



Full wwPDB NMR Structure Validation Report ⓘ

Mar 9, 2026 – 08:29 AM UTC

PDB ID : 2M0D / pdb_00002m0d
BMRB ID : 18806
Title : Solution Structure of Miz-1 zinc finger 5
Authors : Bernard, D.; Bedard, M.; Bilodeau, J.; Lavigne, P.
Deposited on : 2012-10-24

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

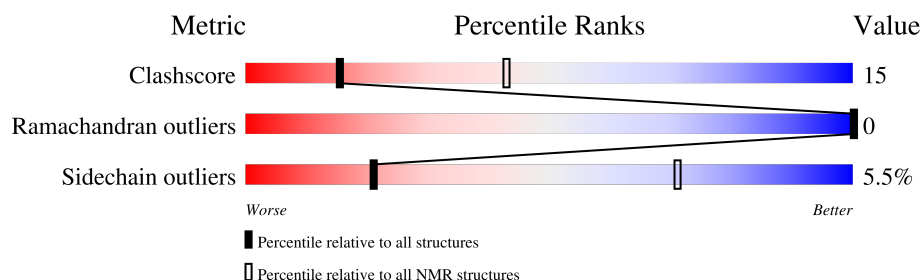
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 80%.

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	112	

2 Ensemble composition and analysis

This entry contains 20 models. Model 4 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:4-A:26 (23)	0.38	4

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

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

The models can be grouped into 3 clusters and 4 single-model clusters were found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 476 atoms, of which 228 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Zinc finger and BTB domain-containing protein 17.

Mol	Chain	Residues	Atoms						Trace
1	A	30	Total	C	H	N	O	S	0
			475	150	228	44	49	4	

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q13105

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

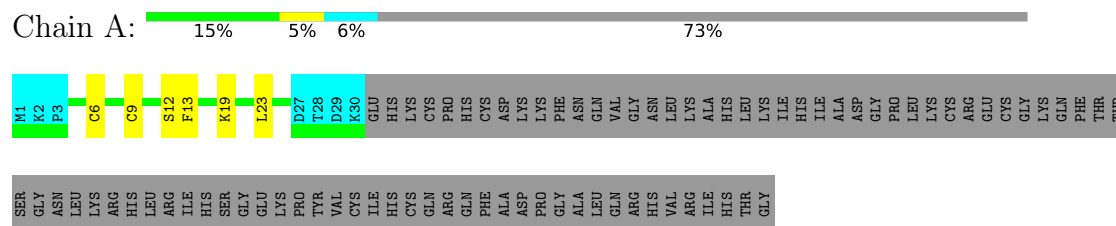
Mol	Chain	Residues	Atoms	
2	A	1	Total	Zn
			1	1

4 Residue-property plots [i](#)

4.1 Average score per residue in the NMR ensemble

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

- Molecule 1: Zinc finger and BTB domain-containing protein 17

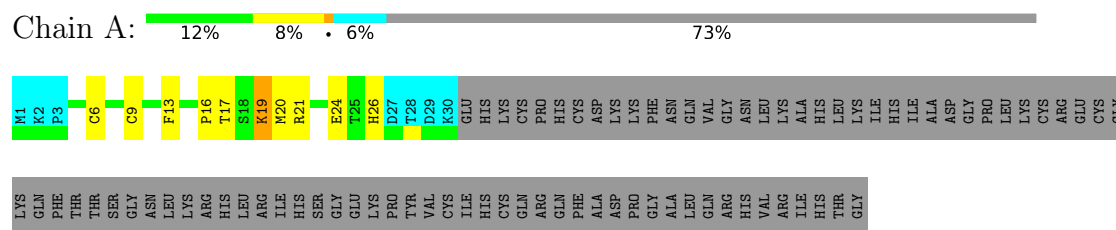


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

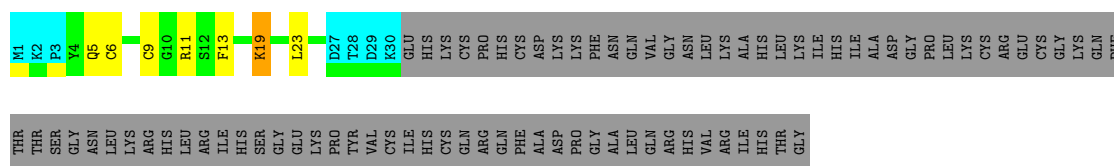
- Molecule 1: Zinc finger and BTB domain-containing protein 17



4.2.2 Score per residue for model 2

- Molecule 1: Zinc finger and BTB domain-containing protein 17

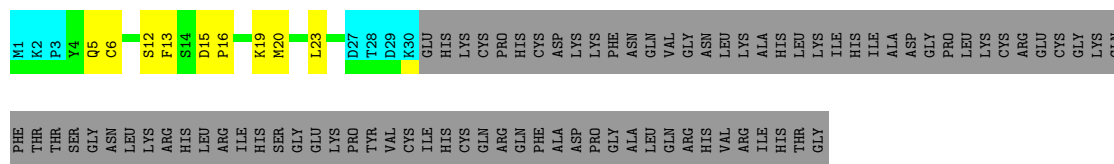




4.2.3 Score per residue for model 3

- Molecule 1: Zinc finger and BTB domain-containing protein 17

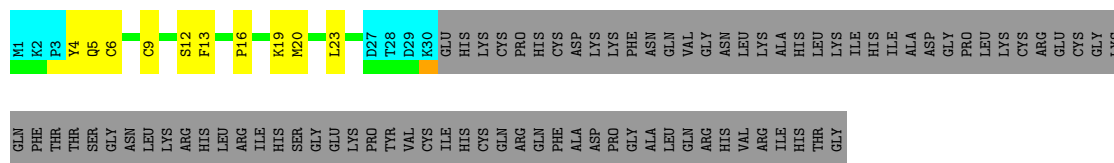
Chain A: 12% 8% 6% 73%



4.2.4 Score per residue for model 4 (medoid)

- Molecule 1: Zinc finger and BTB domain-containing protein 17

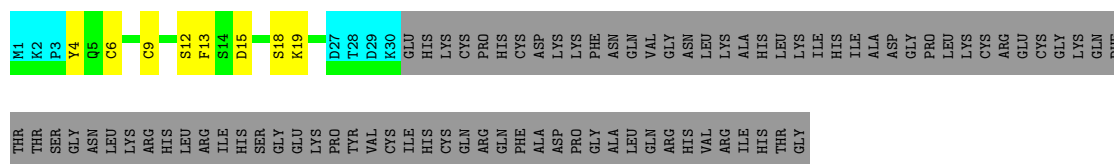
Chain A: 12% 9% 6% 73%



4.2.5 Score per residue for model 5

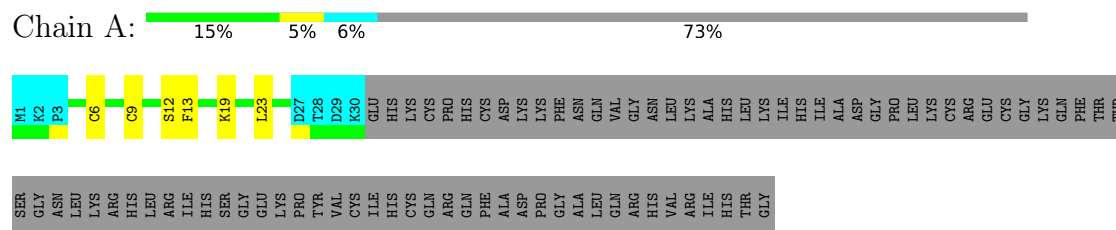
- Molecule 1: Zinc finger and BTB domain-containing protein 17

Chain A: 13% 7% 6% 73%



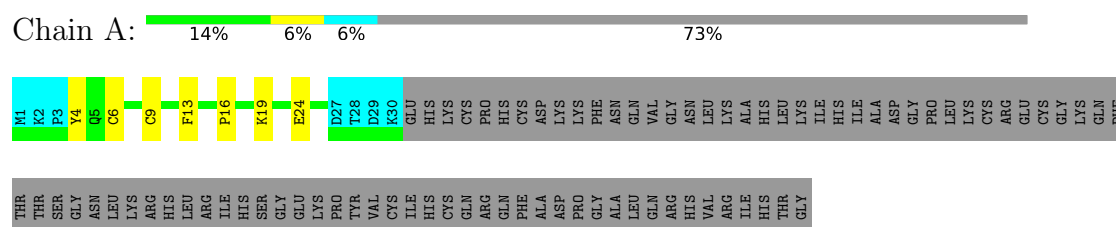
4.2.6 Score per residue for model 6

- Molecule 1: Zinc finger and BTB domain-containing protein 17



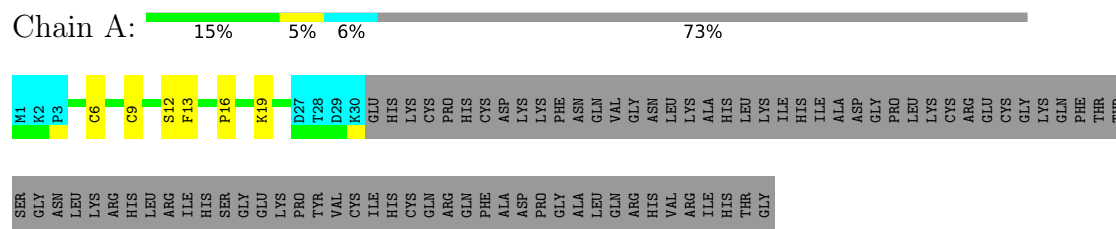
4.2.7 Score per residue for model 7

- Molecule 1: Zinc finger and BTB domain-containing protein 17



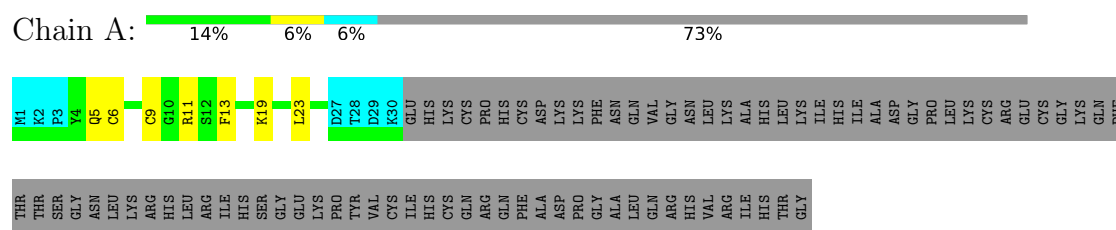
4.2.8 Score per residue for model 8

- Molecule 1: Zinc finger and BTB domain-containing protein 17



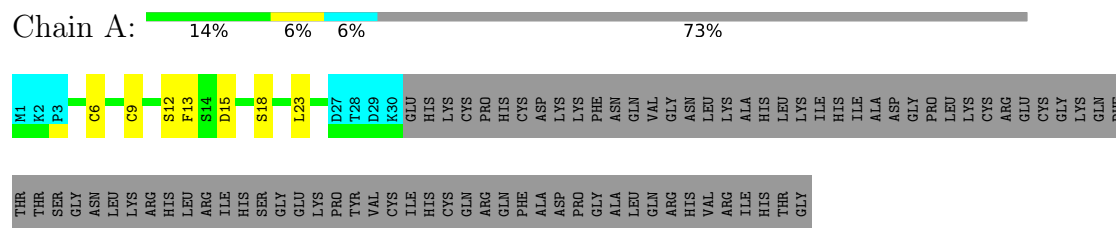
4.2.9 Score per residue for model 9

- Molecule 1: Zinc finger and BTB domain-containing protein 17



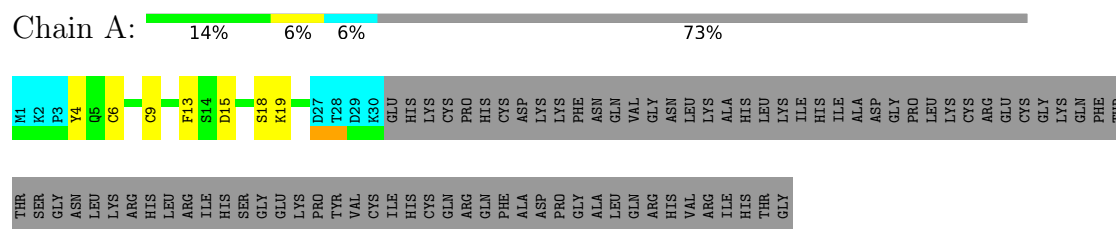
4.2.10 Score per residue for model 10

- Molecule 1: Zinc finger and BTB domain-containing protein 17



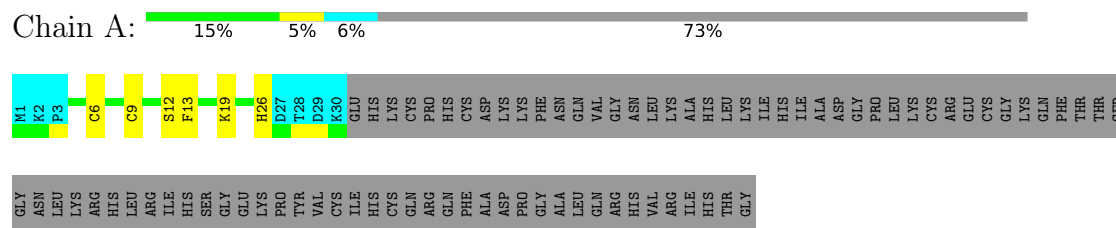
4.2.11 Score per residue for model 11

- Molecule 1: Zinc finger and BTB domain-containing protein 17



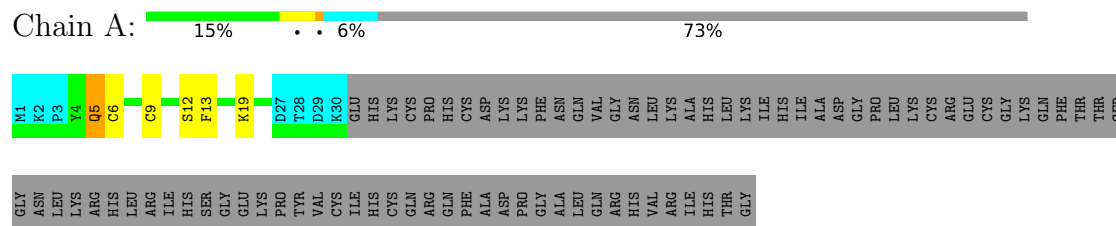
4.2.12 Score per residue for model 12

- Molecule 1: Zinc finger and BTB domain-containing protein 17



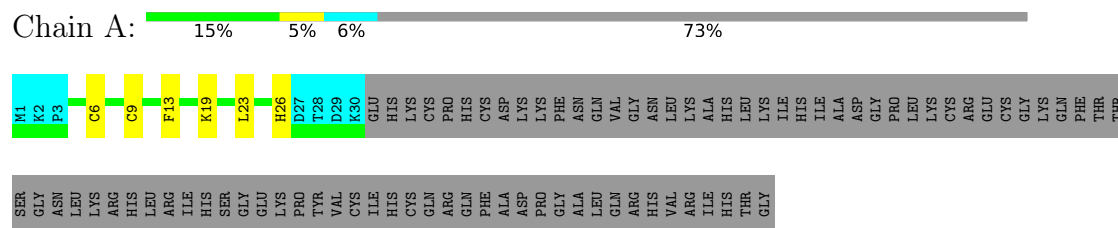
4.2.13 Score per residue for model 13

- Molecule 1: Zinc finger and BTB domain-containing protein 17



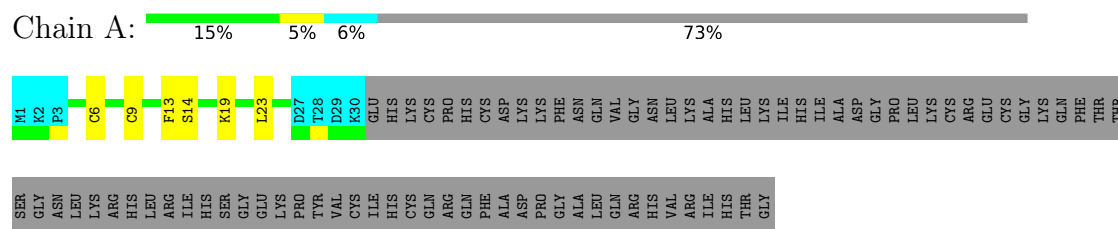
4.2.14 Score per residue for model 14

- Molecule 1: Zinc finger and BTB domain-containing protein 17



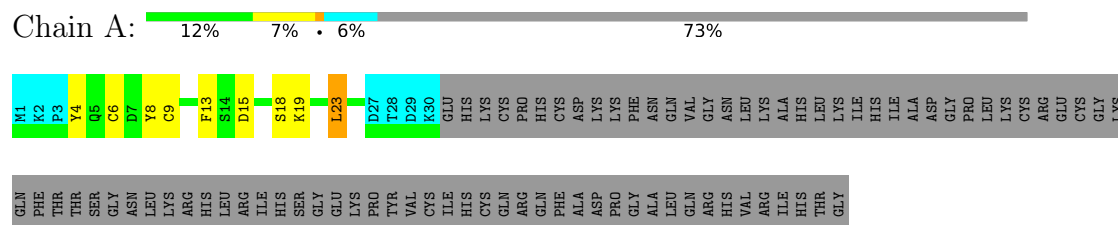
4.2.15 Score per residue for model 15

- Molecule 1: Zinc finger and BTB domain-containing protein 17



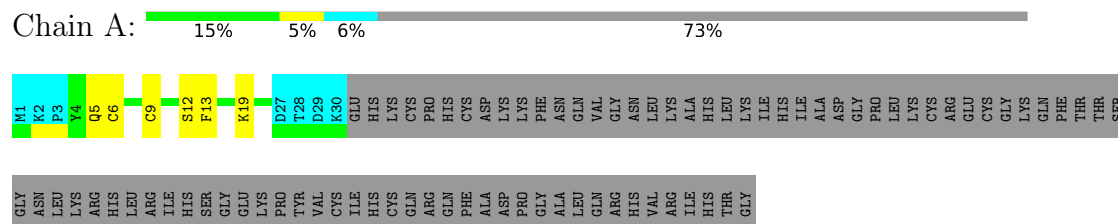
4.2.16 Score per residue for model 16

- Molecule 1: Zinc finger and BTB domain-containing protein 17



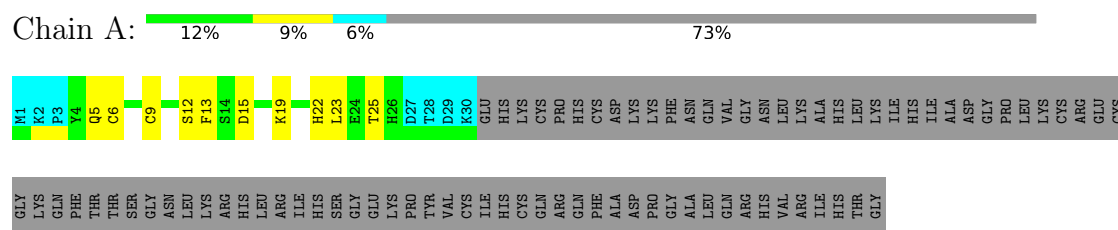
4.2.17 Score per residue for model 17

- Molecule 1: Zinc finger and BTB domain-containing protein 17



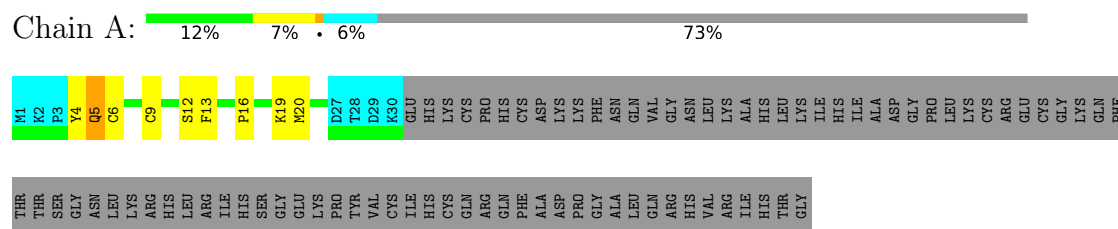
4.2.18 Score per residue for model 18

- Molecule 1: Zinc finger and BTB domain-containing protein 17



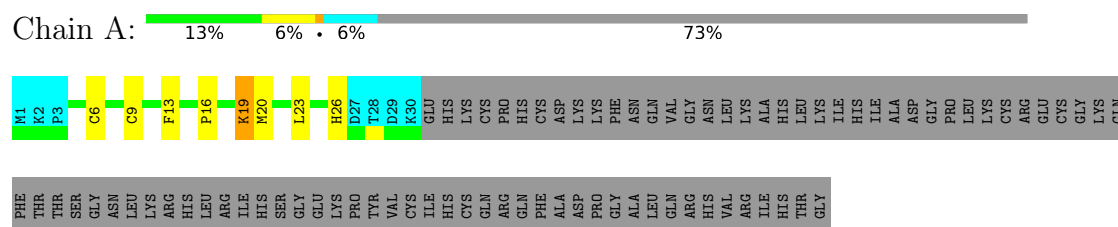
4.2.19 Score per residue for model 19

- Molecule 1: Zinc finger and BTB domain-containing protein 17



4.2.20 Score per residue for model 20

- Molecule 1: Zinc finger and BTB domain-containing protein 17



5 Refinement protocol and experimental data overview

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

Of the 300 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
ARIA	refinement	2.2
CNS	refinement	1.21

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	1186
Number of shifts mapped to atoms	259
Number of unparsed shifts	0
Number of shifts with mapping errors	927
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	80%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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

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

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	191	169	169	5±1
All	All	3840	3380	3380	106

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 15.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:6:CYS:HB2	1:A:13:PHE:HE2	0.89	1.24	12	11
1:A:6:CYS:HB2	1:A:13:PHE:CE2	0.81	2.11	12	9
1:A:6:CYS:HB2	1:A:13:PHE:HE1	0.79	1.38	9	8
1:A:13:PHE:HB2	1:A:19:LYS:HB2	0.73	1.60	18	14
1:A:6:CYS:HB2	1:A:13:PHE:CE1	0.71	2.19	9	8
1:A:6:CYS:HB3	1:A:9:CYS:HB2	0.69	1.64	16	19
1:A:15:ASP:HB2	1:A:18:SER:HB3	0.66	1.67	11	1
1:A:5:GLN:HA	1:A:12:SER:HA	0.64	1.69	13	6
1:A:6:CYS:HA	1:A:23:LEU:HD11	0.61	1.72	14	1
1:A:13:PHE:CB	1:A:19:LYS:HB2	0.57	2.30	20	4
1:A:15:ASP:HB2	1:A:18:SER:OG	0.57	2.00	10	1
1:A:4:TYR:HB3	1:A:19:LYS:CD	0.56	2.30	11	2

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:4:TYR:HB3	1:A:19:LYS:HD3	0.54	1.78	16	2
1:A:16:PRO:O	1:A:20:MET:HB2	0.52	2.04	20	4
1:A:4:TYR:HB3	1:A:19:LYS:HD2	0.50	1.84	4	1
1:A:4:TYR:CE1	1:A:16:PRO:HG3	0.49	2.43	7	1
1:A:15:ASP:O	1:A:19:LYS:HB3	0.48	2.08	16	1
1:A:8:TYR:CE2	1:A:23:LEU:HG	0.47	2.44	16	1
1:A:22:HIS:HA	1:A:25:THR:HG22	0.47	1.86	18	1
1:A:16:PRO:O	1:A:20:MET:HG2	0.47	2.09	19	1
1:A:5:GLN:HA	1:A:11:ARG:O	0.46	2.11	9	2
1:A:15:ASP:CB	1:A:18:SER:HB2	0.46	2.41	16	1
1:A:4:TYR:CE2	1:A:16:PRO:HG3	0.45	2.47	19	1
1:A:4:TYR:O	1:A:12:SER:HA	0.45	2.12	5	1
1:A:19:LYS:O	1:A:23:LEU:HB2	0.43	2.13	2	1
1:A:5:GLN:CD	1:A:5:GLN:H	0.43	2.21	9	1
1:A:4:TYR:HB3	1:A:19:LYS:HE2	0.41	1.92	5	1
1:A:21:ARG:HH21	1:A:24:GLU:CD	0.40	2.24	1	1
1:A:16:PRO:HA	1:A:19:LYS:HE3	0.40	1.93	8	1

6.3 Torsion angles

6.3.1 Protein backbone

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	23/112 (21%)	23±0 (99±2%)	0±0 (1±2%)	0±0 (0±0%)	100	100
All	All	460/2240 (21%)	455 (99%)	5 (1%)	0 (0%)	100	100

There are no Ramachandran outliers.

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	22/100 (22%)	21±1 (95±4%)	1±1 (5±4%)	21	71
All	All	440/2000 (22%)	416 (95%)	24 (5%)	21	71

All 8 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	23	LEU	9
1	A	19	LYS	4
1	A	26	HIS	3
1	A	15	ASP	3
1	A	5	GLN	2
1	A	17	THR	1
1	A	18	SER	1
1	A	24	GLU	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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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 80% for the well-defined parts and 65% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list*

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	1186
Number of shifts mapped to atoms	259
Number of unparsed shifts	0
Number of shifts with mapping errors	927
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

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

- No matching atom found in the structure. All 927 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	32	HIS	H	7.072	0.013	1
1	A	32	HIS	HA	4.467	.	1
1	A	32	HIS	HB2	2.48	0.006	2
1	A	32	HIS	HB3	2.656	0.012	2
1	A	32	HIS	HD2	6.443	0.006	1
1	A	32	HIS	HE1	7.922	0.006	1
1	A	32	HIS	CA	55.261	.	1
1	A	32	HIS	CB	28.642	0.039	1
1	A	32	HIS	CD2	130.448	0.078	1
1	A	32	HIS	CE1	142.848	0.001	1
1	A	32	HIS	N	118.044	0.05	1
1	A	33	LYS	HB2	1.624	.	1
1	A	33	LYS	HB3	1.624	.	1
1	A	33	LYS	HD2	1.379	.	1

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	33	LYS	HD3	1.379	.	1
1	A	33	LYS	HE2	2.805	.	1
1	A	33	LYS	HE3	2.805	.	1
1	A	33	LYS	HG2	1.118	.	1
1	A	33	LYS	HG3	1.118	.	1
1	A	33	LYS	C	175.338	.	1
1	A	33	LYS	CA	55.275	.	1
1	A	33	LYS	CB	34.112	.	1
1	A	33	LYS	CD	28.65	.	1
1	A	33	LYS	CE	41.702	.	1
1	A	33	LYS	CG	24.468	.	1
1	A	34	CYS	H	8.821	0.011	1
1	A	34	CYS	HB2	2.705	.	2
1	A	34	CYS	HB3	3.313	.	2
1	A	34	CYS	CA	57.333	.	1
1	A	34	CYS	CB	30.249	.	1
1	A	34	CYS	N	128.949	0.043	1
1	A	35	PRO	HA	4.338	.	1
1	A	35	PRO	HB2	2.415	.	1
1	A	35	PRO	HB3	2.415	.	1
1	A	35	PRO	HG2	2.017	0.009	1
1	A	35	PRO	HG3	2.017	0.009	1
1	A	35	PRO	C	176.839	.	1
1	A	35	PRO	CA	63.542	0.035	1
1	A	35	PRO	CB	31.808	0.02	1
1	A	35	PRO	CD	50.726	.	1
1	A	35	PRO	CG	26.094	.	1
1	A	36	HIS	H	9.104	0.007	1
1	A	36	HIS	CA	55.905	.	1
1	A	36	HIS	CB	29.729	.	1
1	A	36	HIS	N	118.804	0.039	1
1	A	37	CYS	C	173.009	.	1
1	A	38	ASP	H	7.983	0.005	1
1	A	38	ASP	C	175.924	.	1
1	A	38	ASP	CA	55.54	0.025	1
1	A	38	ASP	CB	40.725	0.06	1
1	A	38	ASP	N	115.754	0.018	1
1	A	39	LYS	H	8.148	0.01	1
1	A	39	LYS	HA	3.822	0.014	1
1	A	39	LYS	HB2	1.28	0.006	1
1	A	39	LYS	HB3	1.28	0.006	1

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	39	LYS	HD2	1.31	0.014	1
1	A	39	LYS	HD3	1.31	0.014	1
1	A	39	LYS	HE2	2.812	0.011	2
1	A	39	LYS	HE3	3.085	0.0	2
1	A	39	LYS	HG2	1.029	0.006	1
1	A	39	LYS	HG3	1.029	0.006	1
1	A	39	LYS	C	174.515	.	1
1	A	39	LYS	CA	57.889	0.053	1
1	A	39	LYS	CB	33.464	0.051	1
1	A	39	LYS	CD	28.7	0.0	1
1	A	39	LYS	CE	42.555	.	1
1	A	39	LYS	CG	26.009	0.02	1
1	A	39	LYS	N	122.198	0.057	1
1	A	40	LYS	H	7.597	0.006	1
1	A	40	LYS	C	175.043	.	1
1	A	40	LYS	CA	54.586	0.073	1
1	A	40	LYS	CB	35.293	0.046	1
1	A	40	LYS	CD	29.274	.	1
1	A	40	LYS	CG	24.785	.	1
1	A	40	LYS	N	118.804	0.053	1
1	A	41	PHE	H	8.395	0.011	1
1	A	41	PHE	HD1	7.095	0.006	3
1	A	41	PHE	HD2	7.095	0.006	3
1	A	41	PHE	HE1	6.713	0.005	3
1	A	41	PHE	HE2	6.713	0.005	3
1	A	41	PHE	HZ	6.14	0.006	1
1	A	41	PHE	CA	57.208	.	1
1	A	41	PHE	CB	43.475	.	1
1	A	41	PHE	CD1	135.112	.	3
1	A	41	PHE	CD2	135.112	.	3
1	A	41	PHE	CE1	133.781	0.005	3
1	A	41	PHE	CE2	133.781	0.005	3
1	A	41	PHE	CZ	131.989	0.056	1
1	A	41	PHE	N	117.05	0.044	1
1	A	42	ASN	HA	4.19	0.002	1
1	A	42	ASN	HB2	2.12	0.01	1
1	A	42	ASN	HB3	2.12	0.01	1
1	A	42	ASN	C	174.947	.	1
1	A	42	ASN	CA	55.807	0.01	1
1	A	42	ASN	CB	42.016	.	1
1	A	43	GLN	H	7.74	0.013	1

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	43	GLN	HG2	2.304	.	1
1	A	43	GLN	HG3	2.304	.	1
1	A	43	GLN	CA	58.492	.	1
1	A	43	GLN	CB	30.33	.	1
1	A	43	GLN	N	118.321	0.06	1
1	A	44	VAL	H	8.859	.	1
1	A	44	VAL	HG11	0.6	0.012	1
1	A	44	VAL	HG12	0.6	0.012	1
1	A	44	VAL	HG13	0.6	0.012	1
1	A	44	VAL	HG21	0.6	0.012	1
1	A	44	VAL	HG22	0.6	0.012	1
1	A	44	VAL	HG23	0.6	0.012	1
1	A	44	VAL	C	177.34	.	1
1	A	44	VAL	CA	65.759	.	1
1	A	44	VAL	CB	31.018	.	1
1	A	44	VAL	N	125.715	.	1
1	A	45	GLY	H	8.87	0.01	1
1	A	45	GLY	HA2	3.563	0.006	2
1	A	45	GLY	HA3	3.765	0.014	2
1	A	45	GLY	C	176.706	.	1
1	A	45	GLY	CA	46.901	0.019	1
1	A	45	GLY	N	108.836	0.06	1
1	A	46	ASN	H	6.995	0.006	1
1	A	46	ASN	HA	4.441	0.015	1
1	A	46	ASN	HB2	2.816	0.013	1
1	A	46	ASN	HB3	2.816	0.013	1
1	A	46	ASN	C	177.372	.	1
1	A	46	ASN	CA	54.836	0.064	1
1	A	46	ASN	CB	37.777	0.041	1
1	A	46	ASN	N	118.342	0.044	1
1	A	47	LEU	H	6.876	0.012	1
1	A	47	LEU	HA	2.937	0.011	1
1	A	47	LEU	HB2	1.866	0.015	2
1	A	47	LEU	HB3	1.071	0.013	2
1	A	47	LEU	HD11	0.822	0.013	1
1	A	47	LEU	HD12	0.822	0.013	1
1	A	47	LEU	HD13	0.822	0.013	1
1	A	47	LEU	HD21	0.822	0.013	1
1	A	47	LEU	HD22	0.822	0.013	1
1	A	47	LEU	HD23	0.822	0.013	1
1	A	47	LEU	HG	1.315	0.014	1

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	47	LEU	C	177.264	.	1
1	A	47	LEU	CA	57.847	0.039	1
1	A	47	LEU	CB	39.999	0.032	1
1	A	47	LEU	CD1	23.478	.	1
1	A	47	LEU	CD2	23.478	.	1
1	A	47	LEU	CG	26.208	.	1
1	A	47	LEU	N	123.407	0.057	1
1	A	48	LYS	H	8.18	0.009	1
1	A	48	LYS	HA	3.665	0.011	1
1	A	48	LYS	HB2	1.68	0.009	1
1	A	48	LYS	HB3	1.68	0.009	1
1	A	48	LYS	HD2	1.458	0.01	1
1	A	48	LYS	HD3	1.458	0.01	1
1	A	48	LYS	HE2	2.733	0.004	1
1	A	48	LYS	HE3	2.733	0.004	1
1	A	48	LYS	HG2	1.226	0.003	1
1	A	48	LYS	HG3	1.226	0.003	1
1	A	48	LYS	C	178.767	.	1
1	A	48	LYS	CA	59.956	0.018	1
1	A	48	LYS	CB	31.843	0.059	1
1	A	48	LYS	CD	29.097	0.009	1
1	A	48	LYS	CE	42.424	0.042	1
1	A	48	LYS	CG	25.703	0.008	1
1	A	48	LYS	N	117.891	0.044	1
1	A	49	ALA	H	7.193	0.011	1
1	A	49	ALA	HA	3.946	0.011	1
1	A	49	ALA	HB1	1.304	0.013	1
1	A	49	ALA	HB2	1.304	0.013	1
1	A	49	ALA	HB3	1.304	0.013	1
1	A	49	ALA	C	179.732	.	1
1	A	49	ALA	CA	54.564	0.067	1
1	A	49	ALA	CB	18.174	0.051	1
1	A	49	ALA	N	119.002	0.03	1
1	A	50	HIS	H	7.324	0.009	1
1	A	50	HIS	HA	4.083	0.015	1
1	A	50	HIS	HB2	3.055	0.014	2
1	A	50	HIS	HB3	2.825	0.012	2
1	A	50	HIS	HD2	7.07	0.007	1
1	A	50	HIS	HE1	7.865	0.015	1
1	A	50	HIS	C	176.003	.	1
1	A	50	HIS	CA	58.898	0.017	1

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	50	HIS	CB	28.544	0.069	1
1	A	50	HIS	CD2	130.56	0.037	1
1	A	50	HIS	N	118.664	0.045	1
1	A	51	LEU	H	8.085	0.007	1
1	A	51	LEU	HA	3.676	0.015	1
1	A	51	LEU	HB2	1.803	0.014	2
1	A	51	LEU	HB3	1.486	0.011	2
1	A	51	LEU	HD11	0.886	0.012	1
1	A	51	LEU	HD12	0.886	0.012	1
1	A	51	LEU	HD13	0.886	0.012	1
1	A	51	LEU	HD21	0.886	0.012	1
1	A	51	LEU	HD22	0.886	0.012	1
1	A	51	LEU	HD23	0.886	0.012	1
1	A	51	LEU	HG	1.137	0.004	1
1	A	51	LEU	C	178.47	.	1
1	A	51	LEU	CA	58.047	0.012	1
1	A	51	LEU	CB	41.905	0.044	1
1	A	51	LEU	CD1	25.642	0.076	1
1	A	51	LEU	CD2	25.642	0.076	1
1	A	51	LEU	CG	24.504	0.013	1
1	A	51	LEU	N	116.715	0.006	1
1	A	52	LYS	H	6.883	0.012	1
1	A	52	LYS	HA	3.832	0.011	1
1	A	52	LYS	HB2	1.689	0.009	1
1	A	52	LYS	HB3	1.689	0.009	1
1	A	52	LYS	HD2	1.553	0.013	1
1	A	52	LYS	HD3	1.553	0.013	1
1	A	52	LYS	HE2	2.849	0.002	1
1	A	52	LYS	HE3	2.849	0.002	1
1	A	52	LYS	HG2	1.328	0.014	1
1	A	52	LYS	HG3	1.328	0.014	1
1	A	52	LYS	C	178.357	.	1
1	A	52	LYS	CA	58.417	0.034	1
1	A	52	LYS	CB	32.112	0.025	1
1	A	52	LYS	CD	28.897	0.007	1
1	A	52	LYS	CE	40.271	.	1
1	A	52	LYS	CG	24.602	0.005	1
1	A	52	LYS	N	115.588	0.055	1
1	A	53	ILE	H	7.655	0.011	1
1	A	53	ILE	HA	3.831	0.009	1
1	A	53	ILE	HB	1.568	0.013	1

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	53	ILE	HG12	0.791	0.011	1
1	A	53	ILE	HG13	0.791	0.011	1
1	A	53	ILE	HG21	0.484	0.014	1
1	A	53	ILE	HG22	0.484	0.014	1
1	A	53	ILE	HG23	0.484	0.014	1
1	A	53	ILE	C	177.054	.	1
1	A	53	ILE	CA	62.683	0.06	1
1	A	53	ILE	CB	37.501	0.044	1
1	A	53	ILE	CD1	14.169	.	1
1	A	53	ILE	CG1	25.093	0.017	1
1	A	53	ILE	CG2	16.399	.	1
1	A	53	ILE	N	115.446	0.037	1
1	A	54	HIS	H	7.1	0.013	1
1	A	54	HIS	HA	4.462	0.004	1
1	A	54	HIS	HB2	2.677	0.013	1
1	A	54	HIS	HB3	2.677	0.013	1
1	A	54	HIS	HD2	6.454	0.002	1
1	A	54	HIS	C	174.896	.	1
1	A	54	HIS	CA	55.395	0.054	1
1	A	54	HIS	CB	28.564	0.065	1
1	A	54	HIS	CD2	130.631	0.005	1
1	A	54	HIS	N	117.283	0.056	1
1	A	55	ILE	H	7.247	0.012	1
1	A	55	ILE	HA	3.884	0.015	1
1	A	55	ILE	HB	1.719	0.01	1
1	A	55	ILE	HD11	0.708	0.012	1
1	A	55	ILE	HD12	0.708	0.012	1
1	A	55	ILE	HD13	0.708	0.012	1
1	A	55	ILE	HG12	1.341	0.013	2
1	A	55	ILE	HG13	1.021	0.011	2
1	A	55	ILE	HG21	0.759	0.013	1
1	A	55	ILE	HG22	0.759	0.013	1
1	A	55	ILE	HG23	0.759	0.013	1
1	A	55	ILE	C	175.788	.	1
1	A	55	ILE	CA	61.915	0.073	1
1	A	55	ILE	CB	38.42	0.068	1
1	A	55	ILE	CD1	12.996	0.057	1
1	A	55	ILE	CG1	27.339	0.034	1
1	A	55	ILE	CG2	17.415	0.074	1
1	A	55	ILE	N	119.709	0.047	1
1	A	56	ALA	H	8.009	0.011	1

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	56	ALA	HA	4.197	0.014	1
1	A	56	ALA	HB1	1.223	0.013	1
1	A	56	ALA	HB2	1.223	0.013	1
1	A	56	ALA	HB3	1.223	0.013	1
1	A	56	ALA	C	177.042	.	1
1	A	56	ALA	CA	52.204	0.056	1
1	A	56	ALA	CB	19.19	0.068	1
1	A	56	ALA	N	126.276	0.056	1
1	A	57	ASP	H	7.924	0.009	1
1	A	57	ASP	HA	4.447	0.008	1
1	A	57	ASP	HB2	2.516	0.013	1
1	A	57	ASP	HB3	2.516	0.013	1
1	A	57	ASP	C	176.2	.	1
1	A	57	ASP	CA	54.257	0.059	1
1	A	57	ASP	CB	41.256	0.041	1
1	A	57	ASP	N	119.736	0.044	1
1	A	58	GLY	H	7.903	0.009	1
1	A	58	GLY	HA2	3.916	0.01	2
1	A	58	GLY	HA3	3.994	0.008	2
1	A	58	GLY	CA	44.961	0.075	1
1	A	58	GLY	N	108.482	0.048	1
1	A	59	PRO	HA	4.352	0.0	1
1	A	59	PRO	HB2	2.093	0.008	1
1	A	59	PRO	HB3	2.093	0.008	1
1	A	59	PRO	HD2	3.483	0.009	1
1	A	59	PRO	HD3	3.483	0.009	1
1	A	59	PRO	HG2	1.822	0.014	1
1	A	59	PRO	HG3	1.822	0.014	1
1	A	59	PRO	C	176.875	.	1
1	A	59	PRO	CA	63.48	0.064	1
1	A	59	PRO	CB	31.639	.	1
1	A	59	PRO	CD	49.803	0.018	1
1	A	59	PRO	CG	26.989	0.039	1
1	A	60	LEU	H	8.314	0.009	1
1	A	60	LEU	HA	4.313	0.011	1
1	A	60	LEU	HB2	1.426	0.01	2
1	A	60	LEU	HB3	1.618	0.015	2
1	A	60	LEU	HD11	0.585	0.015	1
1	A	60	LEU	HD12	0.585	0.015	1
1	A	60	LEU	HD13	0.585	0.015	1
1	A	60	LEU	HD21	0.61	0.012	1

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	60	LEU	HD22	0.61	0.012	1
1	A	60	LEU	HD23	0.61	0.012	1
1	A	60	LEU	HG	1.424	0.013	1
1	A	60	LEU	C	174.836	.	1
1	A	60	LEU	CA	54.188	0.06	1
1	A	60	LEU	CB	41.692	0.037	1
1	A	60	LEU	CD1	23.005	0.045	2
1	A	60	LEU	CD2	25.524	0.06	2
1	A	60	LEU	CG	26.901	0.003	1
1	A	60	LEU	N	120.479	0.034	1
1	A	61	LYS	H	7.587	0.01	1
1	A	61	LYS	HA	4.907	0.014	1
1	A	61	LYS	HB2	1.431	0.013	1
1	A	61	LYS	HB3	1.431	0.013	1
1	A	61	LYS	HD2	1.427	0.011	1
1	A	61	LYS	HD3	1.427	0.011	1
1	A	61	LYS	HE2	2.782	0.012	1
1	A	61	LYS	HE3	2.782	0.012	1
1	A	61	LYS	HG2	0.973	0.012	1
1	A	61	LYS	HG3	0.973	0.012	1
1	A	61	LYS	C	175.533	.	1
1	A	61	LYS	CA	54.322	0.054	1
1	A	61	LYS	CB	35.449	0.035	1
1	A	61	LYS	CD	29.395	0.01	1
1	A	61	LYS	CE	41.411	0.018	1
1	A	61	LYS	CG	25.191	.	1
1	A	61	LYS	N	120.279	0.057	1
1	A	62	CYS	H	9.008	0.012	1
1	A	62	CYS	HA	4.349	0.013	1
1	A	62	CYS	HB2	2.727	0.01	2
1	A	62	CYS	HB3	3.195	0.013	2
1	A	62	CYS	C	177.533	.	1
1	A	62	CYS	CA	59.489	0.046	1
1	A	62	CYS	CB	29.664	0.074	1
1	A	62	CYS	N	127.047	0.06	1
1	A	63	ARG	H	9.213	0.008	1
1	A	63	ARG	HA	3.996	0.015	1
1	A	63	ARG	HB2	1.789	0.013	1
1	A	63	ARG	HB3	1.789	0.013	1
1	A	63	ARG	HD2	3.085	0.013	1
1	A	63	ARG	HD3	3.085	0.013	1

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	63	ARG	HG2	1.586	0.013	1
1	A	63	ARG	HG3	1.586	0.013	1
1	A	63	ARG	C	176.307	.	1
1	A	63	ARG	CA	58.135	0.061	1
1	A	63	ARG	CB	29.869	0.078	1
1	A	63	ARG	CD	43.293	0.028	1
1	A	63	ARG	CG	27.124	0.035	1
1	A	63	ARG	N	131.833	0.032	1
1	A	64	GLU	H	8.674	0.007	1
1	A	64	GLU	HA	4.075	0.012	1
1	A	64	GLU	HB2	1.186	0.009	2
1	A	64	GLU	HB3	1.008	0.004	2
1	A	64	GLU	HG2	1.675	0.014	1
1	A	64	GLU	HG3	1.675	0.014	1
1	A	64	GLU	C	177.231	.	1
1	A	64	GLU	CA	57.835	0.022	1
1	A	64	GLU	CB	29.173	0.048	1
1	A	64	GLU	CG	35.257	0.051	1
1	A	64	GLU	N	120.21	0.058	1
1	A	65	CYS	H	8.115	0.008	1
1	A	65	CYS	HA	5.028	0.01	1
1	A	65	CYS	HB2	2.723	0.011	2
1	A	65	CYS	HB3	3.309	0.012	2
1	A	65	CYS	C	176.295	.	1
1	A	65	CYS	CA	58.223	0.037	1
1	A	65	CYS	CB	32.339	0.061	1
1	A	65	CYS	N	115.424	0.057	1
1	A	66	GLY	H	7.984	0.011	1
1	A	66	GLY	HA2	3.63	0.013	2
1	A	66	GLY	HA3	4.08	0.014	2
1	A	66	GLY	C	173.337	.	1
1	A	66	GLY	CA	46.164	0.06	1
1	A	66	GLY	N	113.249	0.039	1
1	A	67	LYS	H	7.7	0.009	1
1	A	67	LYS	HA	3.824	0.009	1
1	A	67	LYS	HB2	1.082	0.015	2
1	A	67	LYS	HB3	1.317	0.007	2
1	A	67	LYS	HD2	1.335	0.009	1
1	A	67	LYS	HD3	1.335	0.009	1
1	A	67	LYS	HE2	2.798	0.009	2
1	A	67	LYS	HE3	2.836	0.011	2

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	67	LYS	HG2	0.923	0.014	1
1	A	67	LYS	HG3	0.923	0.014	1
1	A	67	LYS	C	174.006	.	1
1	A	67	LYS	CA	57.937	0.071	1
1	A	67	LYS	CB	33.563	0.059	1
1	A	67	LYS	CD	28.967	0.043	1
1	A	67	LYS	CE	42.133	0.037	1
1	A	67	LYS	CG	26.138	.	1
1	A	67	LYS	N	122.126	0.044	1
1	A	68	GLN	H	7.911	0.005	1
1	A	68	GLN	HA	4.678	0.011	1
1	A	68	GLN	HB2	1.603	0.01	2
1	A	68	GLN	HB3	1.738	0.004	2
1	A	68	GLN	HE21	6.72	0.01	1
1	A	68	GLN	HE22	7.445	0.009	1
1	A	68	GLN	HG2	2.037	0.011	1
1	A	68	GLN	HG3	2.037	0.011	1
1	A	68	GLN	C	174.813	.	1
1	A	68	GLN	CA	54.55	0.069	1
1	A	68	GLN	CB	31.199	0.003	1
1	A	68	GLN	CG	34.108	0.045	1
1	A	68	GLN	N	120.787	0.059	1
1	A	68	GLN	NE2	111.914	0.054	1
1	A	69	PHE	H	8.308	0.01	1
1	A	69	PHE	HB2	3.121	0.009	2
1	A	69	PHE	HB3	2.54	0.015	2
1	A	69	PHE	HD1	7.04	0.011	3
1	A	69	PHE	HD2	7.04	0.011	3
1	A	69	PHE	HZ	5.878	0.001	1
1	A	69	PHE	C	175.241	.	1
1	A	69	PHE	CA	57.347	0.051	1
1	A	69	PHE	CB	43.408	0.061	1
1	A	69	PHE	CD1	135.014	0.033	3
1	A	69	PHE	CD2	135.014	0.033	3
1	A	69	PHE	CZ	131.475	.	1
1	A	69	PHE	N	120.205	0.059	1
1	A	70	THR	H	9.023	0.005	1
1	A	70	THR	HA	4.267	0.009	1
1	A	70	THR	HB	4.284	0.007	1
1	A	70	THR	HG21	1.123	0.014	1
1	A	70	THR	HG22	1.123	0.014	1

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	70	THR	HG23	1.123	0.014	1
1	A	70	THR	C	175.435	.	1
1	A	70	THR	CA	62.819	0.028	1
1	A	70	THR	CB	69.591	0.076	1
1	A	70	THR	CG2	22.256	0.075	1
1	A	70	THR	N	108.936	0.034	1
1	A	71	THR	H	7.15	0.011	1
1	A	71	THR	HA	4.732	0.002	1
1	A	71	THR	HB	4.444	0.014	1
1	A	71	THR	HG21	1.107	0.011	1
1	A	71	THR	HG22	1.107	0.011	1
1	A	71	THR	HG23	1.107	0.011	1
1	A	71	THR	C	174.614	.	1
1	A	71	THR	CA	58.874	0.024	1
1	A	71	THR	CB	72.806	0.031	1
1	A	71	THR	N	108.345	0.042	1
1	A	72	SER	H	9.243	0.007	1
1	A	72	SER	HA	3.9	0.013	1
1	A	72	SER	HB2	3.807	0.015	1
1	A	72	SER	HB3	3.807	0.015	1
1	A	72	SER	C	177.313	.	1
1	A	72	SER	CA	61.112	0.052	1
1	A	72	SER	CB	62.316	0.04	1
1	A	72	SER	N	119.177	0.031	1
1	A	73	GLY	H	8.661	0.007	1
1	A	73	GLY	HA2	3.804	0.014	1
1	A	73	GLY	HA3	3.804	0.014	1
1	A	73	GLY	C	176.236	.	1
1	A	73	GLY	CA	46.952	0.067	1
1	A	73	GLY	N	110.453	0.019	1
1	A	74	ASN	H	7.74	0.006	1
1	A	74	ASN	HA	4.397	0.012	1
1	A	74	ASN	HB2	2.821	0.013	1
1	A	74	ASN	HB3	2.821	0.013	1
1	A	74	ASN	C	177.974	.	1
1	A	74	ASN	CA	55.21	0.021	1
1	A	74	ASN	CB	37.623	0.079	1
1	A	74	ASN	N	120.577	0.015	1
1	A	75	LEU	H	7.343	0.009	1
1	A	75	LEU	HA	2.948	0.013	1
1	A	75	LEU	HB2	1.041	0.015	2

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	75	LEU	HB3	1.841	0.013	2
1	A	75	LEU	HD11	0.793	0.011	2
1	A	75	LEU	HD12	0.793	0.011	2
1	A	75	LEU	HD13	0.793	0.011	2
1	A	75	LEU	HD21	0.704	0.013	2
1	A	75	LEU	HD22	0.704	0.013	2
1	A	75	LEU	HD23	0.704	0.013	2
1	A	75	LEU	HG	1.346	0.007	1
1	A	75	LEU	C	177.097	.	1
1	A	75	LEU	CA	57.968	0.078	1
1	A	75	LEU	CB	40.52	0.079	1
1	A	75	LEU	CD1	26.273	0.058	2
1	A	75	LEU	CD2	22.725	0.056	2
1	A	75	LEU	CG	26.908	0.021	1
1	A	75	LEU	N	123.304	0.046	1
1	A	76	LYS	H	8.254	0.01	1
1	A	76	LYS	HA	3.648	0.008	1
1	A	76	LYS	HB2	1.721	0.014	1
1	A	76	LYS	HB3	1.721	0.014	1
1	A	76	LYS	HD2	1.487	0.013	1
1	A	76	LYS	HD3	1.487	0.013	1
1	A	76	LYS	HE2	2.78	0.011	1
1	A	76	LYS	HE3	2.78	0.011	1
1	A	76	LYS	HG2	1.233	0.012	1
1	A	76	LYS	HG3	1.232	0.012	1
1	A	76	LYS	C	179.149	.	1
1	A	76	LYS	CA	60.272	0.053	1
1	A	76	LYS	CB	31.908	0.072	1
1	A	76	LYS	CD	29.27	0.048	1
1	A	76	LYS	CE	41.796	0.008	1
1	A	76	LYS	CG	25.9	0.001	1
1	A	76	LYS	N	118.414	0.03	1
1	A	77	ARG	H	7.452	0.009	1
1	A	77	ARG	HA	3.799	0.008	1
1	A	77	ARG	HB2	1.692	0.014	1
1	A	77	ARG	HB3	1.692	0.014	1
1	A	77	ARG	HD2	3.057	0.012	1
1	A	77	ARG	HD3	3.057	0.012	1
1	A	77	ARG	HG2	1.439	0.009	1
1	A	77	ARG	HG3	1.439	0.009	1
1	A	77	ARG	C	178.514	.	1

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	77	ARG	CA	59.234	0.037	1
1	A	77	ARG	CB	30.442	0.07	1
1	A	77	ARG	CD	43.205	0.01	1
1	A	77	ARG	CG	27.98	0.018	1
1	A	77	ARG	N	117.219	0.057	1
1	A	78	HIS	H	7.306	0.012	1
1	A	78	HIS	HA	4.039	0.011	1
1	A	78	HIS	HB2	2.931	0.01	2
1	A	78	HIS	HB3	2.643	0.015	2
1	A	78	HIS	HD2	6.719	0.015	1
1	A	78	HIS	HE1	7.9	0.003	1
1	A	78	HIS	C	175.93	.	1
1	A	78	HIS	CA	59.113	0.075	1
1	A	78	HIS	CB	28.286	0.065	1
1	A	78	HIS	CD2	130.741	.	1
1	A	78	HIS	CE1	142.456	.	1
1	A	78	HIS	N	119.279	0.042	1
1	A	79	LEU	H	8.084	0.009	1
1	A	79	LEU	HA	3.643	0.013	1
1	A	79	LEU	HB2	1.415	0.014	2
1	A	79	LEU	HB3	1.755	0.011	2
1	A	79	LEU	HD11	0.84	0.013	1
1	A	79	LEU	HD12	0.84	0.013	1
1	A	79	LEU	HD13	0.84	0.013	1
1	A	79	LEU	HD21	0.84	0.013	1
1	A	79	LEU	HD22	0.84	0.013	1
1	A	79	LEU	HD23	0.84	0.013	1
1	A	79	LEU	HG	1.083	0.013	1
1	A	79	LEU	C	178.932	.	1
1	A	79	LEU	CA	57.964	0.034	1
1	A	79	LEU	CB	41.703	0.061	1
1	A	79	LEU	CD1	25.641	0.055	1
1	A	79	LEU	CD2	25.641	0.055	1
1	A	79	LEU	CG	24.335	0.049	1
1	A	79	LEU	N	116.633	0.031	1
1	A	80	ARG	H	6.954	0.011	1
1	A	80	ARG	HA	3.936	0.011	1
1	A	80	ARG	HB2	1.677	0.008	1
1	A	80	ARG	HB3	1.677	0.008	1
1	A	80	ARG	HD2	3.053	0.01	1
1	A	80	ARG	HD3	3.053	0.01	1

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	80	ARG	HG2	1.54	0.012	1
1	A	80	ARG	HG3	1.54	0.012	1
1	A	80	ARG	C	178.644	.	1
1	A	80	ARG	CA	58.327	0.054	1
1	A	80	ARG	CB	29.806	0.043	1
1	A	80	ARG	CD	43.397	0.007	1
1	A	80	ARG	CG	27.104	0.009	1
1	A	80	ARG	N	116.912	0.049	1
1	A	81	ILE	H	7.763	0.009	1
1	A	81	ILE	HA	3.798	0.006	1
1	A	81	ILE	HB	1.536	0.01	1
1	A	81	ILE	HD11	0.564	0.014	1
1	A	81	ILE	HD12	0.564	0.014	1
1	A	81	ILE	HD13	0.564	0.014	1
1	A	81	ILE	HG12	0.786	0.011	1
1	A	81	ILE	HG13	0.786	0.011	1
1	A	81	ILE	HG21	0.443	0.011	1
1	A	81	ILE	HG22	0.443	0.011	1
1	A	81	ILE	HG23	0.443	0.011	1
1	A	81	ILE	C	177.513	.	1
1	A	81	ILE	CA	63.01	0.058	1
1	A	81	ILE	CB	37.27	0.061	1
1	A	81	ILE	N	116.941	0.024	1
1	A	82	HIS	H	6.975	0.013	1
1	A	82	HIS	HA	4.627	0.005	1
1	A	82	HIS	HB2	3.196	0.008	2
1	A	82	HIS	HB3	2.951	0.01	2
1	A	82	HIS	HD2	6.516	0.008	1
1	A	82	HIS	HE1	7.882	0.011	1
1	A	82	HIS	C	175.365	.	1
1	A	82	HIS	CA	55.064	0.047	1
1	A	82	HIS	CB	28.514	0.032	1
1	A	82	HIS	CD2	130.548	0.028	1
1	A	82	HIS	CE1	142.545	0.07	1
1	A	82	HIS	N	117.229	0.046	1
1	A	83	SER	H	7.586	0.007	1
1	A	83	SER	HA	4.261	0.01	1
1	A	83	SER	HB2	3.775	0.012	1
1	A	83	SER	HB3	3.775	0.012	1
1	A	83	SER	C	174.859	.	1
1	A	83	SER	CA	59.132	0.053	1

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	83	SER	CB	63.674	0.037	1
1	A	83	SER	N	114.372	0.051	1
1	A	84	GLY	H	8.061	0.005	1
1	A	84	GLY	HA2	3.816	0.013	1
1	A	84	GLY	HA3	3.816	0.013	1
1	A	84	GLY	C	174.031	.	1
1	A	84	GLY	CA	45.361	0.07	1
1	A	84	GLY	N	110.203	0.018	1
1	A	85	GLU	H	7.881	0.01	1
1	A	85	GLU	HA	4.085	0.012	1
1	A	85	GLU	HB2	1.807	0.012	2
1	A	85	GLU	HB3	1.873	0.012	2
1	A	85	GLU	HG2	2.113	0.014	2
1	A	85	GLU	HG3	2.141	0.009	2
1	A	85	GLU	C	176.197	.	1
1	A	85	GLU	CA	56.641	0.071	1
1	A	85	GLU	CB	30.408	0.042	1
1	A	85	GLU	CG	36.14	0.054	1
1	A	85	GLU	N	119.951	0.02	1
1	A	86	LYS	H	8.079	0.009	1
1	A	86	LYS	HA	4.391	0.012	1
1	A	86	LYS	HB2	1.44	0.013	1
1	A	86	LYS	HB3	1.44	0.013	1
1	A	86	LYS	HD2	1.207	0.014	1
1	A	86	LYS	HD3	1.207	0.014	1
1	A	86	LYS	HG2	1.069	0.007	1
1	A	86	LYS	HG3	1.069	0.007	1
1	A	86	LYS	CA	53.803	0.006	1
1	A	86	LYS	CB	33.098	0.008	1
1	A	86	LYS	N	121.528	0.041	1
1	A	87	PRO	HA	4.165	0.011	1
1	A	87	PRO	HB2	1.871	0.014	1
1	A	87	PRO	HB3	1.871	0.014	1
1	A	87	PRO	HD2	3.451	0.009	1
1	A	87	PRO	HD3	3.451	0.009	1
1	A	87	PRO	HG2	1.677	0.007	1
1	A	87	PRO	HG3	1.677	0.007	1
1	A	87	PRO	C	176.103	.	1
1	A	87	PRO	CA	63.071	0.068	1
1	A	87	PRO	CB	31.922	0.036	1
1	A	87	PRO	CD	49.706	0.016	1

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	87	PRO	CG	26.478	0.076	1
1	A	88	TYR	H	7.917	0.006	1
1	A	88	TYR	HA	4.453	0.014	1
1	A	88	TYR	HB2	2.763	0.011	1
1	A	88	TYR	HB3	2.764	0.011	1
1	A	88	TYR	HD1	6.883	0.01	3
1	A	88	TYR	HD2	6.883	0.01	3
1	A	88	TYR	C	174.419	.	1
1	A	88	TYR	CA	57.597	0.042	1
1	A	88	TYR	CB	37.762	0.058	1
1	A	88	TYR	CD1	136.067	0.026	3
1	A	88	TYR	CD2	136.067	0.026	3
1	A	88	TYR	N	119.446	0.054	1
1	A	89	VAL	H	8.195	0.007	1
1	A	89	VAL	HA	4.578	0.011	1
1	A	89	VAL	HB	1.702	0.013	1
1	A	89	VAL	HG11	0.649	0.011	2
1	A	89	VAL	HG12	0.649	0.011	2
1	A	89	VAL	HG13	0.649	0.011	2
1	A	89	VAL	HG21	0.599	0.013	2
1	A	89	VAL	HG22	0.599	0.013	2
1	A	89	VAL	HG23	0.599	0.013	2
1	A	89	VAL	C	175.019	.	1
1	A	89	VAL	CA	60.879	0.054	1
1	A	89	VAL	CB	34.764	0.029	1
1	A	89	VAL	CG1	21.513	0.065	2
1	A	89	VAL	CG2	20.584	0.048	2
1	A	89	VAL	N	123.957	0.037	1
1	A	90	CYS	H	8.869	0.009	1
1	A	90	CYS	HA	4.504	0.013	1
1	A	90	CYS	HB2	2.753	0.012	2
1	A	90	CYS	HB3	3.275	0.01	2
1	A	90	CYS	C	177.11	.	1
1	A	90	CYS	CA	59.226	0.065	1
1	A	90	CYS	CB	29.983	0.071	1
1	A	90	CYS	N	128.789	0.03	1
1	A	91	ILE	H	8.687	0.007	1
1	A	91	ILE	HA	3.915	0.01	1
1	A	91	ILE	HB	1.7	0.007	1
1	A	91	ILE	HD11	0.749	0.007	1
1	A	91	ILE	HD12	0.749	0.007	1

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	91	ILE	HD13	0.749	0.007	1
1	A	91	ILE	HG12	0.957	0.012	1
1	A	91	ILE	HG13	0.957	0.012	1
1	A	91	ILE	HG21	0.625	0.009	1
1	A	91	ILE	HG22	0.625	0.009	1
1	A	91	ILE	HG23	0.625	0.009	1
1	A	91	ILE	C	175.617	.	1
1	A	91	ILE	CA	62.872	0.064	1
1	A	91	ILE	CB	37.599	0.048	1
1	A	91	ILE	CD1	13.948	.	1
1	A	91	ILE	CG1	28.529	.	1
1	A	91	ILE	CG2	17.542	0.027	1
1	A	91	ILE	N	128.33	0.035	1
1	A	92	HIS	H	8.526	0.015	1
1	A	92	HIS	HA	4.204	0.013	1
1	A	92	HIS	HB2	1.768	0.013	2
1	A	92	HIS	HB3	2.205	0.013	2
1	A	92	HIS	C	176.698	.	1
1	A	92	HIS	CA	57.915	0.038	1
1	A	92	HIS	CB	29.583	0.068	1
1	A	92	HIS	N	121.59	0.059	1
1	A	93	CYS	H	7.958	0.013	1
1	A	93	CYS	HA	5.023	0.007	1
1	A	93	CYS	HB2	3.312	0.015	2
1	A	93	CYS	HB3	2.723	0.014	2
1	A	93	CYS	C	174.973	.	1
1	A	93	CYS	CA	58.432	0.033	1
1	A	93	CYS	CB	32.158	0.072	1
1	A	93	CYS	N	115.876	0.021	1
1	A	94	GLN	H	8.178	0.011	1
1	A	94	GLN	HA	3.876	0.012	1
1	A	94	GLN	HB2	2.306	0.011	2
1	A	94	GLN	HB3	2.186	0.007	2
1	A	94	GLN	HE21	7.129	0.01	1
1	A	94	GLN	HE22	6.368	0.004	1
1	A	94	GLN	HG2	2.099	0.015	1
1	A	94	GLN	HG3	2.099	0.015	1
1	A	94	GLN	C	174.707	.	1
1	A	94	GLN	CA	58.288	0.073	1
1	A	94	GLN	CB	25.429	0.055	1
1	A	94	GLN	CG	34.36	0.054	1

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	94	GLN	N	116.348	0.034	1
1	A	94	GLN	NE2	112.157	0.053	1
1	A	95	ARG	H	7.856	0.011	1
1	A	95	ARG	HA	3.927	0.012	1
1	A	95	ARG	HB2	1.354	0.012	2
1	A	95	ARG	HB3	1.201	0.015	2
1	A	95	ARG	HD2	2.758	0.009	2
1	A	95	ARG	HD3	2.976	0.008	2
1	A	95	ARG	HG2	1.705	0.011	2
1	A	95	ARG	HG3	1.671	0.015	2
1	A	95	ARG	C	174.113	.	1
1	A	95	ARG	CA	57.979	0.031	1
1	A	95	ARG	CB	31.403	0.038	1
1	A	95	ARG	CD	43.547	0.078	1
1	A	95	ARG	CG	28.398	0.018	1
1	A	95	ARG	N	121.105	0.053	1
1	A	96	GLN	H	7.833	0.007	1
1	A	96	GLN	HA	4.845	0.011	1
1	A	96	GLN	HB2	2.034	0.014	1
1	A	96	GLN	HB3	2.034	0.014	1
1	A	96	GLN	HG2	2.189	0.012	1
1	A	96	GLN	HG3	2.189	0.012	1
1	A	96	GLN	C	174.982	.	1
1	A	96	GLN	CA	54.273	0.056	1
1	A	96	GLN	CB	31.188	0.035	1
1	A	96	GLN	CG	34.06	.	1
1	A	96	GLN	N	119.07	0.045	1
1	A	97	PHE	H	8.875	0.008	1
1	A	97	PHE	HA	4.456	0.014	1
1	A	97	PHE	HB2	2.596	0.009	2
1	A	97	PHE	HB3	3.114	0.011	2
1	A	97	PHE	HD1	7.039	0.012	3
1	A	97	PHE	HD2	7.039	0.012	3
1	A	97	PHE	HE1	6.665	0.002	3
1	A	97	PHE	HE2	6.665	0.002	3
1	A	97	PHE	HZ	5.869	0.005	1
1	A	97	PHE	C	174.888	.	1
1	A	97	PHE	CA	57.285	0.011	1
1	A	97	PHE	CB	43.463	0.069	1
1	A	97	PHE	CD1	135.172	0.041	3
1	A	97	PHE	CD2	135.172	0.041	3

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	97	PHE	CZ	131.433	0.017	1
1	A	97	PHE	N	118.706	0.052	1
1	A	98	ALA	H	9.019	0.01	1
1	A	98	ALA	HA	4.462	0.014	1
1	A	98	ALA	HB1	1.454	0.011	1
1	A	98	ALA	HB2	1.454	0.011	1
1	A	98	ALA	HB3	1.454	0.011	1
1	A	98	ALA	C	176.342	.	1
1	A	98	ALA	CA	53.297	0.015	1
1	A	98	ALA	CB	19.97	0.057	1
1	A	98	ALA	N	121.599	0.032	1
1	A	99	ASP	H	7.323	0.006	1
1	A	99	ASP	HA	4.742	0.013	1
1	A	99	ASP	HB2	2.535	0.014	2
1	A	99	ASP	HB3	2.666	0.013	2
1	A	99	ASP	CA	51.162	0.064	1
1	A	99	ASP	CB	42.663	0.035	1
1	A	99	ASP	N	114.064	0.051	1
1	A	100	PRO	HA	3.463	0.014	1
1	A	100	PRO	HB2	1.712	0.012	2
1	A	100	PRO	HB3	1.641	0.011	2
1	A	100	PRO	HD2	3.025	0.008	2
1	A	100	PRO	HD3	3.617	0.01	2
1	A	100	PRO	HG2	1.556	0.007	2
1	A	100	PRO	HG3	1.811	0.014	2
1	A	100	PRO	C	178.935	.	1
1	A	100	PRO	CA	64.03	0.075	1
1	A	100	PRO	CB	31.142	0.071	1
1	A	100	PRO	CD	50.016	0.034	1
1	A	100	PRO	CG	26.824	0.024	1
1	A	101	GLY	H	8.262	0.01	1
1	A	101	GLY	HA2	3.63	0.011	1
1	A	101	GLY	HA3	3.63	0.011	1
1	A	101	GLY	C	175.852	.	1
1	A	101	GLY	CA	46.678	0.054	1
1	A	101	GLY	N	110.226	0.057	1
1	A	102	ALA	H	8.019	0.005	1
1	A	102	ALA	HA	3.817	0.012	1
1	A	102	ALA	HB1	1.465	0.011	1
1	A	102	ALA	HB2	1.465	0.011	1
1	A	102	ALA	HB3	1.465	0.011	1

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	102	ALA	C	180.54	.	1
1	A	102	ALA	CA	54.496	0.046	1
1	A	102	ALA	CB	18.812	0.071	1
1	A	102	ALA	N	125.555	0.035	1
1	A	103	LEU	H	6.789	0.009	1
1	A	103	LEU	HA	2.975	0.008	1
1	A	103	LEU	HB2	1.706	0.013	2
1	A	103	LEU	HB3	1.029	0.009	2
1	A	103	LEU	HD11	0.775	0.01	2
1	A	103	LEU	HD12	0.775	0.01	2
1	A	103	LEU	HD13	0.775	0.01	2
1	A	103	LEU	HD21	0.864	0.015	2
1	A	103	LEU	HD22	0.864	0.015	2
1	A	103	LEU	HD23	0.864	0.015	2
1	A	103	LEU	HG	1.429	0.01	1
1	A	103	LEU	C	176.809	.	1
1	A	103	LEU	CA	57.588	0.064	1
1	A	103	LEU	CB	40.519	0.066	1
1	A	103	LEU	CD1	23.066	0.038	2
1	A	103	LEU	CD2	23.359	0.026	2
1	A	103	LEU	CG	26.606	.	1
1	A	103	LEU	N	118.329	0.033	1
1	A	104	GLN	H	7.861	0.009	1
1	A	104	GLN	HA	3.8	0.011	1
1	A	104	GLN	HB2	1.99	0.014	1
1	A	104	GLN	HB3	1.99	0.014	1
1	A	104	GLN	HE21	6.657	0.015	1
1	A	104	GLN	HE22	7.476	0.011	1
1	A	104	GLN	HG2	2.22	0.015	2
1	A	104	GLN	HG3	2.304	0.009	2
1	A	104	GLN	C	178.34	.	1
1	A	104	GLN	CA	58.869	0.057	1
1	A	104	GLN	CB	27.988	0.053	1
1	A	104	GLN	CG	33.706	0.078	1
1	A	104	GLN	N	118.337	0.053	1
1	A	104	GLN	NE2	111.002	0.052	1
1	A	105	ARG	H	7.707	0.005	1
1	A	105	ARG	HA	3.815	0.009	1
1	A	105	ARG	HB2	1.64	0.011	1
1	A	105	ARG	HB3	1.639	0.011	1
1	A	105	ARG	HD2	3.062	0.008	1

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	105	ARG	HD3	3.062	0.008	1
1	A	105	ARG	HG2	1.332	0.008	1
1	A	105	ARG	HG3	1.332	0.008	1
1	A	105	ARG	C	178.351	.	1
1	A	105	ARG	CA	58.968	0.054	1
1	A	105	ARG	CB	30.21	0.055	1
1	A	105	ARG	CD	43.004	0.009	1
1	A	105	ARG	CG	28.003	0.008	1
1	A	105	ARG	N	116.516	0.04	1
1	A	106	HIS	H	7.363	0.01	1
1	A	106	HIS	HA	4.103	0.014	1
1	A	106	HIS	HB2	2.703	0.011	2
1	A	106	HIS	HB3	2.9	0.01	2
1	A	106	HIS	HD2	6.681	0.004	1
1	A	106	HIS	HE1	7.878	.	1
1	A	106	HIS	C	176.619	.	1
1	A	106	HIS	CA	59.059	0.077	1
1	A	106	HIS	CB	28.524	0.075	1
1	A	106	HIS	N	118.237	0.053	1
1	A	107	VAL	H	8.352	0.008	1
1	A	107	VAL	HA	3.473	0.012	1
1	A	107	VAL	HB	2.207	0.014	1
1	A	107	VAL	HG11	1.257	0.013	2
1	A	107	VAL	HG12	1.257	0.013	2
1	A	107	VAL	HG13	1.257	0.013	2
1	A	107	VAL	HG21	1.191	0.014	2
1	A	107	VAL	HG22	1.191	0.014	2
1	A	107	VAL	HG23	1.191	0.014	2
1	A	107	VAL	C	176.81	.	1
1	A	107	VAL	CA	66.042	0.036	1
1	A	107	VAL	CB	31.888	0.07	1
1	A	107	VAL	CG1	22.376	0.024	2
1	A	107	VAL	CG2	21.848	0.048	2
1	A	107	VAL	N	114.907	0.041	1
1	A	108	ARG	H	6.735	0.008	1
1	A	108	ARG	HA	4.002	0.009	1
1	A	108	ARG	HB2	1.614	0.008	1
1	A	108	ARG	HB3	1.614	0.008	1
1	A	108	ARG	HD2	3.048	0.007	1
1	A	108	ARG	HD3	3.048	0.007	1
1	A	108	ARG	HG2	1.515	0.01	1

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	108	ARG	HG3	1.515	0.01	1
1	A	108	ARG	C	178.341	.	1
1	A	108	ARG	CA	57.871	0.067	1
1	A	108	ARG	CB	29.759	0.041	1
1	A	108	ARG	CD	43.062	0.065	1
1	A	108	ARG	CG	27.003	0.006	1
1	A	108	ARG	N	117.784	0.052	1
1	A	109	ILE	H	7.712	0.01	1
1	A	109	ILE	HA	3.813	0.015	1
1	A	109	ILE	HB	1.548	0.013	1
1	A	109	ILE	HD11	0.526	0.013	1
1	A	109	ILE	HD12	0.526	0.013	1
1	A	109	ILE	HD13	0.526	0.013	1
1	A	109	ILE	HG12	0.754	0.015	2
1	A	109	ILE	HG13	0.815	0.015	2
1	A	109	ILE	HG21	0.441	0.015	1
1	A	109	ILE	HG22	0.441	0.015	1
1	A	109	ILE	HG23	0.441	0.015	1
1	A	109	ILE	C	176.877	.	1
1	A	109	ILE	CA	63.016	0.054	1
1	A	109	ILE	CB	37.442	0.052	1
1	A	109	ILE	CD1	14.638	0.053	1
1	A	109	ILE	CG1	26.404	0.037	1
1	A	109	ILE	CG2	16.582	0.078	1
1	A	109	ILE	N	116.281	0.024	1
1	A	110	HIS	H	7.299	0.008	1
1	A	110	HIS	HA	4.476	0.015	1
1	A	110	HIS	HB2	2.6	0.01	2
1	A	110	HIS	HB3	2.481	0.002	2
1	A	110	HIS	HD2	6.574	0.009	1
1	A	110	HIS	HE1	7.913	.	1
1	A	110	HIS	C	175.597	.	1
1	A	110	HIS	CA	55.29	0.016	1
1	A	110	HIS	CB	28.463	0.032	1
1	A	110	HIS	CD2	131.677	0.047	1
1	A	110	HIS	N	117.512	0.029	1
1	A	111	THR	H	7.528	0.012	1
1	A	111	THR	HA	4.135	0.015	1
1	A	111	THR	HB	4.176	0.014	1
1	A	111	THR	HG21	0.991	0.014	1
1	A	111	THR	HG22	0.991	0.014	1

Continued on next page...

Continued from previous page...

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	111	THR	HG23	0.991	0.014	1
1	A	111	THR	C	174.74	.	1
1	A	111	THR	CA	62.068	0.059	1
1	A	111	THR	CB	69.863	0.068	1
1	A	111	THR	CG2	21.179	0.058	1
1	A	111	THR	N	109.948	0.055	1
1	A	112	GLY	H	7.878	0.009	1
1	A	112	GLY	HA2	3.751	0.011	2
1	A	112	GLY	HA3	3.548	0.014	2
1	A	112	GLY	CA	46.168	0.065	1
1	A	112	GLY	N	117.415	0.04	1

7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	103	-0.71 ± 0.11	Should be checked
$^{13}\text{C}_\beta$	95	0.36 ± 0.16	None needed (< 0.5 ppm)
$^{13}\text{C}'$	94	-0.22 ± 0.20	None needed (< 0.5 ppm)
^{15}N	95	-0.13 ± 0.84	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 80%, i.e. 243 atoms were assigned a chemical shift out of a possible 304. 0 out of 1 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	108/114 (95%)	44/46 (96%)	43/46 (93%)	21/22 (95%)
Sidechain	113/148 (76%)	75/94 (80%)	38/46 (83%)	0/8 (0%)
Aromatic	22/42 (52%)	12/21 (57%)	10/19 (53%)	0/2 (0%)
Overall	243/304 (80%)	131/161 (81%)	91/111 (82%)	21/32 (66%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 65%, i.e. 259 atoms were assigned a chemical shift out of a possible 396. 0 out of 1 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	111/147 (76%)	45/59 (76%)	45/60 (75%)	21/28 (75%)
Sidechain	126/207 (61%)	84/131 (64%)	42/66 (64%)	0/10 (0%)
Aromatic	22/42 (52%)	12/21 (57%)	10/19 (53%)	0/2 (0%)
Overall	259/396 (65%)	141/211 (67%)	97/145 (67%)	21/40 (52%)

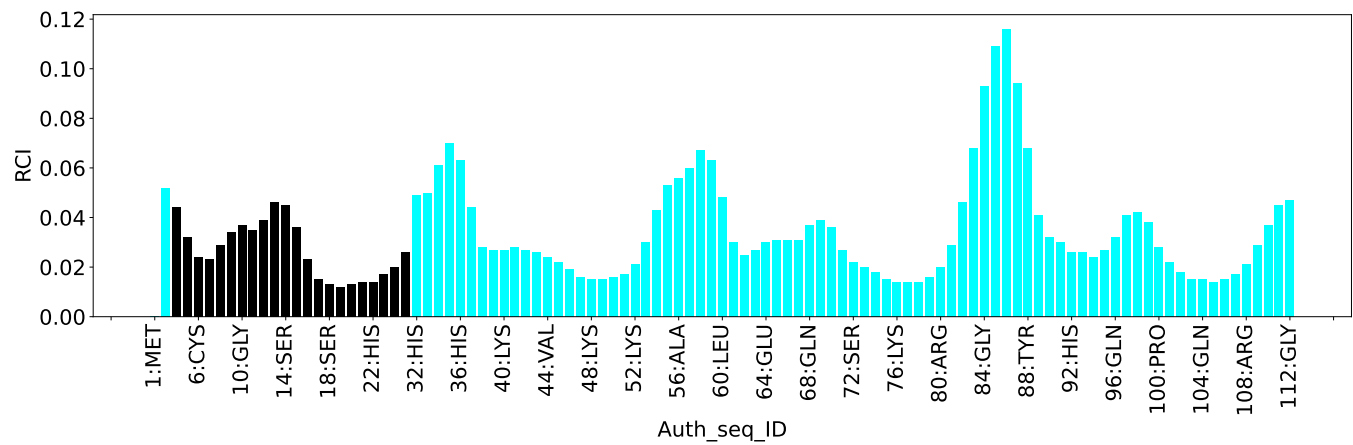
7.1.4 Statistically unusual chemical shifts ⓘ

There are no statistically unusual chemical shifts.

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	436
Intra-residue ($ i-j =0$)	208
Sequential ($ i-j =1$)	106
Medium range ($ i-j >1$ and $ i-j <5$)	90
Long range ($ i-j \geq 5$)	32
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	51
Number of unmapped restraints	0
Number of restraints per residue	4.3
Number of long range restraints per residue ¹	0.3

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)	4.5	0.2
0.2-0.5 (Medium)	6.8	0.5
>0.5 (Large)	2.8	2.27

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)	1.2	4.14
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis ⓘ

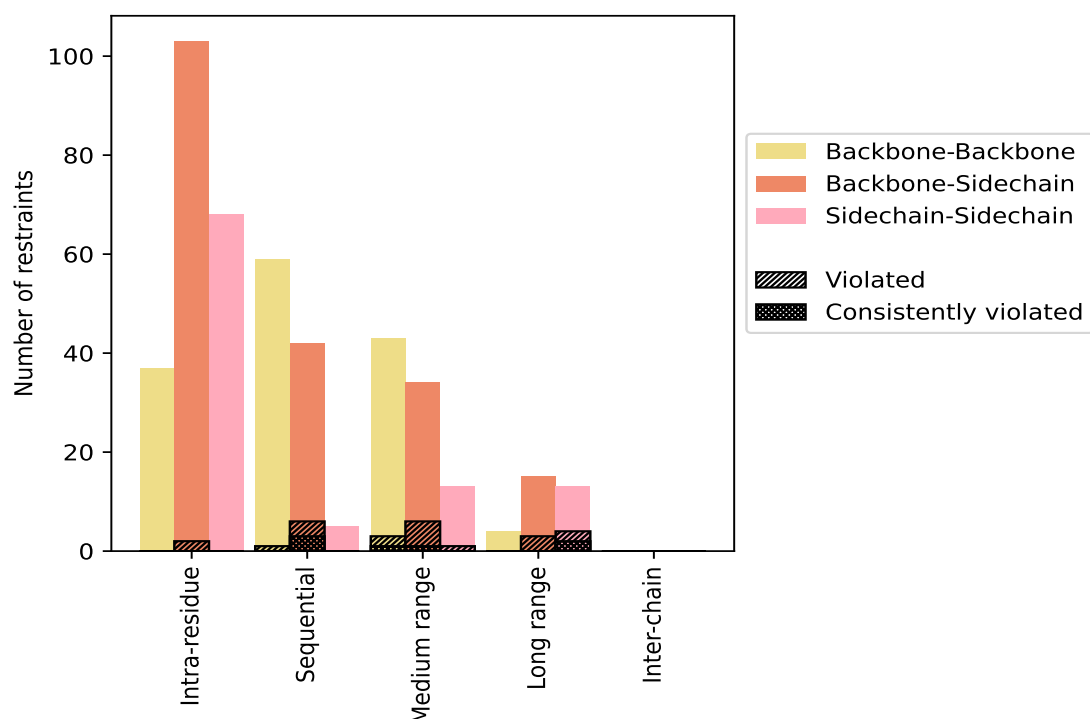
9.1 Summary of distance violations ⓘ

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

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue (i-j =0)	208	47.7	2	1.0	0.5	0	0.0	0.0
Backbone-Backbone	37	8.5	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	103	23.6	2	1.9	0.5	0	0.0	0.0
Sidechain-Sidechain	68	15.6	0	0.0	0.0	0	0.0	0.0
Sequential (i-j =1)	106	24.3	7	6.6	1.6	3	2.8	0.7
Backbone-Backbone	59	13.5	1	1.7	0.2	0	0.0	0.0
Backbone-Sidechain	42	9.6	6	14.3	1.4	3	7.1	0.7
Sidechain-Sidechain	5	1.1	0	0.0	0.0	0	0.0	0.0
Medium range (i-j >1 & i-j <5)	90	20.6	10	11.1	2.3	2	2.2	0.5
Backbone-Backbone	43	9.9	3	7.0	0.7	1	2.3	0.2
Backbone-Sidechain	34	7.8	6	17.6	1.4	1	2.9	0.2
Sidechain-Sidechain	13	3.0	1	7.7	0.2	0	0.0	0.0
Long range (i-j ≥5)	32	7.3	7	21.9	1.6	2	6.2	0.5
Backbone-Backbone	4	0.9	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	15	3.4	3	20.0	0.7	0	0.0	0.0
Sidechain-Sidechain	13	3.0	4	30.8	0.9	2	15.4	0.5
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	0	0.0	0	0.0	0.0	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	436	100.0	26	6.0	6.0	7	1.6	1.6
Backbone-Backbone	143	32.8	4	2.8	0.9	1	0.7	0.2
Backbone-Sidechain	194	44.5	17	8.8	3.9	4	2.1	0.9
Sidechain-Sidechain	99	22.7	5	5.1	1.1	2	2.0	0.5

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	1	4	6	5	0	16	0.31	0.9	0.23	0.24
2	1	3	7	3	0	14	0.49	2.03	0.5	0.28
3	0	4	4	3	0	11	0.58	1.9	0.55	0.25
4	1	4	4	2	0	11	0.39	0.91	0.24	0.32
5	1	6	7	3	0	17	0.33	0.91	0.24	0.24
6	1	4	5	3	0	13	0.33	0.89	0.24	0.21
7	1	5	5	5	0	16	0.35	1.52	0.38	0.18
8	2	4	5	4	0	15	0.31	0.85	0.22	0.23
9	1	6	6	4	0	17	0.45	1.97	0.44	0.3
10	1	4	7	4	0	16	0.41	1.88	0.45	0.24

Continued on next page...

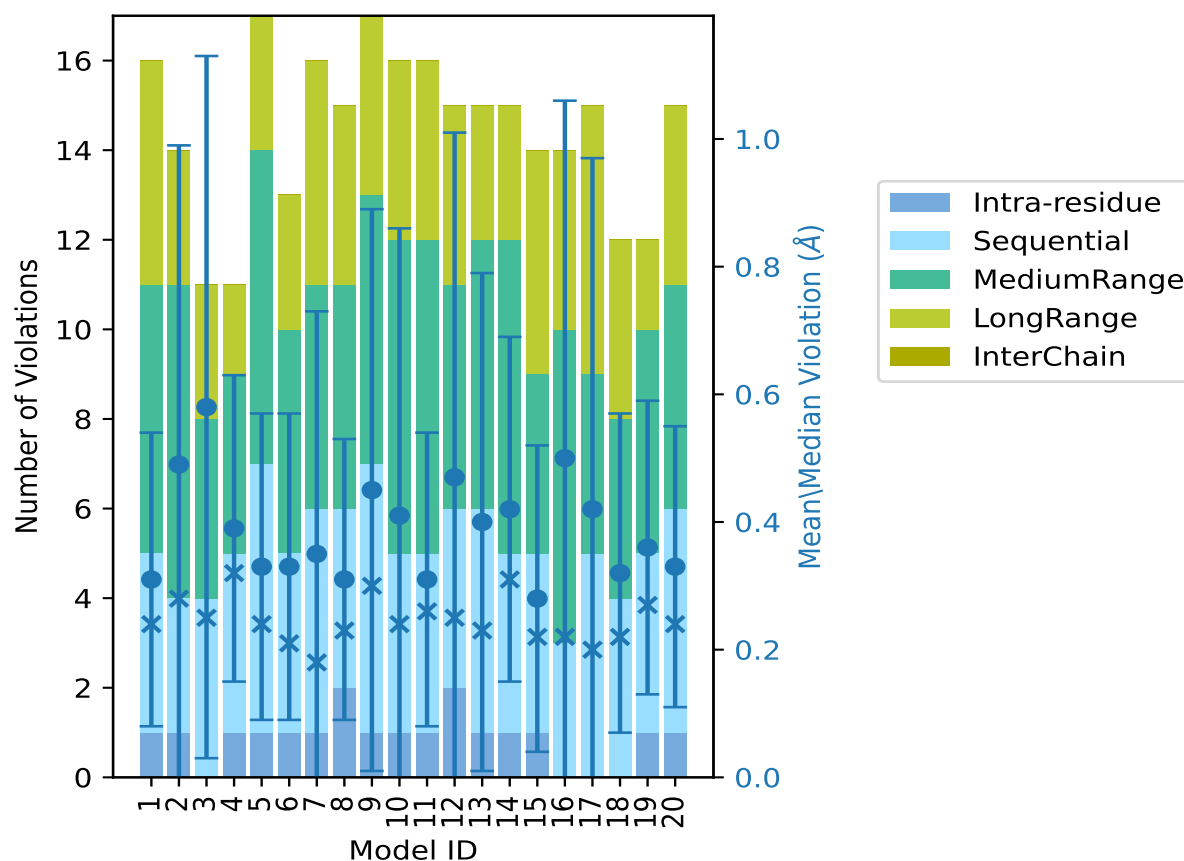
Continued from previous page...

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	1	4	7	4	0	16	0.31	0.9	0.23	0.26
12	2	4	5	4	0	15	0.47	2.26	0.54	0.25
13	1	5	6	3	0	15	0.4	1.59	0.39	0.23
14	1	4	7	3	0	15	0.42	0.95	0.27	0.31
15	1	4	4	5	0	14	0.28	0.88	0.24	0.22
16	0	3	7	4	0	14	0.5	2.21	0.56	0.22
17	0	5	4	6	0	15	0.42	2.27	0.55	0.2
18	0	4	4	4	0	12	0.32	0.92	0.25	0.22
19	1	4	5	2	0	12	0.36	0.89	0.23	0.27
20	1	5	5	4	0	15	0.33	0.87	0.22	0.24

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

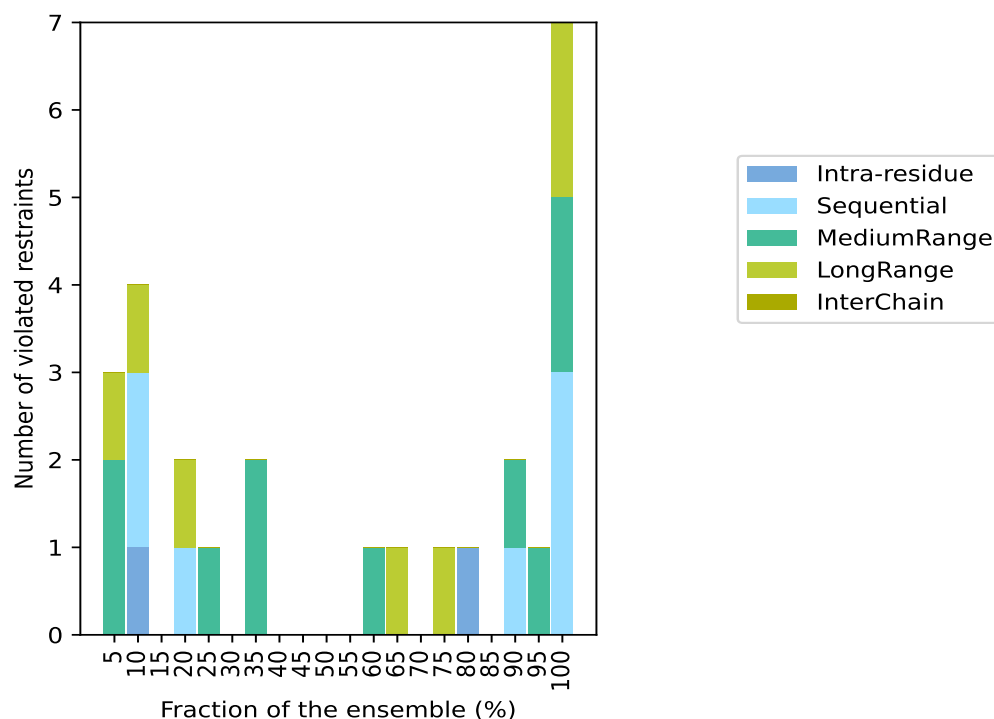
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 410(IR:206, SQ:99, MR:80, LR:25, IC:0) restraints are not 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	%
0	0	2	1	0	3	1	5.0
1	2	0	1	0	4	2	10.0
0	0	0	0	0	0	3	15.0
0	1	0	1	0	2	4	20.0
0	0	1	0	0	1	5	25.0
0	0	0	0	0	0	6	30.0
0	0	2	0	0	2	7	35.0
0	0	0	0	0	0	8	40.0
0	0	0	0	0	0	9	45.0
0	0	0	0	0	0	10	50.0
0	0	0	0	0	0	11	55.0
0	0	1	0	0	1	12	60.0
0	0	0	1	0	1	13	65.0
0	0	0	0	0	0	14	70.0
0	0	0	1	0	1	15	75.0
1	0	0	0	0	1	16	80.0
0	0	0	0	0	0	17	85.0
0	1	1	0	0	2	18	90.0
0	0	1	0	0	1	19	95.0
0	3	2	2	0	7	20	100.0

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

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

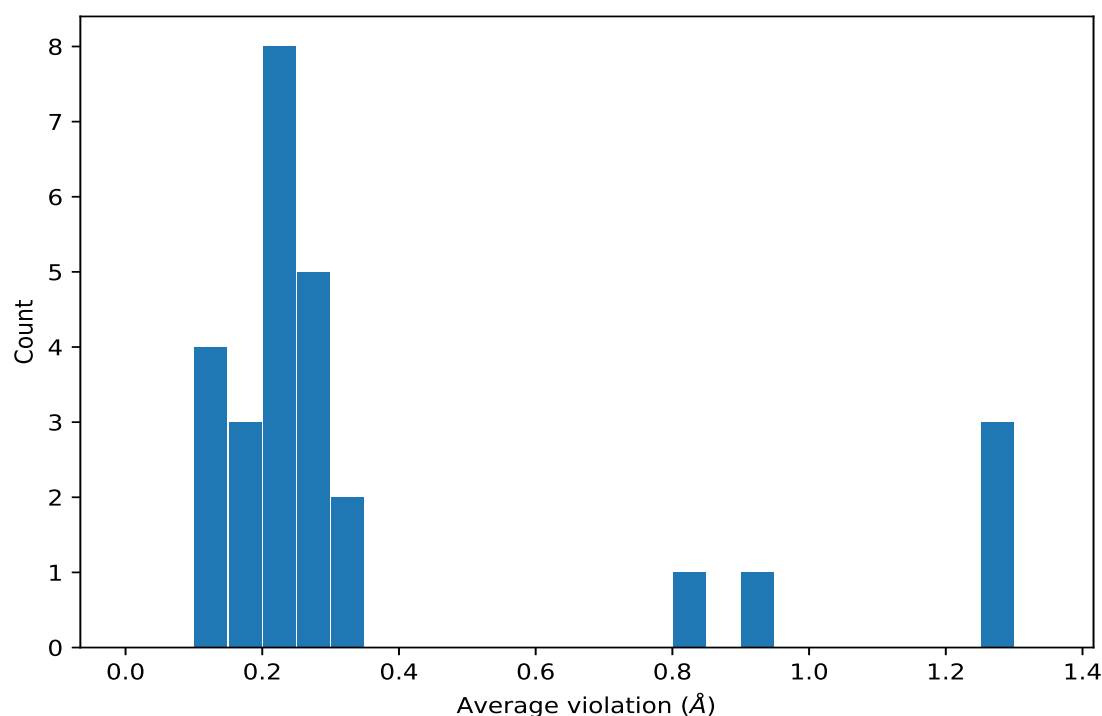
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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)
(1,10)	1:4:A:TYR:H	1:3:A:PRO:HD3	20	0.91	0.04	0.9
(1,250)	1:20:A:MET:H	1:19:A:LYS:HB2	20	0.85	0.03	0.86
(1,119)	1:13:A:PHE:HZ	1:26:A:HIS:HE1	20	0.32	0.16	0.29
(1,135)	1:6:A:CYS:H	1:9:A:CYS:HB3	20	0.31	0.21	0.28
(1,403)	1:20:A:MET:H	1:18:A:SER:HA	20	0.27	0.04	0.28
(1,17)	1:26:A:HIS:HE1	1:9:A:CYS:HB3	20	0.24	0.08	0.24
(1,100)	1:8:A:TYR:H	1:9:A:CYS:HB3	20	0.22	0.03	0.22
(1,229)	1:6:A:CYS:HB3	1:9:A:CYS:HB2	19	0.26	0.05	0.25
(1,404)	1:9:A:CYS:H	1:10:A:GLY:HA3	18	0.22	0.08	0.18
(1,239)	1:15:A:ASP:H	1:13:A:PHE:HA	18	0.18	0.05	0.17
(1,366)	1:11:A:ARG:H	1:11:A:ARG:HG2	16	0.26	0.13	0.3
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD21	15	1.28	0.87	1.59
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD22	15	1.28	0.87	1.59
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD23	15	1.28	0.87	1.59
(1,7)	1:13:A:PHE:H	1:19:A:LYS:HB3	13	0.24	0.05	0.24
(1,225)	1:17:A:THR:H	1:20:A:MET:HB2	12	0.27	0.26	0.13

Continued on next page...

Continued from previous page...

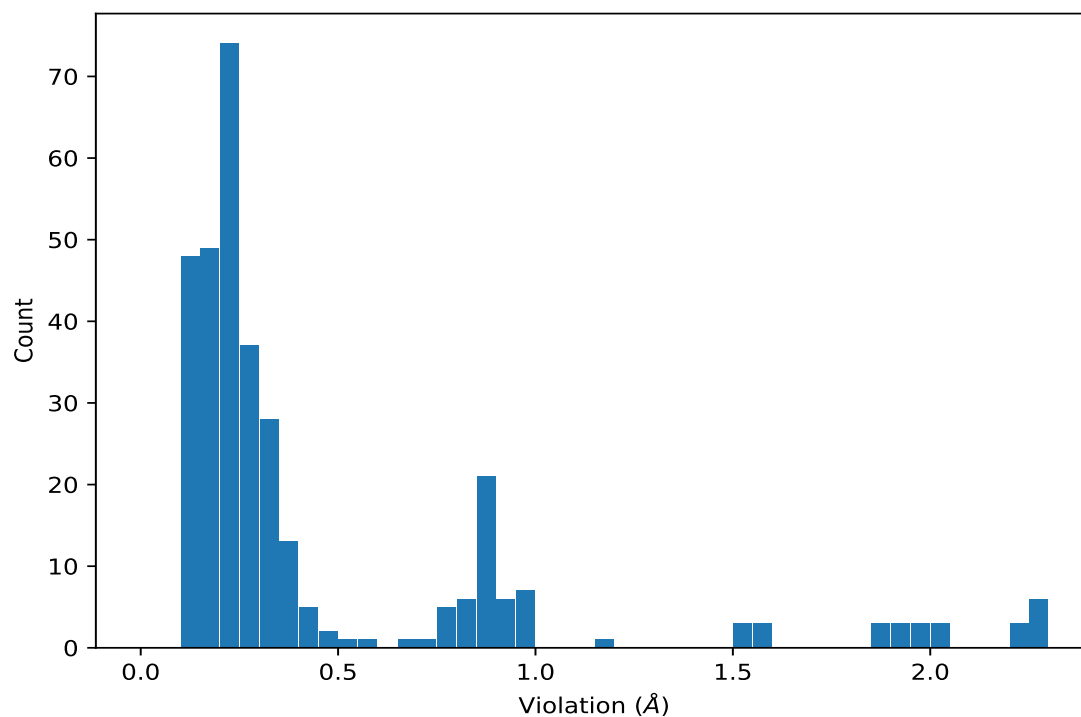
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD21	7	0.21	0.05	0.21
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD22	7	0.21	0.05	0.21
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD23	7	0.21	0.05	0.21
(1,358)	1:9:A:CYS:H	1:6:A:CYS:HB2	7	0.15	0.04	0.15
(1,329)	1:15:A:ASP:H	1:19:A:LYS:HB2	5	0.22	0.03	0.21
(1,154)	1:12:A:SER:H	1:11:A:ARG:HD2	4	0.16	0.05	0.15
(1,387)	1:11:A:ARG:H	1:6:A:CYS:HB2	4	0.12	0.02	0.11
(1,262)	1:6:A:CYS:HB2	1:11:A:ARG:HB2	2	0.28	0.01	0.28
(1,357)	1:18:A:SER:H	1:17:A:THR:HB	2	0.18	0.02	0.18
(1,305)	1:12:A:SER:H	1:11:A:ARG:HB2	2	0.12	0.02	0.12
(1,194)	1:24:A:GLU:H	1:24:A:GLU:HG2	2	0.12	0.01	0.12

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

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)
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD21	17	2.27
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD22	17	2.27
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD23	17	2.27
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD21	12	2.26
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD22	12	2.26
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD23	12	2.26
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD21	16	2.21
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD22	16	2.21
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD23	16	2.21
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD21	2	2.03
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD22	2	2.03
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD23	2	2.03
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD21	9	1.97
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD22	9	1.97
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD23	9	1.97
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD21	3	1.9
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD22	3	1.9
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD23	3	1.9
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD21	10	1.88
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD22	10	1.88
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD23	10	1.88
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD21	13	1.59
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD22	13	1.59
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD23	13	1.59
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD21	7	1.52
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD22	7	1.52
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD23	7	1.52
(1,135)	1:6:A:CYS:H	1:9:A:CYS:HB3	3	1.15
(1,10)	1:4:A:TYR:H	1:3:A:PRO:HD3	3	0.98
(1,10)	1:4:A:TYR:H	1:3:A:PRO:HD3	10	0.97
(1,10)	1:4:A:TYR:H	1:3:A:PRO:HD3	12	0.97
(1,10)	1:4:A:TYR:H	1:3:A:PRO:HD3	2	0.96
(1,10)	1:4:A:TYR:H	1:3:A:PRO:HD3	16	0.96
(1,10)	1:4:A:TYR:H	1:3:A:PRO:HD3	14	0.95
(1,10)	1:4:A:TYR:H	1:3:A:PRO:HD3	17	0.95
(1,119)	1:13:A:PHE:HZ	1:26:A:HIS:HE1	16	0.94
(1,10)	1:4:A:TYR:H	1:3:A:PRO:HD3	18	0.92

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,250)	1:20:A:MET:H	1:19:A:LYS:HB2	5	0.91
(1,10)	1:4:A:TYR:H	1:3:A:PRO:HD3	4	0.91
(1,250)	1:20:A:MET:H	1:19:A:LYS:HB2	1	0.9
(1,10)	1:4:A:TYR:H	1:3:A:PRO:HD3	11	0.9
(1,250)	1:20:A:MET:H	1:19:A:LYS:HB2	2	0.89
(1,10)	1:4:A:TYR:H	1:3:A:PRO:HD3	6	0.89
(1,10)	1:4:A:TYR:H	1:3:A:PRO:HD3	19	0.89
(1,250)	1:20:A:MET:H	1:19:A:LYS:HB2	16	0.88
(1,10)	1:4:A:TYR:H	1:3:A:PRO:HD3	9	0.88
(1,10)	1:4:A:TYR:H	1:3:A:PRO:HD3	15	0.88
(1,250)	1:20:A:MET:H	1:19:A:LYS:HB2	10	0.87
(1,250)	1:20:A:MET:H	1:19:A:LYS:HB2	14	0.87
(1,10)	1:4:A:TYR:H	1:3:A:PRO:HD3	1	0.87
(1,10)	1:4:A:TYR:H	1:3:A:PRO:HD3	5	0.87
(1,10)	1:4:A:TYR:H	1:3:A:PRO:HD3	7	0.87
(1,10)	1:4:A:TYR:H	1:3:A:PRO:HD3	13	0.87
(1,10)	1:4:A:TYR:H	1:3:A:PRO:HD3	20	0.87
(1,250)	1:20:A:MET:H	1:19:A:LYS:HB2	3	0.86
(1,250)	1:20:A:MET:H	1:19:A:LYS:HB2	4	0.86
(1,250)	1:20:A:MET:H	1:19:A:LYS:HB2	6	0.86
(1,250)	1:20:A:MET:H	1:19:A:LYS:HB2	7	0.86
(1,250)	1:20:A:MET:H	1:19:A:LYS:HB2	12	0.86
(1,250)	1:20:A:MET:H	1:19:A:LYS:HB2	17	0.86
(1,250)	1:20:A:MET:H	1:19:A:LYS:HB2	8	0.85
(1,10)	1:4:A:TYR:H	1:3:A:PRO:HD3	8	0.85
(1,250)	1:20:A:MET:H	1:19:A:LYS:HB2	11	0.84
(1,250)	1:20:A:MET:H	1:19:A:LYS:HB2	13	0.84
(1,250)	1:20:A:MET:H	1:19:A:LYS:HB2	18	0.84
(1,250)	1:20:A:MET:H	1:19:A:LYS:HB2	20	0.84
(1,250)	1:20:A:MET:H	1:19:A:LYS:HB2	9	0.83
(1,250)	1:20:A:MET:H	1:19:A:LYS:HB2	15	0.81
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD21	14	0.79
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD22	14	0.79
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD23	14	0.79
(1,250)	1:20:A:MET:H	1:19:A:LYS:HB2	19	0.76
(1,225)	1:17:A:THR:H	1:20:A:MET:HB2	14	0.75
(1,225)	1:17:A:THR:H	1:20:A:MET:HB2	9	0.73
(1,225)	1:17:A:THR:H	1:20:A:MET:HB2	2	0.65
(1,118)	1:17:A:THR:H	1:15:A:ASP:HB3	5	0.58
(1,366)	1:11:A:ARG:H	1:11:A:ARG:HG2	19	0.5
(1,17)	1:26:A:HIS:HE1	1:9:A:CYS:HB3	1	0.46
(1,17)	1:26:A:HIS:HE1	1:9:A:CYS:HB3	20	0.45

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,366)	1:11:A:ARG:H	1:11:A:ARG:HG2	13	0.41
(1,135)	1:6:A:CYS:H	1:9:A:CYS:HB3	2	0.41
(1,119)	1:13:A:PHE:HZ	1:26:A:HIS:HE1	12	0.41
(1,119)	1:13:A:PHE:HZ	1:26:A:HIS:HE1	14	0.41
(1,404)	1:9:A:CYS:H	1:10:A:GLY:HA3	4	0.4
(1,366)	1:11:A:ARG:H	1:11:A:ARG:HG2	1	0.39
(1,135)	1:6:A:CYS:H	1:9:A:CYS:HB3	6	0.39
(1,135)	1:6:A:CYS:H	1:9:A:CYS:HB3	11	0.39
(1,119)	1:13:A:PHE:HZ	1:26:A:HIS:HE1	5	0.39
(1,135)	1:6:A:CYS:H	1:9:A:CYS:HB3	5	0.38
(1,135)	1:6:A:CYS:H	1:9:A:CYS:HB3	9	0.38
(1,366)	1:11:A:ARG:H	1:11:A:ARG:HG2	14	0.37
(1,119)	1:13:A:PHE:HZ	1:26:A:HIS:HE1	11	0.36
(1,366)	1:11:A:ARG:H	1:11:A:ARG:HG2	12	0.35
(1,229)	1:6:A:CYS:HB3	1:9:A:CYS:HB2	9	0.35
(1,135)	1:6:A:CYS:H	1:9:A:CYS:HB3	10	0.35
(1,135)	1:6:A:CYS:H	1:9:A:CYS:HB3	20	0.35
(1,119)	1:13:A:PHE:HZ	1:26:A:HIS:HE1	13	0.35
(1,404)	1:9:A:CYS:H	1:10:A:GLY:HA3	20	0.34
(1,366)	1:11:A:ARG:H	1:11:A:ARG:HG2	4	0.34
(1,7)	1:13:A:PHE:H	1:19:A:LYS:HB3	5	0.34
(1,404)	1:9:A:CYS:H	1:10:A:GLY:HA3	8	0.33
(1,229)	1:6:A:CYS:HB3	1:9:A:CYS:HB2	6	0.33
(1,229)	1:6:A:CYS:HB3	1:9:A:CYS:HB2	16	0.33
(1,403)	1:20:A:MET:H	1:18:A:SER:HA	4	0.32
(1,403)	1:20:A:MET:H	1:18:A:SER:HA	11	0.32
(1,366)	1:11:A:ARG:H	1:11:A:ARG:HG2	5	0.32
(1,229)	1:6:A:CYS:HB3	1:9:A:CYS:HB2	2	0.32
(1,119)	1:13:A:PHE:HZ	1:26:A:HIS:HE1	4	0.32
(1,119)	1:13:A:PHE:HZ	1:26:A:HIS:HE1	9	0.32
(1,119)	1:13:A:PHE:HZ	1:26:A:HIS:HE1	10	0.32
(1,404)	1:9:A:CYS:H	1:10:A:GLY:HA3	19	0.31
(1,403)	1:20:A:MET:H	1:18:A:SER:HA	2	0.31
(1,403)	1:20:A:MET:H	1:18:A:SER:HA	14	0.31
(1,366)	1:11:A:ARG:H	1:11:A:ARG:HG2	8	0.31
(1,135)	1:6:A:CYS:H	1:9:A:CYS:HB3	14	0.31
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD21	9	0.31
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD22	9	0.31
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD23	9	0.31
(1,7)	1:13:A:PHE:H	1:19:A:LYS:HB3	6	0.31
(1,404)	1:9:A:CYS:H	1:10:A:GLY:HA3	17	0.3
(1,403)	1:20:A:MET:H	1:18:A:SER:HA	3	0.3

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,403)	1:20:A:MET:H	1:18:A:SER:HA	9	0.3
(1,366)	1:11:A:ARG:H	1:11:A:ARG:HG2	9	0.3
(1,229)	1:6:A:CYS:HB3	1:9:A:CYS:HB2	12	0.3
(1,135)	1:6:A:CYS:H	1:9:A:CYS:HB3	1	0.3
(1,403)	1:20:A:MET:H	1:18:A:SER:HA	7	0.29
(1,403)	1:20:A:MET:H	1:18:A:SER:HA	15	0.29
(1,262)	1:6:A:CYS:HB2	1:11:A:ARG:HB2	18	0.29
(1,119)	1:13:A:PHE:HZ	1:26:A:HIS:HE1	8	0.29
(1,403)	1:20:A:MET:H	1:18:A:SER:HA	10	0.28
(1,403)	1:20:A:MET:H	1:18:A:SER:HA	12	0.28
(1,403)	1:20:A:MET:H	1:18:A:SER:HA	13	0.28
(1,403)	1:20:A:MET:H	1:18:A:SER:HA	19	0.28
(1,239)	1:15:A:ASP:H	1:13:A:PHE:HA	11	0.28
(1,229)	1:6:A:CYS:HB3	1:9:A:CYS:HB2	14	0.28
(1,119)	1:13:A:PHE:HZ	1:26:A:HIS:HE1	7	0.28
(1,119)	1:13:A:PHE:HZ	1:26:A:HIS:HE1	15	0.28
(1,17)	1:26:A:HIS:HE1	1:9:A:CYS:HB3	5	0.28
(1,403)	1:20:A:MET:H	1:18:A:SER:HA	17	0.27
(1,239)	1:15:A:ASP:H	1:13:A:PHE:HA	19	0.27
(1,229)	1:6:A:CYS:HB3	1:9:A:CYS:HB2	10	0.27
(1,229)	1:6:A:CYS:HB3	1:9:A:CYS:HB2	15	0.27
(1,119)	1:13:A:PHE:HZ	1:26:A:HIS:HE1	19	0.27
(1,100)	1:8:A:TYR:H	1:9:A:CYS:HB3	19	0.27
(1,329)	1:15:A:ASP:H	1:19:A:LYS:HB2	11	0.26
(1,262)	1:6:A:CYS:HB2	1:11:A:ARG:HB2	17	0.26
(1,229)	1:6:A:CYS:HB3	1:9:A:CYS:HB2	8	0.26
(1,100)	1:8:A:TYR:H	1:9:A:CYS:HB3	20	0.26
(1,17)	1:26:A:HIS:HE1	1:9:A:CYS:HB3	9	0.26
(1,17)	1:26:A:HIS:HE1	1:9:A:CYS:HB3	11	0.26
(1,7)	1:13:A:PHE:H	1:19:A:LYS:HB3	7	0.26
(1,403)	1:20:A:MET:H	1:18:A:SER:HA	8	0.25
(1,229)	1:6:A:CYS:HB3	1:9:A:CYS:HB2	4	0.25
(1,229)	1:6:A:CYS:HB3	1:9:A:CYS:HB2	11	0.25
(1,135)	1:6:A:CYS:H	1:9:A:CYS:HB3	18	0.25
(1,119)	1:13:A:PHE:HZ	1:26:A:HIS:HE1	2	0.25
(1,119)	1:13:A:PHE:HZ	1:26:A:HIS:HE1	3	0.25
(1,100)	1:8:A:TYR:H	1:9:A:CYS:HB3	1	0.25
(1,100)	1:8:A:TYR:H	1:9:A:CYS:HB3	3	0.25
(1,100)	1:8:A:TYR:H	1:9:A:CYS:HB3	12	0.25
(1,17)	1:26:A:HIS:HE1	1:9:A:CYS:HB3	18	0.25
(1,7)	1:13:A:PHE:H	1:19:A:LYS:HB3	16	0.25
(1,404)	1:9:A:CYS:H	1:10:A:GLY:HA3	1	0.24

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,229)	1:6:A:CYS:HB3	1:9:A:CYS:HB2	5	0.24
(1,229)	1:6:A:CYS:HB3	1:9:A:CYS:HB2	13	0.24
(1,154)	1:12:A:SER:H	1:11:A:ARG:HD2	20	0.24
(1,135)	1:6:A:CYS:H	1:9:A:CYS:HB3	12	0.24
(1,119)	1:13:A:PHE:HZ	1:26:A:HIS:HE1	20	0.24
(1,100)	1:8:A:TYR:H	1:9:A:CYS:HB3	17	0.24
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD21	10	0.24
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD22	10	0.24
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD23	10	0.24
(1,17)	1:26:A:HIS:HE1	1:9:A:CYS:HB3	4	0.24
(1,17)	1:26:A:HIS:HE1	1:9:A:CYS:HB3	10	0.24
(1,17)	1:26:A:HIS:HE1	1:9:A:CYS:HB3	14	0.24
(1,17)	1:26:A:HIS:HE1	1:9:A:CYS:HB3	19	0.24
(1,7)	1:13:A:PHE:H	1:19:A:LYS:HB3	1	0.24
(1,7)	1:13:A:PHE:H	1:19:A:LYS:HB3	10	0.24
(1,7)	1:13:A:PHE:H	1:19:A:LYS:HB3	20	0.24
(1,404)	1:9:A:CYS:H	1:10:A:GLY:HA3	15	0.23
(1,403)	1:20:A:MET:H	1:18:A:SER:HA	1	0.23
(1,403)	1:20:A:MET:H	1:18:A:SER:HA	6	0.23
(1,403)	1:20:A:MET:H	1:18:A:SER:HA	20	0.23
(1,329)	1:15:A:ASP:H	1:19:A:LYS:HB2	16	0.23
(1,229)	1:6:A:CYS:HB3	1:9:A:CYS:HB2	20	0.23
(1,225)	1:17:A:THR:H	1:20:A:MET:HB2	8	0.23
(1,119)	1:13:A:PHE:HZ	1:26:A:HIS:HE1	1	0.23
(1,100)	1:8:A:TYR:H	1:9:A:CYS:HB3	9	0.23
(1,100)	1:8:A:TYR:H	1:9:A:CYS:HB3	18	0.23
(1,17)	1:26:A:HIS:HE1	1:9:A:CYS:HB3	13	0.23
(1,7)	1:13:A:PHE:H	1:19:A:LYS:HB3	8	0.23
(1,7)	1:13:A:PHE:H	1:19:A:LYS:HB3	15	0.23
(1,404)	1:9:A:CYS:H	1:10:A:GLY:HA3	18	0.22
(1,403)	1:20:A:MET:H	1:18:A:SER:HA	16	0.22
(1,403)	1:20:A:MET:H	1:18:A:SER:HA	18	0.22
(1,358)	1:9:A:CYS:H	1:6:A:CYS:HB2	14	0.22
(1,239)	1:15:A:ASP:H	1:13:A:PHE:HA	4	0.22
(1,239)	1:15:A:ASP:H	1:13:A:PHE:HA	12	0.22
(1,100)	1:8:A:TYR:H	1:9:A:CYS:HB3	8	0.22
(1,100)	1:8:A:TYR:H	1:9:A:CYS:HB3	11	0.22
(1,100)	1:8:A:TYR:H	1:9:A:CYS:HB3	15	0.22
(1,17)	1:26:A:HIS:HE1	1:9:A:CYS:HB3	12	0.22
(1,7)	1:13:A:PHE:H	1:19:A:LYS:HB3	12	0.22
(1,329)	1:15:A:ASP:H	1:19:A:LYS:HB2	1	0.21
(1,329)	1:15:A:ASP:H	1:19:A:LYS:HB2	5	0.21

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,239)	1:15:A:ASP:H	1:13:A:PHE:HA	8	0.21
(1,239)	1:15:A:ASP:H	1:13:A:PHE:HA	14	0.21
(1,229)	1:6:A:CYS:HB3	1:9:A:CYS:HB2	7	0.21
(1,229)	1:6:A:CYS:HB3	1:9:A:CYS:HB2	18	0.21
(1,135)	1:6:A:CYS:H	1:9:A:CYS:HB3	4	0.21
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD21	20	0.21
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD22	20	0.21
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD23	20	0.21
(1,100)	1:8:A:TYR:H	1:9:A:CYS:HB3	10	0.21
(1,100)	1:8:A:TYR:H	1:9:A:CYS:HB3	14	0.21
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD21	3	0.21
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD22	3	0.21
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD23	3	0.21
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD21	14	0.21
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD22	14	0.21
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD23	14	0.21
(1,17)	1:26:A:HIS:HE1	1:9:A:CYS:HB3	6	0.21
(1,7)	1:13:A:PHE:H	1:19:A:LYS:HB3	9	0.21
(1,403)	1:20:A:MET:H	1:18:A:SER:HA	5	0.2
(1,357)	1:18:A:SER:H	1:17:A:THR:HB	5	0.2
(1,239)	1:15:A:ASP:H	1:13:A:PHE:HA	2	0.2
(1,229)	1:6:A:CYS:HB3	1:9:A:CYS:HB2	1	0.2
(1,229)	1:6:A:CYS:HB3	1:9:A:CYS:HB2	19	0.2
(1,135)	1:6:A:CYS:H	1:9:A:CYS:HB3	13	0.2
(1,119)	1:13:A:PHE:HZ	1:26:A:HIS:HE1	18	0.2
(1,100)	1:8:A:TYR:H	1:9:A:CYS:HB3	5	0.2
(1,100)	1:8:A:TYR:H	1:9:A:CYS:HB3	13	0.2
(1,17)	1:26:A:HIS:HE1	1:9:A:CYS:HB3	2	0.2
(1,17)	1:26:A:HIS:HE1	1:9:A:CYS:HB3	3	0.2
(1,17)	1:26:A:HIS:HE1	1:9:A:CYS:HB3	8	0.2
(1,7)	1:13:A:PHE:H	1:19:A:LYS:HB3	17	0.2
(1,404)	1:9:A:CYS:H	1:10:A:GLY:HA3	12	0.19
(1,358)	1:9:A:CYS:H	1:6:A:CYS:HB2	6	0.19
(1,239)	1:15:A:ASP:H	1:13:A:PHE:HA	13	0.19
(1,119)	1:13:A:PHE:HZ	1:26:A:HIS:HE1	6	0.19
(1,100)	1:8:A:TYR:H	1:9:A:CYS:HB3	4	0.19
(1,100)	1:8:A:TYR:H	1:9:A:CYS:HB3	7	0.19
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD21	2	0.19
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD22	2	0.19
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD23	2	0.19
(1,404)	1:9:A:CYS:H	1:10:A:GLY:HA3	6	0.18
(1,404)	1:9:A:CYS:H	1:10:A:GLY:HA3	9	0.18

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,239)	1:15:A:ASP:H	1:13:A:PHE:HA	9	0.18
(1,229)	1:6:A:CYS:HB3	1:9:A:CYS:HB2	17	0.18
(1,135)	1:6:A:CYS:H	1:9:A:CYS:HB3	8	0.18
(1,135)	1:6:A:CYS:H	1:9:A:CYS:HB3	16	0.18
(1,100)	1:8:A:TYR:H	1:9:A:CYS:HB3	16	0.18
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD21	7	0.18
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD22	7	0.18
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD23	7	0.18
(1,404)	1:9:A:CYS:H	1:10:A:GLY:HA3	7	0.17
(1,329)	1:15:A:ASP:H	1:19:A:LYS:HB2	10	0.17
(1,135)	1:6:A:CYS:H	1:9:A:CYS:HB3	7	0.17
(1,100)	1:8:A:TYR:H	1:9:A:CYS:HB3	2	0.17
(1,100)	1:8:A:TYR:H	1:9:A:CYS:HB3	6	0.17
(1,17)	1:26:A:HIS:HE1	1:9:A:CYS:HB3	7	0.17
(1,404)	1:9:A:CYS:H	1:10:A:GLY:HA3	13	0.16
(1,366)	1:11:A:ARG:H	1:11:A:ARG:HG2	6	0.16
(1,357)	1:18:A:SER:H	1:17:A:THR:HB	13	0.16
(1,239)	1:15:A:ASP:H	1:13:A:PHE:HA	3	0.16
(1,239)	1:15:A:ASP:H	1:13:A:PHE:HA	7	0.16
(1,239)	1:15:A:ASP:H	1:13:A:PHE:HA	20	0.16
(1,135)	1:6:A:CYS:H	1:9:A:CYS:HB3	19	0.16
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD21	8	0.16
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD22	8	0.16
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD23	8	0.16
(1,119)	1:13:A:PHE:HZ	1:26:A:HIS:HE1	17	0.16
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD21	13	0.16
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD22	13	0.16
(1,24)	1:26:A:HIS:H	1:23:A:LEU:HD23	13	0.16
(1,404)	1:9:A:CYS:H	1:10:A:GLY:HA3	11	0.15
(1,387)	1:11:A:ARG:H	1:6:A:CYS:HB2	18	0.15
(1,358)	1:9:A:CYS:H	1:6:A:CYS:HB2	10	0.15
(1,358)	1:9:A:CYS:H	1:6:A:CYS:HB2	11	0.15
(1,358)	1:9:A:CYS:H	1:6:A:CYS:HB2	16	0.15
(1,239)	1:15:A:ASP:H	1:13:A:PHE:HA	10	0.15
(1,239)	1:15:A:ASP:H	1:13:A:PHE:HA	16	0.15
(1,154)	1:12:A:SER:H	1:11:A:ARG:HD2	9	0.15
(1,17)	1:26:A:HIS:HE1	1:9:A:CYS:HB3	17	0.15
(1,7)	1:13:A:PHE:H	1:19:A:LYS:HB3	11	0.15
(1,404)	1:9:A:CYS:H	1:10:A:GLY:HA3	10	0.14
(1,366)	1:11:A:ARG:H	1:11:A:ARG:HG2	2	0.14
(1,366)	1:11:A:ARG:H	1:11:A:ARG:HG2	15	0.14
(1,366)	1:11:A:ARG:H	1:11:A:ARG:HG2	20	0.14

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,305)	1:12:A:SER:H	1:11:A:ARG:HB2	9	0.14
(1,154)	1:12:A:SER:H	1:11:A:ARG:HD2	17	0.14
(1,135)	1:6:A:CYS:H	1:9:A:CYS:HB3	15	0.14
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD21	1	0.14
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD22	1	0.14
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD23	1	0.14
(1,17)	1:26:A:HIS:HE1	1:9:A:CYS:HB3	16	0.14
(1,404)	1:9:A:CYS:H	1:10:A:GLY:HA3	5	0.13
(1,404)	1:9:A:CYS:H	1:10:A:GLY:HA3	14	0.13
(1,239)	1:15:A:ASP:H	1:13:A:PHE:HA	6	0.13
(1,225)	1:17:A:THR:H	1:20:A:MET:HB2	11	0.13
(1,225)	1:17:A:THR:H	1:20:A:MET:HB2	13	0.13
(1,225)	1:17:A:THR:H	1:20:A:MET:HB2	19	0.13
(1,194)	1:24:A:GLU:H	1:24:A:GLU:HG2	8	0.13
(1,135)	1:6:A:CYS:H	1:9:A:CYS:HB3	17	0.13
(1,404)	1:9:A:CYS:H	1:10:A:GLY:HA3	3	0.12
(1,366)	1:11:A:ARG:H	1:11:A:ARG:HG2	11	0.12
(1,239)	1:15:A:ASP:H	1:13:A:PHE:HA	1	0.12
(1,239)	1:15:A:ASP:H	1:13:A:PHE:HA	15	0.12
(1,225)	1:17:A:THR:H	1:20:A:MET:HB2	1	0.12
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD21	15	0.12
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD22	15	0.12
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD23	15	0.12
(1,17)	1:26:A:HIS:HE1	1:9:A:CYS:HB3	15	0.12
(1,387)	1:11:A:ARG:H	1:6:A:CYS:HB2	1	0.11
(1,387)	1:11:A:ARG:H	1:6:A:CYS:HB2	7	0.11
(1,366)	1:11:A:ARG:H	1:11:A:ARG:HG2	10	0.11
(1,358)	1:9:A:CYS:H	1:6:A:CYS:HB2	2	0.11
(1,358)	1:9:A:CYS:H	1:6:A:CYS:HB2	5	0.11
(1,336)	1:24:A:GLU:H	1:20:A:MET:HA	20	0.11
(1,305)	1:12:A:SER:H	1:11:A:ARG:HB2	5	0.11
(1,225)	1:17:A:THR:H	1:20:A:MET:HB2	16	0.11
(1,194)	1:24:A:GLU:H	1:24:A:GLU:HG2	12	0.11
(1,154)	1:12:A:SER:H	1:11:A:ARG:HD2	7	0.11
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD21	11	0.11
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD22	11	0.11
(1,129)	1:9:A:CYS:H	1:23:A:LEU:HD23	11	0.11
(1,63)	1:13:A:PHE:HZ	1:22:A:HIS:HB3	15	0.11
(1,387)	1:11:A:ARG:H	1:6:A:CYS:HB2	17	0.1
(1,366)	1:11:A:ARG:H	1:11:A:ARG:HG2	7	0.1
(1,239)	1:15:A:ASP:H	1:13:A:PHE:HA	18	0.1
(1,225)	1:17:A:THR:H	1:20:A:MET:HB2	5	0.1

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,225)	1:17:A:THR:H	1:20:A:MET:HB2	12	0.1
(1,225)	1:17:A:THR:H	1:20:A:MET:HB2	17	0.1

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

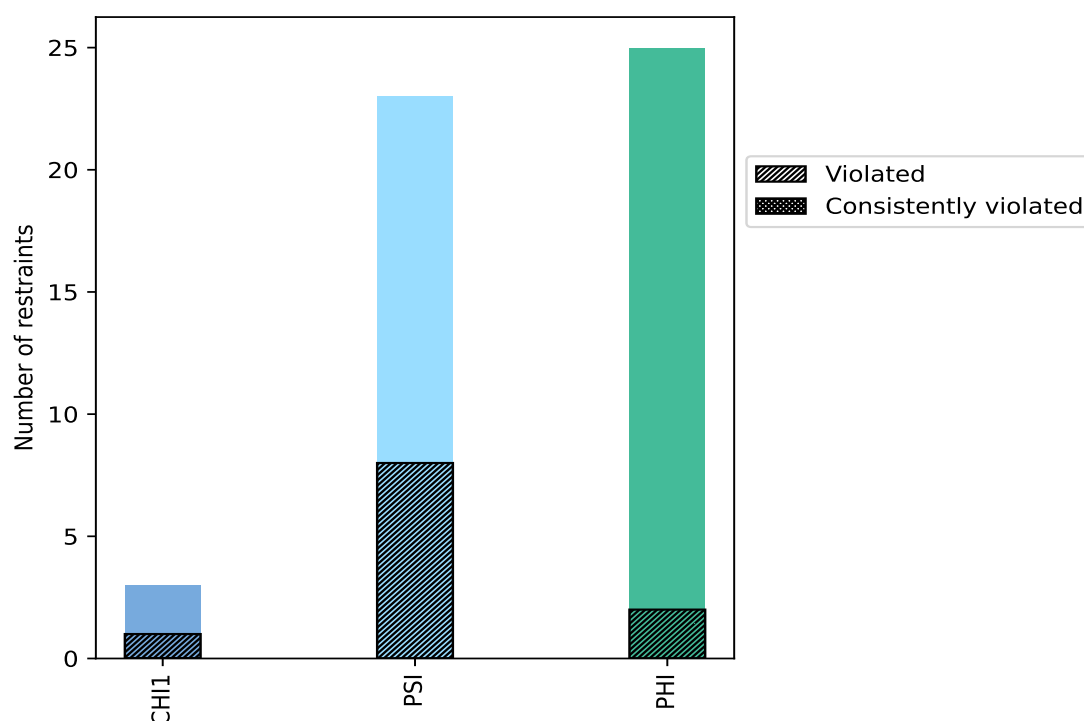
10.1 Summary of dihedral-angle violations [i](#)

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
CHI1	3	5.9	1	33.3	2.0	0	0.0	0.0
PSI	23	45.1	8	34.8	15.7	0	0.0	0.0
PHI	25	49.0	2	8.0	3.9	0	0.0	0.0
Total	51	100.0	11	21.6	21.6	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](#)



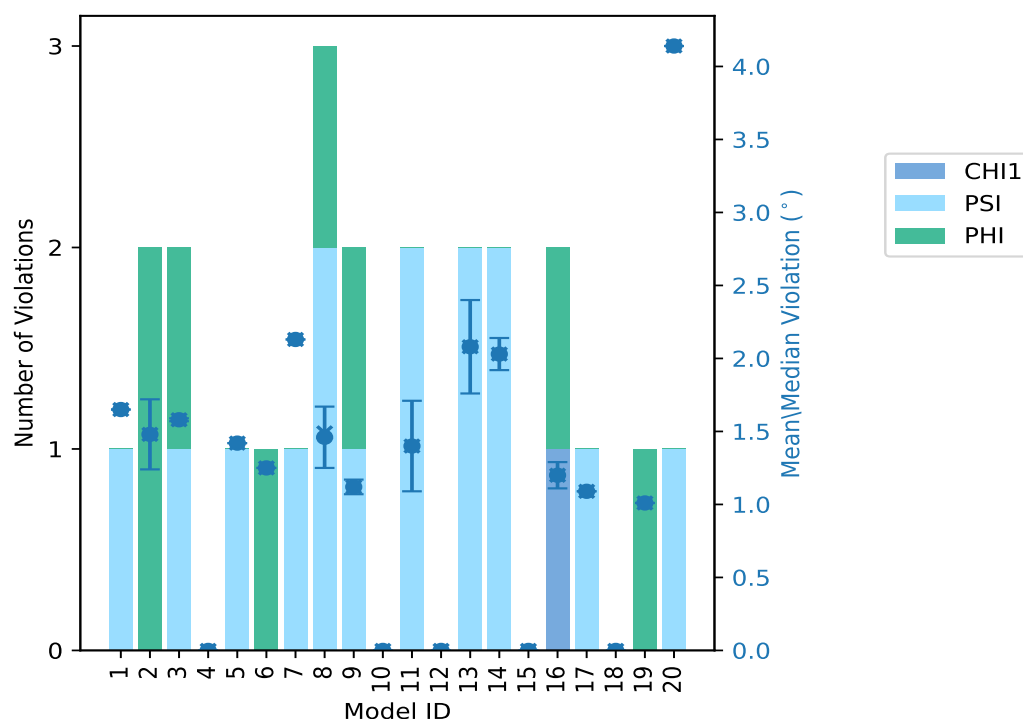
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

10.2 Dihedral-angle violation statistics for each model

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 (°)
	CHI1	PSI	PHI	Total				
1	0	1	0	1	1.65	1.65	0.0	1.65
2	0	0	2	2	1.48	1.72	0.24	1.48
3	0	1	1	2	1.58	1.58	0.01	1.58
4	0	0	0	0	0.0	0.0	0.0	0.0
5	0	1	0	1	1.42	1.42	0.0	1.42
6	0	0	1	1	1.25	1.25	0.0	1.25
7	0	1	0	1	2.13	2.13	0.0	2.13
8	0	2	1	3	1.46	1.7	0.21	1.49
9	0	1	1	2	1.12	1.17	0.05	1.12
10	0	0	0	0	0.0	0.0	0.0	0.0
11	0	2	0	2	1.4	1.71	0.31	1.4
12	0	0	0	0	0.0	0.0	0.0	0.0
13	0	2	0	2	2.08	2.4	0.32	2.08
14	0	2	0	2	2.03	2.14	0.11	2.03
15	0	0	0	0	0.0	0.0	0.0	0.0
16	1	0	1	2	1.2	1.29	0.09	1.2
17	0	1	0	1	1.09	1.09	0.0	1.09
18	0	0	0	0	0.0	0.0	0.0	0.0
19	0	0	1	1	1.01	1.01	0.0	1.01
20	0	1	0	1	4.14	4.14	0.0	4.14

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



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

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

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

Number of violated restraints				Fraction of the ensemble	
CHI1	PSI	PHI	Total	Count ¹	%
1	3	0	4	1	5.0
0	3	0	3	2	10.0
0	2	1	3	3	15.0
0	0	0	0	4	20.0
0	0	1	1	5	25.0
0	0	0	0	6	30.0
0	0	0	0	7	35.0
0	0	0	0	8	40.0
0	0	0	0	9	45.0
0	0	0	0	10	50.0
0	0	0	0	11	55.0

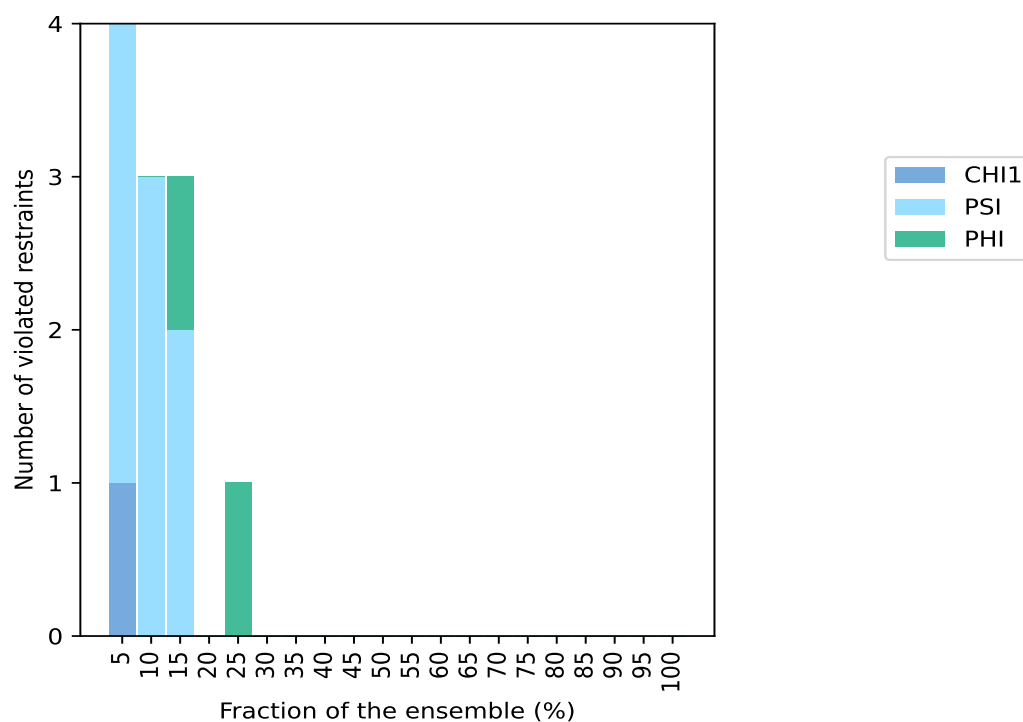
Continued on next page...

Continued from previous page...

Number of violated restraints				Fraction of the ensemble	
CHI1	PSI	PHI	Total	Count ¹	%
0	0	0	0	12	60.0
0	0	0	0	13	65.0
0	0	0	0	14	70.0
0	0	0	0	15	75.0
0	0	0	0	16	80.0
0	0	0	0	17	85.0
0	0	0	0	18	90.0
0	0	0	0	19	95.0
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](#)

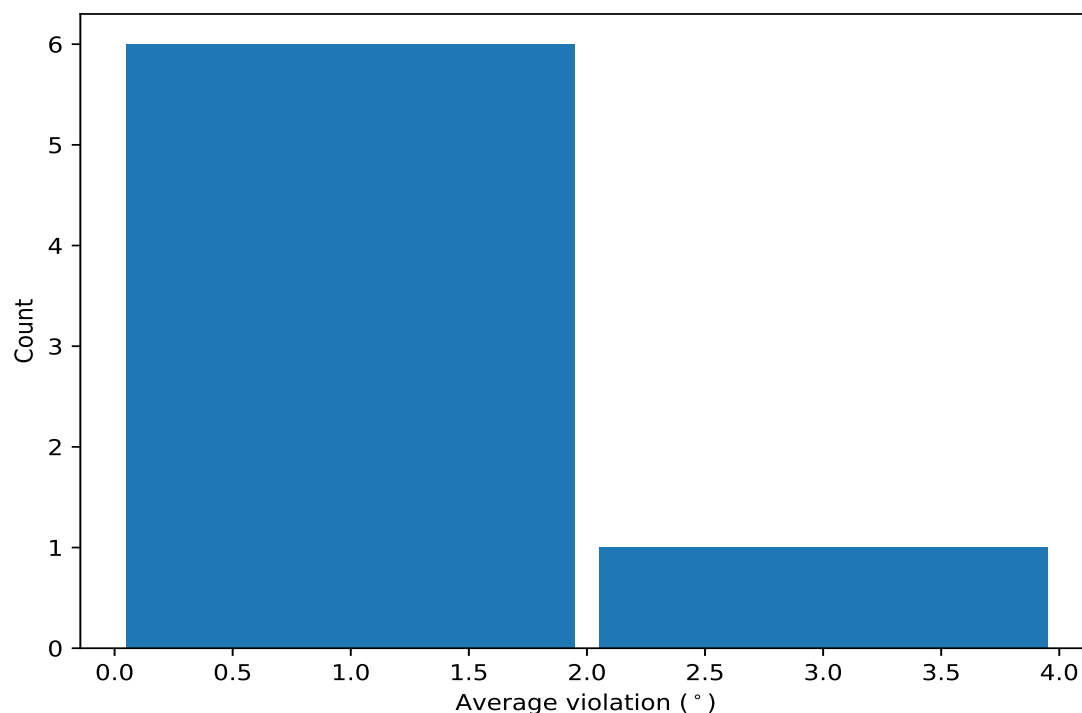


10.4 Most violated dihedral-angle restraints in the ensemble [i](#)

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 [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.

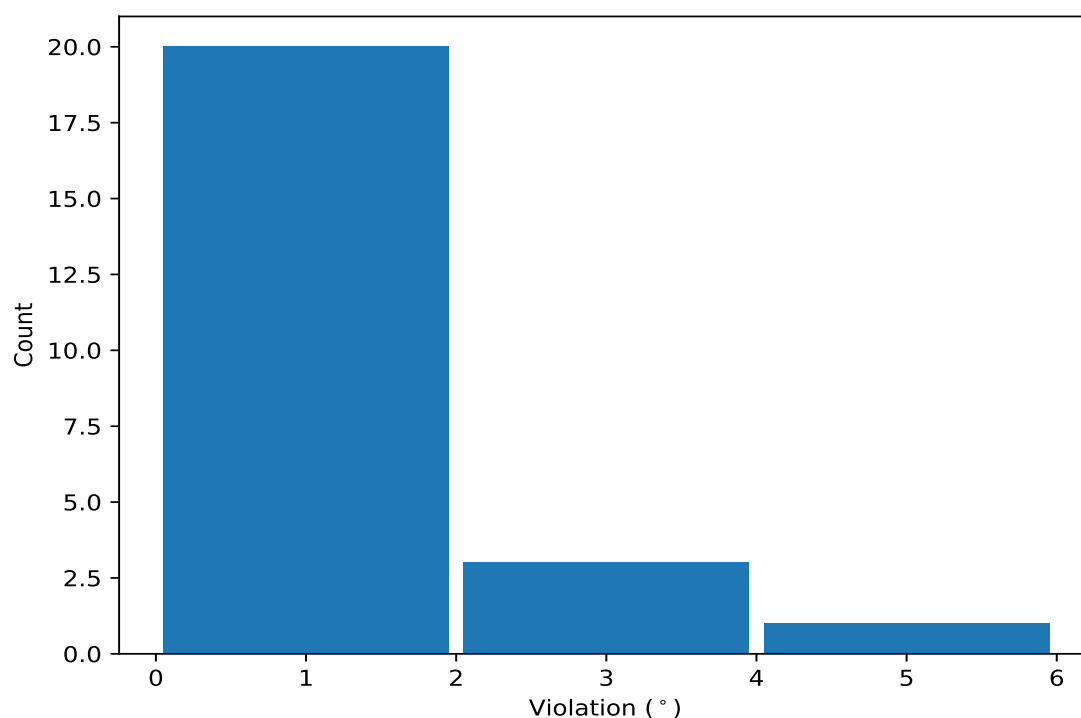
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,9)	1:7:A:ASP:C	1:8:A:TYR:N	1:8:A:TYR:CA	1:8:A:TYR:C	5	1.35	0.26	1.25
(1,2)	1:3:A:PRO:N	1:3:A:PRO:CA	1:3:A:PRO:C	1:4:A:TYR:N	3	1.73	0.54	1.7
(1,12)	1:9:A:CYS:N	1:9:A:CYS:CA	1:9:A:CYS:C	1:10:A:GLY:N	3	1.44	0.27	1.49
(1,1)	1:2:A:LYS:C	1:3:A:PRO:N	1:3:A:PRO:CA	1:3:A:PRO:C	3	1.15	0.1	1.19
(1,43)	1:25:A:THR:N	1:25:A:THR:CA	1:25:A:THR:C	1:26:A:HIS:N	2	3.14	1.0	3.14
(1,8)	1:7:A:ASP:N	1:7:A:ASP:CA	1:7:A:ASP:C	1:8:A:TYR:N	2	1.92	0.21	1.92
(1,31)	1:19:A:LYS:N	1:19:A:LYS:CA	1:19:A:LYS:C	1:20:A:MET:N	2	1.37	0.2	1.37

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 (°)
(1,43)	1:25:A:THR:N	1:25:A:THR:CA	1:25:A:THR:C	1:26:A:HIS:N	20	4.14
(1,2)	1:3:A:PRO:N	1:3:A:PRO:CA	1:3:A:PRO:C	1:4:A:TYR:N	13	2.4
(1,43)	1:25:A:THR:N	1:25:A:THR:CA	1:25:A:THR:C	1:26:A:HIS:N	14	2.14
(1,8)	1:7:A:ASP:N	1:7:A:ASP:CA	1:7:A:ASP:C	1:8:A:TYR:N	7	2.13
(1,45)	1:26:A:HIS:N	1:26:A:HIS:CA	1:26:A:HIS:C	1:27:A:ASP:N	14	1.92
(1,12)	1:9:A:CYS:N	1:9:A:CYS:CA	1:9:A:CYS:C	1:10:A:GLY:N	13	1.75
(1,9)	1:7:A:ASP:C	1:8:A:TYR:N	1:8:A:TYR:CA	1:8:A:TYR:C	2	1.72
(1,8)	1:7:A:ASP:N	1:7:A:ASP:CA	1:7:A:ASP:C	1:8:A:TYR:N	11	1.71
(1,2)	1:3:A:PRO:N	1:3:A:PRO:CA	1:3:A:PRO:C	1:4:A:TYR:N	8	1.7
(1,16)	1:11:A:ARG:N	1:11:A:ARG:CA	1:11:A:ARG:C	1:12:A:SER:N	1	1.65
(1,9)	1:7:A:ASP:C	1:8:A:TYR:N	1:8:A:TYR:CA	1:8:A:TYR:C	3	1.58
(1,31)	1:19:A:LYS:N	1:19:A:LYS:CA	1:19:A:LYS:C	1:20:A:MET:N	3	1.57
(1,12)	1:9:A:CYS:N	1:9:A:CYS:CA	1:9:A:CYS:C	1:10:A:GLY:N	8	1.49
(1,4)	1:5:A:GLN:N	1:5:A:GLN:CA	1:5:A:GLN:C	1:6:A:CYS:N	5	1.42
(1,50)	1:19:A:LYS:N	1:19:A:LYS:CA	1:19:A:LYS:CB	1:19:A:LYS:CG	16	1.29
(1,9)	1:7:A:ASP:C	1:8:A:TYR:N	1:8:A:TYR:CA	1:8:A:TYR:C	6	1.25
(1,1)	1:2:A:LYS:C	1:3:A:PRO:N	1:3:A:PRO:CA	1:3:A:PRO:C	2	1.25
(1,1)	1:2:A:LYS:C	1:3:A:PRO:N	1:3:A:PRO:CA	1:3:A:PRO:C	8	1.19
(1,31)	1:19:A:LYS:N	1:19:A:LYS:CA	1:19:A:LYS:C	1:20:A:MET:N	9	1.17
(1,9)	1:7:A:ASP:C	1:8:A:TYR:N	1:8:A:TYR:CA	1:8:A:TYR:C	16	1.11
(1,12)	1:9:A:CYS:N	1:9:A:CYS:CA	1:9:A:CYS:C	1:10:A:GLY:N	17	1.09

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,2)	1:3:A:PRO:N	1:3:A:PRO:CA	1:3:A:PRO:C	1:4:A:TYR:N	11	1.08
(1,9)	1:7:A:ASP:C	1:8:A:TYR:N	1:8:A:TYR:CA	1:8:A:TYR:C	9	1.07
(1,1)	1:2:A:LYS:C	1:3:A:PRO:N	1:3:A:PRO:CA	1:3:A:PRO:C	19	1.01