wwPDB NMR Structure Validation Summary Report

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BMRB ID	:	36385
Title	:	Solution structure of Gaussia Luciferase by NMR
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Deposited on	:	2020-09-17

This is a wwPDB NMR Structure Validation Summary 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 (i) 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 (1)) were used in the production of this report:

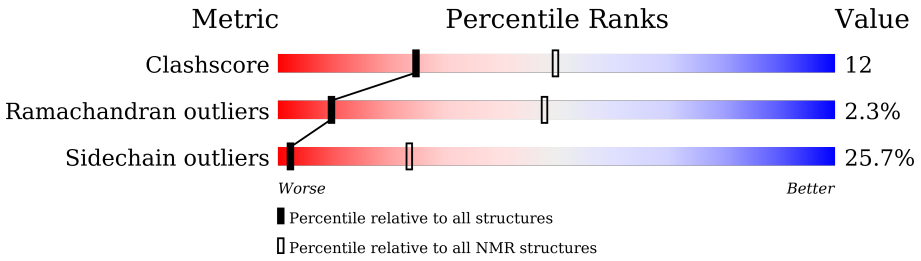
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.33

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
SOLUTION NMR

The overall completeness of chemical shifts assignment is 91%.

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	174	39% 25% 33% .

2 Ensemble composition and analysis

This entry contains 19 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: *target function*.

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:19, A:34-A:81, A:95-A:143 (110)	1.37	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 3 clusters. No single-model clusters were found.

Cluster number	Models
1	1, 2, 3, 4, 5, 6, 7, 10, 11, 13, 15, 16, 18
2	8, 9, 14, 19
3	12, 17

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 2552 atoms, of which 1284 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Luciferase.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	168	2552	793	1284	222	240	13	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	THR	-	expression tag	UNP Q9BLZ2
A	0	GLY	-	expression tag	UNP Q9BLZ2
A	100	ALA	GLU	engineered mutation	UNP Q9BLZ2
A	103	ARG	GLY	engineered mutation	UNP Q9BLZ2
A	169	ILE	-	expression tag	UNP Q9BLZ2
A	170	GLU	-	expression tag	UNP Q9BLZ2
A	171	GLY	-	expression tag	UNP Q9BLZ2
A	172	ARG	-	expression tag	UNP Q9BLZ2

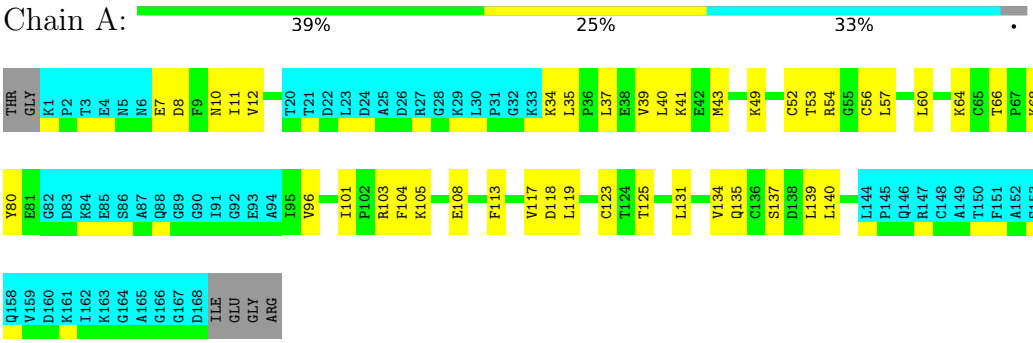
4 Residue-property plots (i)

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: Luciferase

Chain A:

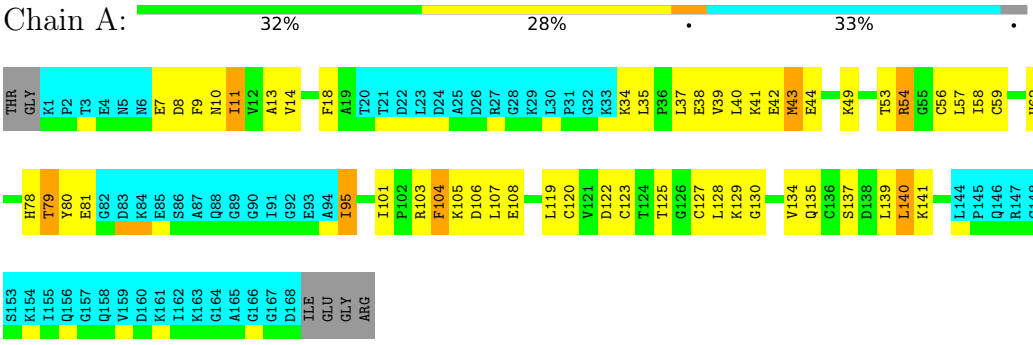


4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 18. Colouring as in section 4.1 above.

• Molecule 1: Luciferase

Chain A:



5 Refinement protocol and experimental data overview

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

Of the 200 calculated structures, 19 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
CYANA	structure calculation	3.98
CYANA	refinement	3.98

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	1960
Number of shifts mapped to atoms	1960
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	91%

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	853	874	874	20±4
All	All	16207	16606	16635	385

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 12.

5 of 202 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:56:CYS:SG	1:A:127:CYS:SG	1.11	2.48	5	6
1:A:123:CYS:SG	1:A:127:CYS:SG	1.07	2.53	11	3
1:A:12:VAL:HG23	1:A:40:LEU:HD12	0.95	1.39	7	1
1:A:35:LEU:HD12	1:A:39:VAL:HG11	0.94	1.39	13	4
1:A:14:VAL:HG11	1:A:60:LEU:HD12	0.87	1.42	14	2

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	110/174 (63%)	98±1 (89±1%)	9±2 (9±2%)	3±2 (2±1%)	9	48
All	All	2090/3306 (63%)	1863 (89%)	178 (9%)	49 (2%)	9	48

5 of 12 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	34	LYS	13
1	A	135	GLN	8
1	A	79	THR	6
1	A	96	VAL	4
1	A	80	TYR	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	96/142 (68%)	71±3 (74±3%)	25±3 (26±3%)	2	23
All	All	1824/2698 (68%)	1355 (74%)	469 (26%)	2	23

5 of 63 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	11	ILE	18
1	A	53	THR	18
1	A	135	GLN	17
1	A	8	ASP	16
1	A	137	SER	16

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 91% for the well-defined parts and 89% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *shift_set_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	1960
Number of shifts mapped to atoms	1960
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	166	-0.13 ± 0.12	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	152	0.19 ± 0.11	None needed (< 0.5 ppm)
$^{13}C'$	164	-0.18 ± 0.09	None needed (< 0.5 ppm)
^{15}N	158	0.58 ± 0.29	None needed (imprecise)

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 91%, i.e. 1362 atoms were assigned a chemical shift out of a possible 1504. 0 out of 18 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	538/543 (99%)	218/219 (100%)	217/220 (99%)	103/104 (99%)
Sidechain	746/876 (85%)	507/572 (89%)	228/274 (83%)	11/30 (37%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	78/85 (92%)	39/43 (91%)	38/39 (97%)	1/3 (33%)
Overall	1362/1504 (91%)	764/834 (92%)	483/533 (91%)	115/137 (84%)

7.1.4 Statistically unusual chemical shifts (i)

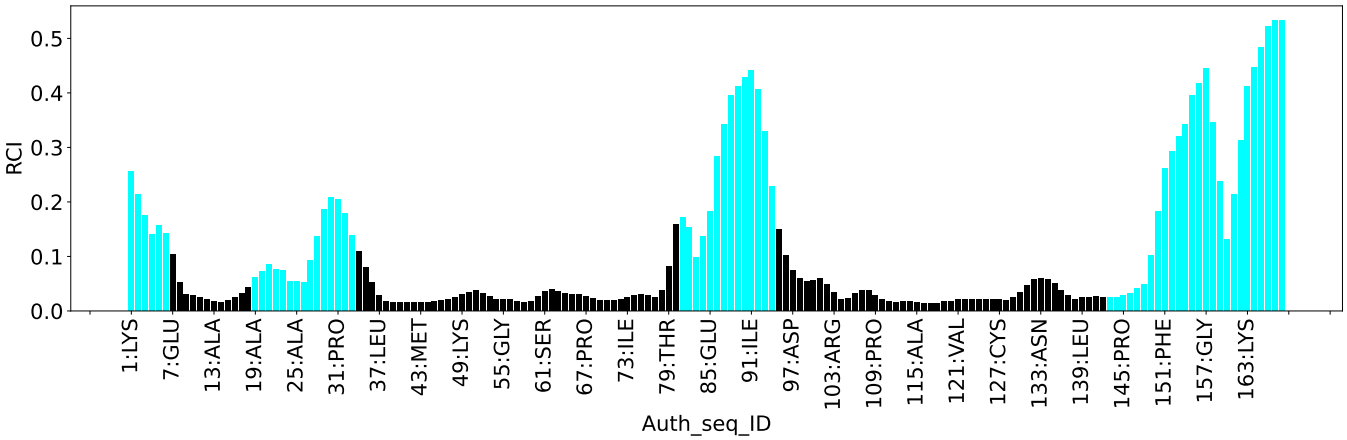
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	66	THR	HG1	6.05	0.08 – 2.19	23.3
1	A	124	THR	HG1	5.55	0.08 – 2.19	20.9

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	47379
Intra-residue (|i-j|=0)	10107
Sequential (|i-j|=1)	13282
Medium range (|i-j|>1 and |i-j|<5)	13121
Long range (|i-j|≥5)	10735
Inter-chain	0
Hydrogen bond restraints	86
Disulfide bond restraints	48
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	272.3
Number of long range restraints per residue[1]	61.9

[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

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)	802.3	0.2
0.2-0.5 (Medium)	1326.8	0.5
>0.5 (Large)	1825.4	12.56

8.2.2 Average number of dihedral-angle violations per model (i)

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

9 Distance violation analysis (i)

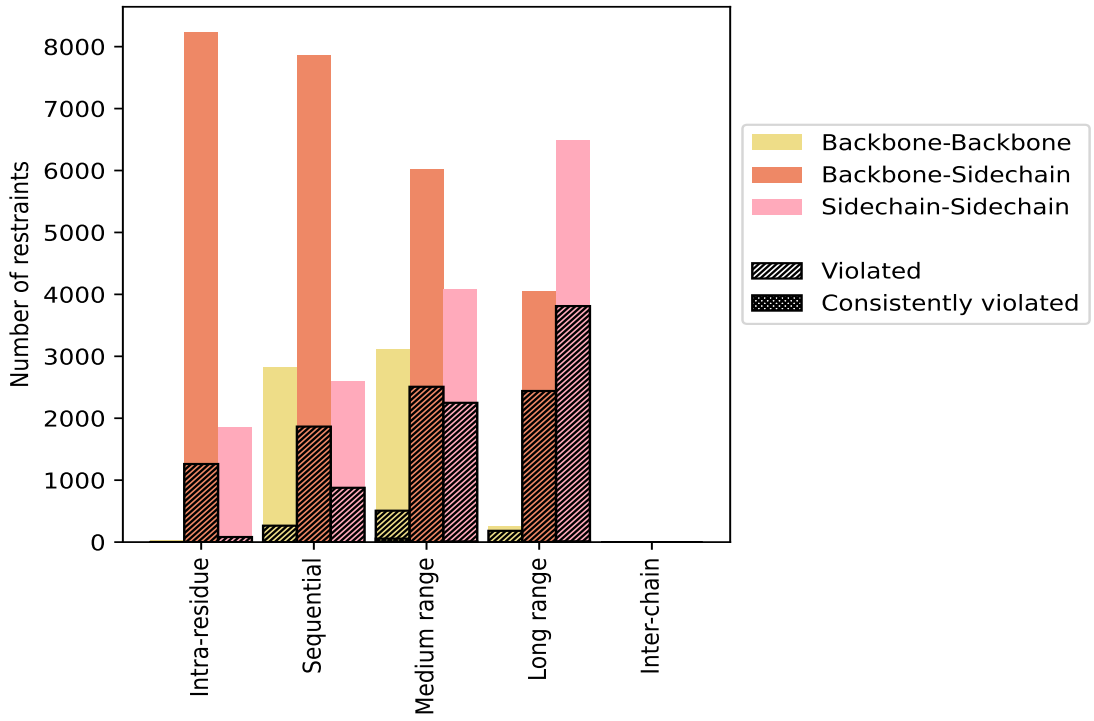
9.1 Summary of distance violations (i)

The following table shows the summary of distance violations in different restraint categories based on the sequence separation of the atoms involved. Each category is further sub-divided into three sub-categories based on the atoms involved. Violations less than 0.1 Å are not included in the statistics.

Restraints type	Count	%[1]	Violated[3]			Consistently Violated[4]		
			Count	%[2]	%[1]	Count	%[2]	%[1]
Intra-residue (|i-j|=0)	10107	21.3	1344	13.3	2.8	0	0.0	0.0
Backbone-Backbone	20	0.0	1	5.0	0.0	0	0.0	0.0
Backbone-Sidechain	8232	17.4	1261	15.3	2.7	0	0.0	0.0
Sidechain-Sidechain	1855	3.9	82	4.4	0.2	0	0.0	0.0
Sequential (|i-j|=1)	13282	28.0	3007	22.6	6.3	0	0.0	0.0
Backbone-Backbone	2826	6.0	265	9.4	0.6	0	0.0	0.0
Backbone-Sidechain	7857	16.6	1865	23.7	3.9	0	0.0	0.0
Sidechain-Sidechain	2599	5.5	877	33.7	1.9	0	0.0	0.0
Medium range (|i-j|>1 & |i-j|<5)	13121	27.7	5221	39.8	11.0	39	0.3	0.1
Backbone-Backbone	3026	6.4	476	15.7	1.0	38	1.3	0.1
Backbone-Sidechain	6024	12.7	2508	41.6	5.3	1	0.0	0.0
Sidechain-Sidechain	4071	8.6	2237	54.9	4.7	0	0.0	0.0
Long range (|i-j|≥5)	10735	22.7	6409	59.7	13.5	4	0.0	0.0
Backbone-Backbone	248	0.5	182	73.4	0.4	0	0.0	0.0
Backbone-Sidechain	4039	8.5	2440	60.4	5.1	3	0.1	0.0
Sidechain-Sidechain	6448	13.6	3787	58.7	8.0	1	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	86	0.2	31	36.0	0.1	18	20.9	0.0
Disulfide bond	48	0.1	36	75.0	0.1	23	47.9	0.0
Total	47379	100.0	16048	33.9	33.9	84	0.2	0.2
Backbone-Backbone	6204	13.1	955	15.4	2.0	56	0.9	0.1
Backbone-Sidechain	26154	55.2	8074	30.9	17.0	4	0.0	0.0
Sidechain-Sidechain	15021	31.7	7019	46.7	14.8	24	0.2	0.1

[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	237	606	1082	1522	0	3447	0.78	8.36	0.89	0.46
2	242	627	1362	1605	0	3836	0.76	10.02	0.93	0.43
3	232	714	1527	1831	0	4304	0.83	11.71	1.04	0.46
4	368	542	1303	1645	0	3858	0.85	10.7	1.18	0.45
5	260	609	1306	1688	0	3863	0.72	9.19	0.86	0.43
6	373	702	1556	1923	0	4554	0.79	12.21	1.05	0.44
7	265	477	1434	1787	0	3963	0.88	9.28	1.13	0.46
8	242	588	1332	1619	0	3781	0.74	9.14	0.99	0.42
9	204	528	1323	1423	0	3478	0.85	12.56	1.11	0.46
10	253	652	1396	1882	0	4183	0.79	10.34	0.9	0.46
11	314	716	1410	1733	0	4173	0.83	10.49	1.0	0.48

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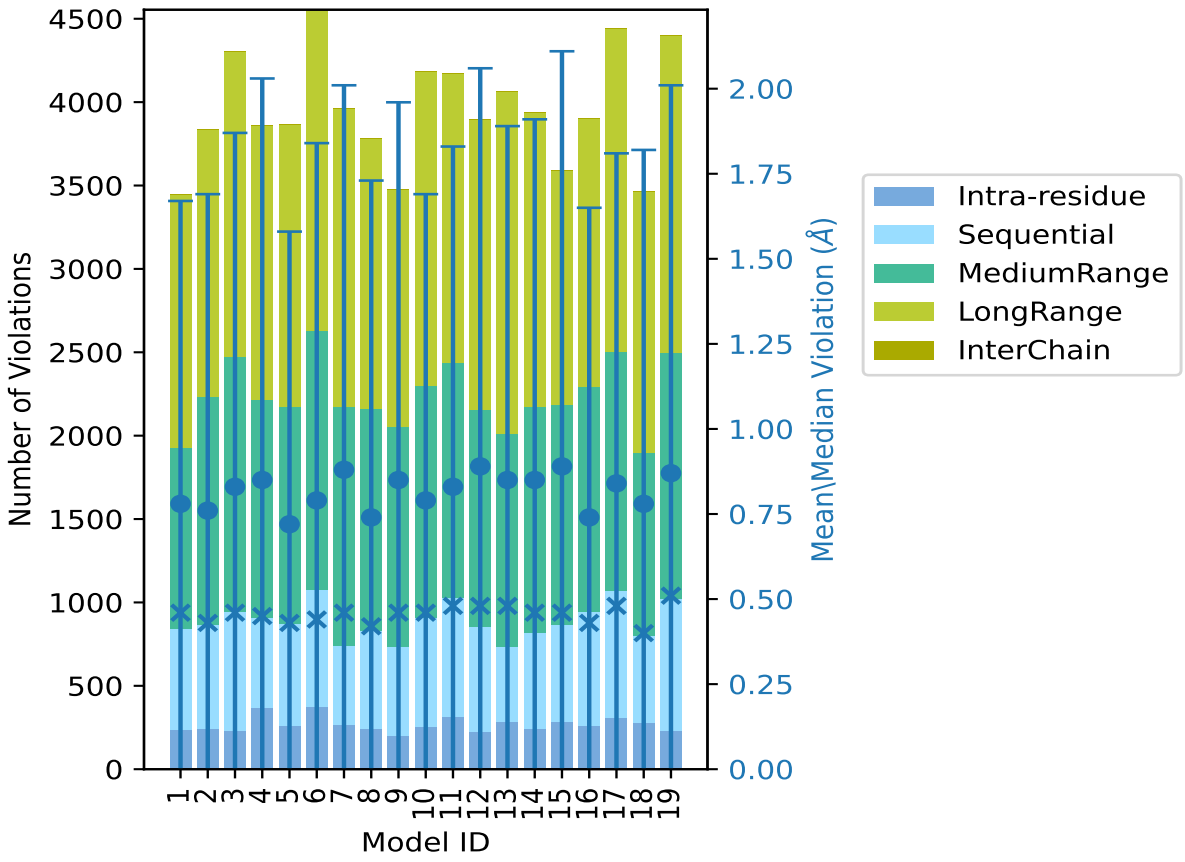
Model ID	Number of violations						Mean (Å)	Max (Å)	SD[6] (Å)	Median (Å)
	IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total				
12	226	629	1304	1734	0	3893	0.89	11.3	1.17	0.48
13	282	455	1274	2051	0	4062	0.85	10.19	1.04	0.48
14	240	578	1354	1767	0	3939	0.85	8.5	1.06	0.46
15	287	582	1314	1408	0	3591	0.89	11.24	1.22	0.46
16	258	687	1349	1610	0	3904	0.74	10.2	0.91	0.43
17	312	757	1436	1936	0	4441	0.84	9.05	0.97	0.48
18	281	517	1102	1563	0	3463	0.78	9.61	1.04	0.4
19	233	789	1478	1902	0	4402	0.87	12.19	1.14	0.51

[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

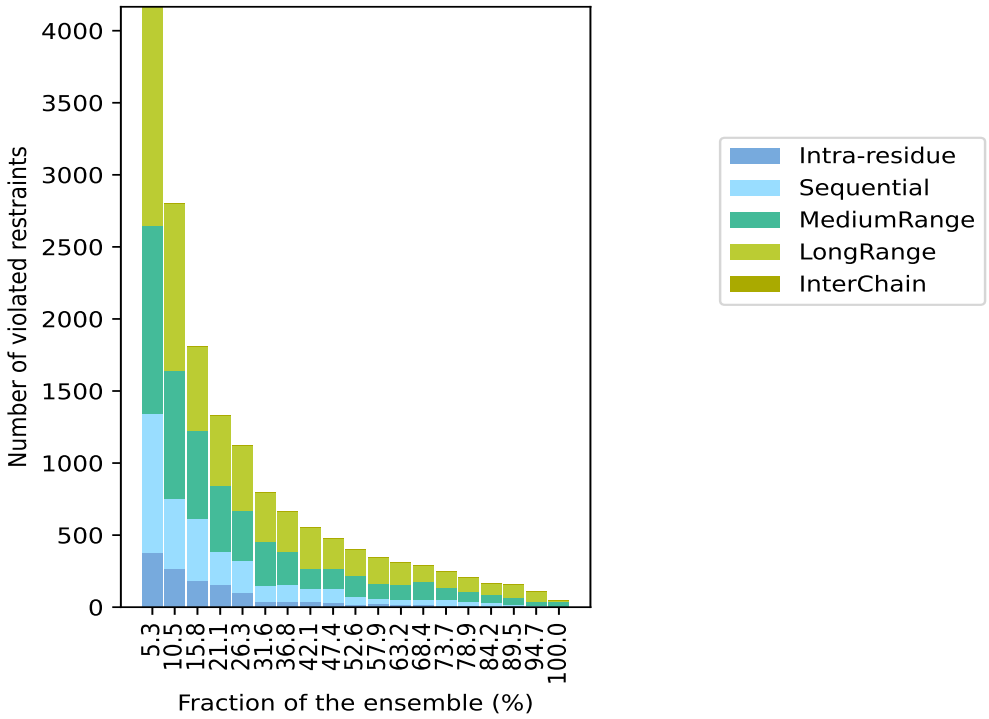
9.3 Distance violation statistics for the ensemble (i)

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, 31264(IR:8763, SQ:10275, MR:7900, LR:4326, 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]	%
378	964	1302	1522	0	4166	1	5.3
266	486	890	1159	0	2801	2	10.5
182	431	609	584	0	1806	3	15.8
154	232	454	490	0	1330	4	21.1
100	224	345	450	0	1119	5	26.3
39	108	306	342	0	795	6	31.6
41	113	229	278	0	661	7	36.8
39	89	139	284	0	551	8	42.1
35	92	138	214	0	479	9	47.4
17	57	143	182	0	399	10	52.6
28	28	106	183	0	345	11	57.9
18	31	108	156	0	313	12	63.2
16	34	129	107	0	286	13	68.4
7	41	87	114	0	249	14	73.7
9	30	70	100	0	209	15	78.9
5	25	55	79	0	164	16	84.2
6	13	44	96	0	159	17	89.5
4	9	28	65	0	106	18	94.7
0	0	39	4	0	43	19	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

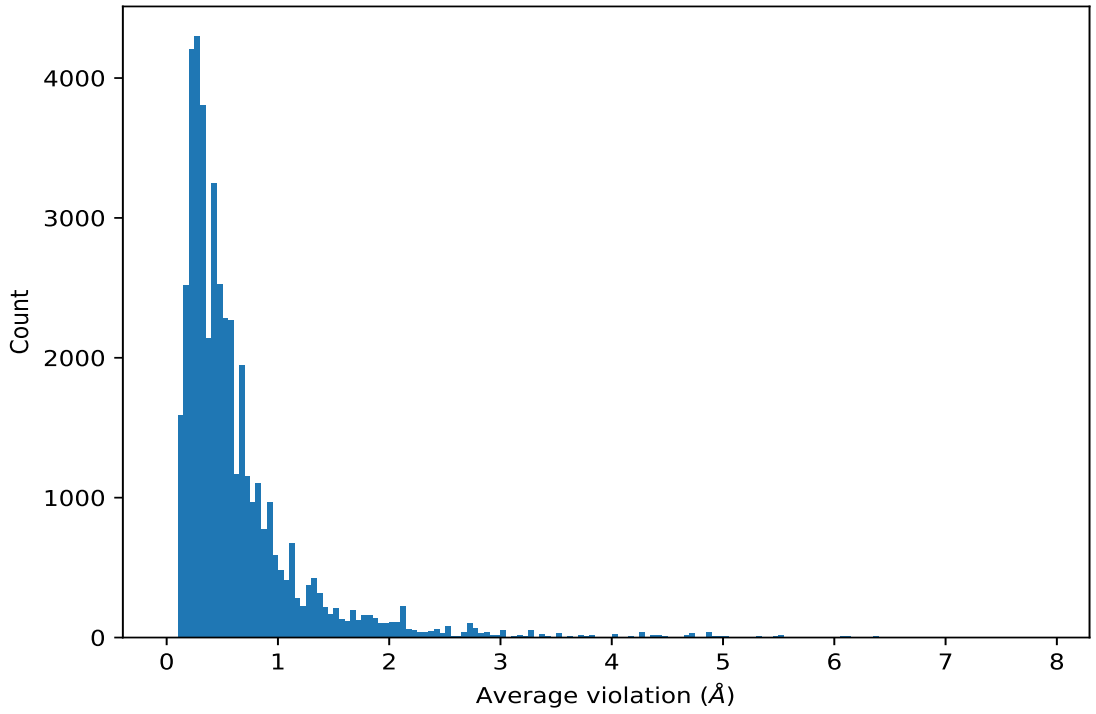
9.3.1 Bar graph : Distance violation statistics for the ensemble



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 (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.

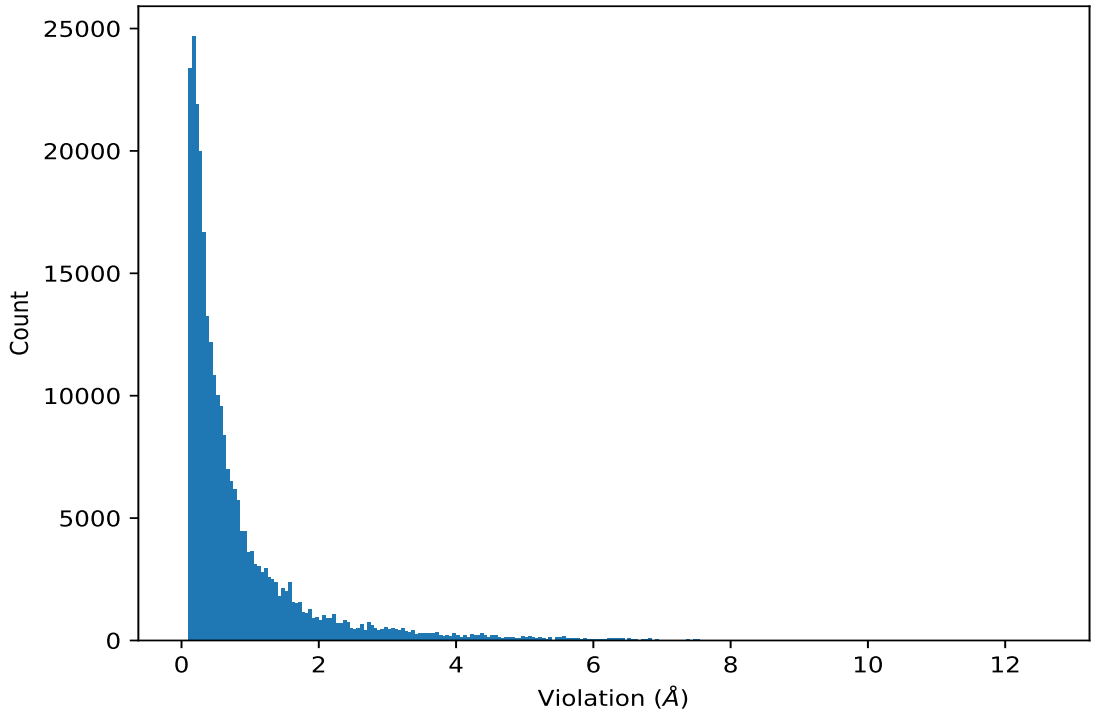
Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(20,7)	1:A:56:CYS:SG	1:A:120:CYS:SG	19	5.68	0.78	5.69
(20,12)	1:A:59:CYS:SG	1:A:123:CYS:SG	19	5.64	1.15	5.96
(20,10)	1:A:56:CYS:SG	1:A:59:CYS:SG	19	5.49	0.33	5.49
(20,1)	1:A:120:CYS:SG	1:A:123:CYS:SG	19	5.38	1.18	5.42
(19,1)	1:A:120:CYS:SG	1:A:56:CYS:CB	19	4.71	0.71	4.85
(19,23)	1:A:59:CYS:SG	1:A:123:CYS:CB	19	4.66	0.89	4.8
(19,3)	1:A:120:CYS:SG	1:A:123:CYS:CB	19	4.44	0.82	4.4
(19,17)	1:A:56:CYS:SG	1:A:120:CYS:CB	19	4.2	0.95	4.44
(19,24)	1:A:59:CYS:SG	1:A:56:CYS:CB	19	4.15	0.18	4.18
(1,913)	1:A:66:THR:HG21	1:A:95:ILE:HB	19	4.14	1.28	4.57

[1]Number of violated models, [2]Standard 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)
(5,748)	1:A:43:MET:HE1	1:A:147:ARG:HE	9	12.56
(5,748)	1:A:43:MET:HE2	1:A:147:ARG:HE	9	12.56
(5,748)	1:A:43:MET:HE3	1:A:147:ARG:HE	9	12.56
(17,756)	1:A:43:MET:HE1	1:A:147:ARG:HE	9	12.3
(17,756)	1:A:43:MET:HE2	1:A:147:ARG:HE	9	12.3
(17,756)	1:A:43:MET:HE3	1:A:147:ARG:HE	9	12.3
(5,748)	1:A:43:MET:HE1	1:A:147:ARG:HE	6	12.21
(5,748)	1:A:43:MET:HE2	1:A:147:ARG:HE	6	12.21
(5,748)	1:A:43:MET:HE3	1:A:147:ARG:HE	6	12.21
(5,748)	1:A:43:MET:HE1	1:A:147:ARG:HE	19	12.19
(5,748)	1:A:43:MET:HE2	1:A:147:ARG:HE	19	12.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(5,748)	1:A:43:MET:HE3	1:A:147:ARG:HE	19	12.19
(17,756)	1:A:43:MET:HE1	1:A:147:ARG:HE	6	11.95
(17,756)	1:A:43:MET:HE2	1:A:147:ARG:HE	6	11.95
(17,756)	1:A:43:MET:HE3	1:A:147:ARG:HE	6	11.95
(17,756)	1:A:43:MET:HE1	1:A:147:ARG:HE	19	11.93
(17,756)	1:A:43:MET:HE2	1:A:147:ARG:HE	19	11.93
(17,756)	1:A:43:MET:HE3	1:A:147:ARG:HE	19	11.93
(5,748)	1:A:43:MET:HE1	1:A:147:ARG:HE	3	11.71
(5,748)	1:A:43:MET:HE2	1:A:147:ARG:HE	3	11.71
(5,748)	1:A:43:MET:HE3	1:A:147:ARG:HE	3	11.71
(17,756)	1:A:43:MET:HE1	1:A:147:ARG:HE	3	11.45
(17,756)	1:A:43:MET:HE2	1:A:147:ARG:HE	3	11.45
(17,756)	1:A:43:MET:HE3	1:A:147:ARG:HE	3	11.45
(1,192)	1:A:68:LYS:HE2	1:A:93:GLU:H	12	11.3
(1,192)	1:A:68:LYS:HE3	1:A:93:GLU:H	12	11.3
(5,748)	1:A:43:MET:HE1	1:A:147:ARG:HE	15	11.24

10 Dihedral-angle violation analysis (i)

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