Full wwPDB NMR Structure Validation Report (i)

Jun 5, 2023 – 04:45 PM EDT

PDB ID	:	2M8J
BMRB ID	:	19259
Title	:	Structure of Pin1 WW domain phospho-mimic S16E
Authors	:	Luh, L.M.; Kirchner, D.K.; Loehr, F.; Haensel, R.; Doetsch, V.
Deposited on	:	2013-05-22

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

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

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

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

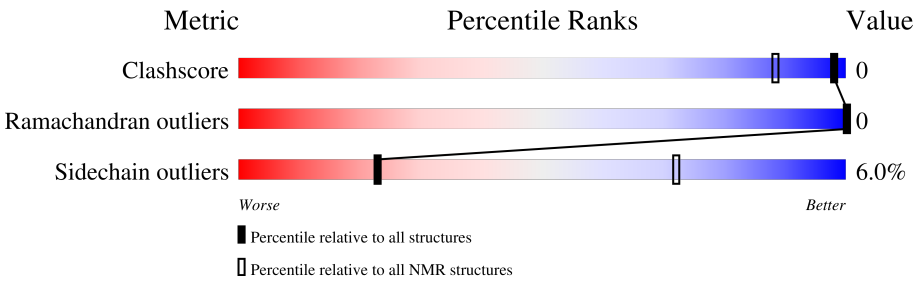
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal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

1 Overall quality at a glance (i)

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

The overall completeness of chemical shifts assignment is 84%.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	43	77% 23%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 1 is the overall representative, medoid model (most similar to other models).

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:10-A:42 (33)	0.24	1

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

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

The models can be grouped into 4 clusters and 1 single-model cluster was found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 686 atoms, of which 329 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	43	686	222	329	66	67	2	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP Q13526
A	2	LEU	-	expression tag	UNP Q13526
A	3	GLU	-	expression tag	UNP Q13526
A	4	HIS	-	expression tag	UNP Q13526
A	20	GLU	SER	engineered mutation	UNP Q13526

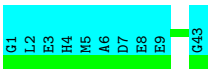
4 Residue-property plots (i)

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: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

Chain A:



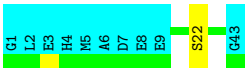
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1 (medoid)

• Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

Chain A:



4.2.2 Score per residue for model 2

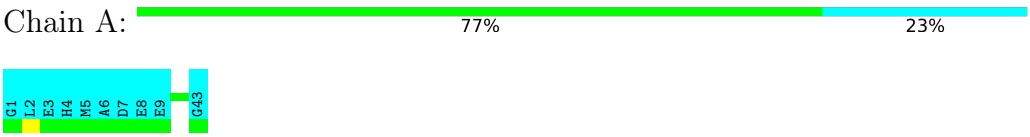
• Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

Chain A:

4.2.3 Score per residue for model 3

• Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

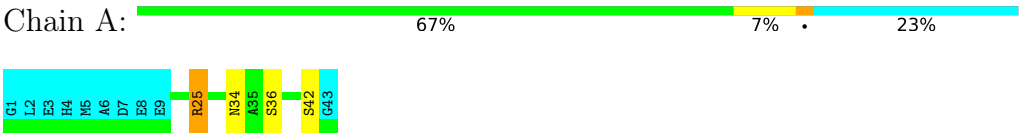
Chain A:



4.2.4 Score per residue for model 4

• Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

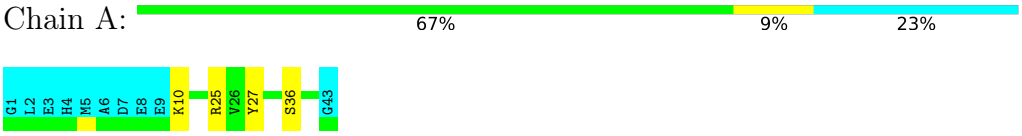
Chain A:



4.2.5 Score per residue for model 5

• Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

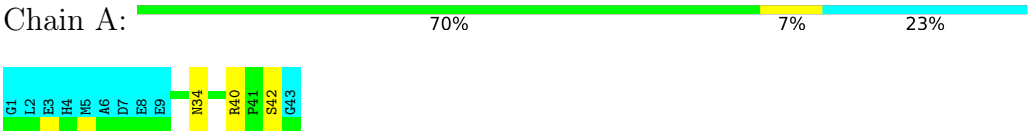
Chain A:



4.2.6 Score per residue for model 6

• Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

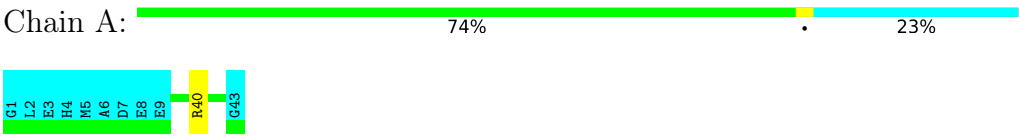
Chain A:



4.2.7 Score per residue for model 7

• Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

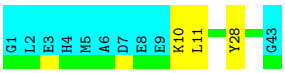
Chain A:



4.2.8 Score per residue for model 8

• Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

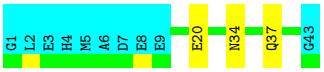
Chain A: 70% 7% 23%



4.2.9 Score per residue for model 9

• Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

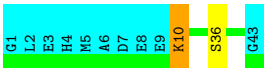
Chain A: 70% 7% 23%



4.2.10 Score per residue for model 10

• Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

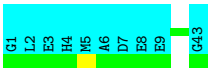
Chain A: 72% • • 23%



4.2.11 Score per residue for model 11

• Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

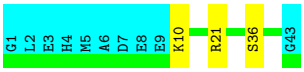
Chain A: 77% 23%



4.2.12 Score per residue for model 12

• Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

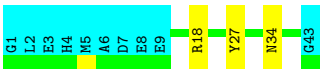
Chain A: 70% 7% 23%



4.2.13 Score per residue for model 13

• Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

Chain A: 70% 7% 23%



4.2.14 Score per residue for model 14

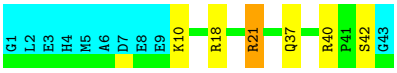
• Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

Chain A: 72% 5% 23%

4.2.15 Score per residue for model 15

• Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

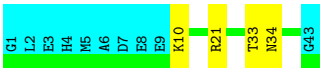
Chain A: 63% 12% • 23%



4.2.16 Score per residue for model 16

• Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

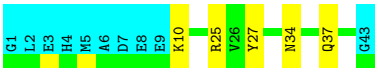
Chain A: 67% 9% 23%



4.2.17 Score per residue for model 17

• Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

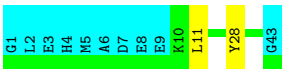
Chain A: 65% 12% 23%



4.2.18 Score per residue for model 18

• Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

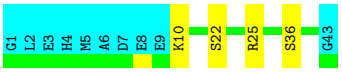
Chain A: 72% 5% 23%



4.2.19 Score per residue for model 19

• Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

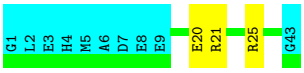
Chain A: 67% 9% 23%



4.2.20 Score per residue for model 20

• Molecule 1: Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1

Chain A: 70% 7% 23%



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *torsion angle dynamics*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
CYANA	structure solution	
TALOS	geometry optimization	
OPAL	refinement	
CYANA	refinement	

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	496
Number of shifts mapped to atoms	496
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	84%

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	0.66±0.01	0±0/294 (0.0± 0.0%)	1.06±0.05	0±1/398 (0.1± 0.2%)
All	All	0.66	0/5880 (0.0%)	1.06	8/7960 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	0.4±0.6
All	All	0	8

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(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	25	ARG	NE-CZ-NH1	7.34	123.97	120.30	19	1
1	A	25	ARG	NE-CZ-NH2	-6.83	116.88	120.30	19	2
1	A	21	ARG	NE-CZ-NH2	-5.71	117.45	120.30	15	2
1	A	18	ARG	NE-CZ-NH1	5.38	122.99	120.30	13	1
1	A	18	ARG	CD-NE-CZ	5.07	130.70	123.60	15	1
1	A	40	ARG	NE-CZ-NH2	-5.04	117.78	120.30	6	1

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	27	TYR	Sidechain	3
1	A	25	ARG	Sidechain	2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group	Models (Total)
1	A	21	ARG	Sidechain	2
1	A	40	ARG	Sidechain	1

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	283	269	269	0±0
All	All	5660	5380	5380	3

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 0.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:10:LYS:HA	1:A:10:LYS:HE3	0.46	1.87	10	1
1:A:11:LEU:HD11	1:A:28:TYR:CD1	0.45	2.47	18	2

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	33/43 (77%)	31±1 (94±3%)	2±1 (6±3%)	0±0 (0±0%)	100	100
All	All	660/860 (77%)	623 (94%)	37 (6%)	0 (0%)	100	100

There are no Ramachandran outliers.

6.3.2 Protein sidechains (i)

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	30/37 (81%)	28±1 (94±4%)	2±1 (6±4%)	23	72
All	All	600/740 (81%)	564 (94%)	36 (6%)	23	72

All 11 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	10	LYS	8
1	A	34	ASN	6
1	A	36	SER	5
1	A	37	GLN	4
1	A	25	ARG	3
1	A	42	SER	3
1	A	22	SER	2
1	A	20	GLU	2
1	A	40	ARG	1
1	A	21	ARG	1
1	A	33	THR	1

6.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates (i)

There are no monosaccharides in this entry.

6.6 Ligand geometry (i)

There are no ligands in this entry.

6.7 Other polymers (i)

There are no such molecules in this entry.

6.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

7 Chemical shift validation (i)

The completeness of assignment taking into account all chemical shift lists is 84% for the well-defined parts and 84% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping (i)

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

Total number of shifts	496
Number of shifts mapped to atoms	496
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	3

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	42	0.11 ± 0.10	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	39	-0.11 ± 0.18	None needed (< 0.5 ppm)
$^{13}C'$	39	0.15 ± 0.17	None needed (< 0.5 ppm)
^{15}N	37	-1.16 ± 0.61	None needed (imprecise)

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 84%, i.e. 401 atoms were assigned a chemical shift out of a possible 476. 0 out of 2 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	156/161 (97%)	64/65 (98%)	63/66 (95%)	29/30 (97%)
Sidechain	197/256 (77%)	132/163 (81%)	65/76 (86%)	0/17 (0%)

Continued on next page...

Continued from previous page...

	Total	^{1}H	^{13}C	^{15}N
Aromatic	48/59 (81%)	27/29 (93%)	19/27 (70%)	2/3 (67%)
Overall	401/476 (84%)	223/257 (87%)	147/169 (87%)	31/50 (62%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 84%, i.e. 495 atoms were assigned a chemical shift out of a possible 590. 0 out of 3 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	200/213 (94%)	82/87 (94%)	81/86 (94%)	37/40 (92%)
Sidechain	244/311 (78%)	164/198 (83%)	80/96 (83%)	0/17 (0%)
Aromatic	51/66 (77%)	29/33 (88%)	20/29 (69%)	2/4 (50%)
Overall	495/590 (84%)	275/318 (86%)	181/211 (86%)	39/61 (64%)

7.1.4 Statistically unusual chemical shifts (i)

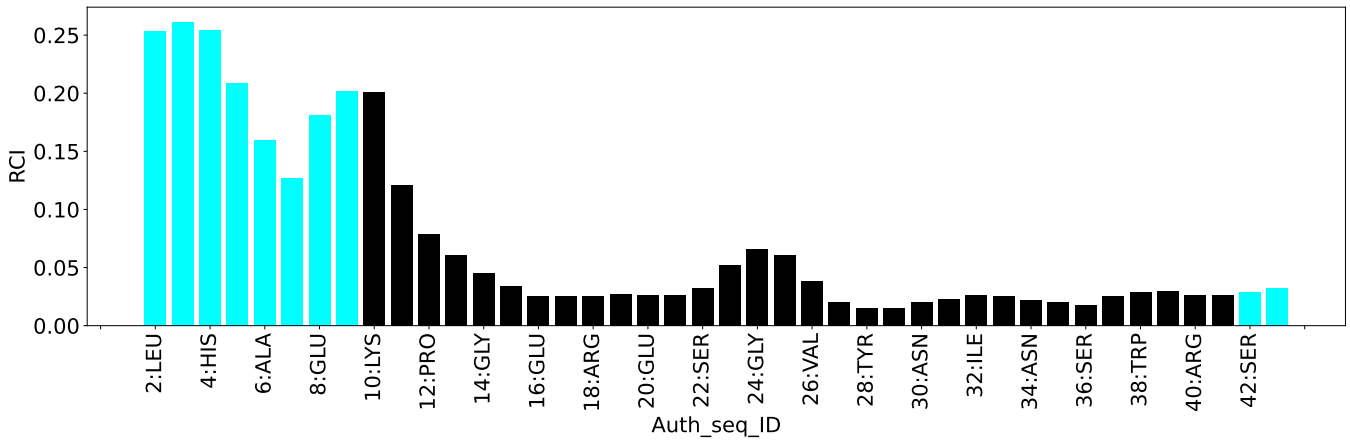
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	30	ASN	HB3	-0.62	1.12 – 4.38	-10.3
1	A	18	ARG	HB3	0.09	0.43 – 3.11	-6.3
1	A	41	PRO	HG3	-0.07	0.33 – 3.48	-6.3

7.1.5 Random Coil Index (RCI) plots (i)

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

Random coil index (RCI) for chain A:


RCI
0.25
0.20
0.15
0.10
0.05
0.00
2:LEU
4:HIS
6:ALA
8:GLU
10:LYS
12:PRO
14:GLY
16:GLU
18:ARG
20:GLU
22:SER
24:GLY
26:VAL
28:TYR
30:ASN
32:ILE
34:ASN
36:SER
38:TRP
40:ARG
42:SER
Auth_seq_ID

8 NMR restraints analysis (i)

8.1 Conformationally restricting restraints (i)

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

Description	Value
Total distance restraints	837
Intra-residue (|i-j|=0)	139
Sequential (|i-j|=1)	251
Medium range (|i-j|>1 and |i-j|<5)	108
Long range (|i-j|≥5)	339
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	19.5
Number of long range restraints per residue[1]	7.9

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

8.2 Residual restraint violations (i)

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

8.2.1 Average number of distance violations per model (i)

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

Bins (Å)	Average number of violations per model	Max (Å)
0.1-0.2 (Small)	0.1	0.11
0.2-0.5 (Medium)	None	None
>0.5 (Large)	None	None

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

Dihedral-angle violations less than 1° are not included in the calculation.There are no dihedral-angle violations

9 Distance violation analysis (i)

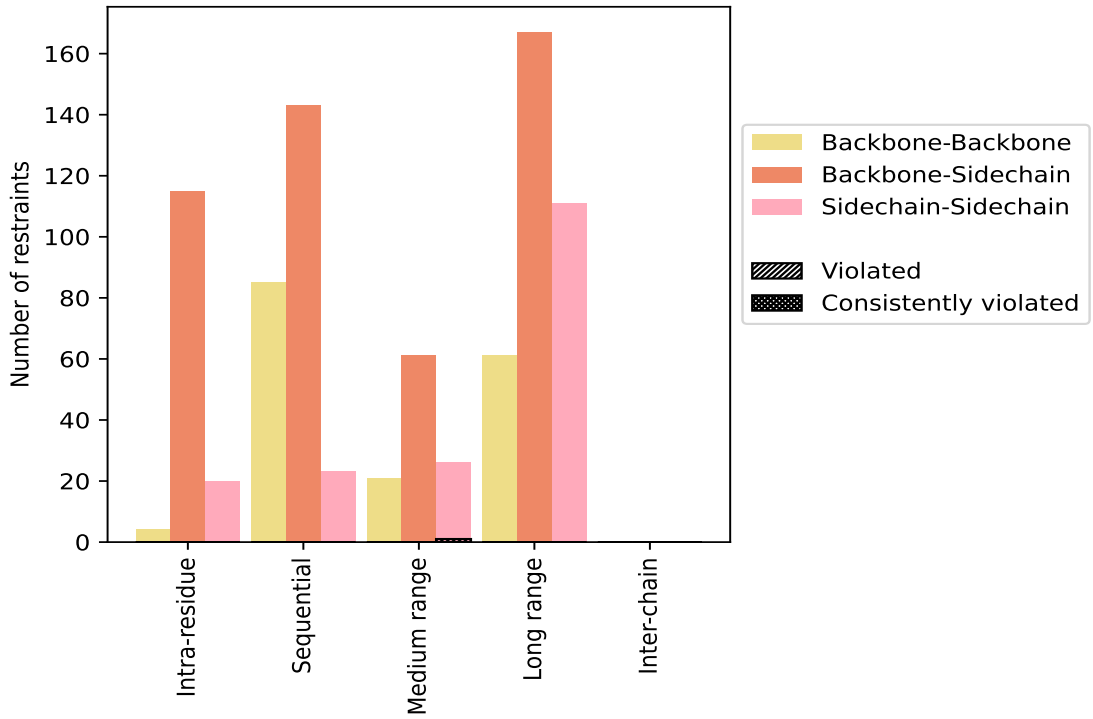
9.1 Summary of distance violations (i)

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

Restraints type	Count	%[1]	Violated[3]			Consistently Violated[4]		
			Count	%[2]	%[1]	Count	%[2]	%[1]
Intra-residue (|i-j|=0)	139	16.6	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	4	0.5	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	115	13.7	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	20	2.4	0	0.0	0.0	0	0.0	0.0
Sequential (|i-j|=1)	251	30.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	85	10.2	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	143	17.1	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	23	2.7	0	0.0	0.0	0	0.0	0.0
Medium range (|i-j|>1 & |i-j|<5)	108	12.9	1	0.9	0.1	0	0.0	0.0
Backbone-Backbone	21	2.5	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	61	7.3	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	26	3.1	1	3.8	0.1	0	0.0	0.0
Long range (|i-j|≥5)	339	40.5	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	61	7.3	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	167	20.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	111	13.3	0	0.0	0.0	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	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	837	100.0	1	0.1	0.1	0	0.0	0.0
Backbone-Backbone	171	20.4	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	486	58.1	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	180	21.5	1	0.6	0.1	0	0.0	0.0

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

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



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

9.2 Distance violation statistics for each model (i)

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

Model ID	Number of violations						Mean (Å)	Max (Å)	SD[6] (Å)	Median (Å)
	IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total				
1	0	0	0	0	0	0	0.0	0.0	0.0	0.0
2	0	0	0	0	0	0	0.0	0.0	0.0	0.0
3	0	0	0	0	0	0	0.0	0.0	0.0	0.0
4	0	0	0	0	0	0	0.0	0.0	0.0	0.0
5	0	0	0	0	0	0	0.0	0.0	0.0	0.0
6	0	0	0	0	0	0	0.0	0.0	0.0	0.0
7	0	0	0	0	0	0	0.0	0.0	0.0	0.0
8	0	0	0	0	0	0	0.0	0.0	0.0	0.0
9	0	0	0	0	0	0	0.0	0.0	0.0	0.0
10	0	0	0	0	0	0	0.0	0.0	0.0	0.0
11	0	0	1	0	0	1	0.11	0.11	0.0	0.11

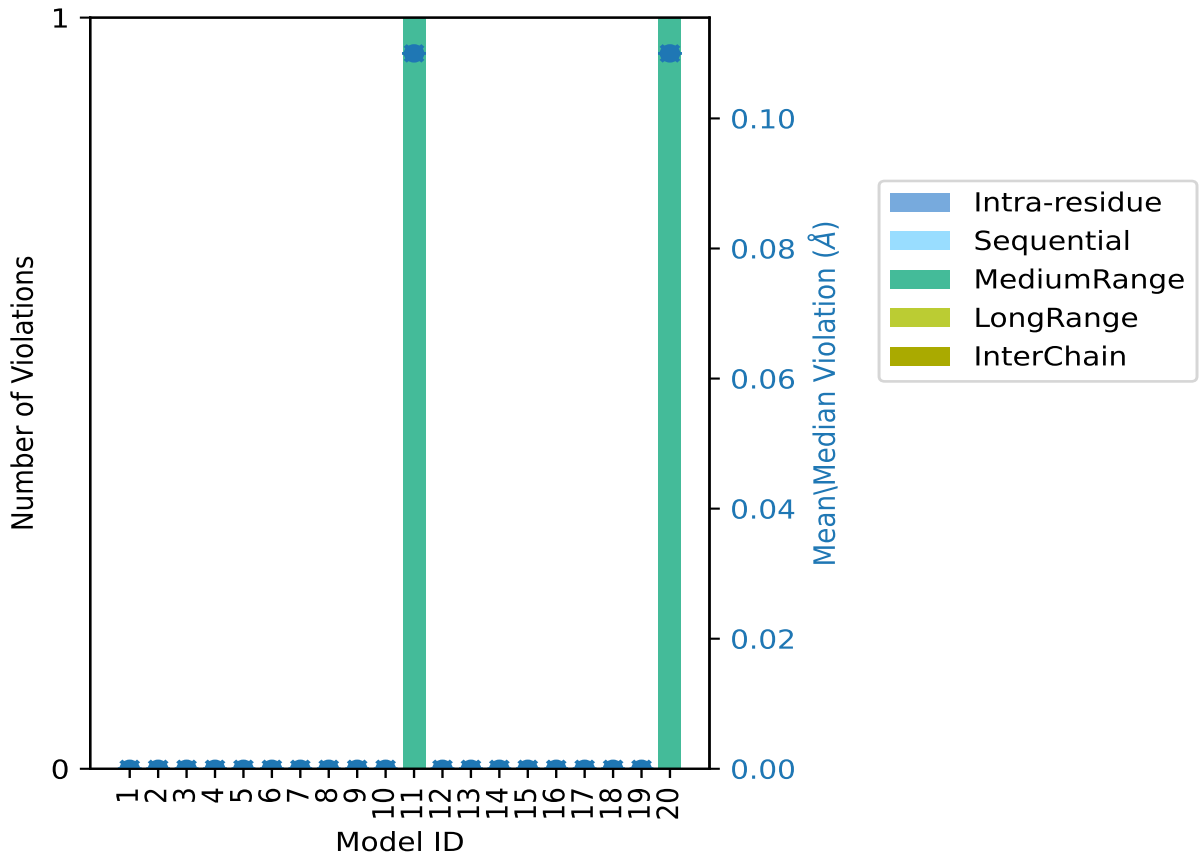
Continued on next page...

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				
12	0	0	0	0	0	0	0.0	0.0	0.0	0.0
13	0	0	0	0	0	0	0.0	0.0	0.0	0.0
14	0	0	0	0	0	0	0.0	0.0	0.0	0.0
15	0	0	0	0	0	0	0.0	0.0	0.0	0.0
16	0	0	0	0	0	0	0.0	0.0	0.0	0.0
17	0	0	0	0	0	0	0.0	0.0	0.0	0.0
18	0	0	0	0	0	0	0.0	0.0	0.0	0.0
19	0	0	0	0	0	0	0.0	0.0	0.0	0.0
20	0	0	1	0	0	1	0.11	0.11	0.0	0.11

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

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



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

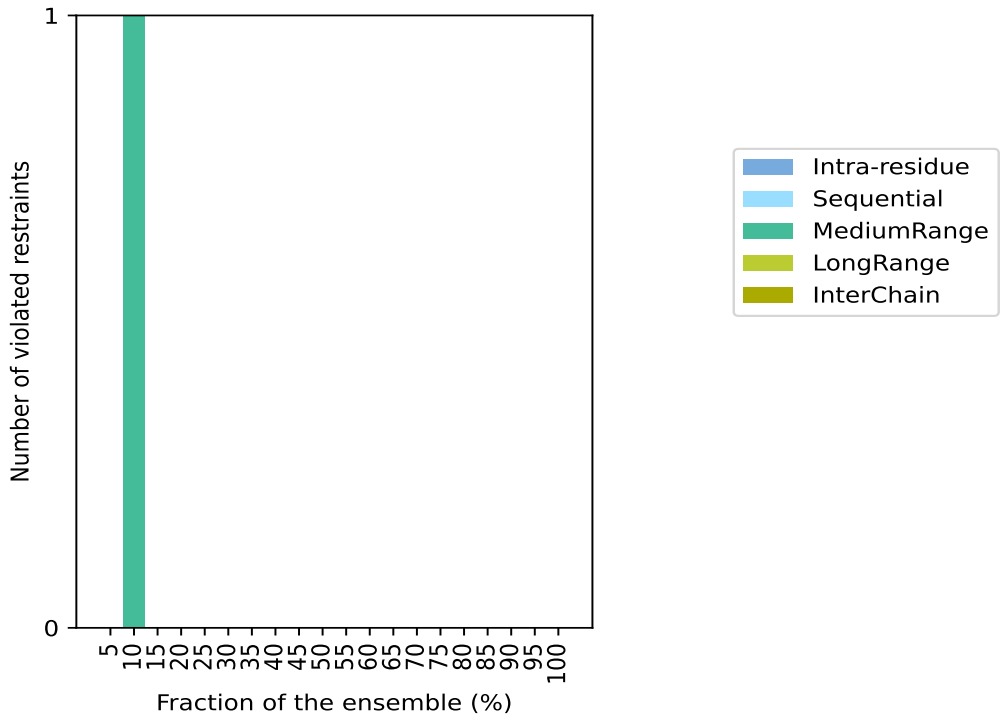
9.3 Distance violation statistics for the ensemble (i)

Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 836(IR:139, SQ:251, MR:107, LR:339, 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	0	0	0	0	1	5.0
0	0	1	0	0	1	2	10.0
0	0	0	0	0	0	3	15.0
0	0	0	0	0	0	4	20.0
0	0	0	0	0	0	5	25.0
0	0	0	0	0	0	6	30.0
0	0	0	0	0	0	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	0	0	0	0	12	60.0
0	0	0	0	0	0	13	65.0
0	0	0	0	0	0	14	70.0
0	0	0	0	0	0	15	75.0
0	0	0	0	0	0	16	80.0
0	0	0	0	0	0	17	85.0
0	0	0	0	0	0	18	90.0
0	0	0	0	0	0	19	95.0
0	0	0	0	0	0	20	100.0

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

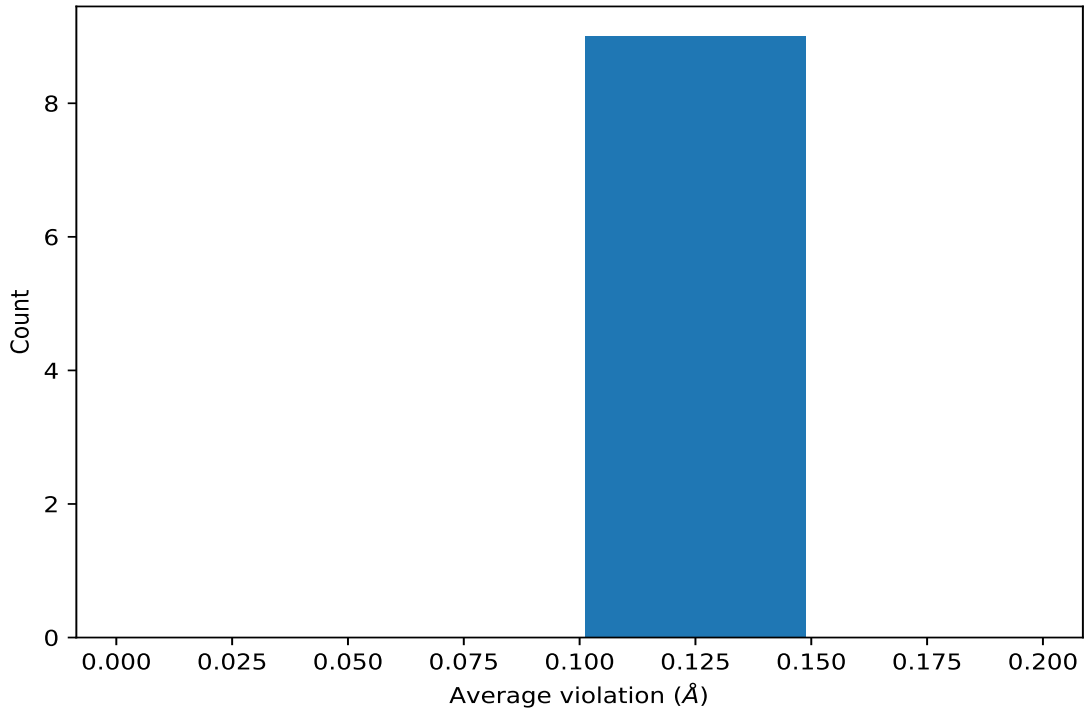
9.3.1 Bar graph : Distance violation statistics for the ensemble (i)



9.4 Most violated distance restraints in the ensemble (i)

9.4.1 Histogram : Distribution of mean distance violations (i)

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



9.4.2 Table: Most violated distance restraints (i)

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

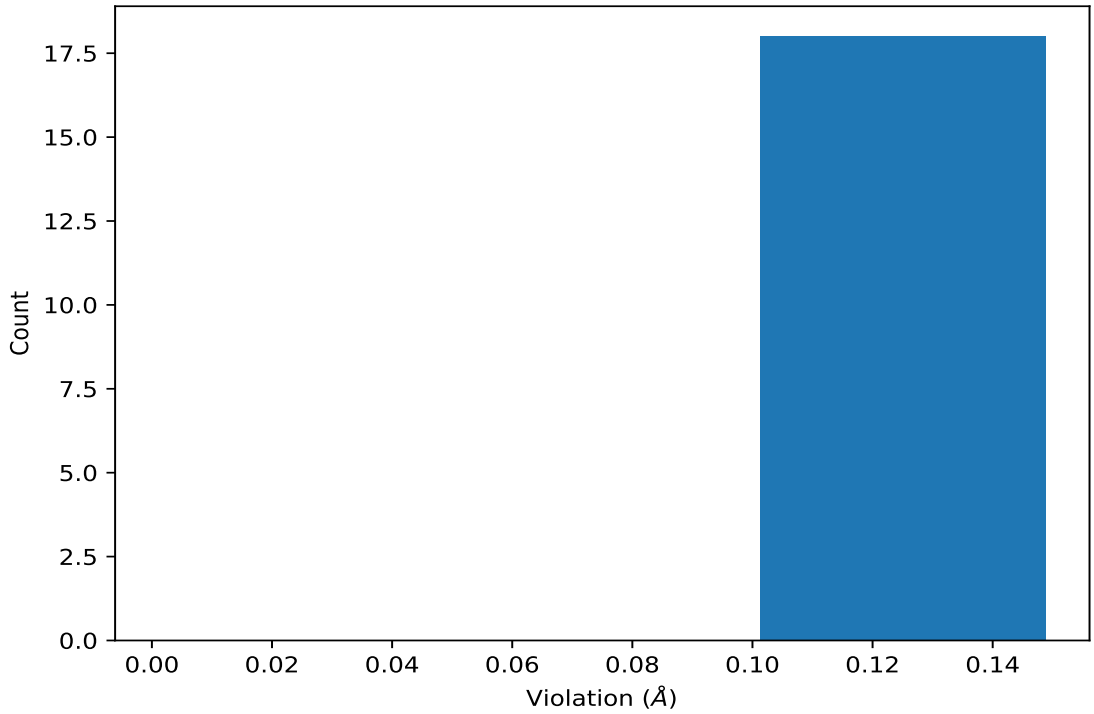
Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(1,32)	1:A:32:ILE:HG21	1:A:35:ALA:HB1	2	0.11	0.0	0.11
(1,32)	1:A:32:ILE:HG21	1:A:35:ALA:HB2	2	0.11	0.0	0.11
(1,32)	1:A:32:ILE:HG21	1:A:35:ALA:HB3	2	0.11	0.0	0.11
(1,32)	1:A:32:ILE:HG22	1:A:35:ALA:HB1	2	0.11	0.0	0.11
(1,32)	1:A:32:ILE:HG22	1:A:35:ALA:HB2	2	0.11	0.0	0.11
(1,32)	1:A:32:ILE:HG22	1:A:35:ALA:HB3	2	0.11	0.0	0.11
(1,32)	1:A:32:ILE:HG23	1:A:35:ALA:HB1	2	0.11	0.0	0.11
(1,32)	1:A:32:ILE:HG23	1:A:35:ALA:HB2	2	0.11	0.0	0.11
(1,32)	1:A:32:ILE:HG23	1:A:35:ALA:HB3	2	0.11	0.0	0.11

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

9.5 All violated distance restraints (i)

9.5.1 Histogram : Distribution of distance violations (i)

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



9.5.2 Table : All distance violations (i)

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

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,32)	1:A:32:ILE:HG21	1:A:35:ALA:HB1	11	0.11
(1,32)	1:A:32:ILE:HG21	1:A:35:ALA:HB2	11	0.11
(1,32)	1:A:32:ILE:HG21	1:A:35:ALA:HB3	11	0.11
(1,32)	1:A:32:ILE:HG22	1:A:35:ALA:HB1	11	0.11
(1,32)	1:A:32:ILE:HG22	1:A:35:ALA:HB2	11	0.11
(1,32)	1:A:32:ILE:HG22	1:A:35:ALA:HB3	11	0.11
(1,32)	1:A:32:ILE:HG23	1:A:35:ALA:HB1	11	0.11
(1,32)	1:A:32:ILE:HG23	1:A:35:ALA:HB2	11	0.11
(1,32)	1:A:32:ILE:HG23	1:A:35:ALA:HB3	11	0.11
(1,32)	1:A:32:ILE:HG21	1:A:35:ALA:HB1	20	0.11

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,32)	1:A:32:ILE:HG21	1:A:35:ALA:HB2	20	0.11
(1,32)	1:A:32:ILE:HG21	1:A:35:ALA:HB3	20	0.11
(1,32)	1:A:32:ILE:HG22	1:A:35:ALA:HB1	20	0.11
(1,32)	1:A:32:ILE:HG22	1:A:35:ALA:HB2	20	0.11
(1,32)	1:A:32:ILE:HG22	1:A:35:ALA:HB3	20	0.11
(1,32)	1:A:32:ILE:HG23	1:A:35:ALA:HB1	20	0.11
(1,32)	1:A:32:ILE:HG23	1:A:35:ALA:HB2	20	0.11
(1,32)	1:A:32:ILE:HG23	1:A:35:ALA:HB3	20	0.11

10 Dihedral-angle violation analysis (i)

Dihedral angle analysis failed due to data error in the dihedral angle restraints, possibly missing target value