



wwPDB NMR Structure Validation Summary Report ⓘ

Mar 5, 2026 – 04:57 PM UTC

PDB ID : 2AN7 / pdb_00002an7
BMRB ID : 4792
Title : Solution structure of the bacterial antidote ParD
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Deposited on : 2005-08-11

This is a wwPDB NMR Structure Validation Summary Report for a publicly released PDB entry.

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with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
BMRB Restraints Analysis : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

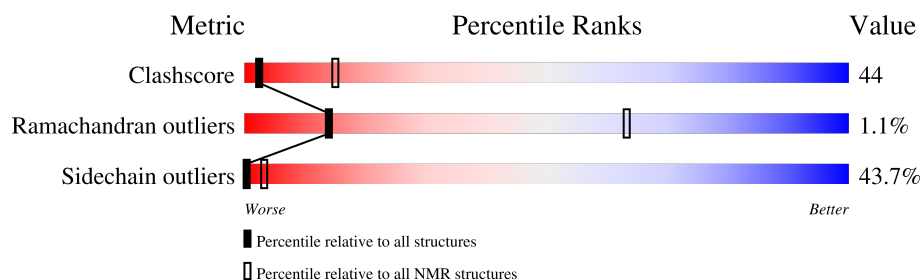
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 77%.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	83	
1	B	83	

2 Ensemble composition and analysis

This entry contains 24 models. Model 1 is the overall representative, medoid model (most similar to other models).

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:2-A:35, B:102-B:135 (68)	0.54	1
2	A:39-A:55 (17)	2.35	24

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.

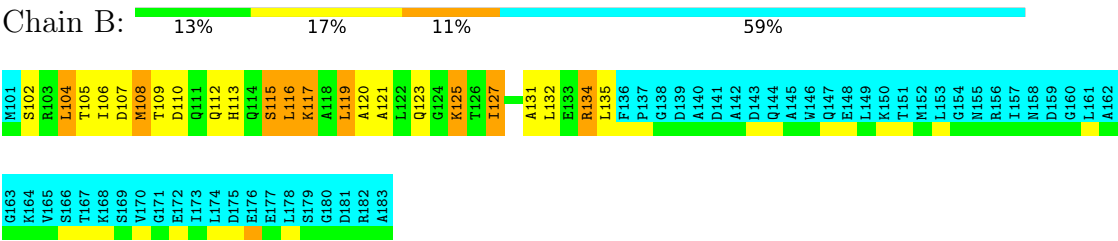
Cluster number	Models
1	1, 4, 7, 8, 9, 12, 14, 15, 17, 18, 19, 21, 22, 23, 24
2	2, 3, 10, 11, 13, 16, 20
3	5, 6

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 2556 atoms, of which 1282 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Protein parD.

Mol	Chain	Residues	Atoms						Trace
1	A	83	Total	C	H	N	O	S	0
			1278	391	641	113	130	3	
1	B	83	Total	C	H	N	O	S	0
			1278	391	641	113	130	3	



5 Refinement protocol and experimental data overview

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

Of the 150 calculated structures, 24 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
CNS	refinement	1.1
CNS	structure solution	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	1
Total number of shifts	1712
Number of shifts mapped to atoms	1712
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	77%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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 [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	402	406	405	40±6
1	B	270	287	286	38±7
All	All	16128	16632	16584	1437

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 44.

5 of 563 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:104:LEU:HD21	1:B:106:ILE:HD11	1.04	1.20	18	10
1:A:4:LEU:HD21	1:A:6:ILE:HD11	0.99	1.34	11	11
1:A:8:MET:HE2	1:B:132:LEU:HD12	0.95	1.38	17	2
1:A:35:LEU:HD12	1:B:108:MET:HE1	0.92	1.36	11	14
1:A:16:LEU:HD13	1:A:17:LYS:N	0.91	1.81	11	4

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	51/83 (61%)	45±2 (89±4%)	5±2 (10±4%)	1±1 (1±2%)	11	57
1	B	34/83 (41%)	32±1 (95±3%)	2±1 (5±3%)	0±0 (0±1%)	26	74
All	All	2040/3984 (51%)	1859 (91%)	159 (8%)	22 (1%)	14	63

5 of 11 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	54	GLY	4
1	A	10	ASP	3
1	B	102	SER	3
1	A	2	SER	2
1	A	52	MET	2

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	42/67 (63%)	24±3 (58±7%)	18±3 (42±7%)	0	4
1	B	29/67 (43%)	16±2 (54±6%)	13±2 (46±6%)	0	2
All	All	1704/3216 (53%)	959 (56%)	745 (44%)	0	3

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	8	MET	24
1	A	19	LEU	24
1	B	104	LEU	24
1	B	108	MET	24
1	B	119	LEU	24

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

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 77% 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	1712
Number of shifts mapped to atoms	1712
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	18

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	160	-1.39 ± 0.06	Should be checked
$^{13}\text{C}_\beta$	146	-0.20 ± 0.05	None needed (< 0.5 ppm)
$^{13}\text{C}'$	158	0.89 ± 0.39	Should be applied
^{15}N	158	0.43 ± 0.18	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 77%, i.e. 913 atoms were assigned a chemical shift out of a possible 1190. 0 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	405/428 (95%)	162/173 (94%)	162/170 (95%)	81/85 (95%)
Sidechain	495/716 (69%)	310/464 (67%)	172/220 (78%)	13/32 (41%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	13/46 (28%)	12/22 (55%)	0/19 (0%)	1/5 (20%)
Overall	913/1190 (77%)	484/659 (73%)	334/409 (82%)	95/122 (78%)

7.1.4 Statistically unusual chemical shifts ⓘ

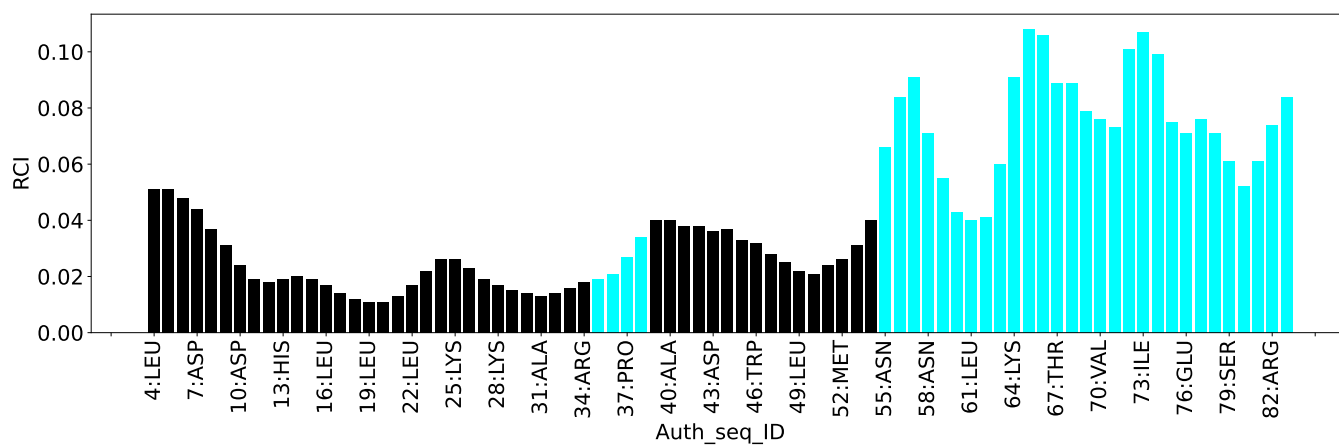
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	19	LEU	CG	67.09	21.37 – 32.19	37.3
1	B	119	LEU	CG	67.09	21.37 – 32.19	37.3
1	A	9	THR	CG2	61.67	16.06 – 27.03	36.6
1	B	109	THR	CG2	61.67	16.06 – 27.03	36.6
1	A	58	ASN	CG	112.29	164.52 – 188.90	-26.4
1	B	158	ASN	CG	112.29	164.52 – 188.90	-26.4
1	A	11	GLN	CD	171.82	173.59 – 185.85	-6.4
1	B	111	GLN	CD	171.82	173.59 – 185.85	-6.4
1	A	44	GLN	CD	171.87	173.59 – 185.85	-6.4
1	B	144	GLN	CD	171.87	173.59 – 185.85	-6.4
1	A	47	GLN	CD	172.04	173.59 – 185.85	-6.3
1	B	147	GLN	CD	172.04	173.59 – 185.85	-6.3
1	A	14	GLN	CD	172.05	173.59 – 185.85	-6.2
1	B	114	GLN	CD	172.05	173.59 – 185.85	-6.2
1	A	23	GLN	CD	172.28	173.59 – 185.85	-6.1
1	B	123	GLN	CD	172.28	173.59 – 185.85	-6.1
1	A	29	GLN	CD	172.37	173.59 – 185.85	-6.0
1	B	129	GLN	CD	172.37	173.59 – 185.85	-6.0

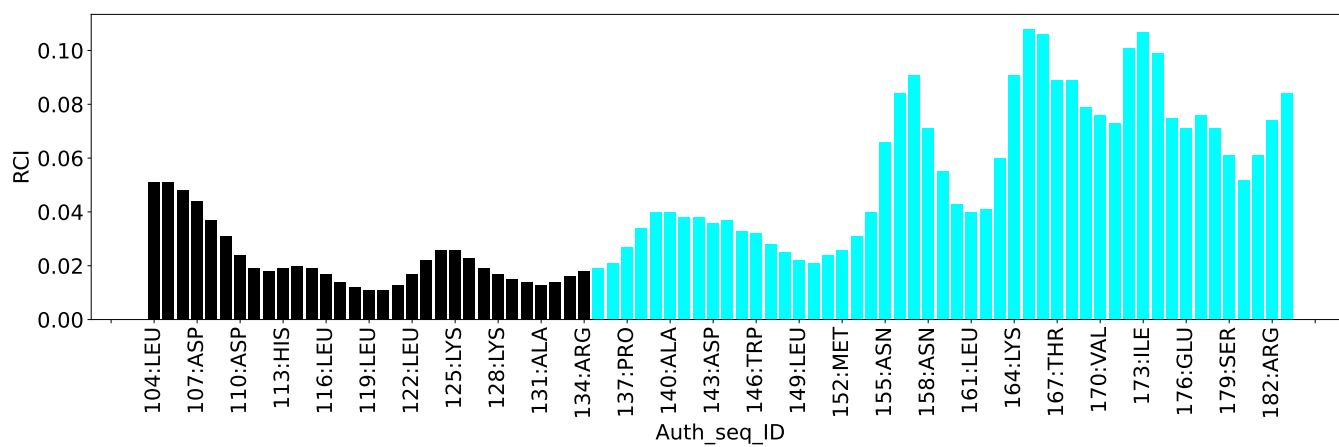
7.1.5 Random Coil Index (RCI) plots ⓘ

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:



Random coil index (RCI) for chain B:



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	2108
Intra-residue ($ i-j =0$)	862
Sequential ($ i-j =1$)	498
Medium range ($ i-j >1$ and $ i-j <5$)	300
Long range ($ i-j \geq 5$)	122
Inter-chain	326
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	12.7
Number of long range restraints per residue ¹	0.7

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)	13.5	0.2
0.2-0.5 (Medium)	2.6	0.5
>0.5 (Large)	2.0	1.53

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 ⓘ

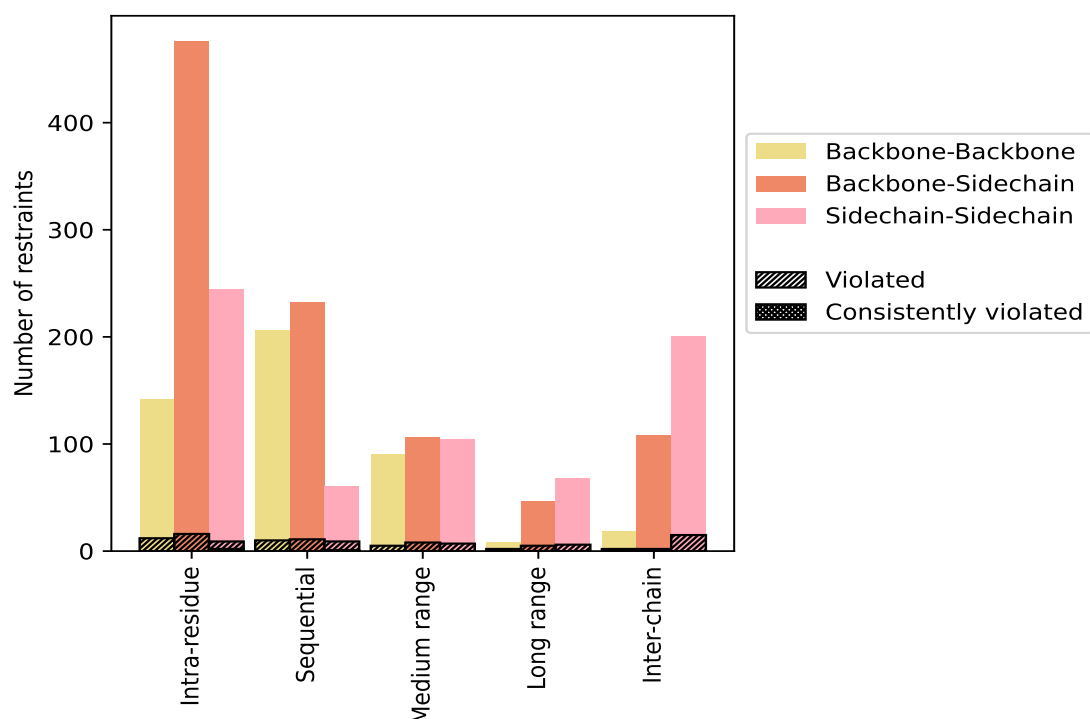
9.1 Summary of distance violations ⓘ

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)	862	40.9	37	4.3	1.8	2	0.2	0.1
Backbone-Backbone	142	6.7	12	8.5	0.6	0	0.0	0.0
Backbone-Sidechain	476	22.6	16	3.4	0.8	0	0.0	0.0
Sidechain-Sidechain	244	11.6	9	3.7	0.4	2	0.8	0.1
Sequential (i-j =1)	498	23.6	30	6.0	1.4	1	0.2	0.0
Backbone-Backbone	206	9.8	10	4.9	0.5	0	0.0	0.0
Backbone-Sidechain	232	11.0	11	4.7	0.5	0	0.0	0.0
Sidechain-Sidechain	60	2.8	9	15.0	0.4	1	1.7	0.0
Medium range (i-j >1 & i-j <5)	300	14.2	20	6.7	0.9	0	0.0	0.0
Backbone-Backbone	90	4.3	5	5.6	0.2	0	0.0	0.0
Backbone-Sidechain	106	5.0	8	7.5	0.4	0	0.0	0.0
Sidechain-Sidechain	104	4.9	7	6.7	0.3	0	0.0	0.0
Long range (i-j ≥5)	122	5.8	13	10.7	0.6	0	0.0	0.0
Backbone-Backbone	8	0.4	2	25.0	0.1	0	0.0	0.0
Backbone-Sidechain	46	2.2	5	10.9	0.2	0	0.0	0.0
Sidechain-Sidechain	68	3.2	6	8.8	0.3	0	0.0	0.0
Inter-chain	326	15.5	19	5.8	0.9	0	0.0	0.0
Backbone-Backbone	18	0.9	2	11.1	0.1	0	0.0	0.0
Backbone-Sidechain	108	5.1	2	1.9	0.1	0	0.0	0.0
Sidechain-Sidechain	200	9.5	15	7.5	0.7	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	2108	100.0	119	5.6	5.6	3	0.1	0.1
Backbone-Backbone	464	22.0	31	6.7	1.5	0	0.0	0.0
Backbone-Sidechain	968	45.9	42	4.3	2.0	0	0.0	0.0
Sidechain-Sidechain	676	32.1	46	6.8	2.2	3	0.4	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 [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	3	4	2	0	3	12	0.29	1.13	0.32	0.12
2	4	6	2	1	6	19	0.25	1.43	0.3	0.13
3	10	8	8	2	2	30	0.2	0.86	0.16	0.13
4	6	5	1	1	5	18	0.17	0.59	0.11	0.14
5	7	5	2	5	3	22	0.17	0.65	0.12	0.14
6	5	6	2	0	5	18	0.22	1.53	0.33	0.12
7	6	6	0	0	4	16	0.3	1.08	0.27	0.15
8	6	6	1	0	4	17	0.33	1.04	0.31	0.16
9	4	7	0	1	5	17	0.29	0.91	0.3	0.13
10	4	9	2	6	4	25	0.19	0.64	0.14	0.14

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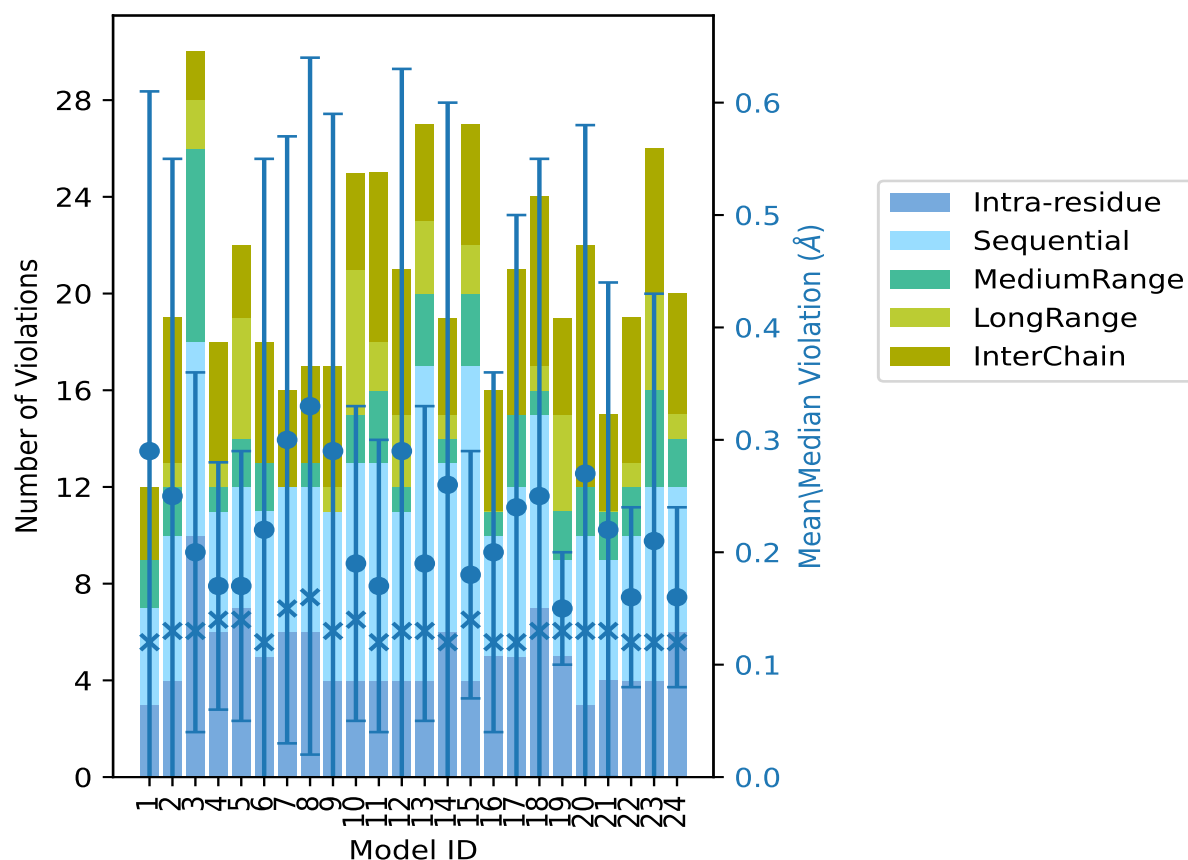
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	4	9	3	2	7	25	0.17	0.65	0.13	0.12
12	4	7	1	3	6	21	0.29	1.35	0.34	0.13
13	4	13	3	3	4	27	0.19	0.65	0.14	0.13
14	6	7	1	1	4	19	0.26	1.5	0.34	0.12
15	4	13	3	2	5	27	0.18	0.55	0.11	0.14
16	5	5	1	0	5	16	0.2	0.59	0.16	0.12
17	5	7	3	0	6	21	0.24	0.95	0.26	0.12
18	7	8	1	1	7	24	0.25	1.47	0.3	0.13
19	5	4	2	4	4	19	0.15	0.3	0.05	0.13
20	3	7	2	0	10	22	0.27	1.31	0.31	0.13
21	4	5	2	0	4	15	0.22	0.94	0.22	0.13
22	4	6	2	1	6	19	0.16	0.44	0.08	0.12
23	4	8	4	4	6	26	0.21	1.1	0.22	0.12
24	6	6	2	1	5	20	0.16	0.41	0.08	0.12

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, 1989(IR:825, SQ:468, MR:280, LR:109, IC:307) 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	%
22	8	14	2	7	53	1	4.2
6	8	4	6	1	25	2	8.3
2	4	0	3	2	11	3	12.5
1	2	0	0	0	3	4	16.7
1	1	0	0	0	2	5	20.8
2	1	0	0	1	4	6	25.0

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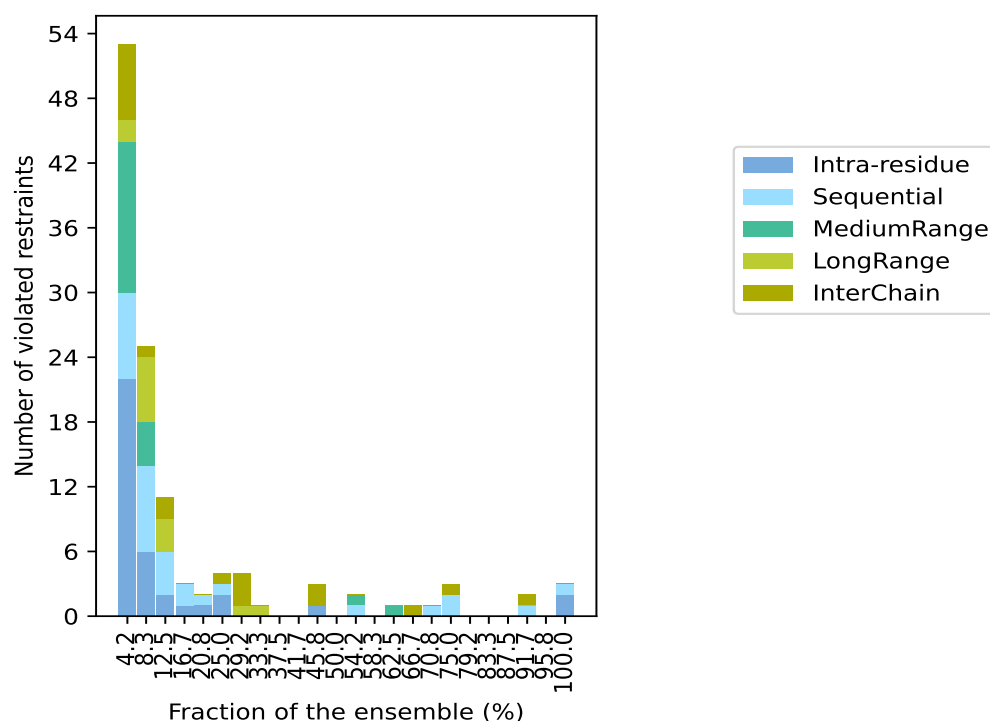
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Number of violated restraints						Fraction of the ensemble	
IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total	Count ⁶	%
0	0	0	1	3	4	7	29.2
0	0	0	1	0	1	8	33.3
0	0	0	0	0	0	9	37.5
0	0	0	0	0	0	10	41.7
1	0	0	0	2	3	11	45.8
0	0	0	0	0	0	12	50.0
0	1	1	0	0	2	13	54.2
0	0	0	0	0	0	14	58.3
0	0	1	0	0	1	15	62.5
0	0	0	0	1	1	16	66.7
0	1	0	0	0	1	17	70.8
0	2	0	0	1	3	18	75.0
0	0	0	0	0	0	19	79.2
0	0	0	0	0	0	20	83.3
0	0	0	0	0	0	21	87.5
0	1	0	0	1	2	22	91.7
0	0	0	0	0	0	23	95.8
2	1	0	0	0	3	24	100.0

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

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

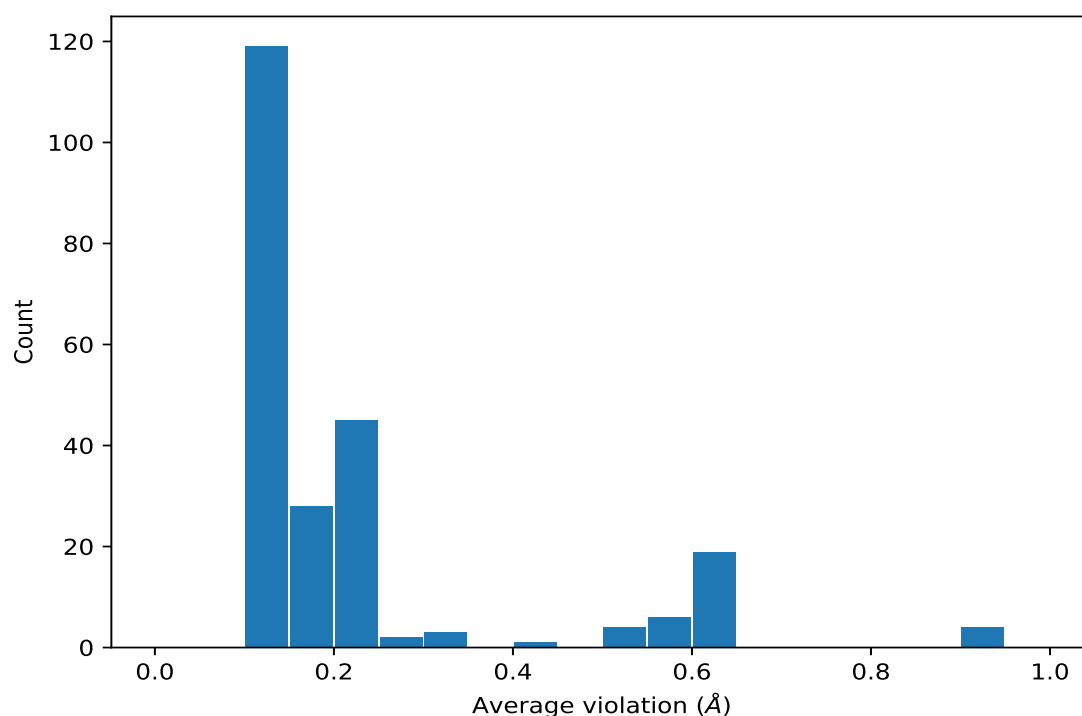
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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)
(1,1474)	1:129:B:GLN:HB2	1:130:B:TYR:HD1	24	0.14	0.02	0.13
(1,1474)	1:129:B:GLN:HB2	1:130:B:TYR:HD2	24	0.14	0.02	0.13
(1,1474)	1:129:B:GLN:HB3	1:130:B:TYR:HD1	24	0.14	0.02	0.13
(1,1474)	1:129:B:GLN:HB3	1:130:B:TYR:HD2	24	0.14	0.02	0.13
(1,553)	1:36:A:PHE:HB2	1:36:A:PHE:HZ	24	0.12	0.0	0.12
(1,553)	1:36:A:PHE:HB3	1:36:A:PHE:HZ	24	0.12	0.0	0.12
(1,1607)	1:136:B:PHE:HB2	1:136:B:PHE:HZ	24	0.12	0.0	0.12
(1,1607)	1:136:B:PHE:HB3	1:136:B:PHE:HZ	24	0.12	0.0	0.12
(1,2038)	1:108:B:MET:HE1	1:27:A:ILE:HD11	22	0.16	0.03	0.15
(1,2038)	1:108:B:MET:HE1	1:27:A:ILE:HD12	22	0.16	0.03	0.15
(1,2038)	1:108:B:MET:HE1	1:27:A:ILE:HD13	22	0.16	0.03	0.15
(1,2038)	1:108:B:MET:HE2	1:27:A:ILE:HD11	22	0.16	0.03	0.15
(1,2038)	1:108:B:MET:HE2	1:27:A:ILE:HD12	22	0.16	0.03	0.15
(1,2038)	1:108:B:MET:HE2	1:27:A:ILE:HD13	22	0.16	0.03	0.15
(1,2038)	1:108:B:MET:HE3	1:27:A:ILE:HD11	22	0.16	0.03	0.15
(1,2038)	1:108:B:MET:HE3	1:27:A:ILE:HD12	22	0.16	0.03	0.15

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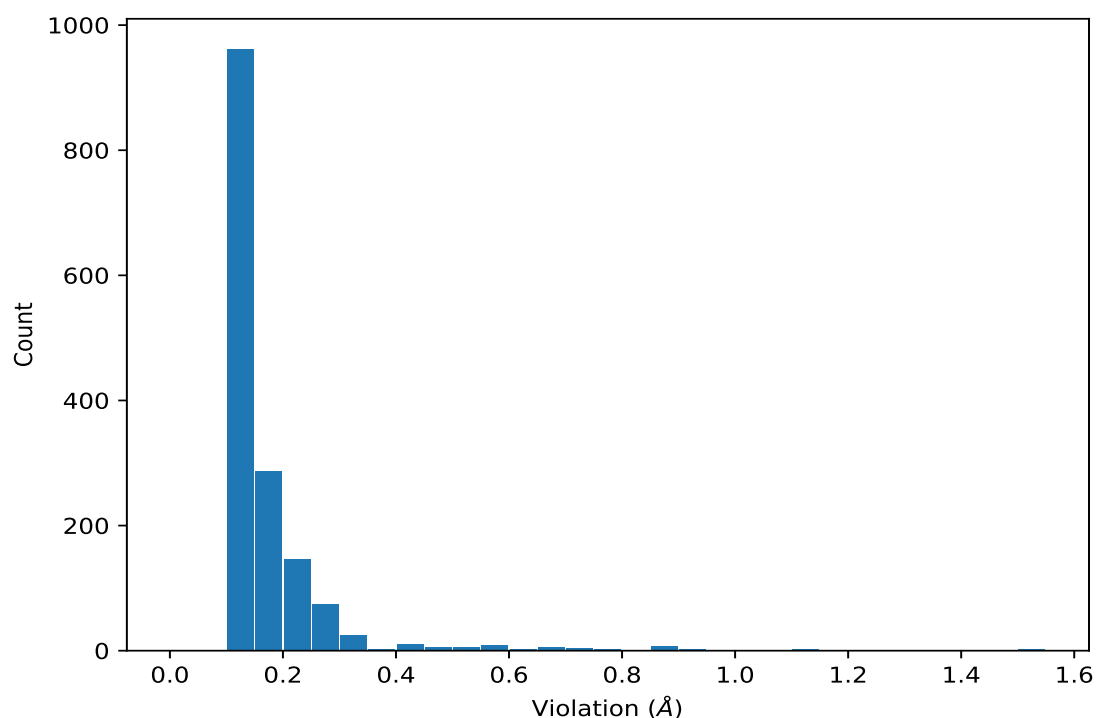
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,2038)	1:108:B:MET:HE3	1:27:A:ILE:HD13	22	0.16	0.03	0.15
(1,420)	1:29:A:GLN:HB2	1:30:A:TYR:HD1	22	0.14	0.03	0.13
(1,420)	1:29:A:GLN:HB2	1:30:A:TYR:HD2	22	0.14	0.03	0.13
(1,420)	1:29:A:GLN:HB3	1:30:A:TYR:HD1	22	0.14	0.03	0.13
(1,420)	1:29:A:GLN:HB3	1:30:A:TYR:HD2	22	0.14	0.03	0.13
(1,636)	1:45:A:ALA:HB1	1:46:A:TRP:HZ3	18	0.62	0.26	0.62
(1,636)	1:45:A:ALA:HB3	1:46:A:TRP:HZ2	18	0.62	0.26	0.62
(1,636)	1:45:A:ALA:HB2	1:46:A:TRP:HZ2	18	0.62	0.26	0.62
(1,636)	1:45:A:ALA:HB3	1:46:A:TRP:HZ3	18	0.62	0.26	0.62
(1,636)	1:45:A:ALA:HB2	1:46:A:TRP:HZ3	18	0.62	0.26	0.62
(1,636)	1:45:A:ALA:HB1	1:46:A:TRP:HZ2	18	0.62	0.26	0.62
(1,1690)	1:145:B:ALA:HB3	1:146:B:TRP:HZ2	18	0.59	0.21	0.55
(1,1690)	1:145:B:ALA:HB2	1:146:B:TRP:HZ2	18	0.59	0.21	0.55
(1,1690)	1:145:B:ALA:HB1	1:146:B:TRP:HZ2	18	0.59	0.21	0.55
(1,1690)	1:145:B:ALA:HB2	1:146:B:TRP:HZ3	18	0.59	0.21	0.55
(1,1690)	1:145:B:ALA:HB1	1:146:B:TRP:HZ3	18	0.59	0.21	0.55
(1,1690)	1:145:B:ALA:HB3	1:146:B:TRP:HZ3	18	0.59	0.21	0.55
(1,984)	1:8:A:MET:HE1	1:127:B:ILE:HD11	18	0.15	0.03	0.15
(1,984)	1:8:A:MET:HE1	1:127:B:ILE:HD12	18	0.15	0.03	0.15
(1,984)	1:8:A:MET:HE1	1:127:B:ILE:HD13	18	0.15	0.03	0.15
(1,984)	1:8:A:MET:HE2	1:127:B:ILE:HD11	18	0.15	0.03	0.15
(1,984)	1:8:A:MET:HE2	1:127:B:ILE:HD12	18	0.15	0.03	0.15
(1,984)	1:8:A:MET:HE2	1:127:B:ILE:HD13	18	0.15	0.03	0.15
(1,984)	1:8:A:MET:HE3	1:127:B:ILE:HD11	18	0.15	0.03	0.15
(1,984)	1:8:A:MET:HE3	1:127:B:ILE:HD12	18	0.15	0.03	0.15
(1,984)	1:8:A:MET:HE3	1:127:B:ILE:HD13	18	0.15	0.03	0.15
(1,1528)	1:132:B:LEU:HA	1:131:B:ALA:H	17	0.11	0.01	0.11
(1,1968)	1:104:B:LEU:HB3	1:6:A:ILE:HG23	16	0.52	0.37	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 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)
(1,914)	1:4:A:LEU:HB3	1:106:B:ILE:HG13	6	1.53
(1,2073)	1:128:B:LYS:HG2	1:6:A:ILE:HG23	14	1.5
(1,914)	1:4:A:LEU:HB3	1:106:B:ILE:HG22	18	1.47
(1,914)	1:4:A:LEU:HB3	1:106:B:ILE:HG21	2	1.43
(1,914)	1:4:A:LEU:HB3	1:106:B:ILE:HG13	12	1.35
(1,1968)	1:104:B:LEU:HB3	1:6:A:ILE:HG13	20	1.31
(1,1690)	1:145:B:ALA:HB2	1:146:B:TRP:HZ2	12	1.18
(1,1019)	1:28:A:LYS:HG3	1:106:B:ILE:HG23	1	1.13
(1,1968)	1:104:B:LEU:HB3	1:6:A:ILE:HG23	23	1.1
(1,636)	1:45:A:ALA:HB1	1:46:A:TRP:HZ3	7	1.08

10 Dihedral-angle violation analysis ⓘ

No dihedral-angle restraints found