



Full wwPDB NMR Structure Validation Report ⓘ

Jun 29, 2026 – 11:22 am BST

PDB ID : 9RLN / pdb_00009rln
BMRB ID : 35001
Title : Synthetic chimeric inhibitor peptide of the AuroraA kinase/N-Myc complex - SCPmod
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Deposited on : 2025-06-17

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) : 2.50

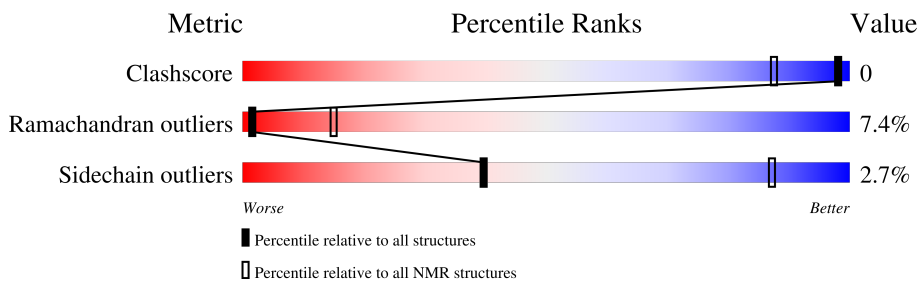
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

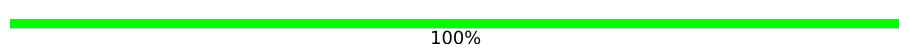
The overall completeness of chemical shifts assignment is 64%.

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	19	 100%

2 Ensemble composition and analysis

This entry contains 20 models.

Cyrange was unable to find well-defined residues.

Error message: Only domains with < 8 residues could be identified.

NmrClust was unable to cluster the ensemble.

Error message: Wrapper check: not enough residues in core to run NmrClust

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 284 atoms, of which 141 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called SCPmod.

Mol	Chain	Residues	Atoms					Trace
			Total	C	H	N	O	
1	A	19	284	83	141	31	29	0

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

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

- Molecule 1: SCPmod

Chain A:  100%

There are no outlier residues in this chain.

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: SCPmod

Chain A:  95% 5%



4.2.2 Score per residue for model 2


- Molecule 1: SCPmod

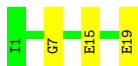
Chain A:  79% 21%



4.2.3 Score per residue for model 3

- Molecule 1: SCPmod

Chain A:  84% 16%



4.2.4 Score per residue for model 4

- Molecule 1: SCPmod

Chain A:  95% 5%



4.2.5 Score per residue for model 5

- Molecule 1: SCPmod

Chain A:  89% 11%



4.2.6 Score per residue for model 6

- Molecule 1: SCPmod

Chain A:  100%

There are no outlier residues in this chain.

4.2.7 Score per residue for model 7

- Molecule 1: SCPmod

Chain A:  95% 5%



4.2.8 Score per residue for model 8


- Molecule 1: SCPmod

Chain A:  100%

There are no outlier residues in this chain.

4.2.9 Score per residue for model 9

- Molecule 1: SCPmod

Chain A:  79% 21%



4.2.10 Score per residue for model 10


- Molecule 1: SCPmod

Chain A:  95% 5%



4.2.11 Score per residue for model 11

- Molecule 1: SCPmod

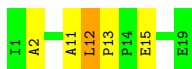
Chain A:  89% 11%



4.2.12 Score per residue for model 12

- Molecule 1: SCPmod

Chain A:  74% 21% 5%



4.2.13 Score per residue for model 13

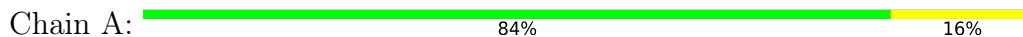
- Molecule 1: SCPmod

Chain A:  89% 11%



4.2.14 Score per residue for model 14

- Molecule 1: SCPmod



4.2.15 Score per residue for model 15

- Molecule 1: SCPmod



There are no outlier residues in this chain.

4.2.16 Score per residue for model 16

- Molecule 1: SCPmod



4.2.17 Score per residue for model 17

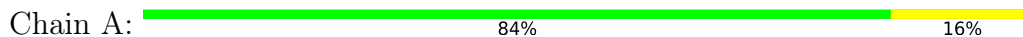
- Molecule 1: SCPmod



There are no outlier residues in this chain.


4.2.18 Score per residue for model 18

- Molecule 1: SCPmod



4.2.19 Score per residue for model 19


- Molecule 1: SCPmod

Chain A:  84% 16%



4.2.20 Score per residue for model 20

- Molecule 1: SCPmod

Chain A:  89% 11%



5 Refinement protocol and experimental data overview

The models were refined using the following method: *Energy minimization with explicit water*.

Of the 500 calculated structures, 20 were deposited, based on the following criterion: *all calculated structures submitted*.

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

Software name	Classification	Version
CNS	refinement	
CYANA	structure calculation	

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	191
Number of shifts mapped to atoms	191
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	64%

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	1.22±0.05	0±0/145 (0.1± 0.2%)	0.94±0.06	0±0/193 (0.0± 0.0%)
All	All	1.22	2/2900 (0.1%)	0.94	0/3860 (0.0%)

All unique bond 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(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	13	PRO	CA-C	5.17	1.55	1.52	20	1
1	A	12	LEU	C-N	5.09	1.39	1.33	12	1

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	143	141	140	0±0
All	All	2860	2820	2800	2

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:12:LEU:HB3	1:A:13:PRO:HD2	0.42	1.92	12	1
1:A:13:PRO:HB2	1:A:16:SER:HB3	0.41	1.93	2	1

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	17/19 (89%)	12±1 (68±8%)	4±1 (25±8%)	1±1 (7±6%)	1	15
All	All	340/380 (89%)	230 (68%)	85 (25%)	25 (7%)	1	15

All 9 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	11	ALA	6
1	A	3	SER	5
1	A	5	ARG	4
1	A	15	GLU	3
1	A	7	GLY	2
1	A	14	PRO	2
1	A	18	HIS	1
1	A	2	ALA	1
1	A	4	GLY	1

6.3.2 Protein sidechains [i](#)

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	15/15 (100%)	15±1 (97±4%)	0±1 (3±4%)	40	87
All	All	300/300 (100%)	292 (97%)	8 (3%)	40	87

All 4 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	12	LEU	4
1	A	15	GLU	2
1	A	19	GLU	1
1	A	10	ASN	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation i

The completeness of assignment taking into account all chemical shift lists is 64% for the well-defined parts and 64% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *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	191
Number of shifts mapped to atoms	191
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	4

- Can not parse the chemical shift value. All 33 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	1	ILE	HG12	1.486	0.00	.
1	A	1	ILE	HG13	1.216	0.00	.
1	A	3	SER	HB3	3.851	0.02	.
1	A	5	ARG	HB2	1.743	0.01	.
1	A	5	ARG	HB3	1.867	0.03	.
1	A	8	ARG	HB2	1.734	0.01	.
1	A	8	ARG	HB3	1.815	0.00	.
1	A	9	ARG	HB2	1.735	0.00	.
1	A	9	ARG	HB3	1.815	0.00	.
1	A	10	ASN	HB2	2.733	0.03	.
1	A	10	ASN	HB3	2.778	0.03	.
1	A	10	ASN	HD21	7.618	0.00	.
1	A	10	ASN	HD22	6.917	0.00	.
1	A	12	LEU	CD1	25.214	0.00	.
1	A	12	LEU	CD2	23.302	0.00	.
1	A	13	PRO	HB2	2.338	0.00	.
1	A	13	PRO	HB3	1.902	0.01	.

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	13	PRO	HD2	3.841	0.00	.
1	A	13	PRO	HD3	3.610	0.00	.
1	A	13	PRO	HG2	2.018	0.00	.
1	A	14	PRO	HB2	2.281	0.00	.
1	A	14	PRO	HB3	1.899	0.01	.
1	A	14	PRO	HD2	3.786	0.00	.
1	A	14	PRO	HD3	3.629	0.01	.
1	A	14	PRO	HG2	2.014	0.00	.
1	A	15	GLU	HB2	1.982	0.00	.
1	A	15	GLU	HB3	2.097	0.01	.
1	A	16	SER	HB3	3.841	0.01	.
1	A	17	SER	HB3	3.839	0.01	.
1	A	18	HIS	HB2	3.265	0.04	.
1	A	18	HIS	HB3	3.208	0.03	.
1	A	19	GLU	HB2	1.927	0.01	.
1	A	19	GLU	HB3	2.142	0.01	.

7.1.2 Chemical shift referencing [i](#)

No chemical shift referencing corrections were calculated (not enough data).

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 64%, i.e. 158 atoms were assigned a chemical shift out of a possible 246. 0 out of 1 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	72/93 (77%)	37/38 (97%)	19/38 (50%)	16/17 (94%)
Sidechain	82/145 (57%)	45/93 (48%)	33/42 (79%)	4/10 (40%)
Aromatic	4/8 (50%)	2/4 (50%)	2/2 (100%)	0/2 (0%)
Overall	158/246 (64%)	84/135 (62%)	54/82 (66%)	20/29 (69%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 64%, i.e. 158 atoms were assigned a chemical shift out of a possible 246. 0 out of 1 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	72/93 (77%)	37/38 (97%)	19/38 (50%)	16/17 (94%)

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	Total	¹ H	¹³ C	¹⁵ N
Sidechain	82/145 (57%)	45/93 (48%)	33/42 (79%)	4/10 (40%)
Aromatic	4/8 (50%)	2/4 (50%)	2/2 (100%)	0/2 (0%)
Overall	158/246 (64%)	84/135 (62%)	54/82 (66%)	20/29 (69%)

7.1.4 Statistically unusual chemical shifts [i](#)

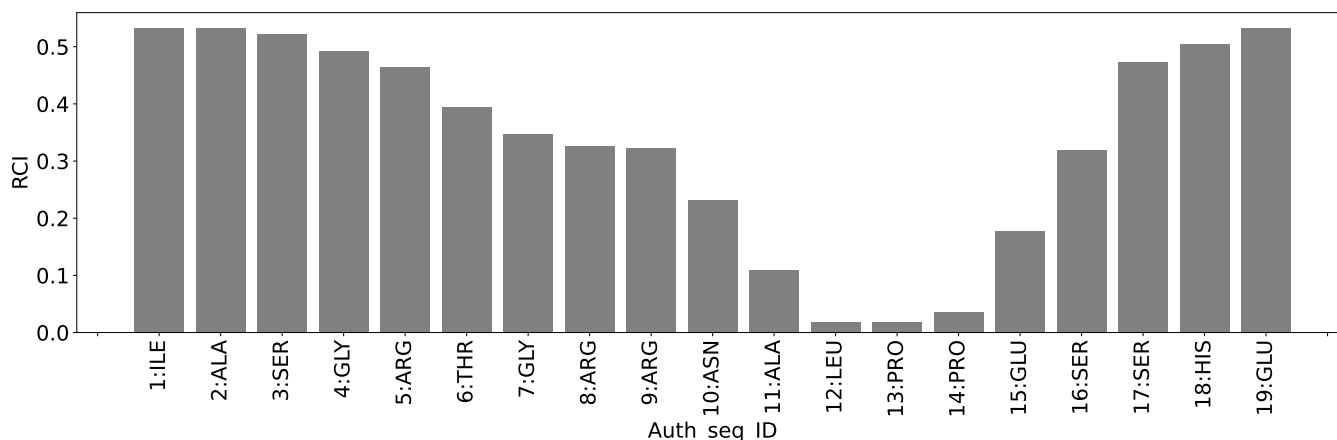
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	5	ARG	NE	119.61	76.53 – 92.65	21.7
1	A	8	ARG	NE	119.61	76.53 – 92.65	21.7
1	A	9	ARG	NE	119.61	76.53 – 92.65	21.7
1	A	12	LEU	N	65.70	102.77 – 140.89	-14.7

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

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

Random coil index (RCI) for chain A:



8 NMR restraints analysis

8.1 Conformationally restricting restraints

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

Description	Value
Total distance restraints	4
Intra-residue ($ i-j =0$)	4
Sequential ($ i-j =1$)	0
Medium range ($ i-j >1$ and $ i-j <5$)	0
Long range ($ i-j \geq 5$)	0
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	0.2
Number of long range restraints per residue ¹	0.0

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. There are no distance violations

8.2.2 Average number of dihedral-angle violations per model

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

9 Distance violation analysis [i](#)

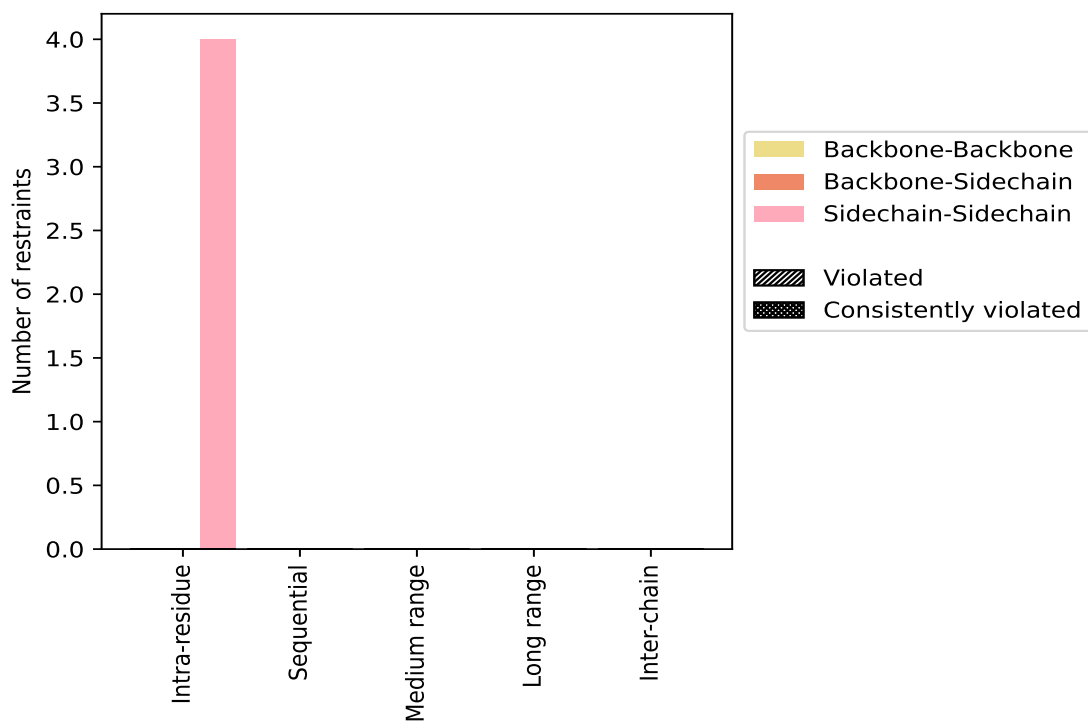
9.1 Summary of distance violations [i](#)

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.

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue (i-j =0)	4	100.0	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	4	100.0	0	0.0	0.0	0	0.0	0.0
Sequential (i-j =1)	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
Medium range (i-j >1 & i-j <5)	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
Long range (i-j ≥5)	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
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	4	100.0	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	4	100.0	0	0.0	0.0	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 disulfid bonds are counted in their appropriate category on the x-axis

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

No violations found

9.3 Distance violation statistics for the ensemble [i](#)

No violations found

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

No violations found

9.5 All violated distance restraints [i](#)

No violations found

10 Dihedral-angle violation analysis

No dihedral-angle restraints found