



Full wwPDB NMR Structure Validation Report ⓘ

Dec 24, 2024 – 05:00 PM EST

PDB ID : 2LOY
BMRB ID : 16833
Title : Refined Miminal Constraint Solution NMR Structure of Translationally-controlled tumor protein (TCTP) from *Caenorhabditis elegans*, Northeast Structural Genomics Consortium Target WR73
Authors : Aramini, J.M.; Rossi, P.; Cort, J.R.; Lee, H.; Janjua, H.; Maglaqui, M.; Cooper, B.; Xiao, R.; Acton, T.B.; Everett, J.K.; Montelione, G.T.; Northeast Structural Genomics Consortium (NESG)
Deposited on : 2012-01-27

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
BMRB Restraints Analysis : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.40

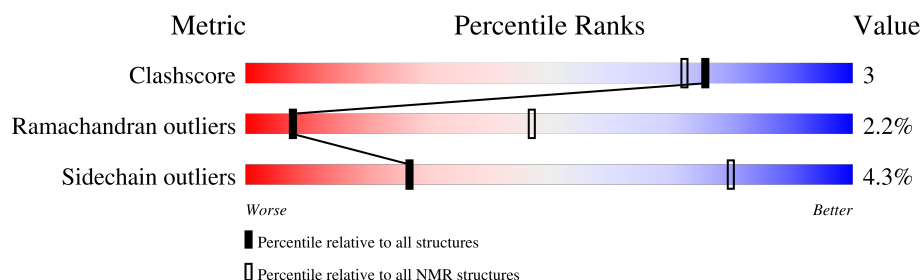
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 51%.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	189	 84% 11%

2 Ensemble composition and analysis

This entry contains 20 models. Model 5 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:1-A:42, A:64-A:183 (162)	1.65	5

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 2 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2902 atoms, of which 1445 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Translationally-controlled tumor protein homolog.

Mol	Chain	Residues	Atoms						Trace
1	A	183	Total	C	H	N	O	S	0
			2902	922	1445	239	287	9	

There are 8 discrepancies between the modelled and reference sequences:

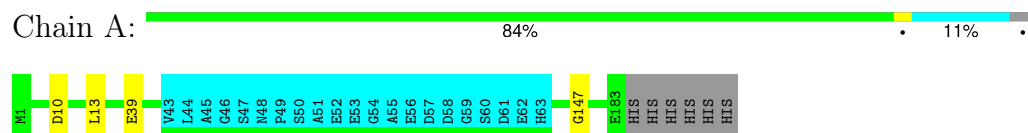
Chain	Residue	Modelled	Actual	Comment	Reference
A	182	LEU	-	expression tag	UNP Q93573
A	183	GLU	-	expression tag	UNP Q93573
A	184	HIS	-	expression tag	UNP Q93573
A	185	HIS	-	expression tag	UNP Q93573
A	186	HIS	-	expression tag	UNP Q93573
A	187	HIS	-	expression tag	UNP Q93573
A	188	HIS	-	expression tag	UNP Q93573
A	189	HIS	-	expression tag	UNP Q93573

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

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

- Molecule 1: Translationally-controlled tumor protein homolog

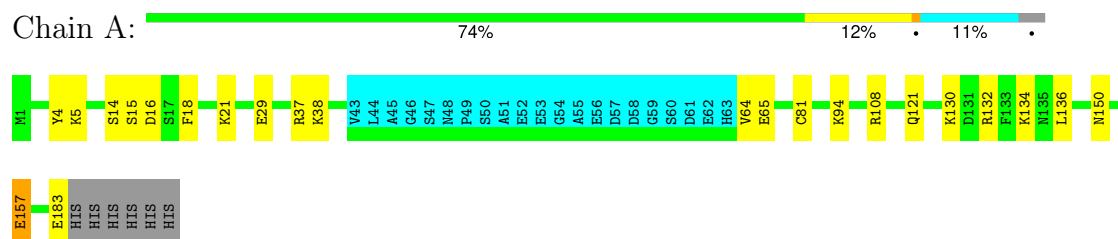


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

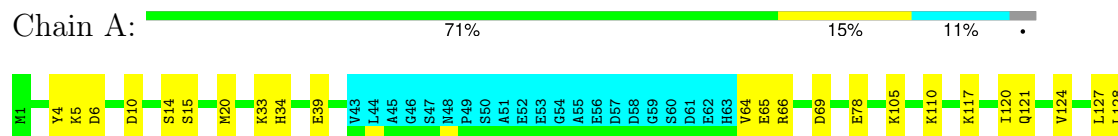
4.2.1 Score per residue for model 1

- Molecule 1: Translationally-controlled tumor protein homolog



4.2.2 Score per residue for model 2

- Molecule 1: Translationally-controlled tumor protein homolog

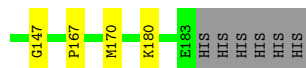
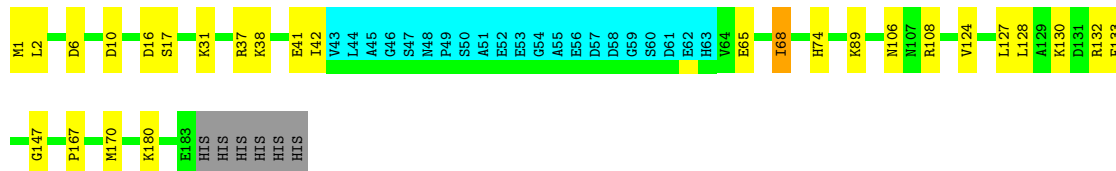




4.2.3 Score per residue for model 3

- Molecule 1: Translationally-controlled tumor protein homolog

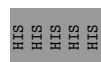
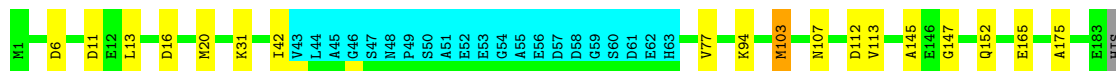
Chain A: 71% 14% 11%



4.2.4 Score per residue for model 4

- Molecule 1: Translationally-controlled tumor protein homolog

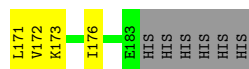
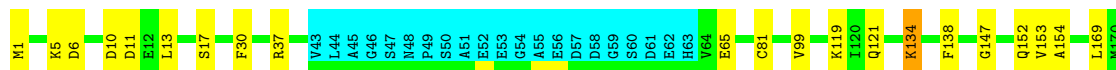
Chain A: 76% 9% 11%



4.2.5 Score per residue for model 5 (medoid)

- Molecule 1: Translationally-controlled tumor protein homolog

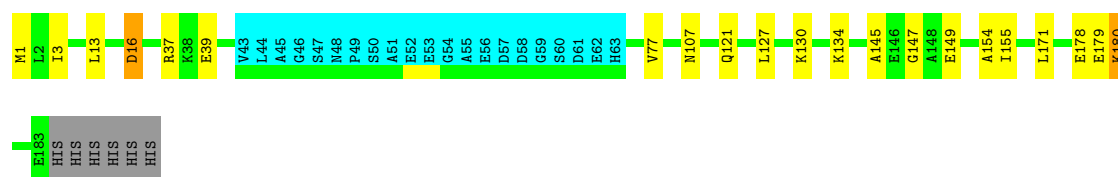
Chain A: 72% 13% 11%



4.2.6 Score per residue for model 6

- Molecule 1: Translationally-controlled tumor protein homolog

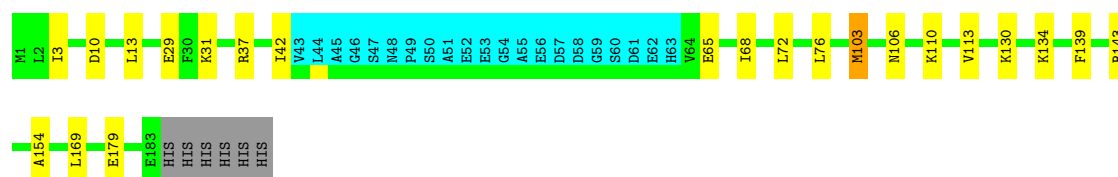
Chain A: 75% 10% 11%



4.2.7 Score per residue for model 7

- Molecule 1: Translationally-controlled tumor protein homolog

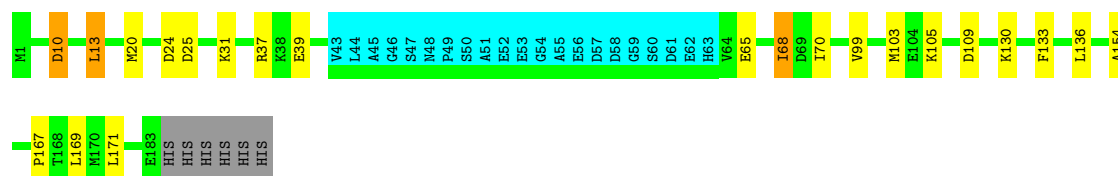
Chain A: 74% 11% 11%



4.2.8 Score per residue for model 8

- Molecule 1: Translationally-controlled tumor protein homolog

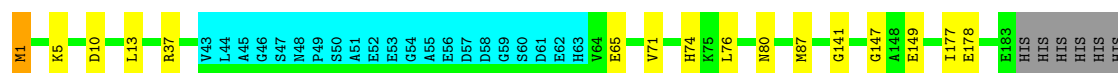
Chain A: 74% 10% 11%



4.2.9 Score per residue for model 9

- Molecule 1: Translationally-controlled tumor protein homolog

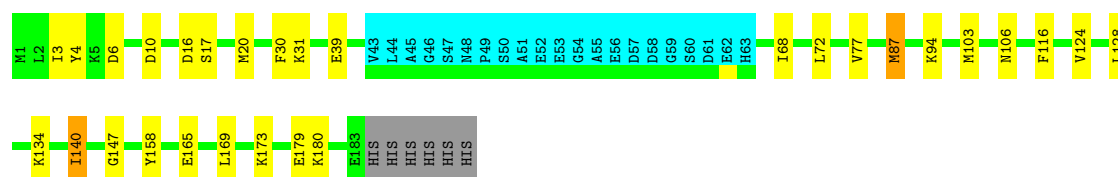
Chain A: 77% 8% 11%



4.2.10 Score per residue for model 10

- Molecule 1: Translationally-controlled tumor protein homolog

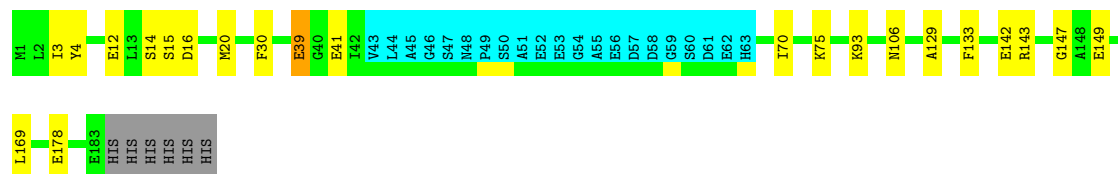
Chain A: 70% 14% 11%



4.2.11 Score per residue for model 11

- Molecule 1: Translationally-controlled tumor protein homolog

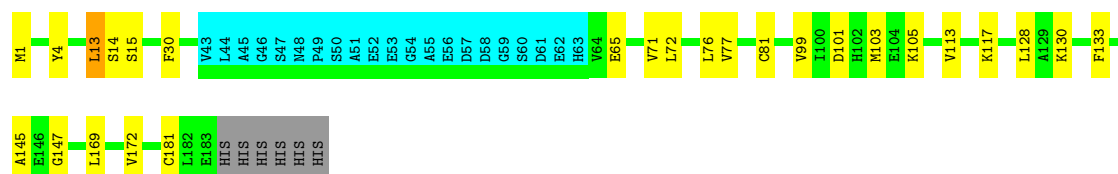
Chain A: 74% 11% 11%



4.2.12 Score per residue for model 12

- Molecule 1: Translationally-controlled tumor protein homolog

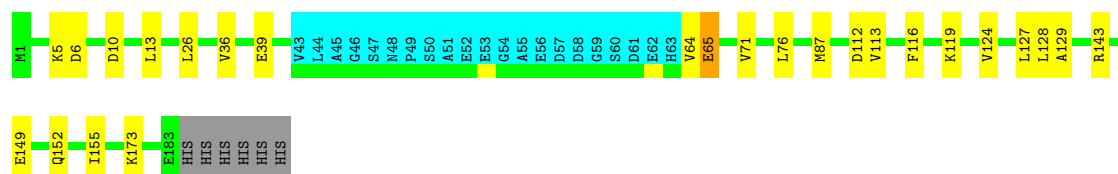
Chain A: 72% 13% 11%



4.2.13 Score per residue for model 13

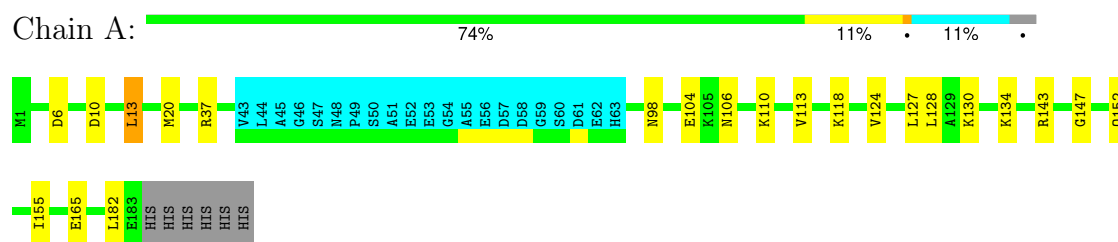
- Molecule 1: Translationally-controlled tumor protein homolog

Chain A: 72% 13% 11%



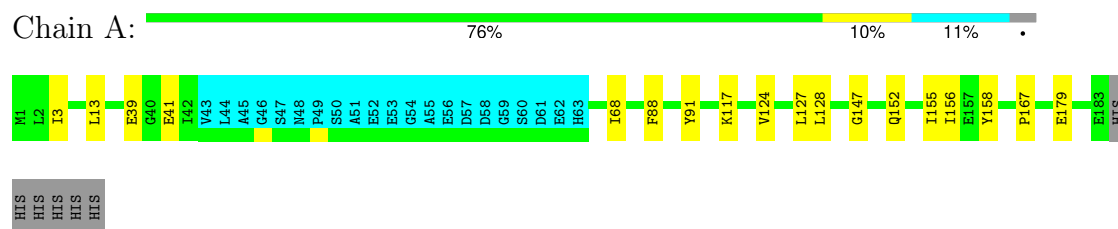
4.2.14 Score per residue for model 14

- Molecule 1: Translationally-controlled tumor protein homolog



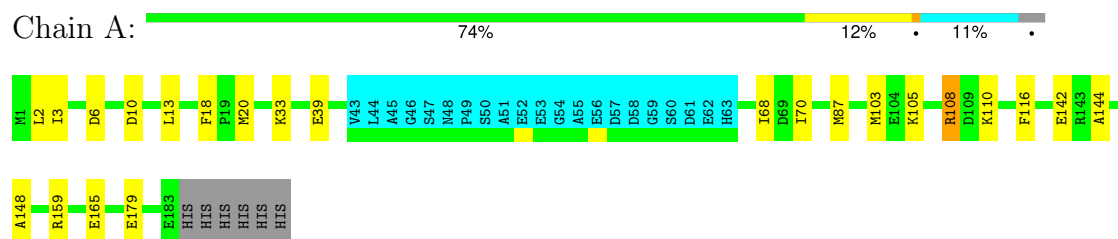
4.2.15 Score per residue for model 15

- Molecule 1: Translationally-controlled tumor protein homolog



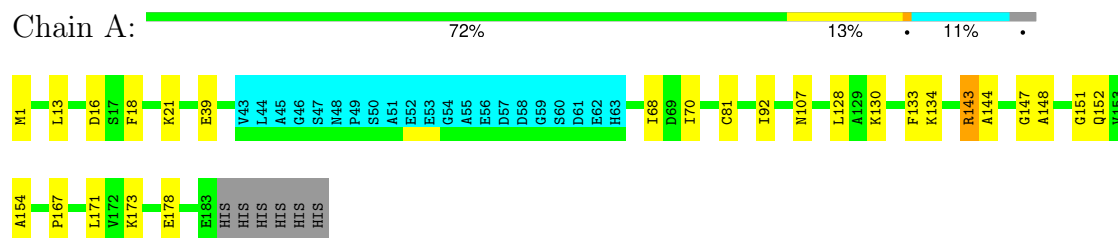
4.2.16 Score per residue for model 16

- Molecule 1: Translationally-controlled tumor protein homolog



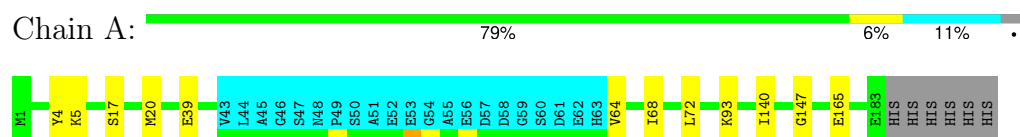
4.2.17 Score per residue for model 17

- Molecule 1: Translationally-controlled tumor protein homolog



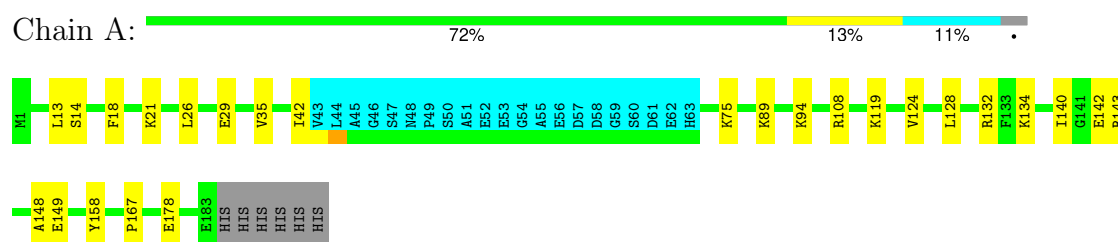
4.2.18 Score per residue for model 18

- Molecule 1: Translationally-controlled tumor protein homolog



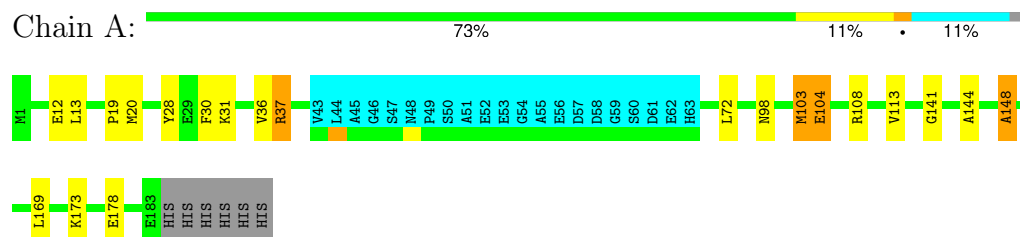
4.2.19 Score per residue for model 19

- Molecule 1: Translationally-controlled tumor protein homolog



4.2.20 Score per residue for model 20

- Molecule 1: Translationally-controlled tumor protein homolog



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
CNS	refinement	1.3
CNS	structure solution	1.3
CNS	geometry optimization	1.3
CYANA	structure solution	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	1275
Number of shifts mapped to atoms	1275
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	51%

6 Model quality

6.1 Standard geometry

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

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	1312	1329	1326	8±2
All	All	26240	26580	26520	154

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 3.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:103:MET:SD	1:A:113:VAL:HG12	0.65	2.31	20	3
1:A:4:TYR:HB3	1:A:20:MET:SD	0.62	2.35	18	1
1:A:37:ARG:HB3	1:A:65:GLU:HB2	0.60	1.73	9	3
1:A:77:VAL:HG11	1:A:145:ALA:HB2	0.59	1.74	6	3
1:A:68:ILE:HD11	1:A:70:ILE:HD12	0.58	1.73	17	2
1:A:68:ILE:HD12	1:A:167:PRO:HB2	0.56	1.76	3	3
1:A:30:PHE:HB3	1:A:169:LEU:HB3	0.56	1.76	5	5
1:A:6:ASP:H	1:A:10:ASP:HA	0.56	1.61	14	1
1:A:92:ILE:HG21	1:A:128:LEU:HD11	0.55	1.76	17	1
1:A:4:TYR:HB3	1:A:14:SER:HB3	0.55	1.79	12	1
1:A:37:ARG:HB2	1:A:72:LEU:HD13	0.54	1.78	20	1
1:A:92:ILE:HG13	1:A:128:LEU:HD21	0.54	1.79	17	1
1:A:26:LEU:HD22	1:A:119:LYS:HG3	0.53	1.80	13	2
1:A:144:ALA:HA	1:A:148:ALA:HB3	0.53	1.80	16	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:65:GLU:HG3	1:A:66:ARG:HG2	0.53	1.79	2	1
1:A:37:ARG:HB2	1:A:65:GLU:HB2	0.52	1.80	8	3
1:A:6:ASP:HB3	1:A:10:ASP:HB3	0.52	1.82	13	1
1:A:107:ASN:HD21	1:A:112:ASP:HB3	0.52	1.65	4	1
1:A:1:MET:SD	1:A:16:ASP:HA	0.52	2.44	17	1
1:A:4:TYR:HB2	1:A:14:SER:HB3	0.52	1.81	1	2
1:A:154:ALA:HA	1:A:171:LEU:HD21	0.51	1.82	5	4
1:A:104:GLU:HA	1:A:113:VAL:HG11	0.51	1.82	20	2
1:A:139:PHE:HB2	1:A:154:ALA:HB3	0.50	1.83	7	1
1:A:5:LYS:HB2	1:A:177:ILE:HB	0.50	1.82	9	1
1:A:87:MET:SD	1:A:87:MET:N	0.49	2.85	10	4
1:A:6:ASP:HB2	1:A:13:LEU:HG	0.49	1.84	14	1
1:A:124:VAL:O	1:A:128:LEU:HG	0.49	2.08	3	7
1:A:38:LYS:HG2	1:A:64:VAL:HG22	0.49	1.85	1	1
1:A:103:MET:SD	1:A:116:PHE:CG	0.48	3.05	16	2
1:A:33:LYS:HG2	1:A:69:ASP:HB2	0.48	1.85	2	1
1:A:75:LYS:HE3	1:A:142:GLU:HG3	0.48	1.85	11	1
1:A:143:ARG:HH11	1:A:148:ALA:HB2	0.47	1.69	17	1
1:A:71:VAL:HG13	1:A:76:LEU:HB2	0.47	1.86	9	3
1:A:173:LYS:HZ3	1:A:173:LYS:HB3	0.47	1.69	13	1
1:A:70:ILE:HD13	1:A:169:LEU:HB2	0.47	1.87	8	2
1:A:94:LYS:HD3	1:A:150:ASN:HA	0.47	1.86	1	1
1:A:6:ASP:O	1:A:10:ASP:HB3	0.47	2.10	2	4
1:A:65:GLU:HB3	1:A:72:LEU:HD22	0.47	1.85	7	2
1:A:103:MET:HA	1:A:106:ASN:ND2	0.47	2.23	10	1
1:A:127:LEU:HD21	1:A:155:ILE:HG21	0.47	1.85	13	5
1:A:99:VAL:HG11	1:A:172:VAL:HG11	0.47	1.87	12	2
1:A:127:LEU:HA	1:A:132:ARG:HD2	0.46	1.87	3	1
1:A:6:ASP:HB3	1:A:10:ASP:HB2	0.46	1.88	5	1
1:A:136:LEU:HD23	1:A:157:GLU:HB3	0.46	1.87	1	1
1:A:3:ILE:HA	1:A:15:SER:HA	0.46	1.88	11	1
1:A:38:LYS:HB3	1:A:41:GLU:HB3	0.46	1.88	3	1
1:A:20:MET:SD	1:A:28:TYR:CD1	0.46	3.08	20	1
1:A:99:VAL:O	1:A:103:MET:HG2	0.46	2.10	8	1
1:A:138:PHE:HB3	1:A:153:VAL:HG11	0.46	1.88	5	1
1:A:3:ILE:HG23	1:A:179:GLU:HB3	0.46	1.88	10	3
1:A:12:GLU:HB2	1:A:143:ARG:HG2	0.46	1.86	11	1
1:A:5:LYS:NZ	1:A:179:GLU:HB2	0.45	2.27	2	1
1:A:6:ASP:HA	1:A:175:ALA:O	0.45	2.11	4	1
1:A:81:CYS:SG	1:A:133:PHE:O	0.45	2.71	17	1
1:A:81:CYS:SG	1:A:130:LYS:HD3	0.45	2.52	1	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:77:VAL:HG13	1:A:140:ILE:HG23	0.44	1.90	10	1
1:A:104:GLU:O	1:A:108:ARG:HB2	0.44	2.12	20	1
1:A:130:LYS:O	1:A:134:LYS:HB2	0.44	2.13	6	2
1:A:76:LEU:HD22	1:A:141:GLY:HA2	0.44	1.89	9	1
1:A:158:TYR:HB2	1:A:165:GLU:HB2	0.44	1.89	10	1
1:A:68:ILE:HD11	1:A:156:ILE:HD12	0.44	1.89	15	1
1:A:130:LYS:HA	1:A:133:PHE:HB2	0.43	1.89	3	3
1:A:16:ASP:HB3	1:A:18:PHE:CE2	0.43	2.48	17	2
1:A:81:CYS:SG	1:A:138:PHE:HE2	0.43	2.37	5	1
1:A:128:LEU:HA	1:A:133:PHE:CE1	0.43	2.49	12	1
1:A:159:ARG:O	1:A:165:GLU:HA	0.43	2.14	16	1
1:A:180:LYS:H	1:A:180:LYS:HD2	0.43	1.73	6	1
1:A:1:MET:SD	1:A:1:MET:N	0.43	2.85	9	1
1:A:173:LYS:HA	1:A:176:ILE:HG22	0.43	1.91	5	1
1:A:21:LYS:HB2	1:A:29:GLU:HB2	0.42	1.90	1	1
1:A:36:VAL:HA	1:A:65:GLU:O	0.42	2.14	13	1
1:A:117:LYS:HA	1:A:120:ILE:HG22	0.42	1.92	2	1
1:A:1:MET:HG3	1:A:181:CYS:SG	0.42	2.53	12	1
1:A:1:MET:HG3	1:A:2:LEU:HG	0.42	1.89	3	1
1:A:29:GLU:HA	1:A:169:LEU:O	0.42	2.14	7	1
1:A:68:ILE:O	1:A:72:LEU:HG	0.42	2.14	18	3
1:A:129:ALA:O	1:A:133:PHE:HB2	0.42	2.14	11	1
1:A:76:LEU:HB3	1:A:139:PHE:HB3	0.42	1.91	7	1
1:A:103:MET:HB3	1:A:113:VAL:HG12	0.42	1.91	12	1
1:A:113:VAL:HA	1:A:116:PHE:HB3	0.42	1.91	13	1
1:A:35:VAL:HB	1:A:42:ILE:HD11	0.42	1.91	19	1
1:A:3:ILE:HB	1:A:179:GLU:HB2	0.42	1.90	6	1
1:A:2:LEU:HD12	1:A:20:MET:SD	0.42	2.55	16	1
1:A:88:PHE:HA	1:A:91:TYR:HD2	0.42	1.75	15	1
1:A:12:GLU:HG3	1:A:141:GLY:HA3	0.42	1.92	20	1
1:A:4:TYR:HB2	1:A:14:SER:HB2	0.41	1.90	11	1
1:A:81:CYS:HG	1:A:138:PHE:HE2	0.41	1.57	5	1
1:A:19:PRO:HB2	1:A:31:LYS:HB2	0.41	1.93	20	1
1:A:1:MET:SD	1:A:17:SER:N	0.41	2.93	5	1
1:A:10:ASP:O	1:A:13:LEU:HG	0.41	2.16	8	1
1:A:133:PHE:HA	1:A:136:LEU:HB2	0.41	1.91	8	1
1:A:14:SER:HB3	1:A:18:PHE:CE2	0.41	2.51	19	1
1:A:3:ILE:HB	1:A:179:GLU:HG3	0.41	1.92	7	1
1:A:81:CYS:SG	1:A:133:PHE:CD2	0.41	3.14	12	1
1:A:101:ASP:O	1:A:105:LYS:HG3	0.41	2.16	12	1
1:A:130:LYS:O	1:A:134:LYS:HG3	0.41	2.16	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:158:TYR:HB2	1:A:165:GLU:HB3	0.41	1.92	20	1
1:A:158:TYR:HA	1:A:167:PRO:HA	0.40	1.93	15	2
1:A:1:MET:HA	1:A:16:ASP:O	0.40	2.16	6	1
1:A:5:LYS:HD2	1:A:11:ASP:HA	0.40	1.93	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	160/189 (85%)	144±3 (90±2%)	12±3 (8±2%)	4±1 (2±1%)	8	47
All	All	3200/3780 (85%)	2881 (90%)	248 (8%)	71 (2%)	8	47

All 23 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	13	LEU	13
1	A	147	GLY	12
1	A	39	GLU	8
1	A	134	LYS	5
1	A	16	ASP	5
1	A	15	SER	3
1	A	110	LYS	3
1	A	17	SER	3
1	A	42	ILE	3
1	A	64	VAL	2
1	A	148	ALA	2
1	A	11	ASP	1
1	A	24	ASP	1
1	A	25	ASP	1
1	A	109	ASP	1
1	A	65	GLU	1
1	A	129	ALA	1
1	A	149	GLU	1

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Mol	Chain	Res	Type	Models (Total)
1	A	182	LEU	1
1	A	18	PHE	1
1	A	108	ARG	1
1	A	151	GLY	1
1	A	163	GLY	1

6.3.2 Protein sidechains ⓘ

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	143/164 (87%)	137±2 (96±2%)	6±2 (4±2%)	27 80
All	All	2860/3280 (87%)	2738 (96%)	122 (4%)	27 80

All 51 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	20	MET	6
1	A	143	ARG	6
1	A	152	GLN	6
1	A	178	GLU	6
1	A	149	GLU	5
1	A	31	LYS	5
1	A	108	ARG	4
1	A	121	GLN	4
1	A	106	ASN	4
1	A	5	LYS	3
1	A	105	LYS	3
1	A	180	LYS	3
1	A	94	LYS	3
1	A	103	MET	3
1	A	165	GLU	3
1	A	37	ARG	3
1	A	10	ASP	3
1	A	140	ILE	3
1	A	173	LYS	3
1	A	132	ARG	2

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Mol	Chain	Res	Type	Models (Total)
1	A	68	ILE	2
1	A	74	HIS	2
1	A	89	LYS	2
1	A	134	LYS	2
1	A	107	ASN	2
1	A	39	GLU	2
1	A	41	GLU	2
1	A	93	LYS	2
1	A	13	LEU	2
1	A	117	LYS	2
1	A	98	ASN	2
1	A	142	GLU	2
1	A	21	LYS	2
1	A	157	GLU	1
1	A	183	GLU	1
1	A	34	HIS	1
1	A	78	GLU	1
1	A	170	MET	1
1	A	119	LYS	1
1	A	110	LYS	1
1	A	130	LYS	1
1	A	1	MET	1
1	A	80	ASN	1
1	A	4	TYR	1
1	A	87	MET	1
1	A	112	ASP	1
1	A	118	LYS	1
1	A	33	LYS	1
1	A	29	GLU	1
1	A	75	LYS	1
1	A	104	GLU	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 51% for the well-defined parts and 51% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping

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

Total number of shifts	1275
Number of shifts mapped to atoms	1275
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	182	-0.63 ± 0.07	Should be checked
$^{13}\text{C}_\beta$	171	0.53 ± 0.07	Should be checked
$^{13}\text{C}'$	180	-0.48 ± 0.11	None needed (< 0.5 ppm)
^{15}N	178	-0.14 ± 0.39	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 51%, i.e. 1165 atoms were assigned a chemical shift out of a possible 2288. 0 out of 27 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	637/814 (78%)	158/330 (48%)	321/324 (99%)	158/160 (99%)
Sidechain	474/1303 (36%)	245/842 (29%)	220/415 (53%)	9/46 (20%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	54/171 (32%)	53/83 (64%)	0/81 (0%)	1/7 (14%)
Overall	1165/2288 (51%)	456/1255 (36%)	541/820 (66%)	168/213 (79%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 51%, i.e. 1275 atoms were assigned a chemical shift out of a possible 2505. 0 out of 29 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	718/920 (78%)	178/374 (48%)	362/366 (99%)	178/180 (99%)
Sidechain	503/1406 (36%)	253/907 (28%)	240/452 (53%)	10/47 (21%)
Aromatic	54/179 (30%)	53/87 (61%)	0/83 (0%)	1/9 (11%)
Overall	1275/2505 (51%)	484/1368 (35%)	602/901 (67%)	189/236 (80%)

7.1.4 Statistically unusual chemical shifts [i](#)

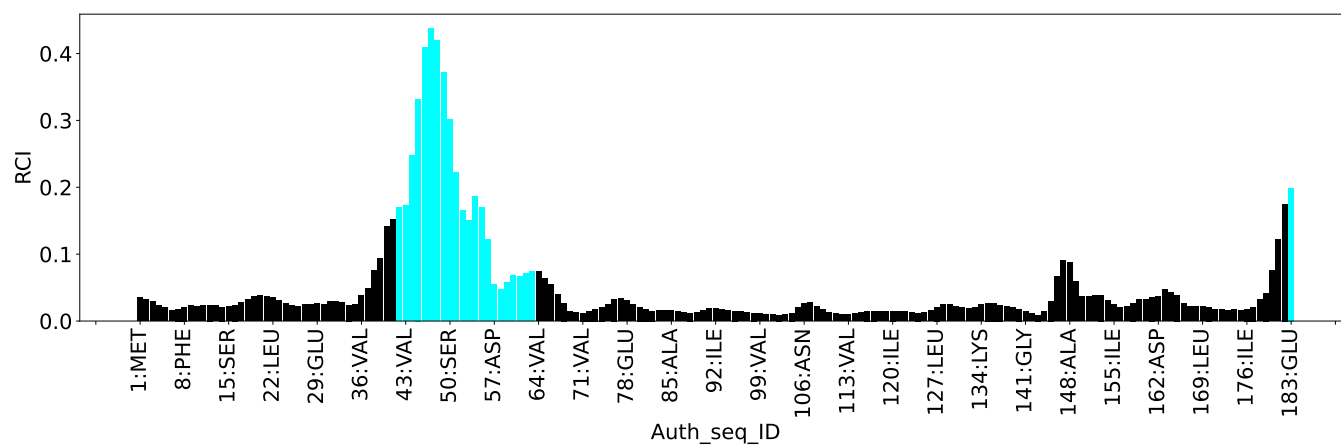
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	143	ARG	H	11.73	5.25 – 11.22	5.9

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

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

Random coil index (RCI) for chain A:



8 NMR restraints analysis

8.1 Conformationally restricting restraints

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

Description	Value
Total distance restraints	1136
Intra-residue ($ i-j =0$)	95
Sequential ($ i-j =1$)	282
Medium range ($ i-j >1$ and $ i-j <5$)	249
Long range ($ i-j \geq 5$)	384
Inter-chain	0
Hydrogen bond restraints	126
Disulfide bond restraints	0
Total dihedral-angle restraints	293
Number of unmapped restraints	0
Number of restraints per residue	7.6
Number of long range restraints per residue ¹	2.4

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

8.2 Residual restraint violations

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

8.2.1 Average number of distance violations per model

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

Bins (Å)	Average number of violations per model	Max (Å)
0.1-0.2 (Small)	6.5	0.2
0.2-0.5 (Medium)	1.1	0.33
>0.5 (Large)	None	None

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

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

Bins (°)	Average number of violations per model	Max (°)
1.0-10.0 (Small)	22.1	9.74
10.0-20.0 (Medium)	0.1	11.56
>20.0 (Large)	1.5	159.47

9 Distance violation analysis

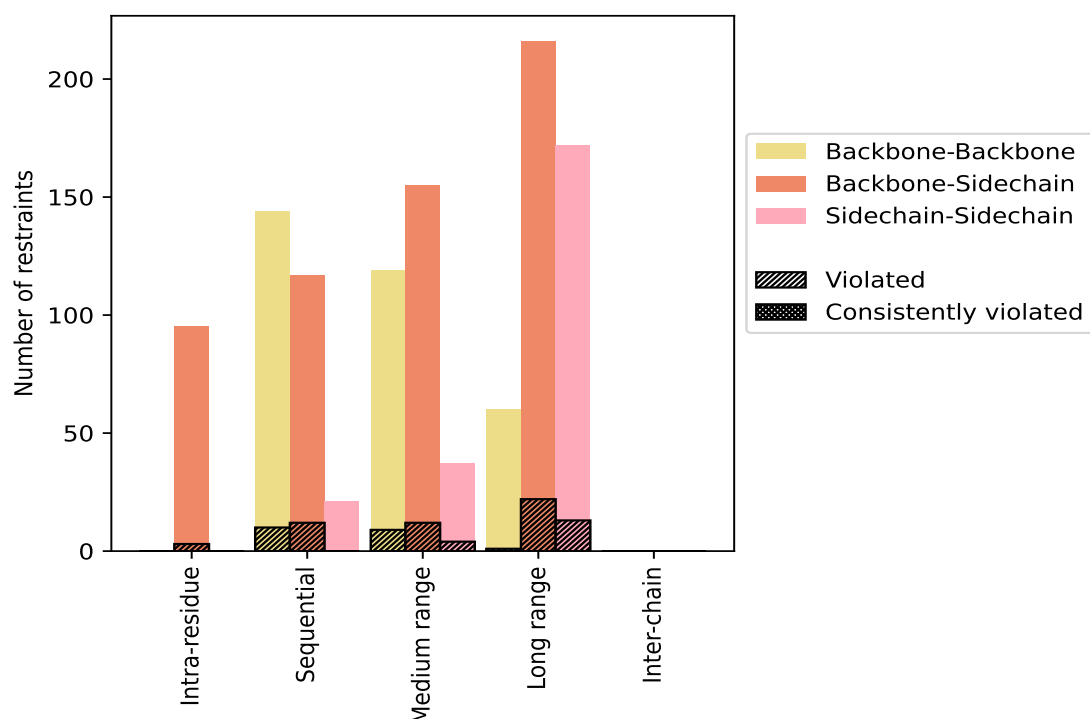
9.1 Summary of distance violations

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

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue ($ i-j =0$)	95	8.4	3	3.2	0.3	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	95	8.4	3	3.2	0.3	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sequential ($ i-j =1$)	282	24.8	22	7.8	1.9	0	0.0	0.0
Backbone-Backbone	144	12.7	10	6.9	0.9	0	0.0	0.0
Backbone-Sidechain	117	10.3	12	10.3	1.1	0	0.0	0.0
Sidechain-Sidechain	21	1.8	0	0.0	0.0	0	0.0	0.0
Medium range ($ i-j >1$ & $ i-j <5$)	249	21.9	25	10.0	2.2	0	0.0	0.0
Backbone-Backbone	119	10.5	9	7.6	0.8	0	0.0	0.0
Backbone-Sidechain	93	8.2	12	12.9	1.1	0	0.0	0.0
Sidechain-Sidechain	37	3.3	4	10.8	0.4	0	0.0	0.0
Long range ($ i-j \geq 5$)	384	33.8	32	8.3	2.8	0	0.0	0.0
Backbone-Backbone	60	5.3	1	1.7	0.1	0	0.0	0.0
Backbone-Sidechain	152	13.4	18	11.8	1.6	0	0.0	0.0
Sidechain-Sidechain	172	15.1	13	7.6	1.1	0	0.0	0.0
Inter-chain	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Hydrogen bond	126	11.1	4	3.2	0.4	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	1136	100.0	86	7.6	7.6	0	0.0	0.0
Backbone-Backbone	323	28.4	20	6.2	1.8	0	0.0	0.0
Backbone-Sidechain	583	51.3	49	8.4	4.3	0	0.0	0.0
Sidechain-Sidechain	230	20.2	17	7.4	1.5	0	0.0	0.0

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

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



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

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

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

Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
1	0	1	2	1	0	4	0.15	0.25	0.06	0.12
2	1	3	5	1	0	10	0.16	0.25	0.04	0.15
3	1	2	4	3	0	10	0.15	0.25	0.04	0.14
4	1	4	1	1	0	7	0.15	0.27	0.05	0.13
5	0	1	1	4	0	6	0.11	0.12	0.01	0.11
6	0	3	2	1	0	6	0.16	0.21	0.03	0.16
7	0	2	3	8	0	13	0.13	0.17	0.02	0.12
8	0	2	2	2	0	6	0.14	0.17	0.02	0.13
9	1	1	2	7	0	11	0.14	0.25	0.04	0.13
10	0	2	4	5	0	11	0.17	0.33	0.06	0.14

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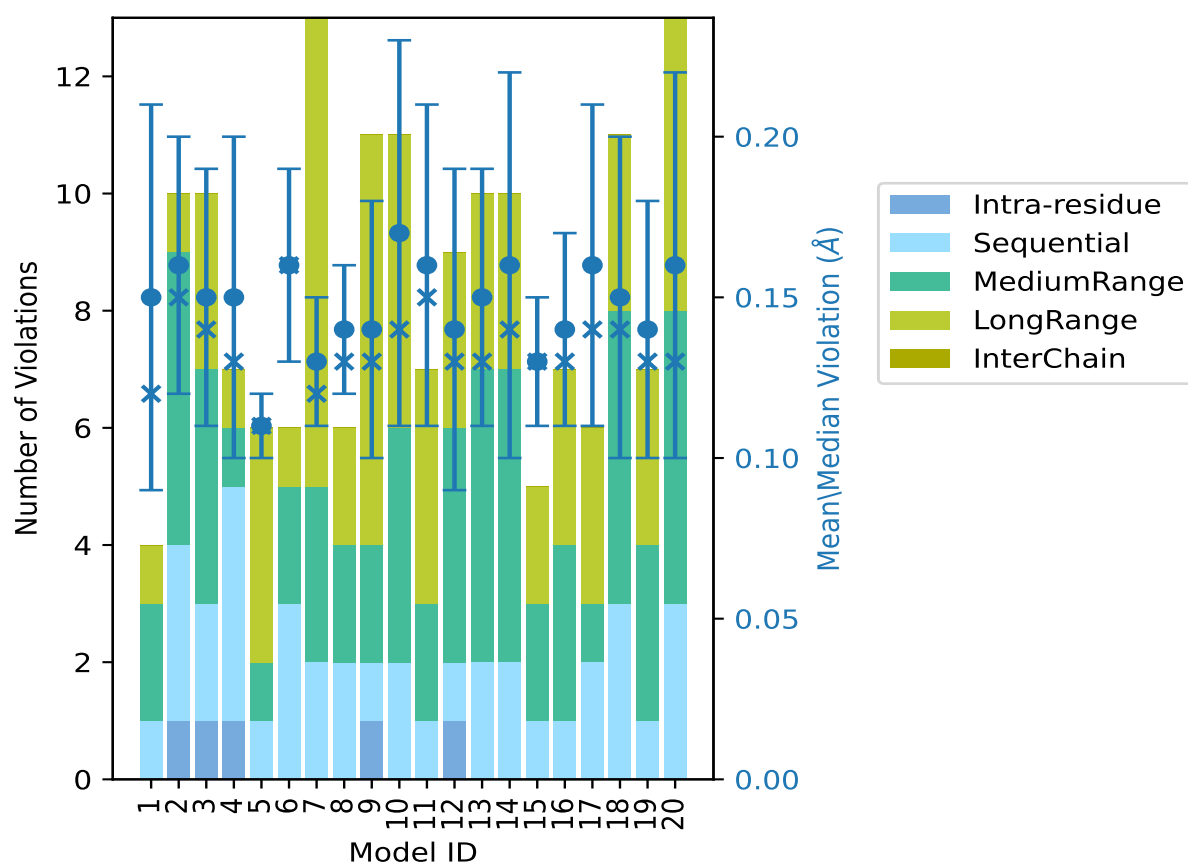
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	0	1	2	4	0	7	0.16	0.27	0.05	0.15
12	1	1	4	3	0	9	0.14	0.26	0.05	0.13
13	0	2	5	3	0	10	0.15	0.21	0.04	0.13
14	0	2	5	3	0	10	0.16	0.32	0.06	0.14
15	0	1	2	2	0	5	0.13	0.16	0.02	0.13
16	0	1	3	3	0	7	0.14	0.21	0.03	0.13
17	0	2	1	3	0	6	0.16	0.25	0.05	0.14
18	0	3	5	3	0	11	0.15	0.26	0.05	0.14
19	0	1	3	3	0	7	0.14	0.21	0.04	0.13
20	0	3	5	5	0	13	0.16	0.31	0.06	0.13

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

⁵Inter-chain restraints, ⁶Standard deviation

9.2.1 Bar graph : Distance Violation statistics for each model ⓘ



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

9.3 Distance violation statistics for the ensemble

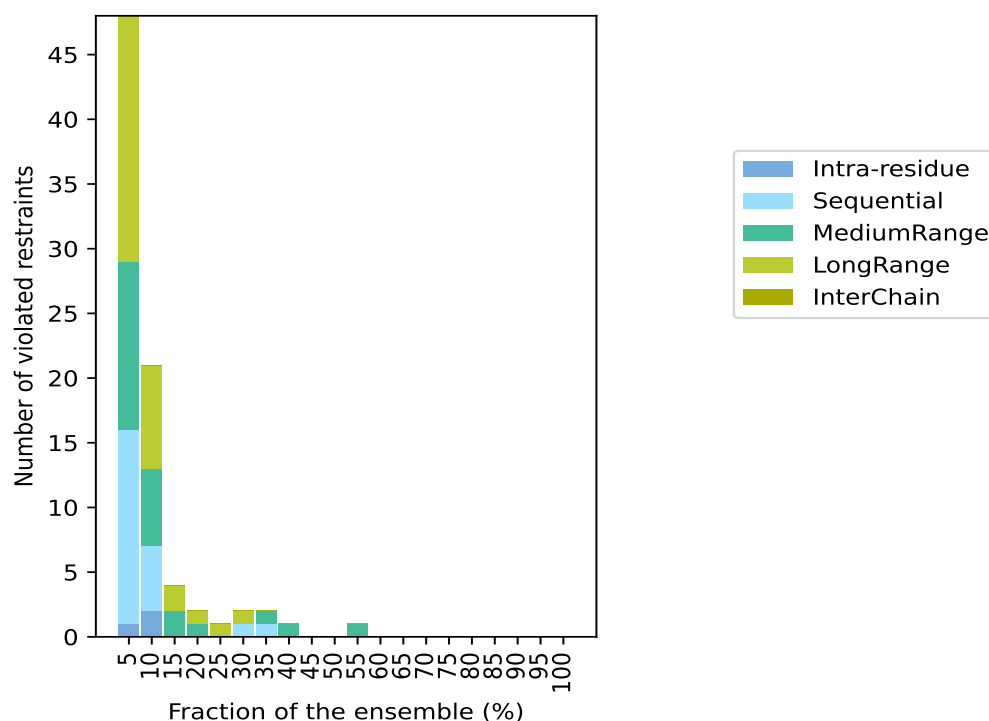
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 928(IR:92, SQ:260, MR:224, LR:352, IC:0) restraints are not violated in the ensemble.

Number of violated restraints						Fraction of the ensemble	
IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total	Count ⁶	%
1	15	13	19	0	48	1	5.0
2	5	6	8	0	21	2	10.0
0	0	2	2	0	4	3	15.0
0	0	1	1	0	2	4	20.0
0	0	0	1	0	1	5	25.0
0	1	0	1	0	2	6	30.0
0	1	1	0	0	2	7	35.0
0	0	1	0	0	1	8	40.0
0	0	0	0	0	0	9	45.0
0	0	0	0	0	0	10	50.0
0	0	1	0	0	1	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	0	0	0	0	0	17	85.0
0	0	0	0	0	0	18	90.0
0	0	0	0	0	0	19	95.0
0	0	0	0	0	0	20	100.0

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

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

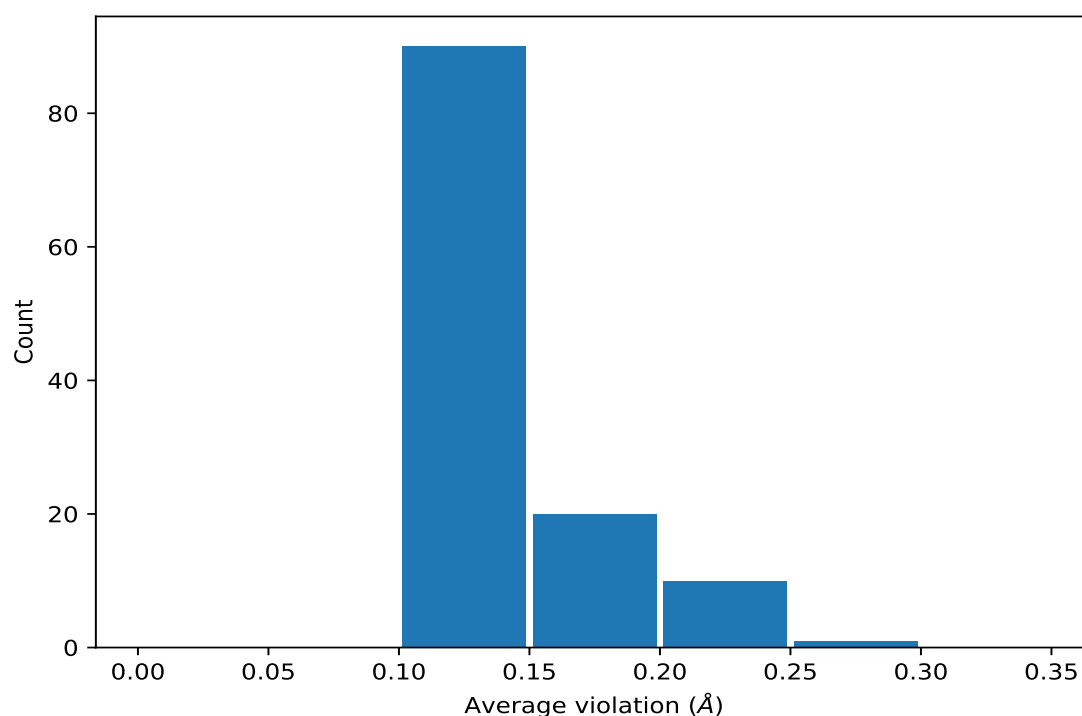
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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

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

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



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

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

Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,455)	1:8:A:PHE:H	1:11:A:ASP:H	11	0.24	0.04	0.23
(1,874)	1:64:A:VAL:HG21	1:66:A:ARG:H	8	0.17	0.06	0.16
(1,874)	1:64:A:VAL:HG22	1:66:A:ARG:H	8	0.17	0.06	0.16
(1,874)	1:64:A:VAL:HG23	1:66:A:ARG:H	8	0.17	0.06	0.16
(1,391)	1:23:A:VAL:HG11	1:26:A:LEU:H	7	0.14	0.02	0.14
(1,391)	1:23:A:VAL:HG12	1:26:A:LEU:H	7	0.14	0.02	0.14
(1,391)	1:23:A:VAL:HG13	1:26:A:LEU:H	7	0.14	0.02	0.14
(1,93)	1:39:A:GLU:H	1:40:A:GLY:H	7	0.14	0.02	0.13
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG11	6	0.19	0.07	0.17
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG12	6	0.19	0.07	0.17
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG13	6	0.19	0.07	0.17
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG21	6	0.19	0.07	0.17
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG22	6	0.19	0.07	0.17
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG23	6	0.19	0.07	0.17
(1,79)	1:13:A:LEU:H	1:14:A:SER:H	6	0.17	0.05	0.15
(1,860)	1:139:A:PHE:H	1:153:A:VAL:HG21	5	0.13	0.01	0.13

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,860)	1:139:A:PHE:H	1:153:A:VAL:HG22	5	0.13	0.01	0.13
(1,860)	1:139:A:PHE:H	1:153:A:VAL:HG23	5	0.13	0.01	0.13
(2,35)	1:155:A:ILE:H	1:170:A:MET:O	5	0.12	0.02	0.13
(1,241)	1:37:A:ARG:H	1:66:A:ARG:H	4	0.15	0.04	0.14
(1,862)	1:62:A:GLU:H	1:64:A:VAL:HG21	4	0.12	0.02	0.12
(1,862)	1:62:A:GLU:H	1:64:A:VAL:HG22	4	0.12	0.02	0.12
(1,862)	1:62:A:GLU:H	1:64:A:VAL:HG23	4	0.12	0.02	0.12
(1,751)	1:36:A:VAL:HG11	1:44:A:LEU:HD21	3	0.2	0.04	0.21
(1,751)	1:36:A:VAL:HG11	1:44:A:LEU:HD22	3	0.2	0.04	0.21
(1,751)	1:36:A:VAL:HG11	1:44:A:LEU:HD23	3	0.2	0.04	0.21
(1,751)	1:36:A:VAL:HG12	1:44:A:LEU:HD21	3	0.2	0.04	0.21
(1,751)	1:36:A:VAL:HG12	1:44:A:LEU:HD22	3	0.2	0.04	0.21
(1,751)	1:36:A:VAL:HG12	1:44:A:LEU:HD23	3	0.2	0.04	0.21
(1,751)	1:36:A:VAL:HG13	1:44:A:LEU:HD21	3	0.2	0.04	0.21
(1,751)	1:36:A:VAL:HG13	1:44:A:LEU:HD22	3	0.2	0.04	0.21
(1,751)	1:36:A:VAL:HG13	1:44:A:LEU:HD23	3	0.2	0.04	0.21
(1,500)	1:138:A:PHE:HD1	1:153:A:VAL:HG21	3	0.12	0.0	0.12
(1,500)	1:138:A:PHE:HD1	1:153:A:VAL:HG22	3	0.12	0.0	0.12
(1,500)	1:138:A:PHE:HD1	1:153:A:VAL:HG23	3	0.12	0.0	0.12
(1,500)	1:138:A:PHE:HD2	1:153:A:VAL:HG21	3	0.12	0.0	0.12
(1,500)	1:138:A:PHE:HD2	1:153:A:VAL:HG22	3	0.12	0.0	0.12
(1,500)	1:138:A:PHE:HD2	1:153:A:VAL:HG23	3	0.12	0.0	0.12
(1,540)	1:133:A:PHE:HD1	1:136:A:LEU:HD21	3	0.12	0.0	0.12
(1,540)	1:133:A:PHE:HD1	1:136:A:LEU:HD22	3	0.12	0.0	0.12
(1,540)	1:133:A:PHE:HD1	1:136:A:LEU:HD23	3	0.12	0.0	0.12
(1,540)	1:133:A:PHE:HD2	1:136:A:LEU:HD21	3	0.12	0.0	0.12
(1,540)	1:133:A:PHE:HD2	1:136:A:LEU:HD22	3	0.12	0.0	0.12
(1,540)	1:133:A:PHE:HD2	1:136:A:LEU:HD23	3	0.12	0.0	0.12
(1,663)	1:149:A:GLU:H	1:151:A:GLY:H	3	0.11	0.0	0.11
(1,50)	1:80:A:ASN:H	1:80:A:ASN:HD22	2	0.26	0.01	0.26
(1,415)	1:131:A:ASP:H	1:134:A:LYS:H	2	0.19	0.02	0.19
(1,243)	1:66:A:ARG:H	1:72:A:LEU:HD21	2	0.18	0.01	0.18
(1,243)	1:66:A:ARG:H	1:72:A:LEU:HD22	2	0.18	0.01	0.18
(1,243)	1:66:A:ARG:H	1:72:A:LEU:HD23	2	0.18	0.01	0.18
(1,322)	1:28:A:TYR:HD1	1:171:A:LEU:H	2	0.16	0.06	0.16
(1,322)	1:28:A:TYR:HD2	1:171:A:LEU:H	2	0.16	0.06	0.16
(1,100)	1:58:A:ASP:H	1:59:A:GLY:H	2	0.16	0.04	0.16
(1,942)	1:135:A:ASN:HD21	1:136:A:LEU:H	2	0.15	0.0	0.15
(1,942)	1:135:A:ASN:HD22	1:136:A:LEU:H	2	0.15	0.0	0.15
(1,160)	1:44:A:LEU:H	1:44:A:LEU:HD11	2	0.14	0.02	0.14
(1,160)	1:44:A:LEU:H	1:44:A:LEU:HD12	2	0.14	0.02	0.14
(1,160)	1:44:A:LEU:H	1:44:A:LEU:HD13	2	0.14	0.02	0.14

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,730)	1:27:A:VAL:HG11	1:120:A:ILE:HD11	2	0.14	0.04	0.14
(1,730)	1:27:A:VAL:HG11	1:120:A:ILE:HD12	2	0.14	0.04	0.14
(1,730)	1:27:A:VAL:HG11	1:120:A:ILE:HD13	2	0.14	0.04	0.14
(1,730)	1:27:A:VAL:HG12	1:120:A:ILE:HD11	2	0.14	0.04	0.14
(1,730)	1:27:A:VAL:HG12	1:120:A:ILE:HD12	2	0.14	0.04	0.14
(1,730)	1:27:A:VAL:HG12	1:120:A:ILE:HD13	2	0.14	0.04	0.14
(1,730)	1:27:A:VAL:HG13	1:120:A:ILE:HD11	2	0.14	0.04	0.14
(1,730)	1:27:A:VAL:HG13	1:120:A:ILE:HD12	2	0.14	0.04	0.14
(1,730)	1:27:A:VAL:HG13	1:120:A:ILE:HD13	2	0.14	0.04	0.14
(1,89)	1:162:A:ASP:H	1:163:A:GLY:H	2	0.13	0.03	0.13
(1,517)	1:127:A:LEU:HD11	1:133:A:PHE:HD1	2	0.13	0.0	0.13
(1,517)	1:127:A:LEU:HD11	1:133:A:PHE:HD2	2	0.13	0.0	0.13
(1,517)	1:127:A:LEU:HD12	1:133:A:PHE:HD1	2	0.13	0.0	0.13
(1,517)	1:127:A:LEU:HD12	1:133:A:PHE:HD2	2	0.13	0.0	0.13
(1,517)	1:127:A:LEU:HD13	1:133:A:PHE:HD1	2	0.13	0.0	0.13
(1,517)	1:127:A:LEU:HD13	1:133:A:PHE:HD2	2	0.13	0.0	0.13
(1,901)	1:156:A:ILE:H	1:169:A:LEU:HD11	2	0.12	0.02	0.12
(1,901)	1:156:A:ILE:H	1:169:A:LEU:HD12	2	0.12	0.02	0.12
(1,901)	1:156:A:ILE:H	1:169:A:LEU:HD13	2	0.12	0.02	0.12
(1,291)	1:182:A:LEU:HD21	1:183:A:GLU:H	2	0.12	0.01	0.12
(1,291)	1:182:A:LEU:HD22	1:183:A:GLU:H	2	0.12	0.01	0.12
(1,291)	1:182:A:LEU:HD23	1:183:A:GLU:H	2	0.12	0.01	0.12
(1,341)	1:95:A:PHE:HD1	1:98:A:ASN:H	2	0.12	0.0	0.12
(1,341)	1:95:A:PHE:HD2	1:98:A:ASN:H	2	0.12	0.0	0.12
(1,609)	1:80:A:ASN:H	1:82:A:TYR:H	2	0.12	0.01	0.12
(1,829)	1:124:A:VAL:HG11	1:128:A:LEU:H	2	0.12	0.0	0.12
(1,829)	1:124:A:VAL:HG12	1:128:A:LEU:H	2	0.12	0.0	0.12
(1,829)	1:124:A:VAL:HG13	1:128:A:LEU:H	2	0.12	0.0	0.12
(1,265)	1:70:A:ILE:H	1:72:A:LEU:HD11	2	0.12	0.0	0.12
(1,265)	1:70:A:ILE:H	1:72:A:LEU:HD12	2	0.12	0.0	0.12
(1,265)	1:70:A:ILE:H	1:72:A:LEU:HD13	2	0.12	0.0	0.12
(1,553)	1:124:A:VAL:HG11	1:128:A:LEU:HD21	2	0.12	0.0	0.12
(1,553)	1:124:A:VAL:HG11	1:128:A:LEU:HD22	2	0.12	0.0	0.12
(1,553)	1:124:A:VAL:HG11	1:128:A:LEU:HD23	2	0.12	0.0	0.12
(1,553)	1:124:A:VAL:HG12	1:128:A:LEU:HD21	2	0.12	0.0	0.12
(1,553)	1:124:A:VAL:HG12	1:128:A:LEU:HD22	2	0.12	0.0	0.12
(1,553)	1:124:A:VAL:HG12	1:128:A:LEU:HD23	2	0.12	0.0	0.12
(1,553)	1:124:A:VAL:HG13	1:128:A:LEU:HD21	2	0.12	0.0	0.12
(1,553)	1:124:A:VAL:HG13	1:128:A:LEU:HD22	2	0.12	0.0	0.12
(1,553)	1:124:A:VAL:HG13	1:128:A:LEU:HD23	2	0.12	0.0	0.12
(1,648)	1:56:A:GLU:H	1:57:A:ASP:H	2	0.12	0.0	0.12
(1,223)	1:6:A:ASP:H	1:13:A:LEU:HD11	2	0.11	0.01	0.11

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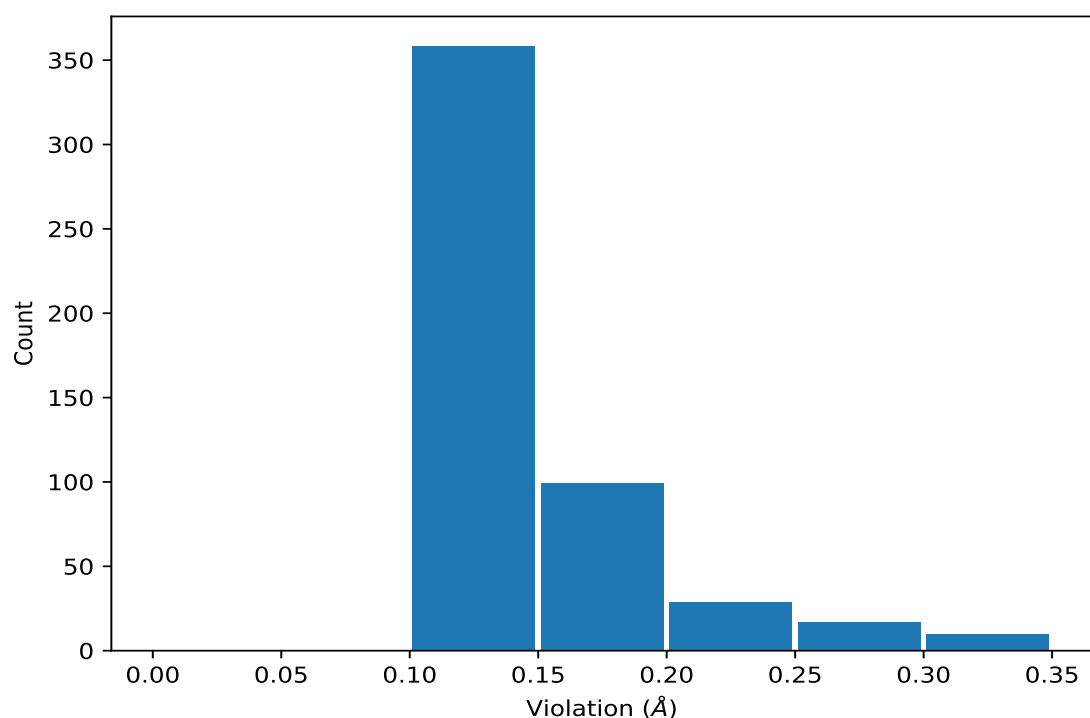
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,223)	1:6:A:ASP:H	1:13:A:LEU:HD12	2	0.11	0.01	0.11
(1,223)	1:6:A:ASP:H	1:13:A:LEU:HD13	2	0.11	0.01	0.11
(1,977)	1:113:A:VAL:HG11	1:100:A:ILE:HD11	2	0.11	0.01	0.11
(1,977)	1:113:A:VAL:HG11	1:100:A:ILE:HD12	2	0.11	0.01	0.11
(1,977)	1:113:A:VAL:HG11	1:100:A:ILE:HD13	2	0.11	0.01	0.11
(1,977)	1:113:A:VAL:HG12	1:100:A:ILE:HD11	2	0.11	0.01	0.11
(1,977)	1:113:A:VAL:HG12	1:100:A:ILE:HD12	2	0.11	0.01	0.11
(1,977)	1:113:A:VAL:HG12	1:100:A:ILE:HD13	2	0.11	0.01	0.11
(1,977)	1:113:A:VAL:HG13	1:100:A:ILE:HD11	2	0.11	0.01	0.11
(1,977)	1:113:A:VAL:HG13	1:100:A:ILE:HD12	2	0.11	0.01	0.11
(1,977)	1:113:A:VAL:HG13	1:100:A:ILE:HD13	2	0.11	0.01	0.11
(1,983)	1:100:A:ILE:HD11	1:113:A:VAL:HG11	2	0.11	0.01	0.11
(1,983)	1:100:A:ILE:HD11	1:113:A:VAL:HG12	2	0.11	0.01	0.11
(1,983)	1:100:A:ILE:HD11	1:113:A:VAL:HG13	2	0.11	0.01	0.11
(1,983)	1:100:A:ILE:HD12	1:113:A:VAL:HG11	2	0.11	0.01	0.11
(1,983)	1:100:A:ILE:HD12	1:113:A:VAL:HG12	2	0.11	0.01	0.11
(1,983)	1:100:A:ILE:HD12	1:113:A:VAL:HG13	2	0.11	0.01	0.11
(1,983)	1:100:A:ILE:HD13	1:113:A:VAL:HG11	2	0.11	0.01	0.11
(1,983)	1:100:A:ILE:HD13	1:113:A:VAL:HG12	2	0.11	0.01	0.11
(1,983)	1:100:A:ILE:HD13	1:113:A:VAL:HG13	2	0.11	0.01	0.11
(2,21)	1:79:A:MET:O	1:138:A:PHE:H	2	0.11	0.01	0.11

¹Number of violated models, ²Standard deviation

9.5 All violated distance restraints [i](#)

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

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



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

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

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG11	10	0.33
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG12	10	0.33
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG13	10	0.33
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG21	10	0.33
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG22	10	0.33
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG23	10	0.33
(1,455)	1:8:A:PHE:H	1:11:A:ASP:H	14	0.32
(1,874)	1:64:A:VAL:HG21	1:66:A:ARG:H	20	0.31
(1,874)	1:64:A:VAL:HG22	1:66:A:ARG:H	20	0.31
(1,874)	1:64:A:VAL:HG23	1:66:A:ARG:H	20	0.31
(1,455)	1:8:A:PHE:H	1:11:A:ASP:H	11	0.27
(1,50)	1:80:A:ASN:H	1:80:A:ASN:HD22	4	0.27
(1,79)	1:13:A:LEU:H	1:14:A:SER:H	18	0.26
(1,50)	1:80:A:ASN:H	1:80:A:ASN:HD22	12	0.26
(1,751)	1:36:A:VAL:HG11	1:44:A:LEU:HD21	9	0.25
(1,751)	1:36:A:VAL:HG11	1:44:A:LEU:HD22	9	0.25

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,751)	1:36:A:VAL:HG11	1:44:A:LEU:HD23	9	0.25
(1,751)	1:36:A:VAL:HG12	1:44:A:LEU:HD21	9	0.25
(1,751)	1:36:A:VAL:HG12	1:44:A:LEU:HD22	9	0.25
(1,751)	1:36:A:VAL:HG12	1:44:A:LEU:HD23	9	0.25
(1,751)	1:36:A:VAL:HG13	1:44:A:LEU:HD21	9	0.25
(1,751)	1:36:A:VAL:HG13	1:44:A:LEU:HD22	9	0.25
(1,751)	1:36:A:VAL:HG13	1:44:A:LEU:HD23	9	0.25
(1,455)	1:8:A:PHE:H	1:11:A:ASP:H	1	0.25
(1,455)	1:8:A:PHE:H	1:11:A:ASP:H	2	0.25
(1,455)	1:8:A:PHE:H	1:11:A:ASP:H	3	0.25
(1,101)	1:150:A:ASN:H	1:151:A:GLY:H	17	0.25
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG11	20	0.23
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG12	20	0.23
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG13	20	0.23
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG21	20	0.23
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG22	20	0.23
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG23	20	0.23
(1,455)	1:8:A:PHE:H	1:11:A:ASP:H	10	0.23
(1,455)	1:8:A:PHE:H	1:11:A:ASP:H	20	0.23
(1,322)	1:28:A:TYR:HD1	1:171:A:LEU:H	20	0.23
(1,322)	1:28:A:TYR:HD2	1:171:A:LEU:H	20	0.23
(1,455)	1:8:A:PHE:H	1:11:A:ASP:H	18	0.22
(1,79)	1:13:A:LEU:H	1:14:A:SER:H	10	0.22
(1,874)	1:64:A:VAL:HG21	1:66:A:ARG:H	13	0.21
(1,874)	1:64:A:VAL:HG22	1:66:A:ARG:H	13	0.21
(1,874)	1:64:A:VAL:HG23	1:66:A:ARG:H	13	0.21
(1,751)	1:36:A:VAL:HG11	1:44:A:LEU:HD21	19	0.21
(1,751)	1:36:A:VAL:HG11	1:44:A:LEU:HD22	19	0.21
(1,751)	1:36:A:VAL:HG11	1:44:A:LEU:HD23	19	0.21
(1,751)	1:36:A:VAL:HG12	1:44:A:LEU:HD21	19	0.21
(1,751)	1:36:A:VAL:HG12	1:44:A:LEU:HD22	19	0.21
(1,751)	1:36:A:VAL:HG12	1:44:A:LEU:HD23	19	0.21
(1,751)	1:36:A:VAL:HG13	1:44:A:LEU:HD21	19	0.21
(1,751)	1:36:A:VAL:HG13	1:44:A:LEU:HD22	19	0.21
(1,751)	1:36:A:VAL:HG13	1:44:A:LEU:HD23	19	0.21
(1,455)	1:8:A:PHE:H	1:11:A:ASP:H	16	0.21
(1,415)	1:131:A:ASP:H	1:134:A:LYS:H	3	0.21
(1,100)	1:58:A:ASP:H	1:59:A:GLY:H	6	0.21
(1,455)	1:8:A:PHE:H	1:11:A:ASP:H	12	0.2
(1,241)	1:37:A:ARG:H	1:66:A:ARG:H	13	0.2
(1,874)	1:64:A:VAL:HG21	1:66:A:ARG:H	2	0.19
(1,874)	1:64:A:VAL:HG22	1:66:A:ARG:H	2	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,874)	1:64:A:VAL:HG23	1:66:A:ARG:H	2	0.19
(1,243)	1:66:A:ARG:H	1:72:A:LEU:HD21	11	0.19
(1,243)	1:66:A:ARG:H	1:72:A:LEU:HD22	11	0.19
(1,243)	1:66:A:ARG:H	1:72:A:LEU:HD23	11	0.19
(1,647)	1:103:A:MET:H	1:105:A:LYS:H	13	0.18
(1,463)	1:16:A:ASP:H	1:18:A:PHE:H	14	0.18
(1,243)	1:66:A:ARG:H	1:72:A:LEU:HD21	17	0.18
(1,243)	1:66:A:ARG:H	1:72:A:LEU:HD22	17	0.18
(1,243)	1:66:A:ARG:H	1:72:A:LEU:HD23	17	0.18
(1,191)	1:64:A:VAL:HG11	1:65:A:GLU:H	18	0.18
(1,191)	1:64:A:VAL:HG12	1:65:A:GLU:H	18	0.18
(1,191)	1:64:A:VAL:HG13	1:65:A:GLU:H	18	0.18
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG11	7	0.17
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG12	7	0.17
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG13	7	0.17
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG21	7	0.17
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG22	7	0.17
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG23	7	0.17
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG11	13	0.17
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG12	13	0.17
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG13	13	0.17
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG21	13	0.17
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG22	13	0.17
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG23	13	0.17
(1,919)	1:18:A:PHE:HZ	1:73:A:ASN:HD21	7	0.17
(1,919)	1:18:A:PHE:HZ	1:73:A:ASN:HD22	7	0.17
(1,730)	1:27:A:VAL:HG11	1:120:A:ILE:HD11	11	0.17
(1,730)	1:27:A:VAL:HG11	1:120:A:ILE:HD12	11	0.17
(1,730)	1:27:A:VAL:HG11	1:120:A:ILE:HD13	11	0.17
(1,730)	1:27:A:VAL:HG12	1:120:A:ILE:HD11	11	0.17
(1,730)	1:27:A:VAL:HG12	1:120:A:ILE:HD12	11	0.17
(1,730)	1:27:A:VAL:HG12	1:120:A:ILE:HD13	11	0.17
(1,730)	1:27:A:VAL:HG13	1:120:A:ILE:HD11	11	0.17
(1,730)	1:27:A:VAL:HG13	1:120:A:ILE:HD12	11	0.17
(1,730)	1:27:A:VAL:HG13	1:120:A:ILE:HD13	11	0.17
(1,455)	1:8:A:PHE:H	1:11:A:ASP:H	19	0.17
(1,415)	1:131:A:ASP:H	1:134:A:LYS:H	8	0.17
(1,405)	1:24:A:ASP:H	1:25:A:ASP:H	8	0.17
(1,241)	1:37:A:ARG:H	1:66:A:ARG:H	10	0.17
(1,108)	1:15:A:SER:H	1:18:A:PHE:HD1	10	0.17
(1,108)	1:15:A:SER:H	1:18:A:PHE:HD2	10	0.17
(1,93)	1:39:A:GLU:H	1:40:A:GLY:H	6	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,874)	1:64:A:VAL:HG21	1:66:A:ARG:H	6	0.16
(1,874)	1:64:A:VAL:HG22	1:66:A:ARG:H	6	0.16
(1,874)	1:64:A:VAL:HG23	1:66:A:ARG:H	6	0.16
(1,874)	1:64:A:VAL:HG21	1:66:A:ARG:H	18	0.16
(1,874)	1:64:A:VAL:HG22	1:66:A:ARG:H	18	0.16
(1,874)	1:64:A:VAL:HG23	1:66:A:ARG:H	18	0.16
(1,462)	1:182:A:LEU:H	1:183:A:GLU:H	14	0.16
(1,391)	1:23:A:VAL:HG11	1:26:A:LEU:H	2	0.16
(1,391)	1:23:A:VAL:HG12	1:26:A:LEU:H	2	0.16
(1,391)	1:23:A:VAL:HG13	1:26:A:LEU:H	2	0.16
(1,391)	1:23:A:VAL:HG11	1:26:A:LEU:H	18	0.16
(1,391)	1:23:A:VAL:HG12	1:26:A:LEU:H	18	0.16
(1,391)	1:23:A:VAL:HG13	1:26:A:LEU:H	18	0.16
(1,160)	1:44:A:LEU:H	1:44:A:LEU:HD11	2	0.16
(1,160)	1:44:A:LEU:H	1:44:A:LEU:HD12	2	0.16
(1,160)	1:44:A:LEU:H	1:44:A:LEU:HD13	2	0.16
(1,93)	1:39:A:GLU:H	1:40:A:GLY:H	15	0.16
(1,89)	1:162:A:ASP:H	1:163:A:GLY:H	3	0.16
(1,947)	1:152:A:GLN:HE21	1:176:A:ILE:HD11	14	0.15
(1,947)	1:152:A:GLN:HE21	1:176:A:ILE:HD12	14	0.15
(1,947)	1:152:A:GLN:HE21	1:176:A:ILE:HD13	14	0.15
(1,947)	1:152:A:GLN:HE22	1:176:A:ILE:HD11	14	0.15
(1,947)	1:152:A:GLN:HE22	1:176:A:ILE:HD12	14	0.15
(1,947)	1:152:A:GLN:HE22	1:176:A:ILE:HD13	14	0.15
(1,942)	1:135:A:ASN:HD21	1:136:A:LEU:H	12	0.15
(1,942)	1:135:A:ASN:HD22	1:136:A:LEU:H	12	0.15
(1,929)	1:106:A:ASN:HD21	1:107:A:ASN:H	2	0.15
(1,929)	1:106:A:ASN:HD22	1:107:A:ASN:H	2	0.15
(1,865)	1:7:A:ILE:HD11	1:8:A:PHE:H	6	0.15
(1,865)	1:7:A:ILE:HD12	1:8:A:PHE:H	6	0.15
(1,865)	1:7:A:ILE:HD13	1:8:A:PHE:H	6	0.15
(1,862)	1:62:A:GLU:H	1:64:A:VAL:HG21	7	0.15
(1,862)	1:62:A:GLU:H	1:64:A:VAL:HG22	7	0.15
(1,862)	1:62:A:GLU:H	1:64:A:VAL:HG23	7	0.15
(1,751)	1:36:A:VAL:HG11	1:44:A:LEU:HD21	3	0.15
(1,751)	1:36:A:VAL:HG11	1:44:A:LEU:HD22	3	0.15
(1,751)	1:36:A:VAL:HG11	1:44:A:LEU:HD23	3	0.15
(1,751)	1:36:A:VAL:HG12	1:44:A:LEU:HD21	3	0.15
(1,751)	1:36:A:VAL:HG12	1:44:A:LEU:HD22	3	0.15
(1,751)	1:36:A:VAL:HG12	1:44:A:LEU:HD23	3	0.15
(1,751)	1:36:A:VAL:HG13	1:44:A:LEU:HD21	3	0.15
(1,751)	1:36:A:VAL:HG13	1:44:A:LEU:HD22	3	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,751)	1:36:A:VAL:HG13	1:44:A:LEU:HD23	3	0.15
(1,655)	1:52:A:GLU:H	1:53:A:GLU:H	7	0.15
(1,391)	1:23:A:VAL:HG11	1:26:A:LEU:H	3	0.15
(1,391)	1:23:A:VAL:HG12	1:26:A:LEU:H	3	0.15
(1,391)	1:23:A:VAL:HG13	1:26:A:LEU:H	3	0.15
(1,384)	1:104:A:GLU:H	1:108:A:ARG:H	16	0.15
(1,194)	1:176:A:ILE:HD11	1:177:A:ILE:H	11	0.15
(1,194)	1:176:A:ILE:HD12	1:177:A:ILE:H	11	0.15
(1,194)	1:176:A:ILE:HD13	1:177:A:ILE:H	11	0.15
(1,192)	1:37:A:ARG:H	1:72:A:LEU:HD21	19	0.15
(1,192)	1:37:A:ARG:H	1:72:A:LEU:HD22	19	0.15
(1,192)	1:37:A:ARG:H	1:72:A:LEU:HD23	19	0.15
(1,79)	1:13:A:LEU:H	1:14:A:SER:H	17	0.15
(2,35)	1:155:A:ILE:H	1:170:A:MET:O	6	0.14
(2,35)	1:155:A:ILE:H	1:170:A:MET:O	11	0.14
(1,942)	1:135:A:ASN:HD21	1:136:A:LEU:H	14	0.14
(1,942)	1:135:A:ASN:HD22	1:136:A:LEU:H	14	0.14
(1,901)	1:156:A:ILE:H	1:169:A:LEU:HD11	8	0.14
(1,901)	1:156:A:ILE:H	1:169:A:LEU:HD12	8	0.14
(1,901)	1:156:A:ILE:H	1:169:A:LEU:HD13	8	0.14
(1,860)	1:139:A:PHE:H	1:153:A:VAL:HG21	7	0.14
(1,860)	1:139:A:PHE:H	1:153:A:VAL:HG22	7	0.14
(1,860)	1:139:A:PHE:H	1:153:A:VAL:HG23	7	0.14
(1,820)	1:76:A:LEU:HD21	1:140:A:ILE:H	9	0.14
(1,820)	1:76:A:LEU:HD22	1:140:A:ILE:H	9	0.14
(1,820)	1:76:A:LEU:HD23	1:140:A:ILE:H	9	0.14
(1,808)	1:121:A:GLN:HE22	1:125:A:VAL:HG11	10	0.14
(1,808)	1:121:A:GLN:HE22	1:125:A:VAL:HG12	10	0.14
(1,808)	1:121:A:GLN:HE22	1:125:A:VAL:HG13	10	0.14
(1,766)	1:77:A:VAL:HG11	1:140:A:ILE:HD11	10	0.14
(1,766)	1:77:A:VAL:HG11	1:140:A:ILE:HD12	10	0.14
(1,766)	1:77:A:VAL:HG11	1:140:A:ILE:HD13	10	0.14
(1,766)	1:77:A:VAL:HG12	1:140:A:ILE:HD11	10	0.14
(1,766)	1:77:A:VAL:HG12	1:140:A:ILE:HD12	10	0.14
(1,766)	1:77:A:VAL:HG12	1:140:A:ILE:HD13	10	0.14
(1,766)	1:77:A:VAL:HG13	1:140:A:ILE:HD11	10	0.14
(1,766)	1:77:A:VAL:HG13	1:140:A:ILE:HD12	10	0.14
(1,766)	1:77:A:VAL:HG13	1:140:A:ILE:HD13	10	0.14
(1,650)	1:38:A:LYS:H	1:41:A:GLU:H	1	0.14
(1,391)	1:23:A:VAL:HG11	1:26:A:LEU:H	9	0.14
(1,391)	1:23:A:VAL:HG12	1:26:A:LEU:H	9	0.14
(1,391)	1:23:A:VAL:HG13	1:26:A:LEU:H	9	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,288)	1:2:A:LEU:HD11	1:3:A:ILE:H	2	0.14
(1,288)	1:2:A:LEU:HD12	1:3:A:ILE:H	2	0.14
(1,288)	1:2:A:LEU:HD13	1:3:A:ILE:H	2	0.14
(1,174)	1:22:A:LEU:H	1:28:A:TYR:HD1	18	0.14
(1,174)	1:22:A:LEU:H	1:28:A:TYR:HD2	18	0.14
(1,98)	1:36:A:VAL:HG11	1:67:A:GLY:H	20	0.14
(1,98)	1:36:A:VAL:HG12	1:67:A:GLY:H	20	0.14
(1,98)	1:36:A:VAL:HG13	1:67:A:GLY:H	20	0.14
(1,93)	1:39:A:GLU:H	1:40:A:GLY:H	16	0.14
(1,90)	1:161:A:VAL:H	1:163:A:GLY:H	9	0.14
(1,79)	1:13:A:LEU:H	1:14:A:SER:H	4	0.14
(1,79)	1:13:A:LEU:H	1:14:A:SER:H	13	0.14
(1,76)	1:4:A:TYR:HD1	1:14:A:SER:H	2	0.14
(1,76)	1:4:A:TYR:HD2	1:14:A:SER:H	2	0.14
(2,35)	1:155:A:ILE:H	1:170:A:MET:O	17	0.13
(2,3)	1:2:A:LEU:H	1:16:A:ASP:O	3	0.13
(1,951)	1:161:A:VAL:H	1:166:A:VAL:HG11	10	0.13
(1,951)	1:161:A:VAL:H	1:166:A:VAL:HG12	10	0.13
(1,951)	1:161:A:VAL:H	1:166:A:VAL:HG13	10	0.13
(1,951)	1:161:A:VAL:H	1:166:A:VAL:HG21	10	0.13
(1,951)	1:161:A:VAL:H	1:166:A:VAL:HG22	10	0.13
(1,951)	1:161:A:VAL:H	1:166:A:VAL:HG23	10	0.13
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG11	14	0.13
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG12	14	0.13
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG13	14	0.13
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG21	14	0.13
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG22	14	0.13
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG23	14	0.13
(1,874)	1:64:A:VAL:HG21	1:66:A:ARG:H	14	0.13
(1,874)	1:64:A:VAL:HG22	1:66:A:ARG:H	14	0.13
(1,874)	1:64:A:VAL:HG23	1:66:A:ARG:H	14	0.13
(1,862)	1:62:A:GLU:H	1:64:A:VAL:HG21	14	0.13
(1,862)	1:62:A:GLU:H	1:64:A:VAL:HG22	14	0.13
(1,862)	1:62:A:GLU:H	1:64:A:VAL:HG23	14	0.13
(1,860)	1:139:A:PHE:H	1:153:A:VAL:HG21	15	0.13
(1,860)	1:139:A:PHE:H	1:153:A:VAL:HG22	15	0.13
(1,860)	1:139:A:PHE:H	1:153:A:VAL:HG23	15	0.13
(1,860)	1:139:A:PHE:H	1:153:A:VAL:HG21	16	0.13
(1,860)	1:139:A:PHE:H	1:153:A:VAL:HG22	16	0.13
(1,860)	1:139:A:PHE:H	1:153:A:VAL:HG23	16	0.13
(1,860)	1:139:A:PHE:H	1:153:A:VAL:HG21	19	0.13
(1,860)	1:139:A:PHE:H	1:153:A:VAL:HG22	19	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,860)	1:139:A:PHE:H	1:153:A:VAL:HG23	19	0.13
(1,797)	1:92:A:ILE:HD11	1:96:A:MET:H	15	0.13
(1,797)	1:92:A:ILE:HD12	1:96:A:MET:H	15	0.13
(1,797)	1:92:A:ILE:HD13	1:96:A:MET:H	15	0.13
(1,756)	1:2:A:LEU:HD21	1:182:A:LEU:HD21	9	0.13
(1,756)	1:2:A:LEU:HD21	1:182:A:LEU:HD22	9	0.13
(1,756)	1:2:A:LEU:HD21	1:182:A:LEU:HD23	9	0.13
(1,756)	1:2:A:LEU:HD22	1:182:A:LEU:HD21	9	0.13
(1,756)	1:2:A:LEU:HD22	1:182:A:LEU:HD22	9	0.13
(1,756)	1:2:A:LEU:HD22	1:182:A:LEU:HD23	9	0.13
(1,756)	1:2:A:LEU:HD23	1:182:A:LEU:HD21	9	0.13
(1,756)	1:2:A:LEU:HD23	1:182:A:LEU:HD22	9	0.13
(1,756)	1:2:A:LEU:HD23	1:182:A:LEU:HD23	9	0.13
(1,743)	1:42:A:ILE:HD11	1:44:A:LEU:HD11	20	0.13
(1,743)	1:42:A:ILE:HD11	1:44:A:LEU:HD12	20	0.13
(1,743)	1:42:A:ILE:HD11	1:44:A:LEU:HD13	20	0.13
(1,743)	1:42:A:ILE:HD12	1:44:A:LEU:HD11	20	0.13
(1,743)	1:42:A:ILE:HD12	1:44:A:LEU:HD12	20	0.13
(1,743)	1:42:A:ILE:HD12	1:44:A:LEU:HD13	20	0.13
(1,743)	1:42:A:ILE:HD13	1:44:A:LEU:HD11	20	0.13
(1,743)	1:42:A:ILE:HD13	1:44:A:LEU:HD12	20	0.13
(1,743)	1:42:A:ILE:HD13	1:44:A:LEU:HD13	20	0.13
(1,609)	1:80:A:ASN:H	1:82:A:TYR:H	2	0.13
(1,601)	1:28:A:TYR:HD1	1:171:A:LEU:HD11	9	0.13
(1,601)	1:28:A:TYR:HD1	1:171:A:LEU:HD12	9	0.13
(1,601)	1:28:A:TYR:HD1	1:171:A:LEU:HD13	9	0.13
(1,601)	1:28:A:TYR:HD2	1:171:A:LEU:HD11	9	0.13
(1,601)	1:28:A:TYR:HD2	1:171:A:LEU:HD12	9	0.13
(1,601)	1:28:A:TYR:HD2	1:171:A:LEU:HD13	9	0.13
(1,517)	1:127:A:LEU:HD11	1:133:A:PHE:HD1	3	0.13
(1,517)	1:127:A:LEU:HD11	1:133:A:PHE:HD2	3	0.13
(1,517)	1:127:A:LEU:HD12	1:133:A:PHE:HD1	3	0.13
(1,517)	1:127:A:LEU:HD12	1:133:A:PHE:HD2	3	0.13
(1,517)	1:127:A:LEU:HD13	1:133:A:PHE:HD1	3	0.13
(1,517)	1:127:A:LEU:HD13	1:133:A:PHE:HD2	3	0.13
(1,517)	1:127:A:LEU:HD11	1:133:A:PHE:HD1	4	0.13
(1,517)	1:127:A:LEU:HD11	1:133:A:PHE:HD2	4	0.13
(1,517)	1:127:A:LEU:HD12	1:133:A:PHE:HD1	4	0.13
(1,517)	1:127:A:LEU:HD12	1:133:A:PHE:HD2	4	0.13
(1,517)	1:127:A:LEU:HD13	1:133:A:PHE:HD1	4	0.13
(1,517)	1:127:A:LEU:HD13	1:133:A:PHE:HD2	4	0.13
(1,500)	1:138:A:PHE:HD1	1:153:A:VAL:HG21	20	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,500)	1:138:A:PHE:HD1	1:153:A:VAL:HG22	20	0.13
(1,500)	1:138:A:PHE:HD1	1:153:A:VAL:HG23	20	0.13
(1,500)	1:138:A:PHE:HD2	1:153:A:VAL:HG21	20	0.13
(1,500)	1:138:A:PHE:HD2	1:153:A:VAL:HG22	20	0.13
(1,500)	1:138:A:PHE:HD2	1:153:A:VAL:HG23	20	0.13
(1,391)	1:23:A:VAL:HG11	1:26:A:LEU:H	12	0.13
(1,391)	1:23:A:VAL:HG12	1:26:A:LEU:H	12	0.13
(1,391)	1:23:A:VAL:HG13	1:26:A:LEU:H	12	0.13
(1,388)	1:116:A:PHE:HD1	1:174:A:GLU:H	12	0.13
(1,388)	1:116:A:PHE:HD2	1:174:A:GLU:H	12	0.13
(1,291)	1:182:A:LEU:HD21	1:183:A:GLU:H	4	0.13
(1,291)	1:182:A:LEU:HD22	1:183:A:GLU:H	4	0.13
(1,291)	1:182:A:LEU:HD23	1:183:A:GLU:H	4	0.13
(1,107)	1:54:A:GLY:H	1:55:A:ALA:H	9	0.13
(1,93)	1:39:A:GLU:H	1:40:A:GLY:H	2	0.13
(2,21)	1:79:A:MET:O	1:138:A:PHE:H	7	0.12
(1,983)	1:100:A:ILE:HD11	1:113:A:VAL:HG11	7	0.12
(1,983)	1:100:A:ILE:HD11	1:113:A:VAL:HG12	7	0.12
(1,983)	1:100:A:ILE:HD11	1:113:A:VAL:HG13	7	0.12
(1,983)	1:100:A:ILE:HD12	1:113:A:VAL:HG11	7	0.12
(1,983)	1:100:A:ILE:HD12	1:113:A:VAL:HG12	7	0.12
(1,983)	1:100:A:ILE:HD12	1:113:A:VAL:HG13	7	0.12
(1,983)	1:100:A:ILE:HD13	1:113:A:VAL:HG11	7	0.12
(1,983)	1:100:A:ILE:HD13	1:113:A:VAL:HG12	7	0.12
(1,983)	1:100:A:ILE:HD13	1:113:A:VAL:HG13	7	0.12
(1,977)	1:113:A:VAL:HG11	1:100:A:ILE:HD11	7	0.12
(1,977)	1:113:A:VAL:HG11	1:100:A:ILE:HD12	7	0.12
(1,977)	1:113:A:VAL:HG11	1:100:A:ILE:HD13	7	0.12
(1,977)	1:113:A:VAL:HG12	1:100:A:ILE:HD11	7	0.12
(1,977)	1:113:A:VAL:HG12	1:100:A:ILE:HD12	7	0.12
(1,977)	1:113:A:VAL:HG12	1:100:A:ILE:HD13	7	0.12
(1,977)	1:113:A:VAL:HG13	1:100:A:ILE:HD11	7	0.12
(1,977)	1:113:A:VAL:HG13	1:100:A:ILE:HD12	7	0.12
(1,977)	1:113:A:VAL:HG13	1:100:A:ILE:HD13	7	0.12
(1,874)	1:64:A:VAL:HG21	1:66:A:ARG:H	15	0.12
(1,874)	1:64:A:VAL:HG22	1:66:A:ARG:H	15	0.12
(1,874)	1:64:A:VAL:HG23	1:66:A:ARG:H	15	0.12
(1,862)	1:62:A:GLU:H	1:64:A:VAL:HG21	4	0.12
(1,862)	1:62:A:GLU:H	1:64:A:VAL:HG22	4	0.12
(1,862)	1:62:A:GLU:H	1:64:A:VAL:HG23	4	0.12
(1,860)	1:139:A:PHE:H	1:153:A:VAL:HG21	8	0.12
(1,860)	1:139:A:PHE:H	1:153:A:VAL:HG22	8	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,860)	1:139:A:PHE:H	1:153:A:VAL:HG23	8	0.12
(1,832)	1:120:A:ILE:HD11	1:174:A:GLU:H	20	0.12
(1,832)	1:120:A:ILE:HD12	1:174:A:GLU:H	20	0.12
(1,832)	1:120:A:ILE:HD13	1:174:A:GLU:H	20	0.12
(1,829)	1:124:A:VAL:HG11	1:128:A:LEU:H	12	0.12
(1,829)	1:124:A:VAL:HG12	1:128:A:LEU:H	12	0.12
(1,829)	1:124:A:VAL:HG13	1:128:A:LEU:H	12	0.12
(1,829)	1:124:A:VAL:HG11	1:128:A:LEU:H	13	0.12
(1,829)	1:124:A:VAL:HG12	1:128:A:LEU:H	13	0.12
(1,829)	1:124:A:VAL:HG13	1:128:A:LEU:H	13	0.12
(1,814)	1:27:A:VAL:HG11	1:173:A:LYS:H	9	0.12
(1,814)	1:27:A:VAL:HG12	1:173:A:LYS:H	9	0.12
(1,814)	1:27:A:VAL:HG13	1:173:A:LYS:H	9	0.12
(1,648)	1:56:A:GLU:H	1:57:A:ASP:H	3	0.12
(1,553)	1:124:A:VAL:HG11	1:128:A:LEU:HD21	19	0.12
(1,553)	1:124:A:VAL:HG11	1:128:A:LEU:HD22	19	0.12
(1,553)	1:124:A:VAL:HG11	1:128:A:LEU:HD23	19	0.12
(1,553)	1:124:A:VAL:HG12	1:128:A:LEU:HD21	19	0.12
(1,553)	1:124:A:VAL:HG12	1:128:A:LEU:HD22	19	0.12
(1,553)	1:124:A:VAL:HG12	1:128:A:LEU:HD23	19	0.12
(1,553)	1:124:A:VAL:HG13	1:128:A:LEU:HD21	19	0.12
(1,553)	1:124:A:VAL:HG13	1:128:A:LEU:HD22	19	0.12
(1,553)	1:124:A:VAL:HG13	1:128:A:LEU:HD23	19	0.12
(1,540)	1:133:A:PHE:HD1	1:136:A:LEU:HD21	8	0.12
(1,540)	1:133:A:PHE:HD1	1:136:A:LEU:HD22	8	0.12
(1,540)	1:133:A:PHE:HD1	1:136:A:LEU:HD23	8	0.12
(1,540)	1:133:A:PHE:HD2	1:136:A:LEU:HD21	8	0.12
(1,540)	1:133:A:PHE:HD2	1:136:A:LEU:HD22	8	0.12
(1,540)	1:133:A:PHE:HD2	1:136:A:LEU:HD23	8	0.12
(1,540)	1:133:A:PHE:HD1	1:136:A:LEU:HD21	17	0.12
(1,540)	1:133:A:PHE:HD1	1:136:A:LEU:HD22	17	0.12
(1,540)	1:133:A:PHE:HD1	1:136:A:LEU:HD23	17	0.12
(1,540)	1:133:A:PHE:HD2	1:136:A:LEU:HD21	17	0.12
(1,540)	1:133:A:PHE:HD2	1:136:A:LEU:HD22	17	0.12
(1,540)	1:133:A:PHE:HD2	1:136:A:LEU:HD23	17	0.12
(1,500)	1:138:A:PHE:HD1	1:153:A:VAL:HG21	10	0.12
(1,500)	1:138:A:PHE:HD1	1:153:A:VAL:HG22	10	0.12
(1,500)	1:138:A:PHE:HD1	1:153:A:VAL:HG23	10	0.12
(1,500)	1:138:A:PHE:HD2	1:153:A:VAL:HG21	10	0.12
(1,500)	1:138:A:PHE:HD2	1:153:A:VAL:HG22	10	0.12
(1,500)	1:138:A:PHE:HD2	1:153:A:VAL:HG23	10	0.12
(1,500)	1:138:A:PHE:HD1	1:153:A:VAL:HG21	16	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,500)	1:138:A:PHE:HD1	1:153:A:VAL:HG22	16	0.12
(1,500)	1:138:A:PHE:HD1	1:153:A:VAL:HG23	16	0.12
(1,500)	1:138:A:PHE:HD2	1:153:A:VAL:HG21	16	0.12
(1,500)	1:138:A:PHE:HD2	1:153:A:VAL:HG22	16	0.12
(1,500)	1:138:A:PHE:HD2	1:153:A:VAL:HG23	16	0.12
(1,449)	1:4:A:TYR:HD1	1:15:A:SER:H	9	0.12
(1,449)	1:4:A:TYR:HD2	1:15:A:SER:H	9	0.12
(1,391)	1:23:A:VAL:HG11	1:26:A:LEU:H	10	0.12
(1,391)	1:23:A:VAL:HG12	1:26:A:LEU:H	10	0.12
(1,391)	1:23:A:VAL:HG13	1:26:A:LEU:H	10	0.12
(1,341)	1:95:A:PHE:HD1	1:98:A:ASN:H	13	0.12
(1,341)	1:95:A:PHE:HD2	1:98:A:ASN:H	13	0.12
(1,341)	1:95:A:PHE:HD1	1:98:A:ASN:H	18	0.12
(1,341)	1:95:A:PHE:HD2	1:98:A:ASN:H	18	0.12
(1,265)	1:70:A:ILE:H	1:72:A:LEU:HD11	11	0.12
(1,265)	1:70:A:ILE:H	1:72:A:LEU:HD12	11	0.12
(1,265)	1:70:A:ILE:H	1:72:A:LEU:HD13	11	0.12
(1,223)	1:6:A:ASP:H	1:13:A:LEU:HD11	14	0.12
(1,223)	1:6:A:ASP:H	1:13:A:LEU:HD12	14	0.12
(1,223)	1:6:A:ASP:H	1:13:A:LEU:HD13	14	0.12
(1,222)	1:109:A:ASP:H	1:113:A:VAL:HG21	7	0.12
(1,222)	1:109:A:ASP:H	1:113:A:VAL:HG22	7	0.12
(1,222)	1:109:A:ASP:H	1:113:A:VAL:HG23	7	0.12
(1,159)	1:2:A:LEU:HD11	1:179:A:GLU:H	18	0.12
(1,159)	1:2:A:LEU:HD12	1:179:A:GLU:H	18	0.12
(1,159)	1:2:A:LEU:HD13	1:179:A:GLU:H	18	0.12
(1,148)	1:71:A:VAL:HG11	1:78:A:GLU:H	5	0.12
(1,148)	1:71:A:VAL:HG12	1:78:A:GLU:H	5	0.12
(1,148)	1:71:A:VAL:HG13	1:78:A:GLU:H	5	0.12
(1,116)	1:74:A:HIS:H	1:76:A:LEU:HD11	2	0.12
(1,116)	1:74:A:HIS:H	1:76:A:LEU:HD12	2	0.12
(1,116)	1:74:A:HIS:H	1:76:A:LEU:HD13	2	0.12
(1,105)	1:127:A:LEU:HD21	1:128:A:LEU:H	4	0.12
(1,105)	1:127:A:LEU:HD22	1:128:A:LEU:H	4	0.12
(1,105)	1:127:A:LEU:HD23	1:128:A:LEU:H	4	0.12
(1,100)	1:58:A:ASP:H	1:59:A:GLY:H	4	0.12
(1,93)	1:39:A:GLU:H	1:40:A:GLY:H	8	0.12
(1,93)	1:39:A:GLU:H	1:40:A:GLY:H	18	0.12
(1,79)	1:13:A:LEU:H	1:14:A:SER:H	20	0.12
(1,40)	1:158:A:TYR:H	1:158:A:TYR:HD1	9	0.12
(1,40)	1:158:A:TYR:H	1:158:A:TYR:HD2	9	0.12
(2,59)	1:35:A:VAL:O	1:67:A:GLY:H	13	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,35)	1:155:A:ILE:H	1:170:A:MET:O	5	0.11
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG11	5	0.11
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG12	5	0.11
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG13	5	0.11
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG21	5	0.11
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG22	5	0.11
(1,950)	1:160:A:ASP:H	1:166:A:VAL:HG23	5	0.11
(1,874)	1:64:A:VAL:HG21	1:66:A:ARG:H	16	0.11
(1,874)	1:64:A:VAL:HG22	1:66:A:ARG:H	16	0.11
(1,874)	1:64:A:VAL:HG23	1:66:A:ARG:H	16	0.11
(1,798)	1:169:A:LEU:HD21	1:170:A:MET:H	5	0.11
(1,798)	1:169:A:LEU:HD22	1:170:A:MET:H	5	0.11
(1,798)	1:169:A:LEU:HD23	1:170:A:MET:H	5	0.11
(1,663)	1:149:A:GLU:H	1:151:A:GLY:H	5	0.11
(1,663)	1:149:A:GLU:H	1:151:A:GLY:H	13	0.11
(1,663)	1:149:A:GLU:H	1:151:A:GLY:H	14	0.11
(1,648)	1:56:A:GLU:H	1:57:A:ASP:H	1	0.11
(1,609)	1:80:A:ASN:H	1:82:A:TYR:H	12	0.11
(1,561)	1:28:A:TYR:HD1	1:176:A:ILE:HD11	17	0.11
(1,561)	1:28:A:TYR:HD1	1:176:A:ILE:HD12	17	0.11
(1,561)	1:28:A:TYR:HD1	1:176:A:ILE:HD13	17	0.11
(1,561)	1:28:A:TYR:HD2	1:176:A:ILE:HD11	17	0.11
(1,561)	1:28:A:TYR:HD2	1:176:A:ILE:HD12	17	0.11
(1,561)	1:28:A:TYR:HD2	1:176:A:ILE:HD13	17	0.11
(1,553)	1:124:A:VAL:HG11	1:128:A:LEU:HD21	20	0.11
(1,553)	1:124:A:VAL:HG11	1:128:A:LEU:HD22	20	0.11
(1,553)	1:124:A:VAL:HG11	1:128:A:LEU:HD23	20	0.11
(1,553)	1:124:A:VAL:HG12	1:128:A:LEU:HD21	20	0.11
(1,553)	1:124:A:VAL:HG12	1:128:A:LEU:HD22	20	0.11
(1,553)	1:124:A:VAL:HG12	1:128:A:LEU:HD23	20	0.11
(1,553)	1:124:A:VAL:HG13	1:128:A:LEU:HD21	20	0.11
(1,553)	1:124:A:VAL:HG13	1:128:A:LEU:HD22	20	0.11
(1,553)	1:124:A:VAL:HG13	1:128:A:LEU:HD23	20	0.11
(1,552)	1:13:A:LEU:HD21	1:169:A:LEU:HD21	9	0.11
(1,552)	1:13:A:LEU:HD21	1:169:A:LEU:HD22	9	0.11
(1,552)	1:13:A:LEU:HD21	1:169:A:LEU:HD23	9	0.11
(1,552)	1:13:A:LEU:HD22	1:169:A:LEU:HD21	9	0.11
(1,552)	1:13:A:LEU:HD22	1:169:A:LEU:HD22	9	0.11
(1,552)	1:13:A:LEU:HD22	1:169:A:LEU:HD23	9	0.11
(1,552)	1:13:A:LEU:HD23	1:169:A:LEU:HD21	9	0.11
(1,552)	1:13:A:LEU:HD23	1:169:A:LEU:HD22	9	0.11
(1,552)	1:13:A:LEU:HD23	1:169:A:LEU:HD23	9	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,540)	1:133:A:PHE:HD1	1:136:A:LEU:HD21	3	0.11
(1,540)	1:133:A:PHE:HD1	1:136:A:LEU:HD22	3	0.11
(1,540)	1:133:A:PHE:HD1	1:136:A:LEU:HD23	3	0.11
(1,540)	1:133:A:PHE:HD2	1:136:A:LEU:HD21	3	0.11
(1,540)	1:133:A:PHE:HD2	1:136:A:LEU:HD22	3	0.11
(1,540)	1:133:A:PHE:HD2	1:136:A:LEU:HD23	3	0.11
(1,391)	1:23:A:VAL:HG11	1:26:A:LEU:H	20	0.11
(1,391)	1:23:A:VAL:HG12	1:26:A:LEU:H	20	0.11
(1,391)	1:23:A:VAL:HG13	1:26:A:LEU:H	20	0.11
(1,291)	1:182:A:LEU:HD21	1:183:A:GLU:H	19	0.11
(1,291)	1:182:A:LEU:HD22	1:183:A:GLU:H	19	0.11
(1,291)	1:182:A:LEU:HD23	1:183:A:GLU:H	19	0.11
(1,265)	1:70:A:ILE:H	1:72:A:LEU:HD11	18	0.11
(1,265)	1:70:A:ILE:H	1:72:A:LEU:HD12	18	0.11
(1,265)	1:70:A:ILE:H	1:72:A:LEU:HD13	18	0.11
(1,241)	1:37:A:ARG:H	1:66:A:ARG:H	7	0.11
(1,183)	1:171:A:LEU:HD21	1:172:A:VAL:H	7	0.11
(1,183)	1:171:A:LEU:HD22	1:172:A:VAL:H	7	0.11
(1,183)	1:171:A:LEU:HD23	1:172:A:VAL:H	7	0.11
(1,160)	1:44:A:LEU:H	1:44:A:LEU:HD11	3	0.11
(1,160)	1:44:A:LEU:H	1:44:A:LEU:HD12	3	0.11
(1,160)	1:44:A:LEU:H	1:44:A:LEU:HD13	3	0.11
(1,93)	1:39:A:GLU:H	1:40:A:GLY:H	13	0.11
(2,35)	1:155:A:ILE:H	1:170:A:MET:O	16	0.1
(2,21)	1:79:A:MET:O	1:138:A:PHE:H	15	0.1
(1,983)	1:100:A:ILE:HD11	1:113:A:VAL:HG11	12	0.1
(1,983)	1:100:A:ILE:HD11	1:113:A:VAL:HG12	12	0.1
(1,983)	1:100:A:ILE:HD11	1:113:A:VAL:HG13	12	0.1
(1,983)	1:100:A:ILE:HD12	1:113:A:VAL:HG11	12	0.1
(1,983)	1:100:A:ILE:HD12	1:113:A:VAL:HG12	12	0.1
(1,983)	1:100:A:ILE:HD12	1:113:A:VAL:HG13	12	0.1
(1,983)	1:100:A:ILE:HD13	1:113:A:VAL:HG11	12	0.1
(1,983)	1:100:A:ILE:HD13	1:113:A:VAL:HG12	12	0.1
(1,983)	1:100:A:ILE:HD13	1:113:A:VAL:HG13	12	0.1
(1,977)	1:113:A:VAL:HG11	1:100:A:ILE:HD11	12	0.1
(1,977)	1:113:A:VAL:HG11	1:100:A:ILE:HD12	12	0.1
(1,977)	1:113:A:VAL:HG11	1:100:A:ILE:HD13	12	0.1
(1,977)	1:113:A:VAL:HG12	1:100:A:ILE:HD11	12	0.1
(1,977)	1:113:A:VAL:HG12	1:100:A:ILE:HD12	12	0.1
(1,977)	1:113:A:VAL:HG12	1:100:A:ILE:HD13	12	0.1
(1,977)	1:113:A:VAL:HG13	1:100:A:ILE:HD11	12	0.1
(1,977)	1:113:A:VAL:HG13	1:100:A:ILE:HD12	12	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,977)	1:113:A:VAL:HG13	1:100:A:ILE:HD13	12	0.1
(1,901)	1:156:A:ILE:H	1:169:A:LEU:HD11	7	0.1
(1,901)	1:156:A:ILE:H	1:169:A:LEU:HD12	7	0.1
(1,901)	1:156:A:ILE:H	1:169:A:LEU:HD13	7	0.1
(1,862)	1:62:A:GLU:H	1:64:A:VAL:HG21	19	0.1
(1,862)	1:62:A:GLU:H	1:64:A:VAL:HG22	19	0.1
(1,862)	1:62:A:GLU:H	1:64:A:VAL:HG23	19	0.1
(1,850)	1:112:A:ASP:H	1:113:A:VAL:HG21	10	0.1
(1,850)	1:112:A:ASP:H	1:113:A:VAL:HG22	10	0.1
(1,850)	1:112:A:ASP:H	1:113:A:VAL:HG23	10	0.1
(1,837)	1:33:A:LYS:H	1:35:A:VAL:HG11	6	0.1
(1,837)	1:33:A:LYS:H	1:35:A:VAL:HG12	6	0.1
(1,837)	1:33:A:LYS:H	1:35:A:VAL:HG13	6	0.1
(1,834)	1:71:A:VAL:HG11	1:75:A:LYS:H	7	0.1
(1,834)	1:71:A:VAL:HG12	1:75:A:LYS:H	7	0.1
(1,834)	1:71:A:VAL:HG13	1:75:A:LYS:H	7	0.1
(1,730)	1:27:A:VAL:HG11	1:120:A:ILE:HD11	18	0.1
(1,730)	1:27:A:VAL:HG11	1:120:A:ILE:HD12	18	0.1
(1,730)	1:27:A:VAL:HG11	1:120:A:ILE:HD13	18	0.1
(1,730)	1:27:A:VAL:HG12	1:120:A:ILE:HD11	18	0.1
(1,730)	1:27:A:VAL:HG12	1:120:A:ILE:HD12	18	0.1
(1,730)	1:27:A:VAL:HG12	1:120:A:ILE:HD13	18	0.1
(1,730)	1:27:A:VAL:HG13	1:120:A:ILE:HD11	18	0.1
(1,730)	1:27:A:VAL:HG13	1:120:A:ILE:HD12	18	0.1
(1,730)	1:27:A:VAL:HG13	1:120:A:ILE:HD13	18	0.1
(1,373)	1:175:A:ALA:H	1:176:A:ILE:HD11	20	0.1
(1,373)	1:175:A:ALA:H	1:176:A:ILE:HD12	20	0.1
(1,373)	1:175:A:ALA:H	1:176:A:ILE:HD13	20	0.1
(1,322)	1:28:A:TYR:HD1	1:171:A:LEU:H	11	0.1
(1,322)	1:28:A:TYR:HD2	1:171:A:LEU:H	11	0.1
(1,241)	1:37:A:ARG:H	1:66:A:ARG:H	1	0.1
(1,223)	1:6:A:ASP:H	1:13:A:LEU:HD11	5	0.1
(1,223)	1:6:A:ASP:H	1:13:A:LEU:HD12	5	0.1
(1,223)	1:6:A:ASP:H	1:13:A:LEU:HD13	5	0.1
(1,89)	1:162:A:ASP:H	1:163:A:GLY:H	20	0.1

10 Dihedral-angle violation analysis ⓘ

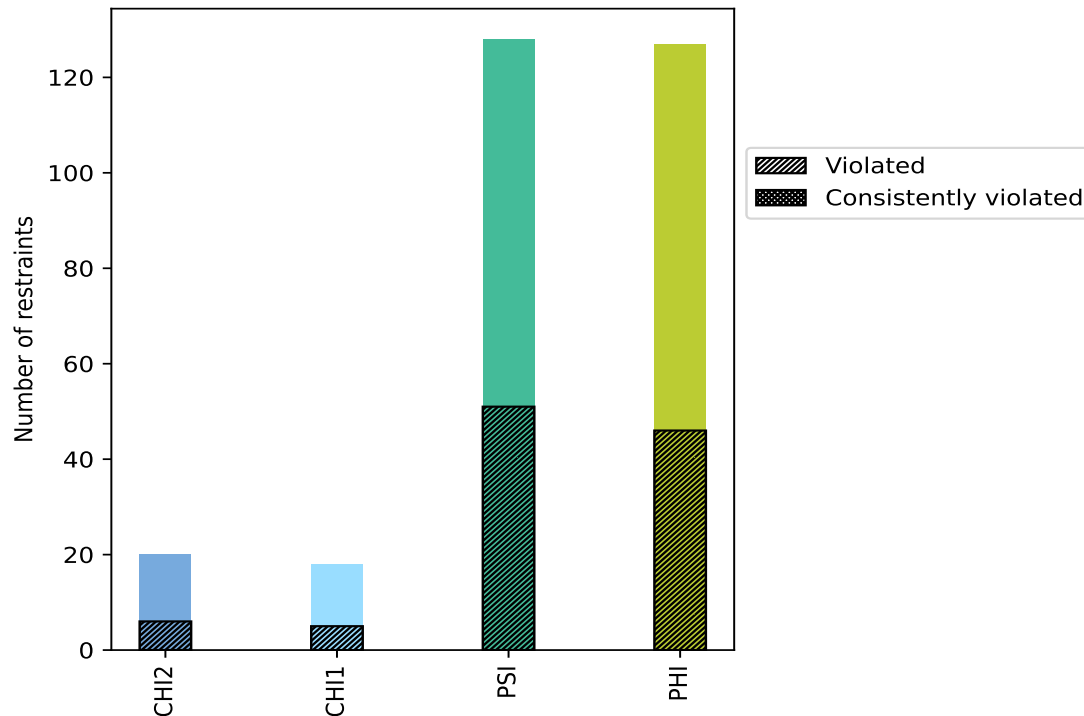
10.1 Summary of dihedral-angle violations ⓘ

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
CHI2	20	6.8	6	30.0	2.0	0	0.0	0.0
CHI1	18	6.1	5	27.8	1.7	0	0.0	0.0
PSI	128	43.7	51	39.8	17.4	0	0.0	0.0
PHI	127	43.3	46	36.2	15.7	0	0.0	0.0
Total	293	100.0	108	36.9	36.9	0	0.0	0.0

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

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



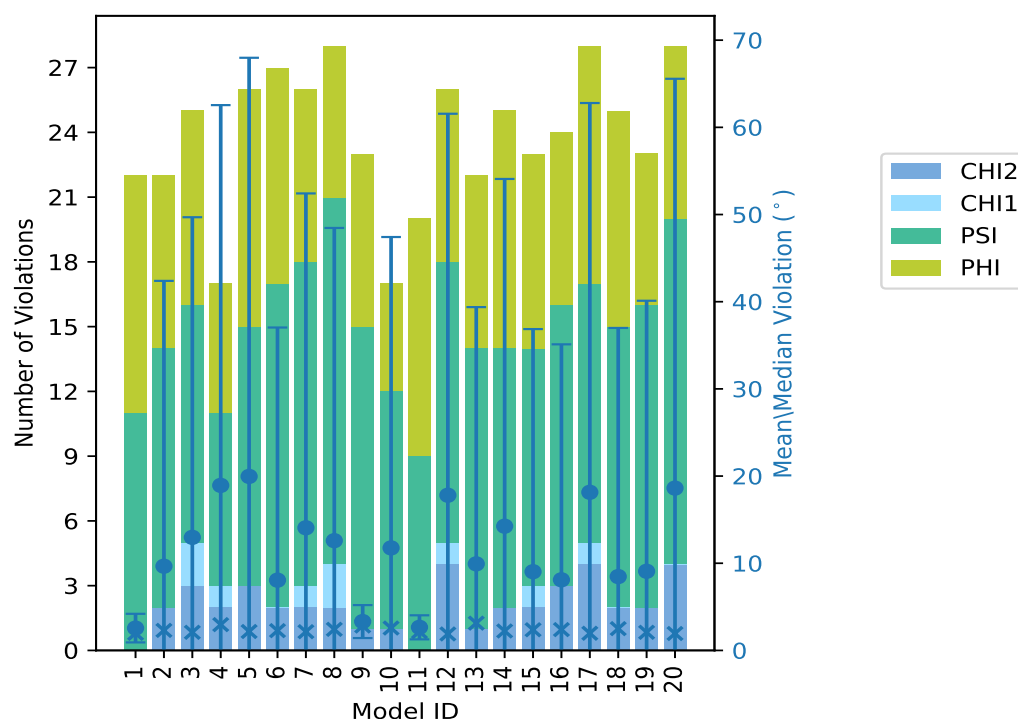
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

10.2 Dihedral-angle violation statistics for each model

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

Model ID	Number of violations					Mean (°)	Max (°)	SD (°)	Median (°)
	CHI2	CHI1	PSI	PHI	Total				
1	0	0	11	11	22	2.56	7.85	1.64	1.96
2	2	0	12	8	22	9.66	159.47	32.73	2.3
3	3	2	11	9	25	12.97	138.56	36.72	2.08
4	2	1	8	6	17	18.93	140.01	43.62	2.96
5	3	0	12	11	26	19.96	158.43	48.02	2.17
6	2	0	15	10	27	8.06	155.72	28.98	2.27
7	2	1	15	8	26	14.07	154.49	38.35	2.15
8	2	2	17	7	28	12.59	147.8	35.87	2.42
9	1	0	14	8	23	3.31	7.82	1.89	2.8
10	1	0	11	5	17	11.76	154.2	35.66	2.57
11	0	0	9	11	20	2.65	6.93	1.38	2.15
12	4	1	13	8	26	17.8	142.11	43.76	1.89
13	1	0	13	8	22	9.93	144.46	29.45	3.13
14	2	0	12	11	25	14.25	157.26	39.83	2.23
15	2	1	11	9	23	9.03	139.15	27.83	2.37
16	3	0	13	8	24	8.1	137.54	27.01	2.39
17	4	1	12	11	28	18.14	155.35	44.65	1.97
18	2	0	13	10	25	8.47	148.02	28.52	2.5
19	2	0	14	7	23	9.08	154.48	31.03	2.08
20	4	0	16	8	28	18.62	156.65	46.95	1.94

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	
CHI2	CHI1	PSI	PHI	Total	Count ¹	%
1	3	15	16	35	1	5.0
1	1	5	9	16	2	10.0
1	0	8	3	12	3	15.0
0	1	4	1	6	4	20.0
0	0	4	4	8	5	25.0
0	0	0	1	1	6	30.0
1	0	1	5	7	7	35.0
0	0	2	1	3	8	40.0
0	0	2	4	6	9	45.0
0	0	1	0	1	10	50.0
0	0	2	2	4	11	55.0

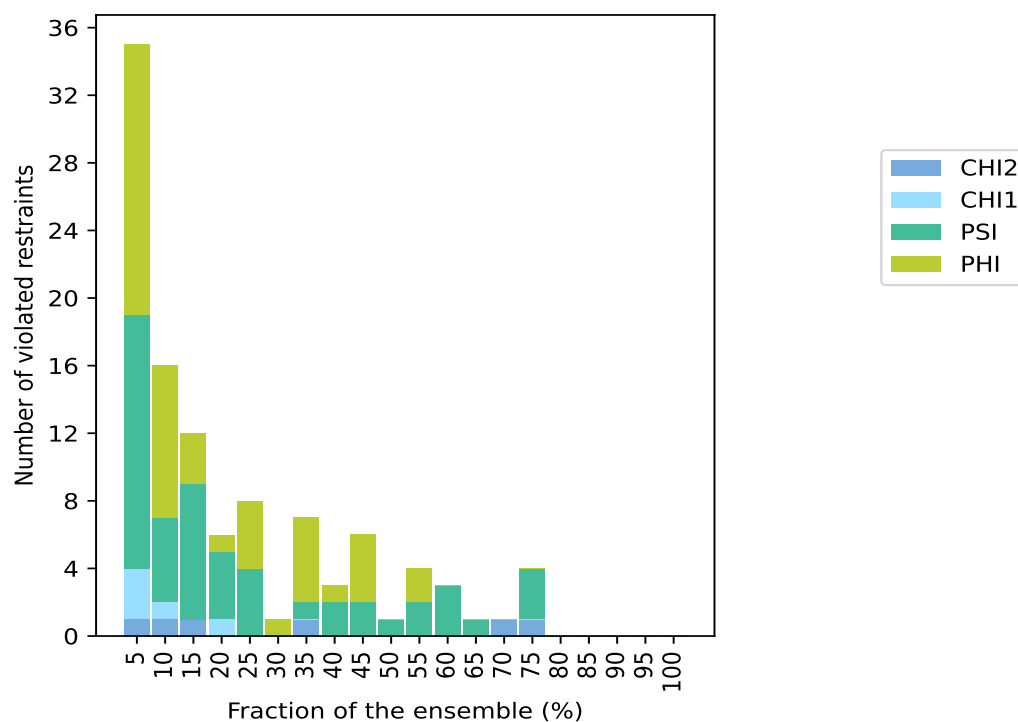
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Number of violated restraints					Fraction of the ensemble	
CHI2	CHI1	PSI	PHI	Total	Count ¹	%
0	0	3	0	3	12	60.0
0	0	1	0	1	13	65.0
1	0	0	0	1	14	70.0
1	0	3	0	4	15	75.0
0	0	0	0	0	16	80.0
0	0	0	0	0	17	85.0
0	0	0	0	0	18	90.0
0	0	0	0	0	19	95.0
0	0	0	0	0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

¹ Number of models with violations

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

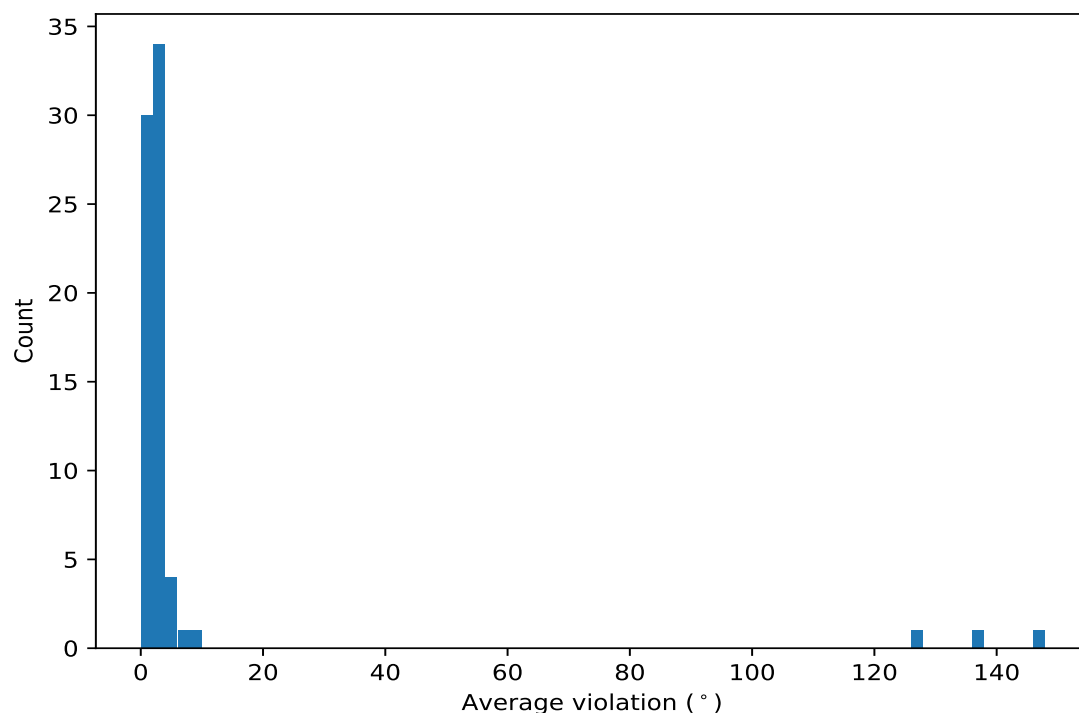


10.4 Most violated dihedral-angle restraints in the ensemble [i](#)

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

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

in the ensemble



10.4.2 Table: Most violated dihedral-angle restraints ⓘ

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

Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Med
(1,293)	1:30:A:PHE:CA	1:30:A:PHE:CB	1:30:A:PHE:CG	1:30:A:PHE:CD1	15	136.11	36.17	140.
(1,175)	1:133:A:PHE:N	1:133:A:PHE:CA	1:133:A:PHE:C	1:134:A:LYS:N	15	6.63	1.05	6.3
(1,230)	1:170:A:MET:N	1:170:A:MET:CA	1:170:A:MET:C	1:171:A:LEU:N	15	2.3	0.7	2.1
(1,167)	1:128:A:LEU:N	1:128:A:LEU:CA	1:128:A:LEU:C	1:129:A:ALA:N	15	2.23	0.73	2.1
(1,271)	1:133:A:PHE:CA	1:133:A:PHE:CB	1:133:A:PHE:CG	1:133:A:PHE:CD1	14	126.67	51.62	144
(1,86)	1:84:A:ASP:N	1:84:A:ASP:CA	1:84:A:ASP:C	1:85:A:ALA:N	13	2.35	1.06	1.8
(1,16)	1:9:A:THR:N	1:9:A:THR:CA	1:9:A:THR:C	1:10:A:ASP:N	12	3.42	1.4	3.5
(1,22)	1:12:A:GLU:N	1:12:A:GLU:CA	1:12:A:GLU:C	1:13:A:LEU:N	12	3.03	1.35	3.3
(1,255)	1:19:A:PRO:N	1:19:A:PRO:CA	1:19:A:PRO:C	1:20:A:MET:N	12	2.77	0.99	2.7
(1,19)	1:10:A:ASP:C	1:11:A:ASP:N	1:11:A:ASP:CA	1:11:A:ASP:C	11	2.52	1.1	2.3
(1,243)	1:177:A:ILE:N	1:177:A:ILE:CA	1:177:A:ILE:C	1:178:A:GLU:N	11	2.43	0.8	2.3
(1,35)	1:27:A:VAL:C	1:28:A:TYR:N	1:28:A:TYR:CA	1:28:A:TYR:C	11	2.27	0.91	1.9
(1,253)	1:26:A:LEU:N	1:26:A:LEU:CA	1:26:A:LEU:C	1:27:A:VAL:N	11	2.22	0.6	2.1
(1,14)	1:8:A:PHE:N	1:8:A:PHE:CA	1:8:A:PHE:C	1:9:A:THR:N	10	5.21	2.64	4.9
(1,13)	1:7:A:ILE:C	1:8:A:PHE:N	1:8:A:PHE:CA	1:8:A:PHE:C	9	4.61	1.3	4.1
(1,52)	1:37:A:ARG:N	1:37:A:ARG:CA	1:37:A:ARG:C	1:38:A:LYS:N	9	2.92	1.03	2.5
(1,172)	1:131:A:ASP:C	1:132:A:ARG:N	1:132:A:ARG:CA	1:132:A:ARG:C	9	2.7	1.26	2.5
(1,4)	1:3:A:ILE:N	1:3:A:ILE:CA	1:3:A:ILE:C	1:4:A:TYR:N	9	2.47	0.87	2.1
(1,180)	1:135:A:ASN:C	1:136:A:LEU:N	1:136:A:LEU:CA	1:136:A:LEU:C	9	2.2	1.05	1.8
(1,83)	1:82:A:TYR:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	9	1.76	0.45	1.7

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Med
(1,18)	1:10:A:ASP:N	1:10:A:ASP:CA	1:10:A:ASP:C	1:11:A:ASP:N	8	8.96	1.33	9.0
(1,57)	1:67:A:GLY:C	1:68:A:ILE:N	1:68:A:ILE:CA	1:68:A:ILE:C	8	2.2	0.84	2.2
(1,251)	1:181:A:CYS:N	1:181:A:CYS:CA	1:181:A:CYS:C	1:182:A:LEU:N	8	2.19	0.83	2.1
(1,15)	1:8:A:PHE:C	1:9:A:THR:N	1:9:A:THR:CA	1:9:A:THR:C	7	5.19	2.59	5.9
(1,54)	1:38:A:LYS:N	1:38:A:LYS:CA	1:38:A:LYS:C	1:39:A:GLU:N	7	2.98	0.9	3.0
(1,53)	1:37:A:ARG:C	1:38:A:LYS:N	1:38:A:LYS:CA	1:38:A:LYS:C	7	1.96	0.67	2.0
(1,214)	1:159:A:ARG:C	1:160:A:ASP:N	1:160:A:ASP:CA	1:160:A:ASP:C	7	1.93	0.68	1.5
(1,77)	1:78:A:GLU:C	1:79:A:MET:N	1:79:A:MET:CA	1:79:A:MET:C	7	1.92	0.78	1.6
(1,227)	1:168:A:THR:C	1:169:A:LEU:N	1:169:A:LEU:CA	1:169:A:LEU:C	7	1.79	0.55	1.6
(1,279)	1:82:A:TYR:CA	1:82:A:TYR:CB	1:82:A:TYR:CG	1:82:A:TYR:CD1	7	1.59	0.36	1.5
(1,21)	1:11:A:ASP:C	1:12:A:GLU:N	1:12:A:GLU:CA	1:12:A:GLU:C	6	3.07	0.77	2.8
(1,17)	1:9:A:THR:C	1:10:A:ASP:N	1:10:A:ASP:CA	1:10:A:ASP:C	5	2.3	0.99	2.6
(1,23)	1:13:A:LEU:C	1:14:A:SER:N	1:14:A:SER:CA	1:14:A:SER:C	5	2.21	1.18	1.8
(1,38)	1:29:A:GLU:N	1:29:A:GLU:CA	1:29:A:GLU:C	1:30:A:PHE:N	5	2.07	0.56	1.9
(1,220)	1:164:A:THR:C	1:165:A:GLU:N	1:165:A:GLU:CA	1:165:A:GLU:C	5	1.94	0.33	1.8
(1,2)	1:2:A:LEU:N	1:2:A:LEU:CA	1:2:A:LEU:C	1:3:A:ILE:N	5	1.88	0.43	2.0
(1,3)	1:2:A:LEU:C	1:3:A:ILE:N	1:3:A:ILE:CA	1:3:A:ILE:C	5	1.86	0.68	1.4
(1,199)	1:146:A:GLU:N	1:146:A:GLU:CA	1:146:A:GLU:C	1:147:A:GLY:N	5	1.56	0.26	1.5
(1,78)	1:79:A:MET:N	1:79:A:MET:CA	1:79:A:MET:C	1:80:A:ASN:N	5	1.4	0.29	1.5
(1,270)	1:133:A:PHE:N	1:133:A:PHE:CA	1:133:A:PHE:CB	1:133:A:PHE:CG	4	4.1	0.46	4.0
(1,25)	1:19:A:PRO:C	1:20:A:MET:N	1:20:A:MET:CA	1:20:A:MET:C	4	2.45	0.35	2.3
(1,223)	1:166:A:VAL:N	1:166:A:VAL:CA	1:166:A:VAL:C	1:167:A:PRO:N	4	2.4	0.77	2.3
(1,36)	1:28:A:TYR:N	1:28:A:TYR:CA	1:28:A:TYR:C	1:29:A:GLU:N	4	2.23	0.17	2.2
(1,171)	1:131:A:ASP:N	1:131:A:ASP:CA	1:131:A:ASP:C	1:132:A:ARG:N	4	1.93	0.46	1.8
(1,40)	1:30:A:PHE:N	1:30:A:PHE:CA	1:30:A:PHE:C	1:31:A:LYS:N	4	1.8	0.57	1.6
(1,265)	1:95:A:PHE:CA	1:95:A:PHE:CB	1:95:A:PHE:CG	1:95:A:PHE:CD1	3	147.05	3.58	148.
(1,24)	1:14:A:SER:N	1:14:A:SER:CA	1:14:A:SER:C	1:15:A:SER:N	3	2.53	0.5	2.3
(1,183)	1:137:A:ALA:N	1:137:A:ALA:CA	1:137:A:ALA:C	1:138:A:PHE:N	3	2.4	0.97	2.3
(1,5)	1:3:A:ILE:C	1:4:A:TYR:N	1:4:A:TYR:CA	1:4:A:TYR:C	3	2.27	0.89	2.4
(1,224)	1:167:A:PRO:N	1:167:A:PRO:CA	1:167:A:PRO:C	1:168:A:THR:N	3	2.22	0.7	2.5
(1,55)	1:65:A:GLU:C	1:66:A:ARG:N	1:66:A:ARG:CA	1:66:A:ARG:C	3	2.14	0.56	2.2
(1,82)	1:82:A:TYR:N	1:82:A:TYR:CA	1:82:A:TYR:C	1:83:A:GLU:N	3	2.14	0.65	1.9
(1,249)	1:180:A:LYS:N	1:180:A:LYS:CA	1:180:A:LYS:C	1:181:A:CYS:N	3	1.83	0.52	1.7
(1,207)	1:155:A:ILE:N	1:155:A:ILE:CA	1:155:A:ILE:C	1:156:A:ILE:N	3	1.78	0.54	2.1
(1,6)	1:4:A:TYR:N	1:4:A:TYR:CA	1:4:A:TYR:C	1:5:A:LYS:N	3	1.74	0.41	1.6
(1,72)	1:75:A:LYS:N	1:75:A:LYS:CA	1:75:A:LYS:C	1:76:A:LEU:N	3	1.43	0.37	1.1
(1,252)	1:25:A:ASP:C	1:26:A:LEU:N	1:26:A:LEU:CA	1:26:A:LEU:C	3	1.26	0.07	1.2
(1,246)	1:178:A:GLU:C	1:179:A:GLU:N	1:179:A:GLU:CA	1:179:A:GLU:C	2	2.94	0.24	2.9
(1,129)	1:105:A:LYS:C	1:106:A:ASN:N	1:106:A:ASN:CA	1:106:A:ASN:C	2	2.1	0.15	2.1
(1,245)	1:178:A:GLU:N	1:178:A:GLU:CA	1:178:A:GLU:C	1:179:A:GLU:N	2	2.1	0.39	2.1
(1,7)	1:4:A:TYR:C	1:5:A:LYS:N	1:5:A:LYS:CA	1:5:A:LYS:C	2	2.07	1.02	2.0
(1,222)	1:165:A:GLU:C	1:166:A:VAL:N	1:166:A:VAL:CA	1:166:A:VAL:C	2	1.94	0.62	1.9
(1,274)	1:91:A:TYR:N	1:91:A:TYR:CA	1:91:A:TYR:CB	1:91:A:TYR:CG	2	1.94	0.65	1.9
(1,200)	1:151:A:GLY:C	1:152:A:GLN:N	1:152:A:GLN:CA	1:152:A:GLN:C	2	1.86	0.26	1.8
(1,70)	1:74:A:HIS:N	1:74:A:HIS:CA	1:74:A:HIS:C	1:75:A:LYS:N	2	1.86	0.73	1.8
(1,216)	1:160:A:ASP:C	1:161:A:VAL:N	1:161:A:VAL:CA	1:161:A:VAL:C	2	1.83	0.72	1.8
(1,275)	1:91:A:TYR:CA	1:91:A:TYR:CB	1:91:A:TYR:CG	1:91:A:TYR:CD1	2	1.79	0.7	1.7
(1,202)	1:152:A:GLN:C	1:153:A:VAL:N	1:153:A:VAL:CA	1:153:A:VAL:C	2	1.7	0.66	1.7
(1,51)	1:36:A:VAL:C	1:37:A:ARG:N	1:37:A:ARG:CA	1:37:A:ARG:C	2	1.6	0.3	1.6
(1,247)	1:179:A:GLU:N	1:179:A:GLU:CA	1:179:A:GLU:C	1:180:A:LYS:N	2	1.58	0.32	1.5
(1,213)	1:158:A:TYR:N	1:158:A:TYR:CA	1:158:A:TYR:C	1:159:A:ARG:N	2	1.56	0.38	1.5

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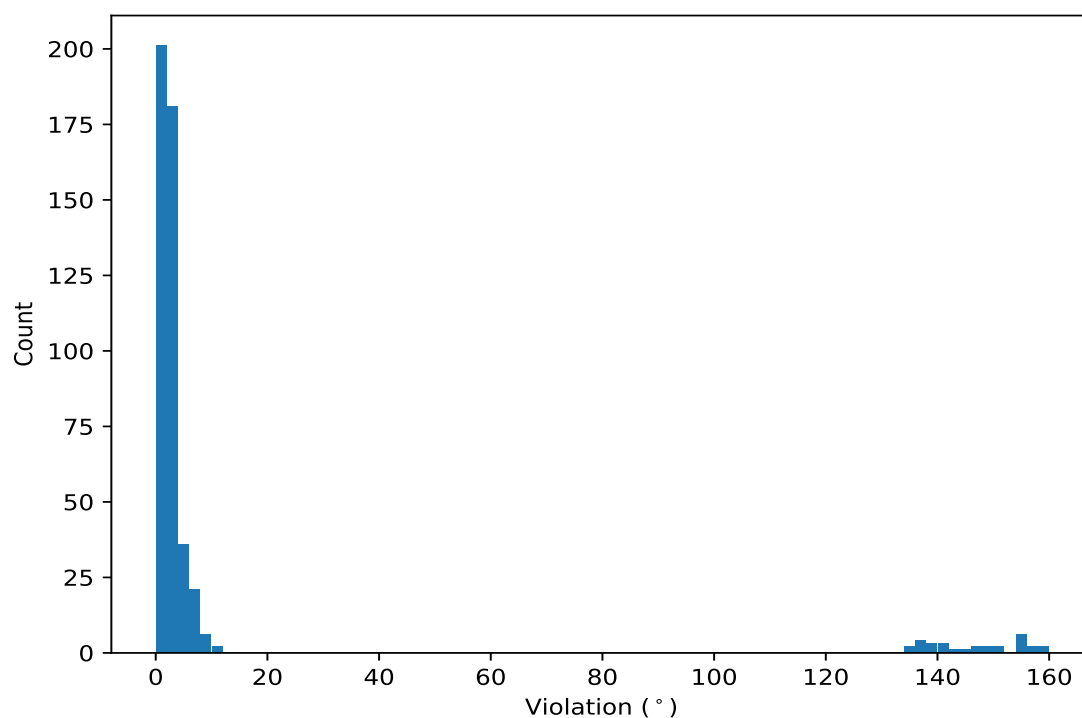
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Med
(1,239)	1:174:A:GLU:C	1:175:A:ALA:N	1:175:A:ALA:CA	1:175:A:ALA:C	2	1.37	0.05	1.3
(1,169)	1:130:A:LYS:N	1:130:A:LYS:CA	1:130:A:LYS:C	1:131:A:ASP:N	2	1.34	0.05	1.3

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

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

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

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



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

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

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,271)	1:133:A:PHE:CA	1:133:A:PHE:CB	1:133:A:PHE:CG	1:133:A:PHE:CD1	2	159.47
(1,293)	1:30:A:PHE:CA	1:30:A:PHE:CB	1:30:A:PHE:CG	1:30:A:PHE:CD1	5	158.43
(1,271)	1:133:A:PHE:CA	1:133:A:PHE:CB	1:133:A:PHE:CG	1:133:A:PHE:CD1	14	157.26
(1,271)	1:133:A:PHE:CA	1:133:A:PHE:CB	1:133:A:PHE:CG	1:133:A:PHE:CD1	20	156.65
(1,271)	1:133:A:PHE:CA	1:133:A:PHE:CB	1:133:A:PHE:CG	1:133:A:PHE:CD1	6	155.72

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,293)	1:30:A:PHE:CA	1:30:A:PHE:CB	1:30:A:PHE:CG	1:30:A:PHE:CD1	17	155.35
(1,293)	1:30:A:PHE:CA	1:30:A:PHE:CB	1:30:A:PHE:CG	1:30:A:PHE:CD1	20	155.08
(1,271)	1:133:A:PHE:CA	1:133:A:PHE:CB	1:133:A:PHE:CG	1:133:A:PHE:CD1	7	154.49
(1,293)	1:30:A:PHE:CA	1:30:A:PHE:CB	1:30:A:PHE:CG	1:30:A:PHE:CD1	19	154.48
(1,271)	1:133:A:PHE:CA	1:133:A:PHE:CB	1:133:A:PHE:CG	1:133:A:PHE:CD1	10	154.2
(1,271)	1:133:A:PHE:CA	1:133:A:PHE:CB	1:133:A:PHE:CG	1:133:A:PHE:CD1	5	151.34
(1,265)	1:95:A:PHE:CA	1:95:A:PHE:CB	1:95:A:PHE:CG	1:95:A:PHE:CD1	20	150.48
(1,265)	1:95:A:PHE:CA	1:95:A:PHE:CB	1:95:A:PHE:CG	1:95:A:PHE:CD1	5	148.57
(1,293)	1:30:A:PHE:CA	1:30:A:PHE:CB	1:30:A:PHE:CG	1:30:A:PHE:CD1	18	148.02
(1,293)	1:30:A:PHE:CA	1:30:A:PHE:CB	1:30:A:PHE:CG	1:30:A:PHE:CD1	8	147.8
(1,281)	1:116:A:PHE:CA	1:116:A:PHE:CB	1:116:A:PHE:CG	1:116:A:PHE:CD1	17	147.76
(1,293)	1:30:A:PHE:CA	1:30:A:PHE:CB	1:30:A:PHE:CG	1:30:A:PHE:CD1	13	144.46
(1,265)	1:95:A:PHE:CA	1:95:A:PHE:CB	1:95:A:PHE:CG	1:95:A:PHE:CD1	12	142.11
(1,293)	1:30:A:PHE:CA	1:30:A:PHE:CB	1:30:A:PHE:CG	1:30:A:PHE:CD1	14	140.77
(1,293)	1:30:A:PHE:CA	1:30:A:PHE:CB	1:30:A:PHE:CG	1:30:A:PHE:CD1	12	140.09
(1,293)	1:30:A:PHE:CA	1:30:A:PHE:CB	1:30:A:PHE:CG	1:30:A:PHE:CD1	4	140.01
(1,293)	1:30:A:PHE:CA	1:30:A:PHE:CB	1:30:A:PHE:CG	1:30:A:PHE:CD1	15	139.15
(1,293)	1:30:A:PHE:CA	1:30:A:PHE:CB	1:30:A:PHE:CG	1:30:A:PHE:CD1	3	138.56
(1,293)	1:30:A:PHE:CA	1:30:A:PHE:CB	1:30:A:PHE:CG	1:30:A:PHE:CD1	7	138.53
(1,293)	1:30:A:PHE:CA	1:30:A:PHE:CB	1:30:A:PHE:CG	1:30:A:PHE:CD1	16	137.54
(1,271)	1:133:A:PHE:CA	1:133:A:PHE:CB	1:133:A:PHE:CG	1:133:A:PHE:CD1	17	136.86
(1,271)	1:133:A:PHE:CA	1:133:A:PHE:CB	1:133:A:PHE:CG	1:133:A:PHE:CD1	4	136.5
(1,271)	1:133:A:PHE:CA	1:133:A:PHE:CB	1:133:A:PHE:CG	1:133:A:PHE:CD1	3	136.37
(1,271)	1:133:A:PHE:CA	1:133:A:PHE:CB	1:133:A:PHE:CG	1:133:A:PHE:CD1	8	135.65
(1,271)	1:133:A:PHE:CA	1:133:A:PHE:CB	1:133:A:PHE:CG	1:133:A:PHE:CD1	12	134.46
(1,18)	1:10:A:ASP:N	1:10:A:ASP:CA	1:10:A:ASP:C	1:11:A:ASP:N	13	11.56
(1,14)	1:8:A:PHE:N	1:8:A:PHE:CA	1:8:A:PHE:C	1:9:A:THR:N	17	10.65
(1,18)	1:10:A:ASP:N	1:10:A:ASP:CA	1:10:A:ASP:C	1:11:A:ASP:N	4	9.74
(1,18)	1:10:A:ASP:N	1:10:A:ASP:CA	1:10:A:ASP:C	1:11:A:ASP:N	7	9.72
(1,18)	1:10:A:ASP:N	1:10:A:ASP:CA	1:10:A:ASP:C	1:11:A:ASP:N	15	9.25
(1,18)	1:10:A:ASP:N	1:10:A:ASP:CA	1:10:A:ASP:C	1:11:A:ASP:N	17	8.84
(1,175)	1:133:A:PHE:N	1:133:A:PHE:CA	1:133:A:PHE:C	1:134:A:LYS:N	5	8.83
(1,175)	1:133:A:PHE:N	1:133:A:PHE:CA	1:133:A:PHE:C	1:134:A:LYS:N	10	8.4
(1,175)	1:133:A:PHE:N	1:133:A:PHE:CA	1:133:A:PHE:C	1:134:A:LYS:N	1	7.85
(1,15)	1:8:A:PHE:C	1:9:A:THR:N	1:9:A:THR:CA	1:9:A:THR:C	9	7.82
(1,15)	1:8:A:PHE:C	1:9:A:THR:N	1:9:A:THR:CA	1:9:A:THR:C	15	7.6
(1,18)	1:10:A:ASP:N	1:10:A:ASP:CA	1:10:A:ASP:C	1:11:A:ASP:N	5	7.57
(1,18)	1:10:A:ASP:N	1:10:A:ASP:CA	1:10:A:ASP:C	1:11:A:ASP:N	8	7.53
(1,18)	1:10:A:ASP:N	1:10:A:ASP:CA	1:10:A:ASP:C	1:11:A:ASP:N	9	7.48
(1,14)	1:8:A:PHE:N	1:8:A:PHE:CA	1:8:A:PHE:C	1:9:A:THR:N	15	7.48
(1,175)	1:133:A:PHE:N	1:133:A:PHE:CA	1:133:A:PHE:C	1:134:A:LYS:N	18	7.04
(1,175)	1:133:A:PHE:N	1:133:A:PHE:CA	1:133:A:PHE:C	1:134:A:LYS:N	11	6.93
(1,15)	1:8:A:PHE:C	1:9:A:THR:N	1:9:A:THR:CA	1:9:A:THR:C	7	6.85
(1,14)	1:8:A:PHE:N	1:8:A:PHE:CA	1:8:A:PHE:C	1:9:A:THR:N	13	6.82
(1,14)	1:8:A:PHE:N	1:8:A:PHE:CA	1:8:A:PHE:C	1:9:A:THR:N	9	6.8
(1,175)	1:133:A:PHE:N	1:133:A:PHE:CA	1:133:A:PHE:C	1:134:A:LYS:N	2	6.73
(1,175)	1:133:A:PHE:N	1:133:A:PHE:CA	1:133:A:PHE:C	1:134:A:LYS:N	14	6.62
(1,13)	1:7:A:ILE:C	1:8:A:PHE:N	1:8:A:PHE:CA	1:8:A:PHE:C	2	6.48
(1,13)	1:7:A:ILE:C	1:8:A:PHE:N	1:8:A:PHE:CA	1:8:A:PHE:C	20	6.41
(1,175)	1:133:A:PHE:N	1:133:A:PHE:CA	1:133:A:PHE:C	1:134:A:LYS:N	6	6.37
(1,175)	1:133:A:PHE:N	1:133:A:PHE:CA	1:133:A:PHE:C	1:134:A:LYS:N	20	6.32

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,175)	1:133:A:PHE:N	1:133:A:PHE:CA	1:133:A:PHE:C	1:134:A:LYS:N	16	6.27
(1,175)	1:133:A:PHE:N	1:133:A:PHE:CA	1:133:A:PHE:C	1:134:A:LYS:N	19	6.23
(1,14)	1:8:A:PHE:N	1:8:A:PHE:CA	1:8:A:PHE:C	1:9:A:THR:N	7	6.11
(1,175)	1:133:A:PHE:N	1:133:A:PHE:CA	1:133:A:PHE:C	1:134:A:LYS:N	9	5.94
(1,15)	1:8:A:PHE:C	1:9:A:THR:N	1:9:A:THR:CA	1:9:A:THR:C	17	5.9
(1,13)	1:7:A:ILE:C	1:8:A:PHE:N	1:8:A:PHE:CA	1:8:A:PHE:C	10	5.83
(1,175)	1:133:A:PHE:N	1:133:A:PHE:CA	1:133:A:PHE:C	1:134:A:LYS:N	13	5.8
(1,16)	1:9:A:THR:N	1:9:A:THR:CA	1:9:A:THR:C	1:10:A:ASP:N	1	5.73
(1,15)	1:8:A:PHE:C	1:9:A:THR:N	1:9:A:THR:CA	1:9:A:THR:C	13	5.58
(1,175)	1:133:A:PHE:N	1:133:A:PHE:CA	1:133:A:PHE:C	1:134:A:LYS:N	7	5.5
(1,16)	1:9:A:THR:N	1:9:A:THR:CA	1:9:A:THR:C	1:10:A:ASP:N	18	5.28
(1,13)	1:7:A:ILE:C	1:8:A:PHE:N	1:8:A:PHE:CA	1:8:A:PHE:C	11	5.13
(1,52)	1:37:A:ARG:N	1:37:A:ARG:CA	1:37:A:ARG:C	1:38:A:LYS:N	13	5.12
(1,22)	1:12:A:GLU:N	1:12:A:GLU:CA	1:12:A:GLU:C	1:13:A:LEU:N	5	4.94
(1,10)	1:6:A:ASP:N	1:6:A:ASP:CA	1:6:A:ASP:C	1:7:A:ILE:N	6	4.84
(1,270)	1:133:A:PHE:N	1:133:A:PHE:CA	1:133:A:PHE:CB	1:133:A:PHE:CG	12	4.82
(1,86)	1:84:A:ASP:N	1:84:A:ASP:CA	1:84:A:ASP:C	1:85:A:ALA:N	2	4.74
(1,54)	1:38:A:LYS:N	1:38:A:LYS:CA	1:38:A:LYS:C	1:39:A:GLU:N	18	4.73
(1,175)	1:133:A:PHE:N	1:133:A:PHE:CA	1:133:A:PHE:C	1:134:A:LYS:N	15	4.69
(1,22)	1:12:A:GLU:N	1:12:A:GLU:CA	1:12:A:GLU:C	1:13:A:LEU:N	4	4.69
(1,172)	1:131:A:ASP:C	1:132:A:ARG:N	1:132:A:ARG:CA	1:132:A:ARG:C	19	4.61
(1,16)	1:9:A:THR:N	1:9:A:THR:CA	1:9:A:THR:C	1:10:A:ASP:N	14	4.53
(1,23)	1:13:A:LEU:C	1:14:A:SER:N	1:14:A:SER:CA	1:14:A:SER:C	7	4.49
(1,21)	1:11:A:ASP:C	1:12:A:GLU:N	1:12:A:GLU:CA	1:12:A:GLU:C	1	4.47
(1,19)	1:10:A:ASP:C	1:11:A:ASP:N	1:11:A:ASP:CA	1:11:A:ASP:C	7	4.42
(1,22)	1:12:A:GLU:N	1:12:A:GLU:CA	1:12:A:GLU:C	1:13:A:LEU:N	15	4.41
(1,172)	1:131:A:ASP:C	1:132:A:ARG:N	1:132:A:ARG:CA	1:132:A:ARG:C	1	4.29
(1,19)	1:10:A:ASP:C	1:11:A:ASP:N	1:11:A:ASP:CA	1:11:A:ASP:C	15	4.26
(1,22)	1:12:A:GLU:N	1:12:A:GLU:CA	1:12:A:GLU:C	1:13:A:LEU:N	14	4.18
(1,255)	1:19:A:PRO:N	1:19:A:PRO:CA	1:19:A:PRO:C	1:20:A:MET:N	4	4.17
(1,264)	1:95:A:PHE:N	1:95:A:PHE:CA	1:95:A:PHE:CB	1:95:A:PHE:CG	8	4.16
(1,255)	1:19:A:PRO:N	1:19:A:PRO:CA	1:19:A:PRO:C	1:20:A:MET:N	20	4.14
(1,16)	1:9:A:THR:N	1:9:A:THR:CA	1:9:A:THR:C	1:10:A:ASP:N	12	4.14
(1,13)	1:7:A:ILE:C	1:8:A:PHE:N	1:8:A:PHE:CA	1:8:A:PHE:C	3	4.13
(1,270)	1:133:A:PHE:N	1:133:A:PHE:CA	1:133:A:PHE:CB	1:133:A:PHE:CG	8	4.08
(1,255)	1:19:A:PRO:N	1:19:A:PRO:CA	1:19:A:PRO:C	1:20:A:MET:N	19	4.04
(1,52)	1:37:A:ARG:N	1:37:A:ARG:CA	1:37:A:ARG:C	1:38:A:LYS:N	7	4.04
(1,16)	1:9:A:THR:N	1:9:A:THR:CA	1:9:A:THR:C	1:10:A:ASP:N	8	4.01
(1,4)	1:3:A:ILE:N	1:3:A:ILE:CA	1:3:A:ILE:C	1:4:A:TYR:N	16	4.01
(1,270)	1:133:A:PHE:N	1:133:A:PHE:CA	1:133:A:PHE:CB	1:133:A:PHE:CG	4	3.93
(1,16)	1:9:A:THR:N	1:9:A:THR:CA	1:9:A:THR:C	1:10:A:ASP:N	19	3.91
(1,172)	1:131:A:ASP:C	1:132:A:ARG:N	1:132:A:ARG:CA	1:132:A:ARG:C	9	3.9
(1,86)	1:84:A:ASP:N	1:84:A:ASP:CA	1:84:A:ASP:C	1:85:A:ALA:N	4	3.9
(1,57)	1:67:A:GLY:C	1:68:A:ILE:N	1:68:A:ILE:CA	1:68:A:ILE:C	10	3.86
(1,13)	1:7:A:ILE:C	1:8:A:PHE:N	1:8:A:PHE:CA	1:8:A:PHE:C	14	3.85
(1,19)	1:10:A:ASP:C	1:11:A:ASP:N	1:11:A:ASP:CA	1:11:A:ASP:C	9	3.83
(1,230)	1:170:A:MET:N	1:170:A:MET:CA	1:170:A:MET:C	1:171:A:LEU:N	11	3.82
(1,251)	1:181:A:CYS:N	1:181:A:CYS:CA	1:181:A:CYS:C	1:182:A:LEU:N	14	3.8
(1,243)	1:177:A:ILE:N	1:177:A:ILE:CA	1:177:A:ILE:C	1:178:A:GLU:N	17	3.79
(1,180)	1:135:A:ASN:C	1:136:A:LEU:N	1:136:A:LEU:CA	1:136:A:LEU:C	6	3.78
(1,180)	1:135:A:ASN:C	1:136:A:LEU:N	1:136:A:LEU:CA	1:136:A:LEU:C	13	3.78

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,14)	1:8:A:PHE:N	1:8:A:PHE:CA	1:8:A:PHE:C	1:9:A:THR:N	4	3.77
(1,17)	1:9:A:THR:C	1:10:A:ASP:N	1:10:A:ASP:CA	1:10:A:ASP:C	14	3.73
(1,230)	1:170:A:MET:N	1:170:A:MET:CA	1:170:A:MET:C	1:171:A:LEU:N	7	3.72
(1,22)	1:12:A:GLU:N	1:12:A:GLU:CA	1:12:A:GLU:C	1:13:A:LEU:N	16	3.71
(1,4)	1:3:A:ILE:N	1:3:A:ILE:CA	1:3:A:ILE:C	1:4:A:TYR:N	11	3.67
(1,86)	1:84:A:ASP:N	1:84:A:ASP:CA	1:84:A:ASP:C	1:85:A:ALA:N	19	3.65
(1,22)	1:12:A:GLU:N	1:12:A:GLU:CA	1:12:A:GLU:C	1:13:A:LEU:N	17	3.62
(1,183)	1:137:A:ALA:N	1:137:A:ALA:CA	1:137:A:ALA:C	1:138:A:PHE:N	13	3.6
(1,35)	1:27:A:VAL:C	1:28:A:TYR:N	1:28:A:TYR:CA	1:28:A:TYR:C	18	3.58
(1,21)	1:11:A:ASP:C	1:12:A:GLU:N	1:12:A:GLU:CA	1:12:A:GLU:C	14	3.58
(1,270)	1:133:A:PHE:N	1:133:A:PHE:CA	1:133:A:PHE:CB	1:133:A:PHE:CG	17	3.56
(1,243)	1:177:A:ILE:N	1:177:A:ILE:CA	1:177:A:ILE:C	1:178:A:GLU:N	18	3.56
(1,54)	1:38:A:LYS:N	1:38:A:LYS:CA	1:38:A:LYS:C	1:39:A:GLU:N	10	3.56
(1,223)	1:166:A:VAL:N	1:166:A:VAL:CA	1:166:A:VAL:C	1:167:A:PRO:N	15	3.53
(1,243)	1:177:A:ILE:N	1:177:A:ILE:CA	1:177:A:ILE:C	1:178:A:GLU:N	13	3.4
(1,77)	1:78:A:GLU:C	1:79:A:MET:N	1:79:A:MET:CA	1:79:A:MET:C	5	3.39
(1,167)	1:128:A:LEU:N	1:128:A:LEU:CA	1:128:A:LEU:C	1:129:A:ALA:N	19	3.36
(1,13)	1:7:A:ILE:C	1:8:A:PHE:N	1:8:A:PHE:CA	1:8:A:PHE:C	16	3.36
(1,293)	1:30:A:PHE:CA	1:30:A:PHE:CB	1:30:A:PHE:CG	1:30:A:PHE:CD1	2	3.33
(1,180)	1:135:A:ASN:C	1:136:A:LEU:N	1:136:A:LEU:CA	1:136:A:LEU:C	9	3.33
(1,167)	1:128:A:LEU:N	1:128:A:LEU:CA	1:128:A:LEU:C	1:129:A:ALA:N	9	3.29
(1,35)	1:27:A:VAL:C	1:28:A:TYR:N	1:28:A:TYR:CA	1:28:A:TYR:C	13	3.29
(1,255)	1:19:A:PRO:N	1:19:A:PRO:CA	1:19:A:PRO:C	1:20:A:MET:N	18	3.28
(1,5)	1:3:A:ILE:C	1:4:A:TYR:N	1:4:A:TYR:CA	1:4:A:TYR:C	9	3.26
(1,35)	1:27:A:VAL:C	1:28:A:TYR:N	1:28:A:TYR:CA	1:28:A:TYR:C	3	3.25
(1,13)	1:7:A:ILE:C	1:8:A:PHE:N	1:8:A:PHE:CA	1:8:A:PHE:C	1	3.25
(1,253)	1:26:A:LEU:N	1:26:A:LEU:CA	1:26:A:LEU:C	1:27:A:VAL:N	9	3.24
(1,24)	1:14:A:SER:N	1:14:A:SER:CA	1:14:A:SER:C	1:15:A:SER:N	13	3.22
(1,172)	1:131:A:ASP:C	1:132:A:ARG:N	1:132:A:ARG:CA	1:132:A:ARG:C	11	3.2
(1,246)	1:178:A:GLU:C	1:179:A:GLU:N	1:179:A:GLU:CA	1:179:A:GLU:C	20	3.18
(1,1)	1:1:A:MET:C	1:2:A:LEU:N	1:2:A:LEU:CA	1:2:A:LEU:C	3	3.17
(1,54)	1:38:A:LYS:N	1:38:A:LYS:CA	1:38:A:LYS:C	1:39:A:GLU:N	12	3.16
(1,230)	1:170:A:MET:N	1:170:A:MET:CA	1:170:A:MET:C	1:171:A:LEU:N	2	3.15
(1,16)	1:9:A:THR:N	1:9:A:THR:CA	1:9:A:THR:C	1:10:A:ASP:N	3	3.13
(1,168)	1:129:A:ALA:C	1:130:A:LYS:N	1:130:A:LYS:CA	1:130:A:LYS:C	11	3.11
(1,214)	1:159:A:ARG:C	1:160:A:ASP:N	1:160:A:ASP:CA	1:160:A:ASP:C	19	3.09
(1,22)	1:12:A:GLU:N	1:12:A:GLU:CA	1:12:A:GLU:C	1:13:A:LEU:N	9	3.09
(1,7)	1:4:A:TYR:C	1:5:A:LYS:N	1:5:A:LYS:CA	1:5:A:LYS:C	8	3.09
(1,52)	1:37:A:ARG:N	1:37:A:ARG:CA	1:37:A:ARG:C	1:38:A:LYS:N	10	3.08
(1,52)	1:37:A:ARG:N	1:37:A:ARG:CA	1:37:A:ARG:C	1:38:A:LYS:N	18	3.07
(1,255)	1:19:A:PRO:N	1:19:A:PRO:CA	1:19:A:PRO:C	1:20:A:MET:N	13	3.04
(1,16)	1:9:A:THR:N	1:9:A:THR:CA	1:9:A:THR:C	1:10:A:ASP:N	6	3.04
(1,54)	1:38:A:LYS:N	1:38:A:LYS:CA	1:38:A:LYS:C	1:39:A:GLU:N	16	3.02
(1,82)	1:82:A:TYR:N	1:82:A:TYR:CA	1:82:A:TYR:C	1:83:A:GLU:N	10	3.01
(1,14)	1:8:A:PHE:N	1:8:A:PHE:CA	1:8:A:PHE:C	1:9:A:THR:N	8	3.01
(1,13)	1:7:A:ILE:C	1:8:A:PHE:N	1:8:A:PHE:CA	1:8:A:PHE:C	18	3.01
(1,35)	1:27:A:VAL:C	1:28:A:TYR:N	1:28:A:TYR:CA	1:28:A:TYR:C	6	3.0
(1,21)	1:11:A:ASP:C	1:12:A:GLU:N	1:12:A:GLU:CA	1:12:A:GLU:C	2	3.0
(1,35)	1:27:A:VAL:C	1:28:A:TYR:N	1:28:A:TYR:CA	1:28:A:TYR:C	8	2.98
(1,25)	1:19:A:PRO:C	1:20:A:MET:N	1:20:A:MET:CA	1:20:A:MET:C	20	2.98
(1,253)	1:26:A:LEU:N	1:26:A:LEU:CA	1:26:A:LEU:C	1:27:A:VAL:N	3	2.97

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,3)	1:2:A:LEU:C	1:3:A:ILE:N	1:3:A:ILE:CA	1:3:A:ILE:C	5	2.97
(1,167)	1:128:A:LEU:N	1:128:A:LEU:CA	1:128:A:LEU:C	1:129:A:ALA:N	4	2.96
(1,16)	1:9:A:THR:N	1:9:A:THR:CA	1:9:A:THR:C	1:10:A:ASP:N	20	2.94
(1,167)	1:128:A:LEU:N	1:128:A:LEU:CA	1:128:A:LEU:C	1:129:A:ALA:N	7	2.93
(1,227)	1:168:A:THR:C	1:169:A:LEU:N	1:169:A:LEU:CA	1:169:A:LEU:C	6	2.91
(1,167)	1:128:A:LEU:N	1:128:A:LEU:CA	1:128:A:LEU:C	1:129:A:ALA:N	8	2.91
(1,53)	1:37:A:ARG:C	1:38:A:LYS:N	1:38:A:LYS:CA	1:38:A:LYS:C	16	2.89
(1,253)	1:26:A:LEU:N	1:26:A:LEU:CA	1:26:A:LEU:C	1:27:A:VAL:N	16	2.88
(1,214)	1:159:A:ARG:C	1:160:A:ASP:N	1:160:A:ASP:CA	1:160:A:ASP:C	8	2.87
(1,4)	1:3:A:ILE:N	1:3:A:ILE:CA	1:3:A:ILE:C	1:4:A:TYR:N	10	2.87
(1,224)	1:167:A:PRO:N	1:167:A:PRO:CA	1:167:A:PRO:C	1:168:A:THR:N	16	2.86
(1,38)	1:29:A:GLU:N	1:29:A:GLU:CA	1:29:A:GLU:C	1:30:A:PHE:N	11	2.86
(1,271)	1:133:A:PHE:CA	1:133:A:PHE:CB	1:133:A:PHE:CG	1:133:A:PHE:CD1	16	2.85
(1,255)	1:19:A:PRO:N	1:19:A:PRO:CA	1:19:A:PRO:C	1:20:A:MET:N	17	2.84
(1,251)	1:181:A:CYS:N	1:181:A:CYS:CA	1:181:A:CYS:C	1:182:A:LEU:N	5	2.81
(1,86)	1:84:A:ASP:N	1:84:A:ASP:CA	1:84:A:ASP:C	1:85:A:ALA:N	9	2.8
(1,55)	1:65:A:GLU:C	1:66:A:ARG:N	1:66:A:ARG:CA	1:66:A:ARG:C	20	2.79
(1,21)	1:11:A:ASP:C	1:12:A:GLU:N	1:12:A:GLU:CA	1:12:A:GLU:C	3	2.77
(1,57)	1:67:A:GLY:C	1:68:A:ILE:N	1:68:A:ILE:CA	1:68:A:ILE:C	15	2.76
(1,17)	1:9:A:THR:C	1:10:A:ASP:N	1:10:A:ASP:CA	1:10:A:ASP:C	18	2.75
(1,77)	1:78:A:GLU:C	1:79:A:MET:N	1:79:A:MET:CA	1:79:A:MET:C	6	2.73
(1,53)	1:37:A:ARG:C	1:38:A:LYS:N	1:38:A:LYS:CA	1:38:A:LYS:C	3	2.73
(1,40)	1:30:A:PHE:N	1:30:A:PHE:CA	1:30:A:PHE:C	1:31:A:LYS:N	1	2.73
(1,246)	1:178:A:GLU:C	1:179:A:GLU:N	1:179:A:GLU:CA	1:179:A:GLU:C	6	2.71
(1,14)	1:8:A:PHE:N	1:8:A:PHE:CA	1:8:A:PHE:C	1:9:A:THR:N	18	2.68
(1,255)	1:19:A:PRO:N	1:19:A:PRO:CA	1:19:A:PRO:C	1:20:A:MET:N	9	2.66
(1,17)	1:9:A:THR:C	1:10:A:ASP:N	1:10:A:ASP:CA	1:10:A:ASP:C	1	2.65
(1,4)	1:3:A:ILE:N	1:3:A:ILE:CA	1:3:A:ILE:C	1:4:A:TYR:N	12	2.64
(1,255)	1:19:A:PRO:N	1:19:A:PRO:CA	1:19:A:PRO:C	1:20:A:MET:N	15	2.62
(1,171)	1:131:A:ASP:N	1:131:A:ASP:CA	1:131:A:ASP:C	1:132:A:ARG:N	11	2.62
(1,274)	1:91:A:TYR:N	1:91:A:TYR:CA	1:91:A:TYR:CB	1:91:A:TYR:CG	7	2.59
(1,70)	1:74:A:HIS:N	1:74:A:HIS:CA	1:74:A:HIS:C	1:75:A:LYS:N	12	2.59
(1,83)	1:82:A:TYR:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	18	2.58
(1,253)	1:26:A:LEU:N	1:26:A:LEU:CA	1:26:A:LEU:C	1:27:A:VAL:N	8	2.57
(1,243)	1:177:A:ILE:N	1:177:A:ILE:CA	1:177:A:ILE:C	1:178:A:GLU:N	10	2.57
(1,222)	1:165:A:GLU:C	1:166:A:VAL:N	1:166:A:VAL:CA	1:166:A:VAL:C	5	2.57
(1,52)	1:37:A:ARG:N	1:37:A:ARG:CA	1:37:A:ARG:C	1:38:A:LYS:N	2	2.57
(1,224)	1:167:A:PRO:N	1:167:A:PRO:CA	1:167:A:PRO:C	1:168:A:THR:N	4	2.56
(1,14)	1:8:A:PHE:N	1:8:A:PHE:CA	1:8:A:PHE:C	1:9:A:THR:N	6	2.56
(1,216)	1:160:A:ASP:C	1:161:A:VAL:N	1:161:A:VAL:CA	1:161:A:VAL:C	11	2.55
(1,251)	1:181:A:CYS:N	1:181:A:CYS:CA	1:181:A:CYS:C	1:182:A:LEU:N	9	2.54
(1,220)	1:164:A:THR:C	1:165:A:GLU:N	1:165:A:GLU:CA	1:165:A:GLU:C	8	2.54
(1,38)	1:29:A:GLU:N	1:29:A:GLU:CA	1:29:A:GLU:C	1:30:A:PHE:N	1	2.54
(1,167)	1:128:A:LEU:N	1:128:A:LEU:CA	1:128:A:LEU:C	1:129:A:ALA:N	2	2.53
(1,57)	1:67:A:GLY:C	1:68:A:ILE:N	1:68:A:ILE:CA	1:68:A:ILE:C	14	2.53
(1,52)	1:37:A:ARG:N	1:37:A:ARG:CA	1:37:A:ARG:C	1:38:A:LYS:N	5	2.53
(1,172)	1:131:A:ASP:C	1:132:A:ARG:N	1:132:A:ARG:CA	1:132:A:ARG:C	15	2.52
(1,25)	1:19:A:PRO:C	1:20:A:MET:N	1:20:A:MET:CA	1:20:A:MET:C	6	2.52
(1,21)	1:11:A:ASP:C	1:12:A:GLU:N	1:12:A:GLU:CA	1:12:A:GLU:C	16	2.52
(1,57)	1:67:A:GLY:C	1:68:A:ILE:N	1:68:A:ILE:CA	1:68:A:ILE:C	18	2.5
(1,275)	1:91:A:TYR:CA	1:91:A:TYR:CB	1:91:A:TYR:CG	1:91:A:TYR:CD1	20	2.49

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,249)	1:180:A:LYS:N	1:180:A:LYS:CA	1:180:A:LYS:C	1:181:A:CYS:N	2	2.49
(1,245)	1:178:A:GLU:N	1:178:A:GLU:CA	1:178:A:GLU:C	1:179:A:GLU:N	2	2.49
(1,223)	1:166:A:VAL:N	1:166:A:VAL:CA	1:166:A:VAL:C	1:167:A:PRO:N	3	2.46
(1,5)	1:3:A:ILE:C	1:4:A:TYR:N	1:4:A:TYR:CA	1:4:A:TYR:C	18	2.45
(1,230)	1:170:A:MET:N	1:170:A:MET:CA	1:170:A:MET:C	1:171:A:LEU:N	9	2.44
(1,251)	1:181:A:CYS:N	1:181:A:CYS:CA	1:181:A:CYS:C	1:182:A:LEU:N	6	2.43
(1,54)	1:38:A:LYS:N	1:38:A:LYS:CA	1:38:A:LYS:C	1:39:A:GLU:N	8	2.43
(1,167)	1:128:A:LEU:N	1:128:A:LEU:CA	1:128:A:LEU:C	1:129:A:ALA:N	20	2.42
(1,43)	1:32:A:GLY:C	1:33:A:LYS:N	1:33:A:LYS:CA	1:33:A:LYS:C	8	2.41
(1,243)	1:177:A:ILE:N	1:177:A:ILE:CA	1:177:A:ILE:C	1:178:A:GLU:N	16	2.4
(1,230)	1:170:A:MET:N	1:170:A:MET:CA	1:170:A:MET:C	1:171:A:LEU:N	18	2.39
(1,183)	1:137:A:ALA:N	1:137:A:ALA:CA	1:137:A:ALA:C	1:138:A:PHE:N	9	2.39
(1,36)	1:28:A:TYR:N	1:28:A:TYR:CA	1:28:A:TYR:C	1:29:A:GLU:N	3	2.39
(1,84)	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	1:84:A:ASP:N	14	2.38
(1,36)	1:28:A:TYR:N	1:28:A:TYR:CA	1:28:A:TYR:C	1:29:A:GLU:N	16	2.38
(1,202)	1:152:A:GLN:C	1:153:A:VAL:N	1:153:A:VAL:CA	1:153:A:VAL:C	15	2.37
(1,19)	1:10:A:ASP:C	1:11:A:ASP:N	1:11:A:ASP:CA	1:11:A:ASP:C	8	2.37
(1,19)	1:10:A:ASP:C	1:11:A:ASP:N	1:11:A:ASP:CA	1:11:A:ASP:C	17	2.35
(1,230)	1:170:A:MET:N	1:170:A:MET:CA	1:170:A:MET:C	1:171:A:LEU:N	12	2.32
(1,24)	1:14:A:SER:N	1:14:A:SER:CA	1:14:A:SER:C	1:15:A:SER:N	6	2.31
(1,3)	1:2:A:LEU:C	1:3:A:ILE:N	1:3:A:ILE:CA	1:3:A:ILE:C	13	2.31
(1,243)	1:177:A:ILE:N	1:177:A:ILE:CA	1:177:A:ILE:C	1:178:A:GLU:N	8	2.3
(1,19)	1:10:A:ASP:C	1:11:A:ASP:N	1:11:A:ASP:CA	1:11:A:ASP:C	19	2.3
(1,253)	1:26:A:LEU:N	1:26:A:LEU:CA	1:26:A:LEU:C	1:27:A:VAL:N	13	2.29
(1,6)	1:4:A:TYR:N	1:4:A:TYR:CA	1:4:A:TYR:C	1:5:A:LYS:N	19	2.29
(1,223)	1:166:A:VAL:N	1:166:A:VAL:CA	1:166:A:VAL:C	1:167:A:PRO:N	6	2.27
(1,83)	1:82:A:TYR:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	14	2.27
(1,53)	1:37:A:ARG:C	1:38:A:LYS:N	1:38:A:LYS:CA	1:38:A:LYS:C	7	2.27
(1,9)	1:5:A:LYS:C	1:6:A:ASP:N	1:6:A:ASP:CA	1:6:A:ASP:C	16	2.27
(1,129)	1:105:A:LYS:C	1:106:A:ASN:N	1:106:A:ASN:CA	1:106:A:ASN:C	15	2.26
(1,50)	1:36:A:VAL:N	1:36:A:VAL:CA	1:36:A:VAL:C	1:37:A:ARG:N	3	2.26
(1,14)	1:8:A:PHE:N	1:8:A:PHE:CA	1:8:A:PHE:C	1:9:A:THR:N	5	2.26
(1,52)	1:37:A:ARG:N	1:37:A:ARG:CA	1:37:A:ARG:C	1:38:A:LYS:N	1	2.25
(1,2)	1:2:A:LEU:N	1:2:A:LEU:CA	1:2:A:LEU:C	1:3:A:ILE:N	14	2.23
(1,86)	1:84:A:ASP:N	1:84:A:ASP:CA	1:84:A:ASP:C	1:85:A:ALA:N	8	2.21
(1,86)	1:84:A:ASP:N	1:84:A:ASP:CA	1:84:A:ASP:C	1:85:A:ALA:N	14	2.21
(1,55)	1:65:A:GLU:C	1:66:A:ARG:N	1:66:A:ARG:CA	1:66:A:ARG:C	13	2.2
(1,25)	1:19:A:PRO:C	1:20:A:MET:N	1:20:A:MET:CA	1:20:A:MET:C	5	2.18
(1,207)	1:155:A:ILE:N	1:155:A:ILE:CA	1:155:A:ILE:C	1:156:A:ILE:N	11	2.17
(1,230)	1:170:A:MET:N	1:170:A:MET:CA	1:170:A:MET:C	1:171:A:LEU:N	8	2.16
(1,207)	1:155:A:ILE:N	1:155:A:ILE:CA	1:155:A:ILE:C	1:156:A:ILE:N	12	2.16
(1,36)	1:28:A:TYR:N	1:28:A:TYR:CA	1:28:A:TYR:C	1:29:A:GLU:N	15	2.16
(1,22)	1:12:A:GLU:N	1:12:A:GLU:CA	1:12:A:GLU:C	1:13:A:LEU:N	8	2.16
(1,19)	1:10:A:ASP:C	1:11:A:ASP:N	1:11:A:ASP:CA	1:11:A:ASP:C	5	2.16
(1,253)	1:26:A:LEU:N	1:26:A:LEU:CA	1:26:A:LEU:C	1:27:A:VAL:N	6	2.15
(1,4)	1:3:A:ILE:N	1:3:A:ILE:CA	1:3:A:ILE:C	1:4:A:TYR:N	8	2.15
(1,200)	1:151:A:GLY:C	1:152:A:GLN:N	1:152:A:GLN:CA	1:152:A:GLN:C	11	2.13
(1,167)	1:128:A:LEU:N	1:128:A:LEU:CA	1:128:A:LEU:C	1:129:A:ALA:N	13	2.13
(1,227)	1:168:A:THR:C	1:169:A:LEU:N	1:169:A:LEU:CA	1:169:A:LEU:C	9	2.12
(1,2)	1:2:A:LEU:N	1:2:A:LEU:CA	1:2:A:LEU:C	1:3:A:ILE:N	19	2.12
(1,230)	1:170:A:MET:N	1:170:A:MET:CA	1:170:A:MET:C	1:171:A:LEU:N	13	2.11

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,52)	1:37:A:ARG:N	1:37:A:ARG:CA	1:37:A:ARG:C	1:38:A:LYS:N	12	2.11
(1,25)	1:19:A:PRO:C	1:20:A:MET:N	1:20:A:MET:CA	1:20:A:MET:C	2	2.1
(1,243)	1:177:A:ILE:N	1:177:A:ILE:CA	1:177:A:ILE:C	1:178:A:GLU:N	9	2.08
(1,54)	1:38:A:LYS:N	1:38:A:LYS:CA	1:38:A:LYS:C	1:39:A:GLU:N	3	2.08
(1,21)	1:11:A:ASP:C	1:12:A:GLU:N	1:12:A:GLU:CA	1:12:A:GLU:C	19	2.08
(1,24)	1:14:A:SER:N	1:14:A:SER:CA	1:14:A:SER:C	1:15:A:SER:N	17	2.07
(1,171)	1:131:A:ASP:N	1:131:A:ASP:CA	1:131:A:ASP:C	1:132:A:ARG:N	1	2.06
(1,53)	1:37:A:ARG:C	1:38:A:LYS:N	1:38:A:LYS:CA	1:38:A:LYS:C	10	2.06
(1,279)	1:82:A:TYR:CA	1:82:A:TYR:CB	1:82:A:TYR:CG	1:82:A:TYR:CD1	15	2.05
(1,8)	1:5:A:LYS:N	1:5:A:LYS:CA	1:5:A:LYS:C	1:6:A:ASP:N	20	2.05
(1,2)	1:2:A:LEU:N	1:2:A:LEU:CA	1:2:A:LEU:C	1:3:A:ILE:N	8	2.04
(1,279)	1:82:A:TYR:CA	1:82:A:TYR:CB	1:82:A:TYR:CG	1:82:A:TYR:CD1	18	2.03
(1,243)	1:177:A:ILE:N	1:177:A:ILE:CA	1:177:A:ILE:C	1:178:A:GLU:N	7	2.03
(1,4)	1:3:A:ILE:N	1:3:A:ILE:CA	1:3:A:ILE:C	1:4:A:TYR:N	19	2.03
(1,167)	1:128:A:LEU:N	1:128:A:LEU:CA	1:128:A:LEU:C	1:129:A:ALA:N	1	2.01
(1,220)	1:164:A:THR:C	1:165:A:GLU:N	1:165:A:GLU:CA	1:165:A:GLU:C	4	2.0
(1,48)	1:35:A:VAL:N	1:35:A:VAL:CA	1:35:A:VAL:C	1:36:A:VAL:N	17	1.99
(1,36)	1:28:A:TYR:N	1:28:A:TYR:CA	1:28:A:TYR:C	1:29:A:GLU:N	17	1.98
(1,19)	1:10:A:ASP:C	1:11:A:ASP:N	1:11:A:ASP:CA	1:11:A:ASP:C	13	1.98
(1,35)	1:27:A:VAL:C	1:28:A:TYR:N	1:28:A:TYR:CA	1:28:A:TYR:C	7	1.97
(1,199)	1:146:A:GLU:N	1:146:A:GLU:CA	1:146:A:GLU:C	1:147:A:GLY:N	20	1.96
(1,167)	1:128:A:LEU:N	1:128:A:LEU:CA	1:128:A:LEU:C	1:129:A:ALA:N	11	1.96
(1,82)	1:82:A:TYR:N	1:82:A:TYR:CA	1:82:A:TYR:C	1:83:A:GLU:N	6	1.96
(1,72)	1:75:A:LYS:N	1:75:A:LYS:CA	1:75:A:LYS:C	1:76:A:LEU:N	5	1.96
(1,38)	1:29:A:GLU:N	1:29:A:GLU:CA	1:29:A:GLU:C	1:30:A:PHE:N	17	1.96
(1,2)	1:2:A:LEU:N	1:2:A:LEU:CA	1:2:A:LEU:C	1:3:A:ILE:N	3	1.96
(1,243)	1:177:A:ILE:N	1:177:A:ILE:CA	1:177:A:ILE:C	1:178:A:GLU:N	6	1.95
(1,230)	1:170:A:MET:N	1:170:A:MET:CA	1:170:A:MET:C	1:171:A:LEU:N	5	1.95
(1,129)	1:105:A:LYS:C	1:106:A:ASN:N	1:106:A:ASN:CA	1:106:A:ASN:C	17	1.95
(1,213)	1:158:A:TYR:N	1:158:A:TYR:CA	1:158:A:TYR:C	1:159:A:ARG:N	16	1.94
(1,57)	1:67:A:GLY:C	1:68:A:ILE:N	1:68:A:ILE:CA	1:68:A:ILE:C	12	1.93
(1,255)	1:19:A:PRO:N	1:19:A:PRO:CA	1:19:A:PRO:C	1:20:A:MET:N	7	1.92
(1,242)	1:176:A:ILE:C	1:177:A:ILE:N	1:177:A:ILE:CA	1:177:A:ILE:C	3	1.92
(1,230)	1:170:A:MET:N	1:170:A:MET:CA	1:170:A:MET:C	1:171:A:LEU:N	1	1.92
(1,77)	1:78:A:GLU:C	1:79:A:MET:N	1:79:A:MET:CA	1:79:A:MET:C	16	1.92
(1,251)	1:181:A:CYS:N	1:181:A:CYS:CA	1:181:A:CYS:C	1:182:A:LEU:N	1	1.91
(1,54)	1:38:A:LYS:N	1:38:A:LYS:CA	1:38:A:LYS:C	1:39:A:GLU:N	20	1.91
(1,23)	1:13:A:LEU:C	1:14:A:SER:N	1:14:A:SER:CA	1:14:A:SER:C	12	1.91
(1,247)	1:179:A:GLU:N	1:179:A:GLU:CA	1:179:A:GLU:C	1:180:A:LYS:N	6	1.9
(1,83)	1:82:A:TYR:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	5	1.9
(1,51)	1:36:A:VAL:C	1:37:A:ARG:N	1:37:A:ARG:CA	1:37:A:ARG:C	11	1.9
(1,253)	1:26:A:LEU:N	1:26:A:LEU:CA	1:26:A:LEU:C	1:27:A:VAL:N	11	1.89
(1,23)	1:13:A:LEU:C	1:14:A:SER:N	1:14:A:SER:CA	1:14:A:SER:C	1	1.89
(1,255)	1:19:A:PRO:N	1:19:A:PRO:CA	1:19:A:PRO:C	1:20:A:MET:N	8	1.88
(1,230)	1:170:A:MET:N	1:170:A:MET:CA	1:170:A:MET:C	1:171:A:LEU:N	20	1.88
(1,180)	1:135:A:ASN:C	1:136:A:LEU:N	1:136:A:LEU:CA	1:136:A:LEU:C	12	1.87
(1,198)	1:145:A:ALA:C	1:146:A:GLU:N	1:146:A:GLU:CA	1:146:A:GLU:C	20	1.86
(1,16)	1:9:A:THR:N	1:9:A:THR:CA	1:9:A:THR:C	1:10:A:ASP:N	10	1.85
(1,4)	1:3:A:ILE:N	1:3:A:ILE:CA	1:3:A:ILE:C	1:4:A:TYR:N	20	1.85
(1,227)	1:168:A:THR:C	1:169:A:LEU:N	1:169:A:LEU:CA	1:169:A:LEU:C	7	1.84
(1,220)	1:164:A:THR:C	1:165:A:GLU:N	1:165:A:GLU:CA	1:165:A:GLU:C	2	1.84

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,201)	1:152:A:GLN:N	1:152:A:GLN:CA	1:152:A:GLN:C	1:153:A:VAL:N	14	1.84
(1,35)	1:27:A:VAL:C	1:28:A:TYR:N	1:28:A:TYR:CA	1:28:A:TYR:C	11	1.84
(1,230)	1:170:A:MET:N	1:170:A:MET:CA	1:170:A:MET:C	1:171:A:LEU:N	14	1.83
(1,4)	1:3:A:ILE:N	1:3:A:ILE:CA	1:3:A:ILE:C	1:4:A:TYR:N	9	1.83
(1,279)	1:82:A:TYR:CA	1:82:A:TYR:CB	1:82:A:TYR:CG	1:82:A:TYR:CD1	16	1.82
(1,83)	1:82:A:TYR:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	11	1.82
(1,86)	1:84:A:ASP:N	1:84:A:ASP:CA	1:84:A:ASP:C	1:85:A:ALA:N	10	1.81
(1,248)	1:179:A:GLU:C	1:180:A:LYS:N	1:180:A:LYS:CA	1:180:A:LYS:C	1	1.8
(1,180)	1:135:A:ASN:C	1:136:A:LEU:N	1:136:A:LEU:CA	1:136:A:LEU:C	18	1.8
(1,19)	1:10:A:ASP:C	1:11:A:ASP:N	1:11:A:ASP:CA	1:11:A:ASP:C	16	1.79
(1,167)	1:128:A:LEU:N	1:128:A:LEU:CA	1:128:A:LEU:C	1:129:A:ALA:N	17	1.78
(1,249)	1:180:A:LYS:N	1:180:A:LYS:CA	1:180:A:LYS:C	1:181:A:CYS:N	20	1.77
(1,86)	1:84:A:ASP:N	1:84:A:ASP:CA	1:84:A:ASP:C	1:85:A:ALA:N	7	1.77
(1,83)	1:82:A:TYR:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	6	1.77
(1,214)	1:159:A:ARG:C	1:160:A:ASP:N	1:160:A:ASP:CA	1:160:A:ASP:C	11	1.76
(1,86)	1:84:A:ASP:N	1:84:A:ASP:CA	1:84:A:ASP:C	1:85:A:ALA:N	5	1.76
(1,266)	1:136:A:LEU:N	1:136:A:LEU:CA	1:136:A:LEU:CB	1:136:A:LEU:CG	3	1.75
(1,78)	1:79:A:MET:N	1:79:A:MET:CA	1:79:A:MET:C	1:80:A:ASN:N	20	1.75
(1,253)	1:26:A:LEU:N	1:26:A:LEU:CA	1:26:A:LEU:C	1:27:A:VAL:N	18	1.73
(1,180)	1:135:A:ASN:C	1:136:A:LEU:N	1:136:A:LEU:CA	1:136:A:LEU:C	15	1.72
(1,83)	1:82:A:TYR:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	2	1.72
(1,40)	1:30:A:PHE:N	1:30:A:PHE:CA	1:30:A:PHE:C	1:31:A:LYS:N	20	1.72
(1,245)	1:178:A:GLU:N	1:178:A:GLU:CA	1:178:A:GLU:C	1:179:A:GLU:N	5	1.71
(1,220)	1:164:A:THR:C	1:165:A:GLU:N	1:165:A:GLU:CA	1:165:A:GLU:C	17	1.71
(1,197)	1:145:A:ALA:N	1:145:A:ALA:CA	1:145:A:ALA:C	1:146:A:GLU:N	8	1.71
(1,253)	1:26:A:LEU:N	1:26:A:LEU:CA	1:26:A:LEU:C	1:27:A:VAL:N	15	1.69
(1,211)	1:157:A:GLU:N	1:157:A:GLU:CA	1:157:A:GLU:C	1:158:A:TYR:N	19	1.68
(1,172)	1:131:A:ASP:C	1:132:A:ARG:N	1:132:A:ARG:CA	1:132:A:ARG:C	16	1.68
(1,39)	1:29:A:GLU:C	1:30:A:PHE:N	1:30:A:PHE:CA	1:30:A:PHE:C	17	1.68
(1,77)	1:78:A:GLU:C	1:79:A:MET:N	1:79:A:MET:CA	1:79:A:MET:C	10	1.67
(1,227)	1:168:A:THR:C	1:169:A:LEU:N	1:169:A:LEU:CA	1:169:A:LEU:C	18	1.65
(1,199)	1:146:A:GLU:N	1:146:A:GLU:CA	1:146:A:GLU:C	1:147:A:GLY:N	1	1.65
(1,230)	1:170:A:MET:N	1:170:A:MET:CA	1:170:A:MET:C	1:171:A:LEU:N	19	1.64
(1,23)	1:13:A:LEU:C	1:14:A:SER:N	1:14:A:SER:CA	1:14:A:SER:C	13	1.64
(1,286)	1:88:A:PHE:N	1:88:A:PHE:CA	1:88:A:PHE:CB	1:88:A:PHE:CG	3	1.63
(1,255)	1:19:A:PRO:N	1:19:A:PRO:CA	1:19:A:PRO:C	1:20:A:MET:N	14	1.63
(1,38)	1:29:A:GLU:N	1:29:A:GLU:CA	1:29:A:GLU:C	1:30:A:PHE:N	9	1.63
(1,78)	1:79:A:MET:N	1:79:A:MET:CA	1:79:A:MET:C	1:80:A:ASN:N	12	1.62
(1,271)	1:133:A:PHE:CA	1:133:A:PHE:CB	1:133:A:PHE:CG	1:133:A:PHE:CD1	19	1.61
(1,86)	1:84:A:ASP:N	1:84:A:ASP:CA	1:84:A:ASP:C	1:85:A:ALA:N	16	1.61
(1,230)	1:170:A:MET:N	1:170:A:MET:CA	1:170:A:MET:C	1:171:A:LEU:N	15	1.6
(1,220)	1:164:A:THR:C	1:165:A:GLU:N	1:165:A:GLU:CA	1:165:A:GLU:C	19	1.6
(1,200)	1:151:A:GLY:C	1:152:A:GLN:N	1:152:A:GLN:CA	1:152:A:GLN:C	14	1.6
(1,86)	1:84:A:ASP:N	1:84:A:ASP:CA	1:84:A:ASP:C	1:85:A:ALA:N	13	1.6
(1,6)	1:4:A:TYR:N	1:4:A:TYR:CA	1:4:A:TYR:C	1:5:A:LYS:N	3	1.6
(1,214)	1:159:A:ARG:C	1:160:A:ASP:N	1:160:A:ASP:CA	1:160:A:ASP:C	3	1.59
(1,253)	1:26:A:LEU:N	1:26:A:LEU:CA	1:26:A:LEU:C	1:27:A:VAL:N	12	1.58
(1,227)	1:168:A:THR:C	1:169:A:LEU:N	1:169:A:LEU:CA	1:169:A:LEU:C	19	1.57
(1,131)	1:108:A:ARG:N	1:108:A:ARG:CA	1:108:A:ARG:C	1:109:A:ASP:N	8	1.57
(1,40)	1:30:A:PHE:N	1:30:A:PHE:CA	1:30:A:PHE:C	1:31:A:LYS:N	14	1.57
(1,199)	1:146:A:GLU:N	1:146:A:GLU:CA	1:146:A:GLU:C	1:147:A:GLY:N	17	1.56

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,172)	1:131:A:ASP:C	1:132:A:ARG:N	1:132:A:ARG:CA	1:132:A:ARG:C	14	1.56
(1,171)	1:131:A:ASP:N	1:131:A:ASP:CA	1:131:A:ASP:C	1:132:A:ARG:N	6	1.56
(1,279)	1:82:A:TYR:CA	1:82:A:TYR:CB	1:82:A:TYR:CG	1:82:A:TYR:CD1	6	1.55
(1,230)	1:170:A:MET:N	1:170:A:MET:CA	1:170:A:MET:C	1:171:A:LEU:N	3	1.55
(1,22)	1:12:A:GLU:N	1:12:A:GLU:CA	1:12:A:GLU:C	1:13:A:LEU:N	11	1.55
(1,167)	1:128:A:LEU:N	1:128:A:LEU:CA	1:128:A:LEU:C	1:129:A:ALA:N	18	1.54
(1,78)	1:79:A:MET:N	1:79:A:MET:CA	1:79:A:MET:C	1:80:A:ASN:N	4	1.53
(1,57)	1:67:A:GLY:C	1:68:A:ILE:N	1:68:A:ILE:CA	1:68:A:ILE:C	7	1.53
(1,53)	1:37:A:ARG:C	1:38:A:LYS:N	1:38:A:LYS:CA	1:38:A:LYS:C	5	1.53
(1,214)	1:159:A:ARG:C	1:160:A:ASP:N	1:160:A:ASP:CA	1:160:A:ASP:C	4	1.52
(1,22)	1:12:A:GLU:N	1:12:A:GLU:CA	1:12:A:GLU:C	1:13:A:LEU:N	7	1.51
(1,15)	1:8:A:PHE:C	1:9:A:THR:N	1:9:A:THR:CA	1:9:A:THR:C	5	1.51
(1,52)	1:37:A:ARG:N	1:37:A:ARG:CA	1:37:A:ARG:C	1:38:A:LYS:N	8	1.5
(1,214)	1:159:A:ARG:C	1:160:A:ASP:N	1:160:A:ASP:CA	1:160:A:ASP:C	2	1.48
(1,199)	1:146:A:GLU:N	1:146:A:GLU:CA	1:146:A:GLU:C	1:147:A:GLY:N	14	1.48
(1,171)	1:131:A:ASP:N	1:131:A:ASP:CA	1:131:A:ASP:C	1:132:A:ARG:N	19	1.48
(1,3)	1:2:A:LEU:C	1:3:A:ILE:N	1:3:A:ILE:CA	1:3:A:ILE:C	3	1.46
(1,172)	1:131:A:ASP:C	1:132:A:ARG:N	1:132:A:ARG:CA	1:132:A:ARG:C	6	1.45
(1,35)	1:27:A:VAL:C	1:28:A:TYR:N	1:28:A:TYR:CA	1:28:A:TYR:C	14	1.45
(1,243)	1:177:A:ILE:N	1:177:A:ILE:CA	1:177:A:ILE:C	1:178:A:GLU:N	12	1.44
(1,82)	1:82:A:TYR:N	1:82:A:TYR:CA	1:82:A:TYR:C	1:83:A:GLU:N	7	1.44
(1,55)	1:65:A:GLU:C	1:66:A:ARG:N	1:66:A:ARG:CA	1:66:A:ARG:C	12	1.43
(1,239)	1:174:A:GLU:C	1:175:A:ALA:N	1:175:A:ALA:CA	1:175:A:ALA:C	17	1.42
(1,279)	1:82:A:TYR:CA	1:82:A:TYR:CB	1:82:A:TYR:CG	1:82:A:TYR:CD1	12	1.41
(1,251)	1:181:A:CYS:N	1:181:A:CYS:CA	1:181:A:CYS:C	1:182:A:LEU:N	7	1.41
(1,218)	1:163:A:GLY:C	1:164:A:THR:N	1:164:A:THR:CA	1:164:A:THR:C	2	1.41
(1,83)	1:82:A:TYR:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	12	1.41
(1,169)	1:130:A:LYS:N	1:130:A:LYS:CA	1:130:A:LYS:C	1:131:A:ASP:N	6	1.4
(1,167)	1:128:A:LEU:N	1:128:A:LEU:CA	1:128:A:LEU:C	1:129:A:ALA:N	12	1.4
(1,28)	1:21:A:LYS:N	1:21:A:LYS:CA	1:21:A:LYS:C	1:22:A:LEU:N	10	1.4
(1,253)	1:26:A:LEU:N	1:26:A:LEU:CA	1:26:A:LEU:C	1:27:A:VAL:N	17	1.38
(1,35)	1:27:A:VAL:C	1:28:A:TYR:N	1:28:A:TYR:CA	1:28:A:TYR:C	4	1.36
(1,223)	1:166:A:VAL:N	1:166:A:VAL:CA	1:166:A:VAL:C	1:167:A:PRO:N	19	1.35
(1,83)	1:82:A:TYR:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	1	1.35
(1,80)	1:81:A:CYS:N	1:81:A:CYS:CA	1:81:A:CYS:C	1:82:A:TYR:N	10	1.35
(1,46)	1:34:A:HIS:N	1:34:A:HIS:CA	1:34:A:HIS:C	1:35:A:VAL:N	18	1.35
(1,58)	1:68:A:ILE:N	1:68:A:ILE:CA	1:68:A:ILE:C	1:69:A:ASP:N	2	1.34
(1,38)	1:29:A:GLU:N	1:29:A:GLU:CA	1:29:A:GLU:C	1:30:A:PHE:N	18	1.34
(1,22)	1:12:A:GLU:N	1:12:A:GLU:CA	1:12:A:GLU:C	1:13:A:LEU:N	19	1.34
(1,252)	1:25:A:ASP:C	1:26:A:LEU:N	1:26:A:LEU:CA	1:26:A:LEU:C	8	1.33
(1,251)	1:181:A:CYS:N	1:181:A:CYS:CA	1:181:A:CYS:C	1:182:A:LEU:N	20	1.33
(1,239)	1:174:A:GLU:C	1:175:A:ALA:N	1:175:A:ALA:CA	1:175:A:ALA:C	13	1.32
(1,227)	1:168:A:THR:C	1:169:A:LEU:N	1:169:A:LEU:CA	1:169:A:LEU:C	5	1.32
(1,222)	1:165:A:GLU:C	1:166:A:VAL:N	1:166:A:VAL:CA	1:166:A:VAL:C	9	1.32
(1,86)	1:84:A:ASP:N	1:84:A:ASP:CA	1:84:A:ASP:C	1:85:A:ALA:N	1	1.32
(1,6)	1:4:A:TYR:N	1:4:A:TYR:CA	1:4:A:TYR:C	1:5:A:LYS:N	20	1.32
(1,274)	1:91:A:TYR:N	1:91:A:TYR:CA	1:91:A:TYR:CB	1:91:A:TYR:CG	15	1.29
(1,169)	1:130:A:LYS:N	1:130:A:LYS:CA	1:130:A:LYS:C	1:131:A:ASP:N	7	1.29
(1,77)	1:78:A:GLU:C	1:79:A:MET:N	1:79:A:MET:CA	1:79:A:MET:C	17	1.29
(1,57)	1:67:A:GLY:C	1:68:A:ILE:N	1:68:A:ILE:CA	1:68:A:ILE:C	5	1.29
(1,51)	1:36:A:VAL:C	1:37:A:ARG:N	1:37:A:ARG:CA	1:37:A:ARG:C	20	1.29

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,16)	1:9:A:THR:N	1:9:A:THR:CA	1:9:A:THR:C	1:10:A:ASP:N	2	1.29
(1,3)	1:2:A:LEU:C	1:3:A:ILE:N	1:3:A:ILE:CA	1:3:A:ILE:C	15	1.29
(1,252)	1:25:A:ASP:C	1:26:A:LEU:N	1:26:A:LEU:CA	1:26:A:LEU:C	12	1.28
(1,180)	1:135:A:ASN:C	1:136:A:LEU:N	1:136:A:LEU:CA	1:136:A:LEU:C	20	1.27
(1,251)	1:181:A:CYS:N	1:181:A:CYS:CA	1:181:A:CYS:C	1:182:A:LEU:N	12	1.26
(1,77)	1:78:A:GLU:C	1:79:A:MET:N	1:79:A:MET:CA	1:79:A:MET:C	1	1.26
(1,35)	1:27:A:VAL:C	1:28:A:TYR:N	1:28:A:TYR:CA	1:28:A:TYR:C	10	1.26
(1,3)	1:2:A:LEU:C	1:3:A:ILE:N	1:3:A:ILE:CA	1:3:A:ILE:C	6	1.26
(1,247)	1:179:A:GLU:N	1:179:A:GLU:CA	1:179:A:GLU:C	1:180:A:LYS:N	20	1.25
(1,224)	1:167:A:PRO:N	1:167:A:PRO:CA	1:167:A:PRO:C	1:168:A:THR:N	5	1.25
(1,279)	1:82:A:TYR:CA	1:82:A:TYR:CB	1:82:A:TYR:CG	1:82:A:TYR:CD1	3	1.24
(1,249)	1:180:A:LYS:N	1:180:A:LYS:CA	1:180:A:LYS:C	1:181:A:CYS:N	7	1.23
(1,243)	1:177:A:ILE:N	1:177:A:ILE:CA	1:177:A:ILE:C	1:178:A:GLU:N	5	1.23
(1,183)	1:137:A:ALA:N	1:137:A:ALA:CA	1:137:A:ALA:C	1:138:A:PHE:N	18	1.22
(1,16)	1:9:A:THR:N	1:9:A:THR:CA	1:9:A:THR:C	1:10:A:ASP:N	16	1.22
(1,206)	1:154:A:ALA:C	1:155:A:ILE:N	1:155:A:ILE:CA	1:155:A:ILE:C	12	1.21
(1,57)	1:67:A:GLY:C	1:68:A:ILE:N	1:68:A:ILE:CA	1:68:A:ILE:C	1	1.21
(1,214)	1:159:A:ARG:C	1:160:A:ASP:N	1:160:A:ASP:CA	1:160:A:ASP:C	17	1.2
(1,86)	1:84:A:ASP:N	1:84:A:ASP:CA	1:84:A:ASP:C	1:85:A:ALA:N	6	1.19
(1,72)	1:75:A:LYS:N	1:75:A:LYS:CA	1:75:A:LYS:C	1:76:A:LEU:N	12	1.19
(1,17)	1:9:A:THR:C	1:10:A:ASP:N	1:10:A:ASP:CA	1:10:A:ASP:C	20	1.19
(1,213)	1:158:A:TYR:N	1:158:A:TYR:CA	1:158:A:TYR:C	1:159:A:ARG:N	7	1.18
(1,182)	1:136:A:LEU:C	1:137:A:ALA:N	1:137:A:ALA:CA	1:137:A:ALA:C	9	1.18
(1,180)	1:135:A:ASN:C	1:136:A:LEU:N	1:136:A:LEU:CA	1:136:A:LEU:C	14	1.18
(1,77)	1:78:A:GLU:C	1:79:A:MET:N	1:79:A:MET:CA	1:79:A:MET:C	19	1.18
(1,252)	1:25:A:ASP:C	1:26:A:LEU:N	1:26:A:LEU:CA	1:26:A:LEU:C	6	1.17
(1,53)	1:37:A:ARG:C	1:38:A:LYS:N	1:38:A:LYS:CA	1:38:A:LYS:C	17	1.17
(1,40)	1:30:A:PHE:N	1:30:A:PHE:CA	1:30:A:PHE:C	1:31:A:LYS:N	16	1.17
(1,22)	1:12:A:GLU:N	1:12:A:GLU:CA	1:12:A:GLU:C	1:13:A:LEU:N	2	1.17
(1,17)	1:9:A:THR:C	1:10:A:ASP:N	1:10:A:ASP:CA	1:10:A:ASP:C	12	1.16
(1,72)	1:75:A:LYS:N	1:75:A:LYS:CA	1:75:A:LYS:C	1:76:A:LEU:N	10	1.15
(1,19)	1:10:A:ASP:C	1:11:A:ASP:N	1:11:A:ASP:CA	1:11:A:ASP:C	3	1.15
(1,199)	1:146:A:GLU:N	1:146:A:GLU:CA	1:146:A:GLU:C	1:147:A:GLY:N	19	1.14
(1,4)	1:3:A:ILE:N	1:3:A:ILE:CA	1:3:A:ILE:C	1:4:A:TYR:N	13	1.14
(1,244)	1:177:A:ILE:C	1:178:A:GLU:N	1:178:A:GLU:CA	1:178:A:GLU:C	2	1.13
(1,172)	1:131:A:ASP:C	1:132:A:ARG:N	1:132:A:ARG:CA	1:132:A:ARG:C	18	1.13
(1,167)	1:128:A:LEU:N	1:128:A:LEU:CA	1:128:A:LEU:C	1:129:A:ALA:N	6	1.13
(1,70)	1:74:A:HIS:N	1:74:A:HIS:CA	1:74:A:HIS:C	1:75:A:LYS:N	3	1.13
(1,11)	1:6:A:ASP:C	1:7:A:ILE:N	1:7:A:ILE:CA	1:7:A:ILE:C	18	1.13
(1,216)	1:160:A:ASP:C	1:161:A:VAL:N	1:161:A:VAL:CA	1:161:A:VAL:C	16	1.11
(1,167)	1:128:A:LEU:N	1:128:A:LEU:CA	1:128:A:LEU:C	1:129:A:ALA:N	16	1.11
(1,78)	1:79:A:MET:N	1:79:A:MET:CA	1:79:A:MET:C	1:80:A:ASN:N	8	1.11
(1,23)	1:13:A:LEU:C	1:14:A:SER:N	1:14:A:SER:CA	1:14:A:SER:C	11	1.1
(1,19)	1:10:A:ASP:C	1:11:A:ASP:N	1:11:A:ASP:CA	1:11:A:ASP:C	1	1.1
(1,5)	1:3:A:ILE:C	1:4:A:TYR:N	1:4:A:TYR:CA	1:4:A:TYR:C	4	1.1
(1,275)	1:91:A:TYR:CA	1:91:A:TYR:CB	1:91:A:TYR:CG	1:91:A:TYR:CD1	17	1.09
(1,227)	1:168:A:THR:C	1:169:A:LEU:N	1:169:A:LEU:CA	1:169:A:LEU:C	1	1.09
(1,178)	1:134:A:LYS:C	1:135:A:ASN:N	1:135:A:ASN:CA	1:135:A:ASN:C	17	1.09
(1,53)	1:37:A:ARG:C	1:38:A:LYS:N	1:38:A:LYS:CA	1:38:A:LYS:C	14	1.09
(1,279)	1:82:A:TYR:CA	1:82:A:TYR:CB	1:82:A:TYR:CG	1:82:A:TYR:CD1	9	1.05
(1,180)	1:135:A:ASN:C	1:136:A:LEU:N	1:136:A:LEU:CA	1:136:A:LEU:C	4	1.05

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,15)	1:8:A:PHE:C	1:9:A:THR:N	1:9:A:THR:CA	1:9:A:THR:C	4	1.05
(1,7)	1:4:A:TYR:C	1:5:A:LYS:N	1:5:A:LYS:CA	1:5:A:LYS:C	5	1.05
(1,250)	1:180:A:LYS:C	1:181:A:CYS:N	1:181:A:CYS:CA	1:181:A:CYS:C	14	1.04
(1,241)	1:176:A:ILE:N	1:176:A:ILE:CA	1:176:A:ILE:C	1:177:A:ILE:N	15	1.04
(1,202)	1:152:A:GLN:C	1:153:A:VAL:N	1:153:A:VAL:CA	1:153:A:VAL:C	11	1.04
(1,2)	1:2:A:LEU:N	1:2:A:LEU:CA	1:2:A:LEU:C	1:3:A:ILE:N	20	1.04
(1,81)	1:81:A:CYS:C	1:82:A:TYR:N	1:82:A:TYR:CA	1:82:A:TYR:C	7	1.03
(1,207)	1:155:A:ILE:N	1:155:A:ILE:CA	1:155:A:ILE:C	1:156:A:ILE:N	15	1.01
(1,78)	1:79:A:MET:N	1:79:A:MET:CA	1:79:A:MET:C	1:80:A:ASN:N	2	1.01
(1,35)	1:27:A:VAL:C	1:28:A:TYR:N	1:28:A:TYR:CA	1:28:A:TYR:C	15	1.01
(1,20)	1:11:A:ASP:N	1:11:A:ASP:CA	1:11:A:ASP:C	1:12:A:GLU:N	3	1.01
(1,255)	1:19:A:PRO:N	1:19:A:PRO:CA	1:19:A:PRO:C	1:20:A:MET:N	2	1.0
(1,83)	1:82:A:TYR:C	1:83:A:GLU:N	1:83:A:GLU:CA	1:83:A:GLU:C	17	1.0