



Full wwPDB NMR Structure Validation Report ⓘ

Mar 9, 2026 – 04:01 AM UTC

PDB ID : 6FIP / pdb_00006fip
BMRB ID : 34235
Title : Solution NMR structure of Pseudomonas aeruginosa TonB CTD
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Deposited on : 2018-01-19

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<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 : 4-5-2 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

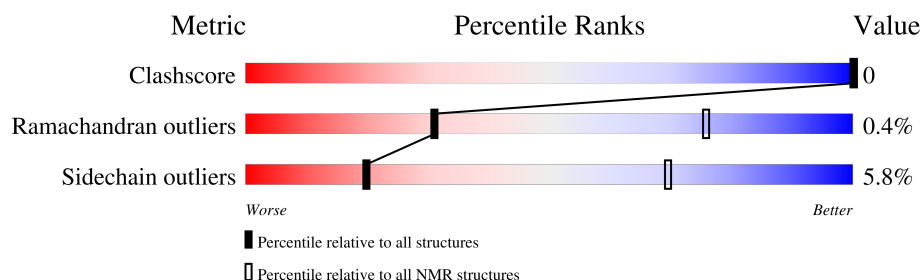
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 89%.

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	99	 91% • 6%

2 Ensemble composition and analysis

This entry contains 20 models. Model 11 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:246-A:338 (93)	0.74	11

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 1 single-model cluster was found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1635 atoms, of which 831 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Protein TonB.

Mol	Chain	Residues	Atoms						Trace
1	A	99	Total	C	H	N	O	S	0
			1635	506	831	153	139	6	

There are 3 discrepancies between the modelled and reference sequences:

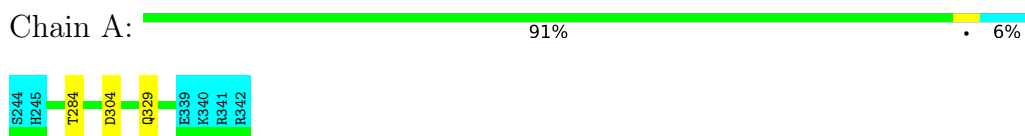
Chain	Residue	Modelled	Actual	Comment	Reference
A	244	SER	-	expression tag	UNP Q51368
A	245	HIS	-	expression tag	UNP Q51368
A	246	MET	-	expression tag	UNP Q51368

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: Protein TonB

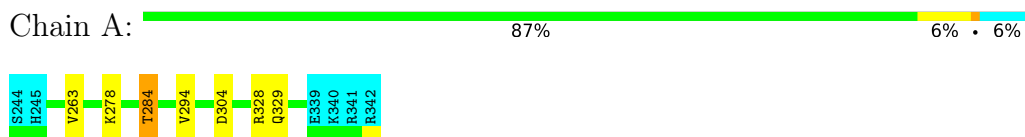


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

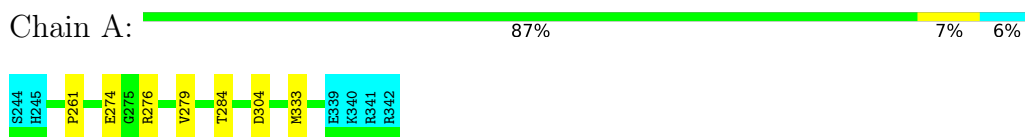
4.2.1 Score per residue for model 1

- Molecule 1: Protein TonB



4.2.2 Score per residue for model 2

- Molecule 1: Protein TonB



4.2.3 Score per residue for model 3

- Molecule 1: Protein TonB

Chain A:  85% 8% 6%



4.2.4 Score per residue for model 4

- Molecule 1: Protein TonB

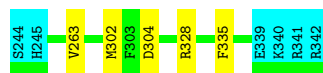
Chain A:  90% 6% 6%



4.2.5 Score per residue for model 5

- Molecule 1: Protein TonB

Chain A:  89% 5% 6%



4.2.6 Score per residue for model 6

- Molecule 1: Protein TonB

Chain A:  87% 7% 6%



4.2.7 Score per residue for model 7

- Molecule 1: Protein TonB

Chain A:  83% 11% 6%



4.2.8 Score per residue for model 8

- Molecule 1: Protein TonB

Chain A:  85% 8% 6%



4.2.9 Score per residue for model 9

- Molecule 1: Protein TonB

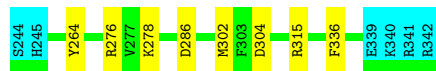
Chain A:  89% 5% 6%



4.2.10 Score per residue for model 10

- Molecule 1: Protein TonB

Chain A:  86% 8% 6%



4.2.11 Score per residue for model 11 (medoid)

- Molecule 1: Protein TonB

Chain A:  90% 0% 6%



4.2.12 Score per residue for model 12

- Molecule 1: Protein TonB

Chain A:  84% 8% 6%



4.2.13 Score per residue for model 13

- Molecule 1: Protein TonB

Chain A:  85% 8% 6%



4.2.14 Score per residue for model 14

- Molecule 1: Protein TonB

Chain A:  88% 6% 6%



4.2.15 Score per residue for model 15

- Molecule 1: Protein TonB

Chain A:  83% 11% 6%



4.2.16 Score per residue for model 16

- Molecule 1: Protein TonB

Chain A:  89% 5% 6%



4.2.17 Score per residue for model 17

- Molecule 1: Protein TonB

Chain A:  88% 5% 6%



4.2.18 Score per residue for model 18

- Molecule 1: Protein TonB

Chain A:  90% • • 6%



4.2.19 Score per residue for model 19

- Molecule 1: Protein TonB

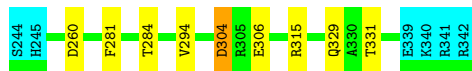
Chain A:  87% 6% • 6%



4.2.20 Score per residue for model 20

- Molecule 1: Protein TonB

Chain A:  85% 8% • 6%



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
Amber	refinement	14
CYANA	structure calculation	3.0

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	1261
Number of shifts mapped to atoms	1261
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	89%

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	0.89±0.02	0±0/763 (0.0± 0.1%)	1.47±0.03	3±2/1024 (0.3± 0.2%)
All	All	0.89	4/15260 (0.0%)	1.47	54/20480 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	0.3±0.5
All	All	0	7

All unique bond outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	261	PRO	CA-C	5.82	1.55	1.51	16	4

All 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	304	ASP	CA-CB-CG	9.11	121.71	112.60	20	5
1	A	260	ASP	CA-C-N	7.17	124.89	119.66	12	9
1	A	260	ASP	C-N-CA	7.17	124.89	119.66	12	9
1	A	286	ASP	CA-CB-CG	7.07	119.67	112.60	6	2
1	A	253	ASP	CA-CB-CG	6.58	119.18	112.60	12	1
1	A	251	ASP	CA-CB-CG	6.43	119.03	112.60	15	2
1	A	264	TYR	N-CA-C	6.24	117.57	109.64	7	2
1	A	304	ASP	N-CA-C	6.16	118.50	111.11	18	2
1	A	261	PRO	N-CA-C	5.94	116.17	110.47	7	2
1	A	329	GLN	OE1-CD-NE2	-5.82	116.78	122.60	12	2

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	259	MET	CA-C-N	5.66	129.13	121.20	3	1
1	A	259	MET	C-N-CA	5.66	129.13	121.20	3	1
1	A	335	PHE	N-CA-C	5.65	117.89	107.73	15	2
1	A	291	ASP	CA-CB-CG	5.51	118.11	112.60	6	1
1	A	294	VAL	N-CA-C	5.36	116.20	108.48	4	1
1	A	291	ASP	CA-C-N	5.32	127.70	120.63	9	1
1	A	291	ASP	C-N-CA	5.32	127.70	120.63	9	1
1	A	251	ASP	N-CA-C	5.30	117.92	110.23	3	1
1	A	316	PHE	N-CA-C	5.27	117.41	109.23	7	2
1	A	263	VAL	N-CA-C	5.08	116.55	109.55	19	2
1	A	261	PRO	N-CA-CB	5.06	106.02	103.19	15	1
1	A	281	PHE	N-CA-C	5.05	115.71	108.74	20	1
1	A	336	PHE	N-CA-C	5.04	116.42	109.15	15	1
1	A	284	THR	N-CA-C	5.03	117.34	110.55	2	2

There are no chirality outliers.

All 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	276	ARG	Sidechain	2
1	A	328	ARG	Sidechain	1
1	A	315	ARG	Sidechain	1
1	A	301	ARG	Sidechain	1
1	A	305	ARG	Sidechain	1
1	A	308	ARG	Sidechain	1

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	748	772	772	0±0
All	All	14960	15440	15440	1

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 0.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:278:LYS:HE3	1:A:333:MET:SD	0.43	2.53	3	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	93/99 (94%)	89±2 (96±2%)	3±2 (4±2%)	0±1 (0±1%)	31	76
All	All	1860/1980 (94%)	1785 (96%)	68 (4%)	7 (0%)	31	76

All 3 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	301	ARG	3
1	A	336	PHE	3
1	A	260	ASP	1

6.3.2 Protein sidechains [i](#)

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	81/87 (93%)	76±2 (94±2%)	5±2 (6±2%)	20	69
All	All	1620/1740 (93%)	1526 (94%)	94 (6%)	20	69

All 28 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	304	ASP	14
1	A	284	THR	10
1	A	329	GLN	10
1	A	263	VAL	8
1	A	294	VAL	6
1	A	278	LYS	5
1	A	333	MET	5
1	A	302	MET	4
1	A	328	ARG	3
1	A	274	GLU	3
1	A	331	THR	3
1	A	306	GLU	3
1	A	279	VAL	2
1	A	313	LYS	2
1	A	309	GLN	2
1	A	276	ARG	2
1	A	266	ARG	1
1	A	308	ARG	1
1	A	319	ARG	1
1	A	257	LEU	1
1	A	326	VAL	1
1	A	305	ARG	1
1	A	317	GLU	1
1	A	280	LEU	1
1	A	255	LYS	1
1	A	307	VAL	1
1	A	267	MET	1
1	A	315	ARG	1

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 oligosaccharides 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 89% for the well-defined parts and 88% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *D_1200008387_cs-upload_P1.str.V4*

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	1261
Number of shifts mapped to atoms	1261
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 $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	98	0.04 ± 0.10	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	92	-0.06 ± 0.16	None needed (< 0.5 ppm)
$^{13}\text{C}'$	95	0.30 ± 0.14	None needed (< 0.5 ppm)
^{15}N	91	0.08 ± 0.28	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 89%, i.e. 1198 atoms were assigned a chemical shift out of a possible 1340. 0 out of 12 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	457/459 (100%)	186/186 (100%)	184/186 (99%)	87/87 (100%)
Sidechain	689/800 (86%)	468/518 (90%)	211/238 (89%)	10/44 (23%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	52/81 (64%)	32/40 (80%)	19/40 (48%)	1/1 (100%)
Overall	1198/1340 (89%)	686/744 (92%)	414/464 (89%)	98/132 (74%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 88%, i.e. 1261 atoms were assigned a chemical shift out of a possible 1439. 0 out of 12 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	479/489 (98%)	195/198 (98%)	193/198 (97%)	91/93 (98%)
Sidechain	726/862 (84%)	492/556 (88%)	224/255 (88%)	10/51 (20%)
Aromatic	56/88 (64%)	34/44 (77%)	21/42 (50%)	1/2 (50%)
Overall	1261/1439 (88%)	721/798 (90%)	438/495 (88%)	102/146 (70%)

7.1.4 Statistically unusual chemical shifts ⓘ

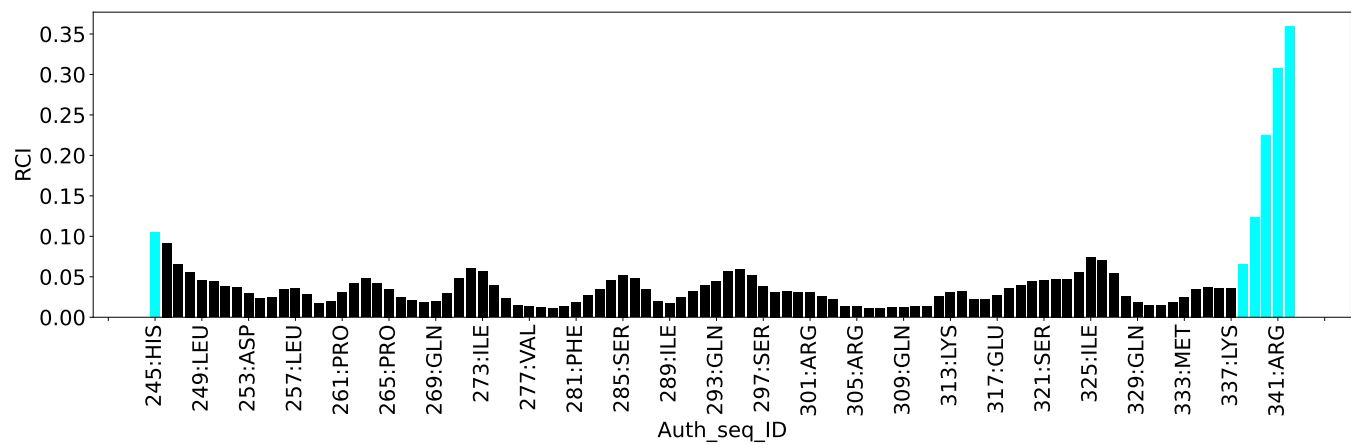
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	311	MET	HG2	0.05	0.65 – 4.19	-6.7
1	A	311	MET	HA	2.09	2.11 – 6.67	-5.0

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:



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	1561
Intra-residue ($ i-j =0$)	413
Sequential ($ i-j =1$)	453
Medium range ($ i-j >1$ and $ i-j <5$)	187
Long range ($ i-j \geq 5$)	508
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	15.8
Number of long range restraints per residue ¹	5.1

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)	1.8	0.18
0.2-0.5 (Medium)	0.2	0.33
>0.5 (Large)	None	None

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 ⓘ

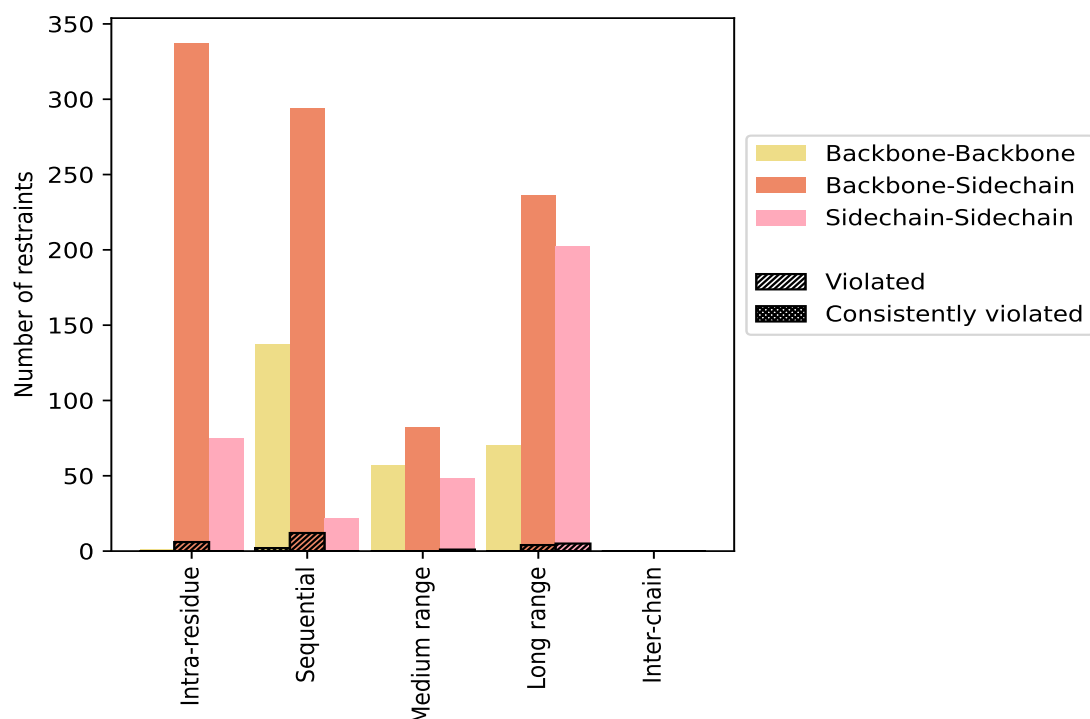
9.1 Summary of distance violations ⓘ

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 ($i-j =0$)	413	26.5	6	1.5	0.4	0	0.0	0.0
Backbone-Backbone	1	0.1	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	337	21.6	6	1.8	0.4	0	0.0	0.0
Sidechain-Sidechain	75	4.8	0	0.0	0.0	0	0.0	0.0
Sequential ($i-j =1$)	453	29.0	14	3.1	0.9	0	0.0	0.0
Backbone-Backbone	137	8.8	2	1.5	0.1	0	0.0	0.0
Backbone-Sidechain	294	18.8	12	4.1	0.8	0	0.0	0.0
Sidechain-Sidechain	22	1.4	0	0.0	0.0	0	0.0	0.0
Medium range ($i-j >1$ & $i-j <5$)	187	12.0	1	0.5	0.1	0	0.0	0.0
Backbone-Backbone	57	3.7	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	82	5.3	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	48	3.1	1	2.1	0.1	0	0.0	0.0
Long range ($i-j \geq 5$)	508	32.5	9	1.8	0.6	0	0.0	0.0
Backbone-Backbone	70	4.5	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	236	15.1	4	1.7	0.3	0	0.0	0.0
Sidechain-Sidechain	202	12.9	5	2.5	0.3	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	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	1561	100.0	30	1.9	1.9	0	0.0	0.0
Backbone-Backbone	265	17.0	2	0.8	0.1	0	0.0	0.0
Backbone-Sidechain	949	60.8	22	2.3	1.4	0	0.0	0.0
Sidechain-Sidechain	347	22.2	6	1.7	0.4	0	0.0	0.0

¹ percentage calculated with respect to the total number of distance restraints, ² percentage calculated with respect to the number of restraints in a particular restraint category, ³ violated in at least one model, ⁴ violated in all the models

9.1.1 Bar chart : Distribution of distance restraints and violations [i](#)



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

9.2 Distance violation statistics for each model [i](#)

The following table provides the distance violation statistics for each model in the ensemble. Violations less than 0.1 Å are not included in the statistics.

Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
1	0	1	0	0	0	1	0.12	0.12	0.0	0.12
2	0	1	0	1	0	2	0.13	0.16	0.03	0.13
3	0	2	0	1	0	3	0.15	0.18	0.02	0.15
4	0	0	0	1	0	1	0.24	0.24	0.0	0.24
5	1	2	0	0	0	3	0.12	0.14	0.02	0.12
6	1	1	1	0	0	3	0.13	0.15	0.02	0.14
7	2	0	0	0	0	2	0.12	0.13	0.01	0.12
8	1	1	0	3	0	5	0.19	0.33	0.08	0.15
9	0	1	0	0	0	1	0.11	0.11	0.0	0.11
10	0	1	0	0	0	1	0.13	0.13	0.0	0.13

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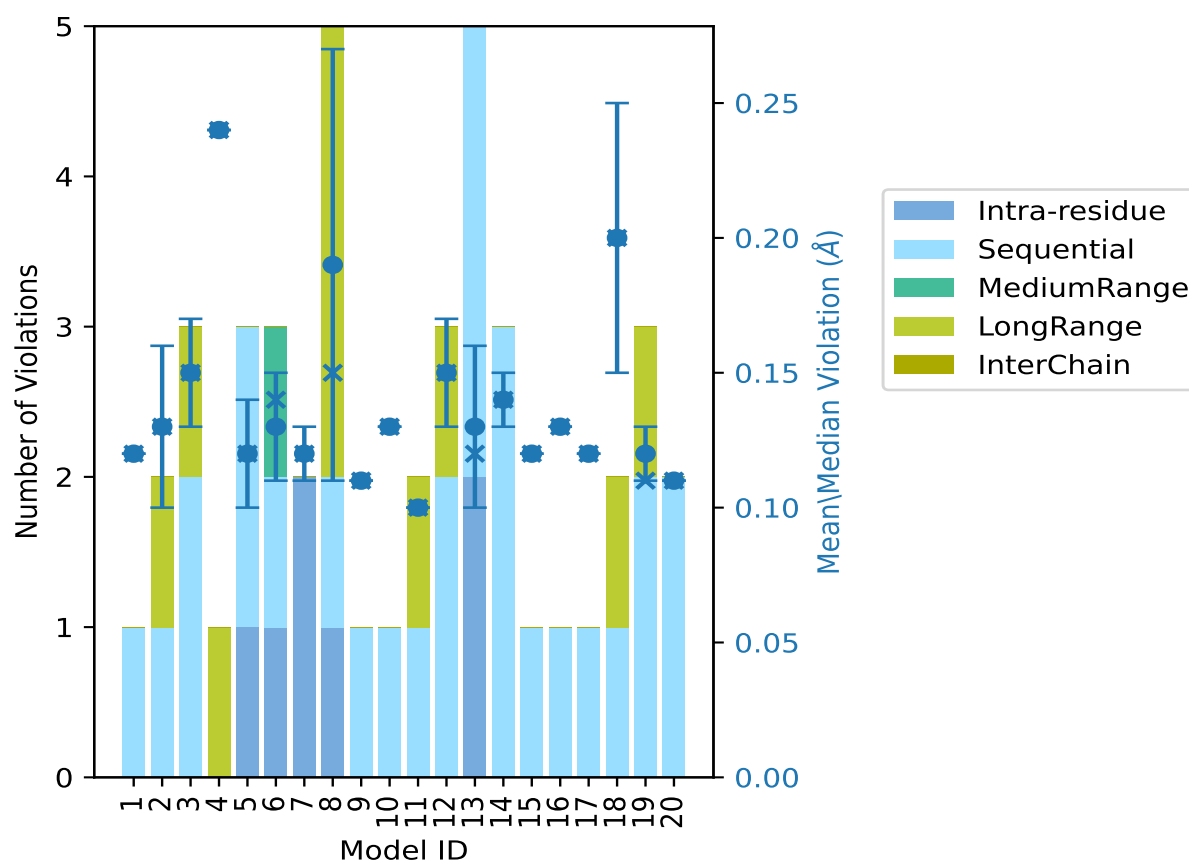
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	0	1	0	1	0	2	0.1	0.1	0.0	0.1
12	0	2	0	1	0	3	0.15	0.18	0.02	0.15
13	2	3	0	0	0	5	0.13	0.17	0.03	0.12
14	0	3	0	0	0	3	0.14	0.15	0.01	0.14
15	0	1	0	0	0	1	0.12	0.12	0.0	0.12
16	0	1	0	0	0	1	0.13	0.13	0.0	0.13
17	0	1	0	0	0	1	0.12	0.12	0.0	0.12
18	0	1	0	1	0	2	0.2	0.25	0.05	0.2
19	0	2	0	1	0	3	0.12	0.14	0.01	0.11
20	0	2	0	0	0	2	0.11	0.11	0.0	0.11

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

⁵Inter-chain restraints, ⁶Standard deviation

9.2.1 Bar graph : Distance Violation statistics for each model ⓘ



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

9.3 Distance violation statistics for the ensemble

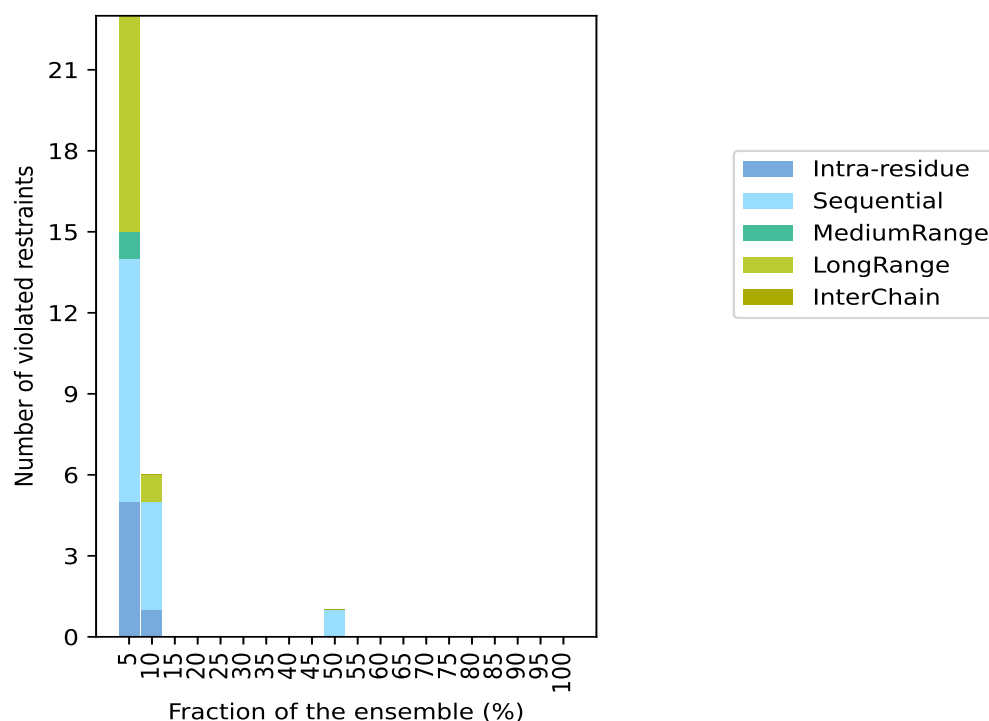
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 1531(IR:407, SQ:439, MR:186, LR:499, IC:0) restraints are 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	%
5	9	1	8	0	23	1	5.0
1	4	0	1	0	6	2	10.0
0	0	0	0	0	0	3	15.0
0	0	0	0	0	0	4	20.0
0	0	0	0	0	0	5	25.0
0	0	0	0	0	0	6	30.0
0	0	0	0	0	0	7	35.0
0	0	0	0	0	0	8	40.0
0	0	0	0	0	0	9	45.0
0	1	0	0	0	1	10	50.0
0	0	0	0	0	0	11	55.0
0	0	0	0	0	0	12	60.0
0	0	0	0	0	0	13	65.0
0	0	0	0	0	0	14	70.0
0	0	0	0	0	0	15	75.0
0	0	0	0	0	0	16	80.0
0	0	0	0	0	0	17	85.0
0	0	0	0	0	0	18	90.0
0	0	0	0	0	0	19	95.0
0	0	0	0	0	0	20	100.0

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

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

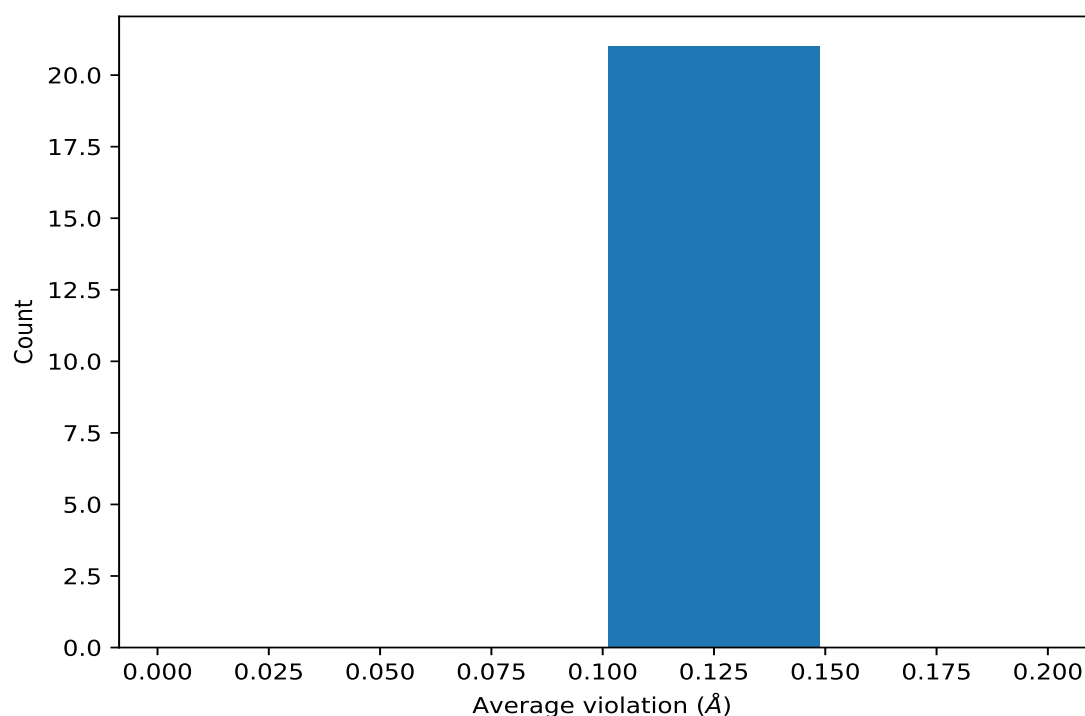
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



9.4 Most violated distance restraints in the ensemble [i](#)

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

The following histogram shows the distribution of the average value of the violation. The average is calculated for each restraint that is violated in more than one model over all the violated models in the ensemble



9.4.2 Table: Most violated distance restraints [i](#)

The following table provides the mean and the standard deviation of the violation for each restraint sorted by number of violated models and the mean value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint. Rows with same key represent combinatorial or ambiguous restraints and are counted as a single restraint.

Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,1217)	1:260:A:ASP:H	1:261:A:PRO:HD2	10	0.13	0.03	0.12
(1,1217)	1:260:A:ASP:H	1:261:A:PRO:HD3	10	0.13	0.03	0.12
(1,322)	1:309:A:GLN:HB2	1:310:A:ALA:H	2	0.15	0.0	0.15
(1,322)	1:309:A:GLN:HB3	1:310:A:ALA:H	2	0.15	0.0	0.15
(1,1302)	1:278:A:LYS:HA	1:279:A:VAL:HG11	2	0.15	0.0	0.15
(1,1302)	1:278:A:LYS:HA	1:279:A:VAL:HG12	2	0.15	0.0	0.15
(1,1302)	1:278:A:LYS:HA	1:279:A:VAL:HG13	2	0.15	0.0	0.15
(1,1302)	1:278:A:LYS:HA	1:279:A:VAL:HG21	2	0.15	0.0	0.15
(1,1302)	1:278:A:LYS:HA	1:279:A:VAL:HG22	2	0.15	0.0	0.15
(1,1302)	1:278:A:LYS:HA	1:279:A:VAL:HG23	2	0.15	0.0	0.15
(1,1558)	1:340:A:LYS:HB2	1:341:A:ARG:H	2	0.14	0.02	0.14
(1,1558)	1:340:A:LYS:HB3	1:341:A:ARG:H	2	0.14	0.02	0.14
(1,1397)	1:293:A:GLN:HA	1:294:A:VAL:HG11	2	0.13	0.01	0.13
(1,1397)	1:293:A:GLN:HA	1:294:A:VAL:HG12	2	0.13	0.01	0.13
(1,1397)	1:293:A:GLN:HA	1:294:A:VAL:HG13	2	0.13	0.01	0.13
(1,1397)	1:293:A:GLN:HA	1:294:A:VAL:HG21	2	0.13	0.01	0.13

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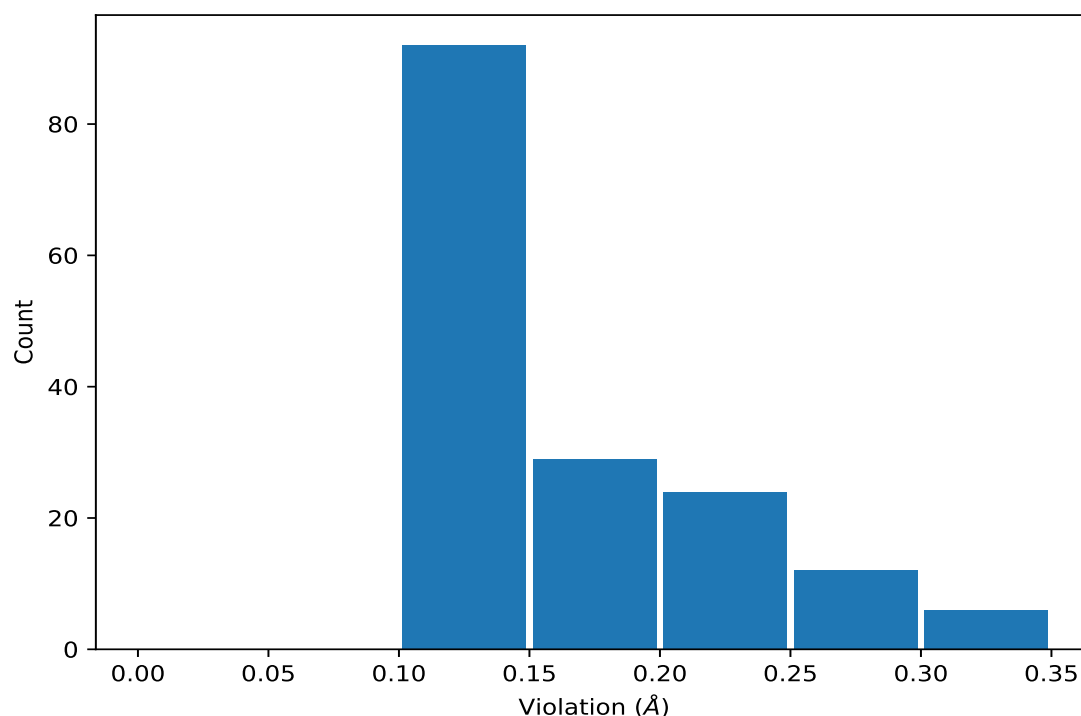
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,1397)	1:293:A:GLN:HA	1:294:A:VAL:HG22	2	0.13	0.01	0.13
(1,1397)	1:293:A:GLN:HA	1:294:A:VAL:HG23	2	0.13	0.01	0.13
(1,317)	1:309:A:GLN:H	1:309:A:GLN:HG3	2	0.12	0.01	0.12
(1,1141)	1:247:A:GLY:H	1:329:A:GLN:HG2	2	0.12	0.01	0.12
(1,1141)	1:247:A:GLY:H	1:329:A:GLN:HG3	2	0.12	0.01	0.12

¹Number of violated models, ²Standard deviation

9.5 All violated distance restraints [i](#)

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

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



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

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

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1153)	1:249:A:LEU:HA	1:249:A:LEU:HD11	8	0.33
(1,1153)	1:249:A:LEU:HA	1:249:A:LEU:HD12	8	0.33
(1,1153)	1:249:A:LEU:HA	1:249:A:LEU:HD13	8	0.33
(1,1153)	1:249:A:LEU:HA	1:249:A:LEU:HD21	8	0.33
(1,1153)	1:249:A:LEU:HA	1:249:A:LEU:HD22	8	0.33
(1,1153)	1:249:A:LEU:HA	1:249:A:LEU:HD23	8	0.33
(1,1321)	1:279:A:VAL:HG11	1:332:A:LYS:HB2	18	0.25
(1,1321)	1:279:A:VAL:HG11	1:332:A:LYS:HB3	18	0.25
(1,1321)	1:279:A:VAL:HG12	1:332:A:LYS:HB2	18	0.25
(1,1321)	1:279:A:VAL:HG12	1:332:A:LYS:HB3	18	0.25
(1,1321)	1:279:A:VAL:HG13	1:332:A:LYS:HB2	18	0.25
(1,1321)	1:279:A:VAL:HG13	1:332:A:LYS:HB3	18	0.25
(1,1321)	1:279:A:VAL:HG21	1:332:A:LYS:HB2	18	0.25
(1,1321)	1:279:A:VAL:HG21	1:332:A:LYS:HB3	18	0.25
(1,1321)	1:279:A:VAL:HG22	1:332:A:LYS:HB2	18	0.25
(1,1321)	1:279:A:VAL:HG22	1:332:A:LYS:HB3	18	0.25
(1,1321)	1:279:A:VAL:HG23	1:332:A:LYS:HB2	18	0.25
(1,1321)	1:279:A:VAL:HG23	1:332:A:LYS:HB3	18	0.25
(1,1310)	1:279:A:VAL:HA	1:295:A:LEU:HD11	4	0.24
(1,1310)	1:279:A:VAL:HA	1:295:A:LEU:HD12	4	0.24
(1,1310)	1:279:A:VAL:HA	1:295:A:LEU:HD13	4	0.24
(1,1310)	1:279:A:VAL:HA	1:295:A:LEU:HD21	4	0.24
(1,1310)	1:279:A:VAL:HA	1:295:A:LEU:HD22	4	0.24
(1,1310)	1:279:A:VAL:HA	1:295:A:LEU:HD23	4	0.24
(1,1159)	1:249:A:LEU:HD11	1:283:A:ILE:HD11	8	0.22
(1,1159)	1:249:A:LEU:HD11	1:283:A:ILE:HD12	8	0.22
(1,1159)	1:249:A:LEU:HD11	1:283:A:ILE:HD13	8	0.22
(1,1159)	1:249:A:LEU:HD12	1:283:A:ILE:HD11	8	0.22
(1,1159)	1:249:A:LEU:HD12	1:283:A:ILE:HD12	8	0.22
(1,1159)	1:249:A:LEU:HD12	1:283:A:ILE:HD13	8	0.22
(1,1159)	1:249:A:LEU:HD13	1:283:A:ILE:HD11	8	0.22
(1,1159)	1:249:A:LEU:HD13	1:283:A:ILE:HD12	8	0.22
(1,1159)	1:249:A:LEU:HD13	1:283:A:ILE:HD13	8	0.22
(1,1159)	1:249:A:LEU:HD21	1:283:A:ILE:HD11	8	0.22
(1,1159)	1:249:A:LEU:HD21	1:283:A:ILE:HD12	8	0.22
(1,1159)	1:249:A:LEU:HD21	1:283:A:ILE:HD13	8	0.22
(1,1159)	1:249:A:LEU:HD22	1:283:A:ILE:HD11	8	0.22
(1,1159)	1:249:A:LEU:HD22	1:283:A:ILE:HD12	8	0.22
(1,1159)	1:249:A:LEU:HD22	1:283:A:ILE:HD13	8	0.22
(1,1159)	1:249:A:LEU:HD23	1:283:A:ILE:HD11	8	0.22
(1,1159)	1:249:A:LEU:HD23	1:283:A:ILE:HD12	8	0.22
(1,1159)	1:249:A:LEU:HD23	1:283:A:ILE:HD13	8	0.22
(1,1217)	1:260:A:ASP:H	1:261:A:PRO:HD2	3	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1217)	1:260:A:ASP:H	1:261:A:PRO:HD3	3	0.18
(1,1217)	1:260:A:ASP:H	1:261:A:PRO:HD2	12	0.18
(1,1217)	1:260:A:ASP:H	1:261:A:PRO:HD3	12	0.18
(1,737)	1:319:A:ARG:HA	1:319:A:ARG:HD2	13	0.17
(1,737)	1:319:A:ARG:HA	1:319:A:ARG:HD3	13	0.17
(1,1319)	1:279:A:VAL:HG11	1:331:A:THR:HB	2	0.16
(1,1319)	1:279:A:VAL:HG12	1:331:A:THR:HB	2	0.16
(1,1319)	1:279:A:VAL:HG13	1:331:A:THR:HB	2	0.16
(1,1319)	1:279:A:VAL:HG21	1:331:A:THR:HB	2	0.16
(1,1319)	1:279:A:VAL:HG22	1:331:A:THR:HB	2	0.16
(1,1319)	1:279:A:VAL:HG23	1:331:A:THR:HB	2	0.16
(1,1558)	1:340:A:LYS:HB2	1:341:A:ARG:H	13	0.15
(1,1558)	1:340:A:LYS:HB3	1:341:A:ARG:H	13	0.15
(1,1302)	1:278:A:LYS:HA	1:279:A:VAL:HG11	12	0.15
(1,1302)	1:278:A:LYS:HA	1:279:A:VAL:HG12	12	0.15
(1,1302)	1:278:A:LYS:HA	1:279:A:VAL:HG13	12	0.15
(1,1302)	1:278:A:LYS:HA	1:279:A:VAL:HG21	12	0.15
(1,1302)	1:278:A:LYS:HA	1:279:A:VAL:HG22	12	0.15
(1,1302)	1:278:A:LYS:HA	1:279:A:VAL:HG23	12	0.15
(1,920)	1:249:A:LEU:HG	1:281:A:PHE:HE1	8	0.15
(1,920)	1:249:A:LEU:HG	1:281:A:PHE:HE2	8	0.15
(1,614)	1:278:A:LYS:HG2	1:333:A:MET:HA	3	0.15
(1,614)	1:278:A:LYS:HG3	1:333:A:MET:HA	3	0.15
(1,466)	1:338:A:ILE:HB	1:339:A:GLU:H	6	0.15
(1,322)	1:309:A:GLN:HB2	1:310:A:ALA:H	14	0.15
(1,322)	1:309:A:GLN:HB3	1:310:A:ALA:H	14	0.15
(1,322)	1:309:A:GLN:HB2	1:310:A:ALA:H	18	0.15
(1,322)	1:309:A:GLN:HB3	1:310:A:ALA:H	18	0.15
(1,1397)	1:293:A:GLN:HA	1:294:A:VAL:HG11	19	0.14
(1,1397)	1:293:A:GLN:HA	1:294:A:VAL:HG12	19	0.14
(1,1397)	1:293:A:GLN:HA	1:294:A:VAL:HG13	19	0.14
(1,1397)	1:293:A:GLN:HA	1:294:A:VAL:HG21	19	0.14
(1,1397)	1:293:A:GLN:HA	1:294:A:VAL:HG22	19	0.14
(1,1397)	1:293:A:GLN:HA	1:294:A:VAL:HG23	19	0.14
(1,1302)	1:278:A:LYS:HA	1:279:A:VAL:HG11	14	0.14
(1,1302)	1:278:A:LYS:HA	1:279:A:VAL:HG12	14	0.14
(1,1302)	1:278:A:LYS:HA	1:279:A:VAL:HG13	14	0.14
(1,1302)	1:278:A:LYS:HA	1:279:A:VAL:HG21	14	0.14
(1,1302)	1:278:A:LYS:HA	1:279:A:VAL:HG22	14	0.14
(1,1302)	1:278:A:LYS:HA	1:279:A:VAL:HG23	14	0.14
(1,1217)	1:260:A:ASP:H	1:261:A:PRO:HD2	5	0.14
(1,1217)	1:260:A:ASP:H	1:261:A:PRO:HD3	5	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,938)	1:284:A:THR:HB	1:286:A:ASP:HB2	6	0.14
(1,938)	1:284:A:THR:HB	1:286:A:ASP:HB3	6	0.14
(1,1318)	1:279:A:VAL:HG11	1:311:A:MET:HE1	8	0.13
(1,1318)	1:279:A:VAL:HG11	1:311:A:MET:HE2	8	0.13
(1,1318)	1:279:A:VAL:HG11	1:311:A:MET:HE3	8	0.13
(1,1318)	1:279:A:VAL:HG12	1:311:A:MET:HE1	8	0.13
(1,1318)	1:279:A:VAL:HG12	1:311:A:MET:HE2	8	0.13
(1,1318)	1:279:A:VAL:HG12	1:311:A:MET:HE3	8	0.13
(1,1318)	1:279:A:VAL:HG13	1:311:A:MET:HE1	8	0.13
(1,1318)	1:279:A:VAL:HG13	1:311:A:MET:HE2	8	0.13
(1,1318)	1:279:A:VAL:HG13	1:311:A:MET:HE3	8	0.13
(1,1318)	1:279:A:VAL:HG21	1:311:A:MET:HE1	8	0.13
(1,1318)	1:279:A:VAL:HG21	1:311:A:MET:HE2	8	0.13
(1,1318)	1:279:A:VAL:HG21	1:311:A:MET:HE3	8	0.13
(1,1318)	1:279:A:VAL:HG22	1:311:A:MET:HE1	8	0.13
(1,1318)	1:279:A:VAL:HG22	1:311:A:MET:HE2	8	0.13
(1,1318)	1:279:A:VAL:HG22	1:311:A:MET:HE3	8	0.13
(1,1318)	1:279:A:VAL:HG23	1:311:A:MET:HE1	8	0.13
(1,1318)	1:279:A:VAL:HG23	1:311:A:MET:HE2	8	0.13
(1,1318)	1:279:A:VAL:HG23	1:311:A:MET:HE3	8	0.13
(1,1217)	1:260:A:ASP:H	1:261:A:PRO:HD2	16	0.13
(1,1217)	1:260:A:ASP:H	1:261:A:PRO:HD3	16	0.13
(1,1141)	1:247:A:GLY:H	1:329:A:GLN:HG2	12	0.13
(1,1141)	1:247:A:GLY:H	1:329:A:GLN:HG3	12	0.13
(1,317)	1:309:A:GLN:H	1:309:A:GLN:HG3	7	0.13
(1,77)	1:259:A:MET:H	1:260:A:ASP:H	10	0.13
(1,1558)	1:340:A:LYS:HB2	1:341:A:ARG:H	3	0.12
(1,1558)	1:340:A:LYS:HB3	1:341:A:ARG:H	3	0.12
(1,1443)	1:306:A:GLU:H	1:307:A:VAL:HG11	17	0.12
(1,1443)	1:306:A:GLU:H	1:307:A:VAL:HG12	17	0.12
(1,1443)	1:306:A:GLU:H	1:307:A:VAL:HG13	17	0.12
(1,1443)	1:306:A:GLU:H	1:307:A:VAL:HG21	17	0.12
(1,1443)	1:306:A:GLU:H	1:307:A:VAL:HG22	17	0.12
(1,1443)	1:306:A:GLU:H	1:307:A:VAL:HG23	17	0.12
(1,1397)	1:293:A:GLN:HA	1:294:A:VAL:HG11	1	0.12
(1,1397)	1:293:A:GLN:HA	1:294:A:VAL:HG12	1	0.12
(1,1397)	1:293:A:GLN:HA	1:294:A:VAL:HG13	1	0.12
(1,1397)	1:293:A:GLN:HA	1:294:A:VAL:HG21	1	0.12
(1,1397)	1:293:A:GLN:HA	1:294:A:VAL:HG22	1	0.12
(1,1397)	1:293:A:GLN:HA	1:294:A:VAL:HG23	1	0.12
(1,1217)	1:260:A:ASP:H	1:261:A:PRO:HD2	13	0.12
(1,1217)	1:260:A:ASP:H	1:261:A:PRO:HD3	13	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1217)	1:260:A:ASP:H	1:261:A:PRO:HD2	14	0.12
(1,1217)	1:260:A:ASP:H	1:261:A:PRO:HD3	14	0.12
(1,471)	1:340:A:LYS:HA	1:341:A:ARG:H	5	0.12
(1,415)	1:328:A:ARG:HG2	1:329:A:GLN:H	15	0.12
(1,415)	1:328:A:ARG:HG3	1:329:A:GLN:H	15	0.12
(1,1251)	1:266:A:ARG:H	1:266:A:ARG:HG2	6	0.11
(1,1251)	1:266:A:ARG:H	1:266:A:ARG:HG3	6	0.11
(1,1217)	1:260:A:ASP:H	1:261:A:PRO:HD2	9	0.11
(1,1217)	1:260:A:ASP:H	1:261:A:PRO:HD3	9	0.11
(1,1217)	1:260:A:ASP:H	1:261:A:PRO:HD2	20	0.11
(1,1217)	1:260:A:ASP:H	1:261:A:PRO:HD3	20	0.11
(1,1141)	1:247:A:GLY:H	1:329:A:GLN:HG2	19	0.11
(1,1141)	1:247:A:GLY:H	1:329:A:GLN:HG3	19	0.11
(1,796)	1:309:A:GLN:HA	1:309:A:GLN:HG2	7	0.11
(1,459)	1:337:A:LYS:HG2	1:338:A:ILE:H	20	0.11
(1,459)	1:337:A:LYS:HG3	1:338:A:ILE:H	20	0.11
(1,317)	1:309:A:GLN:H	1:309:A:GLN:HG3	13	0.11
(1,184)	1:284:A:THR:HG21	1:285:A:SER:H	19	0.11
(1,184)	1:284:A:THR:HG22	1:285:A:SER:H	19	0.11
(1,184)	1:284:A:THR:HG23	1:285:A:SER:H	19	0.11
(1,1523)	1:329:A:GLN:HB2	1:330:A:ALA:H	13	0.1
(1,1523)	1:329:A:GLN:HB3	1:330:A:ALA:H	13	0.1
(1,1340)	1:280:A:LEU:HD11	1:330:A:ALA:H	11	0.1
(1,1340)	1:280:A:LEU:HD12	1:330:A:ALA:H	11	0.1
(1,1340)	1:280:A:LEU:HD13	1:330:A:ALA:H	11	0.1
(1,1340)	1:280:A:LEU:HD21	1:330:A:ALA:H	11	0.1
(1,1340)	1:280:A:LEU:HD22	1:330:A:ALA:H	11	0.1
(1,1340)	1:280:A:LEU:HD23	1:330:A:ALA:H	11	0.1
(1,1217)	1:260:A:ASP:H	1:261:A:PRO:HD2	2	0.1
(1,1217)	1:260:A:ASP:H	1:261:A:PRO:HD3	2	0.1
(1,1217)	1:260:A:ASP:H	1:261:A:PRO:HD2	8	0.1
(1,1217)	1:260:A:ASP:H	1:261:A:PRO:HD3	8	0.1
(1,1048)	1:266:A:ARG:HA	1:266:A:ARG:HD2	5	0.1
(1,1048)	1:266:A:ARG:HA	1:266:A:ARG:HD3	5	0.1
(1,994)	1:278:A:LYS:HG2	1:279:A:VAL:H	11	0.1
(1,994)	1:278:A:LYS:HG3	1:279:A:VAL:H	11	0.1

10 Dihedral-angle violation analysis ⓘ

No dihedral-angle restraints found