



Full wwPDB NMR Structure Validation Report ⓘ

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BMRB ID : 25229
Title : Solution Structure of the Human FAAP20 UBZ
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This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

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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

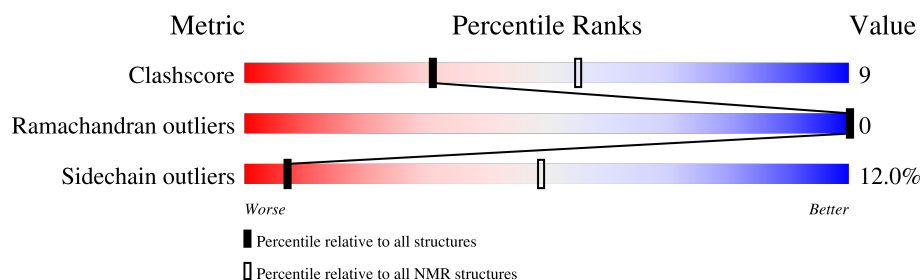
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 83%.

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	44	41% 20% 39%

2 Ensemble composition and analysis

This entry contains 10 models. Model 5 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:9-A:35 (27)	0.16	5

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

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

The models can be grouped into 2 clusters. No single-model clusters were found.

Cluster number	Models
1	1, 2, 3, 5, 7, 8, 9
2	4, 6, 10

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 653 atoms, of which 317 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Fanconi anemia-associated protein of 20 kDa.

Mol	Chain	Residues	Atoms						Trace
1	A	44	Total	C	H	N	O	S	0
			652	205	317	59	66	5	

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	-	expression tag	UNP Q6NZ36
A	2	HIS	-	expression tag	UNP Q6NZ36
A	3	MET	-	expression tag	UNP Q6NZ36

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

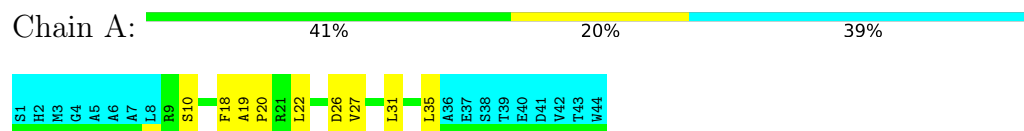
Mol	Chain	Residues	Atoms	
2	A	1	Total	Zn
			1	1

4 Residue-property plots

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: Fanconi anemia-associated protein of 20 kDa

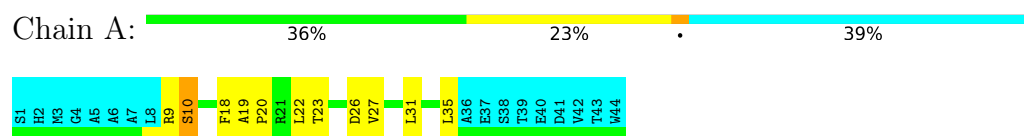


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

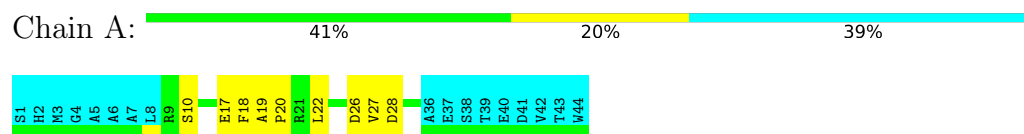
4.2.1 Score per residue for model 1

- Molecule 1: Fanconi anemia-associated protein of 20 kDa



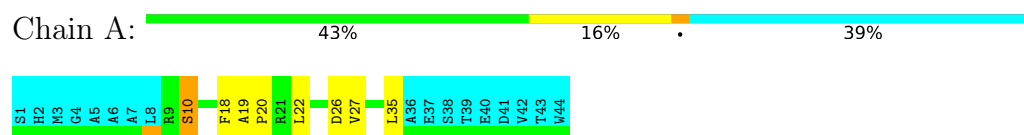
4.2.2 Score per residue for model 2

- Molecule 1: Fanconi anemia-associated protein of 20 kDa



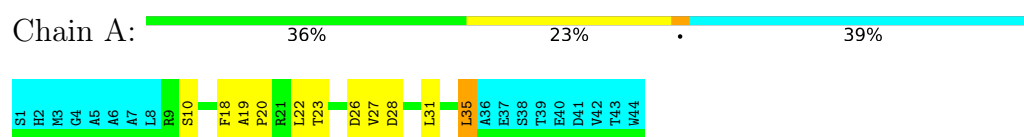
4.2.3 Score per residue for model 3

- Molecule 1: Fanconi anemia-associated protein of 20 kDa



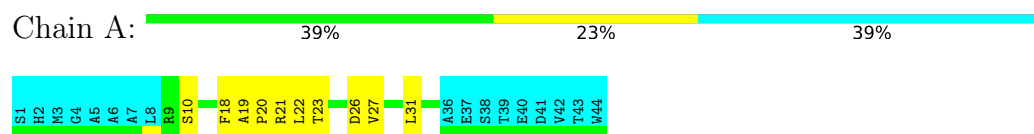
4.2.4 Score per residue for model 4

- Molecule 1: Fanconi anemia-associated protein of 20 kDa



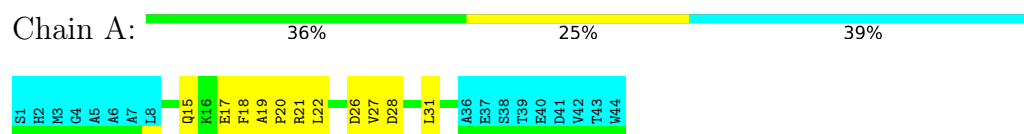
4.2.5 Score per residue for model 5 (medoid)

- Molecule 1: Fanconi anemia-associated protein of 20 kDa



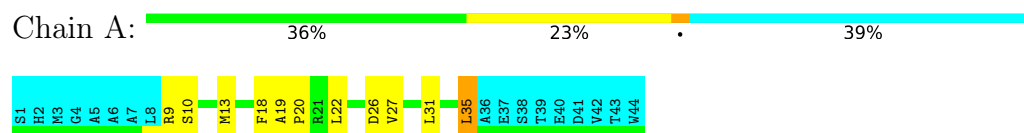
4.2.6 Score per residue for model 6

- Molecule 1: Fanconi anemia-associated protein of 20 kDa



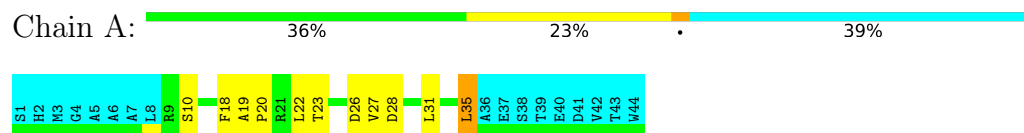
4.2.7 Score per residue for model 7

- Molecule 1: Fanconi anemia-associated protein of 20 kDa



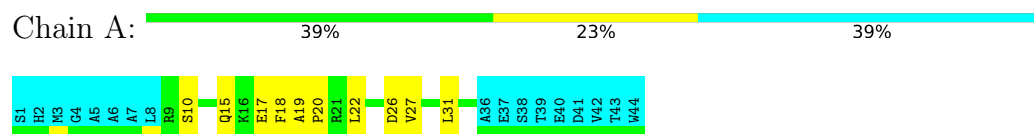
4.2.8 Score per residue for model 8

- Molecule 1: Fanconi anemia-associated protein of 20 kDa



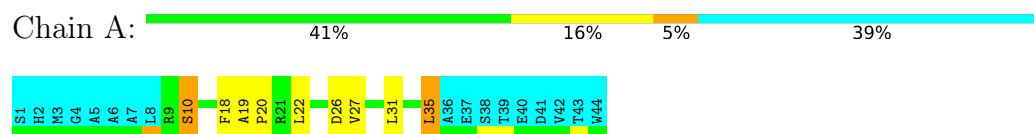
4.2.9 Score per residue for model 9

- Molecule 1: Fanconi anemia-associated protein of 20 kDa



4.2.10 Score per residue for model 10

- Molecule 1: Fanconi anemia-associated protein of 20 kDa



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 10 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
CYANA	refinement	
CYANA	structure solution	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	465
Number of shifts mapped to atoms	465
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	83%

6 Model quality

6.1 Standard geometry

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

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	212	208	208	4±1
All	All	2130	2080	2080	37

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 9.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:18:PHE:CE2	1:A:27:VAL:HG13	0.69	2.23	1	10
1:A:22:LEU:HD22	1:A:26:ASP:HB3	0.61	1.72	10	10
1:A:13:MET:HE1	1:A:31:LEU:HD22	0.54	1.78	7	1
1:A:19:ALA:HB1	1:A:21:ARG:HD3	0.47	1.87	6	1
1:A:27:VAL:HG12	1:A:31:LEU:CD1	0.47	2.40	7	1
1:A:31:LEU:O	1:A:35:LEU:HD23	0.46	2.11	4	4
1:A:19:ALA:HB1	1:A:20:PRO:HD2	0.43	1.90	10	10

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	27/44 (61%)	27±0 (100±0%)	0±0 (0±0%)	0±0 (0±0%)	100	100
All	All	270/440 (61%)	270 (100%)	0 (0%)	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	25/37 (68%)	22±1 (88±3%)	3±1 (12±3%)	7	49
All	All	250/370 (68%)	220 (88%)	30 (12%)	7	49

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	10	SER	8
1	A	35	LEU	6
1	A	23	THR	4
1	A	28	ASP	4
1	A	17	GLU	3
1	A	9	ARG	2
1	A	15	GLN	2
1	A	21	ARG	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 83% for the well-defined parts and 83% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping

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

Total number of shifts	465
Number of shifts mapped to atoms	465
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	43	-0.16 ± 0.24	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	42	0.14 ± 0.12	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	39	-0.90 ± 0.21	Should be applied

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 83%, i.e. 303 atoms were assigned a chemical shift out of a possible 367. 0 out of 5 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	104/131 (79%)	52/52 (100%)	27/54 (50%)	25/25 (100%)
Sidechain	185/219 (84%)	126/142 (89%)	59/67 (88%)	0/10 (0%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	14/17 (82%)	7/9 (78%)	7/7 (100%)	0/1 (0%)
Overall	303/367 (83%)	185/203 (91%)	93/128 (73%)	25/36 (69%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 83%, i.e. 465 atoms were assigned a chemical shift out of a possible 563. 0 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	165/217 (76%)	83/87 (95%)	43/88 (49%)	39/42 (93%)
Sidechain	270/310 (87%)	185/203 (91%)	85/97 (88%)	0/10 (0%)
Aromatic	30/36 (83%)	15/19 (79%)	14/14 (100%)	1/3 (33%)
Overall	465/563 (83%)	283/309 (92%)	142/199 (71%)	40/55 (73%)

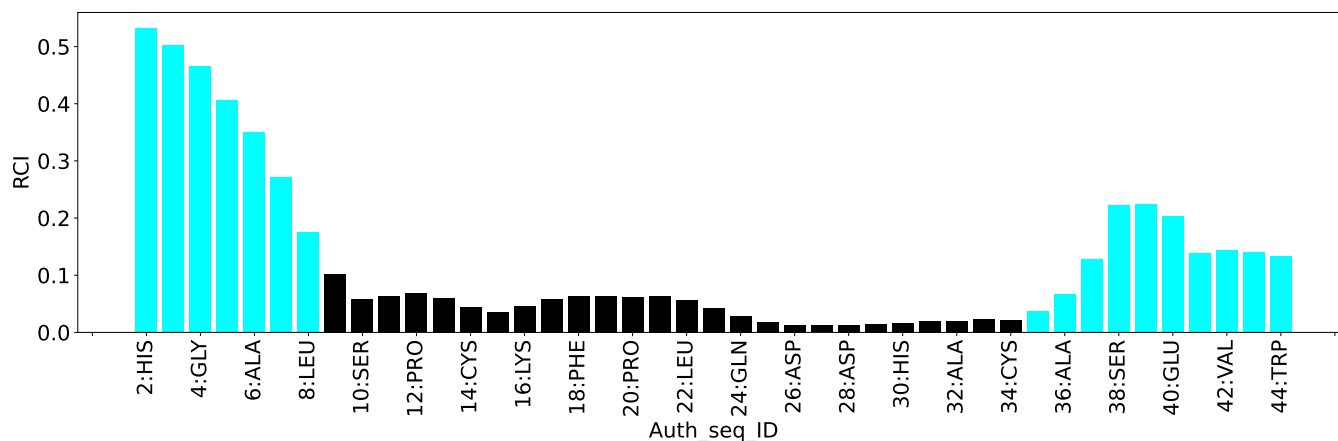
7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

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 [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	708
Intra-residue ($ i-j =0$)	99
Sequential ($ i-j =1$)	199
Medium range ($ i-j >1$ and $ i-j <5$)	238
Long range ($ i-j \geq 5$)	144
Inter-chain	0
Hydrogen bond restraints	28
Disulfide bond restraints	0
Total dihedral-angle restraints	44
Number of unmapped restraints	0
Number of restraints per residue	16.7
Number of long range restraints per residue ¹	3.3

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 [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. There are no distance violations

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](#)

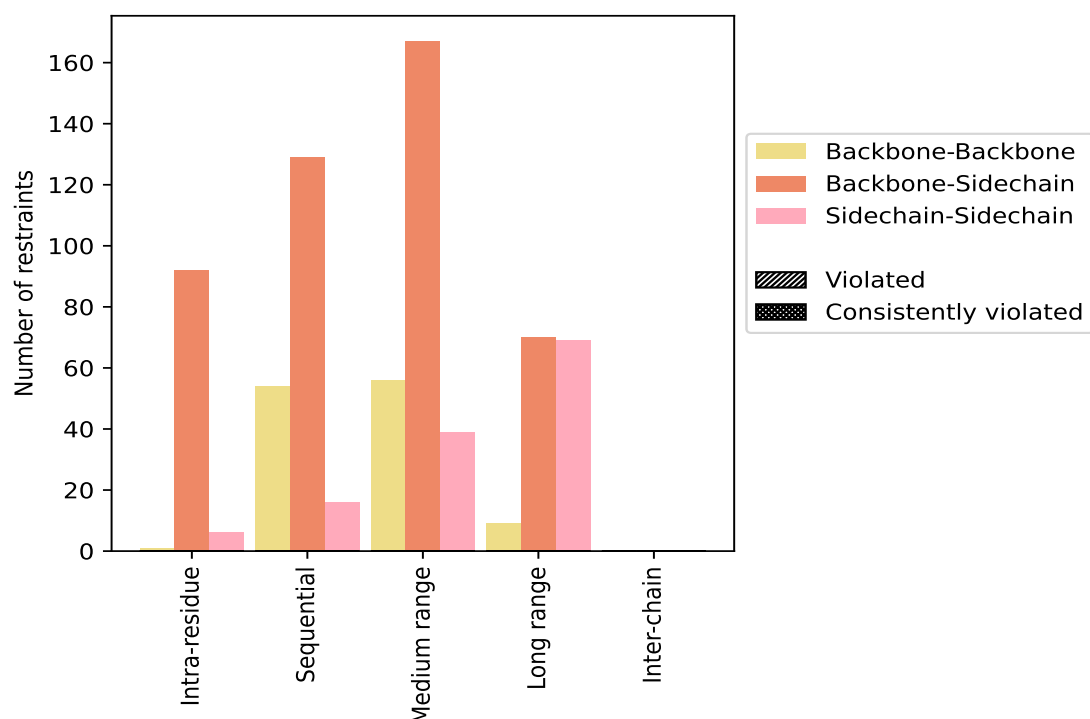
9.1 Summary of distance violations [i](#)

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.

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue (i-j =0)	99	14.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	1	0.1	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	92	13.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	6	0.8	0	0.0	0.0	0	0.0	0.0
Sequential (i-j =1)	199	28.1	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	54	7.6	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	129	18.2	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	16	2.3	0	0.0	0.0	0	0.0	0.0
Medium range (i-j >1 & i-j <5)	238	33.6	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	56	7.9	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	143	20.2	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	39	5.5	0	0.0	0.0	0	0.0	0.0
Long range (i-j ≥5)	144	20.3	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	9	1.3	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	66	9.3	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	69	9.7	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	28	4.0	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	708	100.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	120	16.9	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	458	64.7	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	130	18.4	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 disulfide 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 [i](#)

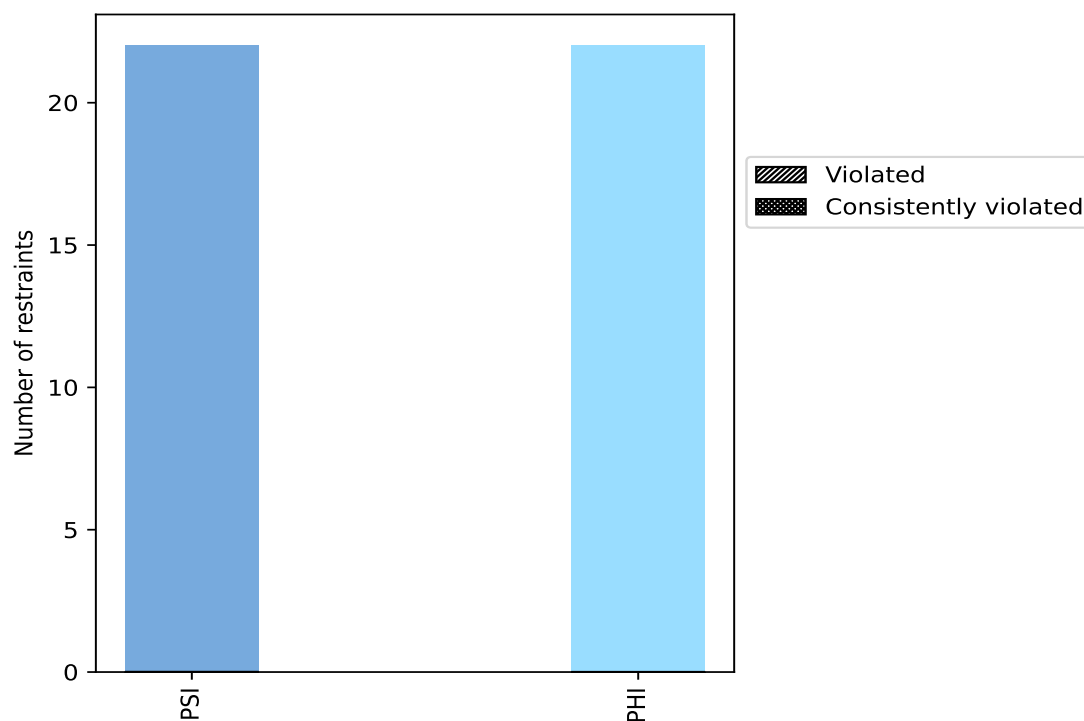
10.1 Summary of dihedral-angle violations [i](#)

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
PSI	22	50.0	0	0.0	0.0	0	0.0	0.0
PHI	22	50.0	0	0.0	0.0	0	0.0	0.0
Total	44	100.0	0	0.0	0.0	0	0.0	0.0

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

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



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

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

No violations found

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

No violations found

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

No violations found

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

No violations found