



wwPDB NMR Structure Validation Summary Report ⓘ

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PDB ID : 5A3G
BMRB ID : 26580
Title : Structure of herpesvirus nuclear egress complex subunit M50
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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 : 4.02b-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

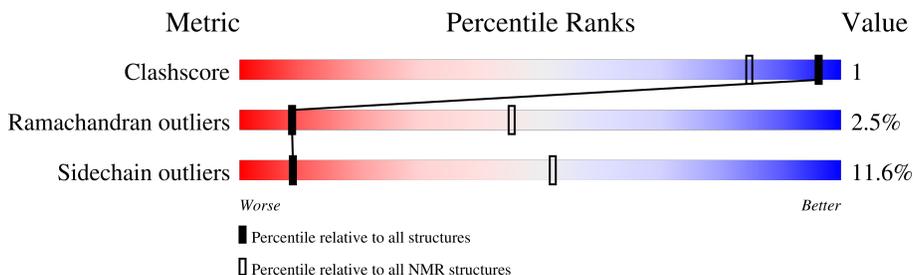
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 13%.

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	171	 79% 16% . .

2 Ensemble composition and analysis

This entry contains 15 models. Model 12 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative.

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:7-A:171 (165)	1.61	12

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	2, 3, 5, 6, 7, 8, 11, 12, 13
2	1, 10, 14, 15
Single-model clusters	4; 9

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2711 atoms, of which 1356 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called M50.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	171	2711	851	1356	234	258	12	0

There are 3 discrepancies between the modelled and reference sequences:

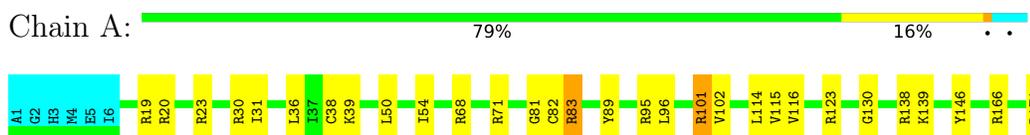
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ALA	-	expression tag	UNP H2A365
A	2	GLY	-	expression tag	UNP H2A365
A	3	HIS	-	expression tag	UNP H2A365

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.

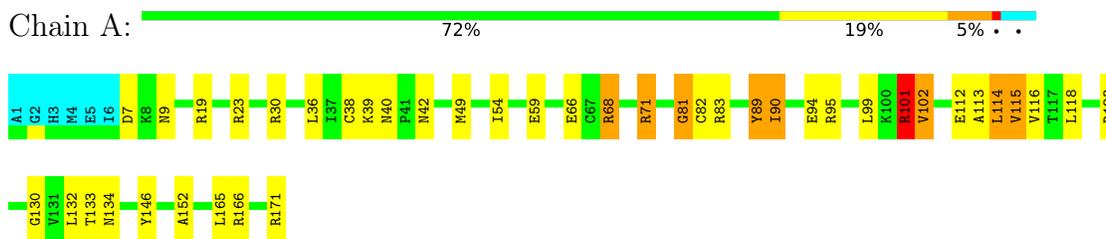
- Molecule 1: M50



4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 12. Colouring as in section 4.1 above.

- Molecule 1: M50



5 Refinement protocol and experimental data overview

The models were refined using the following method: *SIMULATED ANNEALING WITH TORSION ANGLE DYNAMICS SIMULATION FOLLOWED BY RDC AND WATERBOX REFINEMENT*.

Of the 50 calculated structures, 15 were deposited, based on the following criterion: *LOWEST ENERGY*.

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

Software name	Classification	Version
Amber	refinement	
CYANA	structure solution	3.0
NMRDraw	structure solution	11
TALOS+	structure solution	1.2009.0605.17
CcpNmr Analysis	structure solution	2.4
NMRPipe	structure solution	11
hmsIST	structure solution	2.11
CARA	structure solution	1.8.4

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	392
Number of shifts mapped to atoms	392
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	13%

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	0.74±0.01	0±0/1331 (0.0± 0.0%)	1.31±0.03	14±2/1801 (0.8± 0.1%)
All	All	0.74	0/19965 (0.0%)	1.31	208/27015 (0.8%)

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	9.3±2.0
All	All	0	140

There are no bond-length outliers.

5 of 33 unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	101	ARG	NE-CZ-NH1	12.11	126.36	120.30	7	11
1	A	123	ARG	NE-CZ-NH1	10.40	125.50	120.30	5	14
1	A	23	ARG	NE-CZ-NH1	9.38	124.99	120.30	11	14
1	A	19	ARG	NE-CZ-NH1	9.33	124.97	120.30	6	13
1	A	138	ARG	NE-CZ-NH1	9.06	124.83	120.30	7	13

There are no chirality outliers.

5 of 46 unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	89	TYR	Peptide,Sidechain	12
1	A	102	VAL	Peptide	12
1	A	101	ARG	Peptide	9

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Mol	Chain	Res	Type	Group	Models (Total)
1	A	82	CYS	Peptide	7
1	A	83	ARG	Peptide	7

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	1311	1313	1313	2±2
All	All	19665	19695	19695	31

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 1.

5 of 19 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:76:VAL:HG22	1:A:115:VAL:HG22	0.86	1.48	10	3
1:A:113:ALA:C	1:A:114:LEU:HD23	0.62	2.15	13	6
1:A:29:LEU:HD11	1:A:48:ALA:HB1	0.58	1.76	15	2
1:A:139:LYS:HE2	1:A:146:TYR:CD1	0.55	2.36	15	3
1:A:101:ARG:CD	1:A:102:VAL:H	0.53	2.17	5	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	164/171 (96%)	145±2 (88±2%)	15±2 (9±1%)	4±2 (3±1%)	9	45
All	All	2460/2565 (96%)	2176 (88%)	222 (9%)	62 (3%)	9	45

5 of 21 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	81	GLY	15
1	A	130	GLY	8
1	A	38	CYS	7
1	A	126	PRO	4
1	A	125	LYS	4

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	148/152 (97%)	131±3 (88±2%)	17±3 (12±2%)	9 52
All	All	2220/2280 (97%)	1963 (88%)	257 (12%)	9 52

5 of 83 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	139	LYS	13
1	A	36	LEU	12
1	A	114	LEU	12
1	A	101	ARG	11
1	A	54	ILE	9

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation i

The completeness of assignment taking into account all chemical shift lists is 13% for the well-defined parts and 13% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list*

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	392
Number of shifts mapped to atoms	392
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

The following errors were found when reading this chemical shift list.

- Chemical shift has been reported more than once. First 5 (of 0) occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	116	VAL	HG21	0.783	.	2
1	A	116	VAL	HG22	0.783	.	2
1	A	116	VAL	HG23	0.783	.	2
1	A	84	VAL	HG21	0.674	.	2
1	A	84	VAL	HG22	0.674	.	2
1	A	84	VAL	HG23	0.674	.	2
1	A	55	VAL	HG21	0.582	.	2
1	A	55	VAL	HG22	0.582	.	2
1	A	55	VAL	HG23	0.582	.	2
1	A	136	VAL	HG21	0.672	.	2
1	A	136	VAL	HG22	0.672	.	2
1	A	136	VAL	HG23	0.672	.	2
1	A	110	VAL	HG21	0.916	.	2
1	A	110	VAL	HG22	0.916	.	2

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	110	VAL	HG23	0.916	.	2
1	A	115	VAL	HG21	0.821	.	2
1	A	115	VAL	HG22	0.821	.	2
1	A	115	VAL	HG23	0.821	.	2
1	A	150	VAL	HG21	0.677	.	2
1	A	150	VAL	HG22	0.677	.	2
1	A	150	VAL	HG23	0.677	.	2
1	A	151	VAL	HG21	0.636	.	2
1	A	151	VAL	HG22	0.636	.	2
1	A	151	VAL	HG23	0.636	.	2
1	A	10	VAL	HG21	0.901	.	2
1	A	10	VAL	HG22	0.901	.	2
1	A	10	VAL	HG23	0.901	.	2
1	A	58	VAL	HG21	0.950	.	2
1	A	58	VAL	HG22	0.950	.	2
1	A	58	VAL	HG23	0.950	.	2
1	A	131	VAL	HG21	0.722	.	2
1	A	131	VAL	HG22	0.722	.	2
1	A	131	VAL	HG23	0.722	.	2
1	A	76	VAL	HG21	0.753	.	2
1	A	76	VAL	HG22	0.753	.	2
1	A	76	VAL	HG23	0.753	.	2
1	A	137	VAL	HG21	0.657	.	2
1	A	137	VAL	HG22	0.657	.	2
1	A	137	VAL	HG23	0.657	.	2
1	A	50	LEU	HD11	-0.155	.	2
1	A	50	LEU	HD12	-0.155	.	2
1	A	50	LEU	HD13	-0.155	.	2
1	A	62	LEU	HD11	0.172	.	2
1	A	62	LEU	HD12	0.172	.	2
1	A	62	LEU	HD13	0.172	.	2
1	A	45	LEU	HD11	0.714	.	2
1	A	45	LEU	HD12	0.714	.	2
1	A	45	LEU	HD13	0.714	.	2
1	A	96	LEU	HD11	-0.091	.	2
1	A	96	LEU	HD12	-0.091	.	2
1	A	96	LEU	HD13	-0.091	.	2
1	A	86	LEU	HD11	-0.197	.	2
1	A	86	LEU	HD12	-0.197	.	2
1	A	86	LEU	HD13	-0.197	.	2
1	A	14	LEU	HD11	-0.174	.	2

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	14	LEU	HD12	-0.174	.	2
1	A	14	LEU	HD13	-0.174	.	2
1	A	22	LEU	HD11	0.471	.	2
1	A	22	LEU	HD12	0.471	.	2
1	A	22	LEU	HD13	0.471	.	2
1	A	99	LEU	HD11	0.704	.	2
1	A	99	LEU	HD12	0.704	.	2
1	A	99	LEU	HD13	0.704	.	2
1	A	29	LEU	HD11	0.636	.	2
1	A	29	LEU	HD12	0.636	.	2
1	A	29	LEU	HD13	0.636	.	2
1	A	24	LEU	HD11	0.675	.	2
1	A	24	LEU	HD12	0.675	.	2
1	A	24	LEU	HD13	0.675	.	2
1	A	108	LEU	HD11	0.566	.	2
1	A	108	LEU	HD12	0.566	.	2
1	A	108	LEU	HD13	0.566	.	2
1	A	114	LEU	HD11	0.548	.	2
1	A	114	LEU	HD12	0.548	.	2
1	A	114	LEU	HD13	0.548	.	2
1	A	118	LEU	HD11	0.743	.	2
1	A	118	LEU	HD12	0.743	.	2
1	A	118	LEU	HD13	0.743	.	2
1	A	164	LEU	HD11	0.736	.	2
1	A	164	LEU	HD12	0.736	.	2
1	A	164	LEU	HD13	0.736	.	2
1	A	61	LEU	HD11	0.670	.	2
1	A	61	LEU	HD12	0.670	.	2
1	A	61	LEU	HD13	0.670	.	2
1	A	36	LEU	HD12	0.701	.	2
1	A	36	LEU	HD13	0.701	.	2
1	A	165	LEU	HD11	0.522	.	2
1	A	165	LEU	HD12	0.522	.	2
1	A	165	LEU	HD13	0.522	.	2
1	A	102	VAL	HG21	0.789	.	2
1	A	102	VAL	HG22	0.789	.	2
1	A	102	VAL	HG23	0.789	.	2

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 13%, i.e. 296 atoms were assigned a chemical shift out of a possible 2281. 0 out of 32 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	0/822 (0%)	0/332 (0%)	0/330 (0%)	0/160 (0%)
Sidechain	296/1315 (23%)	222/853 (26%)	74/402 (18%)	0/60 (0%)
Aromatic	0/144 (0%)	0/68 (0%)	0/75 (0%)	0/1 (0%)
Overall	296/2281 (13%)	222/1253 (18%)	74/807 (9%)	0/221 (0%)

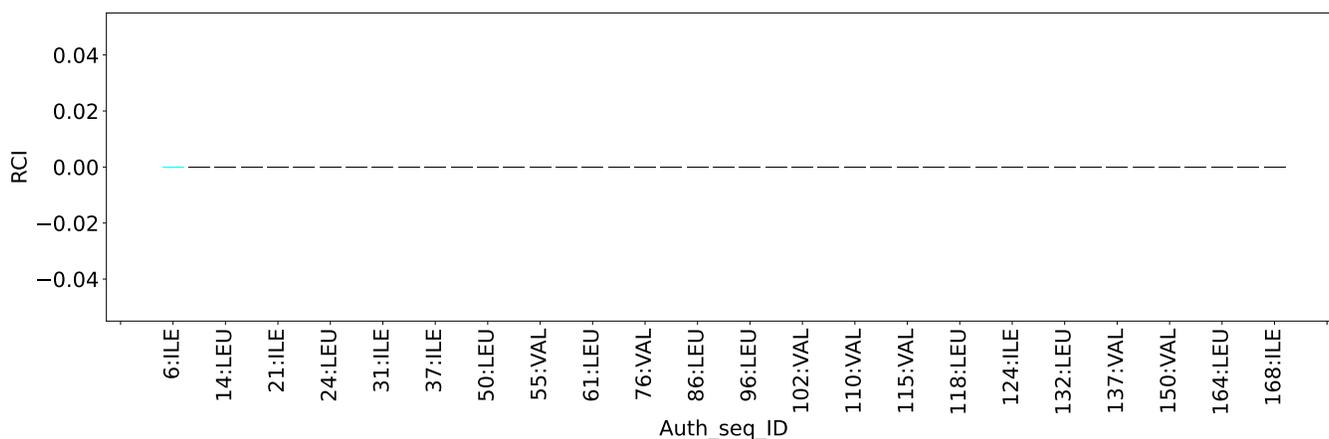
7.1.4 Statistically unusual chemical shifts [i](#)

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:



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	1458
Intra-residue ($ i-j =0$)	300
Sequential ($ i-j =1$)	499
Medium range ($ i-j >1$ and $ i-j <5$)	221
Long range ($ i-j \geq 5$)	350
Inter-chain	0
Hydrogen bond restraints	88
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	8.5
Number of long range restraints per residue ¹	2.3

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

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)	23.4	0.2
0.2-0.5 (Medium)	23.1	0.5
>0.5 (Large)	28.9	2.36

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](#)

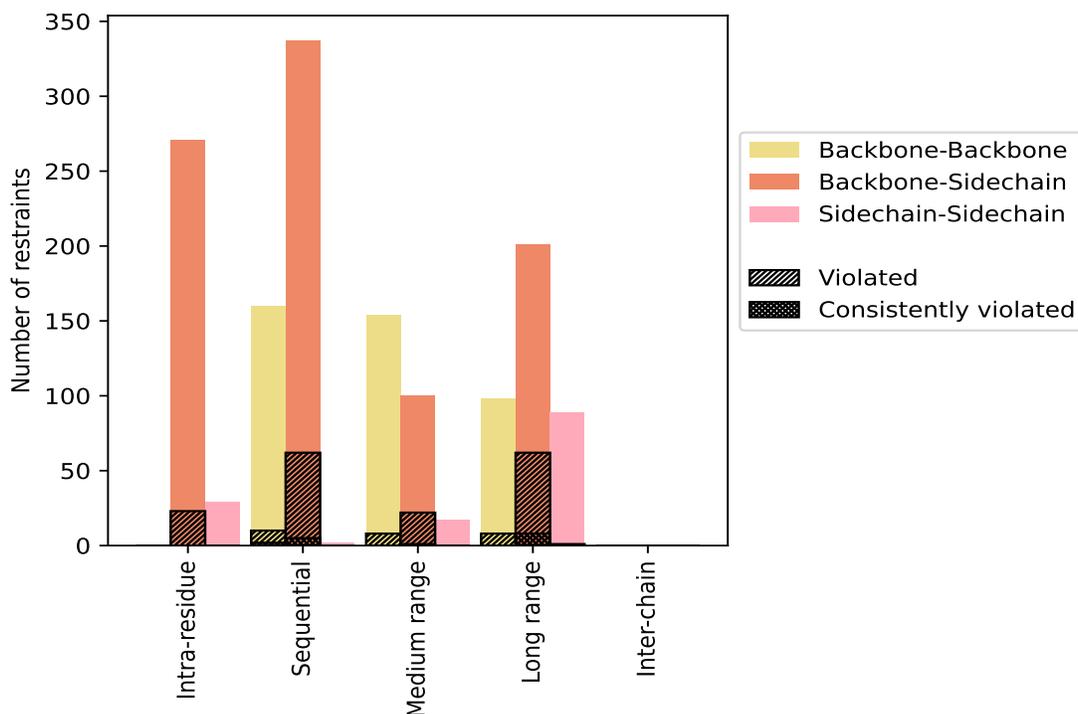
9.1 Summary of distance violations [i](#)

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 ($i-j =0$)	300	20.6	23	7.7	1.6	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	271	18.6	23	8.5	1.6	0	0.0	0.0
Sidechain-Sidechain	29	2.0	0	0.0	0.0	0	0.0	0.0
Sequential ($i-j =1$)	499	34.2	72	14.4	4.9	7	1.4	0.5
Backbone-Backbone	160	11.0	10	6.2	0.7	2	1.2	0.1
Backbone-Sidechain	337	23.1	62	18.4	4.3	5	1.5	0.3
Sidechain-Sidechain	2	0.1	0	0.0	0.0	0	0.0	0.0
Medium range ($i-j >1$ & $i-j <5$)	221	15.2	27	12.2	1.9	1	0.5	0.1
Backbone-Backbone	104	7.1	5	4.8	0.3	0	0.0	0.0
Backbone-Sidechain	100	6.9	22	22.0	1.5	1	1.0	0.1
Sidechain-Sidechain	17	1.2	0	0.0	0.0	0	0.0	0.0
Long range ($i-j \geq 5$)	350	24.0	65	18.6	4.5	8	2.3	0.5
Backbone-Backbone	60	4.1	2	3.3	0.1	0	0.0	0.0
Backbone-Sidechain	201	13.8	62	30.8	4.3	8	4.0	0.5
Sidechain-Sidechain	89	6.1	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	88	6.0	9	10.2	0.6	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	1458	100.0	196	13.4	13.4	16	1.1	1.1
Backbone-Backbone	412	28.3	26	6.3	1.8	2	0.5	0.1
Backbone-Sidechain	909	62.3	169	18.6	11.6	14	1.5	1.0
Sidechain-Sidechain	137	9.4	1	0.7	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 disulfid 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	12	27	5	29	0	73	0.48	1.8	0.36	0.32
2	6	34	8	37	0	85	0.53	2.06	0.46	0.34
3	8	29	5	31	0	73	0.5	1.83	0.41	0.34
4	5	37	5	34	0	81	0.52	2.07	0.45	0.37
5	8	31	6	28	0	73	0.51	1.87	0.4	0.39
6	8	32	7	34	0	81	0.5	1.84	0.43	0.38
7	10	29	4	34	0	77	0.52	1.73	0.43	0.32
8	6	32	8	31	0	77	0.52	1.86	0.46	0.32
9	4	31	7	29	0	71	0.51	1.94	0.47	0.35
10	10	25	5	32	0	72	0.57	1.92	0.5	0.38
11	7	24	9	28	0	68	0.47	1.85	0.4	0.38

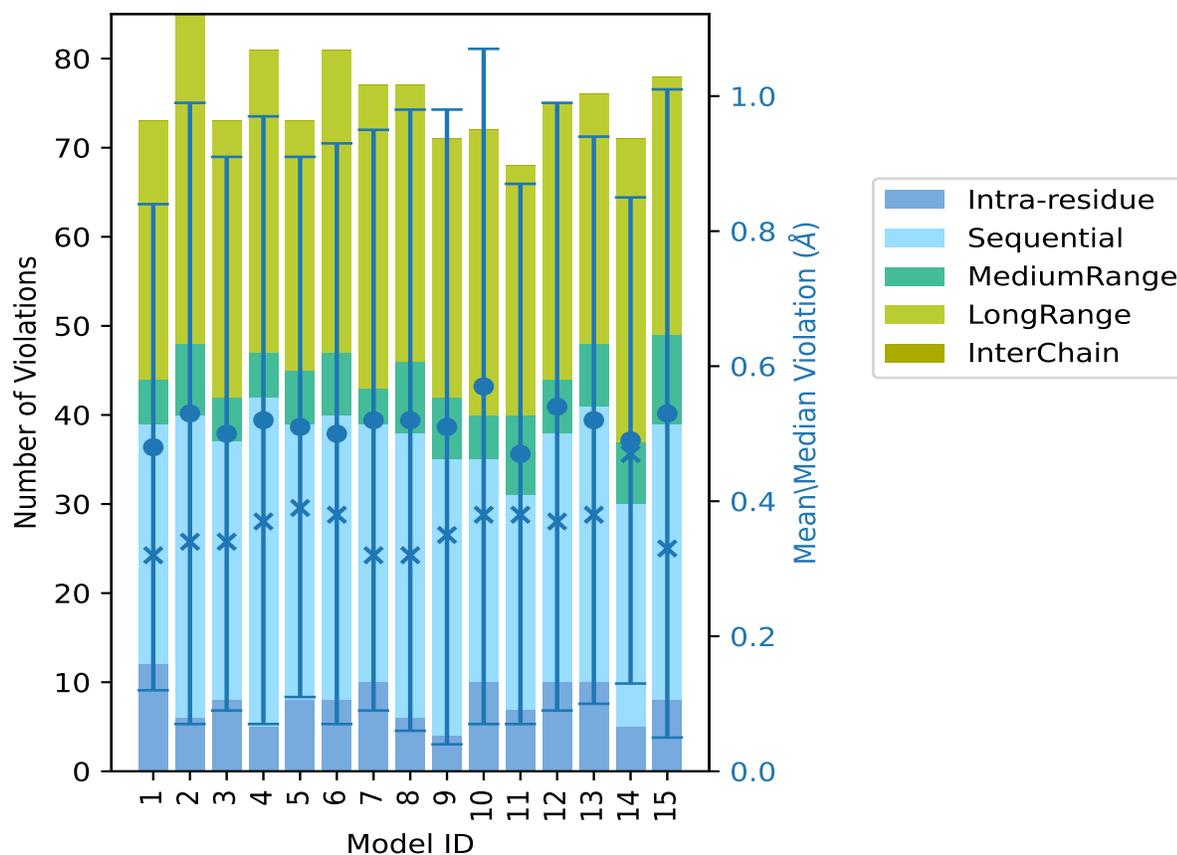
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
12	10	28	6	31	0	75	0.54	1.78	0.45	0.37
13	10	31	7	28	0	76	0.52	1.81	0.42	0.38
14	5	25	7	34	0	71	0.49	1.83	0.36	0.47
15	8	31	10	29	0	78	0.53	2.36	0.48	0.33

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 [i](#)



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

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

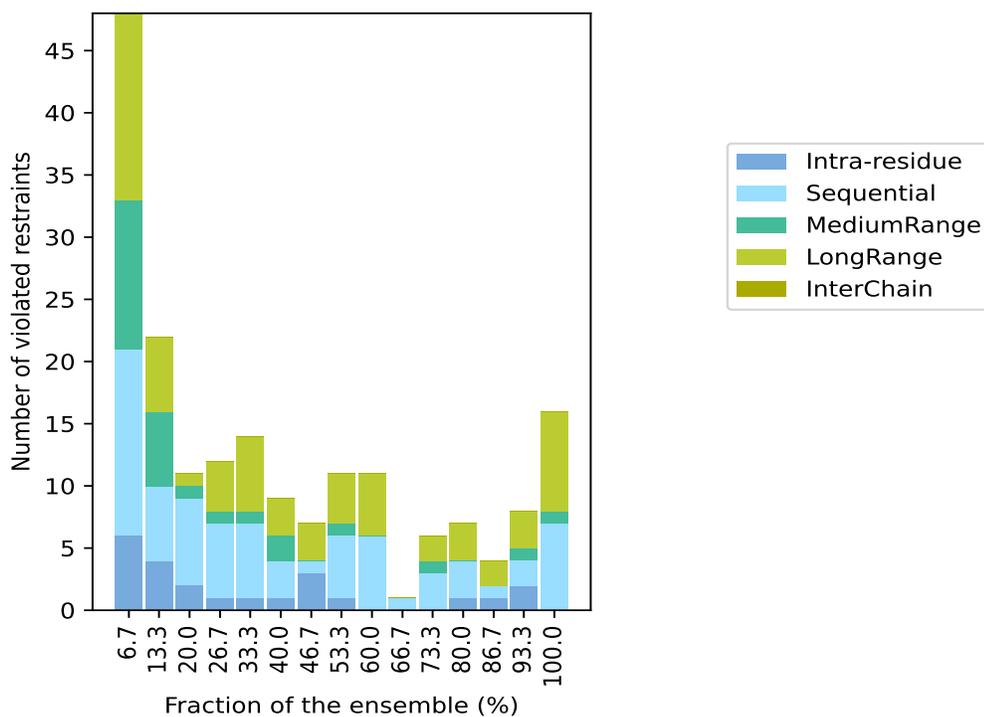
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for

a given fraction of the ensemble. In total, 1183(IR:277, SQ:427, MR:194, LR:285, 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	%
6	15	12	15	0	48	1	6.7
4	6	6	6	0	22	2	13.3
2	7	1	1	0	11	3	20.0
1	6	1	4	0	12	4	26.7
1	6	1	6	0	14	5	33.3
1	3	2	3	0	9	6	40.0
3	1	0	3	0	7	7	46.7
1	5	1	4	0	11	8	53.3
0	6	0	5	0	11	9	60.0
0	1	0	0	0	1	10	66.7
0	3	1	2	0	6	11	73.3
1	3	0	3	0	7	12	80.0
1	1	0	2	0	4	13	86.7
2	2	1	3	0	8	14	93.3
0	7	1	8	0	16	15	100.0

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

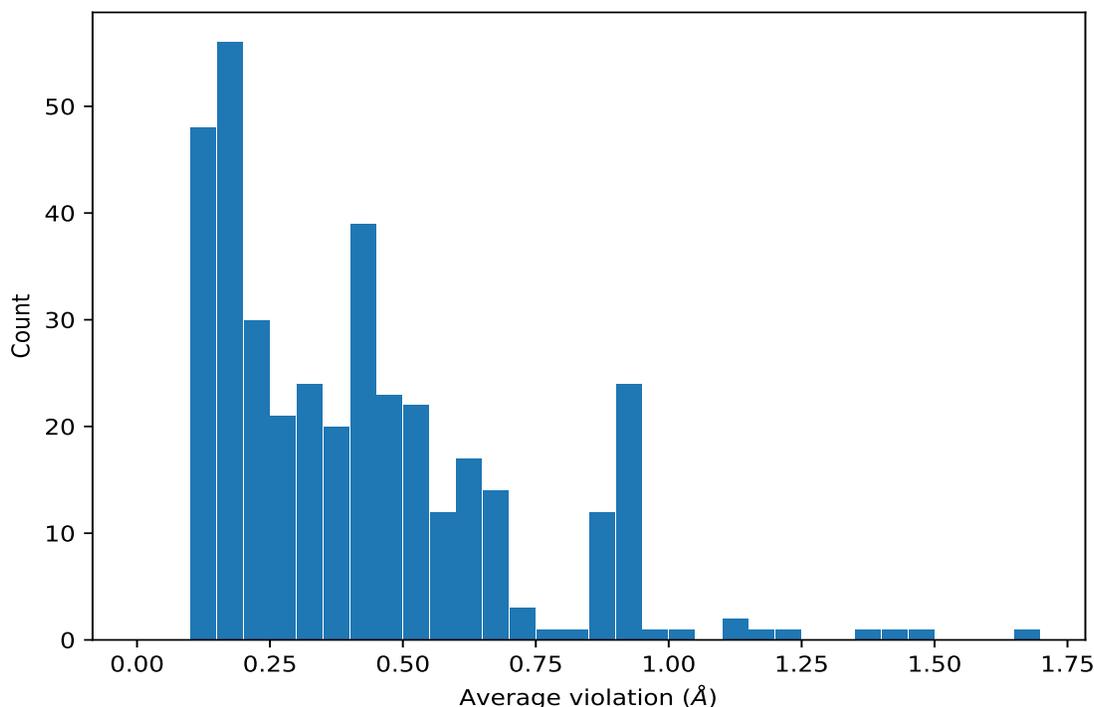
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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 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)
(1,1453)	1:A:78:LYS:HD2	1:A:95:ARG:H	15	1.44	0.5	1.69
(1,508)	1:A:29:LEU:H	1:A:30:ARG:HB3	15	1.39	0.08	1.41
(1,7)	1:A:45:LEU:HB2	1:A:88:CYS:H	15	1.14	0.31	1.09
(1,1188)	1:A:117:THR:H	1:A:118:LEU:HD11	15	0.9	0.41	0.94
(1,1188)	1:A:117:THR:H	1:A:118:LEU:HD12	15	0.9	0.41	0.94
(1,1188)	1:A:117:THR:H	1:A:118:LEU:HD13	15	0.9	0.41	0.94
(1,1188)	1:A:117:THR:H	1:A:118:LEU:HD21	15	0.9	0.41	0.94
(1,1188)	1:A:117:THR:H	1:A:118:LEU:HD22	15	0.9	0.41	0.94
(1,1188)	1:A:117:THR:H	1:A:118:LEU:HD23	15	0.9	0.41	0.94
(1,1090)	1:A:50:LEU:H	1:A:86:LEU:HD21	15	0.9	0.31	0.69
(1,1090)	1:A:50:LEU:H	1:A:86:LEU:HD22	15	0.9	0.31	0.69
(1,1090)	1:A:50:LEU:H	1:A:86:LEU:HD23	15	0.9	0.31	0.69
(1,1090)	1:A:50:LEU:H	1:A:86:LEU:HD11	15	0.9	0.31	0.69
(1,1090)	1:A:50:LEU:H	1:A:86:LEU:HD12	15	0.9	0.31	0.69
(1,1090)	1:A:50:LEU:H	1:A:86:LEU:HD13	15	0.9	0.31	0.69
(1,1141)	1:A:79:ASN:H	1:A:110:VAL:HG11	15	0.89	0.17	0.89

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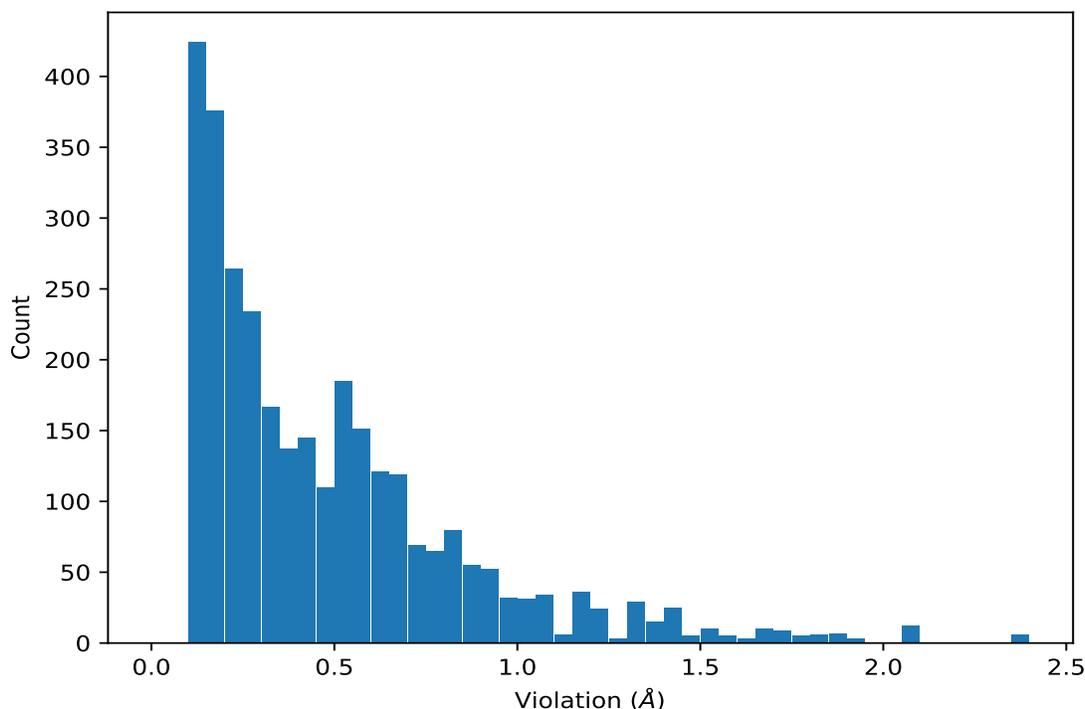
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,1141)	1:A:79:ASN:H	1:A:110:VAL:HG12	15	0.89	0.17	0.89
(1,1141)	1:A:79:ASN:H	1:A:110:VAL:HG13	15	0.89	0.17	0.89
(1,1141)	1:A:79:ASN:H	1:A:110:VAL:HG21	15	0.89	0.17	0.89
(1,1141)	1:A:79:ASN:H	1:A:110:VAL:HG22	15	0.89	0.17	0.89
(1,1141)	1:A:79:ASN:H	1:A:110:VAL:HG23	15	0.89	0.17	0.89
(1,384)	1:A:31:ILE:HG12	1:A:30:ARG:H	15	0.85	0.82	0.19
(1,1151)	1:A:85:SER:H	1:A:86:LEU:HD21	15	0.69	0.22	0.75
(1,1151)	1:A:85:SER:H	1:A:86:LEU:HD22	15	0.69	0.22	0.75
(1,1151)	1:A:85:SER:H	1:A:86:LEU:HD23	15	0.69	0.22	0.75
(1,1151)	1:A:85:SER:H	1:A:86:LEU:HD11	15	0.69	0.22	0.75
(1,1151)	1:A:85:SER:H	1:A:86:LEU:HD12	15	0.69	0.22	0.75
(1,1151)	1:A:85:SER:H	1:A:86:LEU:HD13	15	0.69	0.22	0.75
(1,1129)	1:A:113:ALA:H	1:A:76:VAL:HG21	15	0.64	0.19	0.61
(1,1129)	1:A:113:ALA:H	1:A:76:VAL:HG22	15	0.64	0.19	0.61
(1,1129)	1:A:113:ALA:H	1:A:76:VAL:HG23	15	0.64	0.19	0.61
(1,1129)	1:A:113:ALA:H	1:A:76:VAL:HG11	15	0.64	0.19	0.61
(1,1129)	1:A:113:ALA:H	1:A:76:VAL:HG12	15	0.64	0.19	0.61
(1,1129)	1:A:113:ALA:H	1:A:76:VAL:HG13	15	0.64	0.19	0.61
(1,1080)	1:A:32:THR:H	1:A:45:LEU:HD11	15	0.49	0.2	0.5

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 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)
(1,1114)	1:A:64:TYR:H	1:A:118:LEU:HD11	15	2.36
(1,1114)	1:A:64:TYR:H	1:A:118:LEU:HD12	15	2.36
(1,1114)	1:A:64:TYR:H	1:A:118:LEU:HD13	15	2.36
(1,1114)	1:A:64:TYR:H	1:A:118:LEU:HD21	15	2.36
(1,1114)	1:A:64:TYR:H	1:A:118:LEU:HD22	15	2.36
(1,1114)	1:A:64:TYR:H	1:A:118:LEU:HD23	15	2.36
(1,1114)	1:A:64:TYR:H	1:A:118:LEU:HD11	4	2.07
(1,1114)	1:A:64:TYR:H	1:A:118:LEU:HD12	4	2.07
(1,1114)	1:A:64:TYR:H	1:A:118:LEU:HD13	4	2.07
(1,1114)	1:A:64:TYR:H	1:A:118:LEU:HD21	4	2.07
(1,1114)	1:A:64:TYR:H	1:A:118:LEU:HD22	4	2.07
(1,1114)	1:A:64:TYR:H	1:A:118:LEU:HD23	4	2.07
(1,1114)	1:A:64:TYR:H	1:A:118:LEU:HD11	2	2.06
(1,1114)	1:A:64:TYR:H	1:A:118:LEU:HD12	2	2.06
(1,1114)	1:A:64:TYR:H	1:A:118:LEU:HD13	2	2.06
(1,1114)	1:A:64:TYR:H	1:A:118:LEU:HD21	2	2.06
(1,1114)	1:A:64:TYR:H	1:A:118:LEU:HD22	2	2.06

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1114)	1:A:64:TYR:H	1:A:118:LEU:HD23	2	2.06
(1,889)	1:A:139:LYS:HG2	1:A:145:SER:H	9	1.94
(1,889)	1:A:139:LYS:HG2	1:A:145:SER:H	10	1.92
(1,883)	1:A:145:SER:H	1:A:139:LYS:HE3	15	1.92
(1,883)	1:A:145:SER:H	1:A:139:LYS:HE3	10	1.89
(1,385)	1:A:30:ARG:H	1:A:31:ILE:HG13	4	1.88
(1,384)	1:A:31:ILE:HG12	1:A:30:ARG:H	9	1.88
(1,384)	1:A:31:ILE:HG12	1:A:30:ARG:H	5	1.87

10 Dihedral-angle violation analysis

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