



Full wwPDB NMR Structure Validation Report ⓘ

Jun 5, 2023 – 04:04 AM EDT

PDB ID : 2M0N
BMRB ID : 18812
Title : Solution structure of a DUF3349 annotated protein from Mycobacterium abscessus, MAB_3403c. Seattle Structural Genomics Center for Infectious Disease target MyabA.17112.a.A2
Authors : Buchko, G.W.; Seattle Structural Genomics Center for Infectious Disease (SS-GCID)
Deposited on : 2012-10-30

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 : 4.02b-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

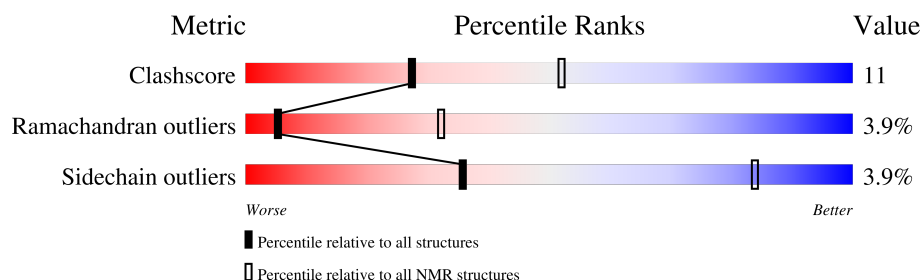
1 Overall quality at a glance

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	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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	112	

2 Ensemble composition and analysis

This entry contains 20 models. Model 18 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:38-A:112 (75)	1.93	18

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1675 atoms, of which 831 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Putative uncharacterized protein.

Mol	Chain	Residues	Atoms						Trace
1	A	112	Total	C	H	N	O	S	0
			1675	521	831	151	170	2	

There are 21 discrepancies between the modelled and reference sequences:

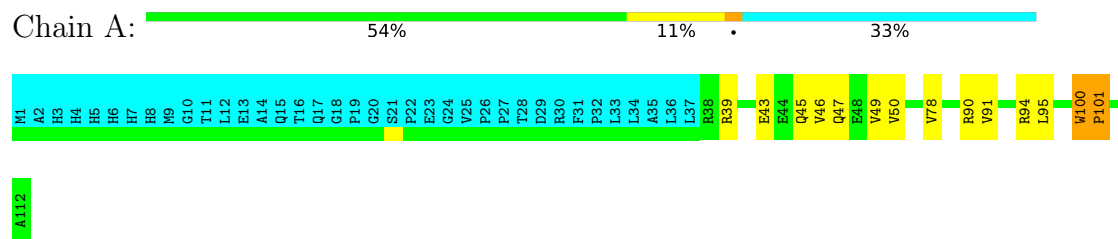
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP B1ME10
A	2	ALA	-	expression tag	UNP B1ME10
A	3	HIS	-	expression tag	UNP B1ME10
A	4	HIS	-	expression tag	UNP B1ME10
A	5	HIS	-	expression tag	UNP B1ME10
A	6	HIS	-	expression tag	UNP B1ME10
A	7	HIS	-	expression tag	UNP B1ME10
A	8	HIS	-	expression tag	UNP B1ME10
A	9	MET	-	expression tag	UNP B1ME10
A	10	GLY	-	expression tag	UNP B1ME10
A	11	THR	-	expression tag	UNP B1ME10
A	12	LEU	-	expression tag	UNP B1ME10
A	13	GLU	-	expression tag	UNP B1ME10
A	14	ALA	-	expression tag	UNP B1ME10
A	15	GLN	-	expression tag	UNP B1ME10
A	16	THR	-	expression tag	UNP B1ME10
A	17	GLN	-	expression tag	UNP B1ME10
A	18	GLY	-	expression tag	UNP B1ME10
A	19	PRO	-	expression tag	UNP B1ME10
A	20	GLY	-	expression tag	UNP B1ME10
A	21	SER	-	expression tag	UNP B1ME10

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: Putative uncharacterized protein

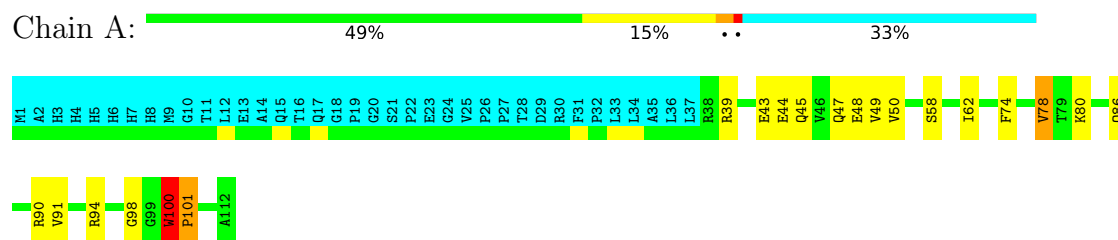


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

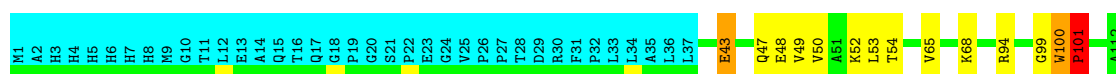
- Molecule 1: Putative uncharacterized protein



4.2.2 Score per residue for model 2

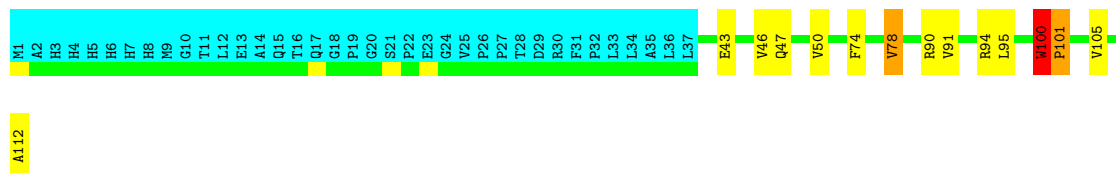
- Molecule 1: Putative uncharacterized protein





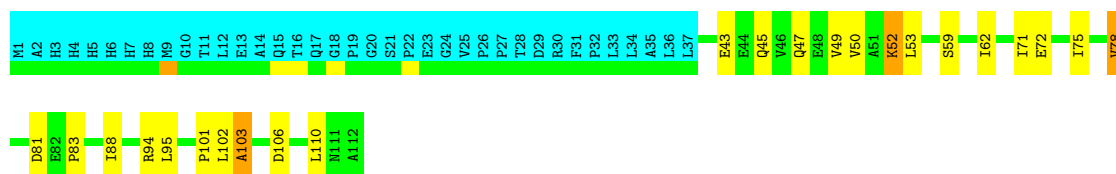
4.2.3 Score per residue for model 3

- Molecule 1: Putative uncharacterized protein



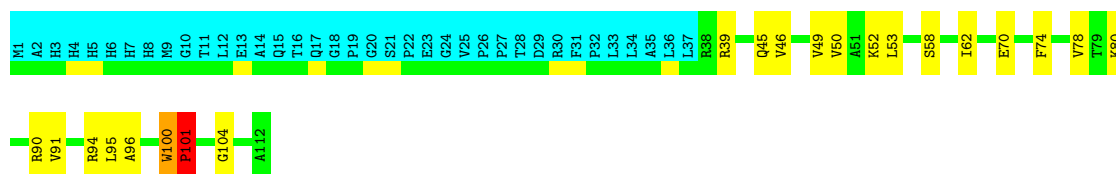
4.2.4 Score per residue for model 4

- Molecule 1: Putative uncharacterized protein



4.2.5 Score per residue for model 5

- Molecule 1: Putative uncharacterized protein



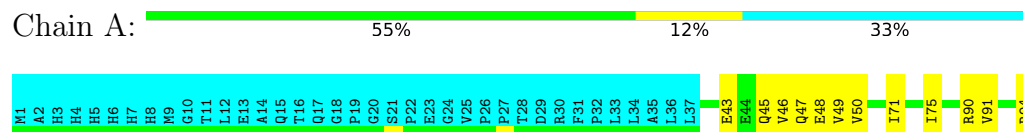
4.2.6 Score per residue for model 6

- Molecule 1: Putative uncharacterized protein



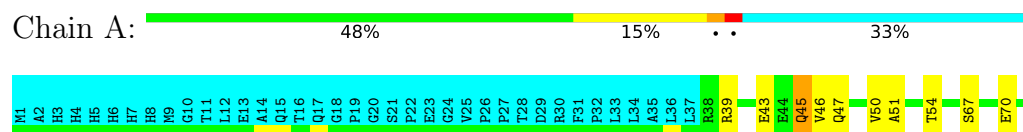
4.2.7 Score per residue for model 7

- Molecule 1: Putative uncharacterized protein



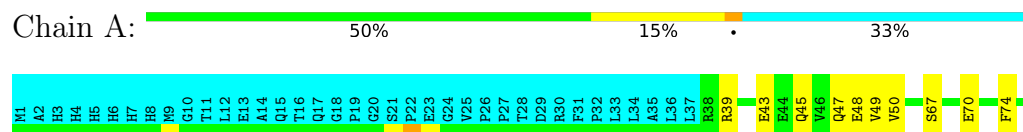
4.2.8 Score per residue for model 8

- Molecule 1: Putative uncharacterized protein



4.2.9 Score per residue for model 9

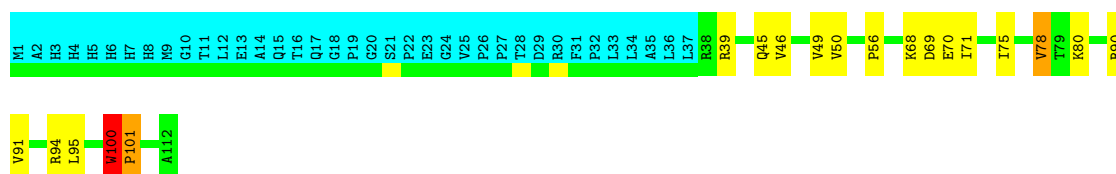
- Molecule 1: Putative uncharacterized protein



4.2.10 Score per residue for model 10

- Molecule 1: Putative uncharacterized protein

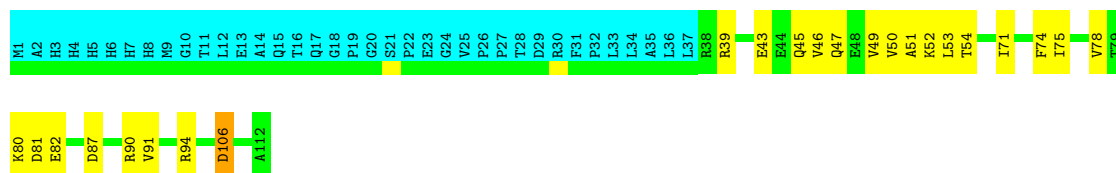




4.2.11 Score per residue for model 11

- Molecule 1: Putative uncharacterized protein

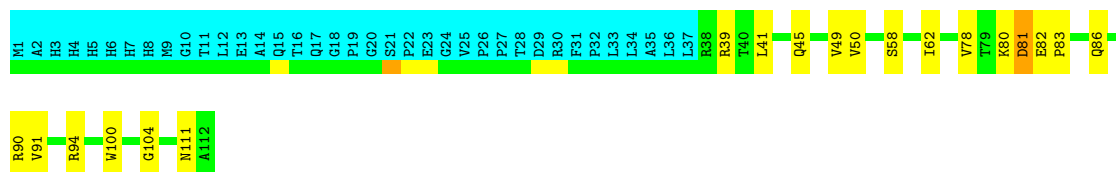
Chain A: 46% 20% 33%



4.2.12 Score per residue for model 12

- Molecule 1: Putative uncharacterized protein

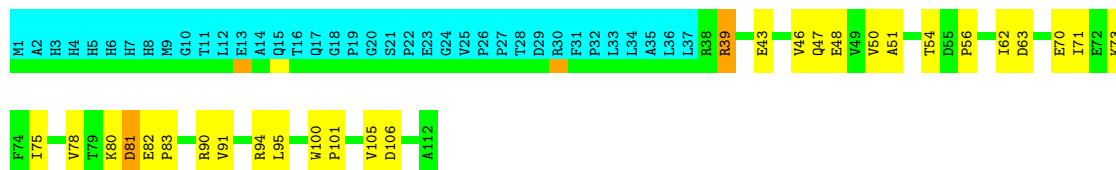
Chain A: 50% 16% 33%



4.2.13 Score per residue for model 13

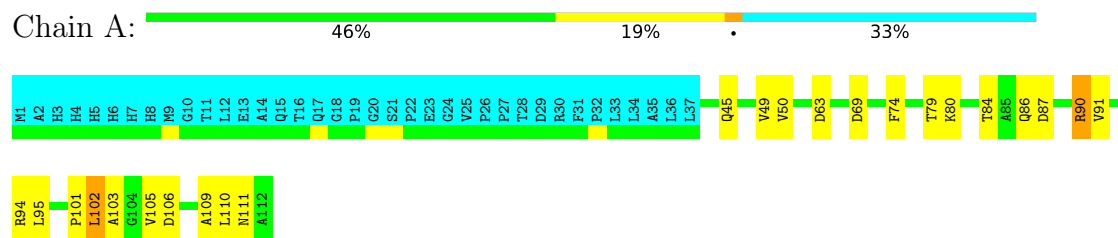
- Molecule 1: Putative uncharacterized protein

Chain A: 42% 23% 33%



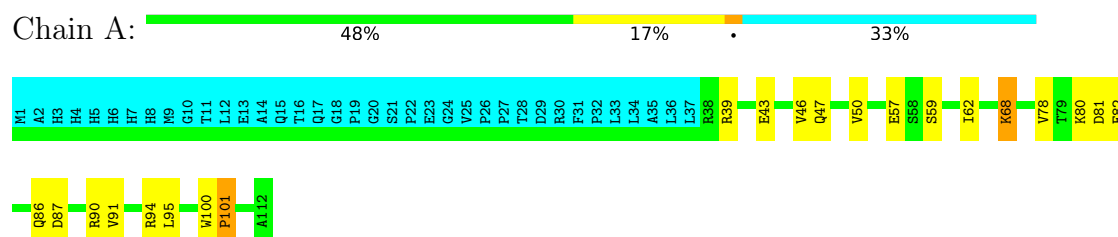
4.2.14 Score per residue for model 14

- Molecule 1: Putative uncharacterized protein



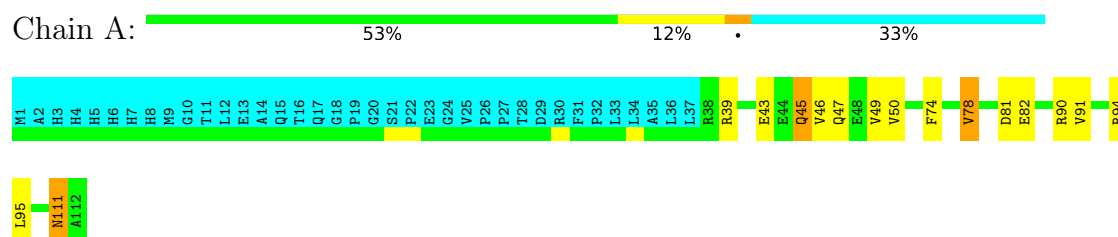
4.2.15 Score per residue for model 15

- Molecule 1: Putative uncharacterized protein



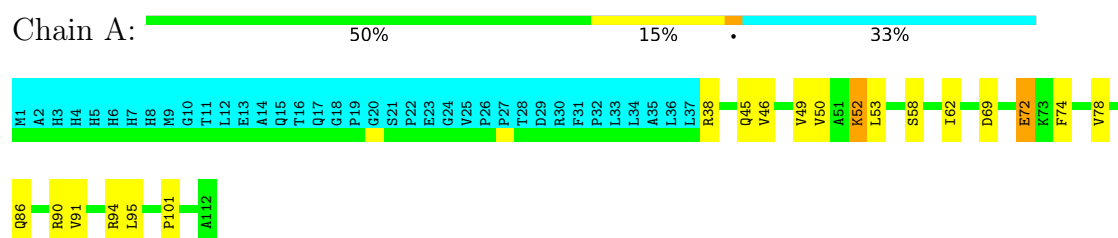
4.2.16 Score per residue for model 16

- Molecule 1: Putative uncharacterized protein



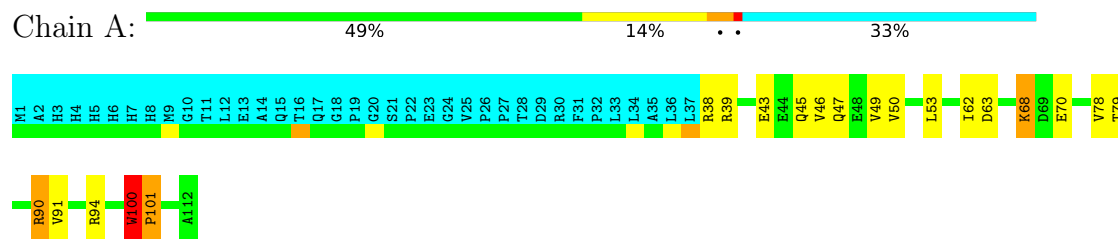
4.2.17 Score per residue for model 17

- Molecule 1: Putative uncharacterized protein



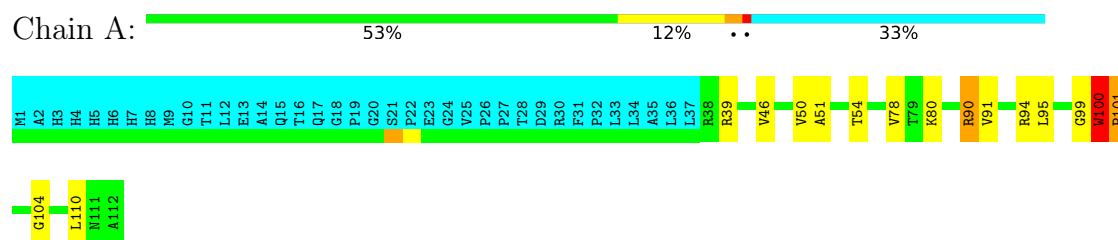
4.2.18 Score per residue for model 18 (medoid)

- Molecule 1: Putative uncharacterized protein



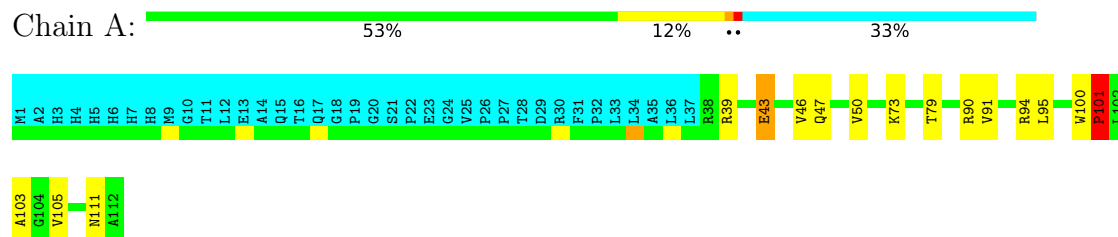
4.2.19 Score per residue for model 19

- Molecule 1: Putative uncharacterized protein



4.2.20 Score per residue for model 20

- Molecule 1: Putative uncharacterized protein



5 Refinement protocol and experimental data overview

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
CNS	refinement	1.1
CYANA	structure solution	2.1

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	1065
Number of shifts mapped to atoms	1065
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 [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	0.34±0.01	0±0/567 (0.0± 0.0%)	0.47±0.02	0±0/769 (0.0± 0.0%)
All	All	0.34	0/11340 (0.0%)	0.47	1/15380 (0.0%)

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	0.6±0.5
All	All	0	11

There are no bond-length outliers.

All unique angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	101	PRO	N-CA-CB	-5.33	96.73	102.60	5	1

There are no chirality outliers.

All unique planar outliers are listed below.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	100	TRP	Peptide	11

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	562	557	557	12±3
All	All	11240	11140	11140	241

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 11.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:100:TRP:HB3	1:A:101:PRO:HD2	0.77	1.57	2	10
1:A:100:TRP:HB2	1:A:101:PRO:HD2	0.71	1.62	20	1
1:A:49:VAL:HG22	1:A:78:VAL:HG21	0.66	1.67	10	3
1:A:50:VAL:HG21	1:A:94:ARG:HB2	0.65	1.69	20	9
1:A:50:VAL:HG12	1:A:91:VAL:HG13	0.64	1.67	15	8
1:A:50:VAL:HG11	1:A:94:ARG:HB2	0.64	1.70	1	11
1:A:50:VAL:HG22	1:A:91:VAL:HG13	0.63	1.71	10	9
1:A:43:GLU:O	1:A:47:GLN:HG3	0.63	1.93	6	5
1:A:43:GLU:O	1:A:47:GLN:HG2	0.62	1.93	1	9
1:A:39:ARG:HH21	1:A:81:ASP:HB3	0.62	1.53	16	1
1:A:39:ARG:HG3	1:A:39:ARG:O	0.62	1.95	15	2
1:A:100:TRP:HB3	1:A:101:PRO:CD	0.61	2.26	6	10
1:A:90:ARG:O	1:A:94:ARG:HG2	0.60	1.96	17	14
1:A:46:VAL:O	1:A:50:VAL:HG23	0.60	1.96	19	8
1:A:70:GLU:HA	1:A:73:LYS:HE2	0.60	1.73	13	1
1:A:86:GLN:NE2	1:A:90:ARG:HH21	0.59	1.94	6	1
1:A:43:GLU:HB3	1:A:112:ALA:HB3	0.56	1.77	9	1
1:A:46:VAL:O	1:A:50:VAL:HG13	0.55	2.02	15	5
1:A:39:ARG:HD2	1:A:80:LYS:O	0.54	2.01	13	2
1:A:39:ARG:O	1:A:40:THR:HG23	0.54	2.02	6	1
1:A:96:ALA:HA	1:A:101:PRO:HG3	0.54	1.78	5	1
1:A:41:LEU:HB2	1:A:80:LYS:NZ	0.53	2.18	12	1
1:A:54:THR:O	1:A:56:PRO:HD3	0.53	2.04	13	1
1:A:74:PHE:O	1:A:78:VAL:HG23	0.52	2.04	6	6
1:A:45:GLN:O	1:A:49:VAL:HG23	0.52	2.05	10	13
1:A:111:ASN:N	1:A:111:ASN:HD22	0.52	2.02	16	1
1:A:52:LYS:HA	1:A:52:LYS:HE3	0.52	1.82	17	1
1:A:71:ILE:O	1:A:75:ILE:HG13	0.52	2.05	6	6
1:A:80:LYS:O	1:A:82:GLU:N	0.51	2.43	13	3
1:A:51:ALA:O	1:A:54:THR:HG22	0.51	2.04	8	3
1:A:39:ARG:O	1:A:80:LYS:HD2	0.51	2.05	8	2
1:A:39:ARG:O	1:A:80:LYS:HE3	0.51	2.07	19	2
1:A:102:LEU:HD13	1:A:102:LEU:H	0.50	1.65	14	1
1:A:67:SER:O	1:A:70:GLU:HG2	0.49	2.07	8	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:39:ARG:NH1	1:A:81:ASP:HB2	0.49	2.23	11	2
1:A:86:GLN:O	1:A:90:ARG:HG3	0.49	2.08	12	1
1:A:110:LEU:HD23	1:A:111:ASN:N	0.49	2.22	14	1
1:A:86:GLN:O	1:A:90:ARG:HD3	0.48	2.09	1	3
1:A:53:LEU:HD13	1:A:53:LEU:O	0.48	2.09	4	1
1:A:59:SER:O	1:A:62:ILE:HG12	0.48	2.07	15	2
1:A:49:VAL:O	1:A:53:LEU:HD23	0.48	2.09	11	3
1:A:68:LYS:HD3	1:A:68:LYS:N	0.48	2.24	6	1
1:A:39:ARG:O	1:A:80:LYS:HA	0.47	2.09	10	1
1:A:100:TRP:HB2	1:A:101:PRO:CD	0.47	2.36	20	1
1:A:58:SER:O	1:A:62:ILE:HG13	0.47	2.09	12	5
1:A:91:VAL:O	1:A:95:LEU:HG	0.47	2.10	15	1
1:A:52:LYS:HE3	1:A:52:LYS:HA	0.47	1.86	4	1
1:A:81:ASP:O	1:A:83:PRO:HD3	0.47	2.10	13	3
1:A:68:LYS:HA	1:A:68:LYS:NZ	0.47	2.24	18	1
1:A:86:GLN:O	1:A:90:ARG:HG2	0.47	2.10	17	1
1:A:62:ILE:HD12	1:A:63:ASP:HB2	0.46	1.87	13	1
1:A:39:ARG:HG3	1:A:79:THR:O	0.46	2.11	18	1
1:A:62:ILE:HD12	1:A:63:ASP:N	0.46	2.25	18	1
1:A:96:ALA:O	1:A:101:PRO:HG3	0.46	2.11	5	1
1:A:53:LEU:HD12	1:A:95:LEU:HD22	0.46	1.89	4	2
1:A:51:ALA:O	1:A:54:THR:HB	0.46	2.10	13	1
1:A:38:ARG:HB3	1:A:45:GLN:NE2	0.46	2.25	17	1
1:A:49:VAL:HG13	1:A:74:PHE:HB3	0.45	1.89	9	3
1:A:110:LEU:O	1:A:111:ASN:HB3	0.45	2.11	14	1
1:A:41:LEU:HD13	1:A:80:LYS:HB2	0.45	1.88	12	1
1:A:102:LEU:H	1:A:102:LEU:HD23	0.45	1.72	9	1
1:A:43:GLU:HB2	1:A:112:ALA:HB3	0.45	1.87	3	1
1:A:48:GLU:O	1:A:52:LYS:HG2	0.45	2.11	2	1
1:A:71:ILE:HG23	1:A:91:VAL:HG11	0.45	1.89	6	1
1:A:53:LEU:O	1:A:53:LEU:HD13	0.44	2.12	17	1
1:A:72:GLU:HB3	1:A:88:ILE:HD11	0.44	1.90	4	1
1:A:76:ALA:HA	1:A:80:LYS:HB3	0.44	1.89	8	1
1:A:53:LEU:HD21	1:A:70:GLU:HG3	0.44	1.90	5	1
1:A:100:TRP:CD1	1:A:100:TRP:N	0.44	2.85	5	1
1:A:102:LEU:O	1:A:103:ALA:HB2	0.43	2.13	4	1
1:A:69:ASP:O	1:A:72:GLU:HG3	0.43	2.13	17	1
1:A:106:ASP:HB3	1:A:109:ALA:HB3	0.43	1.91	14	2
1:A:70:GLU:HG3	1:A:71:ILE:N	0.43	2.29	10	1
1:A:68:LYS:HD3	1:A:68:LYS:H	0.43	1.72	15	1
1:A:78:VAL:O	1:A:78:VAL:HG12	0.43	2.14	12	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:45:GLN:HE21	1:A:45:GLN:HA	0.43	1.74	8	1
1:A:80:LYS:NZ	1:A:87:ASP:OD2	0.43	2.50	11	2
1:A:90:ARG:HA	1:A:90:ARG:NE	0.43	2.29	19	1
1:A:47:GLN:NE2	1:A:94:ARG:HH21	0.43	2.11	20	1
1:A:73:LYS:HB2	1:A:73:LYS:HZ2	0.42	1.73	20	1
1:A:94:ARG:O	1:A:98:GLY:N	0.42	2.52	1	1
1:A:50:VAL:O	1:A:54:THR:HG23	0.42	2.15	2	1
1:A:79:THR:O	1:A:79:THR:HG22	0.42	2.15	14	3
1:A:91:VAL:HG12	1:A:95:LEU:HD23	0.42	1.92	14	1
1:A:50:VAL:HG12	1:A:95:LEU:HD23	0.42	1.91	4	1
1:A:62:ILE:HD12	1:A:74:PHE:CZ	0.41	2.50	5	1
1:A:100:TRP:CB	1:A:101:PRO:HD2	0.41	2.42	15	1
1:A:50:VAL:HG13	1:A:91:VAL:HG13	0.41	1.91	6	1
1:A:38:ARG:NE	1:A:38:ARG:HA	0.41	2.31	18	1
1:A:80:LYS:NZ	1:A:82:GLU:O	0.41	2.48	15	1
1:A:39:ARG:HG2	1:A:79:THR:HG22	0.41	1.93	20	1
1:A:50:VAL:HA	1:A:53:LEU:HB3	0.41	1.93	4	1
1:A:78:VAL:HG12	1:A:78:VAL:O	0.41	2.16	10	1
1:A:68:LYS:HA	1:A:68:LYS:HD2	0.41	1.72	10	1
1:A:106:ASP:HB3	1:A:110:LEU:HB2	0.40	1.92	4	1
1:A:102:LEU:HD13	1:A:102:LEU:N	0.40	2.29	14	1
1:A:49:VAL:O	1:A:53:LEU:HB2	0.40	2.16	4	1
1:A:84:THR:HG23	1:A:86:GLN:HB3	0.40	1.91	14	2
1:A:47:GLN:HA	1:A:50:VAL:HG22	0.40	1.92	18	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	74/112 (66%)	65±2 (88±2%)	6±2 (9±2%)	3±1 (4±2%)	5	32
All	All	1480/2240 (66%)	1297 (88%)	126 (9%)	57 (4%)	5	32

All 14 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	101	PRO	16
1	A	78	VAL	11
1	A	100	TRP	7
1	A	105	VAL	3
1	A	103	ALA	3
1	A	104	GLY	3
1	A	81	ASP	3
1	A	99	GLY	2
1	A	69	ASP	2
1	A	106	ASP	2
1	A	111	ASN	2
1	A	65	VAL	1
1	A	56	PRO	1
1	A	39	ARG	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	61/91 (67%)	59±1 (96±2%)	2±1 (4±2%)	36	84
All	All	1220/1820 (67%)	1172 (96%)	48 (4%)	36	84

All 20 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	95	LEU	8
1	A	68	LYS	4
1	A	101	PRO	4
1	A	52	LYS	4
1	A	48	GLU	4
1	A	90	ARG	4
1	A	43	GLU	3
1	A	110	LEU	2
1	A	45	GLN	2
1	A	82	GLU	2
1	A	105	VAL	2
1	A	100	TRP	1

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Mol	Chain	Res	Type	Models (Total)
1	A	106	ASP	1
1	A	63	ASP	1
1	A	102	LEU	1
1	A	57	GLU	1
1	A	87	ASP	1
1	A	111	ASN	1
1	A	72	GLU	1
1	A	70	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 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

The completeness of assignment taking into account all chemical shift lists is 83% for the well-defined parts and 73% 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	1065
Number of shifts mapped to atoms	1065
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

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	97	-0.21 ± 0.11	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	91	0.12 ± 0.08	None needed (< 0.5 ppm)
$^{13}\text{C}'$	83	-0.31 ± 0.11	None needed (< 0.5 ppm)
^{15}N	91	0.15 ± 0.32	None needed (< 0.5 ppm)

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. 804 atoms were assigned a chemical shift out of a possible 967. 0 out of 13 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	345/373 (92%)	142/151 (94%)	134/150 (89%)	69/72 (96%)
Sidechain	439/572 (77%)	297/371 (80%)	138/180 (77%)	4/21 (19%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	20/22 (91%)	10/11 (91%)	9/10 (90%)	1/1 (100%)
Overall	804/967 (83%)	449/533 (84%)	281/340 (83%)	74/94 (79%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 73%, i.e. 1065 atoms were assigned a chemical shift out of a possible 1454. 0 out of 19 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	462/552 (84%)	191/224 (85%)	180/224 (80%)	91/104 (88%)
Sidechain	579/822 (70%)	390/537 (73%)	185/259 (71%)	4/26 (15%)
Aromatic	24/80 (30%)	12/40 (30%)	11/27 (41%)	1/13 (8%)
Overall	1065/1454 (73%)	593/801 (74%)	376/510 (74%)	96/143 (67%)

7.1.4 Statistically unusual chemical shifts ⓘ

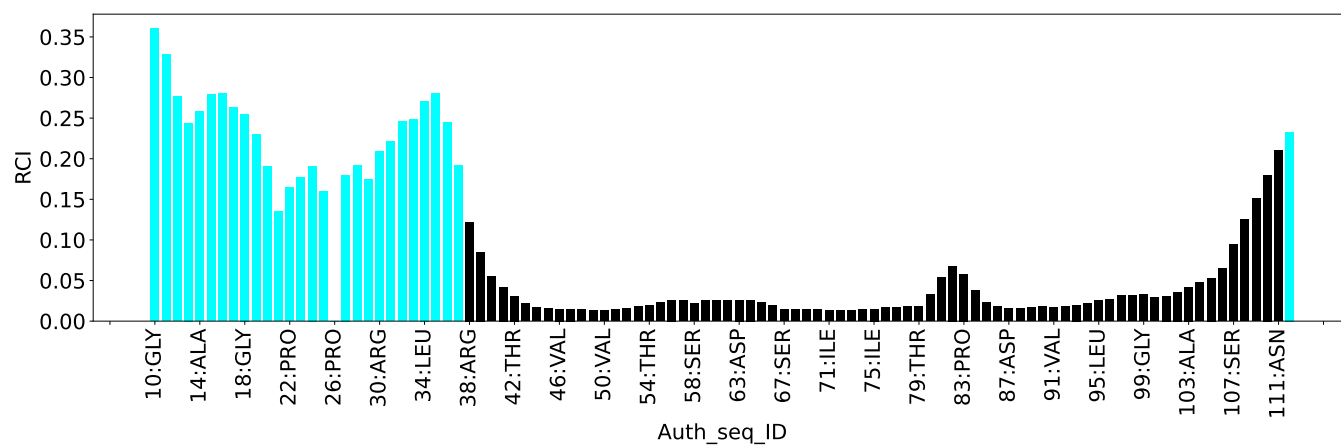
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	100	TRP	CB	52.30	20.06 – 39.75	11.4
1	A	54	THR	HG21	-0.47	0.08 – 2.19	-7.6
1	A	54	THR	HG22	-0.47	0.08 – 2.19	-7.6
1	A	54	THR	HG23	-0.47	0.08 – 2.19	-7.6

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	1118
Intra-residue ($ i-j =0$)	273
Sequential ($ i-j =1$)	355
Medium range ($ i-j >1$ and $ i-j <5$)	270
Long range ($ i-j \geq 5$)	178
Inter-chain	0
Hydrogen bond restraints	42
Disulfide bond restraints	0
Total dihedral-angle restraints	124
Number of unmapped restraints	0
Number of restraints per residue	11.1
Number of long range restraints per residue ¹	1.6

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)	0.1	0.11
0.2-0.5 (Medium)	0.2	0.49
>0.5 (Large)	0.4	2.05

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)	0.8	2.2
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis ⓘ

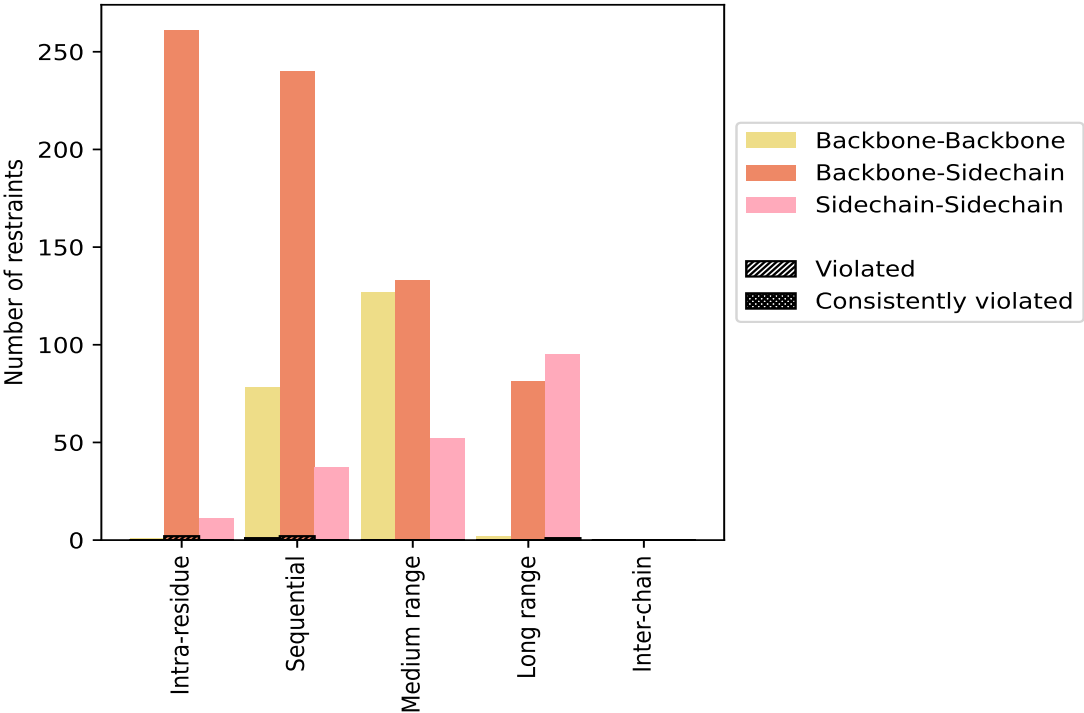
9.1 Summary of distance violations ⓘ

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 ($i-j =0$)	273	24.4	2	0.7	0.2	0	0.0	0.0
Backbone-Backbone	1	0.1	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	261	23.3	2	0.8	0.2	0	0.0	0.0
Sidechain-Sidechain	11	1.0	0	0.0	0.0	0	0.0	0.0
Sequential ($i-j =1$)	355	31.8	3	0.8	0.3	0	0.0	0.0
Backbone-Backbone	78	7.0	1	1.3	0.1	0	0.0	0.0
Backbone-Sidechain	240	21.5	2	0.8	0.2	0	0.0	0.0
Sidechain-Sidechain	37	3.3	0	0.0	0.0	0	0.0	0.0
Medium range ($i-j >1$ & $i-j <5$)	270	24.2	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	85	7.6	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	133	11.9	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	52	4.7	0	0.0	0.0	0	0.0	0.0
Long range ($i-j \geq 5$)	178	15.9	1	0.6	0.1	0	0.0	0.0
Backbone-Backbone	2	0.2	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	81	7.2	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	95	8.5	1	1.1	0.1	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	42	3.8	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	1118	100.0	6	0.5	0.5	0	0.0	0.0
Backbone-Backbone	208	18.6	1	0.5	0.1	0	0.0	0.0
Backbone-Sidechain	715	64.0	4	0.6	0.4	0	0.0	0.0
Sidechain-Sidechain	195	17.4	1	0.5	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	2	2	0	0	0	4	1.16	2.05	0.6	1.04
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	0	0	0	0	0.0	0.0	0.0	0.0

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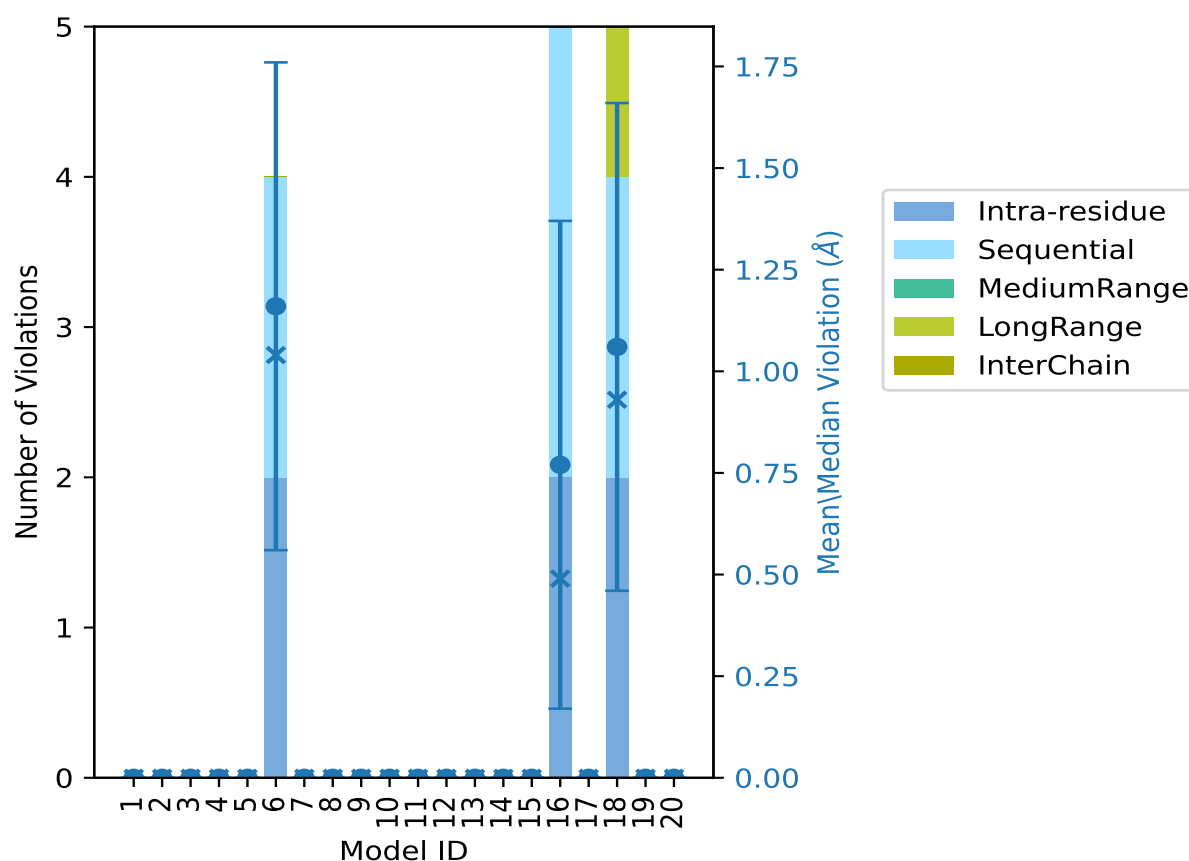
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
12	0	0	0	0	0	0	0.0	0.0	0.0	0.0
13	0	0	0	0	0	0	0.0	0.0	0.0	0.0
14	0	0	0	0	0	0	0.0	0.0	0.0	0.0
15	0	0	0	0	0	0	0.0	0.0	0.0	0.0
16	2	3	0	0	0	5	0.77	1.77	0.6	0.49
17	0	0	0	0	0	0	0.0	0.0	0.0	0.0
18	2	2	0	1	0	5	1.06	2.0	0.6	0.93
19	0	0	0	0	0	0	0.0	0.0	0.0	0.0
20	0	0	0	0	0	0	0.0	0.0	0.0	0.0

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

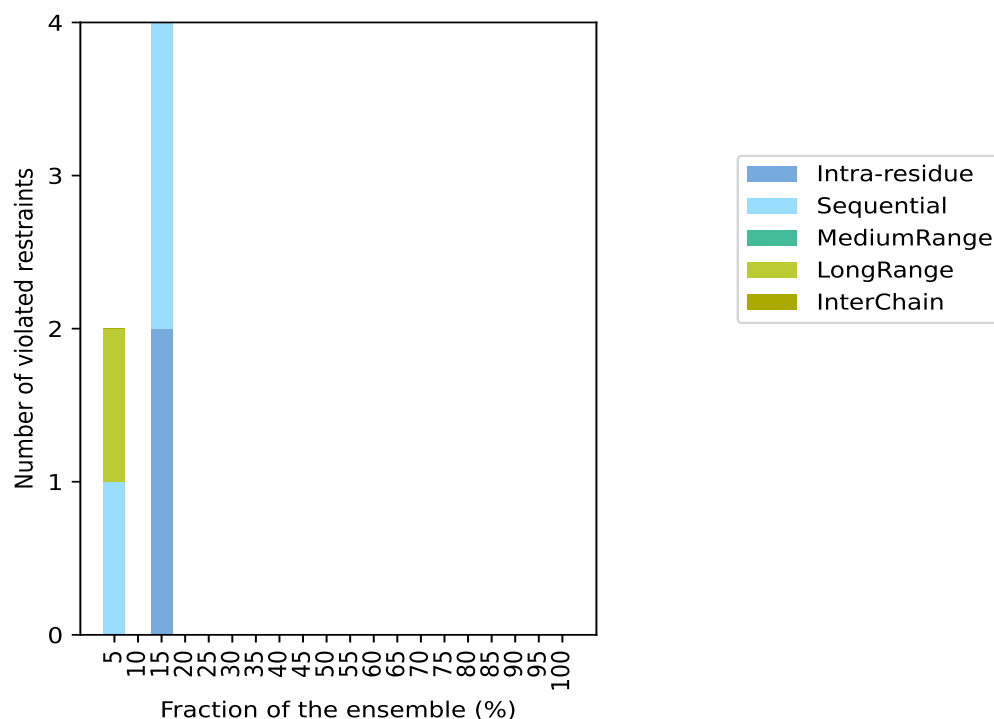
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 1070(IR:271, SQ:352, MR:270, LR:177, IC:0) restraints are 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	1	0	1	0	2	1	5.0
0	0	0	0	0	0	2	10.0
2	2	0	0	0	4	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

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

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

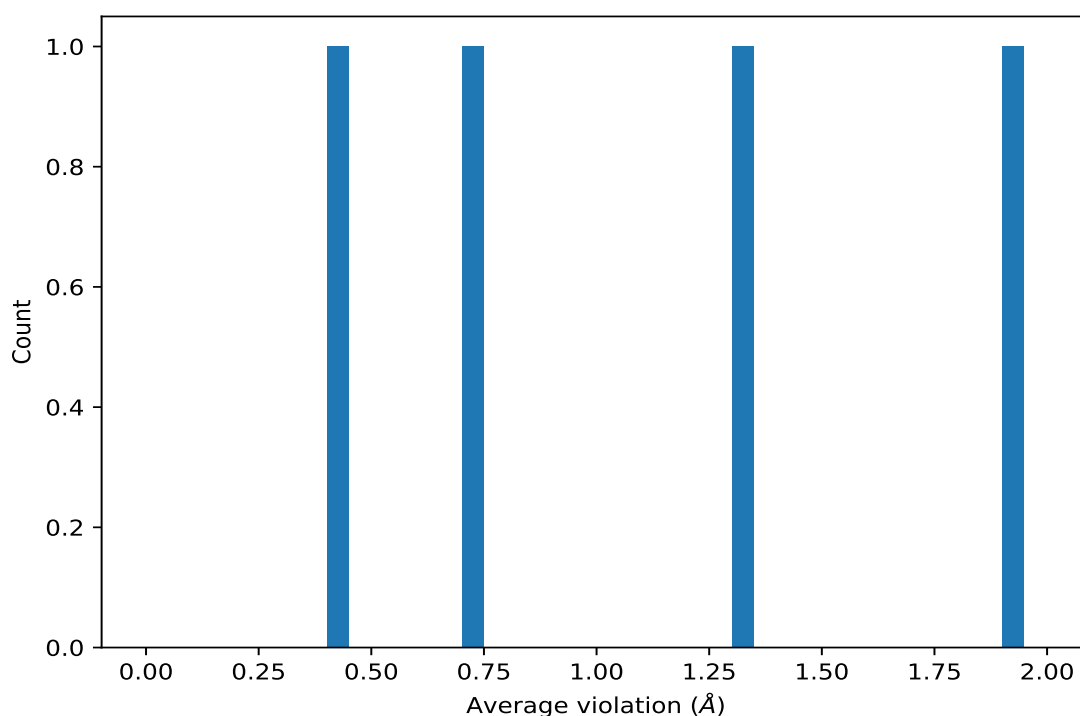
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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.

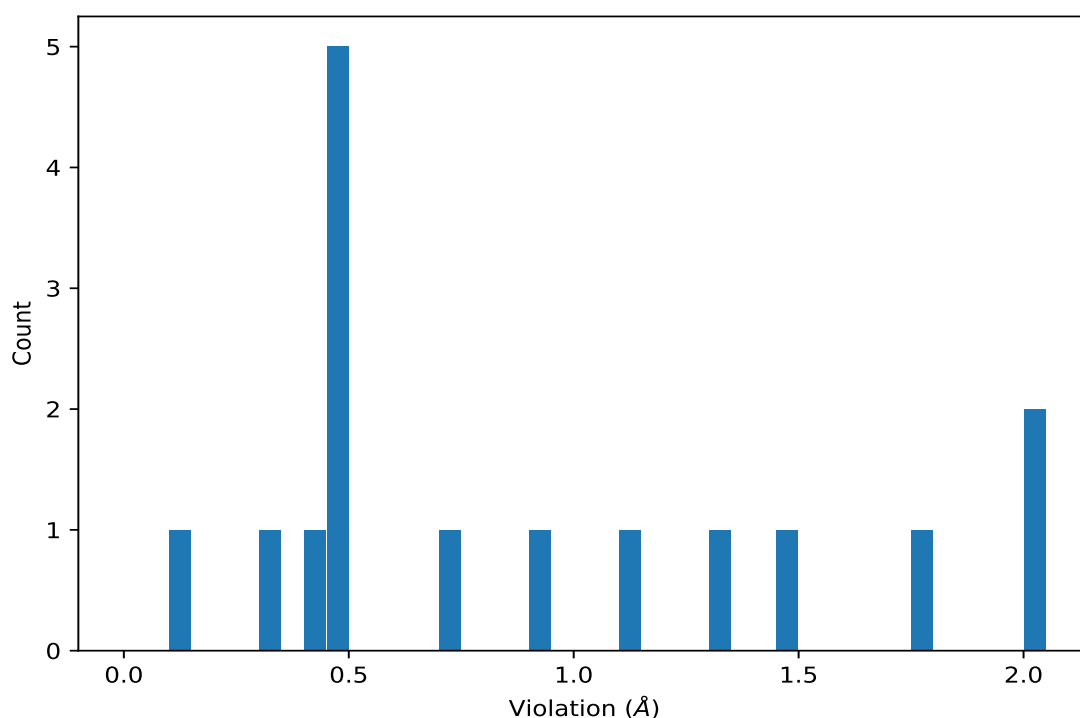
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,616)	1:A:73:LYS:H	1:A:74:PHE:HD1	3	1.94	0.12	2.0
(1,621)	1:A:74:PHE:H	1:A:74:PHE:HD1	3	1.31	0.14	1.34
(1,622)	1:A:74:PHE:H	1:A:74:PHE:HE1	3	0.72	0.18	0.74
(1,631)	1:A:74:PHE:HD1	1:A:75:ILE:H	3	0.42	0.06	0.42

¹Number of violated models, ²Standard deviation

9.5 All violated distance restraints [i](#)

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

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



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

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

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,616)	1:A:73:LYS:H	1:A:74:PHE:HD1	6	2.05
(1,616)	1:A:73:LYS:H	1:A:74:PHE:HD1	18	2.0
(1,616)	1:A:73:LYS:H	1:A:74:PHE:HD1	16	1.77
(1,621)	1:A:74:PHE:H	1:A:74:PHE:HD1	18	1.46
(1,621)	1:A:74:PHE:H	1:A:74:PHE:HD1	6	1.34
(1,621)	1:A:74:PHE:H	1:A:74:PHE:HD1	16	1.12
(1,622)	1:A:74:PHE:H	1:A:74:PHE:HE1	18	0.93
(1,622)	1:A:74:PHE:H	1:A:74:PHE:HE1	6	0.74
(1,631)	1:A:74:PHE:HD1	1:A:75:ILE:H	6	0.49
(1,622)	1:A:74:PHE:H	1:A:74:PHE:HE1	16	0.49
(1,174)	1:A:62:ILE:HD11	1:A:74:PHE:HE1	18	0.47
(1,174)	1:A:62:ILE:HD12	1:A:74:PHE:HE1	18	0.47
(1,174)	1:A:62:ILE:HD13	1:A:74:PHE:HE1	18	0.47
(1,631)	1:A:74:PHE:HD1	1:A:75:ILE:H	18	0.42
(1,631)	1:A:74:PHE:HD1	1:A:75:ILE:H	16	0.34
(1,443)	1:A:28:THR:HA	1:A:29:ASP:H	16	0.11

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

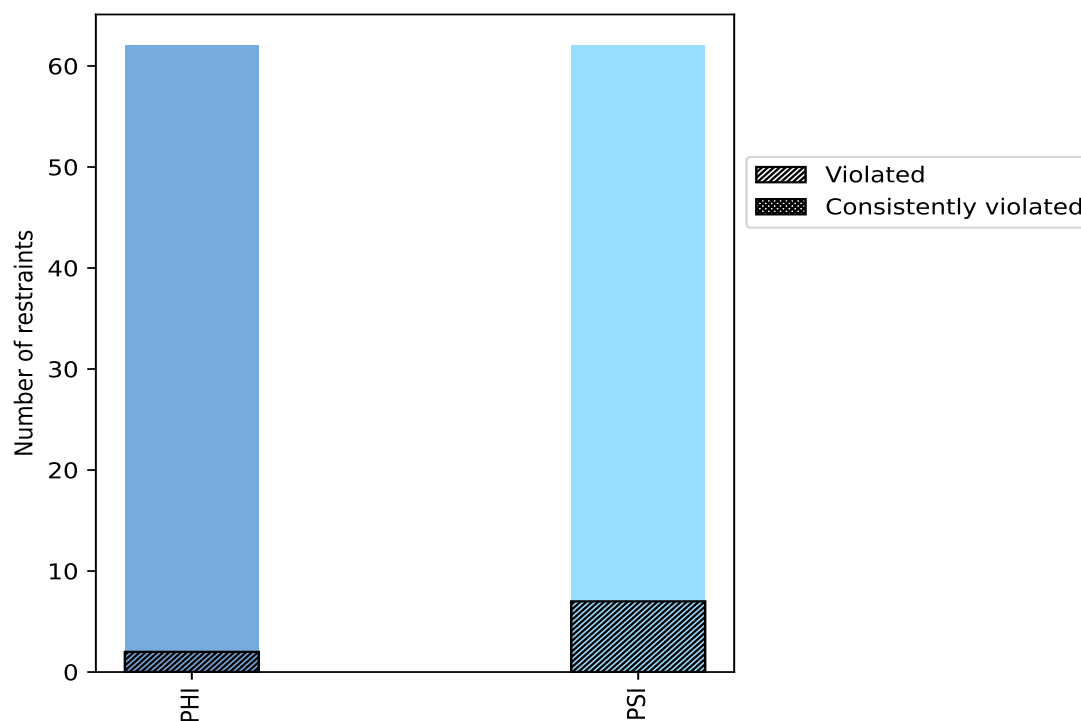
10.1 Summary of dihedral-angle violations [i](#)

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
PHI	62	50.0	2	3.2	1.6	0	0.0	0.0
PSI	62	50.0	7	11.3	5.6	0	0.0	0.0
Total	124	100.0	9	7.3	7.3	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](#)



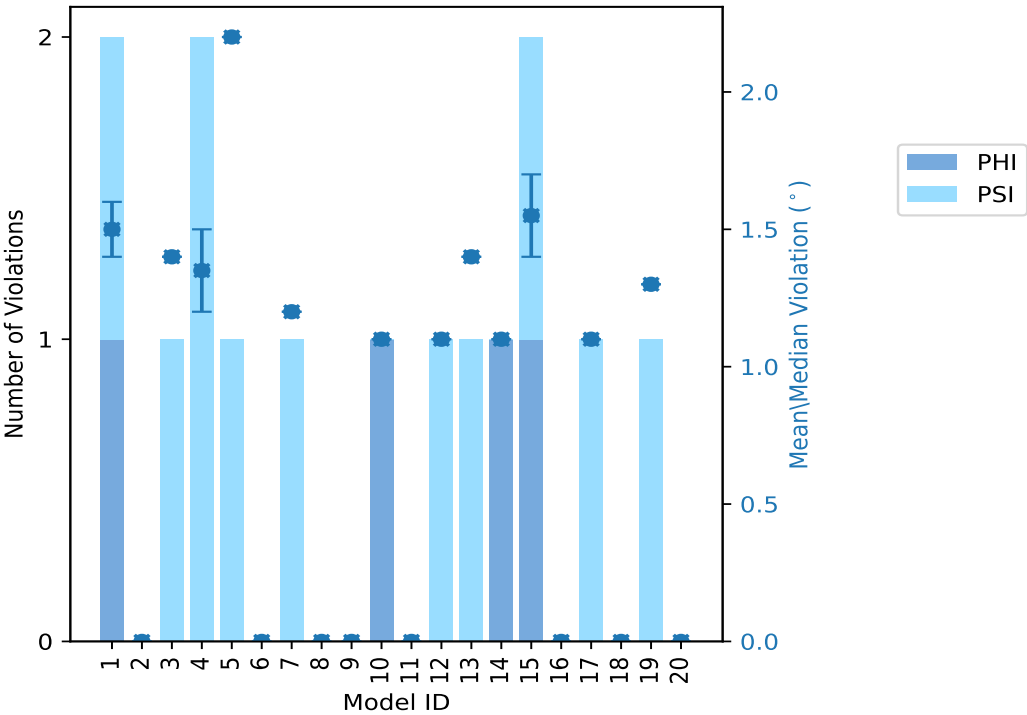
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

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 (°)
	PHI	PSI	Total				
1	1	1	2	1.5	1.6	0.1	1.5
2	0	0	0	0.0	0.0	0.0	0.0
3	0	1	1	1.4	1.4	0.0	1.4
4	0	2	2	1.35	1.5	0.15	1.35
5	0	1	1	2.2	2.2	0.0	2.2
6	0	0	0	0.0	0.0	0.0	0.0
7	0	1	1	1.2	1.2	0.0	1.2
8	0	0	0	0.0	0.0	0.0	0.0
9	0	0	0	0.0	0.0	0.0	0.0
10	1	0	1	1.1	1.1	0.0	1.1
11	0	0	0	0.0	0.0	0.0	0.0
12	0	1	1	1.1	1.1	0.0	1.1
13	0	1	1	1.4	1.4	0.0	1.4
14	1	0	1	1.1	1.1	0.0	1.1
15	1	1	2	1.55	1.7	0.15	1.55
16	0	0	0	0.0	0.0	0.0	0.0
17	0	1	1	1.1	1.1	0.0	1.1
18	0	0	0	0.0	0.0	0.0	0.0
19	0	1	1	1.3	1.3	0.0	1.3
20	0	0	0	0.0	0.0	0.0	0.0

10.2.1 Bar graph : Dihedral 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

10.3 Dihedral-angle violation statistics for the ensemble ⓘ

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	
PHI	PSI	Total	Count ¹	%
1	4	5	1	5.0
0	2	2	2	10.0
1	1	2	3	15.0
0	0	0	4	20.0
0	0	0	5	25.0
0	0	0	6	30.0
0	0	0	7	35.0
0	0	0	8	40.0
0	0	0	9	45.0
0	0	0	10	50.0
0	0	0	11	55.0

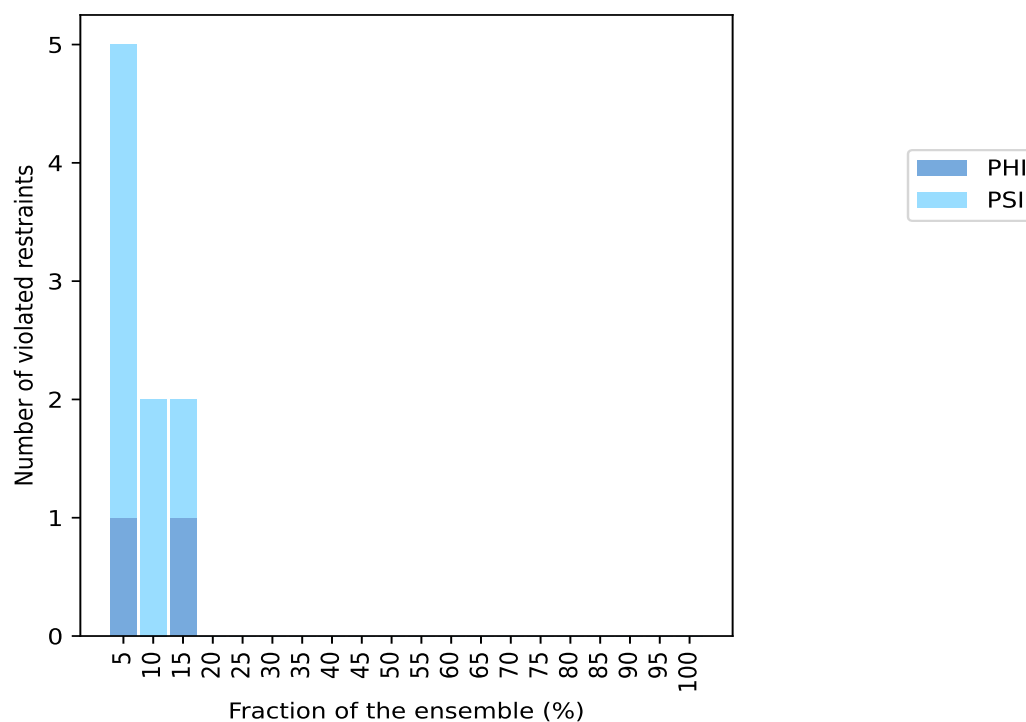
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Number of violated restraints			Fraction of the ensemble	
PHI	PSI	Total	Count ¹	%
0	0	0	12	60.0
0	0	0	13	65.0
0	0	0	14	70.0
0	0	0	15	75.0
0	0	0	16	80.0
0	0	0	17	85.0
0	0	0	18	90.0
0	0	0	19	95.0
0	0	0	20	100.0

¹ Number of models with violations

10.3.1 Bar graph : Dihedral-angle Violation statistics for the ensemble ⓘ

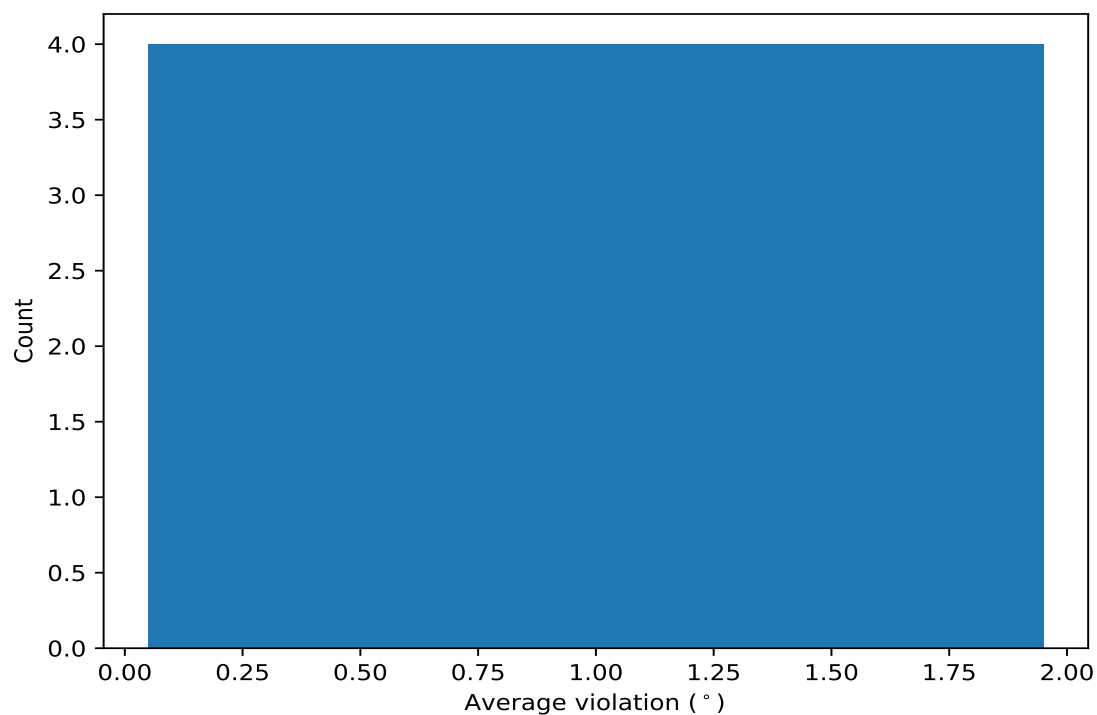


10.4 Most violated dihedral-angle restraints in the ensemble ⓘ

10.4.1 Histogram : Distribution of mean dihedral-angle violations ⓘ

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.

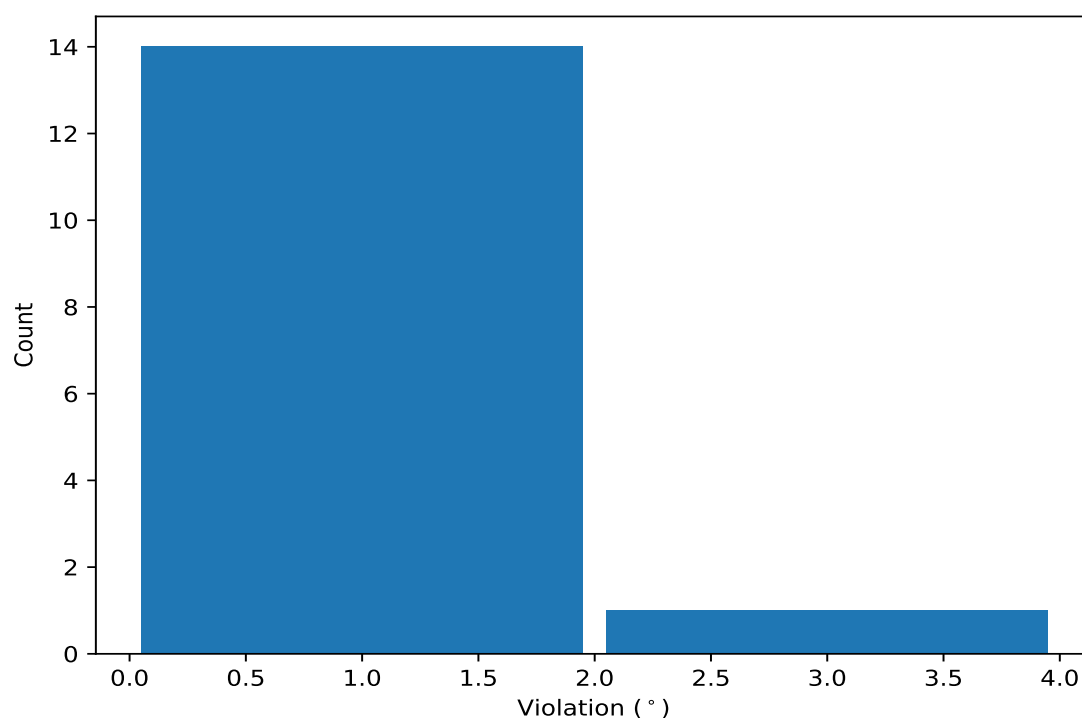
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,116)	1:A:100:TRP:N	1:A:100:TRP:CA	1:A:100:TRP:C	1:A:101:PRO:N	3	1.7	0.36	1.5
(1,61)	1:A:69:ASP:C	1:A:70:GLU:N	1:A:70:GLU:CA	1:A:70:GLU:C	3	1.2	0.14	1.1
(1,48)	1:A:62:ILE:N	1:A:62:ILE:CA	1:A:62:ILE:C	1:A:63:ASP:N	2	1.4	0.3	1.4
(1,60)	1:A:69:ASP:N	1:A:69:ASP:CA	1:A:69:ASP:C	1:A:70:GLU:N	2	1.35	0.25	1.35

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 (°)
(1,116)	1:A:100:TRP:N	1:A:100:TRP:CA	1:A:100:TRP:C	1:A:101:PRO:N	5	2.2
(1,48)	1:A:62:ILE:N	1:A:62:ILE:CA	1:A:62:ILE:C	1:A:63:ASP:N	15	1.7
(1,60)	1:A:69:ASP:N	1:A:69:ASP:CA	1:A:69:ASP:C	1:A:70:GLU:N	1	1.6
(1,116)	1:A:100:TRP:N	1:A:100:TRP:CA	1:A:100:TRP:C	1:A:101:PRO:N	4	1.5
(1,61)	1:A:69:ASP:C	1:A:70:GLU:N	1:A:70:GLU:CA	1:A:70:GLU:C	1	1.4
(1,49)	1:A:62:ILE:C	1:A:63:ASP:N	1:A:63:ASP:CA	1:A:63:ASP:C	15	1.4
(1,116)	1:A:100:TRP:N	1:A:100:TRP:CA	1:A:100:TRP:C	1:A:101:PRO:N	3	1.4
(1,106)	1:A:94:ARG:N	1:A:94:ARG:CA	1:A:94:ARG:C	1:A:95:LEU:N	13	1.4
(1,58)	1:A:68:LYS:N	1:A:68:LYS:CA	1:A:68:LYS:C	1:A:69:ASP:N	19	1.3
(1,80)	1:A:79:THR:N	1:A:79:THR:CA	1:A:79:THR:C	1:A:80:LYS:N	7	1.2
(1,118)	1:A:102:LEU:N	1:A:102:LEU:CA	1:A:102:LEU:C	1:A:103:ALA:N	4	1.2
(1,61)	1:A:69:ASP:C	1:A:70:GLU:N	1:A:70:GLU:CA	1:A:70:GLU:C	10	1.1
(1,61)	1:A:69:ASP:C	1:A:70:GLU:N	1:A:70:GLU:CA	1:A:70:GLU:C	14	1.1
(1,60)	1:A:69:ASP:N	1:A:69:ASP:CA	1:A:69:ASP:C	1:A:70:GLU:N	17	1.1
(1,48)	1:A:62:ILE:N	1:A:62:ILE:CA	1:A:62:ILE:C	1:A:63:ASP:N	12	1.1