



Full wwPDB NMR Structure Validation Report ⓘ

Mar 5, 2026 – 03:52 PM UTC

PDB ID : 2MKJ / pdb_00002mkj
BMRB ID : 19777
Title : Solution structure of tandem RRM domains of cytoplasmic polyadenylation element binding protein 4 (CPEB4) in free state
Authors : Afroz, T.; Skrisovska, L.; Belloc, E.; Boixet, J.G.; Mendez, R.; Allain, F.H.-T.
Deposited on : 2014-02-07

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 : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
BMRB Restraints Analysis : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

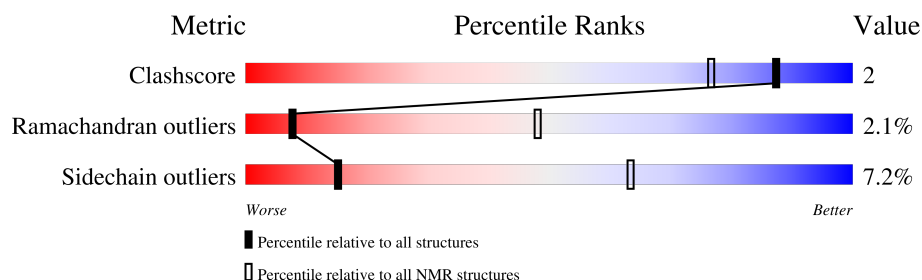
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 68%.

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



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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

Mol	Chain	Length	Quality of chain
1	A	203	

2 Ensemble composition and analysis

This entry contains 20 models. Model 2 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:62-A:95, A:109-A:140, A:145-A:254 (176)	1.75	2

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

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

NmrClust was unable to cluster the ensemble.

Error message: Inconsistent models

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 3182 atoms, of which 1582 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Cytoplasmic polyadenylation element-binding protein 4.

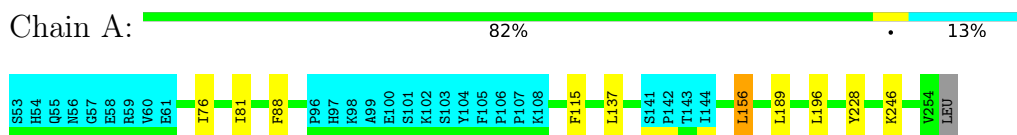
Mol	Chain	Residues	Atoms						Trace
1	A	202	Total	C	H	N	O	S	0
			3182	1023	1582	273	298	6	

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: Cytoplasmic polyadenylation element-binding protein 4

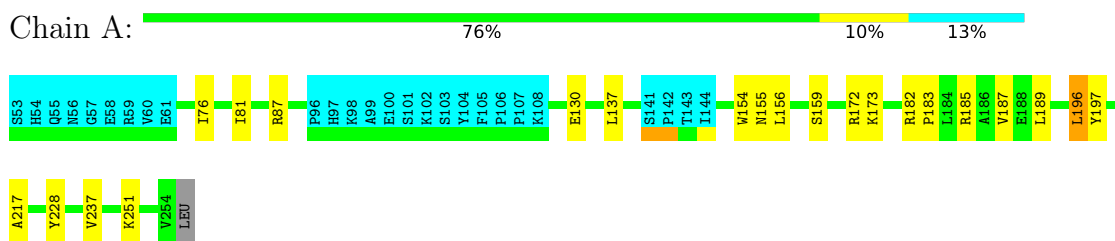


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

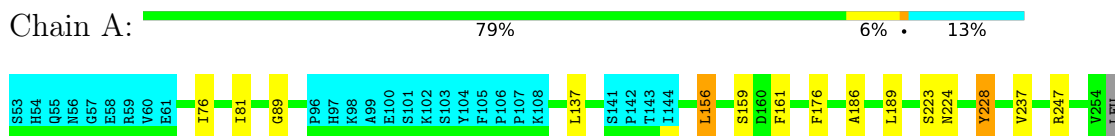
4.2.1 Score per residue for model 1

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 4



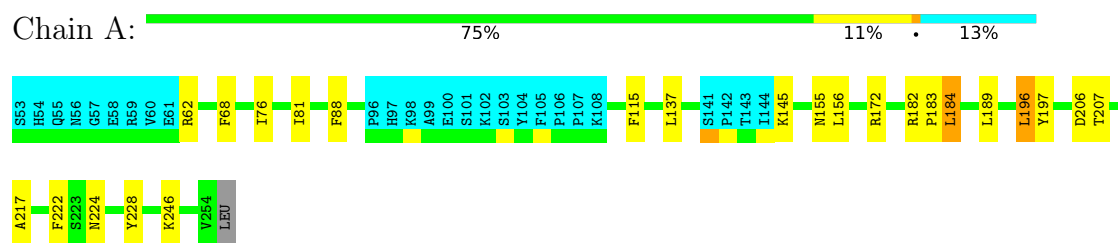
4.2.2 Score per residue for model 2 (medoid)

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 4



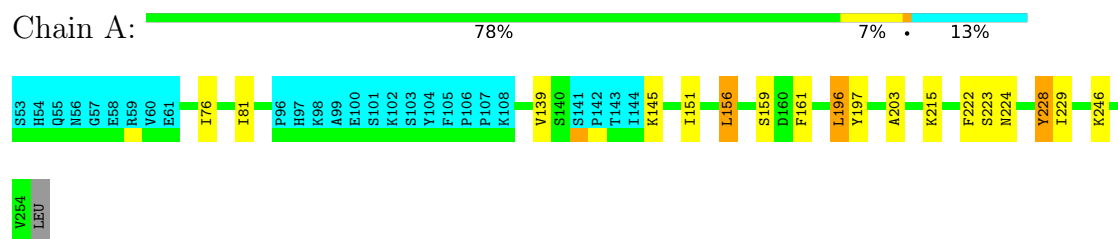
4.2.3 Score per residue for model 3

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 4



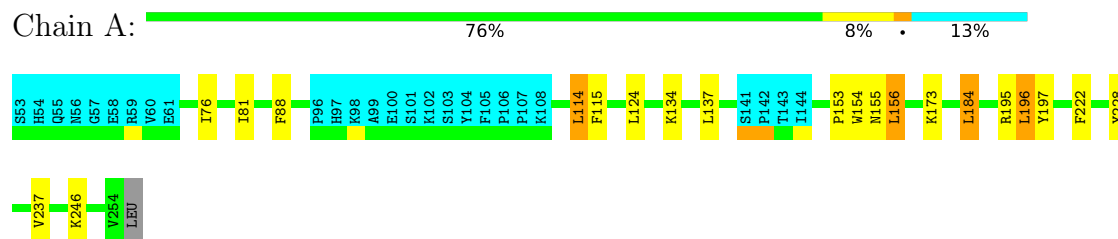
4.2.4 Score per residue for model 4

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 4



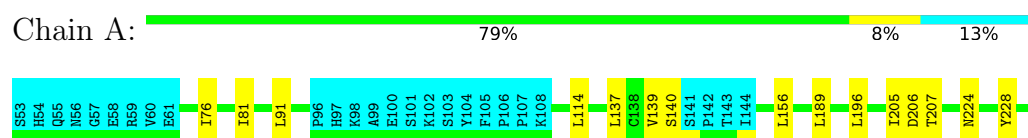
4.2.5 Score per residue for model 5

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 4



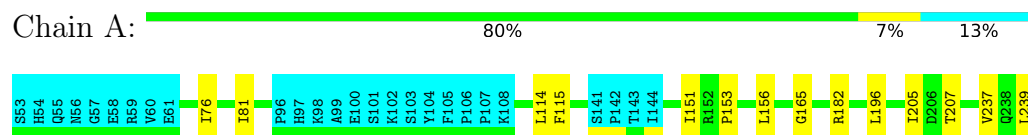
4.2.6 Score per residue for model 6

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 4



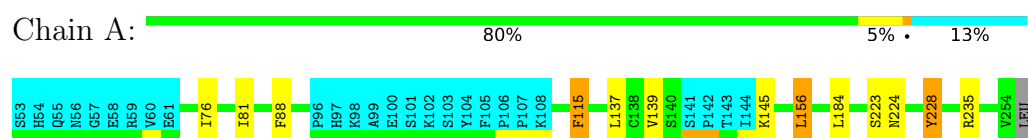
4.2.7 Score per residue for model 7

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 4



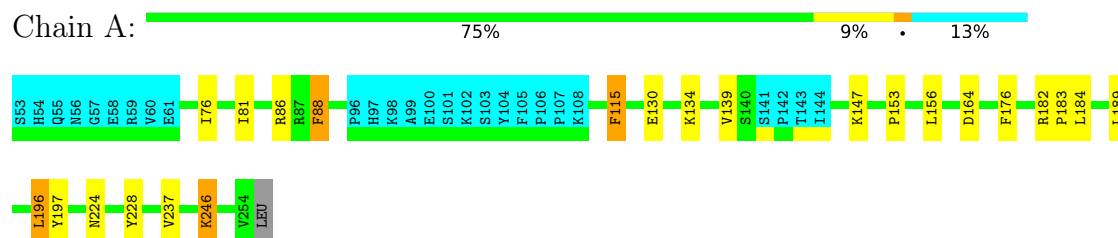
4.2.8 Score per residue for model 8

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 4



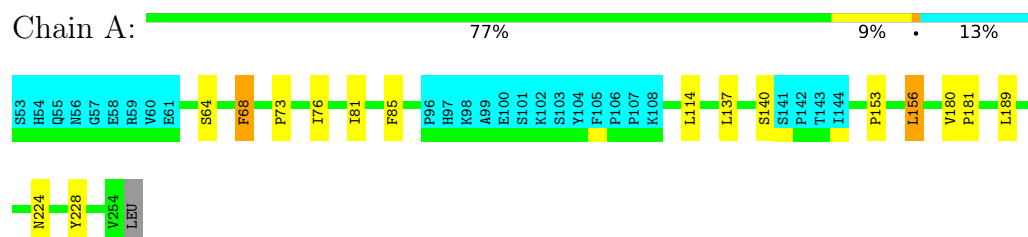
4.2.9 Score per residue for model 9

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 4



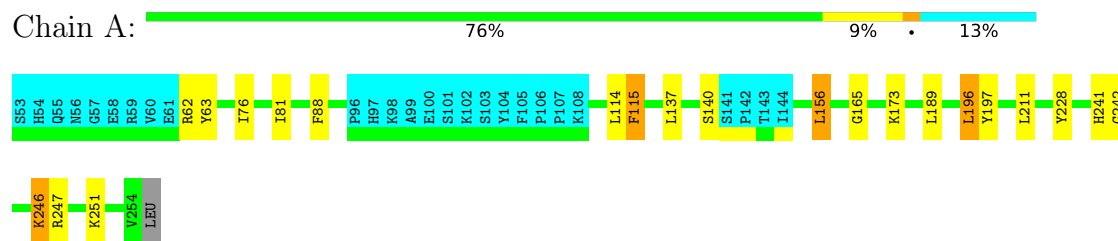
4.2.10 Score per residue for model 10

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 4



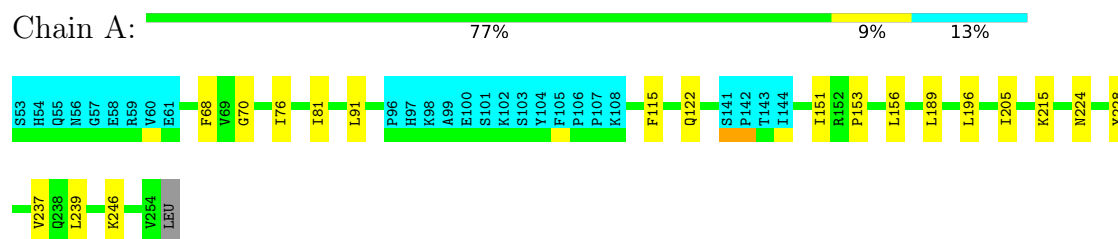
4.2.11 Score per residue for model 11

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 4



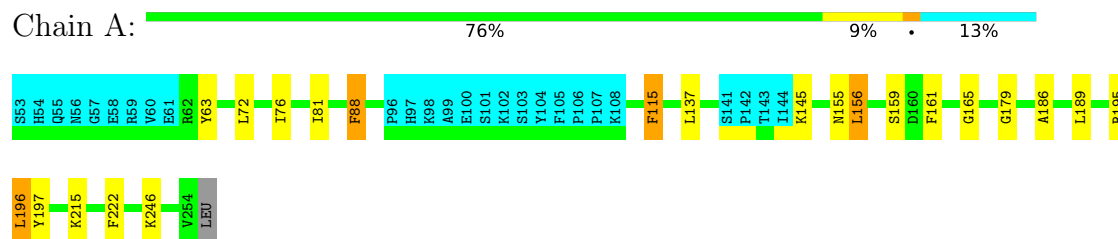
4.2.12 Score per residue for model 12

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 4



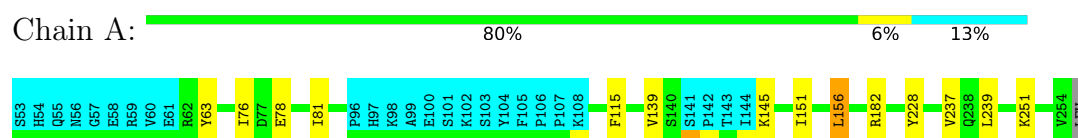
4.2.13 Score per residue for model 13

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 4



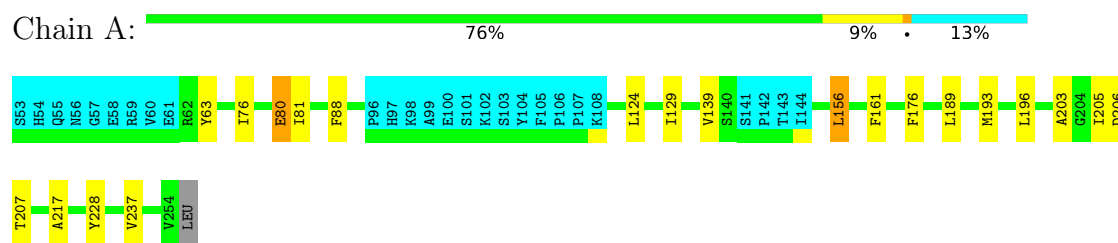
4.2.14 Score per residue for model 14

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 4



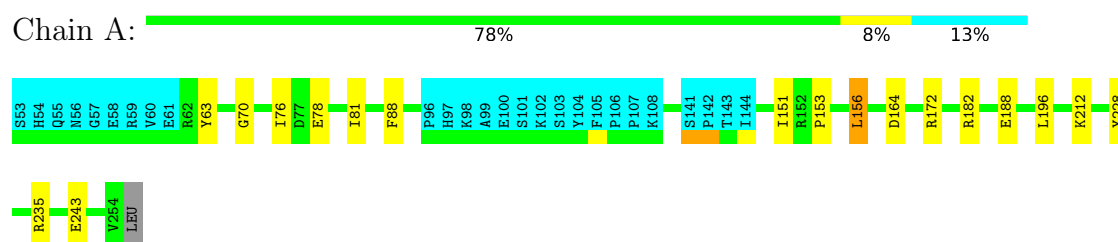
4.2.15 Score per residue for model 15

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 4



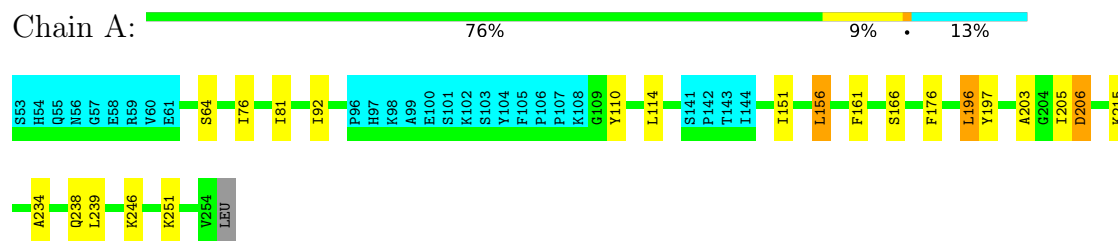
4.2.16 Score per residue for model 16

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 4



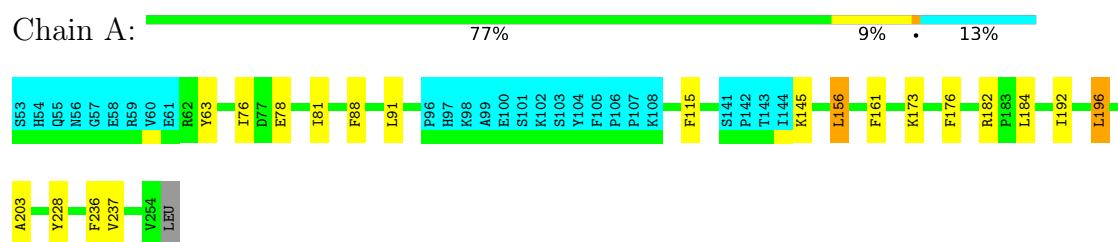
4.2.17 Score per residue for model 17

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 4



4.2.18 Score per residue for model 18

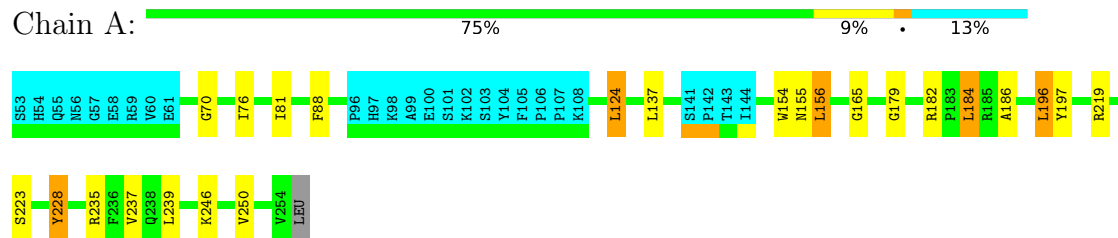
- Molecule 1: Cytoplasmic polyadenylation element-binding protein 4



4.2.19 Score per residue for model 19

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 4

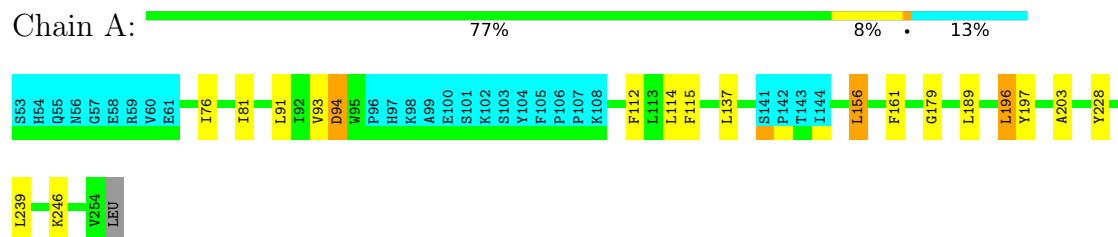
Chain A:



4.2.20 Score per residue for model 20

- Molecule 1: Cytoplasmic polyadenylation element-binding protein 4

Chain A:



5 Refinement protocol and experimental data overview

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

Of the 30 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
Amber	refinement	
CYANA	structure solution	

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	1720
Number of shifts mapped to atoms	1719
Number of unparsed shifts	0
Number of shifts with mapping errors	1
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	68%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.52±0.00	0±0/1425 (0.0± 0.0%)	1.00±0.02	0±1/1932 (0.0± 0.0%)
All	All	0.52	0/28500 (0.0%)	1.00	6/38640 (0.0%)

There are no bond-length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	93	VAL	N-CA-C	6.18	117.37	107.73	20	1
1	A	85	PHE	CA-CB-CG	5.87	119.67	113.80	10	1
1	A	234	ALA	N-CA-C	-5.45	107.18	113.88	17	1
1	A	73	PRO	CA-C-N	5.07	124.79	119.82	10	1
1	A	73	PRO	C-N-CA	5.07	124.79	119.82	10	1
1	A	206	ASP	N-CA-C	5.03	121.52	110.80	17	1

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	1392	1381	1381	6±3
All	All	27840	27620	27620	111

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 2.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:156:LEU:HD13	1:A:156:LEU:H	0.77	1.39	10	12
1:A:196:LEU:CD1	1:A:197:TYR:H	0.63	2.07	11	2
1:A:156:LEU:H	1:A:156:LEU:CD1	0.62	2.08	20	6
1:A:189:LEU:HD23	1:A:189:LEU:C	0.57	2.24	3	7
1:A:156:LEU:HD13	1:A:156:LEU:N	0.57	2.14	16	3
1:A:88:PHE:CD1	1:A:115:PHE:CZ	0.52	2.98	11	4
1:A:189:LEU:C	1:A:189:LEU:HD13	0.51	2.30	2	3
1:A:88:PHE:CE1	1:A:115:PHE:CZ	0.50	3.00	5	3
1:A:161:PHE:CZ	1:A:203:ALA:HB3	0.50	2.40	18	3
1:A:196:LEU:HD12	1:A:197:TYR:H	0.49	1.65	11	5
1:A:154:TRP:CG	1:A:155:ASN:N	0.48	2.81	1	2
1:A:196:LEU:HD13	1:A:197:TYR:CD2	0.48	2.43	1	4
1:A:68:PHE:C	1:A:68:PHE:CD1	0.47	2.92	10	1
1:A:241:HIS:CG	1:A:242:GLY:N	0.47	2.83	11	1
1:A:238:GLN:C	1:A:239:LEU:HD22	0.46	2.36	17	1
1:A:94:ASP:CB	1:A:112:PHE:H	0.46	2.22	20	1
1:A:192:ILE:O	1:A:196:LEU:CD2	0.45	2.64	18	1
1:A:184:LEU:C	1:A:184:LEU:HD12	0.45	2.36	18	1
1:A:223:SER:HA	1:A:228:TYR:CD2	0.45	2.46	8	3
1:A:173:LYS:HA	1:A:173:LYS:HE2	0.45	1.87	18	2
1:A:88:PHE:CZ	1:A:124:LEU:HD12	0.45	2.47	5	1
1:A:62:ARG:C	1:A:63:TYR:CD1	0.45	2.94	11	1
1:A:176:PHE:CD1	1:A:176:PHE:C	0.44	2.95	17	2
1:A:182:ARG:N	1:A:183:PRO:CD	0.44	2.81	9	3
1:A:154:TRP:CD1	1:A:155:ASN:N	0.44	2.85	19	1
1:A:156:LEU:CD1	1:A:156:LEU:N	0.44	2.81	12	4
1:A:114:LEU:HD22	1:A:114:LEU:C	0.44	2.38	5	1
1:A:64:SER:HB2	1:A:156:LEU:HD12	0.43	1.90	17	2
1:A:63:TYR:CD1	1:A:63:TYR:N	0.43	2.85	15	2
1:A:223:SER:HA	1:A:228:TYR:CG	0.43	2.48	4	1
1:A:94:ASP:HA	1:A:112:PHE:O	0.43	2.13	20	1
1:A:161:PHE:CZ	1:A:203:ALA:CB	0.43	3.01	17	2
1:A:184:LEU:C	1:A:184:LEU:CD1	0.43	2.92	3	1
1:A:88:PHE:CE2	1:A:115:PHE:CE2	0.43	3.07	8	1
1:A:246:LYS:HE2	1:A:246:LYS:H	0.43	1.74	11	1
1:A:184:LEU:CD2	1:A:186:ALA:H	0.43	2.27	19	1
1:A:241:HIS:CG	1:A:242:GLY:H	0.42	2.32	11	1
1:A:180:VAL:N	1:A:181:PRO:CD	0.42	2.82	10	1
1:A:94:ASP:CB	1:A:112:PHE:N	0.42	2.82	20	1
1:A:68:PHE:CD1	1:A:68:PHE:C	0.41	2.98	3	2
1:A:196:LEU:CD2	1:A:196:LEU:N	0.41	2.84	18	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:161:PHE:CD1	1:A:186:ALA:CB	0.41	3.04	2	1
1:A:185:ARG:C	1:A:187:VAL:H	0.41	2.23	1	1
1:A:156:LEU:N	1:A:156:LEU:HD12	0.41	2.30	7	1
1:A:196:LEU:HD12	1:A:197:TYR:N	0.41	2.30	20	1
1:A:215:LYS:HD2	1:A:215:LYS:C	0.41	2.40	17	1
1:A:62:ARG:N	1:A:62:ARG:CD	0.41	2.84	3	1
1:A:88:PHE:CG	1:A:115:PHE:CZ	0.41	3.09	11	1
1:A:80:GLU:H	1:A:80:GLU:CD	0.41	2.24	15	1
1:A:156:LEU:N	1:A:156:LEU:CD1	0.41	2.83	16	1
1:A:124:LEU:CD1	1:A:137:LEU:HD21	0.41	2.46	19	1
1:A:205:ILE:O	1:A:207:THR:N	0.40	2.54	10	1
1:A:161:PHE:CE2	1:A:186:ALA:HB3	0.40	2.52	13	1
1:A:92:ILE:HD12	1:A:92:ILE:N	0.40	2.31	17	1
1:A:189:LEU:C	1:A:189:LEU:CD2	0.40	2.94	3	1
1:A:129:ILE:HD12	1:A:129:ILE:N	0.40	2.31	15	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	175/203 (86%)	152±3 (87±2%)	19±4 (11±2%)	4±2 (2±1%)	8	48
All	All	3500/4060 (86%)	3042 (87%)	383 (11%)	75 (2%)	8	48

All 30 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	246	LYS	6
1	A	153	PRO	6
1	A	206	ASP	5
1	A	139	VAL	5
1	A	182	ARG	5
1	A	159	SER	4
1	A	165	GLY	4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	217	ALA	3
1	A	222	PHE	3
1	A	70	GLY	3
1	A	179	GLY	3
1	A	78	GLU	3
1	A	247	ARG	2
1	A	237	VAL	2
1	A	140	SER	2
1	A	164	ASP	2
1	A	239	LEU	2
1	A	145	LYS	2
1	A	235	ARG	2
1	A	87	ARG	1
1	A	89	GLY	1
1	A	184	LEU	1
1	A	86	ARG	1
1	A	63	TYR	1
1	A	243	GLU	1
1	A	110	TYR	1
1	A	166	SER	1
1	A	236	PHE	1
1	A	219	ARG	1
1	A	94	ASP	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	150/175 (86%)	139±2 (93±1%)	11±2 (7±1%)	15	63
All	All	3000/3500 (86%)	2783 (93%)	217 (7%)	15	63

All 45 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	76	ILE	20
1	A	81	ILE	20

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	156	LEU	18
1	A	196	LEU	17
1	A	228	TYR	17
1	A	137	LEU	10
1	A	237	VAL	8
1	A	224	ASN	8
1	A	115	PHE	8
1	A	114	LEU	7
1	A	151	ILE	6
1	A	246	LYS	6
1	A	184	LEU	5
1	A	205	ILE	5
1	A	88	PHE	5
1	A	251	LYS	4
1	A	145	LYS	4
1	A	207	THR	4
1	A	91	LEU	4
1	A	172	ARG	3
1	A	215	LYS	3
1	A	239	LEU	3
1	A	176	PHE	3
1	A	130	GLU	2
1	A	173	LYS	2
1	A	155	ASN	2
1	A	134	LYS	2
1	A	195	ARG	2
1	A	63	TYR	2
1	A	124	LEU	2
1	A	229	ILE	1
1	A	222	PHE	1
1	A	235	ARG	1
1	A	147	LYS	1
1	A	68	PHE	1
1	A	211	LEU	1
1	A	122	GLN	1
1	A	72	LEU	1
1	A	80	GLU	1
1	A	139	VAL	1
1	A	189	LEU	1
1	A	193	MET	1
1	A	188	GLU	1
1	A	212	LYS	1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	250	VAL	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no 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 68% for the well-defined parts and 62% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *CPEB4RRM12_assigned_chemical_shifts*

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	1720
Number of shifts mapped to atoms	1719
Number of unparsed shifts	0
Number of shifts with mapping errors	1
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	9

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- No matching atom found in the structure. All 1 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	255	LEU	H	7.998	0.000	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
$^{13}\text{C}_\alpha$	137	2.96 ± 0.13	Should be applied
$^{13}\text{C}_\beta$	124	2.92 ± 0.14	Should be applied
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	170	-0.52 ± 0.20	Should be applied

7.1.3 Completeness of resonance assignments ⓘ

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 68%, i.e. 1638 atoms were assigned a chemical shift out of a possible 2421. 0 out of 30 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	612/870 (70%)	320/354 (90%)	133/352 (38%)	159/164 (97%)
Sidechain	893/1358 (66%)	625/883 (71%)	260/420 (62%)	8/55 (15%)
Aromatic	133/193 (69%)	81/93 (87%)	50/97 (52%)	2/3 (67%)
Overall	1638/2421 (68%)	1026/1330 (77%)	443/869 (51%)	169/222 (76%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 62%, i.e. 1719 atoms were assigned a chemical shift out of a possible 2765. 0 out of 31 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	642/993 (65%)	335/403 (83%)	137/404 (34%)	170/186 (91%)
Sidechain	931/1546 (60%)	651/1003 (65%)	271/480 (56%)	9/63 (14%)
Aromatic	146/226 (65%)	89/110 (81%)	55/111 (50%)	2/5 (40%)
Overall	1719/2765 (62%)	1075/1516 (71%)	463/995 (47%)	181/254 (71%)

7.1.4 Statistically unusual chemical shifts ⓘ

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

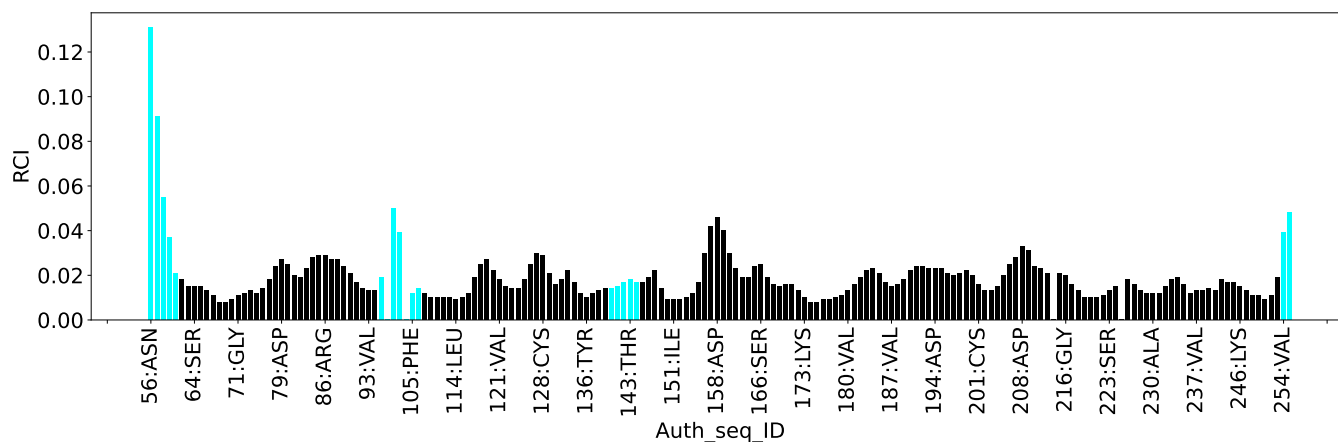
List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	76	ILE	CG1	11.00	19.24 – 36.26	-9.8
1	A	214	PRO	HD3	0.44	1.76 – 5.48	-8.5
1	A	214	PRO	HD2	0.91	1.93 – 5.38	-7.9
1	A	205	ILE	CG1	14.50	19.24 – 36.26	-7.8
1	A	214	PRO	HG3	-0.38	0.33 – 3.48	-7.3
1	A	175	ILE	CG1	17.13	19.24 – 36.26	-6.2
1	A	214	PRO	HG2	0.18	0.41 – 3.45	-5.8
1	A	134	LYS	CE	37.29	37.57 – 46.21	-5.3
1	A	95	TRP	CZ2	121.45	107.20 – 121.33	5.1

7.1.5 Random Coil Index (RCI) plots ⓘ

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from

the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:



8 NMR restraints analysis

8.1 Conformationally restricting restraints

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

Description	Value
Total distance restraints	2493
Intra-residue ($ i-j =0$)	496
Sequential ($ i-j =1$)	718
Medium range ($ i-j >1$ and $ i-j <5$)	426
Long range ($ i-j \geq 5$)	729
Inter-chain	0
Hydrogen bond restraints	124
Disulfide bond restraints	0
Total dihedral-angle restraints	722
Number of unmapped restraints	0
Number of restraints per residue	15.8
Number of long range restraints per residue ¹	3.9

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

8.2 Residual restraint violations

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

8.2.1 Average number of distance violations per model

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

Bins (Å)	Average number of violations per model	Max (Å)
0.1-0.2 (Small)	23.1	0.2
0.2-0.5 (Medium)	15.1	0.48
>0.5 (Large)	1.6	1.56

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)	1.1	4.15
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis [i](#)

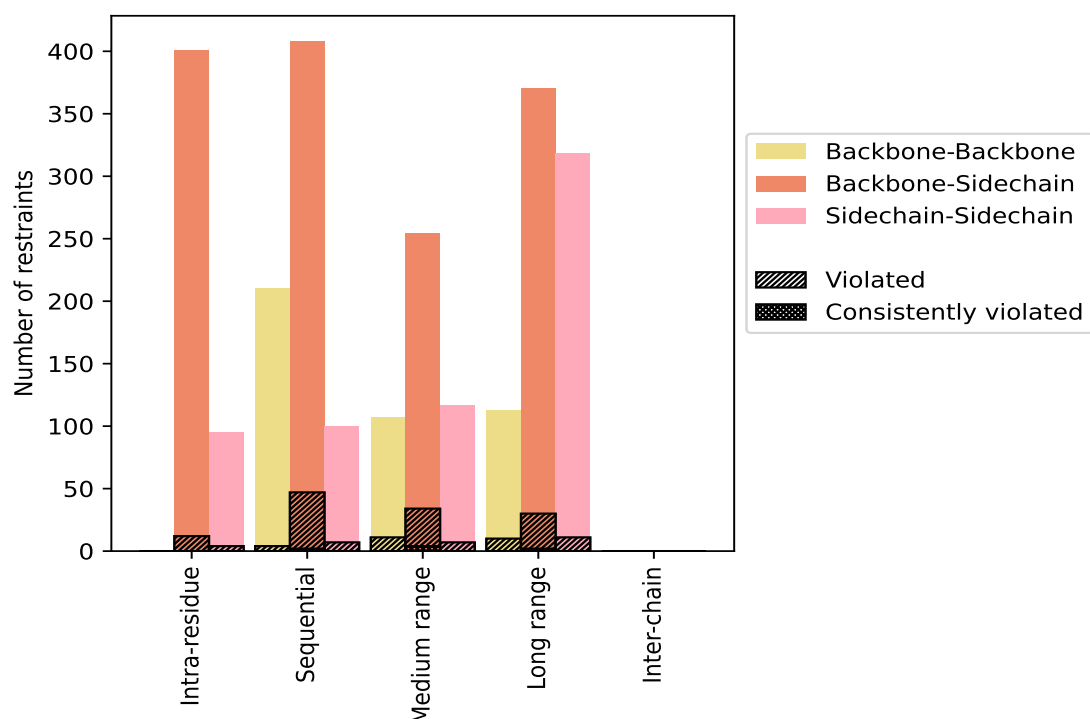
9.1 Summary of distance violations [i](#)

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

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue (i-j =0)	496	19.9	16	3.2	0.6	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	401	16.1	12	3.0	0.5	0	0.0	0.0
Sidechain-Sidechain	95	3.8	4	4.2	0.2	0	0.0	0.0
Sequential (i-j =1)	718	28.8	58	8.1	2.3	2	0.3	0.1
Backbone-Backbone	210	8.4	4	1.9	0.2	0	0.0	0.0
Backbone-Sidechain	408	16.4	47	11.5	1.9	2	0.5	0.1
Sidechain-Sidechain	100	4.0	7	7.0	0.3	0	0.0	0.0
Medium range (i-j >1 & i-j <5)	426	17.1	44	10.3	1.8	4	0.9	0.2
Backbone-Backbone	107	4.3	11	10.3	0.4	0	0.0	0.0
Backbone-Sidechain	202	8.1	26	12.9	1.0	4	2.0	0.2
Sidechain-Sidechain	117	4.7	7	6.0	0.3	0	0.0	0.0
Long range (i-j ≥5)	729	29.2	39	5.3	1.6	0	0.0	0.0
Backbone-Backbone	113	4.5	10	8.8	0.4	0	0.0	0.0
Backbone-Sidechain	300	12.0	18	6.0	0.7	0	0.0	0.0
Sidechain-Sidechain	316	12.7	11	3.5	0.4	0	0.0	0.0
Inter-chain	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Hydrogen bond	124	5.0	20	16.1	0.8	2	1.6	0.1
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	2493	100.0	177	7.1	7.1	8	0.3	0.3
Backbone-Backbone	430	17.2	25	5.8	1.0	0	0.0	0.0
Backbone-Sidechain	1433	57.5	123	8.6	4.9	8	0.6	0.3
Sidechain-Sidechain	630	25.3	29	4.6	1.2	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	2	9	13	8	0	32	0.22	0.76	0.12	0.18
2	3	11	13	10	0	37	0.24	1.56	0.24	0.18
3	2	11	18	8	0	39	0.2	0.4	0.09	0.17
4	2	7	22	13	0	44	0.23	1.25	0.17	0.2
5	2	10	14	12	0	38	0.19	0.83	0.13	0.15
6	6	10	13	13	0	42	0.22	0.58	0.11	0.2
7	5	16	16	10	0	47	0.2	0.98	0.14	0.16
8	4	9	18	11	0	42	0.2	0.55	0.11	0.16
9	2	11	16	9	0	38	0.19	0.99	0.15	0.16
10	2	13	15	9	0	39	0.21	0.46	0.09	0.17

Continued on next page...

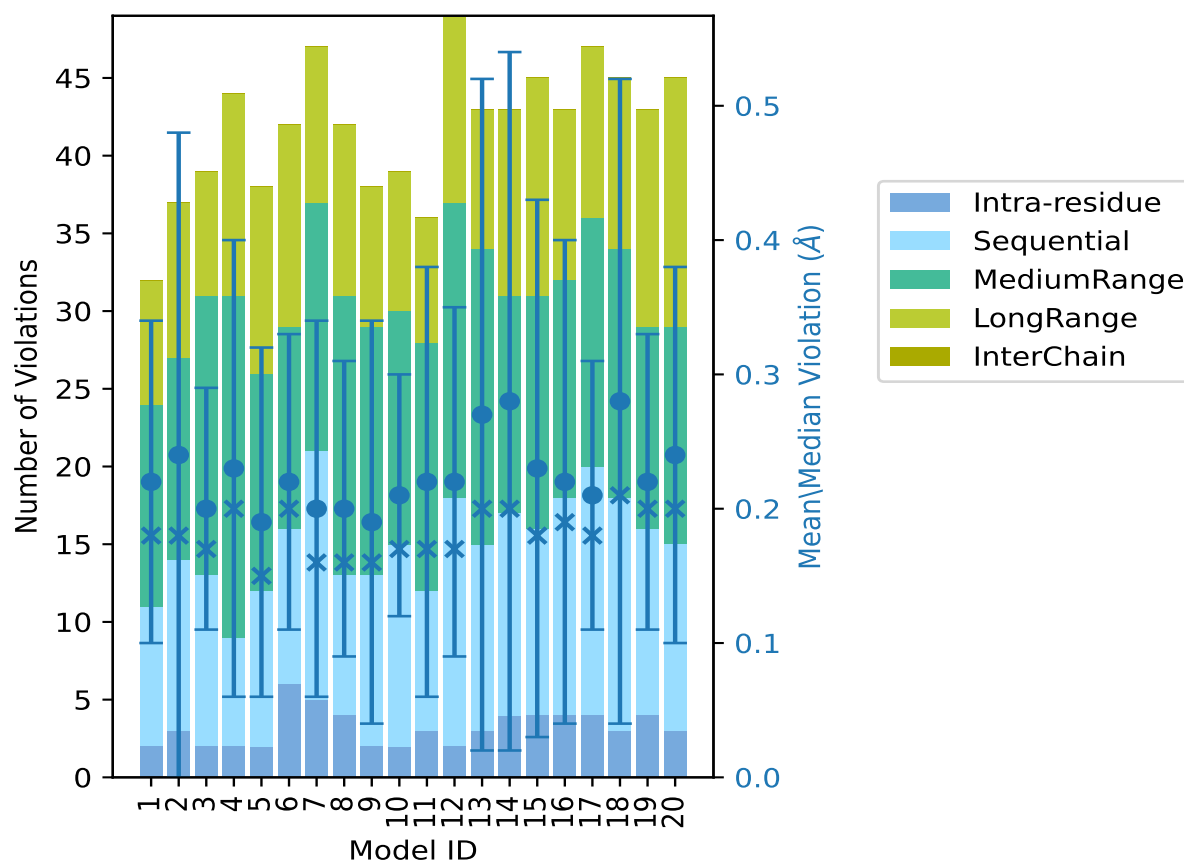
Continued from previous page...

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	3	9	16	8	0	36	0.22	0.93	0.16	0.17
12	2	16	19	12	0	49	0.22	0.77	0.13	0.17
13	3	12	19	9	0	43	0.27	1.5	0.25	0.2
14	4	13	14	12	0	43	0.28	1.23	0.26	0.2
15	4	12	15	14	0	45	0.23	1.42	0.2	0.18
16	4	14	14	11	0	43	0.22	1.23	0.18	0.19
17	4	16	16	11	0	47	0.21	0.55	0.1	0.18
18	3	15	16	11	0	45	0.28	1.42	0.24	0.21
19	4	12	13	14	0	43	0.22	0.61	0.11	0.2
20	3	12	14	16	0	45	0.24	0.8	0.14	0.2

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

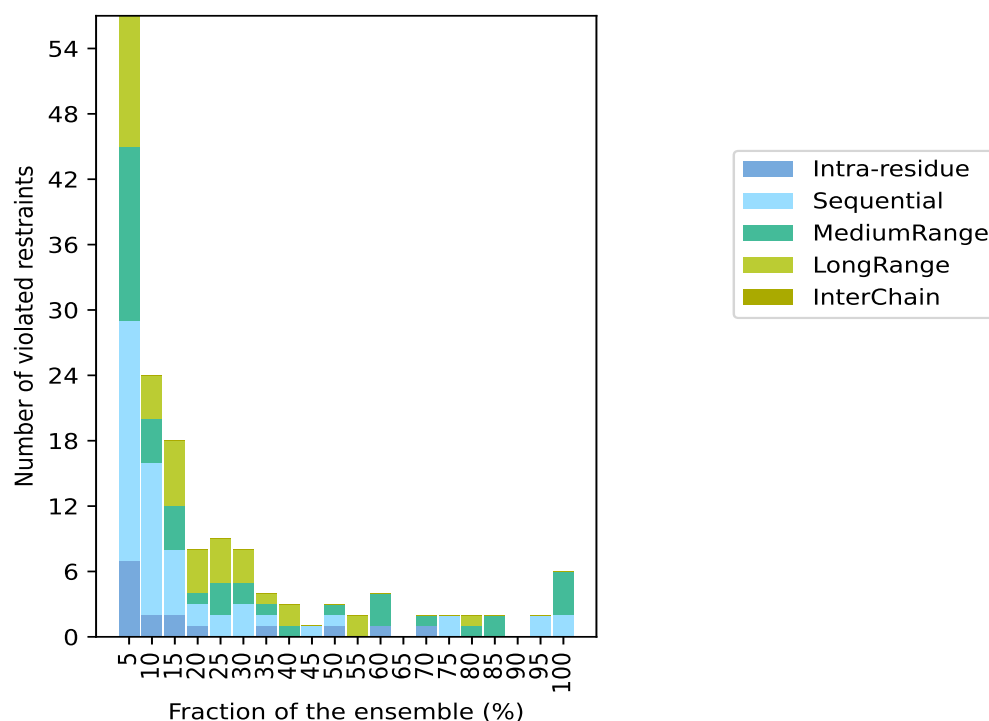
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 2212(IR:480, SQ:660, MR:382, LR:690, IC:0) restraints are 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	%
7	22	16	12	0	57	1	5.0
2	14	4	4	0	24	2	10.0
2	6	4	6	0	18	3	15.0
1	2	1	4	0	8	4	20.0
0	2	3	4	0	9	5	25.0
0	3	2	3	0	8	6	30.0
1	1	1	1	0	4	7	35.0
0	0	1	2	0	3	8	40.0
0	1	0	0	0	1	9	45.0
1	1	1	0	0	3	10	50.0
0	0	0	2	0	2	11	55.0
1	0	3	0	0	4	12	60.0
0	0	0	0	0	0	13	65.0
1	0	1	0	0	2	14	70.0
0	2	0	0	0	2	15	75.0
0	0	1	1	0	2	16	80.0
0	0	2	0	0	2	17	85.0
0	0	0	0	0	0	18	90.0
0	2	0	0	0	2	19	95.0
0	2	4	0	0	6	20	100.0

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

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

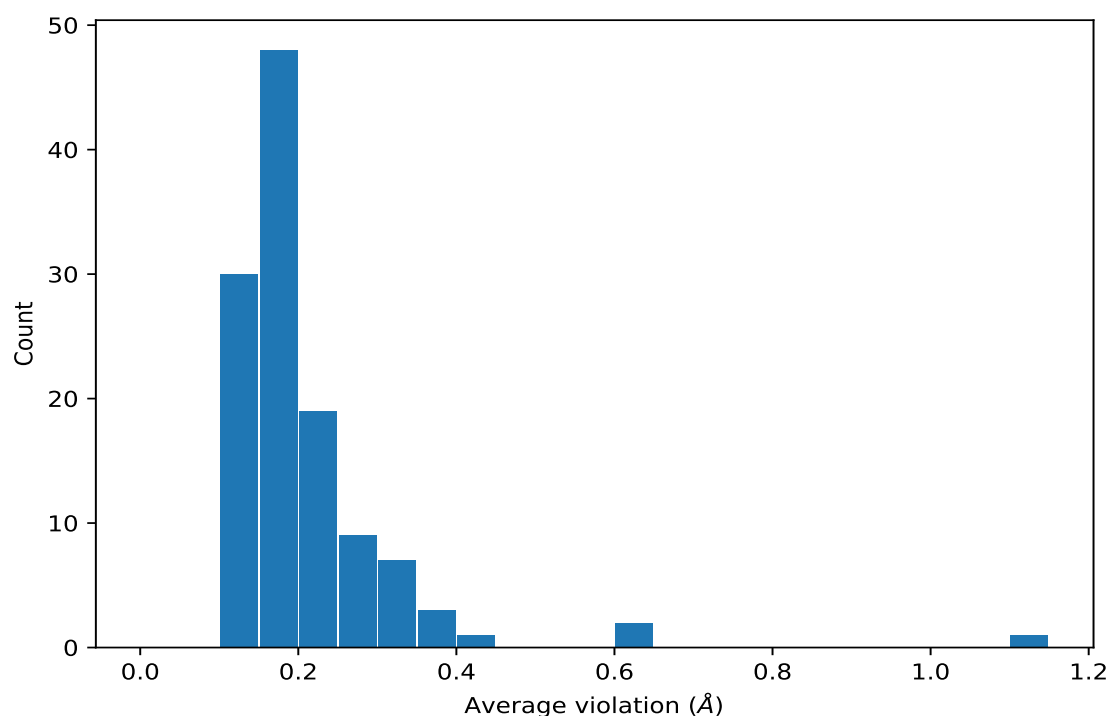
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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)
(1,1225)	1:211:A:LEU:H	1:215:A:LYS:HG2	20	0.63	0.33	0.76
(1,221)	1:194:A:ASP:HA	1:196:A:LEU:HG	20	0.37	0.36	0.26
(1,1180)	1:189:A:LEU:H	1:192:A:ILE:HG13	20	0.32	0.07	0.32
(1,215)	1:248:A:VAL:HA	1:249:A:GLU:HB3	20	0.3	0.04	0.3
(2,109)	1:213:A:TYR:H	1:208:A:ASP:O	20	0.21	0.03	0.2
(2,115)	1:154:A:TRP:H	1:64:A:SER:O	20	0.2	0.03	0.2
(1,2323)	1:210:A:GLU:HB2	1:212:A:LYS:H	20	0.18	0.03	0.19
(1,1790)	1:226:A:GLN:HE22	1:227:A:SER:HA	20	0.13	0.06	0.11
(1,1668)	1:166:A:SER:HB3	1:167:A:GLN:HB3	19	0.29	0.1	0.31
(1,314)	1:193:A:MET:HG2	1:194:A:ASP:HB3	19	0.24	0.05	0.23
(2,116)	1:154:A:TRP:N	1:64:A:SER:O	18	0.15	0.03	0.15
(1,207)	1:159:A:SER:HA	1:161:A:PHE:H	17	0.21	0.08	0.17
(1,1764)	1:187:A:VAL:HA	1:191:A:MET:HB2	17	0.17	0.03	0.17
(1,1446)	1:71:A:GLY:H	1:85:A:PHE:HZ	16	0.25	0.13	0.19
(1,1665)	1:192:A:ILE:HG12	1:195:A:ARG:H	16	0.14	0.02	0.14
(1,527)	1:237:A:VAL:H	1:238:A:GLN:HB2	15	0.43	0.18	0.44

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,1560)	1:187:A:VAL:HA	1:188:A:GLU:HG3	15	0.32	0.08	0.35
(1,484)	1:134:A:LYS:HB3	1:134:A:LYS:HD2	14	0.32	0.02	0.32
(1,1360)	1:231:A:ALA:HA	1:235:A:ARG:H	14	0.26	0.06	0.26
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD13	12	0.28	0.03	0.29
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD11	12	0.28	0.03	0.29
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD12	12	0.28	0.03	0.29
(1,1083)	1:159:A:SER:HB3	1:161:A:PHE:H	12	0.23	0.1	0.22
(1,1983)	1:85:A:PHE:HB2	1:88:A:PHE:HA	12	0.22	0.07	0.2
(1,1373)	1:224:A:ASN:HD22	1:227:A:SER:H	12	0.16	0.05	0.16
(2,65)	1:196:A:LEU:H	1:192:A:ILE:O	12	0.15	0.03	0.16
(1,119)	1:78:A:GLU:HG3	1:95:A:TRP:HZ2	11	0.19	0.06	0.2
(1,127)	1:95:A:TRP:HZ3	1:113:A:LEU:HA	11	0.15	0.05	0.13
(1,120)	1:154:A:TRP:HH2	1:155:A:ASN:H	10	0.21	0.1	0.2
(1,934)	1:168:A:PRO:HA	1:170:A:ASP:H	10	0.19	0.08	0.16
(1,1417)	1:238:A:GLN:HB3	1:238:A:GLN:HE22	10	0.16	0.08	0.14
(2,73)	1:229:A:ILE:H	1:225:A:GLN:O	10	0.12	0.02	0.11
(1,1533)	1:172:A:ARG:HA	1:173:A:LYS:HE2	9	0.19	0.07	0.19
(1,382)	1:180:A:VAL:HA	1:188:A:GLU:HG2	8	0.16	0.07	0.14
(1,1705)	1:140:A:SER:HB2	1:146:A:ASP:HA	8	0.15	0.03	0.15
(1,2246)	1:154:A:TRP:HE1	1:158:A:ASP:H	8	0.12	0.02	0.12
(1,511)	1:167:A:GLN:HB2	1:167:A:GLN:HE22	7	0.24	0.14	0.22
(1,1858)	1:196:A:LEU:HD11	1:197:A:TYR:H	7	0.19	0.08	0.16
(1,1858)	1:196:A:LEU:HD12	1:197:A:TYR:H	7	0.19	0.08	0.16
(1,1858)	1:196:A:LEU:HD13	1:197:A:TYR:H	7	0.19	0.08	0.16
(1,172)	1:74:A:PRO:HA	1:76:A:ILE:H	7	0.15	0.02	0.16
(1,156)	1:174:A:THR:HB	1:253:A:TYR:HA	7	0.11	0.01	0.11
(1,492)	1:234:A:ALA:H	1:235:A:ARG:HB3	6	0.26	0.08	0.24
(1,287)	1:137:A:LEU:HB3	1:149:A:VAL:HB	6	0.22	0.08	0.24
(1,546)	1:134:A:LYS:HG2	1:151:A:ILE:H	6	0.2	0.08	0.16
(1,246)	1:184:A:LEU:HA	1:187:A:VAL:HB	6	0.19	0.05	0.18
(1,1551)	1:141:A:SER:H	1:144:A:ILE:HB	6	0.18	0.09	0.15
(1,1415)	1:238:A:GLN:HE22	1:239:A:LEU:H	6	0.17	0.04	0.15
(1,1438)	1:70:A:GLY:H	1:149:A:VAL:HA	6	0.15	0.05	0.14
(1,2093)	1:136:A:TYR:HA	1:137:A:LEU:HB3	6	0.14	0.02	0.14
(1,305)	1:63:A:TYR:HB3	1:65:A:ARG:H	5	1.1	0.51	1.42
(1,2314)	1:208:A:ASP:HB2	1:212:A:LYS:H	5	0.25	0.05	0.27
(1,1062)	1:206:A:ASP:HB2	1:217:A:ALA:H	5	0.23	0.08	0.24
(1,1652)	1:245:A:ASP:HB2	1:246:A:LYS:HD3	5	0.19	0.03	0.19
(1,1013)	1:141:A:SER:H	1:145:A:LYS:H	5	0.18	0.09	0.12
(1,2171)	1:234:A:ALA:HA	1:235:A:ARG:HA	5	0.18	0.01	0.18
(1,253)	1:91:A:LEU:HA	1:114:A:LEU:H	5	0.17	0.03	0.17
(1,2136)	1:91:A:LEU:HA	1:117:A:ASP:H	5	0.17	0.06	0.16

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,1086)	1:129:A:ILE:H	1:138:A:CYS:HA	5	0.15	0.05	0.12
(2,119)	1:159:A:SER:H	1:155:A:ASN:O	5	0.13	0.02	0.13
(2,61)	1:192:A:ILE:H	1:188:A:GLU:O	5	0.11	0.0	0.11
(1,262)	1:63:A:TYR:HA	1:155:A:ASN:H	4	0.61	0.29	0.56
(1,365)	1:133:A:GLY:H	1:134:A:LYS:HE3	4	0.25	0.04	0.26
(1,2107)	1:63:A:TYR:HA	1:155:A:ASN:HB3	4	0.24	0.11	0.21
(1,1521)	1:208:A:ASP:HB2	1:212:A:LYS:HA	4	0.19	0.03	0.2
(1,407)	1:130:A:GLU:H	1:130:A:GLU:HG3	4	0.18	0.01	0.18
(1,293)	1:206:A:ASP:H	1:218:A:GLY:HA2	4	0.18	0.03	0.17
(1,293)	1:206:A:ASP:H	1:218:A:GLY:HA3	4	0.18	0.03	0.17
(1,303)	1:235:A:ARG:HD3	1:236:A:PHE:H	4	0.17	0.03	0.18
(1,1617)	1:180:A:VAL:HB	1:188:A:GLU:HG2	4	0.16	0.04	0.16
(2,9)	1:123:A:ALA:H	1:119:A:SER:O	4	0.11	0.01	0.11
(1,2155)	1:238:A:GLN:HA	1:239:A:LEU:HB2	3	0.31	0.17	0.29
(1,1048)	1:134:A:LYS:H	1:134:A:LYS:HE3	3	0.21	0.04	0.22
(1,315)	1:184:A:LEU:HB2	1:187:A:VAL:HB	3	0.2	0.1	0.14
(1,1440)	1:70:A:GLY:H	1:85:A:PHE:HZ	3	0.19	0.03	0.18
(1,444)	1:238:A:GLN:HG3	1:239:A:LEU:H	3	0.16	0.07	0.12
(1,1642)	1:208:A:ASP:HB2	1:210:A:GLU:HB3	3	0.16	0.03	0.16
(1,1605)	1:131:A:GLU:HB2	1:134:A:LYS:HG3	3	0.16	0.03	0.17
(1,1655)	1:246:A:LYS:HB3	1:246:A:LYS:HD3	3	0.15	0.04	0.15
(1,1080)	1:129:A:ILE:H	1:138:A:CYS:HB2	3	0.14	0.02	0.13
(1,901)	1:237:A:VAL:HG21	1:238:A:GLN:H	3	0.13	0.01	0.13
(1,901)	1:237:A:VAL:HG22	1:238:A:GLN:H	3	0.13	0.01	0.13
(1,901)	1:237:A:VAL:HG23	1:238:A:GLN:H	3	0.13	0.01	0.13
(1,108)	1:235:A:ARG:HD2	1:236:A:PHE:HZ	3	0.13	0.01	0.13
(1,316)	1:63:A:TYR:HB3	1:155:A:ASN:HA	3	0.13	0.02	0.13
(1,494)	1:77:A:ASP:H	1:80:A:GLU:HB3	3	0.12	0.01	0.12
(1,1022)	1:208:A:ASP:H	1:215:A:LYS:HB2	3	0.12	0.02	0.13
(1,1591)	1:163:A:MET:HB2	1:200:A:VAL:HB	3	0.12	0.01	0.12
(2,63)	1:194:A:ASP:H	1:190:A:ALA:O	3	0.12	0.01	0.11
(1,183)	1:198:A:GLY:H	1:227:A:SER:HA	3	0.11	0.01	0.11
(1,1463)	1:142:A:PRO:HB3	1:143:A:THR:H	3	0.11	0.01	0.11
(1,1463)	1:142:A:PRO:HB2	1:143:A:THR:H	3	0.11	0.01	0.11
(1,1465)	1:199:A:GLY:H	1:200:A:VAL:H	3	0.11	0.01	0.11
(1,1720)	1:195:A:ARG:HA	1:196:A:LEU:HG	2	0.39	0.28	0.39
(1,310)	1:235:A:ARG:H	1:235:A:ARG:HD2	2	0.38	0.02	0.38
(1,1624)	1:168:A:PRO:HB3	1:169:A:LEU:H	2	0.3	0.02	0.3
(1,1583)	1:78:A:GLU:HG3	1:79:A:ASP:HA	2	0.3	0.08	0.3
(1,912)	1:65:A:ARG:H	1:114:A:LEU:HB2	2	0.24	0.1	0.24
(1,1565)	1:184:A:LEU:HB2	1:188:A:GLU:HG3	2	0.22	0.06	0.22
(1,1243)	1:226:A:GLN:HG2	1:229:A:ILE:H	2	0.22	0.02	0.22

Continued on next page...

Continued from previous page...

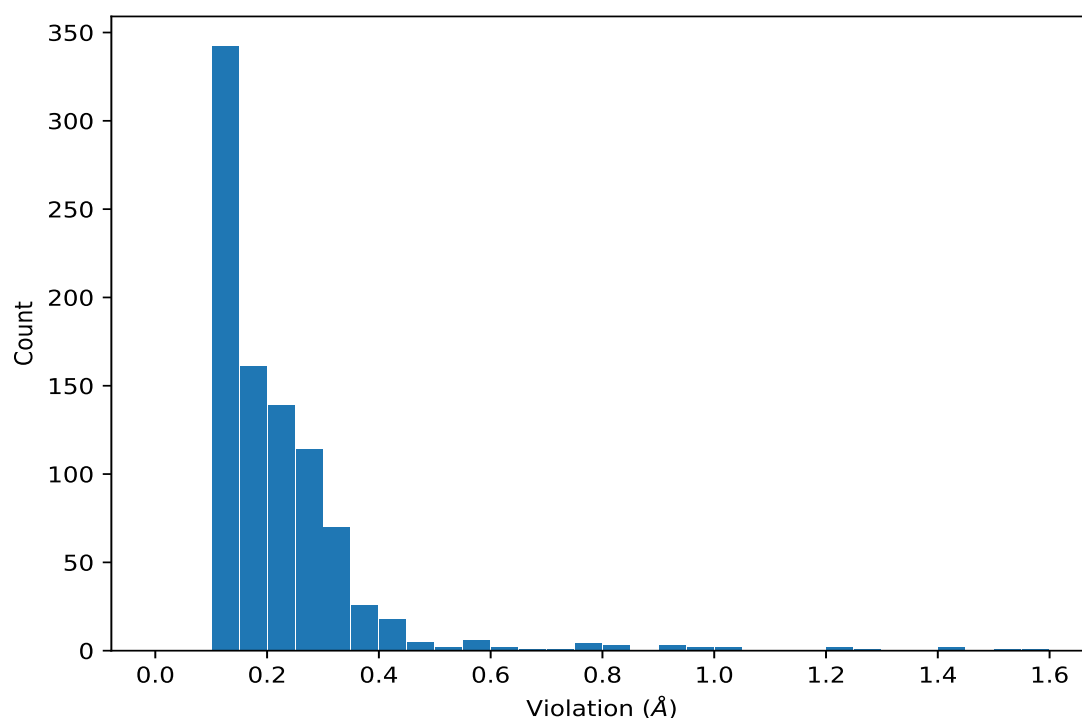
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,2015)	1:194:A:ASP:HA	1:198:A:GLY:H	2	0.22	0.1	0.22
(1,378)	1:63:A:TYR:HA	1:155:A:ASN:HB2	2	0.2	0.04	0.2
(1,612)	1:246:A:LYS:HG2	1:247:A:ARG:H	2	0.19	0.04	0.19
(1,612)	1:246:A:LYS:HG3	1:247:A:ARG:H	2	0.19	0.04	0.19
(1,409)	1:177:A:VAL:H	1:219:A:ARG:HB2	2	0.18	0.03	0.18
(1,1662)	1:251:A:LYS:HA	1:251:A:LYS:HD2	2	0.18	0.08	0.18
(2,28)	1:112:A:PHE:H	1:94:A:ASP:O	2	0.18	0.07	0.18
(1,1441)	1:225:A:GLN:HE22	1:226:A:GLN:H	2	0.18	0.0	0.18
(1,194)	1:244:A:ILE:HA	1:245:A:ASP:HB2	2	0.16	0.04	0.16
(1,312)	1:235:A:ARG:HD2	1:236:A:PHE:H	2	0.16	0.04	0.16
(1,1738)	1:223:A:SER:HB3	1:224:A:ASN:HA	2	0.16	0.05	0.16
(1,1368)	1:196:A:LEU:HG	1:197:A:TYR:H	2	0.15	0.03	0.15
(1,450)	1:238:A:GLN:HG2	1:239:A:LEU:H	2	0.15	0.0	0.15
(2,64)	1:195:A:ARG:H	1:191:A:MET:O	2	0.14	0.01	0.14
(1,443)	1:163:A:MET:HG3	1:164:A:ASP:H	2	0.14	0.01	0.14
(1,950)	1:143:A:THR:H	1:144:A:ILE:H	2	0.14	0.02	0.14
(1,1183)	1:207:A:THR:HB	1:215:A:LYS:H	2	0.13	0.03	0.13
(1,611)	1:81:A:ILE:HG12	1:82:A:THR:HA	2	0.12	0.02	0.12
(1,1554)	1:85:A:PHE:HA	1:88:A:PHE:HB2	2	0.11	0.01	0.11
(1,1034)	1:78:A:GLU:HG3	1:79:A:ASP:H	2	0.11	0.0	0.11

¹Number of violated models, ²Standard deviation

9.5 All violated distance restraints [i](#)

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

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



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

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

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,221)	1:194:A:ASP:HA	1:196:A:LEU:HG	2	1.56
(1,305)	1:63:A:TYR:HB3	1:65:A:ARG:H	13	1.5
(1,305)	1:63:A:TYR:HB3	1:65:A:ARG:H	15	1.42
(1,305)	1:63:A:TYR:HB3	1:65:A:ARG:H	18	1.42
(1,508)	1:226:A:GLN:HG3	1:229:A:ILE:HG12	4	1.25
(1,1225)	1:211:A:LEU:H	1:215:A:LYS:HG2	16	1.23
(1,221)	1:194:A:ASP:HA	1:196:A:LEU:HG	14	1.23
(1,305)	1:63:A:TYR:HB3	1:65:A:ARG:H	14	1.04
(1,262)	1:63:A:TYR:HA	1:155:A:ASN:H	14	1.0
(1,1225)	1:211:A:LEU:H	1:215:A:LYS:HG2	9	0.99
(1,1225)	1:211:A:LEU:H	1:215:A:LYS:HG2	7	0.98
(1,1225)	1:211:A:LEU:H	1:215:A:LYS:HG2	11	0.93
(1,1225)	1:211:A:LEU:H	1:215:A:LYS:HG2	13	0.93
(1,1225)	1:211:A:LEU:H	1:215:A:LYS:HG2	14	0.91
(1,1225)	1:211:A:LEU:H	1:215:A:LYS:HG2	5	0.83
(1,1225)	1:211:A:LEU:H	1:215:A:LYS:HG2	18	0.81

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1225)	1:211:A:LEU:H	1:215:A:LYS:HG2	20	0.8
(1,262)	1:63:A:TYR:HA	1:155:A:ASN:H	18	0.78
(1,1225)	1:211:A:LEU:H	1:215:A:LYS:HG2	12	0.77
(1,527)	1:237:A:VAL:H	1:238:A:GLN:HB2	13	0.77
(1,1225)	1:211:A:LEU:H	1:215:A:LYS:HG2	1	0.76
(1,1494)	1:235:A:ARG:HA	1:235:A:ARG:HD2	20	0.71
(1,1720)	1:195:A:ARG:HA	1:196:A:LEU:HG	18	0.67
(1,527)	1:237:A:VAL:H	1:238:A:GLN:HB2	11	0.64
(1,2160)	1:175:A:ILE:H	1:219:A:ARG:HA	19	0.61
(1,527)	1:237:A:VAL:H	1:238:A:GLN:HB2	12	0.59
(1,1446)	1:71:A:GLY:H	1:85:A:PHE:HZ	16	0.58
(1,527)	1:237:A:VAL:H	1:238:A:GLN:HB2	6	0.58
(1,221)	1:194:A:ASP:HA	1:196:A:LEU:HG	18	0.57
(1,527)	1:237:A:VAL:H	1:238:A:GLN:HB2	8	0.55
(1,511)	1:167:A:GLN:HB2	1:167:A:GLN:HE22	17	0.55
(1,2155)	1:238:A:GLN:HA	1:239:A:LEU:HB2	12	0.52
(1,527)	1:237:A:VAL:H	1:238:A:GLN:HB2	9	0.51
(1,1225)	1:211:A:LEU:H	1:215:A:LYS:HG2	17	0.48
(1,1668)	1:166:A:SER:HB3	1:167:A:GLN:HB3	8	0.47
(1,1446)	1:71:A:GLY:H	1:85:A:PHE:HZ	19	0.47
(2,27)	1:94:A:ASP:H	1:112:A:PHE:O	20	0.46
(1,527)	1:237:A:VAL:H	1:238:A:GLN:HB2	10	0.46
(1,1560)	1:187:A:VAL:HA	1:188:A:GLU:HG3	2	0.44
(1,527)	1:237:A:VAL:H	1:238:A:GLN:HB2	18	0.44
(1,120)	1:154:A:TRP:HH2	1:155:A:ASN:H	19	0.44
(1,1668)	1:166:A:SER:HB3	1:167:A:GLN:HB3	20	0.43
(1,1668)	1:166:A:SER:HB3	1:167:A:GLN:HB3	5	0.42
(1,1560)	1:187:A:VAL:HA	1:188:A:GLU:HG3	6	0.42
(1,2107)	1:63:A:TYR:HA	1:155:A:ASN:HB3	15	0.41
(1,1180)	1:189:A:LEU:H	1:192:A:ILE:HG13	8	0.41
(1,1180)	1:189:A:LEU:H	1:192:A:ILE:HG13	12	0.41
(1,1083)	1:159:A:SER:HB3	1:161:A:PHE:H	18	0.41
(1,527)	1:237:A:VAL:H	1:238:A:GLN:HB2	15	0.41
(1,310)	1:235:A:ARG:H	1:235:A:ARG:HD2	19	0.41
(1,1668)	1:166:A:SER:HB3	1:167:A:GLN:HB3	14	0.4
(1,1417)	1:238:A:GLN:HB3	1:238:A:GLN:HE22	3	0.4
(1,1225)	1:211:A:LEU:H	1:215:A:LYS:HG2	8	0.4
(1,1180)	1:189:A:LEU:H	1:192:A:ILE:HG13	7	0.4
(1,1180)	1:189:A:LEU:H	1:192:A:ILE:HG13	13	0.4
(1,1180)	1:189:A:LEU:H	1:192:A:ILE:HG13	14	0.4
(1,1668)	1:166:A:SER:HB3	1:167:A:GLN:HB3	6	0.39
(1,1560)	1:187:A:VAL:HA	1:188:A:GLU:HG3	17	0.39

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1359)	1:235:A:ARG:H	1:235:A:ARG:HD3	6	0.39
(1,1180)	1:189:A:LEU:H	1:192:A:ILE:HG13	2	0.39
(1,1180)	1:189:A:LEU:H	1:192:A:ILE:HG13	6	0.39
(1,492)	1:234:A:ALA:H	1:235:A:ARG:HB3	17	0.39
(1,1560)	1:187:A:VAL:HA	1:188:A:GLU:HG3	4	0.38
(1,1560)	1:187:A:VAL:HA	1:188:A:GLU:HG3	13	0.38
(1,1083)	1:159:A:SER:HB3	1:161:A:PHE:H	16	0.38
(1,527)	1:237:A:VAL:H	1:238:A:GLN:HB2	3	0.38
(1,221)	1:194:A:ASP:HA	1:196:A:LEU:HG	8	0.38
(1,215)	1:248:A:VAL:HA	1:249:A:GLU:HB3	3	0.38
(1,207)	1:159:A:SER:HA	1:161:A:PHE:H	20	0.38
(1,1668)	1:166:A:SER:HB3	1:167:A:GLN:HB3	19	0.37
(1,1583)	1:78:A:GLU:HG3	1:79:A:ASP:HA	18	0.37
(1,1560)	1:187:A:VAL:HA	1:188:A:GLU:HG3	10	0.37
(1,1446)	1:71:A:GLY:H	1:85:A:PHE:HZ	2	0.37
(1,1180)	1:189:A:LEU:H	1:192:A:ILE:HG13	15	0.37
(1,1078)	1:113:A:LEU:H	1:114:A:LEU:HB3	20	0.37
(1,934)	1:168:A:PRO:HA	1:170:A:ASP:H	4	0.37
(1,546)	1:134:A:LYS:HG2	1:151:A:ILE:H	20	0.37
(1,1560)	1:187:A:VAL:HA	1:188:A:GLU:HG3	3	0.36
(1,1551)	1:141:A:SER:H	1:144:A:ILE:HB	13	0.36
(1,1062)	1:206:A:ASP:HB2	1:217:A:ALA:H	10	0.36
(1,484)	1:134:A:LYS:HB3	1:134:A:LYS:HD2	2	0.36
(1,310)	1:235:A:ARG:H	1:235:A:ARG:HD2	6	0.36
(1,1560)	1:187:A:VAL:HA	1:188:A:GLU:HG3	12	0.35
(1,1360)	1:231:A:ALA:HA	1:235:A:ARG:H	14	0.35
(1,1225)	1:211:A:LEU:H	1:215:A:LYS:HG2	4	0.35
(1,215)	1:248:A:VAL:HA	1:249:A:GLU:HB3	19	0.35
(1,1668)	1:166:A:SER:HB3	1:167:A:GLN:HB3	15	0.34
(1,1668)	1:166:A:SER:HB3	1:167:A:GLN:HB3	18	0.34
(1,1560)	1:187:A:VAL:HA	1:188:A:GLU:HG3	15	0.34
(1,1360)	1:231:A:ALA:HA	1:235:A:ARG:H	11	0.34
(1,1225)	1:211:A:LEU:H	1:215:A:LYS:HG2	19	0.34
(1,1018)	1:140:A:SER:HA	1:146:A:ASP:H	17	0.34
(1,912)	1:65:A:ARG:H	1:114:A:LEU:HB2	20	0.34
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD13	4	0.34
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD11	4	0.34
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD12	4	0.34
(1,484)	1:134:A:LYS:HB3	1:134:A:LYS:HD2	7	0.34
(1,315)	1:184:A:LEU:HB2	1:187:A:VAL:HB	1	0.34
(1,287)	1:137:A:LEU:HB3	1:149:A:VAL:HB	12	0.34
(1,262)	1:63:A:TYR:HA	1:155:A:ASN:H	15	0.34

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,215)	1:248:A:VAL:HA	1:249:A:GLU:HB3	13	0.34
(1,215)	1:248:A:VAL:HA	1:249:A:GLU:HB3	20	0.34
(1,1983)	1:85:A:PHE:HB2	1:88:A:PHE:HA	6	0.33
(1,1858)	1:196:A:LEU:HD11	1:197:A:TYR:H	11	0.33
(1,1858)	1:196:A:LEU:HD12	1:197:A:TYR:H	11	0.33
(1,1858)	1:196:A:LEU:HD13	1:197:A:TYR:H	11	0.33
(1,1668)	1:166:A:SER:HB3	1:167:A:GLN:HB3	10	0.33
(1,1360)	1:231:A:ALA:HA	1:235:A:ARG:H	1	0.33
(1,1180)	1:189:A:LEU:H	1:192:A:ILE:HG13	10	0.33
(1,1180)	1:189:A:LEU:H	1:192:A:ILE:HG13	11	0.33
(1,1013)	1:141:A:SER:H	1:145:A:LYS:H	3	0.33
(1,484)	1:134:A:LYS:HB3	1:134:A:LYS:HD2	15	0.33
(1,484)	1:134:A:LYS:HB3	1:134:A:LYS:HD2	18	0.33
(1,484)	1:134:A:LYS:HB3	1:134:A:LYS:HD2	19	0.33
(1,262)	1:63:A:TYR:HA	1:155:A:ASN:H	13	0.33
(1,215)	1:248:A:VAL:HA	1:249:A:GLU:HB3	4	0.33
(1,215)	1:248:A:VAL:HA	1:249:A:GLU:HB3	5	0.33
(1,215)	1:248:A:VAL:HA	1:249:A:GLU:HB3	6	0.33
(1,215)	1:248:A:VAL:HA	1:249:A:GLU:HB3	16	0.33
(1,207)	1:159:A:SER:HA	1:161:A:PHE:H	2	0.33
(1,2015)	1:194:A:ASP:HA	1:198:A:GLY:H	12	0.32
(1,1983)	1:85:A:PHE:HB2	1:88:A:PHE:HA	13	0.32
(1,1624)	1:168:A:PRO:HB3	1:169:A:LEU:H	15	0.32
(1,1533)	1:172:A:ARG:HA	1:173:A:LYS:HE2	14	0.32
(1,1180)	1:189:A:LEU:H	1:192:A:ILE:HG13	1	0.32
(1,1083)	1:159:A:SER:HB3	1:161:A:PHE:H	12	0.32
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD13	8	0.32
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD11	8	0.32
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD12	8	0.32
(1,492)	1:234:A:ALA:H	1:235:A:ARG:HB3	7	0.32
(1,484)	1:134:A:LYS:HB3	1:134:A:LYS:HD2	1	0.32
(1,484)	1:134:A:LYS:HB3	1:134:A:LYS:HD2	4	0.32
(1,484)	1:134:A:LYS:HB3	1:134:A:LYS:HD2	8	0.32
(1,484)	1:134:A:LYS:HB3	1:134:A:LYS:HD2	10	0.32
(1,484)	1:134:A:LYS:HB3	1:134:A:LYS:HD2	12	0.32
(1,484)	1:134:A:LYS:HB3	1:134:A:LYS:HD2	17	0.32
(1,314)	1:193:A:MET:HG2	1:194:A:ASP:HB3	15	0.32
(1,207)	1:159:A:SER:HA	1:161:A:PHE:H	16	0.32
(1,120)	1:154:A:TRP:HH2	1:155:A:ASN:H	14	0.32
(1,1668)	1:166:A:SER:HB3	1:167:A:GLN:HB3	13	0.31
(1,1636)	1:246:A:LYS:HG2	1:247:A:ARG:HB3	7	0.31
(1,1636)	1:246:A:LYS:HG3	1:247:A:ARG:HB3	7	0.31

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1225)	1:211:A:LEU:H	1:215:A:LYS:HG2	2	0.31
(1,1083)	1:159:A:SER:HB3	1:161:A:PHE:H	13	0.31
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD13	10	0.31
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD11	10	0.31
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD12	10	0.31
(1,382)	1:180:A:VAL:HA	1:188:A:GLU:HG2	3	0.31
(1,314)	1:193:A:MET:HG2	1:194:A:ASP:HB3	18	0.31
(1,221)	1:194:A:ASP:HA	1:196:A:LEU:HG	1	0.31
(1,215)	1:248:A:VAL:HA	1:249:A:GLU:HB3	12	0.31
(1,215)	1:248:A:VAL:HA	1:249:A:GLU:HB3	18	0.31
(1,1858)	1:196:A:LEU:HD11	1:197:A:TYR:H	13	0.3
(1,1858)	1:196:A:LEU:HD12	1:197:A:TYR:H	13	0.3
(1,1858)	1:196:A:LEU:HD13	1:197:A:TYR:H	13	0.3
(1,1790)	1:226:A:GLN:HE22	1:227:A:SER:HA	12	0.3
(1,1560)	1:187:A:VAL:HA	1:188:A:GLU:HG3	18	0.3
(1,1360)	1:231:A:ALA:HA	1:235:A:ARG:H	15	0.3
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD13	18	0.3
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD11	18	0.3
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD12	18	0.3
(1,527)	1:237:A:VAL:H	1:238:A:GLN:HB2	19	0.3
(1,484)	1:134:A:LYS:HB3	1:134:A:LYS:HD2	6	0.3
(1,484)	1:134:A:LYS:HB3	1:134:A:LYS:HD2	13	0.3
(1,365)	1:133:A:GLY:H	1:134:A:LYS:HE3	20	0.3
(1,221)	1:194:A:ASP:HA	1:196:A:LEU:HG	3	0.3
(1,215)	1:248:A:VAL:HA	1:249:A:GLU:HB3	8	0.3
(1,207)	1:159:A:SER:HA	1:161:A:PHE:H	4	0.3
(2,109)	1:213:A:TYR:H	1:208:A:ASP:O	18	0.29
(1,2314)	1:208:A:ASP:HB2	1:212:A:LYS:H	6	0.29
(1,2155)	1:238:A:GLN:HA	1:239:A:LEU:HB2	20	0.29
(1,1983)	1:85:A:PHE:HB2	1:88:A:PHE:HA	18	0.29
(1,1790)	1:226:A:GLN:HE22	1:227:A:SER:HA	4	0.29
(1,1464)	1:199:A:GLY:H	1:200:A:VAL:HB	12	0.29
(1,1360)	1:231:A:ALA:HA	1:235:A:ARG:H	12	0.29
(1,1180)	1:189:A:LEU:H	1:192:A:ILE:HG13	3	0.29
(1,1180)	1:189:A:LEU:H	1:192:A:ILE:HG13	20	0.29
(1,963)	1:234:A:ALA:H	1:236:A:PHE:H	18	0.29
(1,934)	1:168:A:PRO:HA	1:170:A:ASP:H	16	0.29
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD13	11	0.29
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD11	11	0.29
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD12	11	0.29
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD13	14	0.29
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD11	14	0.29

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD12	14	0.29
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD13	19	0.29
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD11	19	0.29
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD12	19	0.29
(1,484)	1:134:A:LYS:HB3	1:134:A:LYS:HD2	14	0.29
(1,314)	1:193:A:MET:HG2	1:194:A:ASP:HB3	7	0.29
(1,314)	1:193:A:MET:HG2	1:194:A:ASP:HB3	14	0.29
(1,221)	1:194:A:ASP:HA	1:196:A:LEU:HG	5	0.29
(1,221)	1:194:A:ASP:HA	1:196:A:LEU:HG	7	0.29
(1,2314)	1:208:A:ASP:HB2	1:212:A:LYS:H	3	0.28
(1,1668)	1:166:A:SER:HB3	1:167:A:GLN:HB3	17	0.28
(1,1624)	1:168:A:PRO:HB3	1:169:A:LEU:H	18	0.28
(1,1565)	1:184:A:LEU:HB2	1:188:A:GLU:HG3	8	0.28
(1,1560)	1:187:A:VAL:HA	1:188:A:GLU:HG3	1	0.28
(1,1462)	1:141:A:SER:H	1:143:A:THR:H	7	0.28
(1,1446)	1:71:A:GLY:H	1:85:A:PHE:HZ	9	0.28
(1,1446)	1:71:A:GLY:H	1:85:A:PHE:HZ	17	0.28
(1,1360)	1:231:A:ALA:HA	1:235:A:ARG:H	2	0.28
(1,1143)	1:227:A:SER:H	1:229:A:ILE:HG12	4	0.28
(1,287)	1:137:A:LEU:HB3	1:149:A:VAL:HB	4	0.28
(1,215)	1:248:A:VAL:HA	1:249:A:GLU:HB3	1	0.28
(1,215)	1:248:A:VAL:HA	1:249:A:GLU:HB3	9	0.28
(1,215)	1:248:A:VAL:HA	1:249:A:GLU:HB3	17	0.28
(2,115)	1:154:A:TRP:H	1:64:A:SER:O	8	0.27
(1,2314)	1:208:A:ASP:HB2	1:212:A:LYS:H	10	0.27
(1,2136)	1:91:A:LEU:HA	1:117:A:ASP:H	17	0.27
(1,1983)	1:85:A:PHE:HB2	1:88:A:PHE:HA	10	0.27
(1,1560)	1:187:A:VAL:HA	1:188:A:GLU:HG3	14	0.27
(1,1373)	1:224:A:ASN:HD22	1:227:A:SER:H	12	0.27
(1,1360)	1:231:A:ALA:HA	1:235:A:ARG:H	3	0.27
(1,1180)	1:189:A:LEU:H	1:192:A:ILE:HG13	17	0.27
(1,1180)	1:189:A:LEU:H	1:192:A:ILE:HG13	19	0.27
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD13	17	0.27
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD11	17	0.27
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD12	17	0.27
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD13	20	0.27
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD11	20	0.27
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD12	20	0.27
(1,527)	1:237:A:VAL:H	1:238:A:GLN:HB2	2	0.27
(1,511)	1:167:A:GLN:HB2	1:167:A:GLN:HE22	6	0.27
(1,365)	1:133:A:GLY:H	1:134:A:LYS:HE3	11	0.27
(1,314)	1:193:A:MET:HG2	1:194:A:ASP:HB3	17	0.27

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,215)	1:248:A:VAL:HA	1:249:A:GLU:HB3	10	0.27
(1,127)	1:95:A:TRP:HZ3	1:113:A:LEU:HA	11	0.27
(1,119)	1:78:A:GLU:HG3	1:95:A:TRP:HZ2	16	0.27
(2,115)	1:154:A:TRP:H	1:64:A:SER:O	16	0.26
(2,109)	1:213:A:TYR:H	1:208:A:ASP:O	3	0.26
(1,2107)	1:63:A:TYR:HA	1:155:A:ASN:HB3	14	0.26
(1,1983)	1:85:A:PHE:HB2	1:88:A:PHE:HA	12	0.26
(1,1668)	1:166:A:SER:HB3	1:167:A:GLN:HB3	7	0.26
(1,1662)	1:251:A:LYS:HA	1:251:A:LYS:HD2	14	0.26
(1,1227)	1:219:A:ARG:HB3	1:220:A:VAL:H	19	0.26
(1,1225)	1:211:A:LEU:H	1:215:A:LYS:HG2	10	0.26
(1,1180)	1:189:A:LEU:H	1:192:A:ILE:HG13	9	0.26
(1,1062)	1:206:A:ASP:HB2	1:217:A:ALA:H	6	0.26
(1,511)	1:167:A:GLN:HB2	1:167:A:GLN:HE22	16	0.26
(1,492)	1:234:A:ALA:H	1:235:A:ARG:HB3	6	0.26
(1,444)	1:238:A:GLN:HG3	1:239:A:LEU:H	13	0.26
(1,314)	1:193:A:MET:HG2	1:194:A:ASP:HB3	4	0.26
(1,314)	1:193:A:MET:HG2	1:194:A:ASP:HB3	6	0.26
(1,314)	1:193:A:MET:HG2	1:194:A:ASP:HB3	19	0.26
(1,287)	1:137:A:LEU:HB3	1:149:A:VAL:HB	14	0.26
(1,246)	1:184:A:LEU:HA	1:187:A:VAL:HB	3	0.26
(1,221)	1:194:A:ASP:HA	1:196:A:LEU:HG	12	0.26
(1,221)	1:194:A:ASP:HA	1:196:A:LEU:HG	16	0.26
(1,119)	1:78:A:GLU:HG3	1:95:A:TRP:HZ2	15	0.26
(2,28)	1:112:A:PHE:H	1:94:A:ASP:O	20	0.25
(1,2314)	1:208:A:ASP:HB2	1:212:A:LYS:H	15	0.25
(1,1668)	1:166:A:SER:HB3	1:167:A:GLN:HB3	4	0.25
(1,1533)	1:172:A:ARG:HA	1:173:A:LYS:HE2	19	0.25
(1,1446)	1:71:A:GLY:H	1:85:A:PHE:HZ	13	0.25
(1,1415)	1:238:A:GLN:HE22	1:239:A:LEU:H	17	0.25
(1,1360)	1:231:A:ALA:HA	1:235:A:ARG:H	4	0.25
(1,1180)	1:189:A:LEU:H	1:192:A:ILE:HG13	4	0.25
(1,1083)	1:159:A:SER:HB3	1:161:A:PHE:H	6	0.25
(1,1048)	1:134:A:LYS:H	1:134:A:LYS:HE3	16	0.25
(1,378)	1:63:A:TYR:HA	1:155:A:ASN:HB2	19	0.25
(1,221)	1:194:A:ASP:HA	1:196:A:LEU:HG	15	0.25
(1,215)	1:248:A:VAL:HA	1:249:A:GLU:HB3	11	0.25
(1,215)	1:248:A:VAL:HA	1:249:A:GLU:HB3	15	0.25
(1,207)	1:159:A:SER:HA	1:161:A:PHE:H	6	0.25
(1,120)	1:154:A:TRP:HH2	1:155:A:ASN:H	10	0.25
(2,109)	1:213:A:TYR:H	1:208:A:ASP:O	4	0.24
(2,84)	1:220:A:VAL:H	1:175:A:ILE:O	19	0.24

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2323)	1:210:A:GLU:HB2	1:212:A:LYS:H	11	0.24
(1,1560)	1:187:A:VAL:HA	1:188:A:GLU:HG3	19	0.24
(1,1446)	1:71:A:GLY:H	1:85:A:PHE:HZ	15	0.24
(1,1243)	1:226:A:GLN:HG2	1:229:A:ILE:H	12	0.24
(1,1062)	1:206:A:ASP:HB2	1:217:A:ALA:H	18	0.24
(1,1013)	1:141:A:SER:H	1:145:A:LYS:H	4	0.24
(1,934)	1:168:A:PRO:HA	1:170:A:ASP:H	6	0.24
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD13	2	0.24
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD11	2	0.24
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD12	2	0.24
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD13	13	0.24
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD11	13	0.24
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD12	13	0.24
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD13	15	0.24
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD11	15	0.24
(1,621)	1:156:A:LEU:H	1:156:A:LEU:HD12	15	0.24
(1,546)	1:134:A:LYS:HG2	1:151:A:ILE:H	7	0.24
(1,527)	1:237:A:VAL:H	1:238:A:GLN:HB2	16	0.24
(1,365)	1:133:A:GLY:H	1:134:A:LYS:HE3	3	0.24
(1,314)	1:193:A:MET:HG2	1:194:A:ASP:HB3	2	0.24
(1,246)	1:184:A:LEU:HA	1:187:A:VAL:HB	9	0.24
(1,221)	1:194:A:ASP:HA	1:196:A:LEU:HG	6	0.24
(1,215)	1:248:A:VAL:HA	1:249:A:GLU:HB3	2	0.24
(1,215)	1:248:A:VAL:HA	1:249:A:GLU:HB3	7	0.24
(1,119)	1:78:A:GLU:HG3	1:95:A:TRP:HZ2	20	0.24
(2,115)	1:154:A:TRP:H	1:64:A:SER:O	17	0.23
(2,65)	1:196:A:LEU:H	1:192:A:ILE:O	18	0.23
(1,1764)	1:187:A:VAL:HA	1:191:A:MET:HB2	4	0.23
(1,1652)	1:245:A:ASP:HB2	1:246:A:LYS:HD3	1	0.23
(1,1617)	1:180:A:VAL:HB	1:188:A:GLU:HG2	5	0.23
(1,1533)	1:172:A:ARG:HA	1:173:A:LYS:HE2	13	0.23
(1,1521)	1:208:A:ASP:HB2	1:212:A:LYS:HA	8	0.23
(1,1510)	1:246:A:LYS:H	1:246:A:LYS:HE3	11	0.23
(1,1510)	1:246:A:LYS:H	1:246:A:LYS:HE2	11	0.23
(1,1440)	1:70:A:GLY:H	1:85:A:PHE:HZ	16	0.23
(1,1438)	1:70:A:GLY:H	1:149:A:VAL:HA	10	0.23
(1,1373)	1:224:A:ASN:HD22	1:227:A:SER:H	15	0.23
(1,1360)	1:231:A:ALA:HA	1:235:A:ARG:H	5	0.23
(1,1180)	1:189:A:LEU:H	1:192:A:ILE:HG13	5	0.23
(1,1180)	1:189:A:LEU:H	1:192:A:ILE:HG13	16	0.23
(1,1180)	1:189:A:LEU:H	1:192:A:ILE:HG13	18	0.23
(1,1083)	1:159:A:SER:HB3	1:161:A:PHE:H	2	0.23

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,612)	1:246:A:LYS:HG2	1:247:A:ARG:H	7	0.23
(1,612)	1:246:A:LYS:HG3	1:247:A:ARG:H	7	0.23
(1,314)	1:193:A:MET:HG2	1:194:A:ASP:HB3	1	0.23
(1,314)	1:193:A:MET:HG2	1:194:A:ASP:HB3	16	0.23
(1,314)	1:193:A:MET:HG2	1:194:A:ASP:HB3	20	0.23
(1,215)	1:248:A:VAL:HA	1:249:A:GLU:HB3	14	0.23
(1,207)	1:159:A:SER:HA	1:161:A:PHE:H	14	0.23
(2,116)	1:154:A:TRP:N	1:64:A:SER:O	8	0.22
(2,115)	1:154:A:TRP:H	1:64:A:SER:O	9	0.22
(2,109)	1:213:A:TYR:H	1:208:A:ASP:O	8	0.22
(2,109)	1:213:A:TYR:H	1:208:A:ASP:O	15	0.22
(2,109)	1:213:A:TYR:H	1:208:A:ASP:O	20	0.22
(1,2323)	1:210:A:GLU:HB2	1:212:A:LYS:H	12	0.22
(1,2323)	1:210:A:GLU:HB2	1:212:A:LYS:H	13	0.22
(1,1764)	1:187:A:VAL:HA	1:191:A:MET:HB2	16	0.22
(1,1668)	1:166:A:SER:HB3	1:167:A:GLN:HB3	16	0.22
(1,1652)	1:245:A:ASP:HB2	1:246:A:LYS:HD3	16	0.22
(1,1583)	1:78:A:GLU:HG3	1:79:A:ASP:HA	17	0.22
(1,1551)	1:141:A:SER:H	1:144:A:ILE:HB	12	0.22
(1,1225)	1:211:A:LEU:H	1:215:A:LYS:HG2	15	0.22
(1,1086)	1:129:A:ILE:H	1:138:A:CYS:HA	20	0.22
(1,1048)	1:134:A:LYS:H	1:134:A:LYS:HE3	11	0.22
(1,511)	1:167:A:GLN:HB2	1:167:A:GLN:HE22	5	0.22
(1,492)	1:234:A:ALA:H	1:235:A:ARG:HB3	9	0.22
(1,314)	1:193:A:MET:HG2	1:194:A:ASP:HB3	10	0.22
(1,293)	1:206:A:ASP:H	1:218:A:GLY:HA2	20	0.22
(1,293)	1:206:A:ASP:H	1:218:A:GLY:HA3	20	0.22
(1,221)	1:194:A:ASP:HA	1:196:A:LEU:HG	19	0.22
(1,120)	1:154:A:TRP:HH2	1:155:A:ASN:H	15	0.22
(1,119)	1:78:A:GLU:HG3	1:95:A:TRP:HZ2	3	0.22
(2,115)	1:154:A:TRP:H	1:64:A:SER:O	2	0.21
(2,115)	1:154:A:TRP:H	1:64:A:SER:O	11	0.21
(2,109)	1:213:A:TYR:H	1:208:A:ASP:O	5	0.21
(2,109)	1:213:A:TYR:H	1:208:A:ASP:O	6	0.21
(2,109)	1:213:A:TYR:H	1:208:A:ASP:O	10	0.21
(2,109)	1:213:A:TYR:H	1:208:A:ASP:O	14	0.21
(2,42)	1:112:A:PHE:N	1:94:A:ASP:O	20	0.21
(1,2323)	1:210:A:GLU:HB2	1:212:A:LYS:H	4	0.21
(1,2323)	1:210:A:GLU:HB2	1:212:A:LYS:H	17	0.21
(1,2186)	1:113:A:LEU:HA	1:114:A:LEU:HB3	20	0.21
(1,1983)	1:85:A:PHE:HB2	1:88:A:PHE:HA	1	0.21
(1,1764)	1:187:A:VAL:HA	1:191:A:MET:HB2	6	0.21

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1764)	1:187:A:VAL:HA	1:191:A:MET:HB2	7	0.21
(1,1521)	1:208:A:ASP:HB2	1:212:A:LYS:HA	19	0.21
(1,1360)	1:231:A:ALA:HA	1:235:A:ARG:H	13	0.21
(1,1360)	1:231:A:ALA:HA	1:235:A:ARG:H	18	0.21
(1,1062)	1:206:A:ASP:HB2	1:217:A:ALA:H	7	0.21
(1,409)	1:177:A:VAL:H	1:219:A:ARG:HB2	8	0.21
(1,382)	1:180:A:VAL:HA	1:188:A:GLU:HG2	6	0.21
(1,314)	1:193:A:MET:HG2	1:194:A:ASP:HB3	3	0.21
(1,287)	1:137:A:LEU:HB3	1:149:A:VAL:HB	18	0.21
(1,253)	1:91:A:LEU:HA	1:114:A:LEU:H	4	0.21
(1,221)	1:194:A:ASP:HA	1:196:A:LEU:HG	13	0.21
(1,194)	1:244:A:ILE:HA	1:245:A:ASP:HB2	13	0.21
(1,127)	1:95:A:TRP:HZ3	1:113:A:LEU:HA	19	0.21
(1,119)	1:78:A:GLU:HG3	1:95:A:TRP:HZ2	1	0.21
(2,115)	1:154:A:TRP:H	1:64:A:SER:O	3	0.2
(2,115)	1:154:A:TRP:H	1:64:A:SER:O	6	0.2
(2,115)	1:154:A:TRP:H	1:64:A:SER:O	10	0.2
(2,115)	1:154:A:TRP:H	1:64:A:SER:O	19	0.2
(2,109)	1:213:A:TYR:H	1:208:A:ASP:O	1	0.2
(2,109)	1:213:A:TYR:H	1:208:A:ASP:O	2	0.2
(2,109)	1:213:A:TYR:H	1:208:A:ASP:O	11	0.2
(2,109)	1:213:A:TYR:H	1:208:A:ASP:O	13	0.2
(2,109)	1:213:A:TYR:H	1:208:A:ASP:O	17	0.2
(2,109)	1:213:A:TYR:H	1:208:A:ASP:O	19	0.2
(1,2323)	1:210:A:GLU:HB2	1:212:A:LYS:H	7	0.2
(1,2323)	1:210:A:GLU:HB2	1:212:A:LYS:H	14	0.2
(1,2171)	1:234:A:ALA:HA	1:235:A:ARG:HA	17	0.2
(1,1983)	1:85:A:PHE:HB2	1:88:A:PHE:HA	11	0.2
(1,1764)	1:187:A:VAL:HA	1:191:A:MET:HB2	14	0.2
(1,1738)	1:223:A:SER:HB3	1:224:A:ASN:HA	14	0.2
(1,1705)	1:140:A:SER:HB2	1:146:A:ASP:HA	2	0.2
(1,1705)	1:140:A:SER:HB2	1:146:A:ASP:HA	20	0.2
(1,1655)	1:246:A:LYS:HB3	1:246:A:LYS:HD3	7	0.2
(1,1642)	1:208:A:ASP:HB2	1:210:A:GLU:HB3	4	0.2
(1,1533)	1:172:A:ARG:HA	1:173:A:LYS:HE2	17	0.2
(1,1415)	1:238:A:GLN:HE22	1:239:A:LEU:H	5	0.2
(1,1360)	1:231:A:ALA:HA	1:235:A:ARG:H	9	0.2
(1,1360)	1:231:A:ALA:HA	1:235:A:ARG:H	20	0.2
(1,1243)	1:226:A:GLN:HG2	1:229:A:ILE:H	4	0.2
(1,1086)	1:129:A:ILE:H	1:138:A:CYS:HA	18	0.2
(1,1083)	1:159:A:SER:HB3	1:161:A:PHE:H	1	0.2
(1,934)	1:168:A:PRO:HA	1:170:A:ASP:H	2	0.2

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,495)	1:79:A:ASP:HB3	1:80:A:GLU:HB3	16	0.2
(1,492)	1:234:A:ALA:H	1:235:A:ARG:HB3	10	0.2
(1,407)	1:130:A:GLU:H	1:130:A:GLU:HG3	20	0.2
(1,314)	1:193:A:MET:HG2	1:194:A:ASP:HB3	9	0.2
(1,314)	1:193:A:MET:HG2	1:194:A:ASP:HB3	13	0.2
(1,312)	1:235:A:ARG:HD2	1:236:A:PHE:H	20	0.2
(1,303)	1:235:A:ARG:HD3	1:236:A:PHE:H	9	0.2
(1,303)	1:235:A:ARG:HD3	1:236:A:PHE:H	17	0.2
(1,221)	1:194:A:ASP:HA	1:196:A:LEU:HG	4	0.2
(1,120)	1:154:A:TRP:HH2	1:155:A:ASN:H	8	0.2
(1,119)	1:78:A:GLU:HG3	1:95:A:TRP:HZ2	5	0.2
(2,115)	1:154:A:TRP:H	1:64:A:SER:O	4	0.19
(2,115)	1:154:A:TRP:H	1:64:A:SER:O	5	0.19
(2,115)	1:154:A:TRP:H	1:64:A:SER:O	7	0.19
(2,115)	1:154:A:TRP:H	1:64:A:SER:O	12	0.19
(2,115)	1:154:A:TRP:H	1:64:A:SER:O	13	0.19
(2,109)	1:213:A:TYR:H	1:208:A:ASP:O	16	0.19
(1,2323)	1:210:A:GLU:HB2	1:212:A:LYS:H	1	0.19
(1,2323)	1:210:A:GLU:HB2	1:212:A:LYS:H	5	0.19
(1,2323)	1:210:A:GLU:HB2	1:212:A:LYS:H	9	0.19
(1,2323)	1:210:A:GLU:HB2	1:212:A:LYS:H	20	0.19
(1,1764)	1:187:A:VAL:HA	1:191:A:MET:HB2	13	0.19
(1,1741)	1:156:A:LEU:H	1:156:A:LEU:HD21	16	0.19
(1,1741)	1:156:A:LEU:H	1:156:A:LEU:HD22	16	0.19
(1,1741)	1:156:A:LEU:H	1:156:A:LEU:HD23	16	0.19
(1,1668)	1:166:A:SER:HB3	1:167:A:GLN:HB3	3	0.19
(1,1652)	1:245:A:ASP:HB2	1:246:A:LYS:HD3	7	0.19
(1,1533)	1:172:A:ARG:HA	1:173:A:LYS:HE2	12	0.19
(1,1521)	1:208:A:ASP:HB2	1:212:A:LYS:HA	2	0.19
(1,1446)	1:71:A:GLY:H	1:85:A:PHE:HZ	1	0.19
(1,1446)	1:71:A:GLY:H	1:85:A:PHE:HZ	5	0.19
(1,1446)	1:71:A:GLY:H	1:85:A:PHE:HZ	6	0.19
(1,1446)	1:71:A:GLY:H	1:85:A:PHE:HZ	8	0.19
(1,1446)	1:71:A:GLY:H	1:85:A:PHE:HZ	11	0.19
(1,1438)	1:70:A:GLY:H	1:149:A:VAL:HA	13	0.19
(1,934)	1:168:A:PRO:HA	1:170:A:ASP:H	14	0.19
(1,527)	1:237:A:VAL:H	1:238:A:GLN:HB2	5	0.19
(1,407)	1:130:A:GLU:H	1:130:A:GLU:HG3	8	0.19
(1,365)	1:133:A:GLY:H	1:134:A:LYS:HE3	16	0.19
(1,253)	1:91:A:LEU:HA	1:114:A:LEU:H	10	0.19
(1,246)	1:184:A:LEU:HA	1:187:A:VAL:HB	17	0.19
(1,221)	1:194:A:ASP:HA	1:196:A:LEU:HG	17	0.19

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,207)	1:159:A:SER:HA	1:161:A:PHE:H	18	0.19
(1,120)	1:154:A:TRP:HH2	1:155:A:ASN:H	7	0.19
(2,116)	1:154:A:TRP:N	1:64:A:SER:O	3	0.18
(2,116)	1:154:A:TRP:N	1:64:A:SER:O	4	0.18
(2,115)	1:154:A:TRP:H	1:64:A:SER:O	1	0.18
(2,109)	1:213:A:TYR:H	1:208:A:ASP:O	9	0.18
(2,65)	1:196:A:LEU:H	1:192:A:ILE:O	4	0.18
(2,65)	1:196:A:LEU:H	1:192:A:ILE:O	10	0.18
(1,2323)	1:210:A:GLU:HB2	1:212:A:LYS:H	16	0.18
(1,2171)	1:234:A:ALA:HA	1:235:A:ARG:HA	6	0.18
(1,2171)	1:234:A:ALA:HA	1:235:A:ARG:HA	16	0.18
(1,2028)	1:189:A:LEU:HA	1:193:A:MET:HG3	8	0.18
(1,1983)	1:85:A:PHE:HB2	1:88:A:PHE:HA	8	0.18
(1,1983)	1:85:A:PHE:HB2	1:88:A:PHE:HA	14	0.18
(1,1858)	1:196:A:LEU:HD11	1:197:A:TYR:H	20	0.18
(1,1858)	1:196:A:LEU:HD12	1:197:A:TYR:H	20	0.18
(1,1858)	1:196:A:LEU:HD13	1:197:A:TYR:H	20	0.18
(1,1764)	1:187:A:VAL:HA	1:191:A:MET:HB2	5	0.18
(1,1652)	1:245:A:ASP:HB2	1:246:A:LYS:HD3	15	0.18
(1,1605)	1:131:A:GLU:HB2	1:134:A:LYS:HG3	9	0.18
(1,1570)	1:245:A:ASP:HA	1:246:A:LYS:HB3	15	0.18
(1,1441)	1:225:A:GLN:HE22	1:226:A:GLN:H	3	0.18
(1,1440)	1:70:A:GLY:H	1:85:A:PHE:HZ	20	0.18
(1,1417)	1:238:A:GLN:HB3	1:238:A:GLN:HE22	17	0.18
(1,1373)	1:224:A:ASN:HD22	1:227:A:SER:H	1	0.18
(1,1373)	1:224:A:ASN:HD22	1:227:A:SER:H	2	0.18
(1,1373)	1:224:A:ASN:HD22	1:227:A:SER:H	4	0.18
(1,1373)	1:224:A:ASN:HD22	1:227:A:SER:H	20	0.18
(1,1368)	1:196:A:LEU:HG	1:197:A:TYR:H	2	0.18
(1,1268)	1:234:A:ALA:HA	1:236:A:PHE:H	18	0.18
(1,1083)	1:159:A:SER:HB3	1:161:A:PHE:H	20	0.18
(1,546)	1:134:A:LYS:HG2	1:151:A:ILE:H	1	0.18
(1,493)	1:167:A:GLN:HB3	1:201:A:CYS:HB3	2	0.18
(1,382)	1:180:A:VAL:HA	1:188:A:GLU:HG2	12	0.18
(1,342)	1:208:A:ASP:HB3	1:215:A:LYS:HG2	19	0.18
(1,314)	1:193:A:MET:HG2	1:194:A:ASP:HB3	12	0.18
(1,221)	1:194:A:ASP:HA	1:196:A:LEU:HG	11	0.18
(1,207)	1:159:A:SER:HA	1:161:A:PHE:H	17	0.18
(1,127)	1:95:A:TRP:HZ3	1:113:A:LEU:HA	8	0.18
(2,116)	1:154:A:TRP:N	1:64:A:SER:O	6	0.17
(2,116)	1:154:A:TRP:N	1:64:A:SER:O	9	0.17
(2,116)	1:154:A:TRP:N	1:64:A:SER:O	11	0.17

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,115)	1:154:A:TRP:H	1:64:A:SER:O	15	0.17
(2,115)	1:154:A:TRP:H	1:64:A:SER:O	18	0.17
(2,109)	1:213:A:TYR:H	1:208:A:ASP:O	12	0.17
(2,65)	1:196:A:LEU:H	1:192:A:ILE:O	20	0.17
(1,2323)	1:210:A:GLU:HB2	1:212:A:LYS:H	2	0.17
(1,2171)	1:234:A:ALA:HA	1:235:A:ARG:HA	19	0.17
(1,2136)	1:91:A:LEU:HA	1:117:A:ASP:H	1	0.17
(1,1764)	1:187:A:VAL:HA	1:191:A:MET:HB2	2	0.17
(1,1764)	1:187:A:VAL:HA	1:191:A:MET:HB2	12	0.17
(1,1764)	1:187:A:VAL:HA	1:191:A:MET:HB2	19	0.17
(1,1665)	1:192:A:ILE:HG12	1:195:A:ARG:H	7	0.17
(1,1665)	1:192:A:ILE:HG12	1:195:A:ARG:H	9	0.17
(1,1665)	1:192:A:ILE:HG12	1:195:A:ARG:H	14	0.17
(1,1665)	1:192:A:ILE:HG12	1:195:A:ARG:H	17	0.17
(1,1617)	1:180:A:VAL:HB	1:188:A:GLU:HG2	7	0.17
(1,1605)	1:131:A:GLU:HB2	1:134:A:LYS:HG3	5	0.17
(1,1560)	1:187:A:VAL:HA	1:188:A:GLU:HG3	9	0.17
(1,1551)	1:141:A:SER:H	1:144:A:ILE:HB	14	0.17
(1,1441)	1:225:A:GLN:HE22	1:226:A:GLN:H	18	0.17
(1,1256)	1:117:A:ASP:H	1:120:A:SER:HB3	3	0.17
(1,511)	1:167:A:GLN:HB2	1:167:A:GLN:HE22	1	0.17
(1,407)	1:130:A:GLU:H	1:130:A:GLU:HG3	14	0.17
(1,407)	1:130:A:GLU:H	1:130:A:GLU:HG3	19	0.17
(1,293)	1:206:A:ASP:H	1:218:A:GLY:HA2	8	0.17
(1,293)	1:206:A:ASP:H	1:218:A:GLY:HA3	8	0.17
(1,293)	1:206:A:ASP:H	1:218:A:GLY:HA2	14	0.17
(1,293)	1:206:A:ASP:H	1:218:A:GLY:HA3	14	0.17
(1,253)	1:91:A:LEU:HA	1:114:A:LEU:H	16	0.17
(1,253)	1:91:A:LEU:HA	1:114:A:LEU:H	19	0.17
(1,246)	1:184:A:LEU:HA	1:187:A:VAL:HB	13	0.17
(1,221)	1:194:A:ASP:HA	1:196:A:LEU:HG	10	0.17
(1,207)	1:159:A:SER:HA	1:161:A:PHE:H	10	0.17
(1,207)	1:159:A:SER:HA	1:161:A:PHE:H	11	0.17
(1,172)	1:74:A:PRO:HA	1:76:A:ILE:H	10	0.17
(2,116)	1:154:A:TRP:N	1:64:A:SER:O	12	0.16
(2,116)	1:154:A:TRP:N	1:64:A:SER:O	17	0.16
(2,109)	1:213:A:TYR:H	1:208:A:ASP:O	7	0.16
(2,73)	1:229:A:ILE:H	1:225:A:GLN:O	12	0.16
(2,65)	1:196:A:LEU:H	1:192:A:ILE:O	1	0.16
(2,65)	1:196:A:LEU:H	1:192:A:ILE:O	3	0.16
(2,65)	1:196:A:LEU:H	1:192:A:ILE:O	15	0.16
(1,2323)	1:210:A:GLU:HB2	1:212:A:LYS:H	3	0.16

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2323)	1:210:A:GLU:HB2	1:212:A:LYS:H	18	0.16
(1,2323)	1:210:A:GLU:HB2	1:212:A:LYS:H	19	0.16
(1,2171)	1:234:A:ALA:HA	1:235:A:ARG:HA	7	0.16
(1,2136)	1:91:A:LEU:HA	1:117:A:ASP:H	16	0.16
(1,2107)	1:63:A:TYR:HA	1:155:A:ASN:HB3	2	0.16
(1,2093)	1:136:A:TYR:HA	1:137:A:LEU:HB3	12	0.16
(1,1858)	1:196:A:LEU:HD11	1:197:A:TYR:H	17	0.16
(1,1858)	1:196:A:LEU:HD12	1:197:A:TYR:H	17	0.16
(1,1858)	1:196:A:LEU:HD13	1:197:A:TYR:H	17	0.16
(1,1824)	1:239:A:LEU:HD11	1:240:A:GLN:H	7	0.16
(1,1824)	1:239:A:LEU:HD12	1:240:A:GLN:H	7	0.16
(1,1824)	1:239:A:LEU:HD13	1:240:A:GLN:H	7	0.16
(1,1764)	1:187:A:VAL:HA	1:191:A:MET:HB2	10	0.16
(1,1764)	1:187:A:VAL:HA	1:191:A:MET:HB2	18	0.16
(1,1705)	1:140:A:SER:HB2	1:146:A:ASP:HA	9	0.16
(1,1665)	1:192:A:ILE:HG12	1:195:A:ARG:H	10	0.16
(1,1665)	1:192:A:ILE:HG12	1:195:A:ARG:H	12	0.16
(1,1642)	1:208:A:ASP:HB2	1:210:A:GLU:HB3	2	0.16
(1,1588)	1:78:A:GLU:HG2	1:80:A:GLU:H	17	0.16
(1,1565)	1:184:A:LEU:HB2	1:188:A:GLU:HG3	11	0.16
(1,1557)	1:80:A:GLU:HG3	1:81:A:ILE:HB	16	0.16
(1,1527)	1:240:A:GLN:HG3	1:245:A:ASP:HB3	5	0.16
(1,1438)	1:70:A:GLY:H	1:149:A:VAL:HA	18	0.16
(1,1417)	1:238:A:GLN:HB3	1:238:A:GLN:HE22	9	0.16
(1,1415)	1:238:A:GLN:HE22	1:239:A:LEU:H	1	0.16
(1,1356)	1:232:A:ILE:HA	1:235:A:ARG:H	13	0.16
(1,1183)	1:207:A:THR:HB	1:215:A:LYS:H	15	0.16
(1,1080)	1:129:A:ILE:H	1:138:A:CYS:HB2	8	0.16
(1,1048)	1:134:A:LYS:H	1:134:A:LYS:HE3	3	0.16
(1,1014)	1:141:A:SER:H	1:145:A:LYS:HA	17	0.16
(1,1011)	1:239:A:LEU:HD11	1:240:A:GLN:H	7	0.16
(1,1011)	1:239:A:LEU:HD12	1:240:A:GLN:H	7	0.16
(1,1011)	1:239:A:LEU:HD13	1:240:A:GLN:H	7	0.16
(1,1011)	1:239:A:LEU:HD21	1:240:A:GLN:H	7	0.16
(1,1011)	1:239:A:LEU:HD22	1:240:A:GLN:H	7	0.16
(1,1011)	1:239:A:LEU:HD23	1:240:A:GLN:H	7	0.16
(1,378)	1:63:A:TYR:HA	1:155:A:ASN:HB2	12	0.16
(1,350)	1:249:A:GLU:H	1:249:A:GLU:HG3	12	0.16
(1,303)	1:235:A:ARG:HD3	1:236:A:PHE:H	10	0.16
(1,221)	1:194:A:ASP:HA	1:196:A:LEU:HG	20	0.16
(1,207)	1:159:A:SER:HA	1:161:A:PHE:H	7	0.16
(1,207)	1:159:A:SER:HA	1:161:A:PHE:H	19	0.16

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,172)	1:74:A:PRO:HA	1:76:A:ILE:H	8	0.16
(1,172)	1:74:A:PRO:HA	1:76:A:ILE:H	11	0.16
(1,172)	1:74:A:PRO:HA	1:76:A:ILE:H	13	0.16
(1,127)	1:95:A:TRP:HZ3	1:113:A:LEU:HA	14	0.16
(2,119)	1:159:A:SER:H	1:155:A:ASN:O	16	0.15
(2,119)	1:159:A:SER:H	1:155:A:ASN:O	18	0.15
(2,116)	1:154:A:TRP:N	1:64:A:SER:O	1	0.15
(2,116)	1:154:A:TRP:N	1:64:A:SER:O	2	0.15
(2,116)	1:154:A:TRP:N	1:64:A:SER:O	10	0.15
(2,116)	1:154:A:TRP:N	1:64:A:SER:O	18	0.15
(2,115)	1:154:A:TRP:H	1:64:A:SER:O	20	0.15
(2,96)	1:220:A:VAL:N	1:175:A:ILE:O	19	0.15
(2,73)	1:229:A:ILE:H	1:225:A:GLN:O	4	0.15
(2,65)	1:196:A:LEU:H	1:192:A:ILE:O	9	0.15
(2,64)	1:195:A:ARG:H	1:191:A:MET:O	5	0.15
(1,2323)	1:210:A:GLU:HB2	1:212:A:LYS:H	6	0.15
(1,2323)	1:210:A:GLU:HB2	1:212:A:LYS:H	8	0.15
(1,2323)	1:210:A:GLU:HB2	1:212:A:LYS:H	10	0.15
(1,2246)	1:154:A:TRP:HE1	1:158:A:ASP:H	17	0.15
(1,2202)	1:144:A:ILE:HD11	1:145:A:LYS:H	10	0.15
(1,2202)	1:144:A:ILE:HD12	1:145:A:LYS:H	10	0.15
(1,2202)	1:144:A:ILE:HD13	1:145:A:LYS:H	10	0.15
(1,2093)	1:136:A:TYR:HA	1:137:A:LEU:HB3	18	0.15
(1,2093)	1:136:A:TYR:HA	1:137:A:LEU:HB3	19	0.15
(1,1764)	1:187:A:VAL:HA	1:191:A:MET:HB2	9	0.15
(1,1764)	1:187:A:VAL:HA	1:191:A:MET:HB2	11	0.15
(1,1764)	1:187:A:VAL:HA	1:191:A:MET:HB2	15	0.15
(1,1749)	1:184:A:LEU:HD22	1:188:A:GLU:H	7	0.15
(1,1749)	1:184:A:LEU:HD23	1:188:A:GLU:H	7	0.15
(1,1749)	1:184:A:LEU:HD21	1:188:A:GLU:H	7	0.15
(1,1705)	1:140:A:SER:HB2	1:146:A:ASP:HA	11	0.15
(1,1705)	1:140:A:SER:HB2	1:146:A:ASP:HA	12	0.15
(1,1668)	1:166:A:SER:HB3	1:167:A:GLN:HB3	2	0.15
(1,1655)	1:246:A:LYS:HB3	1:246:A:LYS:HD3	15	0.15
(1,1652)	1:245:A:ASP:HB2	1:246:A:LYS:HD3	10	0.15
(1,1651)	1:167:A:GLN:HB3	1:201:A:CYS:HB2	16	0.15
(1,1533)	1:172:A:ARG:HA	1:173:A:LYS:HE2	20	0.15
(1,1521)	1:208:A:ASP:HB2	1:212:A:LYS:HA	4	0.15
(1,1446)	1:71:A:GLY:H	1:85:A:PHE:HZ	10	0.15
(1,1440)	1:70:A:GLY:H	1:85:A:PHE:HZ	4	0.15
(1,1225)	1:211:A:LEU:H	1:215:A:LYS:HG2	3	0.15
(1,1049)	1:131:A:GLU:HB2	1:134:A:LYS:H	20	0.15

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,950)	1:143:A:THR:H	1:144:A:ILE:H	9	0.15
(1,912)	1:65:A:ARG:H	1:114:A:LEU:HB2	9	0.15
(1,901)	1:237:A:VAL:HG21	1:238:A:GLN:H	5	0.15
(1,901)	1:237:A:VAL:HG22	1:238:A:GLN:H	5	0.15
(1,901)	1:237:A:VAL:HG23	1:238:A:GLN:H	5	0.15
(1,612)	1:246:A:LYS:HG2	1:247:A:ARG:H	15	0.15
(1,612)	1:246:A:LYS:HG3	1:247:A:ARG:H	15	0.15
(1,546)	1:134:A:LYS:HG2	1:151:A:ILE:H	4	0.15
(1,450)	1:238:A:GLN:HG2	1:239:A:LEU:H	3	0.15
(1,409)	1:177:A:VAL:H	1:219:A:ARG:HB2	20	0.15
(1,382)	1:180:A:VAL:HA	1:188:A:GLU:HG2	2	0.15
(1,367)	1:128:A:CYS:HA	1:129:A:ILE:HB	18	0.15
(1,316)	1:63:A:TYR:HB3	1:155:A:ASN:HA	17	0.15
(1,314)	1:193:A:MET:HG2	1:194:A:ASP:HB3	5	0.15
(1,314)	1:193:A:MET:HG2	1:194:A:ASP:HB3	11	0.15
(1,293)	1:206:A:ASP:H	1:218:A:GLY:HA2	13	0.15
(1,293)	1:206:A:ASP:H	1:218:A:GLY:HA3	13	0.15
(1,246)	1:184:A:LEU:HA	1:187:A:VAL:HB	11	0.15
(1,221)	1:194:A:ASP:HA	1:196:A:LEU:HG	9	0.15
(1,207)	1:159:A:SER:HA	1:161:A:PHE:H	8	0.15
(1,127)	1:95:A:TRP:HZ3	1:113:A:LEU:HA	5	0.15
(1,119)	1:78:A:GLU:HG3	1:95:A:TRP:HZ2	6	0.15
(2,116)	1:154:A:TRP:N	1:64:A:SER:O	13	0.14
(2,116)	1:154:A:TRP:N	1:64:A:SER:O	16	0.14
(2,115)	1:154:A:TRP:H	1:64:A:SER:O	14	0.14
(2,63)	1:194:A:ASP:H	1:190:A:ALA:O	13	0.14
(1,2323)	1:210:A:GLU:HB2	1:212:A:LYS:H	15	0.14
(1,2314)	1:208:A:ASP:HB2	1:212:A:LYS:H	16	0.14
(1,2246)	1:154:A:TRP:HE1	1:158:A:ASP:H	15	0.14
(1,2136)	1:91:A:LEU:HA	1:117:A:ASP:H	12	0.14
(1,1983)	1:85:A:PHE:HB2	1:88:A:PHE:HA	17	0.14
(1,1858)	1:196:A:LEU:HD11	1:197:A:TYR:H	3	0.14
(1,1858)	1:196:A:LEU:HD12	1:197:A:TYR:H	3	0.14
(1,1858)	1:196:A:LEU:HD13	1:197:A:TYR:H	3	0.14
(1,1764)	1:187:A:VAL:HA	1:191:A:MET:HB2	8	0.14
(1,1718)	1:195:A:ARG:H	1:196:A:LEU:HG	2	0.14
(1,1668)	1:166:A:SER:HB3	1:167:A:GLN:HB3	1	0.14
(1,1668)	1:166:A:SER:HB3	1:167:A:GLN:HB3	11	0.14
(1,1668)	1:166:A:SER:HB3	1:167:A:GLN:HB3	12	0.14
(1,1665)	1:192:A:ILE:HG12	1:195:A:ARG:H	1	0.14
(1,1665)	1:192:A:ILE:HG12	1:195:A:ARG:H	13	0.14
(1,1665)	1:192:A:ILE:HG12	1:195:A:ARG:H	20	0.14

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1617)	1:180:A:VAL:HB	1:188:A:GLU:HG2	18	0.14
(1,1560)	1:187:A:VAL:HA	1:188:A:GLU:HG3	16	0.14
(1,1417)	1:238:A:GLN:HB3	1:238:A:GLN:HE22	5	0.14
(1,1417)	1:238:A:GLN:HB3	1:238:A:GLN:HE22	13	0.14
(1,1373)	1:224:A:ASN:HD22	1:227:A:SER:H	9	0.14
(1,1360)	1:231:A:ALA:HA	1:235:A:ARG:H	10	0.14
(1,1225)	1:211:A:LEU:H	1:215:A:LYS:HG2	6	0.14
(1,1083)	1:159:A:SER:HB3	1:161:A:PHE:H	8	0.14
(1,1083)	1:159:A:SER:HB3	1:161:A:PHE:H	9	0.14
(1,1022)	1:208:A:ASP:H	1:215:A:LYS:HB2	3	0.14
(1,934)	1:168:A:PRO:HA	1:170:A:ASP:H	7	0.14
(1,934)	1:168:A:PRO:HA	1:170:A:ASP:H	17	0.14
(1,552)	1:134:A:LYS:HG2	1:136:A:TYR:HB2	12	0.14
(1,546)	1:134:A:LYS:HG2	1:151:A:ILE:H	6	0.14
(1,494)	1:77:A:ASP:H	1:80:A:GLU:HB3	16	0.14
(1,492)	1:234:A:ALA:H	1:235:A:ARG:HB3	18	0.14
(1,450)	1:238:A:GLN:HG2	1:239:A:LEU:H	12	0.14
(1,443)	1:163:A:MET:HG3	1:164:A:ASP:H	14	0.14
(1,315)	1:184:A:LEU:HB2	1:187:A:VAL:HB	15	0.14
(1,207)	1:159:A:SER:HA	1:161:A:PHE:H	13	0.14
(1,172)	1:74:A:PRO:HA	1:76:A:ILE:H	4	0.14
(1,156)	1:174:A:THR:HB	1:253:A:TYR:HA	14	0.14
(1,120)	1:154:A:TRP:HH2	1:155:A:ASN:H	12	0.14
(1,119)	1:78:A:GLU:HG3	1:95:A:TRP:HZ2	19	0.14
(1,108)	1:235:A:ARG:HD2	1:236:A:PHE:HZ	1	0.14
(2,119)	1:159:A:SER:H	1:155:A:ASN:O	20	0.13
(2,116)	1:154:A:TRP:N	1:64:A:SER:O	5	0.13
(2,116)	1:154:A:TRP:N	1:64:A:SER:O	15	0.13
(2,73)	1:229:A:ILE:H	1:225:A:GLN:O	15	0.13
(2,65)	1:196:A:LEU:H	1:192:A:ILE:O	17	0.13
(2,64)	1:195:A:ARG:H	1:191:A:MET:O	12	0.13
(2,56)	1:203:A:ALA:H	1:161:A:PHE:O	15	0.13
(2,48)	1:129:A:ILE:H	1:136:A:TYR:O	13	0.13
(2,9)	1:123:A:ALA:H	1:119:A:SER:O	7	0.13
(1,2246)	1:154:A:TRP:HE1	1:158:A:ASP:H	6	0.13
(1,2246)	1:154:A:TRP:HE1	1:158:A:ASP:H	11	0.13
(1,2093)	1:136:A:TYR:HA	1:137:A:LEU:HB3	4	0.13
(1,1983)	1:85:A:PHE:HB2	1:88:A:PHE:HA	7	0.13
(1,1858)	1:196:A:LEU:HD11	1:197:A:TYR:H	9	0.13
(1,1858)	1:196:A:LEU:HD12	1:197:A:TYR:H	9	0.13
(1,1858)	1:196:A:LEU:HD13	1:197:A:TYR:H	9	0.13
(1,1790)	1:226:A:GLN:HE22	1:227:A:SER:HA	17	0.13

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1765)	1:187:A:VAL:HA	1:188:A:GLU:HG2	16	0.13
(1,1705)	1:140:A:SER:HB2	1:146:A:ASP:HA	14	0.13
(1,1665)	1:192:A:ILE:HG12	1:195:A:ARG:H	4	0.13
(1,1665)	1:192:A:ILE:HG12	1:195:A:ARG:H	5	0.13
(1,1591)	1:163:A:MET:HB2	1:200:A:VAL:HB	3	0.13
(1,1446)	1:71:A:GLY:H	1:85:A:PHE:HZ	7	0.13
(1,1417)	1:238:A:GLN:HB3	1:238:A:GLN:HE22	2	0.13
(1,1417)	1:238:A:GLN:HB3	1:238:A:GLN:HE22	6	0.13
(1,1417)	1:238:A:GLN:HB3	1:238:A:GLN:HE22	7	0.13
(1,1417)	1:238:A:GLN:HB3	1:238:A:GLN:HE22	16	0.13
(1,1415)	1:238:A:GLN:HE22	1:239:A:LEU:H	8	0.13
(1,1415)	1:238:A:GLN:HE22	1:239:A:LEU:H	11	0.13
(1,1415)	1:238:A:GLN:HE22	1:239:A:LEU:H	12	0.13
(1,1373)	1:224:A:ASN:HD22	1:227:A:SER:H	7	0.13
(1,1080)	1:129:A:ILE:H	1:138:A:CYS:HB2	11	0.13
(1,1022)	1:208:A:ASP:H	1:215:A:LYS:HB2	17	0.13
(1,934)	1:168:A:PRO:HA	1:170:A:ASP:H	3	0.13
(1,934)	1:168:A:PRO:HA	1:170:A:ASP:H	19	0.13
(1,901)	1:237:A:VAL:HG21	1:238:A:GLN:H	9	0.13
(1,901)	1:237:A:VAL:HG22	1:238:A:GLN:H	9	0.13
(1,901)	1:237:A:VAL:HG23	1:238:A:GLN:H	9	0.13
(1,695)	1:237:A:VAL:HG11	1:238:A:GLN:H	7	0.13
(1,695)	1:237:A:VAL:HG12	1:238:A:GLN:H	7	0.13
(1,695)	1:237:A:VAL:HG13	1:238:A:GLN:H	7	0.13
(1,611)	1:81:A:ILE:HG12	1:82:A:THR:HA	14	0.13
(1,546)	1:134:A:LYS:HG2	1:151:A:ILE:H	14	0.13
(1,511)	1:167:A:GLN:HB2	1:167:A:GLN:HE22	9	0.13
(1,443)	1:163:A:MET:HG3	1:164:A:ASP:H	8	0.13
(1,382)	1:180:A:VAL:HA	1:188:A:GLU:HG2	10	0.13
(1,316)	1:63:A:TYR:HB3	1:155:A:ASN:HA	12	0.13
(1,305)	1:63:A:TYR:HB3	1:65:A:ARG:H	6	0.13
(1,207)	1:159:A:SER:HA	1:161:A:PHE:H	12	0.13
(1,183)	1:198:A:GLY:H	1:227:A:SER:HA	4	0.13
(1,172)	1:74:A:PRO:HA	1:76:A:ILE:H	12	0.13
(1,156)	1:174:A:THR:HB	1:253:A:TYR:HA	8	0.13
(1,127)	1:95:A:TRP:HZ3	1:113:A:LEU:HA	1	0.13
(1,127)	1:95:A:TRP:HZ3	1:113:A:LEU:HA	7	0.13
(1,119)	1:78:A:GLU:HG3	1:95:A:TRP:HZ2	2	0.13
(1,108)	1:235:A:ARG:HD2	1:236:A:PHE:HZ	8	0.13
(2,73)	1:229:A:ILE:H	1:225:A:GLN:O	1	0.12
(2,65)	1:196:A:LEU:H	1:192:A:ILE:O	19	0.12
(2,9)	1:123:A:ALA:H	1:119:A:SER:O	1	0.12

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2246)	1:154:A:TRP:HE1	1:158:A:ASP:H	8	0.12
(1,2107)	1:63:A:TYR:HA	1:155:A:ASN:HB3	8	0.12
(1,2015)	1:194:A:ASP:HA	1:198:A:GLY:H	11	0.12
(1,1983)	1:85:A:PHE:HB2	1:88:A:PHE:HA	3	0.12
(1,1858)	1:196:A:LEU:HD11	1:197:A:TYR:H	7	0.12
(1,1858)	1:196:A:LEU:HD12	1:197:A:TYR:H	7	0.12
(1,1858)	1:196:A:LEU:HD13	1:197:A:TYR:H	7	0.12
(1,1790)	1:226:A:GLN:HE22	1:227:A:SER:HA	1	0.12
(1,1790)	1:226:A:GLN:HE22	1:227:A:SER:HA	2	0.12
(1,1790)	1:226:A:GLN:HE22	1:227:A:SER:HA	5	0.12
(1,1790)	1:226:A:GLN:HE22	1:227:A:SER:HA	10	0.12
(1,1790)	1:226:A:GLN:HE22	1:227:A:SER:HA	15	0.12
(1,1790)	1:226:A:GLN:HE22	1:227:A:SER:HA	16	0.12
(1,1705)	1:140:A:SER:HB2	1:146:A:ASP:HA	19	0.12
(1,1691)	1:247:A:ARG:HG2	1:248:A:VAL:H	16	0.12
(1,1665)	1:192:A:ILE:HG12	1:195:A:ARG:H	11	0.12
(1,1665)	1:192:A:ILE:HG12	1:195:A:ARG:H	15	0.12
(1,1665)	1:192:A:ILE:HG12	1:195:A:ARG:H	19	0.12
(1,1642)	1:208:A:ASP:HB2	1:210:A:GLU:HB3	8	0.12
(1,1617)	1:180:A:VAL:HB	1:188:A:GLU:HG2	13	0.12
(1,1605)	1:131:A:GLU:HB2	1:134:A:LYS:HG3	20	0.12
(1,1591)	1:163:A:MET:HB2	1:200:A:VAL:HB	6	0.12
(1,1586)	1:78:A:GLU:HG3	1:80:A:GLU:H	4	0.12
(1,1554)	1:85:A:PHE:HA	1:88:A:PHE:HB2	5	0.12
(1,1551)	1:141:A:SER:H	1:144:A:ILE:HB	5	0.12
(1,1533)	1:172:A:ARG:HA	1:173:A:LYS:HE2	7	0.12
(1,1465)	1:199:A:GLY:H	1:200:A:VAL:H	17	0.12
(1,1463)	1:142:A:PRO:HB3	1:143:A:THR:H	5	0.12
(1,1463)	1:142:A:PRO:HB2	1:143:A:THR:H	5	0.12
(1,1446)	1:71:A:GLY:H	1:85:A:PHE:HZ	12	0.12
(1,1425)	1:88:A:PHE:HD1	1:89:A:GLY:H	13	0.12
(1,1425)	1:88:A:PHE:HD2	1:89:A:GLY:H	13	0.12
(1,1375)	1:224:A:ASN:HA	1:224:A:ASN:HD22	7	0.12
(1,1373)	1:224:A:ASN:HD22	1:227:A:SER:H	3	0.12
(1,1373)	1:224:A:ASN:HD22	1:227:A:SER:H	16	0.12
(1,1368)	1:196:A:LEU:HG	1:197:A:TYR:H	14	0.12
(1,1316)	1:163:A:MET:H	1:164:A:ASP:H	10	0.12
(1,1278)	1:122:A:GLN:HE22	1:123:A:ALA:HA	5	0.12
(1,1112)	1:134:A:LYS:HD3	1:135:A:LEU:H	5	0.12
(1,1086)	1:129:A:ILE:H	1:138:A:CYS:HA	5	0.12
(1,1086)	1:129:A:ILE:H	1:138:A:CYS:HA	9	0.12
(1,1083)	1:159:A:SER:HB3	1:161:A:PHE:H	3	0.12

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1080)	1:129:A:ILE:H	1:138:A:CYS:HB2	12	0.12
(1,1013)	1:141:A:SER:H	1:145:A:LYS:H	10	0.12
(1,1012)	1:141:A:SER:H	1:146:A:ASP:H	17	0.12
(1,950)	1:143:A:THR:H	1:144:A:ILE:H	4	0.12
(1,901)	1:237:A:VAL:HG21	1:238:A:GLN:H	1	0.12
(1,901)	1:237:A:VAL:HG22	1:238:A:GLN:H	1	0.12
(1,901)	1:237:A:VAL:HG23	1:238:A:GLN:H	1	0.12
(1,494)	1:77:A:ASP:H	1:80:A:GLU:HB3	17	0.12
(1,444)	1:238:A:GLN:HG3	1:239:A:LEU:H	8	0.12
(1,406)	1:131:A:GLU:HG3	1:134:A:LYS:HE3	8	0.12
(1,382)	1:180:A:VAL:HA	1:188:A:GLU:HG2	4	0.12
(1,315)	1:184:A:LEU:HB2	1:187:A:VAL:HB	7	0.12
(1,312)	1:235:A:ARG:HD2	1:236:A:PHE:H	12	0.12
(1,303)	1:235:A:ARG:HD3	1:236:A:PHE:H	6	0.12
(1,287)	1:137:A:LEU:HB3	1:149:A:VAL:HB	7	0.12
(1,253)	1:91:A:LEU:HA	1:114:A:LEU:H	15	0.12
(1,246)	1:184:A:LEU:HA	1:187:A:VAL:HB	12	0.12
(1,207)	1:159:A:SER:HA	1:161:A:PHE:H	3	0.12
(1,207)	1:159:A:SER:HA	1:161:A:PHE:H	9	0.12
(1,194)	1:244:A:ILE:HA	1:245:A:ASP:HB2	7	0.12
(1,108)	1:235:A:ARG:HD2	1:236:A:PHE:HZ	2	0.12
(2,119)	1:159:A:SER:H	1:155:A:ASN:O	4	0.11
(2,119)	1:159:A:SER:H	1:155:A:ASN:O	13	0.11
(2,116)	1:154:A:TRP:N	1:64:A:SER:O	14	0.11
(2,116)	1:154:A:TRP:N	1:64:A:SER:O	20	0.11
(2,73)	1:229:A:ILE:H	1:225:A:GLN:O	3	0.11
(2,73)	1:229:A:ILE:H	1:225:A:GLN:O	7	0.11
(2,73)	1:229:A:ILE:H	1:225:A:GLN:O	8	0.11
(2,73)	1:229:A:ILE:H	1:225:A:GLN:O	17	0.11
(2,65)	1:196:A:LEU:H	1:192:A:ILE:O	6	0.11
(2,63)	1:194:A:ASP:H	1:190:A:ALA:O	11	0.11
(2,63)	1:194:A:ASP:H	1:190:A:ALA:O	18	0.11
(2,61)	1:192:A:ILE:H	1:188:A:GLU:O	9	0.11
(2,61)	1:192:A:ILE:H	1:188:A:GLU:O	10	0.11
(2,61)	1:192:A:ILE:H	1:188:A:GLU:O	14	0.11
(2,61)	1:192:A:ILE:H	1:188:A:GLU:O	17	0.11
(2,61)	1:192:A:ILE:H	1:188:A:GLU:O	19	0.11
(2,28)	1:112:A:PHE:H	1:94:A:ASP:O	4	0.11
(2,22)	1:152:A:ARG:H	1:68:A:PHE:O	17	0.11
(1,2301)	1:205:A:ILE:H	1:154:A:TRP:HZ2	4	0.11
(1,2246)	1:154:A:TRP:HE1	1:158:A:ASP:H	13	0.11
(1,2246)	1:154:A:TRP:HE1	1:158:A:ASP:H	19	0.11

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2155)	1:238:A:GLN:HA	1:239:A:LEU:HB2	2	0.11
(1,2093)	1:136:A:TYR:HA	1:137:A:LEU:HB3	14	0.11
(1,2093)	1:136:A:TYR:HA	1:137:A:LEU:HB3	17	0.11
(1,1790)	1:226:A:GLN:HE22	1:227:A:SER:HA	3	0.11
(1,1790)	1:226:A:GLN:HE22	1:227:A:SER:HA	7	0.11
(1,1790)	1:226:A:GLN:HE22	1:227:A:SER:HA	8	0.11
(1,1790)	1:226:A:GLN:HE22	1:227:A:SER:HA	9	0.11
(1,1790)	1:226:A:GLN:HE22	1:227:A:SER:HA	13	0.11
(1,1790)	1:226:A:GLN:HE22	1:227:A:SER:HA	19	0.11
(1,1790)	1:226:A:GLN:HE22	1:227:A:SER:HA	20	0.11
(1,1764)	1:187:A:VAL:HA	1:191:A:MET:HB2	3	0.11
(1,1738)	1:223:A:SER:HB3	1:224:A:ASN:HA	17	0.11
(1,1720)	1:195:A:ARG:HA	1:196:A:LEU:HG	14	0.11
(1,1709)	1:140:A:SER:HB3	1:141:A:SER:H	10	0.11
(1,1705)	1:140:A:SER:HB2	1:146:A:ASP:HA	7	0.11
(1,1665)	1:192:A:ILE:HG12	1:195:A:ARG:H	2	0.11
(1,1665)	1:192:A:ILE:HG12	1:195:A:ARG:H	3	0.11
(1,1655)	1:246:A:LYS:HB3	1:246:A:LYS:HD3	6	0.11
(1,1591)	1:163:A:MET:HB2	1:200:A:VAL:HB	16	0.11
(1,1551)	1:141:A:SER:H	1:144:A:ILE:HB	4	0.11
(1,1533)	1:172:A:ARG:HA	1:173:A:LYS:HE2	3	0.11
(1,1520)	1:208:A:ASP:HB2	1:215:A:LYS:HB2	16	0.11
(1,1465)	1:199:A:GLY:H	1:200:A:VAL:H	20	0.11
(1,1463)	1:142:A:PRO:HB3	1:143:A:THR:H	19	0.11
(1,1463)	1:142:A:PRO:HB2	1:143:A:THR:H	19	0.11
(1,1446)	1:71:A:GLY:H	1:85:A:PHE:HZ	20	0.11
(1,1438)	1:70:A:GLY:H	1:149:A:VAL:HA	9	0.11
(1,1417)	1:238:A:GLN:HB3	1:238:A:GLN:HE22	15	0.11
(1,1373)	1:224:A:ASN:HD22	1:227:A:SER:H	19	0.11
(1,1083)	1:159:A:SER:HB3	1:161:A:PHE:H	5	0.11
(1,1034)	1:78:A:GLU:HG3	1:79:A:ASP:H	13	0.11
(1,1013)	1:141:A:SER:H	1:145:A:LYS:H	5	0.11
(1,548)	1:244:A:ILE:H	1:244:A:ILE:HG13	7	0.11
(1,538)	1:247:A:ARG:HG3	1:248:A:VAL:H	12	0.11
(1,511)	1:167:A:GLN:HB2	1:167:A:GLN:HE22	8	0.11
(1,494)	1:77:A:ASP:H	1:80:A:GLU:HB3	20	0.11
(1,431)	1:240:A:GLN:HG2	1:245:A:ASP:HB3	12	0.11
(1,382)	1:180:A:VAL:HA	1:188:A:GLU:HG2	7	0.11
(1,316)	1:63:A:TYR:HB3	1:155:A:ASN:HA	20	0.11
(1,287)	1:137:A:LEU:HB3	1:149:A:VAL:HB	9	0.11
(1,183)	1:198:A:GLY:H	1:227:A:SER:HA	19	0.11
(1,182)	1:197:A:TYR:HB2	1:227:A:SER:HA	18	0.11

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,172)	1:74:A:PRO:HA	1:76:A:ILE:H	15	0.11
(1,156)	1:174:A:THR:HB	1:253:A:TYR:HA	3	0.11
(1,156)	1:174:A:THR:HB	1:253:A:TYR:HA	6	0.11
(1,127)	1:95:A:TRP:HZ3	1:113:A:LEU:HA	2	0.11
(1,127)	1:95:A:TRP:HZ3	1:113:A:LEU:HA	4	0.11
(1,127)	1:95:A:TRP:HZ3	1:113:A:LEU:HA	15	0.11
(1,120)	1:154:A:TRP:HH2	1:155:A:ASN:H	6	0.11
(1,120)	1:154:A:TRP:HH2	1:155:A:ASN:H	9	0.11
(1,119)	1:78:A:GLU:HG3	1:95:A:TRP:HZ2	8	0.11
(1,119)	1:78:A:GLU:HG3	1:95:A:TRP:HZ2	11	0.11
(2,123)	1:241:A:HIS:H	1:244:A:ILE:O	16	0.1
(2,113)	1:206:A:ASP:H	1:217:A:ALA:O	15	0.1
(2,73)	1:229:A:ILE:H	1:225:A:GLN:O	9	0.1
(2,73)	1:229:A:ILE:H	1:225:A:GLN:O	10	0.1
(2,65)	1:196:A:LEU:H	1:192:A:ILE:O	8	0.1
(2,9)	1:123:A:ALA:H	1:119:A:SER:O	5	0.1
(2,9)	1:123:A:ALA:H	1:119:A:SER:O	18	0.1
(1,2246)	1:154:A:TRP:HE1	1:158:A:ASP:H	9	0.1
(1,2136)	1:91:A:LEU:HA	1:117:A:ASP:H	15	0.1
(1,1790)	1:226:A:GLN:HE22	1:227:A:SER:HA	6	0.1
(1,1790)	1:226:A:GLN:HE22	1:227:A:SER:HA	11	0.1
(1,1790)	1:226:A:GLN:HE22	1:227:A:SER:HA	14	0.1
(1,1790)	1:226:A:GLN:HE22	1:227:A:SER:HA	18	0.1
(1,1662)	1:251:A:LYS:HA	1:251:A:LYS:HD2	18	0.1
(1,1594)	1:176:A:PHE:HB3	1:251:A:LYS:HB2	19	0.1
(1,1556)	1:78:A:GLU:HA	1:81:A:ILE:HB	14	0.1
(1,1554)	1:85:A:PHE:HA	1:88:A:PHE:HB2	7	0.1
(1,1551)	1:141:A:SER:H	1:144:A:ILE:HB	8	0.1
(1,1533)	1:172:A:ARG:HA	1:173:A:LYS:HE2	2	0.1
(1,1465)	1:199:A:GLY:H	1:200:A:VAL:H	15	0.1
(1,1463)	1:142:A:PRO:HB3	1:143:A:THR:H	16	0.1
(1,1463)	1:142:A:PRO:HB2	1:143:A:THR:H	16	0.1
(1,1438)	1:70:A:GLY:H	1:149:A:VAL:HA	5	0.1
(1,1438)	1:70:A:GLY:H	1:149:A:VAL:HA	14	0.1
(1,1373)	1:224:A:ASN:HD22	1:227:A:SER:H	13	0.1
(1,1183)	1:207:A:THR:HB	1:215:A:LYS:H	6	0.1
(1,1086)	1:129:A:ILE:H	1:138:A:CYS:HA	17	0.1
(1,1062)	1:206:A:ASP:HB2	1:217:A:ALA:H	15	0.1
(1,1034)	1:78:A:GLU:HG3	1:79:A:ASP:H	12	0.1
(1,1022)	1:208:A:ASP:H	1:215:A:LYS:HB2	10	0.1
(1,1013)	1:141:A:SER:H	1:145:A:LYS:H	16	0.1
(1,934)	1:168:A:PRO:HA	1:170:A:ASP:H	11	0.1

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,611)	1:81:A:ILE:HG12	1:82:A:THR:HA	18	0.1
(1,527)	1:237:A:VAL:H	1:238:A:GLN:HB2	17	0.1
(1,444)	1:238:A:GLN:HG3	1:239:A:LEU:H	11	0.1
(1,382)	1:180:A:VAL:HA	1:188:A:GLU:HG2	5	0.1
(1,183)	1:198:A:GLY:H	1:227:A:SER:HA	6	0.1
(1,156)	1:174:A:THR:HB	1:253:A:TYR:HA	4	0.1
(1,156)	1:174:A:THR:HB	1:253:A:TYR:HA	5	0.1
(1,156)	1:174:A:THR:HB	1:253:A:TYR:HA	18	0.1
(1,127)	1:95:A:TRP:HZ3	1:113:A:LEU:HA	6	0.1
(1,120)	1:154:A:TRP:HH2	1:155:A:ASN:H	18	0.1

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

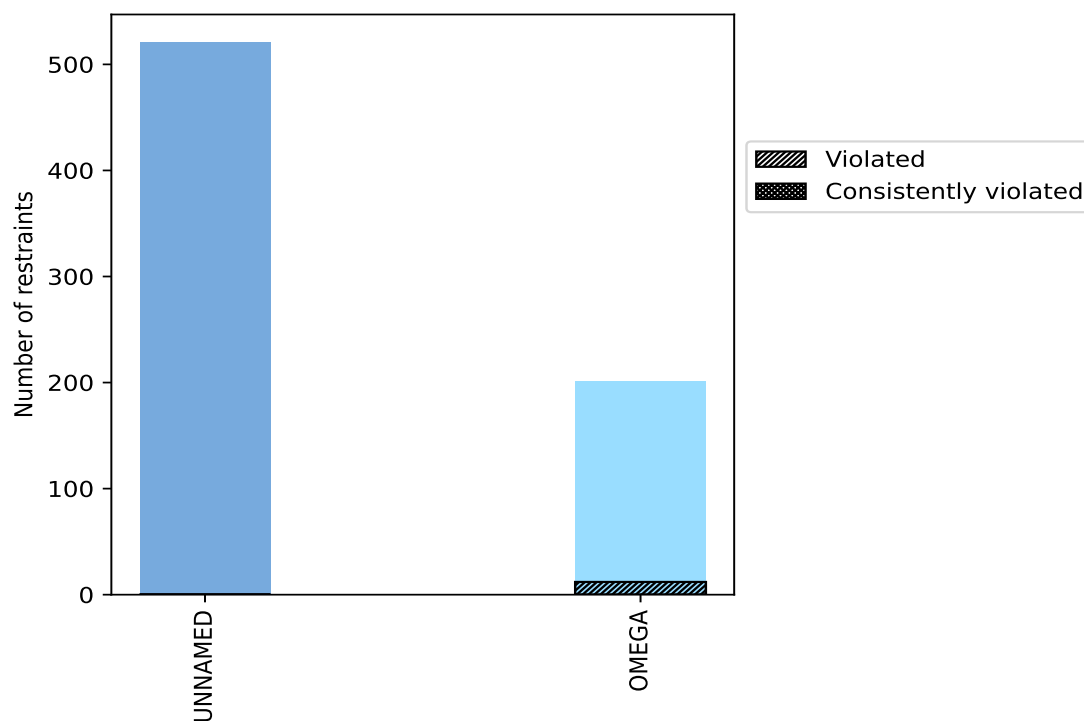
10.1 Summary of dihedral-angle violations [i](#)

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

Angle type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
UNNAMED	521	72.2	0	0.0	0.0	0	0.0	0.0
OMEGA	201	27.8	12	6.0	1.7	0	0.0	0.0
Total	722	100.0	12	1.7	1.7	0	0.0	0.0

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

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



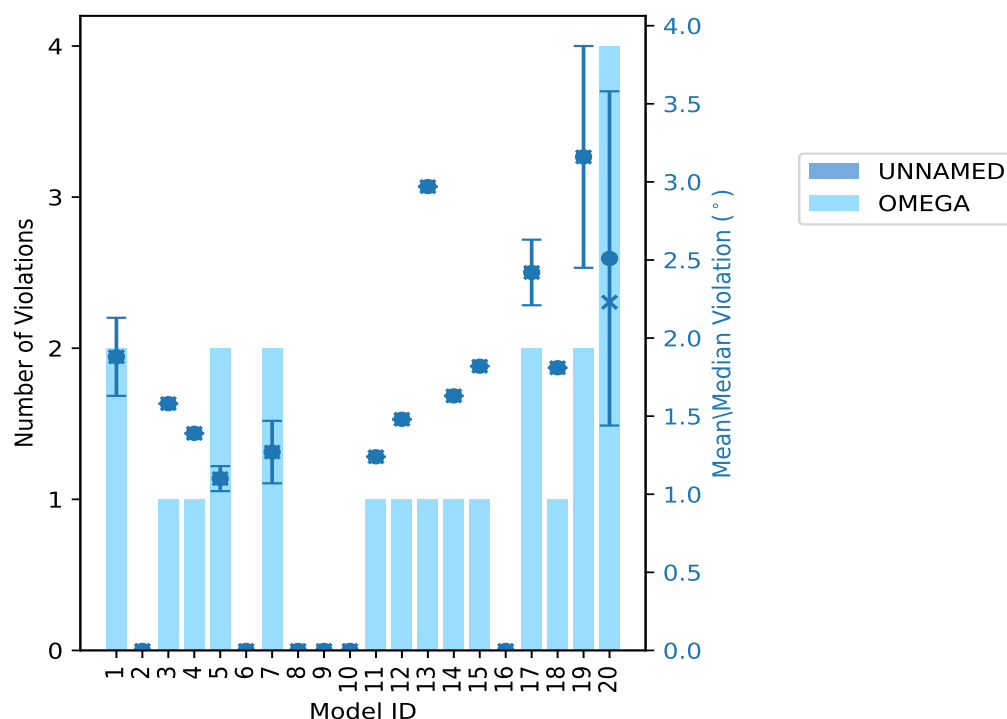
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

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

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

Model ID	Number of violations			Mean (°)	Max (°)	SD (°)	Median (°)
	UNNAMED	OMEGA	Total				
1	0	2	2	1.88	2.13	0.25	1.88
2	0	0	0	0.0	0.0	0.0	0.0
3	0	1	1	1.58	1.58	0.0	1.58
4	0	1	1	1.39	1.39	0.0	1.39
5	0	2	2	1.1	1.18	0.08	1.1
6	0	0	0	0.0	0.0	0.0	0.0
7	0	2	2	1.27	1.48	0.2	1.27
8	0	0	0	0.0	0.0	0.0	0.0
9	0	0	0	0.0	0.0	0.0	0.0
10	0	0	0	0.0	0.0	0.0	0.0
11	0	1	1	1.24	1.24	0.0	1.24
12	0	1	1	1.48	1.48	0.0	1.48
13	0	1	1	2.97	2.97	0.0	2.97
14	0	1	1	1.63	1.63	0.0	1.63
15	0	1	1	1.82	1.82	0.0	1.82
16	0	0	0	0.0	0.0	0.0	0.0
17	0	2	2	2.42	2.63	0.21	2.42
18	0	1	1	1.81	1.81	0.0	1.81
19	0	2	2	3.16	3.88	0.71	3.16
20	0	4	4	2.51	4.15	1.07	2.23

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



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

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

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

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

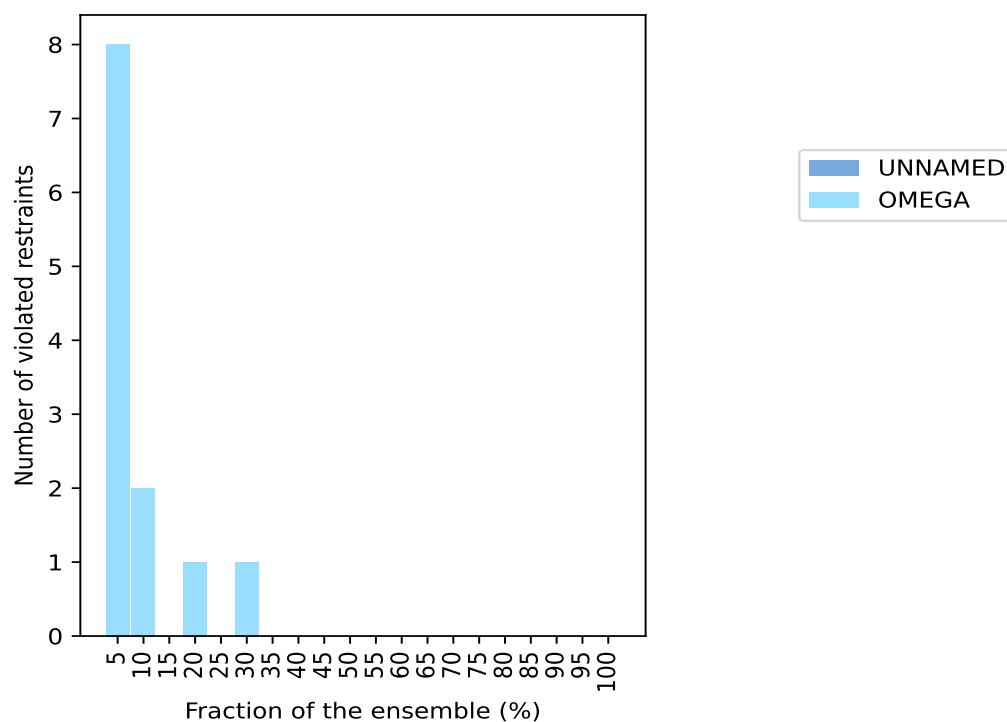
Continued on next page...

Continued from previous page...

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

¹ Number of models with violations

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

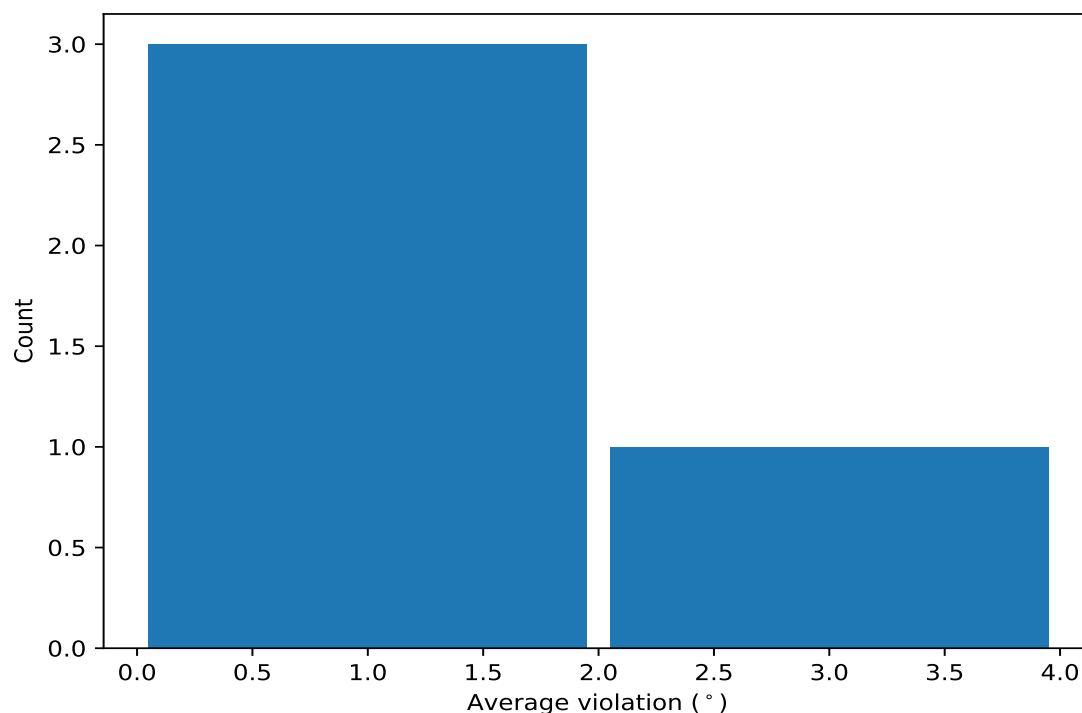


10.4 Most violated dihedral-angle restraints in the ensemble [i](#)

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

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

in the ensemble



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

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

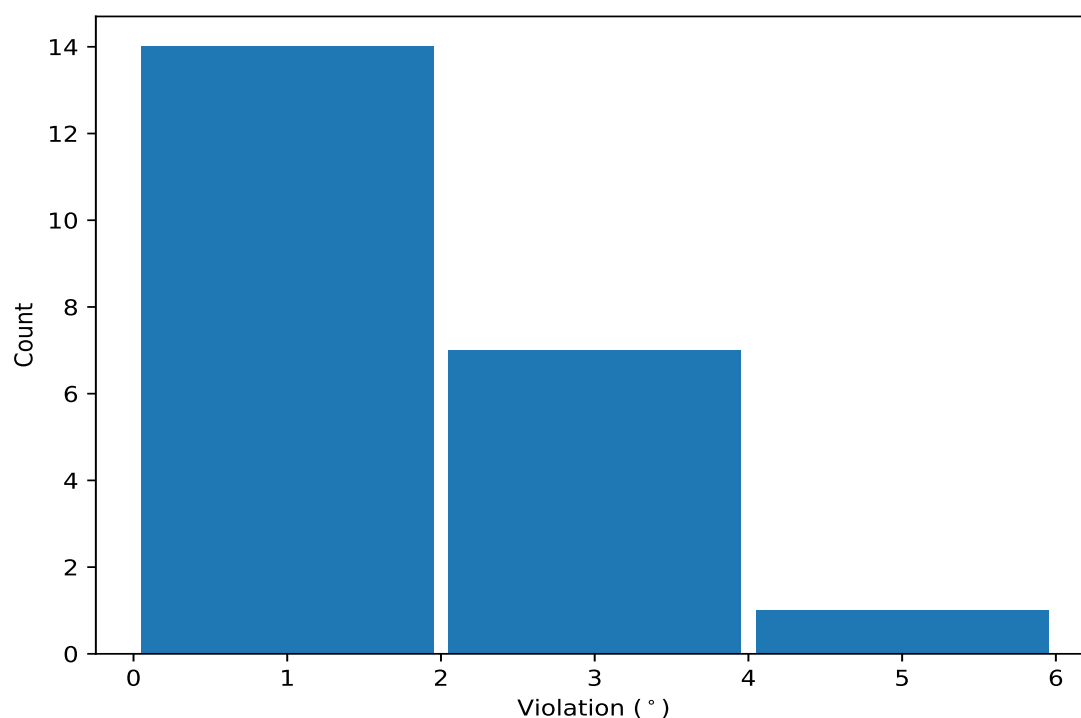
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,621)	1:153:A:PRO:CA	1:153:A:PRO:N	1:152:A:ARG:C	1:152:A:ARG:CA	6	2.02	0.53	1.82
(1,622)	1:154:A:TRP:CA	1:154:A:TRP:N	1:153:A:PRO:C	1:153:A:PRO:CA	4	1.35	0.14	1.36
(1,584)	1:116:A:GLN:CA	1:116:A:GLN:N	1:115:A:PHE:C	1:115:A:PHE:CA	2	1.86	0.27	1.86
(1,714)	1:246:A:LYS:CA	1:246:A:LYS:N	1:245:A:ASP:C	1:245:A:ASP:CA	2	1.32	0.3	1.32

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 (°)
(1,561)	1:93:A:VAL:CA	1:93:A:VAL:N	1:92:A:ILE:C	1:92:A:ILE:CA	20	4.15
(1,688)	1:220:A:VAL:CA	1:220:A:VAL:N	1:219:A:ARG:C	1:219:A:ARG:CA	19	3.88
(1,621)	1:153:A:PRO:CA	1:153:A:PRO:N	1:152:A:ARG:C	1:152:A:ARG:CA	13	2.97
(1,560)	1:92:A:ILE:CA	1:92:A:ILE:N	1:91:A:LEU:C	1:91:A:LEU:CA	20	2.76
(1,630)	1:162:A:VAL:CA	1:162:A:VAL:N	1:161:A:PHE:C	1:161:A:PHE:CA	17	2.63
(1,621)	1:153:A:PRO:CA	1:153:A:PRO:N	1:152:A:ARG:C	1:152:A:ARG:CA	19	2.45
(1,582)	1:114:A:LEU:CA	1:114:A:LEU:N	1:113:A:LEU:C	1:113:A:LEU:CA	17	2.2
(1,584)	1:116:A:GLN:CA	1:116:A:GLN:N	1:115:A:PHE:C	1:115:A:PHE:CA	1	2.13
(1,621)	1:153:A:PRO:CA	1:153:A:PRO:N	1:152:A:ARG:C	1:152:A:ARG:CA	15	1.82
(1,621)	1:153:A:PRO:CA	1:153:A:PRO:N	1:152:A:ARG:C	1:152:A:ARG:CA	18	1.81
(1,562)	1:94:A:ASP:CA	1:94:A:ASP:N	1:93:A:VAL:C	1:93:A:VAL:CA	20	1.7
(1,621)	1:153:A:PRO:CA	1:153:A:PRO:N	1:152:A:ARG:C	1:152:A:ARG:CA	14	1.63
(1,714)	1:246:A:LYS:CA	1:246:A:LYS:N	1:245:A:ASP:C	1:245:A:ASP:CA	1	1.62
(1,584)	1:116:A:GLN:CA	1:116:A:GLN:N	1:115:A:PHE:C	1:115:A:PHE:CA	3	1.58
(1,622)	1:154:A:TRP:CA	1:154:A:TRP:N	1:153:A:PRO:C	1:153:A:PRO:CA	7	1.48
(1,622)	1:154:A:TRP:CA	1:154:A:TRP:N	1:153:A:PRO:C	1:153:A:PRO:CA	12	1.48
(1,621)	1:153:A:PRO:CA	1:153:A:PRO:N	1:152:A:ARG:C	1:152:A:ARG:CA	20	1.42
(1,680)	1:212:A:LYS:CA	1:212:A:LYS:N	1:211:A:LEU:C	1:211:A:LEU:CA	4	1.39
(1,622)	1:154:A:TRP:CA	1:154:A:TRP:N	1:153:A:PRO:C	1:153:A:PRO:CA	11	1.24
(1,622)	1:154:A:TRP:CA	1:154:A:TRP:N	1:153:A:PRO:C	1:153:A:PRO:CA	5	1.18
(1,610)	1:142:A:PRO:CA	1:142:A:PRO:N	1:141:A:SER:C	1:141:A:SER:CA	7	1.07
(1,714)	1:246:A:LYS:CA	1:246:A:LYS:N	1:245:A:ASP:C	1:245:A:ASP:CA	5	1.02