HA	1:A:46:GLU:HG2	16	0.17
(1,1829)	1:A:45:ASP:HA	1:A:46:GLU:HG3	16	0.17
(1,1581)	1:A:11:ALA:HB1	1:A:58:LYS:HE2	3	0.17
(1,1581)	1:A:11:ALA:HB1	1:A:58:LYS:HE3	3	0.17
(1,1581)	1:A:11:ALA:HB2	1:A:58:LYS:HE2	3	0.17
(1,1581)	1:A:11:ALA:HB2	1:A:58:LYS:HE3	3	0.17
(1,1581)	1:A:11:ALA:HB3	1:A:58:LYS:HE2	3	0.17
(1,1581)	1:A:11:ALA:HB3	1:A:58:LYS:HE3	3	0.17
(1,1441)	1:A:101:ALA:HB1	2:B:211:ASP:H	8	0.17
(1,1441)	1:A:101:ALA:HB2	2:B:211:ASP:H	8	0.17
(1,1441)	1:A:101:ALA:HB3	2:B:211:ASP:H	8	0.17
(1,1441)	1:A:101:ALA:HB1	2:B:211:ASP:H	20	0.17
(1,1441)	1:A:101:ALA:HB2	2:B:211:ASP:H	20	0.17
(1,1441)	1:A:101:ALA:HB3	2:B:211:ASP:H	20	0.17
(1,1388)	1:A:111:VAL:H	1:A:112:SER:H	16	0.17
(1,1387)	1:A:111:VAL:HB	1:A:112:SER:H	1	0.17
(1,135)	1:A:31:PHE:HA	1:A:57:LEU:HD11	7	0.17
(1,135)	1:A:31:PHE:HA	1:A:57:LEU:HD12	7	0.17
(1,135)	1:A:31:PHE:HA	1:A:57:LEU:HD13	7	0.17
(1,127)	1:A:57:LEU:HD21	1:A:60:GLU:H	8	0.17
(1,127)	1:A:57:LEU:HD22	1:A:60:GLU:H	8	0.17
(1,127)	1:A:57:LEU:HD23	1:A:60:GLU:H	8	0.17
(1,1061)	1:A:28:LEU:HG	1:A:32:SER:H	13	0.17
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG21	1	0.16
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG22	1	0.16
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG23	1	0.16
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG21	3	0.16
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG22	3	0.16
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG23	3	0.16
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG21	4	0.16
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG22	4	0.16
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG23	4	0.16
(1,709)	2:B:215:SER:HA	2:B:217:LEU:HG	8	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE1	8	0.16
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE2	8	0.16
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE3	8	0.16
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE1	8	0.16
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE2	8	0.16
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE3	8	0.16
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE1	9	0.16
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE2	9	0.16
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE3	9	0.16
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE1	9	0.16
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE2	9	0.16
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE3	9	0.16
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE1	19	0.16
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE2	19	0.16
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE3	19	0.16
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE1	19	0.16
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE2	19	0.16
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE3	19	0.16
(1,521)	1:A:38:VAL:HG21	1:A:60:GLU:HB2	10	0.16
(1,521)	1:A:38:VAL:HG22	1:A:60:GLU:HB2	10	0.16
(1,521)	1:A:38:VAL:HG23	1:A:60:GLU:HB2	10	0.16
(1,424)	1:A:67:LEU:HD21	1:A:71:ASN:HD22	19	0.16
(1,424)	1:A:67:LEU:HD22	1:A:71:ASN:HD22	19	0.16
(1,424)	1:A:67:LEU:HD23	1:A:71:ASN:HD22	19	0.16
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD11	9	0.16
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD12	9	0.16
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD13	9	0.16
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD11	9	0.16
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD12	9	0.16
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD13	9	0.16
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD11	9	0.16
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD12	9	0.16
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD13	9	0.16
(1,375)	1:A:38:VAL:HG11	1:A:58:LYS:HD2	4	0.16
(1,375)	1:A:38:VAL:HG12	1:A:58:LYS:HD2	4	0.16
(1,375)	1:A:38:VAL:HG13	1:A:58:LYS:HD2	4	0.16
(1,375)	1:A:38:VAL:HG11	1:A:58:LYS:HD2	17	0.16
(1,375)	1:A:38:VAL:HG12	1:A:58:LYS:HD2	17	0.16
(1,375)	1:A:38:VAL:HG13	1:A:58:LYS:HD2	17	0.16
(1,334)	1:A:13:ILE:HB	1:A:15:ILE:HD11	7	0.16
(1,334)	1:A:13:ILE:HB	1:A:15:ILE:HD12	7	0.16
(1,334)	1:A:13:ILE:HB	1:A:15:ILE:HD13	7	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,334)	1:A:13:ILE:HB	1:A:15:ILE:HD11	15	0.16
(1,334)	1:A:13:ILE:HB	1:A:15:ILE:HD12	15	0.16
(1,334)	1:A:13:ILE:HB	1:A:15:ILE:HD13	15	0.16
(1,323)	1:A:29:THR:HG21	1:A:30:VAL:HB	7	0.16
(1,323)	1:A:29:THR:HG22	1:A:30:VAL:HB	7	0.16
(1,323)	1:A:29:THR:HG23	1:A:30:VAL:HB	7	0.16
(1,323)	1:A:29:THR:HG21	1:A:30:VAL:HB	12	0.16
(1,323)	1:A:29:THR:HG22	1:A:30:VAL:HB	12	0.16
(1,323)	1:A:29:THR:HG23	1:A:30:VAL:HB	12	0.16
(1,323)	1:A:29:THR:HG21	1:A:30:VAL:HB	15	0.16
(1,323)	1:A:29:THR:HG22	1:A:30:VAL:HB	15	0.16
(1,323)	1:A:29:THR:HG23	1:A:30:VAL:HB	15	0.16
(1,242)	1:A:40:VAL:H	1:A:41:ILE:HD11	20	0.16
(1,242)	1:A:40:VAL:H	1:A:41:ILE:HD12	20	0.16
(1,242)	1:A:40:VAL:H	1:A:41:ILE:HD13	20	0.16
(1,2115)	1:A:102:VAL:HG11	1:A:106:LEU:HG	4	0.16
(1,2115)	1:A:102:VAL:HG12	1:A:106:LEU:HG	4	0.16
(1,2115)	1:A:102:VAL:HG13	1:A:106:LEU:HG	4	0.16
(1,2115)	1:A:102:VAL:HG21	1:A:106:LEU:HG	4	0.16
(1,2115)	1:A:102:VAL:HG22	1:A:106:LEU:HG	4	0.16
(1,2115)	1:A:102:VAL:HG23	1:A:106:LEU:HG	4	0.16
(1,2002)	1:A:80:ARG:H	1:A:80:ARG:HG2	10	0.16
(1,2002)	1:A:80:ARG:H	1:A:80:ARG:HG3	10	0.16
(1,1896)	1:A:63:ARG:H	1:A:63:ARG:HG2	17	0.16
(1,1896)	1:A:63:ARG:H	1:A:63:ARG:HG3	17	0.16
(1,1494)	2:B:221:GLU:H	2:B:222:SER:H	2	0.16
(1,127)	1:A:57:LEU:HD21	1:A:60:GLU:H	9	0.16
(1,127)	1:A:57:LEU:HD22	1:A:60:GLU:H	9	0.16
(1,127)	1:A:57:LEU:HD23	1:A:60:GLU:H	9	0.16
(1,127)	1:A:57:LEU:HD21	1:A:60:GLU:H	19	0.16
(1,127)	1:A:57:LEU:HD22	1:A:60:GLU:H	19	0.16
(1,127)	1:A:57:LEU:HD23	1:A:60:GLU:H	19	0.16
(1,127)	1:A:57:LEU:HD21	1:A:60:GLU:H	20	0.16
(1,127)	1:A:57:LEU:HD22	1:A:60:GLU:H	20	0.16
(1,127)	1:A:57:LEU:HD23	1:A:60:GLU:H	20	0.16
(1,126)	1:A:57:LEU:HD21	1:A:59:TYR:HH	10	0.16
(1,126)	1:A:57:LEU:HD22	1:A:59:TYR:HH	10	0.16
(1,126)	1:A:57:LEU:HD23	1:A:59:TYR:HH	10	0.16
(1,1166)	1:A:59:TYR:H	1:A:68:ALA:HB1	15	0.16
(1,1166)	1:A:59:TYR:H	1:A:68:ALA:HB2	15	0.16
(1,1166)	1:A:59:TYR:H	1:A:68:ALA:HB3	15	0.16
(1,1086)	1:A:38:VAL:HG11	1:A:39:ASP:H	3	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1086)	1:A:38:VAL:HG12	1:A:39:ASP:H	3	0.16
(1,1086)	1:A:38:VAL:HG13	1:A:39:ASP:H	3	0.16
(1,1086)	1:A:38:VAL:HG11	1:A:39:ASP:H	4	0.16
(1,1086)	1:A:38:VAL:HG12	1:A:39:ASP:H	4	0.16
(1,1086)	1:A:38:VAL:HG13	1:A:39:ASP:H	4	0.16
(1,1086)	1:A:38:VAL:HG11	1:A:39:ASP:H	12	0.16
(1,1086)	1:A:38:VAL:HG12	1:A:39:ASP:H	12	0.16
(1,1086)	1:A:38:VAL:HG13	1:A:39:ASP:H	12	0.16
(1,1086)	1:A:38:VAL:HG11	1:A:39:ASP:H	13	0.16
(1,1086)	1:A:38:VAL:HG12	1:A:39:ASP:H	13	0.16
(1,1086)	1:A:38:VAL:HG13	1:A:39:ASP:H	13	0.16
(1,1086)	1:A:38:VAL:HG11	1:A:39:ASP:H	14	0.16
(1,1086)	1:A:38:VAL:HG12	1:A:39:ASP:H	14	0.16
(1,1086)	1:A:38:VAL:HG13	1:A:39:ASP:H	14	0.16
(1,1086)	1:A:38:VAL:HG11	1:A:39:ASP:H	17	0.16
(1,1086)	1:A:38:VAL:HG12	1:A:39:ASP:H	17	0.16
(1,1086)	1:A:38:VAL:HG13	1:A:39:ASP:H	17	0.16
(2,31)	1:A:63:ARG:O	1:A:67:LEU:H	5	0.15
(2,11)	1:A:15:ILE:O	1:A:55:ALA:H	16	0.15
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG21	8	0.15
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG22	8	0.15
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG23	8	0.15
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG21	10	0.15
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG22	10	0.15
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG23	10	0.15
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG21	15	0.15
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG22	15	0.15
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG23	15	0.15
(1,794)	1:A:23:THR:HG21	2:B:215:SER:HA	10	0.15
(1,794)	1:A:23:THR:HG22	2:B:215:SER:HA	10	0.15
(1,794)	1:A:23:THR:HG23	2:B:215:SER:HA	10	0.15
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE1	15	0.15
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE2	15	0.15
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE3	15	0.15
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE1	15	0.15
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE2	15	0.15
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE3	15	0.15
(1,396)	1:A:48:THR:HG21	1:A:50:GLU:HB2	14	0.15
(1,396)	1:A:48:THR:HG22	1:A:50:GLU:HB2	14	0.15
(1,396)	1:A:48:THR:HG23	1:A:50:GLU:HB2	14	0.15
(1,375)	1:A:38:VAL:HG11	1:A:58:LYS:HD2	8	0.15
(1,375)	1:A:38:VAL:HG12	1:A:58:LYS:HD2	8	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,375)	1:A:38:VAL:HG13	1:A:58:LYS:HD2	8	0.15
(1,323)	1:A:29:THR:HG21	1:A:30:VAL:HB	2	0.15
(1,323)	1:A:29:THR:HG22	1:A:30:VAL:HB	2	0.15
(1,323)	1:A:29:THR:HG23	1:A:30:VAL:HB	2	0.15
(1,323)	1:A:29:THR:HG21	1:A:30:VAL:HB	9	0.15
(1,323)	1:A:29:THR:HG22	1:A:30:VAL:HB	9	0.15
(1,323)	1:A:29:THR:HG23	1:A:30:VAL:HB	9	0.15
(1,1878)	1:A:60:GLU:HG2	1:A:61:ASP:H	18	0.15
(1,1878)	1:A:60:GLU:HG3	1:A:61:ASP:H	18	0.15
(1,1763)	1:A:34:TYR:HB2	1:A:68:ALA:HB1	9	0.15
(1,1763)	1:A:34:TYR:HB2	1:A:68:ALA:HB2	9	0.15
(1,1763)	1:A:34:TYR:HB2	1:A:68:ALA:HB3	9	0.15
(1,1763)	1:A:34:TYR:HB3	1:A:68:ALA:HB1	9	0.15
(1,1763)	1:A:34:TYR:HB3	1:A:68:ALA:HB2	9	0.15
(1,1763)	1:A:34:TYR:HB3	1:A:68:ALA:HB3	9	0.15
(1,16)	1:A:77:ILE:HD11	1:A:78:GLY:H	12	0.15
(1,16)	1:A:77:ILE:HD12	1:A:78:GLY:H	12	0.15
(1,16)	1:A:77:ILE:HD13	1:A:78:GLY:H	12	0.15
(1,1580)	1:A:10:ASN:HD21	1:A:11:ALA:HB1	18	0.15
(1,1580)	1:A:10:ASN:HD21	1:A:11:ALA:HB2	18	0.15
(1,1580)	1:A:10:ASN:HD21	1:A:11:ALA:HB3	18	0.15
(1,1580)	1:A:10:ASN:HD22	1:A:11:ALA:HB1	18	0.15
(1,1580)	1:A:10:ASN:HD22	1:A:11:ALA:HB2	18	0.15
(1,1580)	1:A:10:ASN:HD22	1:A:11:ALA:HB3	18	0.15
(1,1580)	1:A:10:ASN:HD21	1:A:11:ALA:HB1	20	0.15
(1,1580)	1:A:10:ASN:HD21	1:A:11:ALA:HB2	20	0.15
(1,1580)	1:A:10:ASN:HD21	1:A:11:ALA:HB3	20	0.15
(1,1580)	1:A:10:ASN:HD22	1:A:11:ALA:HB1	20	0.15
(1,1580)	1:A:10:ASN:HD22	1:A:11:ALA:HB2	20	0.15
(1,1580)	1:A:10:ASN:HD22	1:A:11:ALA:HB3	20	0.15
(1,1570)	1:A:8:LYS:H	1:A:8:LYS:HG2	5	0.15
(1,1570)	1:A:8:LYS:H	1:A:8:LYS:HG3	5	0.15
(1,127)	1:A:57:LEU:HD21	1:A:60:GLU:H	6	0.15
(1,127)	1:A:57:LEU:HD22	1:A:60:GLU:H	6	0.15
(1,127)	1:A:57:LEU:HD23	1:A:60:GLU:H	6	0.15
(1,1131)	1:A:45:ASP:HB2	1:A:50:GLU:H	10	0.15
(1,1086)	1:A:38:VAL:HG11	1:A:39:ASP:H	8	0.15
(1,1086)	1:A:38:VAL:HG12	1:A:39:ASP:H	8	0.15
(1,1086)	1:A:38:VAL:HG13	1:A:39:ASP:H	8	0.15
(1,101)	1:A:11:ALA:HB1	1:A:58:LYS:HG3	20	0.15
(1,101)	1:A:11:ALA:HB2	1:A:58:LYS:HG3	20	0.15
(1,101)	1:A:11:ALA:HB3	1:A:58:LYS:HG3	20	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,968)	1:A:28:LEU:H	2:B:212:PHE:HZ	7	0.14
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG21	14	0.14
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG22	14	0.14
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG23	14	0.14
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG21	18	0.14
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG22	18	0.14
(1,960)	1:A:28:LEU:H	1:A:29:THR:HG23	18	0.14
(1,774)	2:B:206:ILE:HG21	2:B:208:ILE:HD11	1	0.14
(1,774)	2:B:206:ILE:HG21	2:B:208:ILE:HD12	1	0.14
(1,774)	2:B:206:ILE:HG21	2:B:208:ILE:HD13	1	0.14
(1,774)	2:B:206:ILE:HG22	2:B:208:ILE:HD11	1	0.14
(1,774)	2:B:206:ILE:HG22	2:B:208:ILE:HD12	1	0.14
(1,774)	2:B:206:ILE:HG22	2:B:208:ILE:HD13	1	0.14
(1,774)	2:B:206:ILE:HG23	2:B:208:ILE:HD11	1	0.14
(1,774)	2:B:206:ILE:HG23	2:B:208:ILE:HD12	1	0.14
(1,774)	2:B:206:ILE:HG23	2:B:208:ILE:HD13	1	0.14
(1,709)	2:B:215:SER:HA	2:B:217:LEU:HG	14	0.14
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE1	10	0.14
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE2	10	0.14
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE3	10	0.14
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE1	10	0.14
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE2	10	0.14
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE3	10	0.14
(1,644)	1:A:59:TYR:HD1	1:A:65:THR:HA	13	0.14
(1,644)	1:A:59:TYR:HD2	1:A:65:THR:HA	13	0.14
(1,477)	1:A:97:LYS:HA	1:A:97:LYS:HE2	5	0.14
(1,428)	1:A:67:LEU:HD11	1:A:71:ASN:HD22	2	0.14
(1,428)	1:A:67:LEU:HD12	1:A:71:ASN:HD22	2	0.14
(1,428)	1:A:67:LEU:HD13	1:A:71:ASN:HD22	2	0.14
(1,428)	1:A:67:LEU:HD11	1:A:71:ASN:HD22	13	0.14
(1,428)	1:A:67:LEU:HD12	1:A:71:ASN:HD22	13	0.14
(1,428)	1:A:67:LEU:HD13	1:A:71:ASN:HD22	13	0.14
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD11	7	0.14
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD12	7	0.14
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD13	7	0.14
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD11	7	0.14
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD12	7	0.14
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD13	7	0.14
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD11	7	0.14
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD12	7	0.14
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD13	7	0.14
(1,408)	1:A:65:THR:HB	1:A:66:ILE:HD11	2	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,408)	1:A:65:THR:HB	1:A:66:ILE:HD12	2	0.14
(1,408)	1:A:65:THR:HB	1:A:66:ILE:HD13	2	0.14
(1,323)	1:A:29:THR:HG21	1:A:30:VAL:HB	4	0.14
(1,323)	1:A:29:THR:HG22	1:A:30:VAL:HB	4	0.14
(1,323)	1:A:29:THR:HG23	1:A:30:VAL:HB	4	0.14
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG11	16	0.14
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG12	16	0.14
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG13	16	0.14
(1,2214)	2:B:213:SER:HB2	2:B:214:PRO:HG2	13	0.14
(1,2214)	2:B:213:SER:HB2	2:B:214:PRO:HG3	13	0.14
(1,2214)	2:B:213:SER:HB3	2:B:214:PRO:HG2	13	0.14
(1,2214)	2:B:213:SER:HB3	2:B:214:PRO:HG3	13	0.14
(1,2090)	1:A:100:GLU:H	1:A:100:GLU:HG2	5	0.14
(1,2090)	1:A:100:GLU:H	1:A:100:GLU:HG3	5	0.14
(1,1896)	1:A:63:ARG:H	1:A:63:ARG:HG2	7	0.14
(1,1896)	1:A:63:ARG:H	1:A:63:ARG:HG3	7	0.14
(1,1894)	1:A:62:GLN:HG2	1:A:86:HIS:HE1	19	0.14
(1,1894)	1:A:62:GLN:HG3	1:A:86:HIS:HE1	19	0.14
(1,1860)	1:A:51:SER:HB2	1:A:54:PHE:H	20	0.14
(1,1860)	1:A:51:SER:HB3	1:A:54:PHE:H	20	0.14
(1,1834)	1:A:46:GLU:H	1:A:47:ASN:HD21	3	0.14
(1,1834)	1:A:46:GLU:H	1:A:47:ASN:HD22	3	0.14
(1,1472)	1:A:97:LYS:HE2	2:B:209:MET:HE1	17	0.14
(1,1472)	1:A:97:LYS:HE2	2:B:209:MET:HE2	17	0.14
(1,1472)	1:A:97:LYS:HE2	2:B:209:MET:HE3	17	0.14
(1,1396)	1:A:115:ASN:H	1:A:116:ALA:H	15	0.14
(1,1304)	1:A:76:LYS:HB3	1:A:80:ARG:H	18	0.14
(1,127)	1:A:57:LEU:HD21	1:A:60:GLU:H	4	0.14
(1,127)	1:A:57:LEU:HD22	1:A:60:GLU:H	4	0.14
(1,127)	1:A:57:LEU:HD23	1:A:60:GLU:H	4	0.14
(1,1223)	1:A:34:TYR:HD1	1:A:68:ALA:H	2	0.14
(1,1223)	1:A:34:TYR:HD2	1:A:68:ALA:H	2	0.14
(1,1181)	1:A:61:ASP:H	1:A:63:ARG:H	13	0.14
(1,1086)	1:A:38:VAL:HG11	1:A:39:ASP:H	6	0.14
(1,1086)	1:A:38:VAL:HG12	1:A:39:ASP:H	6	0.14
(1,1086)	1:A:38:VAL:HG13	1:A:39:ASP:H	6	0.14
(1,1086)	1:A:38:VAL:HG11	1:A:39:ASP:H	7	0.14
(1,1086)	1:A:38:VAL:HG12	1:A:39:ASP:H	7	0.14
(1,1086)	1:A:38:VAL:HG13	1:A:39:ASP:H	7	0.14
(1,1086)	1:A:38:VAL:HG11	1:A:39:ASP:H	9	0.14
(1,1086)	1:A:38:VAL:HG12	1:A:39:ASP:H	9	0.14
(1,1086)	1:A:38:VAL:HG13	1:A:39:ASP:H	9	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1086)	1:A:38:VAL:HG11	1:A:39:ASP:H	20	0.14
(1,1086)	1:A:38:VAL:HG12	1:A:39:ASP:H	20	0.14
(1,1086)	1:A:38:VAL:HG13	1:A:39:ASP:H	20	0.14
(1,728)	1:A:19:ASN:HB2	2:B:217:LEU:HD11	18	0.13
(1,728)	1:A:19:ASN:HB2	2:B:217:LEU:HD12	18	0.13
(1,728)	1:A:19:ASN:HB2	2:B:217:LEU:HD13	18	0.13
(1,697)	2:B:206:ILE:HD11	2:B:207:ASP:H	17	0.13
(1,697)	2:B:206:ILE:HD12	2:B:207:ASP:H	17	0.13
(1,697)	2:B:206:ILE:HD13	2:B:207:ASP:H	17	0.13
(1,664)	1:A:12:TYR:HE1	1:A:41:ILE:H	5	0.13
(1,664)	1:A:12:TYR:HE2	1:A:41:ILE:H	5	0.13
(1,553)	1:A:34:TYR:HE1	1:A:72:LEU:HG	2	0.13
(1,553)	1:A:34:TYR:HE2	1:A:72:LEU:HG	2	0.13
(1,520)	1:A:38:VAL:HG11	1:A:60:GLU:HA	1	0.13
(1,520)	1:A:38:VAL:HG12	1:A:60:GLU:HA	1	0.13
(1,520)	1:A:38:VAL:HG13	1:A:60:GLU:HA	1	0.13
(1,453)	1:A:76:LYS:H	1:A:76:LYS:HE2	14	0.13
(1,432)	1:A:68:ALA:HB1	1:A:71:ASN:HB3	7	0.13
(1,432)	1:A:68:ALA:HB2	1:A:71:ASN:HB3	7	0.13
(1,432)	1:A:68:ALA:HB3	1:A:71:ASN:HB3	7	0.13
(1,428)	1:A:67:LEU:HD11	1:A:71:ASN:HD22	18	0.13
(1,428)	1:A:67:LEU:HD12	1:A:71:ASN:HD22	18	0.13
(1,428)	1:A:67:LEU:HD13	1:A:71:ASN:HD22	18	0.13
(1,426)	1:A:34:TYR:HA	1:A:67:LEU:HD11	15	0.13
(1,426)	1:A:34:TYR:HA	1:A:67:LEU:HD12	15	0.13
(1,426)	1:A:34:TYR:HA	1:A:67:LEU:HD13	15	0.13
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD11	19	0.13
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD12	19	0.13
(1,410)	1:A:65:THR:HG21	1:A:66:ILE:HD13	19	0.13
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD11	19	0.13
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD12	19	0.13
(1,410)	1:A:65:THR:HG22	1:A:66:ILE:HD13	19	0.13
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD11	19	0.13
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD12	19	0.13
(1,410)	1:A:65:THR:HG23	1:A:66:ILE:HD13	19	0.13
(1,319)	1:A:28:LEU:HD21	2:B:212:PHE:HZ	7	0.13
(1,319)	1:A:28:LEU:HD22	2:B:212:PHE:HZ	7	0.13
(1,319)	1:A:28:LEU:HD23	2:B:212:PHE:HZ	7	0.13
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG11	6	0.13
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG12	6	0.13
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG13	6	0.13
(1,242)	1:A:40:VAL:H	1:A:41:ILE:HD11	9	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,242)	1:A:40:VAL:H	1:A:41:ILE:HD12	9	0.13
(1,242)	1:A:40:VAL:H	1:A:41:ILE:HD13	9	0.13
(1,2180)	1:A:111:VAL:HG11	1:A:113:LYS:H	20	0.13
(1,2180)	1:A:111:VAL:HG12	1:A:113:LYS:H	20	0.13
(1,2180)	1:A:111:VAL:HG13	1:A:113:LYS:H	20	0.13
(1,2180)	1:A:111:VAL:HG21	1:A:113:LYS:H	20	0.13
(1,2180)	1:A:111:VAL:HG22	1:A:113:LYS:H	20	0.13
(1,2180)	1:A:111:VAL:HG23	1:A:113:LYS:H	20	0.13
(1,2137)	1:A:105:GLU:H	1:A:106:LEU:HD11	8	0.13
(1,2137)	1:A:105:GLU:H	1:A:106:LEU:HD12	8	0.13
(1,2137)	1:A:105:GLU:H	1:A:106:LEU:HD13	8	0.13
(1,2137)	1:A:105:GLU:H	1:A:106:LEU:HD21	8	0.13
(1,2137)	1:A:105:GLU:H	1:A:106:LEU:HD22	8	0.13
(1,2137)	1:A:105:GLU:H	1:A:106:LEU:HD23	8	0.13
(1,210)	1:A:107:ASP:HA	1:A:110:ILE:HG13	7	0.13
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD11	4	0.13
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD12	4	0.13
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD13	4	0.13
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD21	4	0.13
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD22	4	0.13
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD23	4	0.13
(1,1902)	1:A:63:ARG:HD2	1:A:64:SER:H	3	0.13
(1,1902)	1:A:63:ARG:HD3	1:A:64:SER:H	3	0.13
(1,1828)	1:A:45:ASP:H	1:A:50:GLU:HG2	20	0.13
(1,1828)	1:A:45:ASP:H	1:A:50:GLU:HG3	20	0.13
(1,1760)	1:A:34:TYR:HA	1:A:67:LEU:HD11	9	0.13
(1,1760)	1:A:34:TYR:HA	1:A:67:LEU:HD12	9	0.13
(1,1760)	1:A:34:TYR:HA	1:A:67:LEU:HD13	9	0.13
(1,1760)	1:A:34:TYR:HA	1:A:67:LEU:HD21	9	0.13
(1,1760)	1:A:34:TYR:HA	1:A:67:LEU:HD22	9	0.13
(1,1760)	1:A:34:TYR:HA	1:A:67:LEU:HD23	9	0.13
(1,1738)	1:A:30:VAL:HG11	1:A:77:ILE:HG21	16	0.13
(1,1738)	1:A:30:VAL:HG11	1:A:77:ILE:HG22	16	0.13
(1,1738)	1:A:30:VAL:HG11	1:A:77:ILE:HG23	16	0.13
(1,1738)	1:A:30:VAL:HG12	1:A:77:ILE:HG21	16	0.13
(1,1738)	1:A:30:VAL:HG12	1:A:77:ILE:HG22	16	0.13
(1,1738)	1:A:30:VAL:HG12	1:A:77:ILE:HG23	16	0.13
(1,1738)	1:A:30:VAL:HG13	1:A:77:ILE:HG21	16	0.13
(1,1738)	1:A:30:VAL:HG13	1:A:77:ILE:HG22	16	0.13
(1,1738)	1:A:30:VAL:HG13	1:A:77:ILE:HG23	16	0.13
(1,1738)	1:A:30:VAL:HG21	1:A:77:ILE:HG21	16	0.13
(1,1738)	1:A:30:VAL:HG21	1:A:77:ILE:HG22	16	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1738)	1:A:30:VAL:HG21	1:A:77:ILE:HG23	16	0.13
(1,1738)	1:A:30:VAL:HG22	1:A:77:ILE:HG21	16	0.13
(1,1738)	1:A:30:VAL:HG22	1:A:77:ILE:HG22	16	0.13
(1,1738)	1:A:30:VAL:HG22	1:A:77:ILE:HG23	16	0.13
(1,1738)	1:A:30:VAL:HG23	1:A:77:ILE:HG21	16	0.13
(1,1738)	1:A:30:VAL:HG23	1:A:77:ILE:HG22	16	0.13
(1,1738)	1:A:30:VAL:HG23	1:A:77:ILE:HG23	16	0.13
(1,1657)	1:A:22:LEU:HD11	2:B:217:LEU:HA	6	0.13
(1,1657)	1:A:22:LEU:HD12	2:B:217:LEU:HA	6	0.13
(1,1657)	1:A:22:LEU:HD13	2:B:217:LEU:HA	6	0.13
(1,1657)	1:A:22:LEU:HD21	2:B:217:LEU:HA	6	0.13
(1,1657)	1:A:22:LEU:HD22	2:B:217:LEU:HA	6	0.13
(1,1657)	1:A:22:LEU:HD23	2:B:217:LEU:HA	6	0.13
(1,1654)	1:A:22:LEU:HD11	2:B:215:SER:H	18	0.13
(1,1654)	1:A:22:LEU:HD12	2:B:215:SER:H	18	0.13
(1,1654)	1:A:22:LEU:HD13	2:B:215:SER:H	18	0.13
(1,1654)	1:A:22:LEU:HD21	2:B:215:SER:H	18	0.13
(1,1654)	1:A:22:LEU:HD22	2:B:215:SER:H	18	0.13
(1,1654)	1:A:22:LEU:HD23	2:B:215:SER:H	18	0.13
(1,1566)	1:A:6:GLU:HG2	1:A:7:TYR:HE1	18	0.13
(1,1566)	1:A:6:GLU:HG2	1:A:7:TYR:HE2	18	0.13
(1,1566)	1:A:6:GLU:HG3	1:A:7:TYR:HE1	18	0.13
(1,1566)	1:A:6:GLU:HG3	1:A:7:TYR:HE2	18	0.13
(1,1509)	2:B:218:LEU:HG	2:B:219:GLU:H	6	0.13
(1,1397)	1:A:6:GLU:H	1:A:6:GLU:HG2	2	0.13
(1,135)	1:A:31:PHE:HA	1:A:57:LEU:HD11	11	0.13
(1,135)	1:A:31:PHE:HA	1:A:57:LEU:HD12	11	0.13
(1,135)	1:A:31:PHE:HA	1:A:57:LEU:HD13	11	0.13
(1,1279)	1:A:74:GLY:H	1:A:84:ILE:HD11	15	0.13
(1,1279)	1:A:74:GLY:H	1:A:84:ILE:HD12	15	0.13
(1,1279)	1:A:74:GLY:H	1:A:84:ILE:HD13	15	0.13
(1,1279)	1:A:74:GLY:H	1:A:84:ILE:HD11	18	0.13
(1,1279)	1:A:74:GLY:H	1:A:84:ILE:HD12	18	0.13
(1,1279)	1:A:74:GLY:H	1:A:84:ILE:HD13	18	0.13
(1,1220)	1:A:68:ALA:H	1:A:71:ASN:HB2	9	0.13
(1,1181)	1:A:61:ASP:H	1:A:63:ARG:H	14	0.13
(1,1166)	1:A:59:TYR:H	1:A:68:ALA:HB1	7	0.13
(1,1166)	1:A:59:TYR:H	1:A:68:ALA:HB2	7	0.13
(1,1166)	1:A:59:TYR:H	1:A:68:ALA:HB3	7	0.13
(1,1166)	1:A:59:TYR:H	1:A:68:ALA:HB1	18	0.13
(1,1166)	1:A:59:TYR:H	1:A:68:ALA:HB2	18	0.13
(1,1166)	1:A:59:TYR:H	1:A:68:ALA:HB3	18	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1086)	1:A:38:VAL:HG11	1:A:39:ASP:H	15	0.13
(1,1086)	1:A:38:VAL:HG12	1:A:39:ASP:H	15	0.13
(1,1086)	1:A:38:VAL:HG13	1:A:39:ASP:H	15	0.13
(2,35)	1:A:65:THR:O	1:A:69:VAL:H	4	0.12
(2,31)	1:A:63:ARG:O	1:A:67:LEU:H	2	0.12
(2,21)	1:A:43:SER:H	1:A:54:PHE:O	8	0.12
(1,721)	1:A:19:ASN:HB2	2:B:217:LEU:HD21	3	0.12
(1,721)	1:A:19:ASN:HB2	2:B:217:LEU:HD22	3	0.12
(1,721)	1:A:19:ASN:HB2	2:B:217:LEU:HD23	3	0.12
(1,721)	1:A:19:ASN:HB2	2:B:217:LEU:HD21	12	0.12
(1,721)	1:A:19:ASN:HB2	2:B:217:LEU:HD22	12	0.12
(1,721)	1:A:19:ASN:HB2	2:B:217:LEU:HD23	12	0.12
(1,721)	1:A:19:ASN:HB2	2:B:217:LEU:HD21	17	0.12
(1,721)	1:A:19:ASN:HB2	2:B:217:LEU:HD22	17	0.12
(1,721)	1:A:19:ASN:HB2	2:B:217:LEU:HD23	17	0.12
(1,716)	1:A:21:GLU:H	2:B:217:LEU:HD21	1	0.12
(1,716)	1:A:21:GLU:H	2:B:217:LEU:HD22	1	0.12
(1,716)	1:A:21:GLU:H	2:B:217:LEU:HD23	1	0.12
(1,709)	2:B:215:SER:HA	2:B:217:LEU:HG	2	0.12
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE1	7	0.12
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE2	7	0.12
(1,707)	1:A:98:TYR:HD1	2:B:209:MET:HE3	7	0.12
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE1	7	0.12
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE2	7	0.12
(1,707)	1:A:98:TYR:HD2	2:B:209:MET:HE3	7	0.12
(1,651)	1:A:88:PHE:HD1	1:A:89:TYR:H	14	0.12
(1,651)	1:A:88:PHE:HD2	1:A:89:TYR:H	14	0.12
(1,647)	1:A:86:HIS:H	1:A:86:HIS:HD2	2	0.12
(1,643)	1:A:59:TYR:HD1	1:A:60:GLU:HB3	15	0.12
(1,643)	1:A:59:TYR:HD2	1:A:60:GLU:HB3	15	0.12
(1,520)	1:A:38:VAL:HG11	1:A:60:GLU:HA	14	0.12
(1,520)	1:A:38:VAL:HG12	1:A:60:GLU:HA	14	0.12
(1,520)	1:A:38:VAL:HG13	1:A:60:GLU:HA	14	0.12
(1,424)	1:A:67:LEU:HD21	1:A:71:ASN:HD22	3	0.12
(1,424)	1:A:67:LEU:HD22	1:A:71:ASN:HD22	3	0.12
(1,424)	1:A:67:LEU:HD23	1:A:71:ASN:HD22	3	0.12
(1,375)	1:A:38:VAL:HG11	1:A:58:LYS:HD2	12	0.12
(1,375)	1:A:38:VAL:HG12	1:A:58:LYS:HD2	12	0.12
(1,375)	1:A:38:VAL:HG13	1:A:58:LYS:HD2	12	0.12
(1,348)	1:A:13:ILE:HG21	1:A:84:ILE:HA	11	0.12
(1,348)	1:A:13:ILE:HG22	1:A:84:ILE:HA	11	0.12
(1,348)	1:A:13:ILE:HG23	1:A:84:ILE:HA	11	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,323)	1:A:29:THR:HG21	1:A:30:VAL:HB	16	0.12
(1,323)	1:A:29:THR:HG22	1:A:30:VAL:HB	16	0.12
(1,323)	1:A:29:THR:HG23	1:A:30:VAL:HB	16	0.12
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG11	12	0.12
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG12	12	0.12
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG13	12	0.12
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG11	13	0.12
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG12	13	0.12
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG13	13	0.12
(1,267)	1:A:18:LEU:HD11	1:A:27:ILE:H	9	0.12
(1,267)	1:A:18:LEU:HD12	1:A:27:ILE:H	9	0.12
(1,267)	1:A:18:LEU:HD13	1:A:27:ILE:H	9	0.12
(1,242)	1:A:40:VAL:H	1:A:41:ILE:HD11	1	0.12
(1,242)	1:A:40:VAL:H	1:A:41:ILE:HD12	1	0.12
(1,242)	1:A:40:VAL:H	1:A:41:ILE:HD13	1	0.12
(1,242)	1:A:40:VAL:H	1:A:41:ILE:HD11	8	0.12
(1,242)	1:A:40:VAL:H	1:A:41:ILE:HD12	8	0.12
(1,242)	1:A:40:VAL:H	1:A:41:ILE:HD13	8	0.12
(1,2241)	2:B:219:GLU:H	2:B:220:LEU:HD11	9	0.12
(1,2241)	2:B:219:GLU:H	2:B:220:LEU:HD12	9	0.12
(1,2241)	2:B:219:GLU:H	2:B:220:LEU:HD13	9	0.12
(1,2241)	2:B:219:GLU:H	2:B:220:LEU:HD21	9	0.12
(1,2241)	2:B:219:GLU:H	2:B:220:LEU:HD22	9	0.12
(1,2241)	2:B:219:GLU:H	2:B:220:LEU:HD23	9	0.12
(1,2210)	2:B:211:ASP:HB2	2:B:213:SER:H	7	0.12
(1,2210)	2:B:211:ASP:HB3	2:B:213:SER:H	7	0.12
(1,2185)	1:A:113:LYS:H	1:A:113:LYS:HG2	10	0.12
(1,2185)	1:A:113:LYS:H	1:A:113:LYS:HG3	10	0.12
(1,2185)	1:A:113:LYS:H	1:A:113:LYS:HG2	12	0.12
(1,2185)	1:A:113:LYS:H	1:A:113:LYS:HG3	12	0.12
(1,2182)	1:A:112:SER:H	1:A:113:LYS:HG2	10	0.12
(1,2182)	1:A:112:SER:H	1:A:113:LYS:HG3	10	0.12
(1,2180)	1:A:111:VAL:HG11	1:A:113:LYS:H	16	0.12
(1,2180)	1:A:111:VAL:HG12	1:A:113:LYS:H	16	0.12
(1,2180)	1:A:111:VAL:HG13	1:A:113:LYS:H	16	0.12
(1,2180)	1:A:111:VAL:HG21	1:A:113:LYS:H	16	0.12
(1,2180)	1:A:111:VAL:HG22	1:A:113:LYS:H	16	0.12
(1,2180)	1:A:111:VAL:HG23	1:A:113:LYS:H	16	0.12
(1,2180)	1:A:111:VAL:HG11	1:A:113:LYS:H	19	0.12
(1,2180)	1:A:111:VAL:HG12	1:A:113:LYS:H	19	0.12
(1,2180)	1:A:111:VAL:HG13	1:A:113:LYS:H	19	0.12
(1,2180)	1:A:111:VAL:HG21	1:A:113:LYS:H	19	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2180)	1:A:111:VAL:HG22	1:A:113:LYS:H	19	0.12
(1,2180)	1:A:111:VAL:HG23	1:A:113:LYS:H	19	0.12
(1,2090)	1:A:100:GLU:H	1:A:100:GLU:HG2	4	0.12
(1,2090)	1:A:100:GLU:H	1:A:100:GLU:HG3	4	0.12
(1,2079)	1:A:97:LYS:HE2	2:B:209:MET:HE1	5	0.12
(1,2079)	1:A:97:LYS:HE2	2:B:209:MET:HE2	5	0.12
(1,2079)	1:A:97:LYS:HE2	2:B:209:MET:HE3	5	0.12
(1,2079)	1:A:97:LYS:HE3	2:B:209:MET:HE1	5	0.12
(1,2079)	1:A:97:LYS:HE3	2:B:209:MET:HE2	5	0.12
(1,2079)	1:A:97:LYS:HE3	2:B:209:MET:HE3	5	0.12
(1,20)	1:A:30:VAL:HB	1:A:77:ILE:HD11	13	0.12
(1,20)	1:A:30:VAL:HB	1:A:77:ILE:HD12	13	0.12
(1,20)	1:A:30:VAL:HB	1:A:77:ILE:HD13	13	0.12
(1,1878)	1:A:60:GLU:HG2	1:A:61:ASP:H	5	0.12
(1,1878)	1:A:60:GLU:HG3	1:A:61:ASP:H	5	0.12
(1,1803)	1:A:40:VAL:HG11	2:B:212:PHE:HZ	7	0.12
(1,1803)	1:A:40:VAL:HG12	2:B:212:PHE:HZ	7	0.12
(1,1803)	1:A:40:VAL:HG13	2:B:212:PHE:HZ	7	0.12
(1,1803)	1:A:40:VAL:HG21	2:B:212:PHE:HZ	7	0.12
(1,1803)	1:A:40:VAL:HG22	2:B:212:PHE:HZ	7	0.12
(1,1803)	1:A:40:VAL:HG23	2:B:212:PHE:HZ	7	0.12
(1,1383)	1:A:109:ASP:H	1:A:109:ASP:HB3	2	0.12
(1,1372)	1:A:77:ILE:HB	1:A:80:ARG:H	17	0.12
(1,127)	1:A:57:LEU:HD21	1:A:60:GLU:H	16	0.12
(1,127)	1:A:57:LEU:HD22	1:A:60:GLU:H	16	0.12
(1,127)	1:A:57:LEU:HD23	1:A:60:GLU:H	16	0.12
(1,127)	1:A:57:LEU:HD21	1:A:60:GLU:H	17	0.12
(1,127)	1:A:57:LEU:HD22	1:A:60:GLU:H	17	0.12
(1,127)	1:A:57:LEU:HD23	1:A:60:GLU:H	17	0.12
(1,1161)	1:A:11:ALA:HB1	1:A:59:TYR:H	5	0.12
(1,1161)	1:A:11:ALA:HB2	1:A:59:TYR:H	5	0.12
(1,1161)	1:A:11:ALA:HB3	1:A:59:TYR:H	5	0.12
(1,1086)	1:A:38:VAL:HG11	1:A:39:ASP:H	1	0.12
(1,1086)	1:A:38:VAL:HG12	1:A:39:ASP:H	1	0.12
(1,1086)	1:A:38:VAL:HG13	1:A:39:ASP:H	1	0.12
(1,101)	1:A:11:ALA:HB1	1:A:58:LYS:HG3	2	0.12
(1,101)	1:A:11:ALA:HB2	1:A:58:LYS:HG3	2	0.12
(1,101)	1:A:11:ALA:HB3	1:A:58:LYS:HG3	2	0.12
(1,101)	1:A:11:ALA:HB1	1:A:58:LYS:HG3	13	0.12
(1,101)	1:A:11:ALA:HB2	1:A:58:LYS:HG3	13	0.12
(1,101)	1:A:11:ALA:HB3	1:A:58:LYS:HG3	13	0.12
(2,35)	1:A:65:THR:O	1:A:69:VAL:H	11	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,31)	1:A:63:ARG:O	1:A:67:LEU:H	11	0.11
(2,27)	1:A:27:ILE:O	1:A:31:PHE:H	2	0.11
(2,11)	1:A:15:ILE:O	1:A:55:ALA:H	5	0.11
(2,11)	1:A:15:ILE:O	1:A:55:ALA:H	18	0.11
(2,11)	1:A:15:ILE:O	1:A:55:ALA:H	20	0.11
(1,934)	1:A:41:ILE:H	1:A:57:LEU:HB2	12	0.11
(1,794)	1:A:23:THR:HG21	2:B:215:SER:HA	19	0.11
(1,794)	1:A:23:THR:HG22	2:B:215:SER:HA	19	0.11
(1,794)	1:A:23:THR:HG23	2:B:215:SER:HA	19	0.11
(1,709)	2:B:215:SER:HA	2:B:217:LEU:HG	20	0.11
(1,701)	1:A:101:ALA:HA	2:B:209:MET:HE1	14	0.11
(1,701)	1:A:101:ALA:HA	2:B:209:MET:HE2	14	0.11
(1,701)	1:A:101:ALA:HA	2:B:209:MET:HE3	14	0.11
(1,644)	1:A:59:TYR:HD1	1:A:65:THR:HA	16	0.11
(1,644)	1:A:59:TYR:HD2	1:A:65:THR:HA	16	0.11
(1,553)	1:A:34:TYR:HE1	1:A:72:LEU:HG	12	0.11
(1,553)	1:A:34:TYR:HE2	1:A:72:LEU:HG	12	0.11
(1,521)	1:A:38:VAL:HG21	1:A:60:GLU:HB2	14	0.11
(1,521)	1:A:38:VAL:HG22	1:A:60:GLU:HB2	14	0.11
(1,521)	1:A:38:VAL:HG23	1:A:60:GLU:HB2	14	0.11
(1,426)	1:A:34:TYR:HA	1:A:67:LEU:HD11	17	0.11
(1,426)	1:A:34:TYR:HA	1:A:67:LEU:HD12	17	0.11
(1,426)	1:A:34:TYR:HA	1:A:67:LEU:HD13	17	0.11
(1,424)	1:A:67:LEU:HD21	1:A:71:ASN:HD22	17	0.11
(1,424)	1:A:67:LEU:HD22	1:A:71:ASN:HD22	17	0.11
(1,424)	1:A:67:LEU:HD23	1:A:71:ASN:HD22	17	0.11
(1,415)	1:A:58:LYS:HA	1:A:65:THR:HG21	17	0.11
(1,415)	1:A:58:LYS:HA	1:A:65:THR:HG22	17	0.11
(1,415)	1:A:58:LYS:HA	1:A:65:THR:HG23	17	0.11
(1,393)	1:A:47:ASN:HB3	1:A:48:THR:HG21	15	0.11
(1,393)	1:A:47:ASN:HB3	1:A:48:THR:HG22	15	0.11
(1,393)	1:A:47:ASN:HB3	1:A:48:THR:HG23	15	0.11
(1,36)	1:A:76:LYS:HE3	1:A:81:ALA:HB1	2	0.11
(1,36)	1:A:76:LYS:HE3	1:A:81:ALA:HB2	2	0.11
(1,36)	1:A:76:LYS:HE3	1:A:81:ALA:HB3	2	0.11
(1,334)	1:A:13:ILE:HB	1:A:15:ILE:HD11	8	0.11
(1,334)	1:A:13:ILE:HB	1:A:15:ILE:HD12	8	0.11
(1,334)	1:A:13:ILE:HB	1:A:15:ILE:HD13	8	0.11
(1,334)	1:A:13:ILE:HB	1:A:15:ILE:HD11	10	0.11
(1,334)	1:A:13:ILE:HB	1:A:15:ILE:HD12	10	0.11
(1,334)	1:A:13:ILE:HB	1:A:15:ILE:HD13	10	0.11
(1,334)	1:A:13:ILE:HB	1:A:15:ILE:HD11	19	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,334)	1:A:13:ILE:HB	1:A:15:ILE:HD12	19	0.11
(1,334)	1:A:13:ILE:HB	1:A:15:ILE:HD13	19	0.11
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG11	4	0.11
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG12	4	0.11
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG13	4	0.11
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG11	5	0.11
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG12	5	0.11
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG13	5	0.11
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG11	9	0.11
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG12	9	0.11
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG13	9	0.11
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG11	17	0.11
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG12	17	0.11
(1,284)	1:A:29:THR:H	1:A:30:VAL:HG13	17	0.11
(1,2253)	2:B:221:GLU:H	2:B:221:GLU:HG2	8	0.11
(1,2253)	2:B:221:GLU:H	2:B:221:GLU:HG3	8	0.11
(1,2171)	1:A:110:ILE:H	1:A:110:ILE:HG12	7	0.11
(1,2171)	1:A:110:ILE:H	1:A:110:ILE:HG13	7	0.11
(1,2090)	1:A:100:GLU:H	1:A:100:GLU:HG2	9	0.11
(1,2090)	1:A:100:GLU:H	1:A:100:GLU:HG3	9	0.11
(1,2005)	1:A:80:ARG:HD2	1:A:81:ALA:H	17	0.11
(1,2005)	1:A:80:ARG:HD3	1:A:81:ALA:H	17	0.11
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD11	11	0.11
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD12	11	0.11
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD13	11	0.11
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD21	11	0.11
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD22	11	0.11
(1,1994)	1:A:77:ILE:HG12	2:B:218:LEU:HD23	11	0.11
(1,1981)	1:A:76:LYS:HD2	1:A:81:ALA:H	11	0.11
(1,1981)	1:A:76:LYS:HD3	1:A:81:ALA:H	11	0.11
(1,1894)	1:A:62:GLN:HG2	1:A:86:HIS:HE1	17	0.11
(1,1894)	1:A:62:GLN:HG3	1:A:86:HIS:HE1	17	0.11
(1,1878)	1:A:60:GLU:HG2	1:A:61:ASP:H	8	0.11
(1,1878)	1:A:60:GLU:HG3	1:A:61:ASP:H	8	0.11
(1,1878)	1:A:60:GLU:HG2	1:A:61:ASP:H	19	0.11
(1,1878)	1:A:60:GLU:HG3	1:A:61:ASP:H	19	0.11
(1,1860)	1:A:51:SER:HB2	1:A:54:PHE:H	6	0.11
(1,1860)	1:A:51:SER:HB3	1:A:54:PHE:H	6	0.11
(1,1829)	1:A:45:ASP:HA	1:A:46:GLU:HG2	19	0.11
(1,1829)	1:A:45:ASP:HA	1:A:46:GLU:HG3	19	0.11
(1,1828)	1:A:45:ASP:H	1:A:50:GLU:HG2	8	0.11
(1,1828)	1:A:45:ASP:H	1:A:50:GLU:HG3	8	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1705)	1:A:28:LEU:HD11	1:A:37:PRO:HG2	15	0.11
(1,1705)	1:A:28:LEU:HD11	1:A:37:PRO:HG3	15	0.11
(1,1705)	1:A:28:LEU:HD12	1:A:37:PRO:HG2	15	0.11
(1,1705)	1:A:28:LEU:HD12	1:A:37:PRO:HG3	15	0.11
(1,1705)	1:A:28:LEU:HD13	1:A:37:PRO:HG2	15	0.11
(1,1705)	1:A:28:LEU:HD13	1:A:37:PRO:HG3	15	0.11
(1,1705)	1:A:28:LEU:HD21	1:A:37:PRO:HG2	15	0.11
(1,1705)	1:A:28:LEU:HD21	1:A:37:PRO:HG3	15	0.11
(1,1705)	1:A:28:LEU:HD22	1:A:37:PRO:HG2	15	0.11
(1,1705)	1:A:28:LEU:HD22	1:A:37:PRO:HG3	15	0.11
(1,1705)	1:A:28:LEU:HD23	1:A:37:PRO:HG2	15	0.11
(1,1705)	1:A:28:LEU:HD23	1:A:37:PRO:HG3	15	0.11
(1,1500)	2:B:220:LEU:HD21	2:B:221:GLU:H	5	0.11
(1,1500)	2:B:220:LEU:HD22	2:B:221:GLU:H	5	0.11
(1,1500)	2:B:220:LEU:HD23	2:B:221:GLU:H	5	0.11
(1,1441)	1:A:101:ALA:HB1	2:B:211:ASP:H	7	0.11
(1,1441)	1:A:101:ALA:HB2	2:B:211:ASP:H	7	0.11
(1,1441)	1:A:101:ALA:HB3	2:B:211:ASP:H	7	0.11
(1,1422)	1:A:46:GLU:H	1:A:52:GLN:HE21	1	0.11
(1,140)	1:A:39:ASP:H	1:A:57:LEU:HD11	10	0.11
(1,140)	1:A:39:ASP:H	1:A:57:LEU:HD12	10	0.11
(1,140)	1:A:39:ASP:H	1:A:57:LEU:HD13	10	0.11
(1,1388)	1:A:111:VAL:H	1:A:112:SER:H	12	0.11
(1,135)	1:A:31:PHE:HA	1:A:57:LEU:HD11	2	0.11
(1,135)	1:A:31:PHE:HA	1:A:57:LEU:HD12	2	0.11
(1,135)	1:A:31:PHE:HA	1:A:57:LEU:HD13	2	0.11
(1,1345)	1:A:41:ILE:HG21	1:A:99:TYR:H	5	0.11
(1,1345)	1:A:41:ILE:HG22	1:A:99:TYR:H	5	0.11
(1,1345)	1:A:41:ILE:HG23	1:A:99:TYR:H	5	0.11
(1,1279)	1:A:74:GLY:H	1:A:84:ILE:HD11	8	0.11
(1,1279)	1:A:74:GLY:H	1:A:84:ILE:HD12	8	0.11
(1,1279)	1:A:74:GLY:H	1:A:84:ILE:HD13	8	0.11
(1,127)	1:A:57:LEU:HD21	1:A:60:GLU:H	3	0.11
(1,127)	1:A:57:LEU:HD22	1:A:60:GLU:H	3	0.11
(1,127)	1:A:57:LEU:HD23	1:A:60:GLU:H	3	0.11
(1,1219)	1:A:68:ALA:H	1:A:71:ASN:HB3	1	0.11
(1,1219)	1:A:68:ALA:H	1:A:71:ASN:HB3	7	0.11
(1,1168)	1:A:58:LYS:HE3	1:A:59:TYR:H	4	0.11
(1,1167)	1:A:58:LYS:HE2	1:A:59:TYR:H	17	0.11
(1,1161)	1:A:11:ALA:HB1	1:A:59:TYR:H	1	0.11
(1,1161)	1:A:11:ALA:HB2	1:A:59:TYR:H	1	0.11
(1,1161)	1:A:11:ALA:HB3	1:A:59:TYR:H	1	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1086)	1:A:38:VAL:HG11	1:A:39:ASP:H	5	0.11
(1,1086)	1:A:38:VAL:HG12	1:A:39:ASP:H	5	0.11
(1,1086)	1:A:38:VAL:HG13	1:A:39:ASP:H	5	0.11
(1,1086)	1:A:38:VAL:HG11	1:A:39:ASP:H	10	0.11
(1,1086)	1:A:38:VAL:HG12	1:A:39:ASP:H	10	0.11
(1,1086)	1:A:38:VAL:HG13	1:A:39:ASP:H	10	0.11
(1,1086)	1:A:38:VAL:HG11	1:A:39:ASP:H	18	0.11
(1,1086)	1:A:38:VAL:HG12	1:A:39:ASP:H	18	0.11
(1,1086)	1:A:38:VAL:HG13	1:A:39:ASP:H	18	0.11

10 Dihedral-angle violation analysis (i)

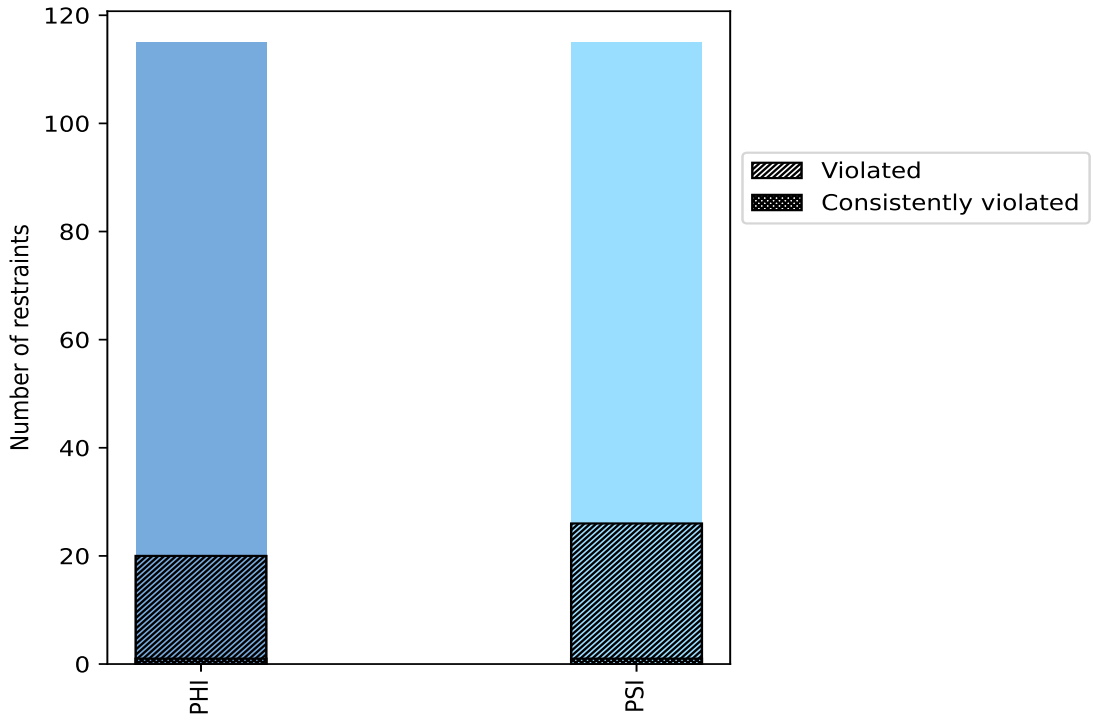
10.1 Summary of dihedral-angle violations (i)

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

Angle type	Count	%[1]	Violated[3]			Consistently Violated[4]		
			Count	%[2]	%[1]	Count	%[2]	%[1]
PHI	115	50.0	20	17.4	8.7	1	0.9	0.4
PSI	115	50.0	26	22.6	11.3	1	0.9	0.4
Total	230	100.0	46	20.0	20.0	2	0.9	0.9

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

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



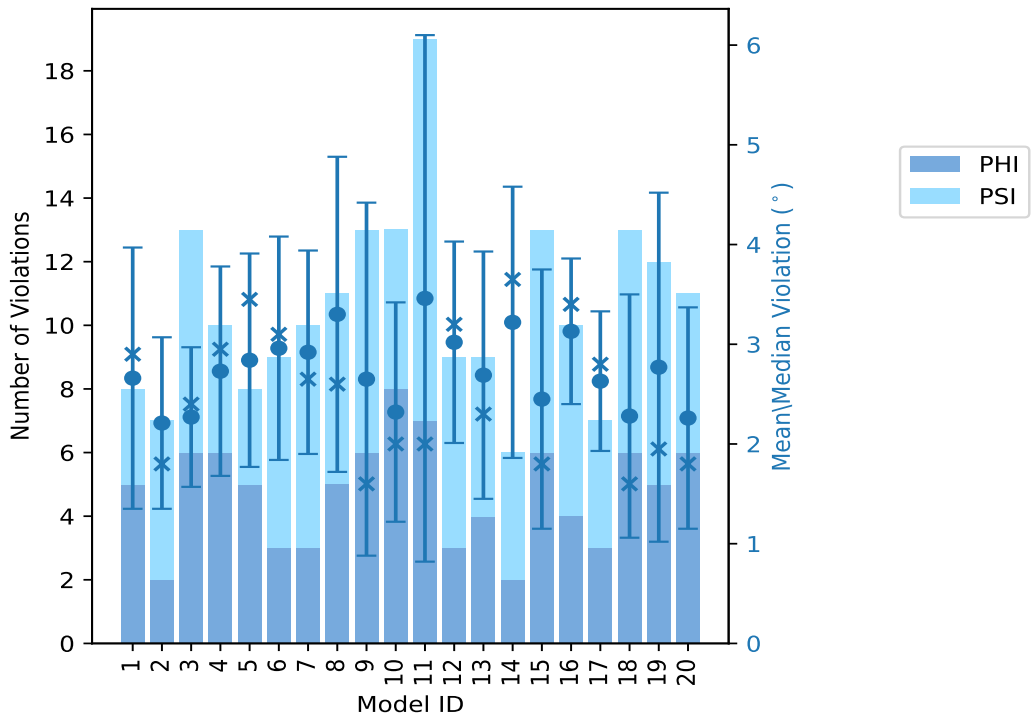
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

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

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

Model ID	Number of violations			Mean (°)	Max (°)	SD (°)	Median (°)
	PHI	PSI	Total				
1	5	3	8	2.66	4.7	1.31	2.9
2	2	5	7	2.21	3.6	0.86	1.8
3	6	7	13	2.27	3.4	0.7	2.4
4	6	4	10	2.73	4.1	1.05	2.95
5	5	3	8	2.84	3.9	1.07	3.45
6	3	6	9	2.96	4.7	1.12	3.1
7	3	7	10	2.92	4.5	1.02	2.65
8	5	6	11	3.3	6.6	1.58	2.6
9	6	7	13	2.65	6.4	1.77	1.6
10	8	5	13	2.32	5.0	1.1	2.0
11	7	12	19	3.46	10.1	2.64	2.0
12	3	6	9	3.02	4.5	1.01	3.2
13	4	5	9	2.69	4.6	1.24	2.3
14	2	4	6	3.22	4.7	1.36	3.65
15	6	7	13	2.45	5.4	1.3	1.8
16	4	6	10	3.13	3.8	0.73	3.4
17	3	4	7	2.63	3.5	0.7	2.8
18	6	7	13	2.28	4.7	1.22	1.6
19	5	7	12	2.77	6.0	1.75	1.95
20	6	5	11	2.26	4.2	1.11	1.8

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



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

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

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

Number of violated restraints			Fraction of the ensemble	
PHI	PSI	Total	Count[1]	%
10	12	22	1	5.0
1	3	4	2	10.0
2	2	4	3	15.0
2	3	5	4	20.0
1	0	1	5	25.0
0	0	0	6	30.0
0	0	0	7	35.0
0	2	2	8	40.0
0	0	0	9	45.0
0	0	0	10	50.0
0	0	0	11	55.0

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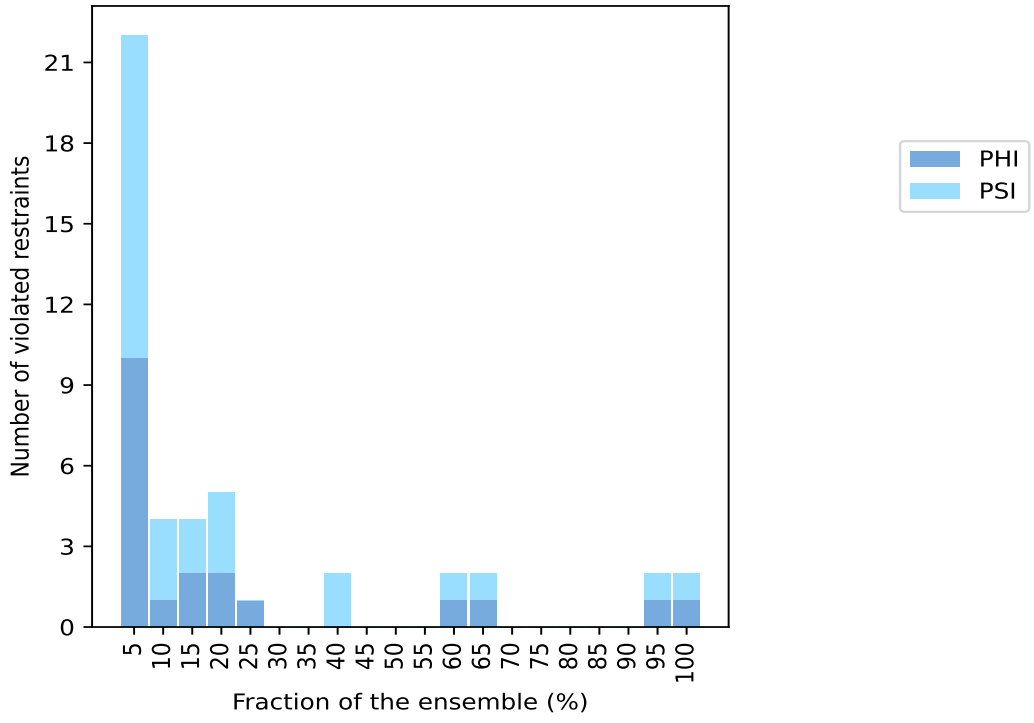
Number of violated restraints			Fraction of the ensemble	
PHI	PSI	Total	Count[1]	%
1	1	2	12	60.0
1	1	2	13	65.0
0	0	0	14	70.0
0	0	0	15	75.0
0	0	0	16	80.0
0	0	0	17	85.0
0	0	0	18	90.0
1	1	2	19	95.0
1	1	2	20	100.0

[1] Number of models with violations

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

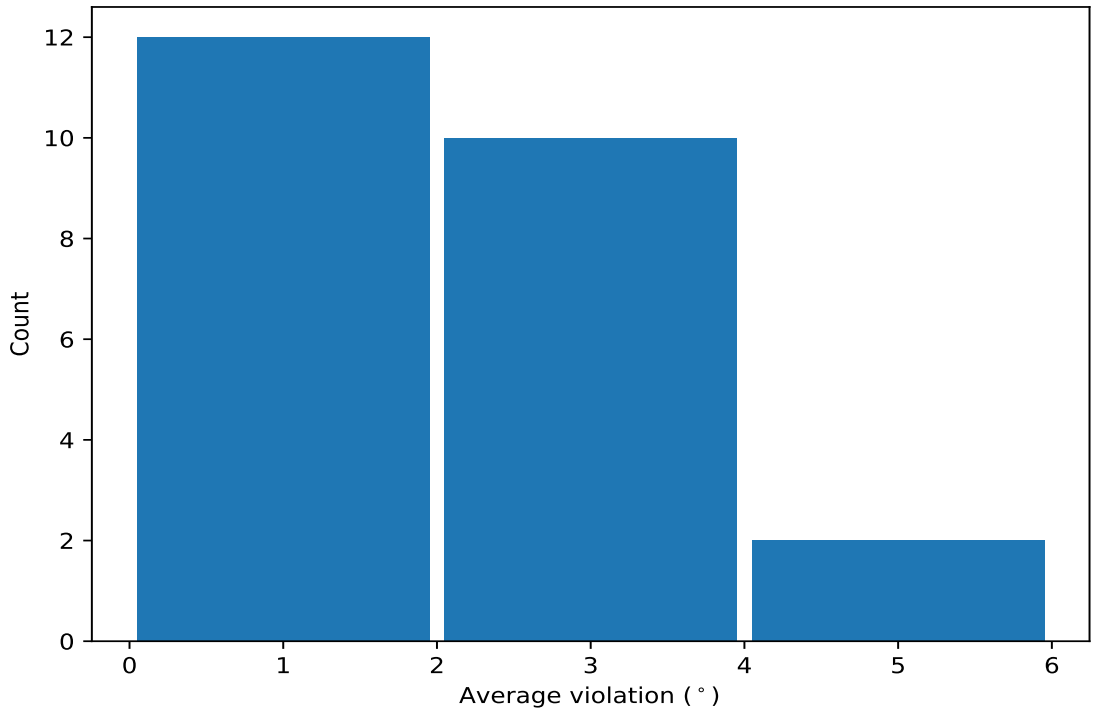


10.4 Most violated dihedral-angle restraints in the ensemble (i)

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

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

in the ensemble



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

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

Key	Atom-1	Atom-2	Atom-3	Atom-4	Models[1]	Mean	SD[2]	Median
(1,92)	1:A:38:VAL:N	1:A:38:VAL:CA	1:A:38:VAL:C	1:A:39:ASP:N	20	3.63	0.75	3.5
(1,51)	1:A:15:ILE:C	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	20	3.03	0.69	3.15
(1,132)	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	1:A:61:ASP:N	19	4.33	0.98	4.3
(1,133)	1:A:60:GLU:C	1:A:61:ASP:N	1:A:61:ASP:CA	1:A:61:ASP:C	19	3.98	1.18	4.3
(1,42)	1:A:11:ALA:N	1:A:11:ALA:CA	1:A:11:ALA:C	1:A:12:TYR:N	13	2.16	0.81	2.1
(1,131)	1:A:59:TYR:C	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	13	2.09	0.77	2.0
(1,18)	2:B:212:PHE:N	2:B:212:PHE:CA	2:B:212:PHE:C	2:B:213:SER:N	12	3.04	1.43	2.9
(1,19)	2:B:212:PHE:C	2:B:213:SER:N	2:B:213:SER:CA	2:B:213:SER:C	12	2.68	0.82	2.5
(1,52)	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	1:A:17:ASN:N	8	1.86	0.56	1.75
(1,186)	1:A:87:THR:N	1:A:87:THR:CA	1:A:87:THR:C	1:A:88:PHE:N	8	1.64	0.41	1.45
(1,107)	1:A:45:ASP:C	1:A:46:GLU:N	1:A:46:GLU:CA	1:A:46:GLU:C	5	1.6	0.3	1.6
(1,113)	1:A:49:GLY:C	1:A:50:GLU:N	1:A:50:GLU:CA	1:A:50:GLU:C	4	2.05	1.09	1.6
(1,22)	2:B:215:SER:N	2:B:215:SER:CA	2:B:215:SER:C	2:B:216:GLY:N	4	1.82	0.84	1.5
(1,7)	2:B:204:GLN:C	2:B:205:TYR:N	2:B:205:TYR:CA	2:B:205:TYR:C	4	1.58	0.5	1.4
(1,194)	1:A:92:LYS:N	1:A:92:LYS:CA	1:A:92:LYS:C	1:A:93:ARG:N	4	1.35	0.15	1.3
(1,12)	2:B:207:ASP:N	2:B:207:ASP:CA	2:B:207:ASP:C	2:B:208:ILE:N	4	1.18	0.08	1.15
(1,88)	1:A:35:GLY:N	1:A:35:GLY:CA	1:A:35:GLY:C	1:A:36:VAL:N	3	4.2	4.17	1.3
(1,20)	2:B:213:SER:N	2:B:213:SER:CA	2:B:213:SER:C	2:B:214:PRO:N	3	2.1	0.14	2.0
(1,119)	1:A:53:GLY:C	1:A:54:PHE:N	1:A:54:PHE:CA	1:A:54:PHE:C	3	2.03	0.65	2.1
(1,35)	1:A:5:ASN:C	1:A:6:GLU:N	1:A:6:GLU:CA	1:A:6:GLU:C	3	1.3	0.22	1.2

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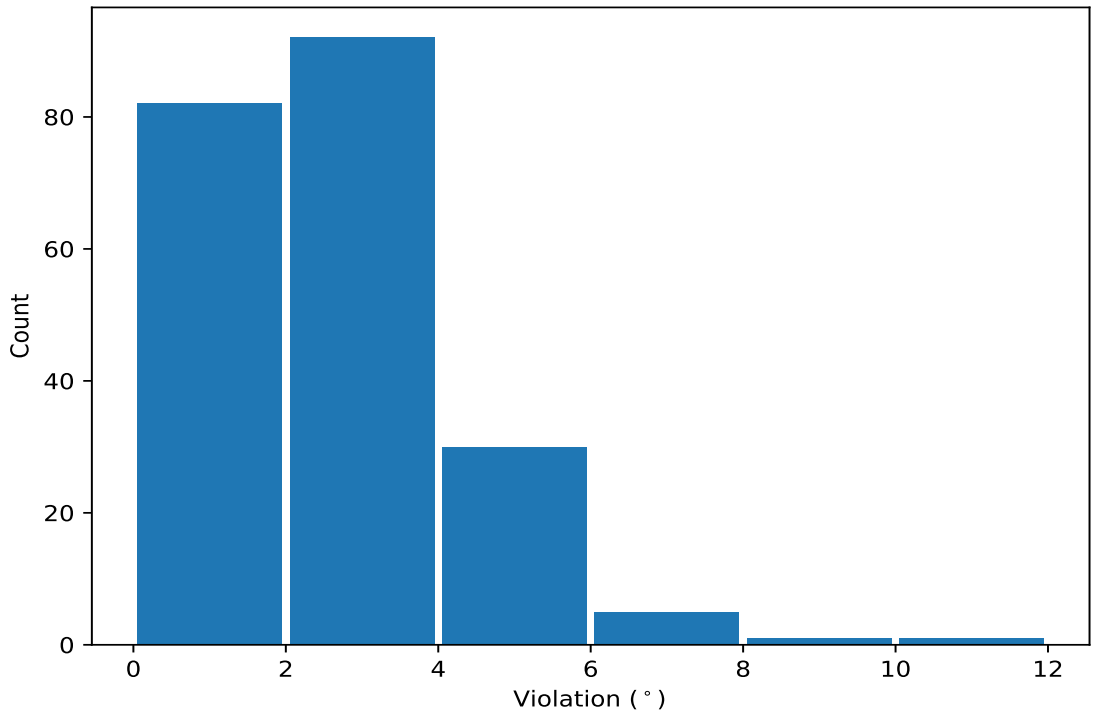
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models[1]	Mean	SD[2]	Median
(1,10)	2:B:206:ILE:N	2:B:206:ILE:CA	2:B:206:ILE:C	2:B:207:ASP:N	2	1.6	0.0	1.6
(1,90)	1:A:36:VAL:N	1:A:36:VAL:CA	1:A:36:VAL:C	1:A:37:PRO:N	2	1.6	0.1	1.6
(1,158)	1:A:73:ASN:N	1:A:73:ASN:CA	1:A:73:ASN:C	1:A:74:GLY:N	2	1.55	0.25	1.55
(1,27)	2:B:218:LEU:C	2:B:219:GLU:N	2:B:219:GLU:CA	2:B:219:GLU:C	2	1.4	0.3	1.4

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

10.5 All violated dihedral-angle restraints (i)

10.5.1 Histogram : Distribution of violations (i)

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



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

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

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,88)	1:A:35:GLY:N	1:A:35:GLY:CA	1:A:35:GLY:C	1:A:36:VAL:N	11	10.1
(1,87)	1:A:34:TYR:C	1:A:35:GLY:N	1:A:35:GLY:CA	1:A:35:GLY:C	11	8.7
(1,18)	2:B:212:PHE:N	2:B:212:PHE:CA	2:B:212:PHE:C	2:B:213:SER:N	8	6.6

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,86)	1:A:34:TYR:N	1:A:34:TYR:CA	1:A:34:TYR:C	1:A:35:GLY:N	11	6.4
(1,132)	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	1:A:61:ASP:N	9	6.4
(1,89)	1:A:35:GLY:C	1:A:36:VAL:N	1:A:36:VAL:CA	1:A:36:VAL:C	11	6.0
(1,133)	1:A:60:GLU:C	1:A:61:ASP:N	1:A:61:ASP:CA	1:A:61:ASP:C	19	6.0
(1,132)	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	1:A:61:ASP:N	19	5.8
(1,133)	1:A:60:GLU:C	1:A:61:ASP:N	1:A:61:ASP:CA	1:A:61:ASP:C	9	5.7
(1,132)	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	1:A:61:ASP:N	8	5.6
(1,92)	1:A:38:VAL:N	1:A:38:VAL:CA	1:A:38:VAL:C	1:A:39:ASP:N	11	5.5
(1,133)	1:A:60:GLU:C	1:A:61:ASP:N	1:A:61:ASP:CA	1:A:61:ASP:C	15	5.4
(1,132)	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	1:A:61:ASP:N	10	5.0
(1,92)	1:A:38:VAL:N	1:A:38:VAL:CA	1:A:38:VAL:C	1:A:39:ASP:N	19	4.9
(1,133)	1:A:60:GLU:C	1:A:61:ASP:N	1:A:61:ASP:CA	1:A:61:ASP:C	1	4.7
(1,133)	1:A:60:GLU:C	1:A:61:ASP:N	1:A:61:ASP:CA	1:A:61:ASP:C	14	4.7
(1,132)	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	1:A:61:ASP:N	6	4.7
(1,132)	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	1:A:61:ASP:N	18	4.7
(1,133)	1:A:60:GLU:C	1:A:61:ASP:N	1:A:61:ASP:CA	1:A:61:ASP:C	13	4.6
(1,133)	1:A:60:GLU:C	1:A:61:ASP:N	1:A:61:ASP:CA	1:A:61:ASP:C	8	4.5
(1,133)	1:A:60:GLU:C	1:A:61:ASP:N	1:A:61:ASP:CA	1:A:61:ASP:C	11	4.5
(1,132)	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	1:A:61:ASP:N	7	4.5
(1,132)	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	1:A:61:ASP:N	12	4.5
(1,132)	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	1:A:61:ASP:N	13	4.5
(1,92)	1:A:38:VAL:N	1:A:38:VAL:CA	1:A:38:VAL:C	1:A:39:ASP:N	14	4.4
(1,133)	1:A:60:GLU:C	1:A:61:ASP:N	1:A:61:ASP:CA	1:A:61:ASP:C	7	4.3
(1,133)	1:A:60:GLU:C	1:A:61:ASP:N	1:A:61:ASP:CA	1:A:61:ASP:C	12	4.3
(1,132)	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	1:A:61:ASP:N	14	4.3
(1,132)	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	1:A:61:ASP:N	15	4.3
(1,92)	1:A:38:VAL:N	1:A:38:VAL:CA	1:A:38:VAL:C	1:A:39:ASP:N	7	4.2
(1,132)	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	1:A:61:ASP:N	11	4.2
(1,132)	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	1:A:61:ASP:N	20	4.2
(1,92)	1:A:38:VAL:N	1:A:38:VAL:CA	1:A:38:VAL:C	1:A:39:ASP:N	15	4.1
(1,51)	1:A:15:ILE:C	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	20	4.1
(1,18)	2:B:212:PHE:N	2:B:212:PHE:CA	2:B:212:PHE:C	2:B:213:SER:N	4	4.1
(1,92)	1:A:38:VAL:N	1:A:38:VAL:CA	1:A:38:VAL:C	1:A:39:ASP:N	13	4.0
(1,133)	1:A:60:GLU:C	1:A:61:ASP:N	1:A:61:ASP:CA	1:A:61:ASP:C	6	4.0
(1,92)	1:A:38:VAL:N	1:A:38:VAL:CA	1:A:38:VAL:C	1:A:39:ASP:N	5	3.9
(1,92)	1:A:38:VAL:N	1:A:38:VAL:CA	1:A:38:VAL:C	1:A:39:ASP:N	9	3.9
(1,51)	1:A:15:ILE:C	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	1	3.9
(1,132)	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	1:A:61:ASP:N	4	3.9
(1,113)	1:A:49:GLY:C	1:A:50:GLU:N	1:A:50:GLU:CA	1:A:50:GLU:C	9	3.9
(1,42)	1:A:11:ALA:N	1:A:11:ALA:CA	1:A:11:ALA:C	1:A:12:TYR:N	16	3.8
(1,18)	2:B:212:PHE:N	2:B:212:PHE:CA	2:B:212:PHE:C	2:B:213:SER:N	6	3.8
(1,18)	2:B:212:PHE:N	2:B:212:PHE:CA	2:B:212:PHE:C	2:B:213:SER:N	16	3.8
(1,133)	1:A:60:GLU:C	1:A:61:ASP:N	1:A:61:ASP:CA	1:A:61:ASP:C	18	3.8
(1,132)	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	1:A:61:ASP:N	5	3.8
(1,132)	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	1:A:61:ASP:N	16	3.8
(1,51)	1:A:15:ILE:C	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	18	3.7
(1,19)	2:B:212:PHE:C	2:B:213:SER:N	2:B:213:SER:CA	2:B:213:SER:C	4	3.7
(1,19)	2:B:212:PHE:C	2:B:213:SER:N	2:B:213:SER:CA	2:B:213:SER:C	12	3.7
(1,92)	1:A:38:VAL:N	1:A:38:VAL:CA	1:A:38:VAL:C	1:A:39:ASP:N	16	3.6
(1,51)	1:A:15:ILE:C	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	2	3.6
(1,51)	1:A:15:ILE:C	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	5	3.6

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,51)	1:A:15:ILE:C	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	9	3.6
(1,19)	2:B:212:PHE:C	2:B:213:SER:N	2:B:213:SER:CA	2:B:213:SER:C	8	3.6
(1,19)	2:B:212:PHE:C	2:B:213:SER:N	2:B:213:SER:CA	2:B:213:SER:C	16	3.6
(1,133)	1:A:60:GLU:C	1:A:61:ASP:N	1:A:61:ASP:CA	1:A:61:ASP:C	10	3.6
(1,92)	1:A:38:VAL:N	1:A:38:VAL:CA	1:A:38:VAL:C	1:A:39:ASP:N	1	3.5
(1,92)	1:A:38:VAL:N	1:A:38:VAL:CA	1:A:38:VAL:C	1:A:39:ASP:N	10	3.5
(1,42)	1:A:11:ALA:N	1:A:11:ALA:CA	1:A:11:ALA:C	1:A:12:TYR:N	17	3.5
(1,18)	2:B:212:PHE:N	2:B:212:PHE:CA	2:B:212:PHE:C	2:B:213:SER:N	19	3.5
(1,133)	1:A:60:GLU:C	1:A:61:ASP:N	1:A:61:ASP:CA	1:A:61:ASP:C	5	3.5
(1,92)	1:A:38:VAL:N	1:A:38:VAL:CA	1:A:38:VAL:C	1:A:39:ASP:N	3	3.4
(1,92)	1:A:38:VAL:N	1:A:38:VAL:CA	1:A:38:VAL:C	1:A:39:ASP:N	17	3.4
(1,131)	1:A:59:TYR:C	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	5	3.4
(1,92)	1:A:38:VAL:N	1:A:38:VAL:CA	1:A:38:VAL:C	1:A:39:ASP:N	4	3.3
(1,92)	1:A:38:VAL:N	1:A:38:VAL:CA	1:A:38:VAL:C	1:A:39:ASP:N	18	3.3
(1,51)	1:A:15:ILE:C	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	3	3.3
(1,51)	1:A:15:ILE:C	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	8	3.3
(1,92)	1:A:38:VAL:N	1:A:38:VAL:CA	1:A:38:VAL:C	1:A:39:ASP:N	20	3.2
(1,51)	1:A:15:ILE:C	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	12	3.2
(1,51)	1:A:15:ILE:C	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	16	3.2
(1,22)	2:B:215:SER:N	2:B:215:SER:CA	2:B:215:SER:C	2:B:216:GLY:N	18	3.2
(1,18)	2:B:212:PHE:N	2:B:212:PHE:CA	2:B:212:PHE:C	2:B:213:SER:N	12	3.2
(1,132)	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	1:A:61:ASP:N	1	3.2
(1,130)	1:A:59:TYR:N	1:A:59:TYR:CA	1:A:59:TYR:C	1:A:60:GLU:N	2	3.2
(1,51)	1:A:15:ILE:C	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	6	3.1
(1,19)	2:B:212:PHE:C	2:B:213:SER:N	2:B:213:SER:CA	2:B:213:SER:C	6	3.1
(1,133)	1:A:60:GLU:C	1:A:61:ASP:N	1:A:61:ASP:CA	1:A:61:ASP:C	16	3.1
(1,131)	1:A:59:TYR:C	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	7	3.1
(1,80)	1:A:31:PHE:N	1:A:31:PHE:CA	1:A:31:PHE:C	1:A:32:SER:N	11	3.0
(1,51)	1:A:15:ILE:C	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	4	3.0
(1,51)	1:A:15:ILE:C	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	10	3.0
(1,51)	1:A:15:ILE:C	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	14	3.0
(1,42)	1:A:11:ALA:N	1:A:11:ALA:CA	1:A:11:ALA:C	1:A:12:TYR:N	6	3.0
(1,131)	1:A:59:TYR:C	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	20	3.0
(1,133)	1:A:60:GLU:C	1:A:61:ASP:N	1:A:61:ASP:CA	1:A:61:ASP:C	4	2.9
(1,131)	1:A:59:TYR:C	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	17	2.9
(1,92)	1:A:38:VAL:N	1:A:38:VAL:CA	1:A:38:VAL:C	1:A:39:ASP:N	12	2.8
(1,51)	1:A:15:ILE:C	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	17	2.8
(1,133)	1:A:60:GLU:C	1:A:61:ASP:N	1:A:61:ASP:CA	1:A:61:ASP:C	3	2.8
(1,119)	1:A:53:GLY:C	1:A:54:PHE:N	1:A:54:PHE:CA	1:A:54:PHE:C	3	2.8
(1,8)	2:B:205:TYR:N	2:B:205:TYR:CA	2:B:205:TYR:C	2:B:206:ILE:N	16	2.7
(1,52)	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	1:A:17:ASN:N	7	2.7
(1,92)	1:A:38:VAL:N	1:A:38:VAL:CA	1:A:38:VAL:C	1:A:39:ASP:N	2	2.6
(1,92)	1:A:38:VAL:N	1:A:38:VAL:CA	1:A:38:VAL:C	1:A:39:ASP:N	8	2.6
(1,51)	1:A:15:ILE:C	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	7	2.6
(1,19)	2:B:212:PHE:C	2:B:213:SER:N	2:B:213:SER:CA	2:B:213:SER:C	1	2.6
(1,18)	2:B:212:PHE:N	2:B:212:PHE:CA	2:B:212:PHE:C	2:B:213:SER:N	3	2.6
(1,18)	2:B:212:PHE:N	2:B:212:PHE:CA	2:B:212:PHE:C	2:B:213:SER:N	15	2.6
(1,92)	1:A:38:VAL:N	1:A:38:VAL:CA	1:A:38:VAL:C	1:A:39:ASP:N	6	2.5
(1,52)	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	1:A:17:ASN:N	15	2.5
(1,51)	1:A:15:ILE:C	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	15	2.5
(1,186)	1:A:87:THR:N	1:A:87:THR:CA	1:A:87:THR:C	1:A:88:PHE:N	7	2.5

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,117)	1:A:52:GLN:C	1:A:53:GLY:N	1:A:53:GLY:CA	1:A:53:GLY:C	4	2.5
(1,7)	2:B:204:GLN:C	2:B:205:TYR:N	2:B:205:TYR:CA	2:B:205:TYR:C	8	2.4
(1,52)	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	1:A:17:ASN:N	19	2.4
(1,42)	1:A:11:ALA:N	1:A:11:ALA:CA	1:A:11:ALA:C	1:A:12:TYR:N	8	2.4
(1,19)	2:B:212:PHE:C	2:B:213:SER:N	2:B:213:SER:CA	2:B:213:SER:C	3	2.4
(1,19)	2:B:212:PHE:C	2:B:213:SER:N	2:B:213:SER:CA	2:B:213:SER:C	10	2.4
(1,19)	2:B:212:PHE:C	2:B:213:SER:N	2:B:213:SER:CA	2:B:213:SER:C	13	2.4
(1,132)	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	1:A:61:ASP:N	3	2.4
(1,132)	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	1:A:61:ASP:N	17	2.4
(1,131)	1:A:59:TYR:C	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	8	2.4
(1,42)	1:A:11:ALA:N	1:A:11:ALA:CA	1:A:11:ALA:C	1:A:12:TYR:N	12	2.3
(1,20)	2:B:213:SER:N	2:B:213:SER:CA	2:B:213:SER:C	2:B:214:PRO:N	13	2.3
(1,51)	1:A:15:ILE:C	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	11	2.1
(1,42)	1:A:11:ALA:N	1:A:11:ALA:CA	1:A:11:ALA:C	1:A:12:TYR:N	10	2.1
(1,42)	1:A:11:ALA:N	1:A:11:ALA:CA	1:A:11:ALA:C	1:A:12:TYR:N	19	2.1
(1,131)	1:A:59:TYR:C	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	16	2.1
(1,119)	1:A:53:GLY:C	1:A:54:PHE:N	1:A:54:PHE:CA	1:A:54:PHE:C	20	2.1
(1,85)	1:A:33:GLU:C	1:A:34:TYR:N	1:A:34:TYR:CA	1:A:34:TYR:C	11	2.0
(1,42)	1:A:11:ALA:N	1:A:11:ALA:CA	1:A:11:ALA:C	1:A:12:TYR:N	3	2.0
(1,20)	2:B:213:SER:N	2:B:213:SER:CA	2:B:213:SER:C	2:B:214:PRO:N	3	2.0
(1,20)	2:B:213:SER:N	2:B:213:SER:CA	2:B:213:SER:C	2:B:214:PRO:N	7	2.0
(1,186)	1:A:87:THR:N	1:A:87:THR:CA	1:A:87:THR:C	1:A:88:PHE:N	17	2.0
(1,18)	2:B:212:PHE:N	2:B:212:PHE:CA	2:B:212:PHE:C	2:B:213:SER:N	13	2.0
(1,131)	1:A:59:TYR:C	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	10	2.0
(1,36)	1:A:6:GLU:N	1:A:6:GLU:CA	1:A:6:GLU:C	1:A:7:TYR:N	11	1.9
(1,118)	1:A:53:GLY:N	1:A:53:GLY:CA	1:A:53:GLY:C	1:A:54:PHE:N	12	1.9
(1,107)	1:A:45:ASP:C	1:A:46:GLU:N	1:A:46:GLU:CA	1:A:46:GLU:C	3	1.9
(1,107)	1:A:45:ASP:C	1:A:46:GLU:N	1:A:46:GLU:CA	1:A:46:GLU:C	5	1.9
(1,52)	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	1:A:17:ASN:N	9	1.8
(1,22)	2:B:215:SER:N	2:B:215:SER:CA	2:B:215:SER:C	2:B:216:GLY:N	2	1.8
(1,19)	2:B:212:PHE:C	2:B:213:SER:N	2:B:213:SER:CA	2:B:213:SER:C	19	1.8
(1,186)	1:A:87:THR:N	1:A:87:THR:CA	1:A:87:THR:C	1:A:88:PHE:N	15	1.8
(1,18)	2:B:212:PHE:N	2:B:212:PHE:CA	2:B:212:PHE:C	2:B:213:SER:N	11	1.8
(1,158)	1:A:73:ASN:N	1:A:73:ASN:CA	1:A:73:ASN:C	1:A:74:GLY:N	15	1.8
(1,133)	1:A:60:GLU:C	1:A:61:ASP:N	1:A:61:ASP:CA	1:A:61:ASP:C	20	1.8
(1,90)	1:A:36:VAL:N	1:A:36:VAL:CA	1:A:36:VAL:C	1:A:37:PRO:N	7	1.7
(1,52)	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	1:A:17:ASN:N	2	1.7
(1,27)	2:B:218:LEU:C	2:B:219:GLU:N	2:B:219:GLU:CA	2:B:219:GLU:C	13	1.7
(1,137)	1:A:62:GLN:C	1:A:63:ARG:N	1:A:63:ARG:CA	1:A:63:ARG:C	11	1.7
(1,131)	1:A:59:TYR:C	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	18	1.7
(1,51)	1:A:15:ILE:C	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	19	1.6
(1,42)	1:A:11:ALA:N	1:A:11:ALA:CA	1:A:11:ALA:C	1:A:12:TYR:N	9	1.6
(1,4)	2:B:203:SER:N	2:B:203:SER:CA	2:B:203:SER:C	2:B:204:GLN:N	14	1.6
(1,35)	1:A:5:ASN:C	1:A:6:GLU:N	1:A:6:GLU:CA	1:A:6:GLU:C	10	1.6
(1,24)	2:B:217:LEU:N	2:B:217:LEU:CA	2:B:217:LEU:C	2:B:218:LEU:N	16	1.6
(1,194)	1:A:92:LYS:N	1:A:92:LYS:CA	1:A:92:LYS:C	1:A:93:ARG:N	8	1.6
(1,186)	1:A:87:THR:N	1:A:87:THR:CA	1:A:87:THR:C	1:A:88:PHE:N	20	1.6
(1,131)	1:A:59:TYR:C	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	3	1.6
(1,131)	1:A:59:TYR:C	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	4	1.6
(1,113)	1:A:49:GLY:C	1:A:50:GLU:N	1:A:50:GLU:CA	1:A:50:GLU:C	10	1.6
(1,113)	1:A:49:GLY:C	1:A:50:GLU:N	1:A:50:GLU:CA	1:A:50:GLU:C	18	1.6

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,107)	1:A:45:ASP:C	1:A:46:GLU:N	1:A:46:GLU:CA	1:A:46:GLU:C	9	1.6
(1,10)	2:B:206:ILE:N	2:B:206:ILE:CA	2:B:206:ILE:C	2:B:207:ASP:N	7	1.6
(1,10)	2:B:206:ILE:N	2:B:206:ILE:CA	2:B:206:ILE:C	2:B:207:ASP:N	18	1.6
(1,90)	1:A:36:VAL:N	1:A:36:VAL:CA	1:A:36:VAL:C	1:A:37:PRO:N	5	1.5
(1,7)	2:B:204:GLN:C	2:B:205:TYR:N	2:B:205:TYR:CA	2:B:205:TYR:C	15	1.5
(1,42)	1:A:11:ALA:N	1:A:11:ALA:CA	1:A:11:ALA:C	1:A:12:TYR:N	15	1.5
(1,3)	2:B:202:LYS:C	2:B:203:SER:N	2:B:203:SER:CA	2:B:203:SER:C	19	1.5
(1,19)	2:B:212:PHE:C	2:B:213:SER:N	2:B:213:SER:CA	2:B:213:SER:C	15	1.5
(1,168)	1:A:78:GLY:N	1:A:78:GLY:CA	1:A:78:GLY:C	1:A:79:GLY:N	10	1.5
(1,107)	1:A:45:ASP:C	1:A:46:GLU:N	1:A:46:GLU:CA	1:A:46:GLU:C	10	1.5
(1,52)	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	1:A:17:ASN:N	11	1.4
(1,51)	1:A:15:ILE:C	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	13	1.4
(1,42)	1:A:11:ALA:N	1:A:11:ALA:CA	1:A:11:ALA:C	1:A:12:TYR:N	20	1.4
(1,19)	2:B:212:PHE:C	2:B:213:SER:N	2:B:213:SER:CA	2:B:213:SER:C	11	1.4
(1,18)	2:B:212:PHE:N	2:B:212:PHE:CA	2:B:212:PHE:C	2:B:213:SER:N	18	1.4
(1,133)	1:A:60:GLU:C	1:A:61:ASP:N	1:A:61:ASP:CA	1:A:61:ASP:C	17	1.4
(1,88)	1:A:35:GLY:N	1:A:35:GLY:CA	1:A:35:GLY:C	1:A:36:VAL:N	9	1.3
(1,7)	2:B:204:GLN:C	2:B:205:TYR:N	2:B:205:TYR:CA	2:B:205:TYR:C	2	1.3
(1,58)	1:A:20:ARG:N	1:A:20:ARG:CA	1:A:20:ARG:C	1:A:21:GLU:N	12	1.3
(1,42)	1:A:11:ALA:N	1:A:11:ALA:CA	1:A:11:ALA:C	1:A:12:TYR:N	11	1.3
(1,194)	1:A:92:LYS:N	1:A:92:LYS:CA	1:A:92:LYS:C	1:A:93:ARG:N	2	1.3
(1,194)	1:A:92:LYS:N	1:A:92:LYS:CA	1:A:92:LYS:C	1:A:93:ARG:N	11	1.3
(1,186)	1:A:87:THR:N	1:A:87:THR:CA	1:A:87:THR:C	1:A:88:PHE:N	8	1.3
(1,186)	1:A:87:THR:N	1:A:87:THR:CA	1:A:87:THR:C	1:A:88:PHE:N	13	1.3
(1,186)	1:A:87:THR:N	1:A:87:THR:CA	1:A:87:THR:C	1:A:88:PHE:N	14	1.3
(1,186)	1:A:87:THR:N	1:A:87:THR:CA	1:A:87:THR:C	1:A:88:PHE:N	19	1.3
(1,158)	1:A:73:ASN:N	1:A:73:ASN:CA	1:A:73:ASN:C	1:A:74:GLY:N	11	1.3
(1,12)	2:B:207:ASP:N	2:B:207:ASP:CA	2:B:207:ASP:C	2:B:208:ILE:N	10	1.3
(1,114)	1:A:50:GLU:N	1:A:50:GLU:CA	1:A:50:GLU:C	1:A:51:SER:N	9	1.3
(1,88)	1:A:35:GLY:N	1:A:35:GLY:CA	1:A:35:GLY:C	1:A:36:VAL:N	6	1.2
(1,52)	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	1:A:17:ASN:N	3	1.2
(1,52)	1:A:16:GLY:N	1:A:16:GLY:CA	1:A:16:GLY:C	1:A:17:ASN:N	18	1.2
(1,35)	1:A:5:ASN:C	1:A:6:GLU:N	1:A:6:GLU:CA	1:A:6:GLU:C	15	1.2
(1,29)	2:B:219:GLU:C	2:B:220:LEU:N	2:B:220:LEU:CA	2:B:220:LEU:C	18	1.2
(1,22)	2:B:215:SER:N	2:B:215:SER:CA	2:B:215:SER:C	2:B:216:GLY:N	6	1.2
(1,194)	1:A:92:LYS:N	1:A:92:LYS:CA	1:A:92:LYS:C	1:A:93:ARG:N	19	1.2
(1,185)	1:A:86:HIS:C	1:A:87:THR:N	1:A:87:THR:CA	1:A:87:THR:C	1	1.2
(1,17)	2:B:211:ASP:C	2:B:212:PHE:N	2:B:212:PHE:CA	2:B:212:PHE:C	20	1.2
(1,136)	1:A:62:GLN:N	1:A:62:GLN:CA	1:A:62:GLN:C	1:A:63:ARG:N	11	1.2
(1,131)	1:A:59:TYR:C	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	9	1.2
(1,12)	2:B:207:ASP:N	2:B:207:ASP:CA	2:B:207:ASP:C	2:B:208:ILE:N	20	1.2
(1,119)	1:A:53:GLY:C	1:A:54:PHE:N	1:A:54:PHE:CA	1:A:54:PHE:C	4	1.2
(1,7)	2:B:204:GLN:C	2:B:205:TYR:N	2:B:205:TYR:CA	2:B:205:TYR:C	10	1.1
(1,55)	1:A:18:LEU:C	1:A:19:ASN:N	1:A:19:ASN:CA	1:A:19:ASN:C	9	1.1
(1,42)	1:A:11:ALA:N	1:A:11:ALA:CA	1:A:11:ALA:C	1:A:12:TYR:N	4	1.1
(1,35)	1:A:5:ASN:C	1:A:6:GLU:N	1:A:6:GLU:CA	1:A:6:GLU:C	5	1.1
(1,27)	2:B:218:LEU:C	2:B:219:GLU:N	2:B:219:GLU:CA	2:B:219:GLU:C	15	1.1
(1,22)	2:B:215:SER:N	2:B:215:SER:CA	2:B:215:SER:C	2:B:216:GLY:N	9	1.1
(1,18)	2:B:212:PHE:N	2:B:212:PHE:CA	2:B:212:PHE:C	2:B:213:SER:N	1	1.1
(1,131)	1:A:59:TYR:C	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	1	1.1
(1,131)	1:A:59:TYR:C	1:A:60:GLU:N	1:A:60:GLU:CA	1:A:60:GLU:C	19	1.1

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,12)	2:B:207:ASP:N	2:B:207:ASP:CA	2:B:207:ASP:C	2:B:208:ILE:N	3	1.1
(1,12)	2:B:207:ASP:N	2:B:207:ASP:CA	2:B:207:ASP:C	2:B:208:ILE:N	18	1.1
(1,113)	1:A:49:GLY:C	1:A:50:GLU:N	1:A:50:GLU:CA	1:A:50:GLU:C	20	1.1
(1,107)	1:A:45:ASP:C	1:A:46:GLU:N	1:A:46:GLU:CA	1:A:46:GLU:C	18	1.1