



# Full wwPDB NMR Structure Validation Report ⓘ

Jun 3, 2023 – 06:08 PM EDT

PDB ID : 2MT3  
BMRB ID : 25147  
Title : Structure of -24 DNA binding domain of sigma 54 from E.coli  
Authors : Wemmer, D.; Gao, Z.; Pelton, J.  
Deposited on : 2014-08-12

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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 ⓘ symbol.

The types of validation reports are described at

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

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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

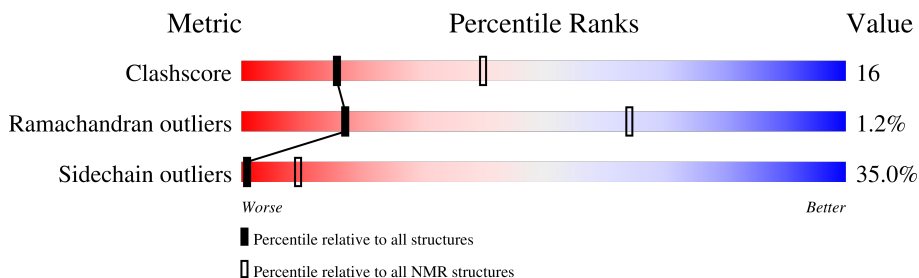
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 82%.

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  $\geq 3$ , 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	84	

## 2 Ensemble composition and analysis i

This entry contains 20 models. Model 7 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:414-A:465 (52)	1.56	7

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 and 1 single-model cluster was found.

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

### 3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1309 atoms, of which 667 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called RNA polymerase sigma-54 factor.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	84	1309	397	667	124	120	1	0

There are 20 discrepancies between the modelled and reference sequences:

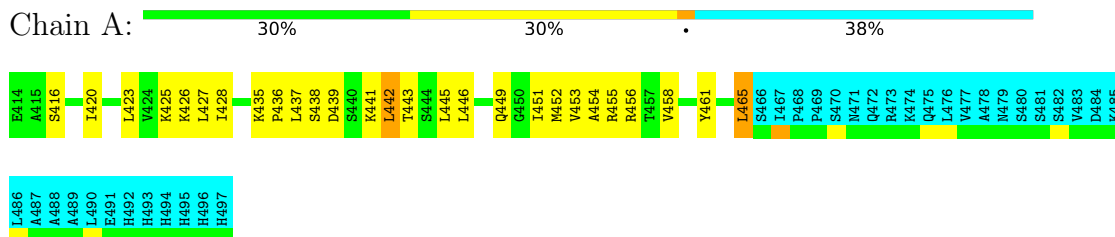
Chain	Residue	Modelled	Actual	Comment	Reference
A	478	ALA	-	expression tag	UNP C3SS82
A	479	ASN	-	expression tag	UNP C3SS82
A	480	SER	-	expression tag	UNP C3SS82
A	481	SER	-	expression tag	UNP C3SS82
A	482	SER	-	expression tag	UNP C3SS82
A	483	VAL	-	expression tag	UNP C3SS82
A	484	ASP	-	expression tag	UNP C3SS82
A	485	LYS	-	expression tag	UNP C3SS82
A	486	LEU	-	expression tag	UNP C3SS82
A	487	ALA	-	expression tag	UNP C3SS82
A	488	ALA	-	expression tag	UNP C3SS82
A	489	ALA	-	expression tag	UNP C3SS82
A	490	LEU	-	expression tag	UNP C3SS82
A	491	GLU	-	expression tag	UNP C3SS82
A	492	HIS	-	expression tag	UNP C3SS82
A	493	HIS	-	expression tag	UNP C3SS82
A	494	HIS	-	expression tag	UNP C3SS82
A	495	HIS	-	expression tag	UNP C3SS82
A	496	HIS	-	expression tag	UNP C3SS82
A	497	HIS	-	expression tag	UNP C3SS82

## 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: RNA polymerase sigma-54 factor

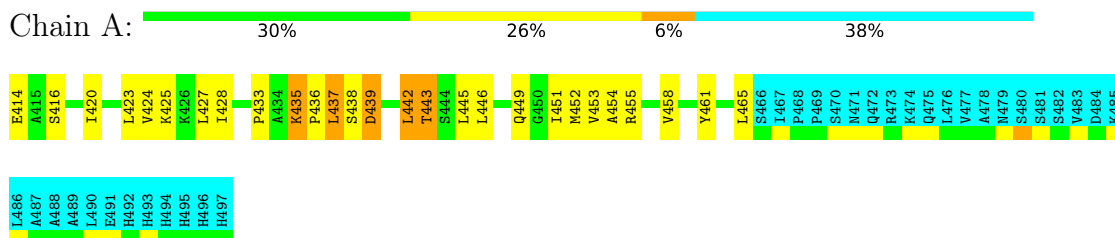


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

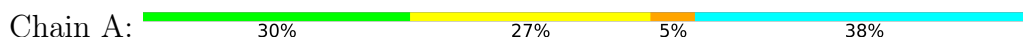
#### 4.2.1 Score per residue for model 1

- Molecule 1: RNA polymerase sigma-54 factor



#### 4.2.2 Score per residue for model 2

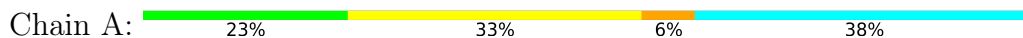
- Molecule 1: RNA polymerase sigma-54 factor





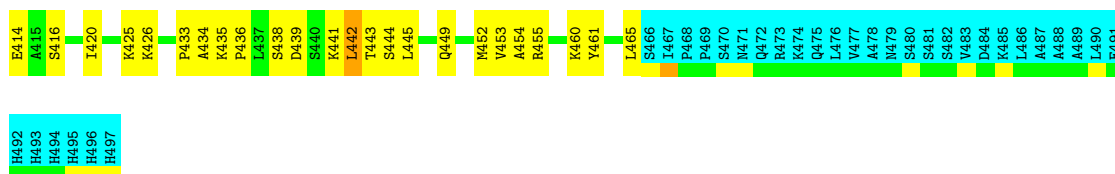
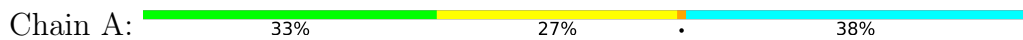
### 4.2.3 Score per residue for model 3

- Molecule 1: RNA polymerase sigma-54 factor



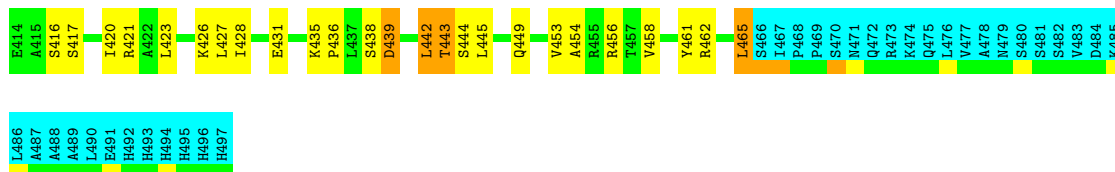
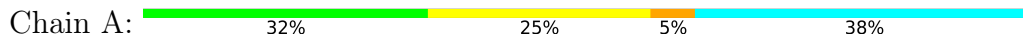
### 4.2.4 Score per residue for model 4

- Molecule 1: RNA polymerase sigma-54 factor



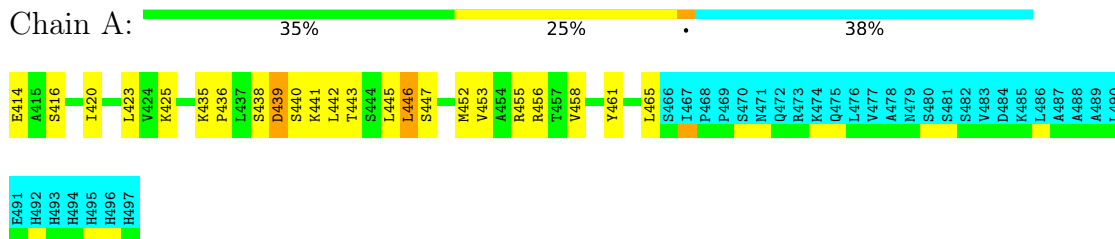
### 4.2.5 Score per residue for model 5

- Molecule 1: RNA polymerase sigma-54 factor



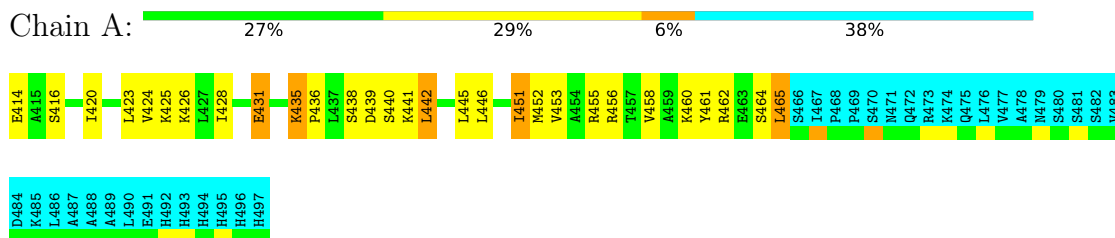
### 4.2.6 Score per residue for model 6

- Molecule 1: RNA polymerase sigma-54 factor



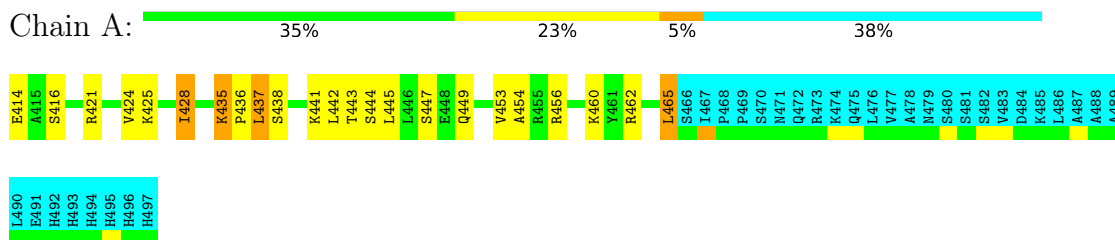
#### 4.2.7 Score per residue for model 7 (medoid)

- Molecule 1: RNA polymerase sigma-54 factor



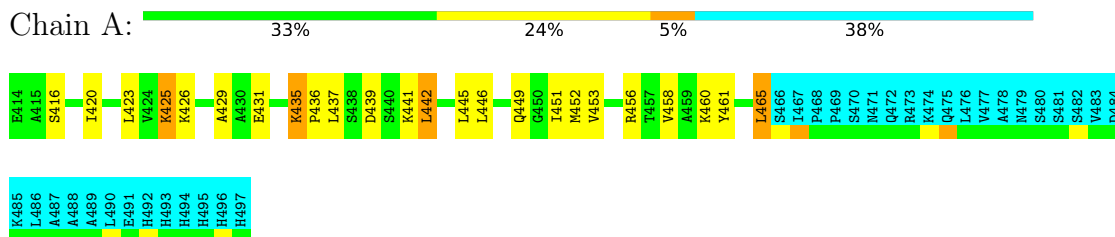
#### 4.2.8 Score per residue for model 8

- Molecule 1: RNA polymerase sigma-54 factor



#### 4.2.9 Score per residue for model 9

- Molecule 1: RNA polymerase sigma-54 factor

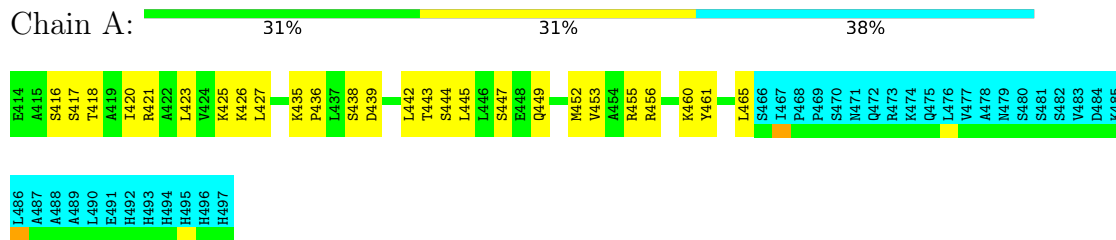






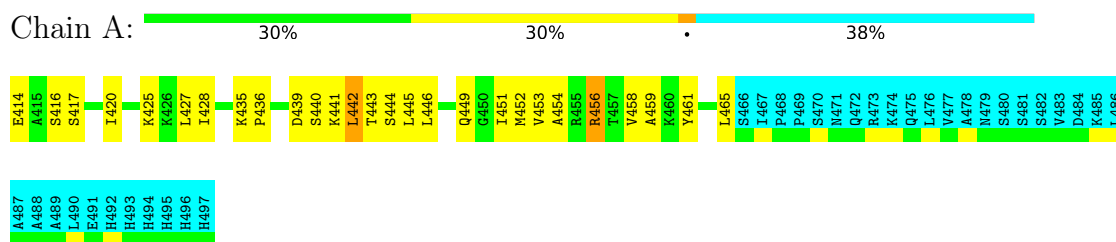
### 4.2.14 Score per residue for model 14

- Molecule 1: RNA polymerase sigma-54 factor



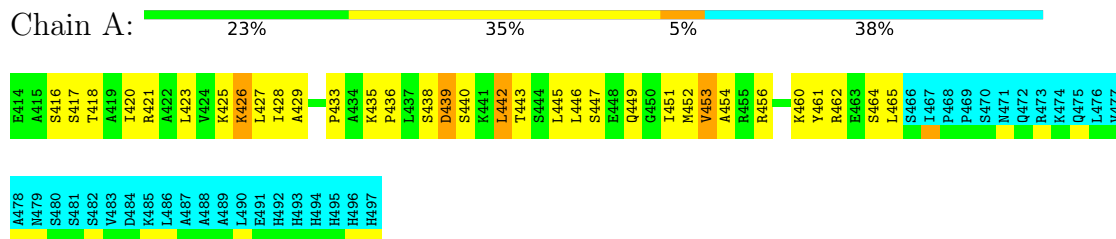
### 4.2.15 Score per residue for model 15

- Molecule 1: RNA polymerase sigma-54 factor



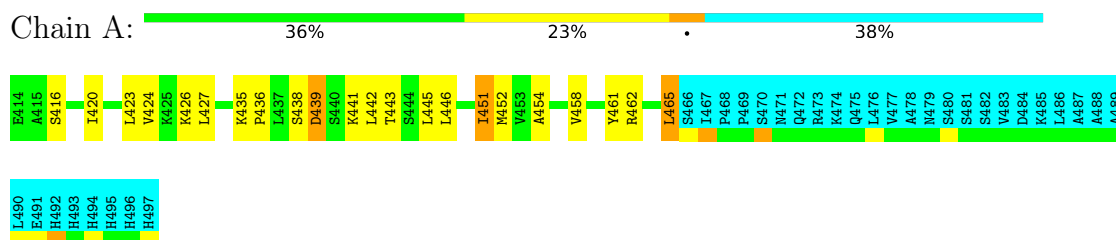
### 4.2.16 Score per residue for model 16

- Molecule 1: RNA polymerase sigma-54 factor



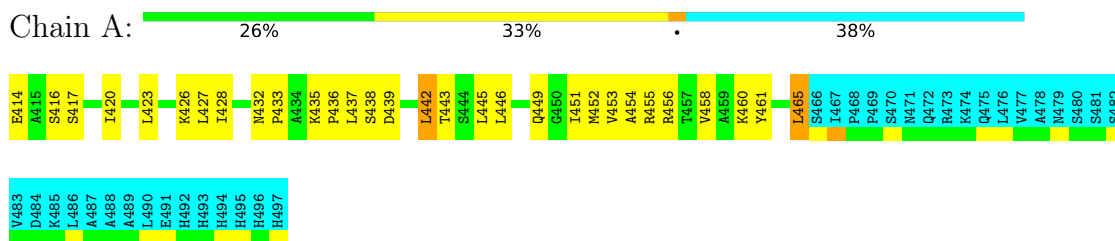
### 4.2.17 Score per residue for model 17

- Molecule 1: RNA polymerase sigma-54 factor



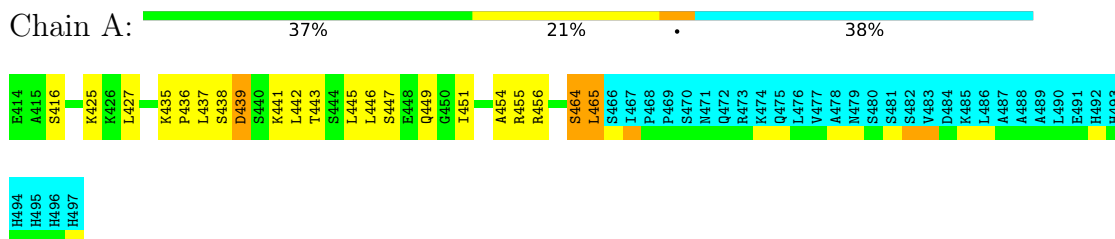
### 4.2.18 Score per residue for model 18

- Molecule 1: RNA polymerase sigma-54 factor



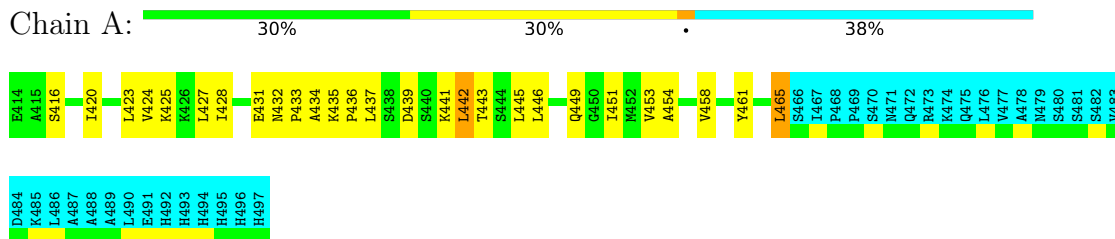
### 4.2.19 Score per residue for model 19

- Molecule 1: RNA polymerase sigma-54 factor



### 4.2.20 Score per residue for model 20

- Molecule 1: RNA polymerase sigma-54 factor



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *na*.

Of the 200 calculated structures, 20 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
CYANA	structure solution	
CYANA	refinement	

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	854
Number of shifts mapped to atoms	854
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	82%

## 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	392	427	426	13±4
All	All	7840	8540	8520	265

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 16.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:443:THR:HG23	1:A:454:ALA:HB3	0.88	1.43	5	4
1:A:443:THR:HG22	1:A:454:ALA:HB3	0.81	1.50	20	8
1:A:424:VAL:HG13	1:A:458:VAL:HG13	0.74	1.59	7	2
1:A:442:LEU:HD12	1:A:443:THR:HG23	0.73	1.60	17	2
1:A:446:LEU:HD22	1:A:451:ILE:HG21	0.72	1.62	10	12
1:A:420:ILE:HG21	1:A:461:TYR:CZ	0.68	2.23	20	14
1:A:424:VAL:HG12	1:A:428:ILE:HD12	0.67	1.65	20	1
1:A:420:ILE:HG21	1:A:461:TYR:CE1	0.67	2.25	15	5
1:A:420:ILE:HG23	1:A:423:LEU:HD12	0.65	1.68	5	2
1:A:439:ASP:OD2	1:A:458:VAL:HG11	0.64	1.93	6	1
1:A:442:LEU:CD1	1:A:458:VAL:HG21	0.64	2.23	13	5
1:A:420:ILE:HG21	1:A:461:TYR:CE2	0.63	2.29	14	5
1:A:442:LEU:HD11	1:A:458:VAL:HG21	0.63	1.71	20	3
1:A:443:THR:HG22	1:A:454:ALA:CB	0.63	2.24	16	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:442:LEU:H	1:A:442:LEU:HD13	0.63	1.53	3	1
1:A:439:ASP:OD2	1:A:459:ALA:HB2	0.61	1.95	3	2
1:A:428:ILE:HG23	1:A:431:GLU:OE2	0.60	1.97	12	3
1:A:427:LEU:HG	1:A:442:LEU:HD13	0.60	1.74	2	1
1:A:428:ILE:HG23	1:A:431:GLU:CD	0.60	2.17	12	2
1:A:446:LEU:HD23	1:A:447:SER:N	0.60	2.12	6	1
1:A:446:LEU:HD22	1:A:451:ILE:CB	0.59	2.28	19	12
1:A:443:THR:CG2	1:A:454:ALA:HB3	0.58	2.28	17	2
1:A:420:ILE:HD13	1:A:423:LEU:HD12	0.58	1.74	14	1
1:A:439:ASP:CB	1:A:442:LEU:HD11	0.57	2.30	7	5
1:A:462:ARG:O	1:A:465:LEU:HD23	0.57	1.99	5	6
1:A:446:LEU:HD22	1:A:451:ILE:CG2	0.57	2.30	2	12
1:A:442:LEU:HD13	1:A:458:VAL:HG21	0.56	1.77	9	1
1:A:461:TYR:O	1:A:465:LEU:HD12	0.56	2.00	14	4
1:A:420:ILE:HG21	1:A:461:TYR:OH	0.55	2.02	12	1
1:A:427:LEU:HD12	1:A:428:ILE:N	0.55	2.17	20	2
1:A:442:LEU:CD1	1:A:443:THR:HG23	0.55	2.32	18	2
1:A:439:ASP:HB2	1:A:442:LEU:HD11	0.54	1.78	7	5
1:A:451:ILE:O	1:A:453:VAL:HG22	0.54	2.03	16	1
1:A:427:LEU:HD13	1:A:442:LEU:HD22	0.54	1.78	19	1
1:A:446:LEU:HD12	1:A:451:ILE:HG21	0.53	1.78	12	1
1:A:428:ILE:HG23	1:A:433:PRO:HG3	0.53	1.80	16	2
1:A:420:ILE:CD1	1:A:423:LEU:HD12	0.53	2.33	14	1
1:A:437:LEU:HD12	1:A:438:SER:N	0.53	2.19	3	1
1:A:427:LEU:HD13	1:A:442:LEU:HD13	0.52	1.80	16	3
1:A:424:VAL:HA	1:A:427:LEU:HD23	0.52	1.81	3	3
1:A:439:ASP:CB	1:A:442:LEU:HD23	0.52	2.35	19	1
1:A:461:TYR:O	1:A:465:LEU:HD22	0.52	2.05	20	1
1:A:443:THR:HA	1:A:446:LEU:HD22	0.51	1.81	6	1
1:A:442:LEU:HD13	1:A:442:LEU:N	0.51	2.21	3	1
1:A:443:THR:CB	1:A:454:ALA:HB3	0.51	2.36	3	2
1:A:442:LEU:HD12	1:A:443:THR:N	0.50	2.21	10	2
1:A:427:LEU:HD12	1:A:442:LEU:HB2	0.50	1.83	18	6
1:A:439:ASP:HB3	1:A:442:LEU:HD11	0.50	1.83	9	2
1:A:442:LEU:HD12	1:A:454:ALA:HB1	0.50	1.83	5	1
1:A:439:ASP:HA	1:A:442:LEU:HD11	0.49	1.84	3	1
1:A:433:PRO:O	1:A:436:PRO:HD2	0.49	2.07	20	5
1:A:435:LYS:CB	1:A:436:PRO:CD	0.49	2.91	1	20
1:A:439:ASP:HA	1:A:442:LEU:HD21	0.48	1.85	7	8
1:A:442:LEU:HD22	1:A:458:VAL:HG21	0.48	1.84	18	1
1:A:437:LEU:HD12	1:A:437:LEU:O	0.48	2.08	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:443:THR:HG21	1:A:455:ARG:HB2	0.48	1.86	19	2
1:A:454:ALA:HA	1:A:458:VAL:HG23	0.47	1.85	15	1
1:A:433:PRO:O	1:A:434:ALA:HB3	0.47	2.10	10	5
1:A:465:LEU:HD12	1:A:465:LEU:O	0.47	2.10	19	1
1:A:424:VAL:HG12	1:A:428:ILE:HG12	0.47	1.86	8	1
1:A:427:LEU:CD1	1:A:458:VAL:HG21	0.47	2.39	17	1
1:A:443:THR:HB	1:A:454:ALA:HB3	0.47	1.86	13	1
1:A:426:LYS:HA	1:A:429:ALA:HB3	0.47	1.87	16	1
1:A:442:LEU:CD1	1:A:454:ALA:HB1	0.47	2.40	10	3
1:A:439:ASP:O	1:A:440:SER:CB	0.46	2.63	11	1
1:A:439:ASP:CB	1:A:442:LEU:HD21	0.46	2.41	14	1
1:A:439:ASP:O	1:A:443:THR:HG22	0.46	2.10	14	1
1:A:443:THR:HG21	1:A:455:ARG:CB	0.46	2.40	3	2
1:A:442:LEU:HD22	1:A:443:THR:N	0.45	2.26	3	1
1:A:451:ILE:HG22	1:A:453:VAL:HG22	0.45	1.88	7	1
1:A:424:VAL:CG1	1:A:458:VAL:HG13	0.45	2.37	7	1
1:A:428:ILE:HG23	1:A:438:SER:OG	0.45	2.12	11	1
1:A:427:LEU:HB3	1:A:442:LEU:HD22	0.45	1.88	2	1
1:A:435:LYS:N	1:A:436:PRO:HD2	0.45	2.27	9	19
1:A:446:LEU:HD13	1:A:453:VAL:CG2	0.45	2.42	16	1
1:A:425:LYS:O	1:A:429:ALA:HB2	0.45	2.12	9	3
1:A:427:LEU:HD11	1:A:458:VAL:HG21	0.44	1.89	17	1
1:A:424:VAL:O	1:A:428:ILE:HD12	0.44	2.11	20	1
1:A:442:LEU:HD21	1:A:458:VAL:HG11	0.44	1.89	18	1
1:A:465:LEU:HD13	1:A:465:LEU:N	0.43	2.28	20	1
1:A:427:LEU:HD22	1:A:458:VAL:HG21	0.43	1.91	15	1
1:A:446:LEU:HD22	1:A:451:ILE:HB	0.42	1.91	16	2
1:A:439:ASP:CA	1:A:442:LEU:HD21	0.42	2.45	3	1
1:A:420:ILE:HD12	1:A:423:LEU:HD12	0.42	1.92	6	1
1:A:451:ILE:O	1:A:452:MET:C	0.42	2.58	7	1
1:A:465:LEU:HD22	1:A:465:LEU:H	0.42	1.74	20	1
1:A:431:GLU:OE1	1:A:442:LEU:HD23	0.42	2.15	7	1
1:A:428:ILE:HG23	1:A:433:PRO:HB3	0.42	1.91	3	1
1:A:424:VAL:HG13	1:A:458:VAL:CG1	0.41	2.40	7	1
1:A:426:LYS:O	1:A:429:ALA:HB3	0.41	2.16	10	1
1:A:456:ARG:O	1:A:459:ALA:HB3	0.41	2.15	15	1
1:A:424:VAL:HG12	1:A:428:ILE:CD1	0.41	2.40	20	1
1:A:427:LEU:HD22	1:A:458:VAL:HG22	0.40	1.93	20	1
1:A:428:ILE:HG22	1:A:433:PRO:HG3	0.40	1.93	1	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	51/84 (61%)	41±1 (81±3%)	9±1 (18±3%)	1±1 (1±2%)	17	64
All	All	1020/1680 (61%)	826 (81%)	182 (18%)	12 (1%)	17	64

All 6 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	437	LEU	5
1	A	439	ASP	2
1	A	451	ILE	2
1	A	438	SER	1
1	A	452	MET	1
1	A	464	SER	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	43/71 (61%)	28±3 (65±6%)	15±3 (35±6%)	1	9
All	All	860/1420 (61%)	559 (65%)	301 (35%)	1	9

All 32 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	416	SER	20
1	A	445	LEU	20
1	A	449	GLN	17
1	A	425	LYS	16

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Mol	Chain	Res	Type	Models (Total)
1	A	438	SER	16
1	A	442	LEU	16
1	A	465	LEU	16
1	A	441	LYS	15
1	A	456	ARG	15
1	A	453	VAL	14
1	A	452	MET	13
1	A	455	ARG	12
1	A	423	LEU	11
1	A	426	LYS	10
1	A	460	LYS	10
1	A	414	GLU	8
1	A	439	ASP	8
1	A	444	SER	7
1	A	447	SER	7
1	A	440	SER	6
1	A	417	SER	6
1	A	435	LYS	5
1	A	437	LEU	5
1	A	421	ARG	5
1	A	443	THR	4
1	A	462	ARG	4
1	A	464	SER	4
1	A	431	GLU	4
1	A	432	ASN	3
1	A	418	THR	2
1	A	446	LEU	1
1	A	428	ILE	1

### 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 82% for the well-defined parts and 75% 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 [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	854
Number of shifts mapped to atoms	854
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

#### 7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	71	$-0.48 \pm 0.23$	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	69	$0.21 \pm 0.12$	None needed (< 0.5 ppm)
$^{13}\text{C}'$	43	$-0.48 \pm 0.13$	None needed (< 0.5 ppm)
$^{15}\text{N}$	71	$-0.34 \pm 0.34$	None needed (< 0.5 ppm)

#### 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 82%, i.e. 585 atoms were assigned a chemical shift out of a possible 714. 0 out of 10 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	225/257 (88%)	97/103 (94%)	81/104 (78%)	47/50 (94%)
Sidechain	352/448 (79%)	241/294 (82%)	111/135 (82%)	0/19 (0%)

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	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Aromatic	8/9 (89%)	4/4 (100%)	4/5 (80%)	0/0 (—%)
Overall	585/714 (82%)	342/401 (85%)	196/244 (80%)	47/69 (68%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 75%, i.e. 854 atoms were assigned a chemical shift out of a possible 1140. 0 out of 15 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	329/413 (80%)	144/165 (87%)	114/168 (68%)	71/80 (89%)
Sidechain	517/676 (76%)	354/443 (80%)	163/205 (80%)	0/28 (0%)
Aromatic	8/51 (16%)	4/28 (14%)	4/17 (24%)	0/6 (0%)
Overall	854/1140 (75%)	502/636 (79%)	281/390 (72%)	71/114 (62%)

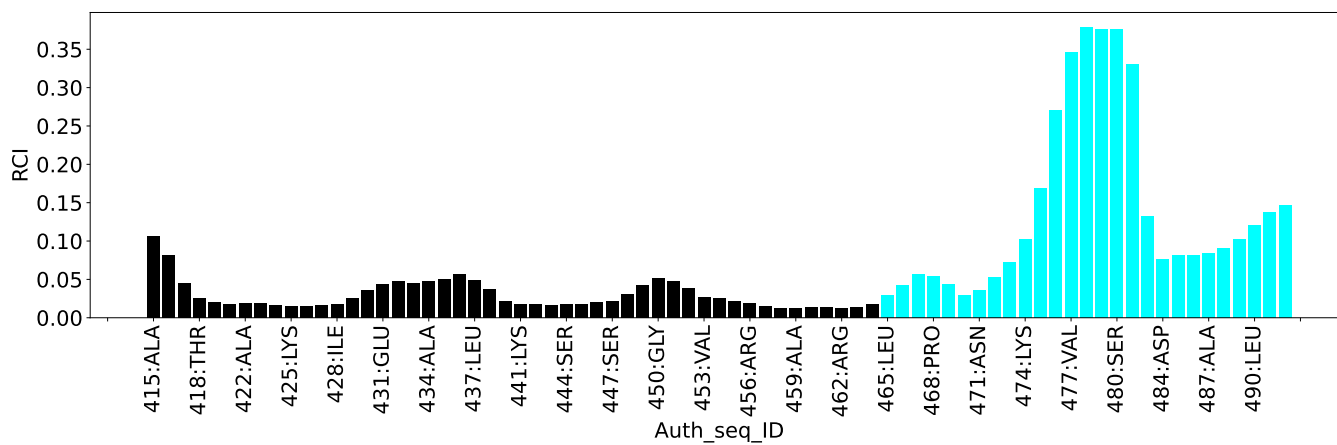
### 7.1.4 Statistically unusual chemical shifts [i](#)

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	499
Intra-residue ( $ i-j =0$ )	185
Sequential ( $ i-j =1$ )	187
Medium range ( $ i-j >1$ and $ i-j <5$ )	101
Long range ( $ i-j \geq 5$ )	26
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	5.9
Number of long range restraints per residue <sup>1</sup>	0.3

<sup>1</sup>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)	10.4	0.2
0.2-0.5 (Medium)	3.0	0.44
>0.5 (Large)	0.2	0.66

### 8.2.2 Average number of dihedral-angle violations per model

Dihedral-angle violations less than  $1^\circ$  are not included in the calculation. There are no dihedral-angle violations

## 9 Distance violation analysis [i](#)

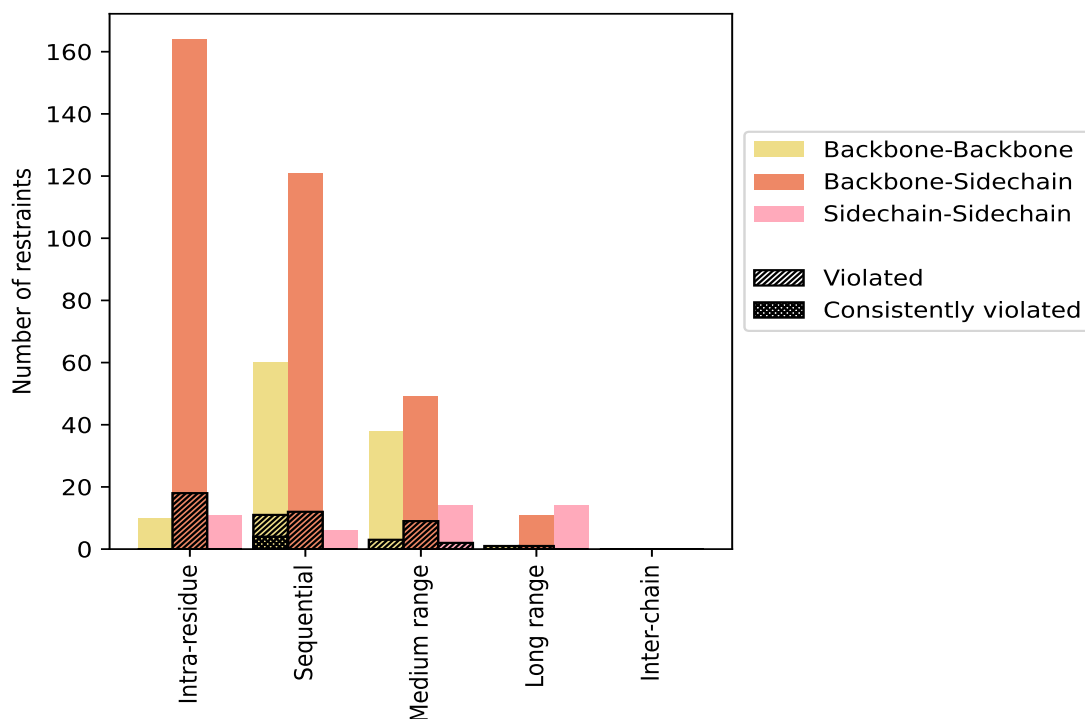
### 9.1 Summary of distance violations [i](#)

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	% <sup>1</sup>	Violated <sup>3</sup>			Consistently Violated <sup>4</sup>		
			Count	% <sup>2</sup>	% <sup>1</sup>	Count	% <sup>2</sup>	% <sup>1</sup>
<b>Intra-residue (<math> i-j =0</math>)</b>	<b>185</b>	<b>37.1</b>	<b>18</b>	<b>9.7</b>	<b>3.6</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>
Backbone-Backbone	10	2.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	164	32.9	18	11.0	3.6	0	0.0	0.0
Sidechain-Sidechain	11	2.2	0	0.0	0.0	0	0.0	0.0
<b>Sequential (<math> i-j =1</math>)</b>	<b>187</b>	<b>37.5</b>	<b>23</b>	<b>12.3</b>	<b>4.6</b>	<b>4</b>	<b>2.1</b>	<b>0.8</b>
Backbone-Backbone	60	12.0	11	18.3	2.2	4	6.7	0.8
Backbone-Sidechain	121	24.2	12	9.9	2.4	0	0.0	0.0
Sidechain-Sidechain	6	1.2	0	0.0	0.0	0	0.0	0.0
<b>Medium range (<math> i-j &gt;1</math> &amp; <math> i-j &lt;5</math>)</b>	<b>101</b>	<b>20.2</b>	<b>14</b>	<b>13.9</b>	<b>2.8</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>
Backbone-Backbone	38	7.6	3	7.9	0.6	0	0.0	0.0
Backbone-Sidechain	49	9.8	9	18.4	1.8	0	0.0	0.0
Sidechain-Sidechain	14	2.8	2	14.3	0.4	0	0.0	0.0
<b>Long range (<math> i-j \geq 5</math>)</b>	<b>26</b>	<b>5.2</b>	<b>2</b>	<b>7.7</b>	<b>0.4</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>
Backbone-Backbone	1	0.2	1	100.0	0.2	0	0.0	0.0
Backbone-Sidechain	11	2.2	1	9.1	0.2	0	0.0	0.0
Sidechain-Sidechain	14	2.8	0	0.0	0.0	0	0.0	0.0
<b>Inter-chain</b>	<b>0</b>	<b>0.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>
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
<b>Hydrogen bond</b>	<b>0</b>	<b>0.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>
<b>Disulfide bond</b>	<b>0</b>	<b>0.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>
<b>Total</b>	<b>499</b>	<b>100.0</b>	<b>57</b>	<b>11.4</b>	<b>11.4</b>	<b>4</b>	<b>0.8</b>	<b>0.8</b>
Backbone-Backbone	109	21.8	15	13.8	3.0	4	3.7	0.8
Backbone-Sidechain	345	69.1	40	11.6	8.0	0	0.0	0.0
Sidechain-Sidechain	45	9.0	2	4.4	0.4	0	0.0	0.0

<sup>1</sup> percentage calculated with respect to the total number of distance restraints, <sup>2</sup> percentage calculated with respect to the number of restraints in a particular restraint category, <sup>3</sup> violated in at least one model, <sup>4</sup> 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 <sup>6</sup> (Å)	Median (Å)
	IR <sup>1</sup>	SQ <sup>2</sup>	MR <sup>3</sup>	LR <sup>4</sup>	IC <sup>5</sup>	Total				
1	1	7	2	0	0	10	0.18	0.31	0.05	0.16
2	3	5	3	0	0	11	0.16	0.29	0.05	0.14
3	2	8	1	1	0	12	0.18	0.4	0.08	0.14
4	3	6	1	0	0	10	0.2	0.42	0.08	0.18
5	4	5	3	0	0	12	0.18	0.37	0.06	0.17
6	5	7	8	2	0	22	0.17	0.3	0.05	0.16
7	3	6	2	0	0	11	0.2	0.66	0.15	0.14
8	5	5	3	0	0	13	0.17	0.39	0.07	0.15
9	2	7	1	0	0	10	0.19	0.41	0.09	0.14
10	3	7	3	0	0	13	0.23	0.66	0.15	0.19
11	7	6	5	1	0	19	0.18	0.4	0.06	0.15

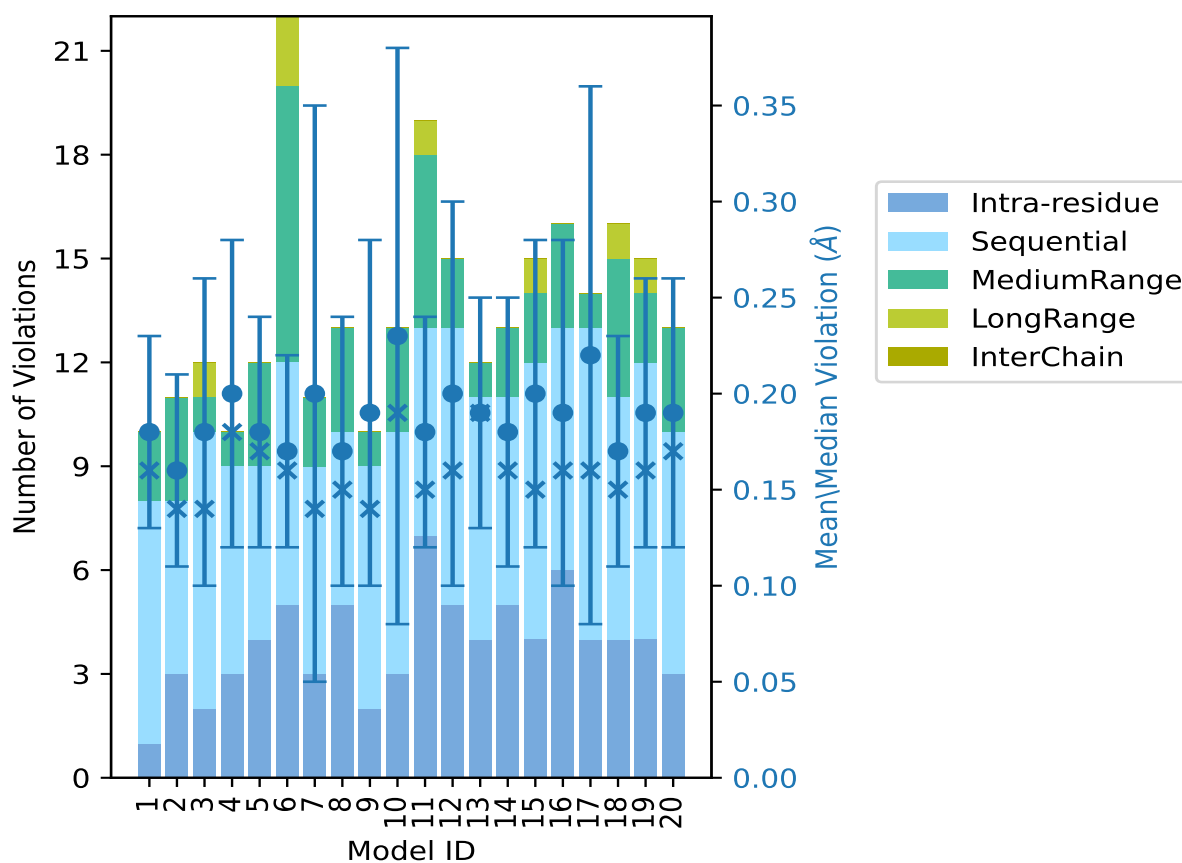
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Model ID	Number of violations					Total	Mean (Å)	Max (Å)	SD <sup>6</sup> (Å)	Median (Å)
	IR <sup>1</sup>	SQ <sup>2</sup>	MR <sup>3</sup>	LR <sup>4</sup>	IC <sup>5</sup>					
12	5	8	2	0	0	15	0.2	0.51	0.1	0.16
13	4	7	1	0	0	12	0.19	0.29	0.06	0.19
14	5	6	2	0	0	13	0.18	0.39	0.07	0.16
15	4	8	2	1	0	15	0.2	0.37	0.08	0.15
16	6	7	3	0	0	16	0.19	0.41	0.09	0.16
17	4	9	1	0	0	14	0.22	0.66	0.14	0.16
18	4	7	4	1	0	16	0.17	0.33	0.06	0.15
19	4	8	2	1	0	15	0.19	0.44	0.07	0.16
20	3	7	3	0	0	13	0.19	0.37	0.07	0.17

<sup>1</sup>Intra-residue restraints, <sup>2</sup>Sequential restraints, <sup>3</sup>Medium range restraints, <sup>4</sup>Long range restraints, <sup>5</sup>Inter-chain restraints, <sup>6</sup>Standard 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



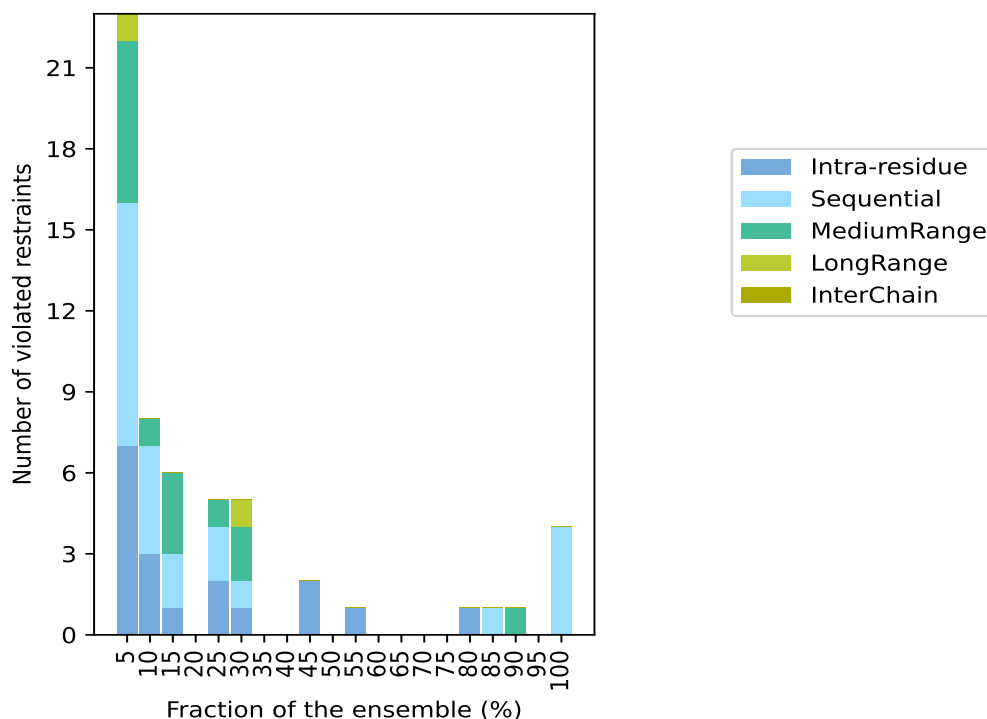
### 9.3 Distance violation statistics for the ensemble

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, 442(IR:167, SQ:164, MR:87, LR:24, IC:0) restraints are not violated in the ensemble.

Number of violated restraints						Fraction of the ensemble	
IR <sup>1</sup>	SQ <sup>2</sup>	MR <sup>3</sup>	LR <sup>4</sup>	IC <sup>5</sup>	Total	Count <sup>6</sup>	%
7	9	6	1	0	23	1	5.0
3	4	1	0	0	8	2	10.0
1	2	3	0	0	6	3	15.0
0	0	0	0	0	0	4	20.0
2	2	1	0	0	5	5	25.0
1	1	2	1	0	5	6	30.0
0	0	0	0	0	0	7	35.0
0	0	0	0	0	0	8	40.0
2	0	0	0	0	2	9	45.0
0	0	0	0	0	0	10	50.0
1	0	0	0	0	1	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
1	0	0	0	0	1	16	80.0
0	1	0	0	0	1	17	85.0
0	0	1	0	0	1	18	90.0
0	0	0	0	0	0	19	95.0
0	4	0	0	0	4	20	100.0

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

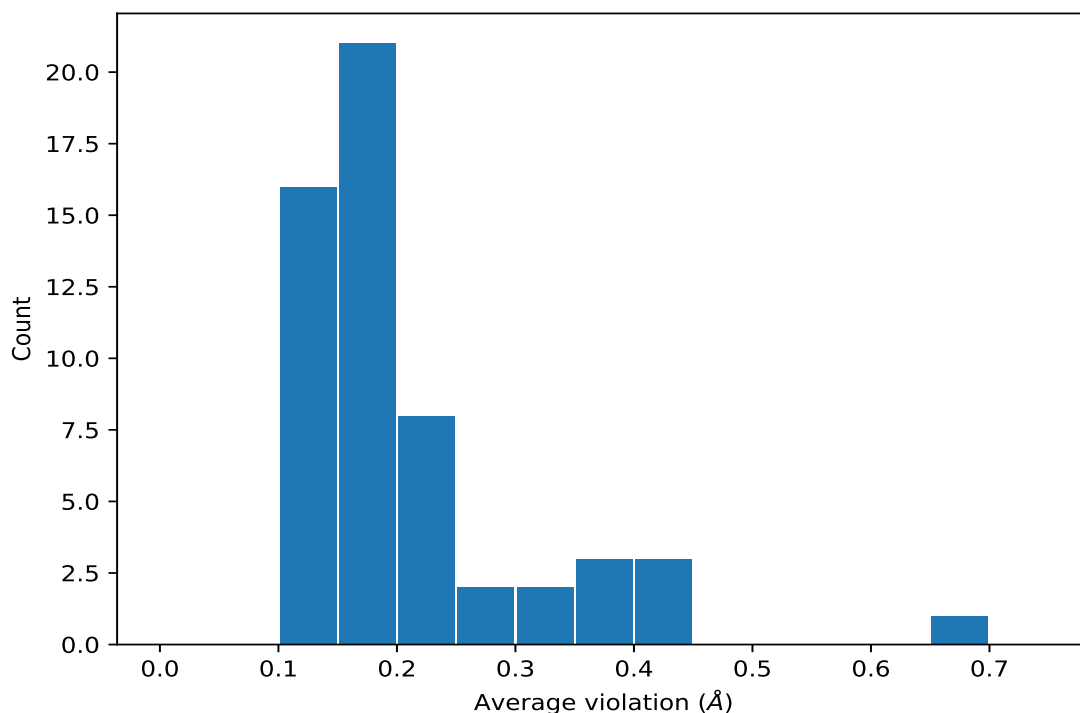
### 9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



## 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 <sup>1</sup>	Mean (Å)	SD <sup>1</sup> (Å)	Median (Å)
(1,411)	1:A:456:ARG:HA	1:A:457:THR:H	20	0.19	0.03	0.19
(1,402)	1:A:454:ALA:HA	1:A:455:ARG:H	20	0.17	0.02	0.18
(1,264)	1:A:416:SER:HA	1:A:417:SER:H	20	0.14	0.0	0.14
(1,490)	1:A:487:ALA:HA	1:A:488:ALA:H	20	0.14	0.0	0.14
(1,184)	1:A:453:VAL:HB	1:A:457:THR:HB	18	0.14	0.06	0.13
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG21	17	0.16	0.04	0.14
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG22	17	0.16	0.04	0.14
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG23	17	0.16	0.04	0.14
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG12	16	0.22	0.04	0.21
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG13	16	0.22	0.04	0.21
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG21	11	0.19	0.06	0.2
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG22	11	0.19	0.06	0.2
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG23	11	0.19	0.06	0.2
(1,131)	1:A:446:LEU:H	1:A:446:LEU:HB3	9	0.16	0.05	0.15
(1,179)	1:A:456:ARG:HA	1:A:456:ARG:HD2	9	0.16	0.02	0.15
(1,179)	1:A:456:ARG:HA	1:A:456:ARG:HD3	9	0.16	0.02	0.15

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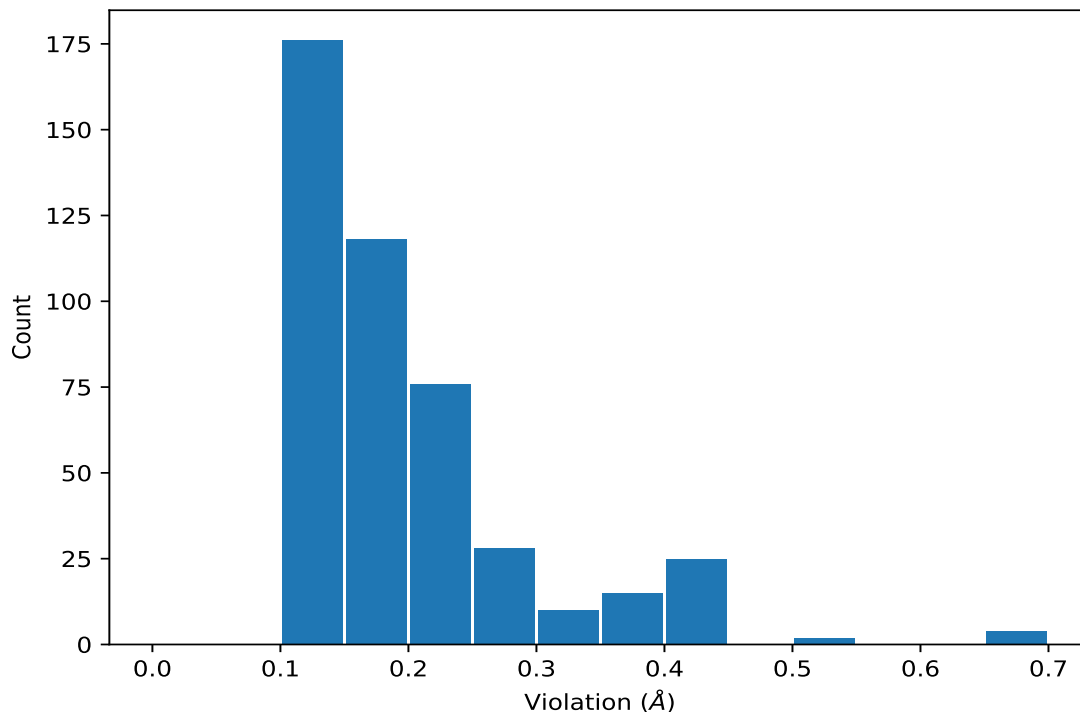
Key	Atom-1	Atom-2	Models <sup>1</sup>	Mean (Å)	SD <sup>1</sup> (Å)	Median (Å)
(1,59)	1:A:427:LEU:HA	1:A:427:LEU:HD11	6	0.39	0.05	0.41
(1,59)	1:A:427:LEU:HA	1:A:427:LEU:HD12	6	0.39	0.05	0.41
(1,59)	1:A:427:LEU:HA	1:A:427:LEU:HD13	6	0.39	0.05	0.41
(1,278)	1:A:421:ARG:HD2	1:A:422:ALA:H	6	0.35	0.19	0.32
(1,278)	1:A:421:ARG:HD3	1:A:422:ALA:H	6	0.35	0.19	0.32
(1,340)	1:A:438:SER:HB2	1:A:441:LYS:H	6	0.2	0.09	0.16
(1,340)	1:A:438:SER:HB3	1:A:441:LYS:H	6	0.2	0.09	0.16
(1,156)	1:A:446:LEU:HA	1:A:451:ILE:HD11	6	0.14	0.02	0.14
(1,156)	1:A:446:LEU:HA	1:A:451:ILE:HD12	6	0.14	0.02	0.14
(1,156)	1:A:446:LEU:HA	1:A:451:ILE:HD13	6	0.14	0.02	0.14
(1,293)	1:A:423:LEU:HD21	1:A:425:LYS:H	6	0.13	0.02	0.14
(1,293)	1:A:423:LEU:HD22	1:A:425:LYS:H	6	0.13	0.02	0.14
(1,293)	1:A:423:LEU:HD23	1:A:425:LYS:H	6	0.13	0.02	0.14
(1,159)	1:A:451:ILE:HA	1:A:451:ILE:HD11	5	0.4	0.02	0.39
(1,159)	1:A:451:ILE:HA	1:A:451:ILE:HD12	5	0.4	0.02	0.39
(1,159)	1:A:451:ILE:HA	1:A:451:ILE:HD13	5	0.4	0.02	0.39
(1,86)	1:A:433:PRO:HA	1:A:434:ALA:H	5	0.27	0.0	0.27
(1,147)	1:A:449:GLN:H	1:A:449:GLN:HG3	5	0.19	0.01	0.2
(1,239)	1:A:473:ARG:HA	1:A:474:LYS:H	5	0.16	0.02	0.15
(1,118)	1:A:439:ASP:HA	1:A:442:LEU:HB2	5	0.13	0.02	0.12
(1,123)	1:A:442:LEU:HB2	1:A:443:THR:H	3	0.23	0.12	0.16
(1,123)	1:A:442:LEU:HB3	1:A:443:THR:H	3	0.23	0.12	0.16
(1,121)	1:A:442:LEU:H	1:A:442:LEU:HG	3	0.21	0.0	0.21
(1,384)	1:A:449:GLN:HB2	1:A:451:ILE:H	3	0.18	0.09	0.12
(1,384)	1:A:449:GLN:HB3	1:A:451:ILE:H	3	0.18	0.09	0.12
(1,328)	1:A:432:ASN:HB2	1:A:434:ALA:H	3	0.15	0.02	0.14
(1,328)	1:A:432:ASN:HB3	1:A:434:ALA:H	3	0.15	0.02	0.14
(1,398)	1:A:453:VAL:HB	1:A:454:ALA:H	3	0.13	0.03	0.11
(1,193)	1:A:459:ALA:HA	1:A:462:ARG:H	3	0.11	0.0	0.11
(1,389)	1:A:451:ILE:HA	1:A:452:MET:H	2	0.66	0.0	0.66
(1,452)	1:A:465:LEU:H	1:A:465:LEU:HG	2	0.25	0.12	0.25
(1,459)	1:A:466:SER:H	1:A:467:ILE:H	2	0.2	0.0	0.2
(1,84)	1:A:432:ASN:H	1:A:432:ASN:HB3	2	0.18	0.06	0.18
(1,250)	1:A:475:GLN:HB2	1:A:476:LEU:H	2	0.18	0.02	0.18
(1,250)	1:A:475:GLN:HB3	1:A:476:LEU:H	2	0.18	0.02	0.18
(1,120)	1:A:439:ASP:HA	1:A:442:LEU:HB3	2	0.17	0.01	0.17
(1,65)	1:A:427:LEU:HB2	1:A:428:ILE:H	2	0.16	0.01	0.16
(1,65)	1:A:427:LEU:HB3	1:A:428:ILE:H	2	0.16	0.01	0.16
(1,211)	1:A:462:ARG:HA	1:A:462:ARG:HG2	2	0.12	0.0	0.12
(1,211)	1:A:462:ARG:HA	1:A:462:ARG:HG3	2	0.12	0.0	0.12

<sup>1</sup>Number of violated models, <sup>2</sup>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 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)
(1,389)	1:A:451:ILE:HA	1:A:452:MET:H	7	0.66
(1,389)	1:A:451:ILE:HA	1:A:452:MET:H	17	0.66
(1,278)	1:A:421:ARG:HD2	1:A:422:ALA:H	10	0.66
(1,278)	1:A:421:ARG:HD3	1:A:422:ALA:H	10	0.66
(1,278)	1:A:421:ARG:HD2	1:A:422:ALA:H	12	0.51
(1,278)	1:A:421:ARG:HD3	1:A:422:ALA:H	12	0.51
(1,59)	1:A:427:LEU:HA	1:A:427:LEU:HD11	19	0.44
(1,59)	1:A:427:LEU:HA	1:A:427:LEU:HD12	19	0.44
(1,59)	1:A:427:LEU:HA	1:A:427:LEU:HD13	19	0.44
(1,59)	1:A:427:LEU:HA	1:A:427:LEU:HD11	17	0.43

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,59)	1:A:427:LEU:HA	1:A:427:LEU:HD12	17	0.43
(1,59)	1:A:427:LEU:HA	1:A:427:LEU:HD13	17	0.43
(1,159)	1:A:451:ILE:HA	1:A:451:ILE:HD11	4	0.42
(1,159)	1:A:451:ILE:HA	1:A:451:ILE:HD12	4	0.42
(1,159)	1:A:451:ILE:HA	1:A:451:ILE:HD13	4	0.42
(1,59)	1:A:427:LEU:HA	1:A:427:LEU:HD11	10	0.41
(1,59)	1:A:427:LEU:HA	1:A:427:LEU:HD12	10	0.41
(1,59)	1:A:427:LEU:HA	1:A:427:LEU:HD13	10	0.41
(1,59)	1:A:427:LEU:HA	1:A:427:LEU:HD11	16	0.41
(1,59)	1:A:427:LEU:HA	1:A:427:LEU:HD12	16	0.41
(1,59)	1:A:427:LEU:HA	1:A:427:LEU:HD13	16	0.41
(1,478)	1:A:477:VAL:H	1:A:477:VAL:HG21	9	0.41
(1,478)	1:A:477:VAL:H	1:A:477:VAL:HG22	9	0.41
(1,478)	1:A:477:VAL:H	1:A:477:VAL:HG23	9	0.41
(1,159)	1:A:451:ILE:HA	1:A:451:ILE:HD11	16	0.41
(1,159)	1:A:451:ILE:HA	1:A:451:ILE:HD12	16	0.41
(1,159)	1:A:451:ILE:HA	1:A:451:ILE:HD13	16	0.41
(1,340)	1:A:438:SER:HB2	1:A:441:LYS:H	11	0.4
(1,340)	1:A:438:SER:HB3	1:A:441:LYS:H	11	0.4
(1,123)	1:A:442:LEU:HB2	1:A:443:THR:H	3	0.4
(1,123)	1:A:442:LEU:HB3	1:A:443:THR:H	3	0.4
(1,159)	1:A:451:ILE:HA	1:A:451:ILE:HD11	8	0.39
(1,159)	1:A:451:ILE:HA	1:A:451:ILE:HD12	8	0.39
(1,159)	1:A:451:ILE:HA	1:A:451:ILE:HD13	8	0.39
(1,159)	1:A:451:ILE:HA	1:A:451:ILE:HD11	14	0.39
(1,159)	1:A:451:ILE:HA	1:A:451:ILE:HD12	14	0.39
(1,159)	1:A:451:ILE:HA	1:A:451:ILE:HD13	14	0.39
(1,452)	1:A:465:LEU:H	1:A:465:LEU:HG	20	0.37
(1,184)	1:A:453:VAL:HB	1:A:457:THR:HB	15	0.37
(1,159)	1:A:451:ILE:HA	1:A:451:ILE:HD11	5	0.37
(1,159)	1:A:451:ILE:HA	1:A:451:ILE:HD12	5	0.37
(1,159)	1:A:451:ILE:HA	1:A:451:ILE:HD13	5	0.37
(1,132)	1:A:446:LEU:HA	1:A:446:LEU:HG	12	0.36
(1,59)	1:A:427:LEU:HA	1:A:427:LEU:HD11	15	0.35
(1,59)	1:A:427:LEU:HA	1:A:427:LEU:HD12	15	0.35
(1,59)	1:A:427:LEU:HA	1:A:427:LEU:HD13	15	0.35
(1,278)	1:A:421:ARG:HD2	1:A:422:ALA:H	18	0.33
(1,278)	1:A:421:ARG:HD3	1:A:422:ALA:H	18	0.33
(1,185)	1:A:457:THR:H	1:A:457:THR:HB	15	0.32
(1,278)	1:A:421:ARG:HD2	1:A:422:ALA:H	1	0.31
(1,278)	1:A:421:ARG:HD3	1:A:422:ALA:H	1	0.31
(1,59)	1:A:427:LEU:HA	1:A:427:LEU:HD11	20	0.3

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,59)	1:A:427:LEU:HA	1:A:427:LEU:HD12	20	0.3
(1,59)	1:A:427:LEU:HA	1:A:427:LEU:HD13	20	0.3
(1,384)	1:A:449:GLN:HB2	1:A:451:ILE:H	6	0.3
(1,384)	1:A:449:GLN:HB3	1:A:451:ILE:H	6	0.3
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG12	18	0.29
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG13	18	0.29
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG21	2	0.29
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG22	2	0.29
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG23	2	0.29
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG21	13	0.29
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG22	13	0.29
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG23	13	0.29
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG12	9	0.28
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG13	9	0.28
(1,131)	1:A:446:LEU:H	1:A:446:LEU:HB3	13	0.28
(1,86)	1:A:433:PRO:HA	1:A:434:ALA:H	4	0.27
(1,86)	1:A:433:PRO:HA	1:A:434:ALA:H	10	0.27
(1,86)	1:A:433:PRO:HA	1:A:434:ALA:H	12	0.27
(1,86)	1:A:433:PRO:HA	1:A:434:ALA:H	13	0.27
(1,86)	1:A:433:PRO:HA	1:A:434:ALA:H	20	0.27
(1,411)	1:A:456:ARG:HA	1:A:457:THR:H	3	0.27
(1,411)	1:A:456:ARG:HA	1:A:457:THR:H	15	0.27
(1,84)	1:A:432:ASN:H	1:A:432:ASN:HB3	18	0.25
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG12	6	0.25
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG13	6	0.25
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG12	8	0.25
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG13	8	0.25
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG12	14	0.25
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG13	14	0.25
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG21	16	0.25
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG22	16	0.25
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG23	16	0.25
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG12	7	0.24
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG13	7	0.24
(1,125)	1:A:443:THR:HA	1:A:453:VAL:H	6	0.24
(1,395)	1:A:451:ILE:HA	1:A:453:VAL:H	6	0.23
(1,348)	1:A:442:LEU:H	1:A:442:LEU:HD11	11	0.23
(1,348)	1:A:442:LEU:H	1:A:442:LEU:HD12	11	0.23
(1,348)	1:A:442:LEU:H	1:A:442:LEU:HD13	11	0.23
(1,348)	1:A:442:LEU:H	1:A:442:LEU:HD21	11	0.23
(1,348)	1:A:442:LEU:H	1:A:442:LEU:HD22	11	0.23
(1,348)	1:A:442:LEU:H	1:A:442:LEU:HD23	11	0.23

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,411)	1:A:456:ARG:HA	1:A:457:THR:H	10	0.22
(1,411)	1:A:456:ARG:HA	1:A:457:THR:H	11	0.22
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG21	1	0.22
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG22	1	0.22
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG23	1	0.22
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG21	4	0.22
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG22	4	0.22
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG23	4	0.22
(1,371)	1:A:448:GLU:HB2	1:A:449:GLN:H	1	0.22
(1,371)	1:A:448:GLU:HB3	1:A:449:GLN:H	1	0.22
(1,337)	1:A:437:LEU:HA	1:A:438:SER:H	3	0.22
(1,121)	1:A:442:LEU:H	1:A:442:LEU:HG	6	0.22
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG12	5	0.21
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG13	5	0.21
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG12	16	0.21
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG13	16	0.21
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG12	17	0.21
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG13	17	0.21
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG12	19	0.21
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG13	19	0.21
(1,459)	1:A:466:SER:H	1:A:467:ILE:H	17	0.21
(1,250)	1:A:475:GLN:HB2	1:A:476:LEU:H	19	0.21
(1,250)	1:A:475:GLN:HB3	1:A:476:LEU:H	19	0.21
(1,239)	1:A:473:ARG:HA	1:A:474:LYS:H	16	0.21
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG21	10	0.21
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG22	10	0.21
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG23	10	0.21
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG21	12	0.21
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG22	12	0.21
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG23	12	0.21
(1,121)	1:A:442:LEU:H	1:A:442:LEU:HG	3	0.21
(1,121)	1:A:442:LEU:H	1:A:442:LEU:HG	11	0.21
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG12	10	0.2
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG13	10	0.2
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG12	11	0.2
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG13	11	0.2
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG12	12	0.2
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG13	12	0.2
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG12	15	0.2
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG13	15	0.2
(1,459)	1:A:466:SER:H	1:A:467:ILE:H	5	0.2
(1,430)	1:A:460:LYS:HB2	1:A:461:TYR:H	14	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,430)	1:A:460:LYS:HB3	1:A:461:TYR:H	14	0.2
(1,411)	1:A:456:ARG:HA	1:A:457:THR:H	1	0.2
(1,411)	1:A:456:ARG:HA	1:A:457:THR:H	13	0.2
(1,411)	1:A:456:ARG:HA	1:A:457:THR:H	16	0.2
(1,411)	1:A:456:ARG:HA	1:A:457:THR:H	17	0.2
(1,411)	1:A:456:ARG:HA	1:A:457:THR:H	20	0.2
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG21	6	0.2
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG22	6	0.2
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG23	6	0.2
(1,251)	1:A:476:LEU:HA	1:A:477:VAL:H	13	0.2
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG21	11	0.2
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG22	11	0.2
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG23	11	0.2
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG21	15	0.2
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG22	15	0.2
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG23	15	0.2
(1,199)	1:A:460:LYS:H	1:A:460:LYS:HG2	16	0.2
(1,199)	1:A:460:LYS:H	1:A:460:LYS:HG3	16	0.2
(1,179)	1:A:456:ARG:HA	1:A:456:ARG:HD2	19	0.2
(1,179)	1:A:456:ARG:HA	1:A:456:ARG:HD3	19	0.2
(1,147)	1:A:449:GLN:H	1:A:449:GLN:HG3	4	0.2
(1,147)	1:A:449:GLN:H	1:A:449:GLN:HG3	13	0.2
(1,147)	1:A:449:GLN:H	1:A:449:GLN:HG3	14	0.2
(1,112)	1:A:441:LYS:HA	1:A:444:SER:H	18	0.2
(1,411)	1:A:456:ARG:HA	1:A:457:THR:H	9	0.19
(1,411)	1:A:456:ARG:HA	1:A:457:THR:H	19	0.19
(1,402)	1:A:454:ALA:HA	1:A:455:ARG:H	10	0.19
(1,402)	1:A:454:ALA:HA	1:A:455:ARG:H	14	0.19
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG21	12	0.19
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG22	12	0.19
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG23	12	0.19
(1,411)	1:A:456:ARG:HA	1:A:457:THR:H	14	0.18
(1,402)	1:A:454:ALA:HA	1:A:455:ARG:H	1	0.18
(1,402)	1:A:454:ALA:HA	1:A:455:ARG:H	2	0.18
(1,402)	1:A:454:ALA:HA	1:A:455:ARG:H	4	0.18
(1,402)	1:A:454:ALA:HA	1:A:455:ARG:H	5	0.18
(1,402)	1:A:454:ALA:HA	1:A:455:ARG:H	7	0.18
(1,402)	1:A:454:ALA:HA	1:A:455:ARG:H	8	0.18
(1,402)	1:A:454:ALA:HA	1:A:455:ARG:H	9	0.18
(1,402)	1:A:454:ALA:HA	1:A:455:ARG:H	11	0.18
(1,402)	1:A:454:ALA:HA	1:A:455:ARG:H	13	0.18
(1,402)	1:A:454:ALA:HA	1:A:455:ARG:H	16	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,402)	1:A:454:ALA:HA	1:A:455:ARG:H	17	0.18
(1,402)	1:A:454:ALA:HA	1:A:455:ARG:H	18	0.18
(1,402)	1:A:454:ALA:HA	1:A:455:ARG:H	19	0.18
(1,402)	1:A:454:ALA:HA	1:A:455:ARG:H	20	0.18
(1,340)	1:A:438:SER:HB2	1:A:441:LYS:H	5	0.18
(1,340)	1:A:438:SER:HB3	1:A:441:LYS:H	5	0.18
(1,328)	1:A:432:ASN:HB2	1:A:434:ALA:H	20	0.18
(1,328)	1:A:432:ASN:HB3	1:A:434:ALA:H	20	0.18
(1,221)	1:A:465:LEU:HB2	1:A:467:ILE:HD11	19	0.18
(1,221)	1:A:465:LEU:HB2	1:A:467:ILE:HD12	19	0.18
(1,221)	1:A:465:LEU:HB2	1:A:467:ILE:HD13	19	0.18
(1,221)	1:A:465:LEU:HB3	1:A:467:ILE:HD11	19	0.18
(1,221)	1:A:465:LEU:HB3	1:A:467:ILE:HD12	19	0.18
(1,221)	1:A:465:LEU:HB3	1:A:467:ILE:HD13	19	0.18
(1,179)	1:A:456:ARG:HA	1:A:456:ARG:HD2	6	0.18
(1,179)	1:A:456:ARG:HA	1:A:456:ARG:HD3	6	0.18
(1,147)	1:A:449:GLN:H	1:A:449:GLN:HG3	11	0.18
(1,147)	1:A:449:GLN:H	1:A:449:GLN:HG3	17	0.18
(1,120)	1:A:439:ASP:HA	1:A:442:LEU:HB3	11	0.18
(1,411)	1:A:456:ARG:HA	1:A:457:THR:H	4	0.17
(1,411)	1:A:456:ARG:HA	1:A:457:THR:H	5	0.17
(1,411)	1:A:456:ARG:HA	1:A:457:THR:H	6	0.17
(1,411)	1:A:456:ARG:HA	1:A:457:THR:H	8	0.17
(1,402)	1:A:454:ALA:HA	1:A:455:ARG:H	12	0.17
(1,398)	1:A:453:VAL:HB	1:A:454:ALA:H	8	0.17
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG21	15	0.17
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG22	15	0.17
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG23	15	0.17
(1,340)	1:A:438:SER:HB2	1:A:441:LYS:H	20	0.17
(1,340)	1:A:438:SER:HB3	1:A:441:LYS:H	20	0.17
(1,131)	1:A:446:LEU:H	1:A:446:LEU:HB3	5	0.17
(1,65)	1:A:427:LEU:HB2	1:A:428:ILE:H	20	0.16
(1,65)	1:A:427:LEU:HB3	1:A:428:ILE:H	20	0.16
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG12	2	0.16
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG13	2	0.16
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG12	13	0.16
(1,460)	1:A:467:ILE:H	1:A:467:ILE:HG13	13	0.16
(1,453)	1:A:465:LEU:H	1:A:465:LEU:HD11	19	0.16
(1,453)	1:A:465:LEU:H	1:A:465:LEU:HD12	19	0.16
(1,453)	1:A:465:LEU:H	1:A:465:LEU:HD13	19	0.16
(1,453)	1:A:465:LEU:H	1:A:465:LEU:HD21	19	0.16
(1,453)	1:A:465:LEU:H	1:A:465:LEU:HD22	19	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,453)	1:A:465:LEU:H	1:A:465:LEU:HD23	19	0.16
(1,411)	1:A:456:ARG:HA	1:A:457:THR:H	2	0.16
(1,411)	1:A:456:ARG:HA	1:A:457:THR:H	7	0.16
(1,411)	1:A:456:ARG:HA	1:A:457:THR:H	12	0.16
(1,411)	1:A:456:ARG:HA	1:A:457:THR:H	18	0.16
(1,402)	1:A:454:ALA:HA	1:A:455:ARG:H	6	0.16
(1,340)	1:A:438:SER:HB2	1:A:441:LYS:H	2	0.16
(1,340)	1:A:438:SER:HB3	1:A:441:LYS:H	2	0.16
(1,293)	1:A:423:LEU:HD21	1:A:425:LYS:H	6	0.16
(1,293)	1:A:423:LEU:HD22	1:A:425:LYS:H	6	0.16
(1,293)	1:A:423:LEU:HD23	1:A:425:LYS:H	6	0.16
(1,250)	1:A:475:GLN:HB2	1:A:476:LEU:H	3	0.16
(1,250)	1:A:475:GLN:HB3	1:A:476:LEU:H	3	0.16
(1,239)	1:A:473:ARG:HA	1:A:474:LYS:H	12	0.16
(1,179)	1:A:456:ARG:HA	1:A:456:ARG:HD2	5	0.16
(1,179)	1:A:456:ARG:HA	1:A:456:ARG:HD3	5	0.16
(1,179)	1:A:456:ARG:HA	1:A:456:ARG:HD2	14	0.16
(1,179)	1:A:456:ARG:HA	1:A:456:ARG:HD3	14	0.16
(1,156)	1:A:446:LEU:HA	1:A:451:ILE:HD11	19	0.16
(1,156)	1:A:446:LEU:HA	1:A:451:ILE:HD12	19	0.16
(1,156)	1:A:446:LEU:HA	1:A:451:ILE:HD13	19	0.16
(1,131)	1:A:446:LEU:H	1:A:446:LEU:HB3	7	0.16
(1,123)	1:A:442:LEU:HB2	1:A:443:THR:H	18	0.16
(1,123)	1:A:442:LEU:HB3	1:A:443:THR:H	18	0.16
(1,120)	1:A:439:ASP:HA	1:A:442:LEU:HB3	6	0.16
(1,65)	1:A:427:LEU:HB2	1:A:428:ILE:H	15	0.15
(1,65)	1:A:427:LEU:HB3	1:A:428:ILE:H	15	0.15
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG21	18	0.15
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG22	18	0.15
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG23	18	0.15
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG21	19	0.15
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG22	19	0.15
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG23	19	0.15
(1,340)	1:A:438:SER:HB2	1:A:441:LYS:H	10	0.15
(1,340)	1:A:438:SER:HB3	1:A:441:LYS:H	10	0.15
(1,335)	1:A:437:LEU:H	1:A:437:LEU:HD11	11	0.15
(1,335)	1:A:437:LEU:H	1:A:437:LEU:HD12	11	0.15
(1,335)	1:A:437:LEU:H	1:A:437:LEU:HD13	11	0.15
(1,239)	1:A:473:ARG:HA	1:A:474:LYS:H	14	0.15
(1,239)	1:A:473:ARG:HA	1:A:474:LYS:H	15	0.15
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG21	1	0.15
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG22	1	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG23	1	0.15
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG21	4	0.15
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG22	4	0.15
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG23	4	0.15
(1,184)	1:A:453:VAL:HB	1:A:457:THR:HB	19	0.15
(1,179)	1:A:456:ARG:HA	1:A:456:ARG:HD2	8	0.15
(1,179)	1:A:456:ARG:HA	1:A:456:ARG:HD3	8	0.15
(1,156)	1:A:446:LEU:HA	1:A:451:ILE:HD11	6	0.15
(1,156)	1:A:446:LEU:HA	1:A:451:ILE:HD12	6	0.15
(1,156)	1:A:446:LEU:HA	1:A:451:ILE:HD13	6	0.15
(1,156)	1:A:446:LEU:HA	1:A:451:ILE:HD11	11	0.15
(1,156)	1:A:446:LEU:HA	1:A:451:ILE:HD12	11	0.15
(1,156)	1:A:446:LEU:HA	1:A:451:ILE:HD13	11	0.15
(1,131)	1:A:446:LEU:H	1:A:446:LEU:HB3	8	0.15
(1,131)	1:A:446:LEU:H	1:A:446:LEU:HB3	11	0.15
(1,118)	1:A:439:ASP:HA	1:A:442:LEU:HB2	1	0.15
(1,490)	1:A:487:ALA:HA	1:A:488:ALA:H	1	0.14
(1,490)	1:A:487:ALA:HA	1:A:488:ALA:H	2	0.14
(1,490)	1:A:487:ALA:HA	1:A:488:ALA:H	3	0.14
(1,490)	1:A:487:ALA:HA	1:A:488:ALA:H	4	0.14
(1,490)	1:A:487:ALA:HA	1:A:488:ALA:H	5	0.14
(1,490)	1:A:487:ALA:HA	1:A:488:ALA:H	6	0.14
(1,490)	1:A:487:ALA:HA	1:A:488:ALA:H	7	0.14
(1,490)	1:A:487:ALA:HA	1:A:488:ALA:H	8	0.14
(1,490)	1:A:487:ALA:HA	1:A:488:ALA:H	9	0.14
(1,490)	1:A:487:ALA:HA	1:A:488:ALA:H	10	0.14
(1,490)	1:A:487:ALA:HA	1:A:488:ALA:H	11	0.14
(1,490)	1:A:487:ALA:HA	1:A:488:ALA:H	12	0.14
(1,490)	1:A:487:ALA:HA	1:A:488:ALA:H	13	0.14
(1,490)	1:A:487:ALA:HA	1:A:488:ALA:H	14	0.14
(1,490)	1:A:487:ALA:HA	1:A:488:ALA:H	15	0.14
(1,490)	1:A:487:ALA:HA	1:A:488:ALA:H	16	0.14
(1,490)	1:A:487:ALA:HA	1:A:488:ALA:H	17	0.14
(1,490)	1:A:487:ALA:HA	1:A:488:ALA:H	18	0.14
(1,490)	1:A:487:ALA:HA	1:A:488:ALA:H	19	0.14
(1,490)	1:A:487:ALA:HA	1:A:488:ALA:H	20	0.14
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG21	3	0.14
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG22	3	0.14
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG23	3	0.14
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG21	11	0.14
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG22	11	0.14
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG23	11	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG21	17	0.14
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG22	17	0.14
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG23	17	0.14
(1,366)	1:A:446:LEU:HB2	1:A:447:SER:H	6	0.14
(1,366)	1:A:446:LEU:HB3	1:A:447:SER:H	6	0.14
(1,350)	1:A:442:LEU:HG	1:A:443:THR:H	11	0.14
(1,328)	1:A:432:ASN:HB2	1:A:434:ALA:H	10	0.14
(1,328)	1:A:432:ASN:HB3	1:A:434:ALA:H	10	0.14
(1,328)	1:A:432:ASN:HB2	1:A:434:ALA:H	12	0.14
(1,328)	1:A:432:ASN:HB3	1:A:434:ALA:H	12	0.14
(1,293)	1:A:423:LEU:HD21	1:A:425:LYS:H	5	0.14
(1,293)	1:A:423:LEU:HD22	1:A:425:LYS:H	5	0.14
(1,293)	1:A:423:LEU:HD23	1:A:425:LYS:H	5	0.14
(1,293)	1:A:423:LEU:HD21	1:A:425:LYS:H	14	0.14
(1,293)	1:A:423:LEU:HD22	1:A:425:LYS:H	14	0.14
(1,293)	1:A:423:LEU:HD23	1:A:425:LYS:H	14	0.14
(1,278)	1:A:421:ARG:HD2	1:A:422:ALA:H	19	0.14
(1,278)	1:A:421:ARG:HD3	1:A:422:ALA:H	19	0.14
(1,264)	1:A:416:SER:HA	1:A:417:SER:H	1	0.14
(1,264)	1:A:416:SER:HA	1:A:417:SER:H	2	0.14
(1,264)	1:A:416:SER:HA	1:A:417:SER:H	3	0.14
(1,264)	1:A:416:SER:HA	1:A:417:SER:H	4	0.14
(1,264)	1:A:416:SER:HA	1:A:417:SER:H	5	0.14
(1,264)	1:A:416:SER:HA	1:A:417:SER:H	6	0.14
(1,264)	1:A:416:SER:HA	1:A:417:SER:H	7	0.14
(1,264)	1:A:416:SER:HA	1:A:417:SER:H	8	0.14
(1,264)	1:A:416:SER:HA	1:A:417:SER:H	9	0.14
(1,264)	1:A:416:SER:HA	1:A:417:SER:H	10	0.14
(1,264)	1:A:416:SER:HA	1:A:417:SER:H	11	0.14
(1,264)	1:A:416:SER:HA	1:A:417:SER:H	12	0.14
(1,264)	1:A:416:SER:HA	1:A:417:SER:H	13	0.14
(1,264)	1:A:416:SER:HA	1:A:417:SER:H	14	0.14
(1,264)	1:A:416:SER:HA	1:A:417:SER:H	15	0.14
(1,264)	1:A:416:SER:HA	1:A:417:SER:H	16	0.14
(1,264)	1:A:416:SER:HA	1:A:417:SER:H	17	0.14
(1,264)	1:A:416:SER:HA	1:A:417:SER:H	18	0.14
(1,264)	1:A:416:SER:HA	1:A:417:SER:H	19	0.14
(1,264)	1:A:416:SER:HA	1:A:417:SER:H	20	0.14
(1,239)	1:A:473:ARG:HA	1:A:474:LYS:H	9	0.14
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG21	3	0.14
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG22	3	0.14
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG23	3	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG21	20	0.14
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG22	20	0.14
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG23	20	0.14
(1,190)	1:A:457:THR:H	1:A:458:VAL:HB	15	0.14
(1,184)	1:A:453:VAL:HB	1:A:457:THR:HB	4	0.14
(1,184)	1:A:453:VAL:HB	1:A:457:THR:HB	6	0.14
(1,184)	1:A:453:VAL:HB	1:A:457:THR:HB	7	0.14
(1,184)	1:A:453:VAL:HB	1:A:457:THR:HB	11	0.14
(1,184)	1:A:453:VAL:HB	1:A:457:THR:HB	17	0.14
(1,179)	1:A:456:ARG:HA	1:A:456:ARG:HD2	2	0.14
(1,179)	1:A:456:ARG:HA	1:A:456:ARG:HD3	2	0.14
(1,179)	1:A:456:ARG:HA	1:A:456:ARG:HD2	7	0.14
(1,179)	1:A:456:ARG:HA	1:A:456:ARG:HD3	7	0.14
(1,179)	1:A:456:ARG:HA	1:A:456:ARG:HD2	12	0.14
(1,179)	1:A:456:ARG:HA	1:A:456:ARG:HD3	12	0.14
(1,179)	1:A:456:ARG:HA	1:A:456:ARG:HD2	18	0.14
(1,179)	1:A:456:ARG:HA	1:A:456:ARG:HD3	18	0.14
(1,131)	1:A:446:LEU:H	1:A:446:LEU:HB3	17	0.14
(1,123)	1:A:442:LEU:HB2	1:A:443:THR:H	19	0.14
(1,123)	1:A:442:LEU:HB3	1:A:443:THR:H	19	0.14
(1,118)	1:A:439:ASP:HA	1:A:442:LEU:HB2	15	0.14
(1,452)	1:A:465:LEU:H	1:A:465:LEU:HG	6	0.13
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG21	2	0.13
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG22	2	0.13
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG23	2	0.13
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG21	7	0.13
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG22	7	0.13
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG23	7	0.13
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG21	9	0.13
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG22	9	0.13
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG23	9	0.13
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG21	10	0.13
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG22	10	0.13
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG23	10	0.13
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG21	20	0.13
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG22	20	0.13
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG23	20	0.13
(1,377)	1:A:448:GLU:HB2	1:A:450:GLY:H	6	0.13
(1,377)	1:A:448:GLU:HB3	1:A:450:GLY:H	6	0.13
(1,340)	1:A:438:SER:HB2	1:A:441:LYS:H	16	0.13
(1,340)	1:A:438:SER:HB3	1:A:441:LYS:H	16	0.13
(1,293)	1:A:423:LEU:HD21	1:A:425:LYS:H	11	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,293)	1:A:423:LEU:HD22	1:A:425:LYS:H	11	0.13
(1,293)	1:A:423:LEU:HD23	1:A:425:LYS:H	11	0.13
(1,278)	1:A:421:ARG:HD2	1:A:422:ALA:H	17	0.13
(1,278)	1:A:421:ARG:HD3	1:A:422:ALA:H	17	0.13
(1,254)	1:A:477:VAL:HA	1:A:478:ALA:H	9	0.13
(1,184)	1:A:453:VAL:HB	1:A:457:THR:HB	9	0.13
(1,184)	1:A:453:VAL:HB	1:A:457:THR:HB	12	0.13
(1,184)	1:A:453:VAL:HB	1:A:457:THR:HB	13	0.13
(1,156)	1:A:446:LEU:HA	1:A:451:ILE:HD11	3	0.13
(1,156)	1:A:446:LEU:HA	1:A:451:ILE:HD12	3	0.13
(1,156)	1:A:446:LEU:HA	1:A:451:ILE:HD13	3	0.13
(1,131)	1:A:446:LEU:H	1:A:446:LEU:HB3	16	0.13
(1,84)	1:A:432:ASN:H	1:A:432:ASN:HB3	8	0.12
(1,402)	1:A:454:ALA:HA	1:A:455:ARG:H	3	0.12
(1,384)	1:A:449:GLN:HB2	1:A:451:ILE:H	11	0.12
(1,384)	1:A:449:GLN:HB3	1:A:451:ILE:H	11	0.12
(1,375)	1:A:449:GLN:H	1:A:451:ILE:HB	6	0.12
(1,293)	1:A:423:LEU:HD21	1:A:425:LYS:H	2	0.12
(1,293)	1:A:423:LEU:HD22	1:A:425:LYS:H	2	0.12
(1,293)	1:A:423:LEU:HD23	1:A:425:LYS:H	2	0.12
(1,211)	1:A:462:ARG:HA	1:A:462:ARG:HG2	18	0.12
(1,211)	1:A:462:ARG:HA	1:A:462:ARG:HG3	18	0.12
(1,193)	1:A:459:ALA:HA	1:A:462:ARG:H	18	0.12
(1,184)	1:A:453:VAL:HB	1:A:457:THR:HB	1	0.12
(1,184)	1:A:453:VAL:HB	1:A:457:THR:HB	5	0.12
(1,184)	1:A:453:VAL:HB	1:A:457:THR:HB	14	0.12
(1,184)	1:A:453:VAL:HB	1:A:457:THR:HB	16	0.12
(1,184)	1:A:453:VAL:HB	1:A:457:THR:HB	20	0.12
(1,169)	1:A:454:ALA:HB1	1:A:456:ARG:H	6	0.12
(1,169)	1:A:454:ALA:HB2	1:A:456:ARG:H	6	0.12
(1,169)	1:A:454:ALA:HB3	1:A:456:ARG:H	6	0.12
(1,156)	1:A:446:LEU:HA	1:A:451:ILE:HD11	15	0.12
(1,156)	1:A:446:LEU:HA	1:A:451:ILE:HD12	15	0.12
(1,156)	1:A:446:LEU:HA	1:A:451:ILE:HD13	15	0.12
(1,131)	1:A:446:LEU:H	1:A:446:LEU:HB3	12	0.12
(1,118)	1:A:439:ASP:HA	1:A:442:LEU:HB2	3	0.12
(1,402)	1:A:454:ALA:HA	1:A:455:ARG:H	15	0.11
(1,398)	1:A:453:VAL:HB	1:A:454:ALA:H	16	0.11
(1,398)	1:A:453:VAL:HB	1:A:454:ALA:H	17	0.11
(1,384)	1:A:449:GLN:HB2	1:A:451:ILE:H	7	0.11
(1,384)	1:A:449:GLN:HB3	1:A:451:ILE:H	7	0.11
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG21	13	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG22	13	0.11
(1,383)	1:A:450:GLY:H	1:A:451:ILE:HG23	13	0.11
(1,293)	1:A:423:LEU:HD21	1:A:425:LYS:H	8	0.11
(1,293)	1:A:423:LEU:HD22	1:A:425:LYS:H	8	0.11
(1,293)	1:A:423:LEU:HD23	1:A:425:LYS:H	8	0.11
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG21	6	0.11
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG22	6	0.11
(1,227)	1:A:467:ILE:H	1:A:467:ILE:HG23	6	0.11
(1,222)	1:A:466:SER:HA	1:A:467:ILE:HD11	6	0.11
(1,222)	1:A:466:SER:HA	1:A:467:ILE:HD12	6	0.11
(1,222)	1:A:466:SER:HA	1:A:467:ILE:HD13	6	0.11
(1,211)	1:A:462:ARG:HA	1:A:462:ARG:HG2	16	0.11
(1,211)	1:A:462:ARG:HA	1:A:462:ARG:HG3	16	0.11
(1,193)	1:A:459:ALA:HA	1:A:462:ARG:H	8	0.11
(1,193)	1:A:459:ALA:HA	1:A:462:ARG:H	16	0.11
(1,184)	1:A:453:VAL:HB	1:A:457:THR:HB	2	0.11
(1,184)	1:A:453:VAL:HB	1:A:457:THR:HB	10	0.11
(1,184)	1:A:453:VAL:HB	1:A:457:THR:HB	18	0.11
(1,156)	1:A:446:LEU:HA	1:A:451:ILE:HD11	18	0.11
(1,156)	1:A:446:LEU:HA	1:A:451:ILE:HD12	18	0.11
(1,156)	1:A:446:LEU:HA	1:A:451:ILE:HD13	18	0.11
(1,131)	1:A:446:LEU:H	1:A:446:LEU:HB3	14	0.11
(1,118)	1:A:439:ASP:HA	1:A:442:LEU:HB2	8	0.11
(1,118)	1:A:439:ASP:HA	1:A:442:LEU:HB2	18	0.11



## 10 Dihedral-angle violation analysis

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