WORLDWIDE wwPDB PROTEIN DATA BANK

wwPDB NMR Structure Validation Summary Report ⓘ

Jun 3, 2023 – 06:09 PM EDT

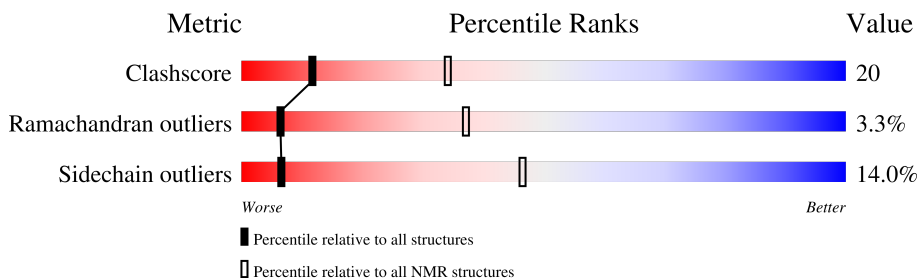|		
PDB ID	:	2KIS
BMRB ID	:	16293
Title	:	Solution structure of CA150 FF1 domain and FF1-FF2 interdomain linker
Authors	:	Murphy, J.M.; Hansen, D.; Wiesner, S.; Muhandiram, D.; Borg, M.; Smith, M.J.; Sicheri, F.; Kay, L.E.; Forman-Kay, J.D.; Pawson, T.
Deposited on	:	2009-05-08

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 81%.

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	Percentile Ranks	Value
Clashscore		20
Ramachandran outliers		3.3%
Sidechain outliers		14.0%

Worse   *Better*

■ Percentile relative to all structures

▯ Percentile relative to all NMR structures

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	71	46% 31% • 20%

2   Ensemble composition and analysis ⓘ

This entry contains 7 models. Model 2 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:618-A:674 (57)	0.31	2

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 and 2 single-model clusters were found.

Cluster number	Models
1	1, 2, 7
2	3, 6
Single-model clusters	4; 5

3 Entry composition ⓘ

There is only 1 type of molecule in this entry. The entry contains 1221 atoms, of which 619 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Transcription elongation regulator 1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	71	1221	381	619	110	108	3	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	613	GLY	-	linker	UNP O14776
A	614	ALA	-	linker	UNP O14776
A	615	MET	-	linker	UNP O14776
A	616	GLY	-	linker	UNP O14776
A	617	SER	-	linker	UNP O14776

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.
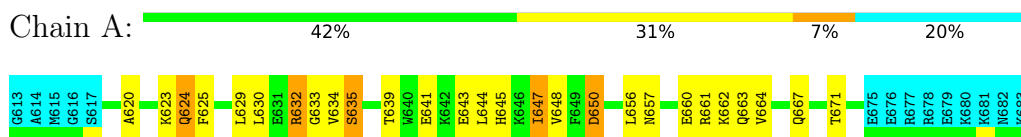
• Molecule 1: Transcription elongation regulator 1
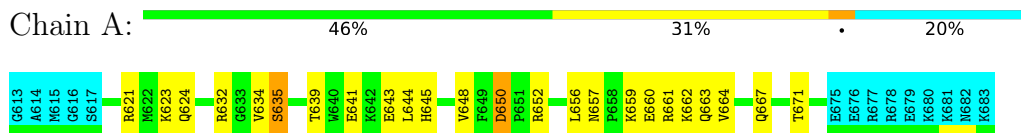
4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 2. Colouring as in section 4.1 above.

• Molecule 1: Transcription elongation regulator 1

5 Refinement protocol and experimental data overview ⓘ

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

Of the 20 calculated structures, 7 were deposited, based on the following criterion: *structures with the lowest energy.*

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

Software name	Classification	Version
ARIA	refinement	1.1

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	2
Total number of shifts	1270
Number of shifts mapped to atoms	1270
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	81%

6 Model quality ⓘ

6.1 Standard geometry ⓘ

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	490	503	503	20±4
All	All	3430	3521	3521	137

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 20.

5 of 51 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models Worst	Total
1:A:634:VAL:HG13	1:A:643:GLU:HB3	0.75	1.55	2	7
1:A:644:LEU:O	1:A:648:VAL:HG13	0.71	1.84	4	5
1:A:660:GLU:O	1:A:664:VAL:HG23	0.67	1.90	7	5
1:A:645:HIS:HA	1:A:648:VAL:HG22	0.62	1.71	4	5
1:A:667:GLN:O	1:A:671:THR:HG22	0.59	1.98	1	7

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	57/71 (80%)	44±1 (77±1%)	11±1 (19±2%)	2±1 (3±1%)	6	37
All	All	399/497 (80%)	309 (77%)	77 (19%)	13 (3%)	6	37

All 5 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	635	SER	7
1	A	633	GLY	3
1	A	658	PRO	1
1	A	640	TRP	1
1	A	644	LEU	1

6.3.2   Protein sidechains ⓘ

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	53/64 (83%)	46±2 (86±4%)	7±2 (14±4%)	6	46
All	All	371/448 (83%)	319 (86%)	52 (14%)	6	46

5 of 22 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	650	ASP	7
1	A	662	LYS	6
1	A	632	ARG	5
1	A	639	THR	5
1	A	623	LYS	4

6.3.3   RNA ⓘ

There are no RNA molecules in this entry.

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

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

6.5   Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.6   Ligand geometry ⓘ

There are no ligands in this entry.

6.7   Other polymers ⓘ

There are no such molecules in this entry.

6.8   Polymer linkage issues ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation ⓘ

The completeness of assignment taking into account all chemical shift lists is 81% for the well-defined parts and 77% 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	736
Number of shifts mapped to atoms	736
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 ± precision, *ppm*	Suggested action
$^{13}C_\alpha$	67	-0.07 ± 0.15	None needed ($<$ 0.5 ppm)
$^{13}C_\beta$	68	-0.30 ± 0.17	None needed ($<$ 0.5 ppm)
$^{13}C'$	0	—	None (insufficient data)
^{15}N	0	—	None (insufficient data)

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 73%, i.e. 634 atoms were assigned a chemical shift out of a possible 867. 0 out of 11 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	167/282 (59%)	112/113 (99%)	55/114 (48%)	0/55 (0%)
Sidechain	413/508 (81%)	276/326 (85%)	137/156 (88%)	0/26 (0%)

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|	**Total**	^{1}**H**	^{13}**C**	^{15}**N**
Aromatic	54/77 (70%)	31/38 (82%)	23/37 (62%)	0/2 (0%)
Overall	634/867 (73%)	419/477 (88%)	215/307 (70%)	0/83 (0%)

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:
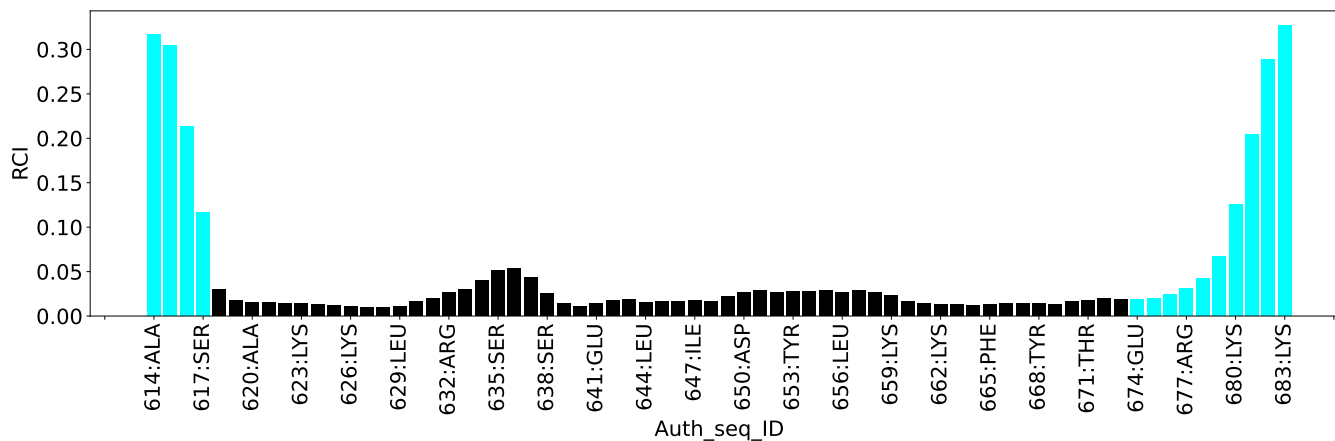
7.2   Chemical shift list 2

File name: working_cs.cif

Chemical shift list name: *assigned_ chem_ shift_ list_ 2*

7.2.1   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	534
Number of shifts mapped to atoms	534
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	5

7.2.2   Chemical shift referencing ⓘ

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_\alpha$	0	—	None (insufficient data)
$^{13}C_\beta$	0	—	None (insufficient data)
$^{13}C'$	0	—	None (insufficient data)
^{15}N	67	0.03 ± 0.38	None needed (< 0.5 ppm)

7.2.3   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 53%, i.e. 459 atoms were assigned a chemical shift out of a possible 867. 0 out of 11 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	166/282 (59%)	111/113 (98%)	0/114 (0%)	55/55 (100%)
Sidechain	266/508 (52%)	257/326 (79%)	0/156 (0%)	9/26 (35%)
Aromatic	27/77 (35%)	26/38 (68%)	0/37 (0%)	1/2 (50%)
Overall	459/867 (53%)	394/477 (83%)	0/307 (0%)	65/83 (78%)

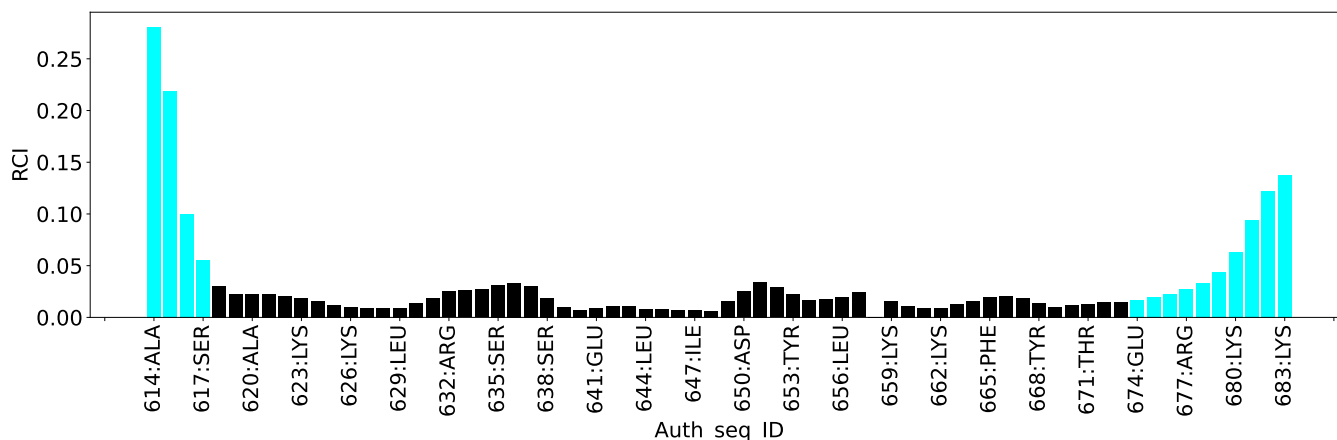### 7.2.4   Statistically unusual chemical shifts ⓘ

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
2	A	661	ARG	NE	111.83	$76.53 - 92.65$	16.9
2	A	672	ARG	NE	110.81	$76.53 - 92.65$	16.3
2	A	632	ARG	NE	110.61	$76.53 - 92.65$	16.1
2	A	652	ARG	NE	110.20	$76.53 - 92.65$	15.9
2	A	621	ARG	NE	109.80	$76.53 - 92.65$	15.6

7.2.5 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 (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	2426
Intra-residue ($\lvert$i-j$\rvert$=0)	931
Sequential ($\lvert$i-j$\rvert$=1)	567
Medium range ($\lvert$i-j$\rvert$>1 and $\lvert$i-j$\rvert$<5)	500
Long range ($\lvert$i-j$\rvert$$\geq$5)	428
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	34.2
Number of long range restraints per residue[1]	6.0

[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)	7.4	0.2
0.2-0.5 (Medium)	32.7	0.5
>0.5 (Large)	1691.7	6.35

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.

Restraints type	Count	$\%^1$	Violated[3]			Consistently Violated[4]		
			Count	$\%^2$	$\%^1$	Count	$\%^2$	$\%^1$
Intra-residue (|i-j|=0)	931	38.4	430	46.2	17.7	408	43.8	16.8
Backbone-Backbone	68	2.8	19	27.9	0.8	19	27.9	0.8
Backbone-Sidechain	453	18.7	264	58.3	10.9	250	55.2	10.3
Sidechain-Sidechain	410	16.9	147	35.9	6.1	139	33.9	5.7
Sequential (|i-j|=1)	567	23.4	478	84.3	19.7	462	81.5	19.0
Backbone-Backbone	167	6.9	107	64.1	4.4	107	64.1	4.4
Backbone-Sidechain	315	13.0	293	93.0	12.1	286	90.8	11.8
Sidechain-Sidechain	85	3.5	78	91.8	3.2	69	81.2	2.8
Medium range (|i-j|>1 & |i-j|<5)	500	20.6	472	94.4	19.5	455	91.0	18.8
Backbone-Backbone	169	7.0	169	100.0	7.0	168	99.4	6.9
Backbone-Sidechain	207	8.5	190	91.8	7.8	184	88.9	7.6
Sidechain-Sidechain	124	5.1	113	91.1	4.7	103	83.1	4.2
Long range (|i-j|≥5)	428	17.6	381	89.0	15.7	357	83.4	14.7
Backbone-Backbone	5	0.2	5	100.0	0.2	5	100.0	0.2
Backbone-Sidechain	144	5.9	131	91.0	5.4	126	87.5	5.2
Sidechain-Sidechain	279	11.5	245	87.8	10.1	226	81.0	9.3
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	2426	100.0	1761	72.6	72.6	1682	69.3	69.3
Backbone-Backbone	409	16.9	300	73.3	12.4	299	73.1	12.3
Backbone-Sidechain	1119	46.1	878	78.5	36.2	846	75.6	34.9
Sidechain-Sidechain	898	37.0	583	64.9	24.0	537	59.8	22.1

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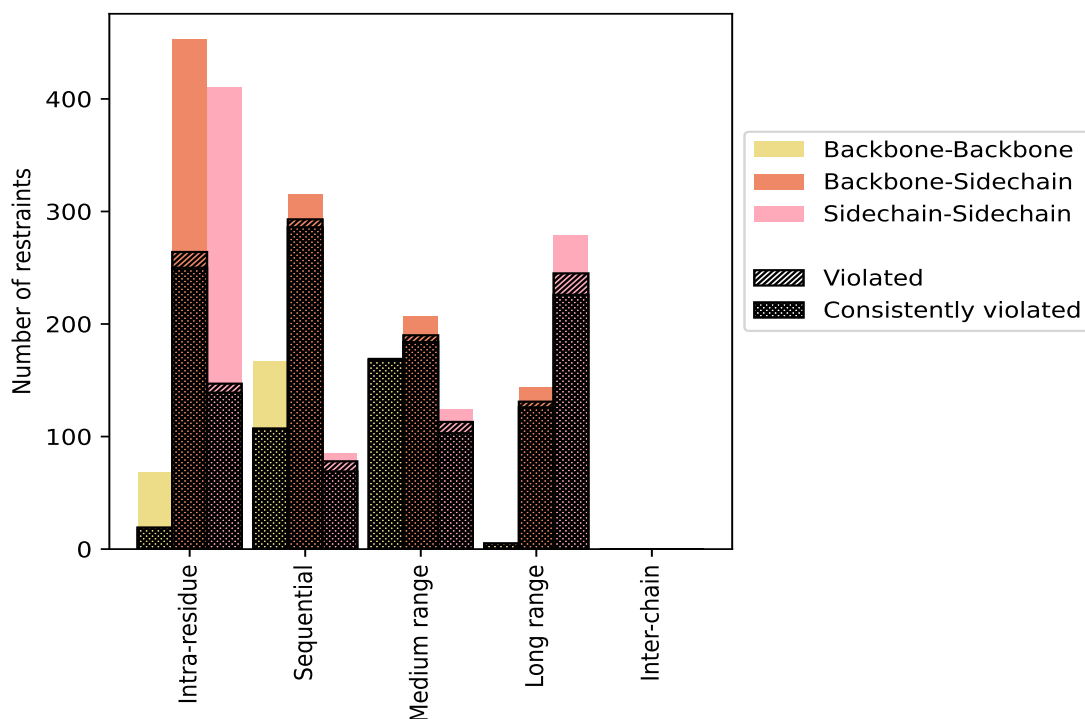
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories. The hydrogen bonds and disulfied bonds are counted in their appropriate category on the x-axis

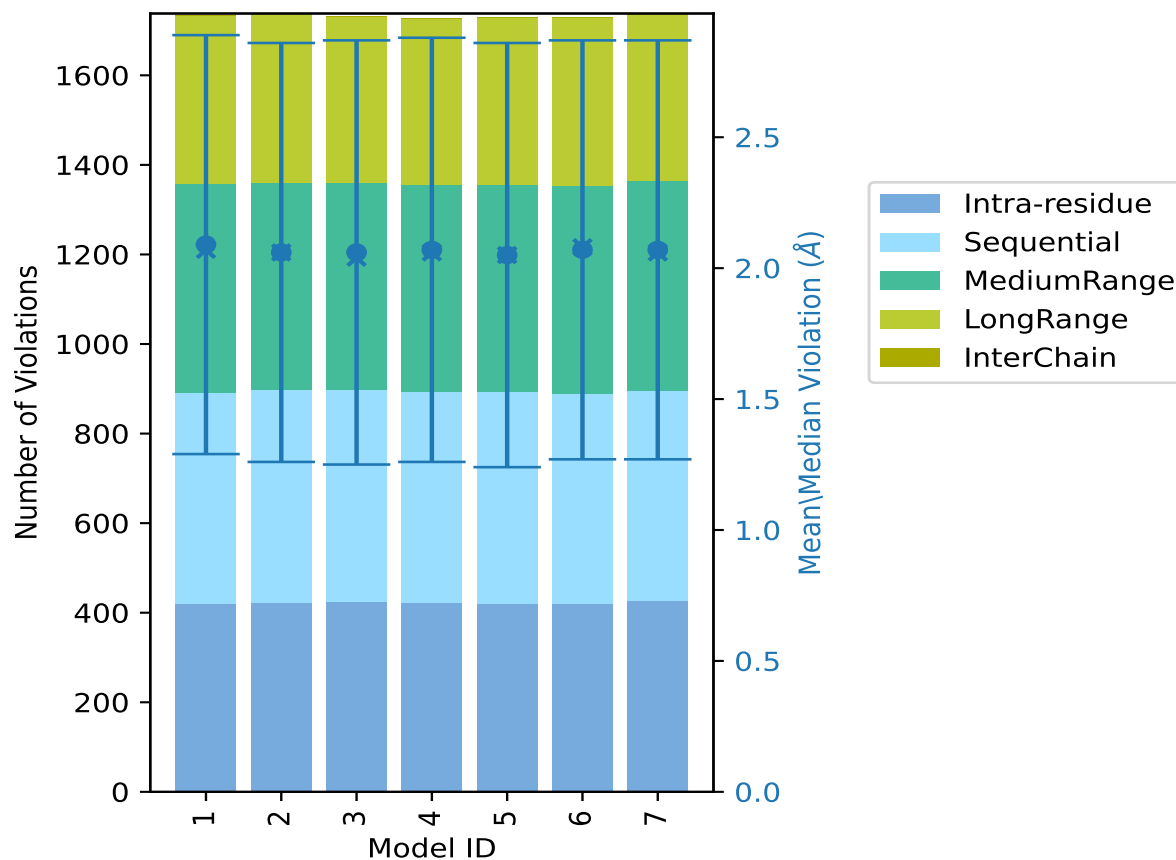## 9.2   Distance violation statistics for each model ⓘ

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	420	472	467	374	0	1733	2.09	5.05	0.8	2.07
2	423	474	463	377	0	1737	2.06	5.55	0.8	2.06
3	425	474	461	371	0	1731	2.06	6.35	0.81	2.04
4	422	472	461	372	0	1727	2.07	6.19	0.81	2.06
5	420	473	463	373	0	1729	2.05	5.71	0.81	2.05
6	420	470	463	375	0	1728	2.07	5.73	0.8	2.08
7	427	469	467	375	0	1738	2.07	5.0	0.8	2.06

[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   ⓘ

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, 665(IR:501, SQ:89, MR:28, LR:47, 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	2	3	1	0	6	1	14.3
3	2	4	2	0	11	2	28.6
1	0	1	0	0	2	3	42.9
5	2	2	3	0	12	4	57.1
6	4	4	7	0	21	5	71.4
7	6	3	11	0	27	6	85.7
408	462	455	357	0	1682	7	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 ⓘ
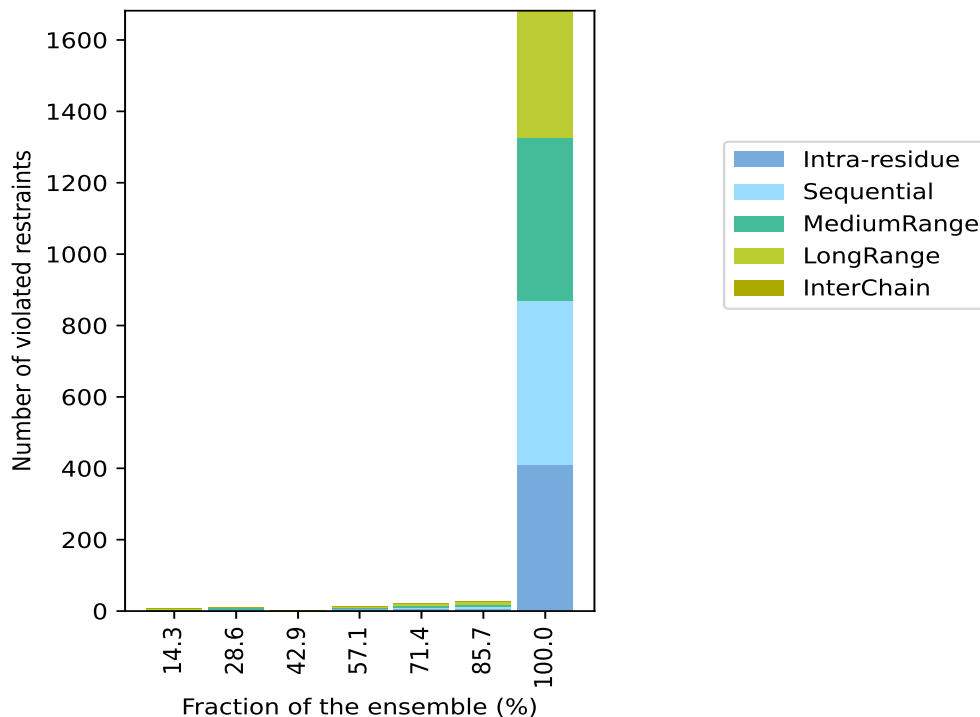
9.4 Most violated distance restraints in the ensemble ⓘ

9.4.1 Histogram : Distribution of mean distance 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
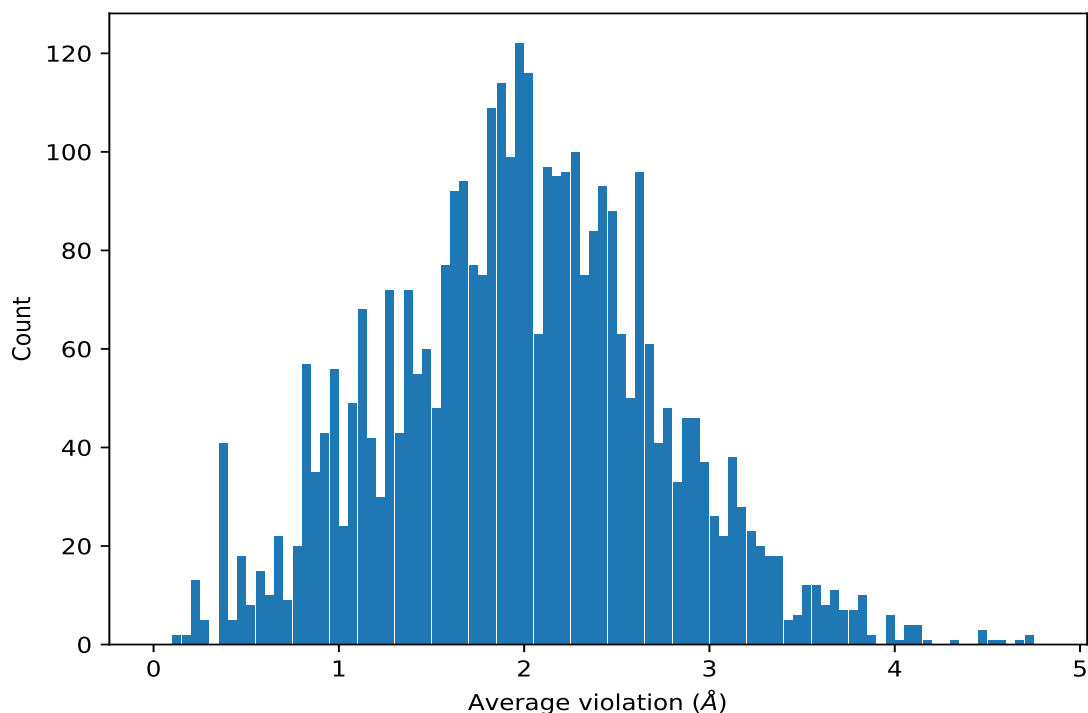
9.4.2 Table: Most violated distance restraints ⓘ

The following table provides the mean and the standard deviation of the violations for the 10 worst performing restraints, sorted by number of violated models and the mean violation 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)
(3,132)	1:A:661:ARG:H	1:A:658:PRO:HG3	7	4.74	0.32	4.86
(3,73)	1:A:664:VAL:H	1:A:662:LYS:HE2	7	4.73	0.6	4.98
(3,472)	1:A:674:GLU:HB3	1:A:673:ALA:HA	7	4.69	0.05	4.7
(1,1019)	1:A:634:VAL:HA	1:A:629:LEU:HB2	7	4.56	0.43	4.75
(1,326)	1:A:675:GLU:H	1:A:678:ARG:HB2	7	4.53	0.16	4.56
(3,233)	1:A:629:LEU:HD11	1:A:647:ILE:HA	7	4.45	1.15	3.77
(3,233)	1:A:629:LEU:HD12	1:A:647:ILE:HA	7	4.45	1.15	3.77
(3,233)	1:A:629:LEU:HD13	1:A:647:ILE:HA	7	4.45	1.15	3.77
(1,978)	1:A:669:VAL:HA	1:A:668:TYR:HB2	7	4.34	0.02	4.34
(1,1200)	1:A:671:THR:HA	1:A:670:LYS:HB2	7	4.17	0.41	4.33
(1,1111)	1:A:671:THR:HB	1:A:670:LYS:HB2	7	4.12	0.57	4.34
(3,445)	1:A:653:TYR:HE1	1:A:654:LEU:HB2	7	4.11	0.27	4.14

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

9.5 All violated distance restraints ⓘ

9.5.1 Histogram : Distribution of distance violations ⓘ

The following histogram shows the distribution of the absolute value of the violation for all violated restraints in the ensemble.
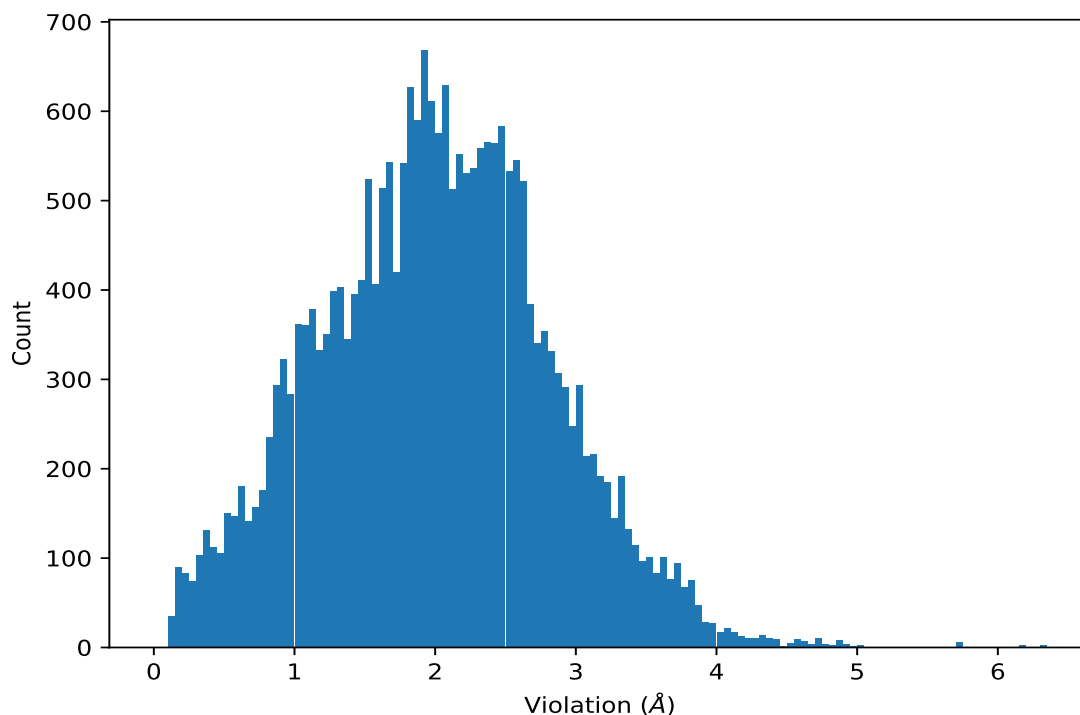
9.5.2 Table : All distance violations ⓘ

The following table provides the 10 worst performing restraints, sorted by the violation 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)
(3,233)	1:A:629:LEU:HD11	1:A:647:ILE:HA	3	6.35
(3,233)	1:A:629:LEU:HD12	1:A:647:ILE:HA	3	6.35
(3,233)	1:A:629:LEU:HD13	1:A:647:ILE:HA	3	6.35
(3,233)	1:A:629:LEU:HD11	1:A:647:ILE:HA	4	6.19
(3,233)	1:A:629:LEU:HD12	1:A:647:ILE:HA	4	6.19
(3,233)	1:A:629:LEU:HD13	1:A:647:ILE:HA	4	6.19
(1,1174)	1:A:640:TRP:HH2	1:A:648:VAL:HG11	6	5.73
(1,1174)	1:A:640:TRP:HH2	1:A:648:VAL:HG12	6	5.73
(1,1174)	1:A:640:TRP:HH2	1:A:648:VAL:HG13	6	5.73
(1,1174)	1:A:640:TRP:HH2	1:A:648:VAL:HG11	5	5.71
(1,1174)	1:A:640:TRP:HH2	1:A:648:VAL:HG12	5	5.71

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1174)	1:A:640:TRP:HH2	1:A:648:VAL:HG13	5	5.71
(3,73)	1:A:664:VAL:H	1:A:662:LYS:HE2	2	5.55
(3,74)	1:A:665:PHE:H	1:A:662:LYS:HE2	6	5.32
(3,73)	1:A:664:VAL:H	1:A:662:LYS:HE2	1	5.05
(3,74)	1:A:665:PHE:H	1:A:662:LYS:HE2	3	5.03
(3,73)	1:A:664:VAL:H	1:A:662:LYS:HE2	4	5.03
(1,322)	1:A:657:ASN:HD22	1:A:659:LYS:HB2	7	5.0

10 Dihedral-angle violation analysis ⓘ

No dihedral-angle restraints found