



Full wwPDB NMR Structure Validation Report ⓘ

Mar 9, 2026 – 06:52 AM UTC

PDB ID : 2LVO / pdb_00002lvo
BMRB ID : 18582
Title : Structure of the gp78CUE domain bound to monubiquitin
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Byrd, R.A.; Das, R.
Deposited on : 2012-07-09

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ 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

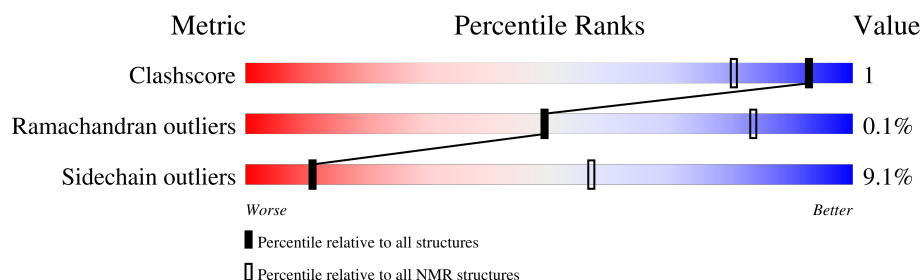
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 42%.

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	76	 88% 7% 5%
2	C	52	 77% . 21%

2 Ensemble composition and analysis

This entry contains 20 models. Model 9 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:1-A:72, C:457-C:497 (113)	0.47	9

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 4 clusters. No single-model clusters were found.

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

3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 2067 atoms, of which 1046 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms						Trace
1	A	76	Total	C	H	N	O	S	0
			1231	378	629	105	118	1	

- Molecule 2 is a protein called E3 ubiquitin-protein ligase AMFR.

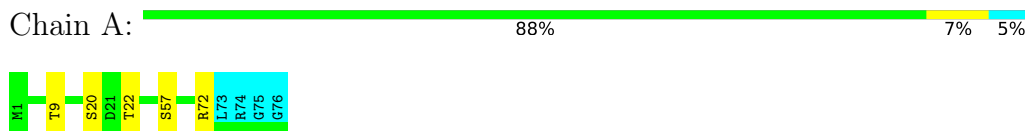
Mol	Chain	Residues	Atoms						Trace
2	C	52	Total	C	H	N	O	S	0
			836	264	417	72	81	2	

4 Residue-property plots [i](#)

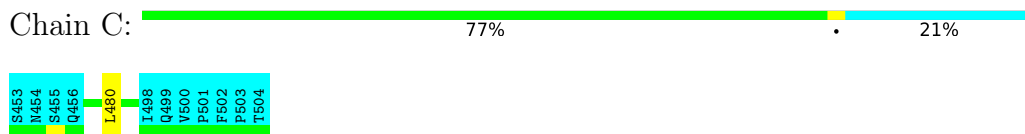
4.1 Average score per residue in the NMR ensemble

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: Ubiquitin



- Molecule 2: E3 ubiquitin-protein ligase AMFR

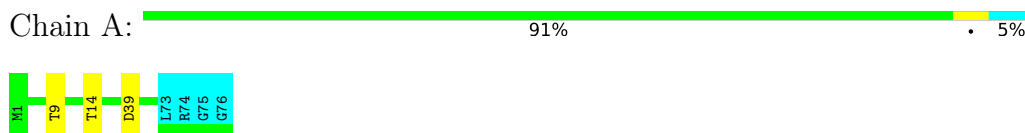


4.2 Scores per residue for each member of the ensemble

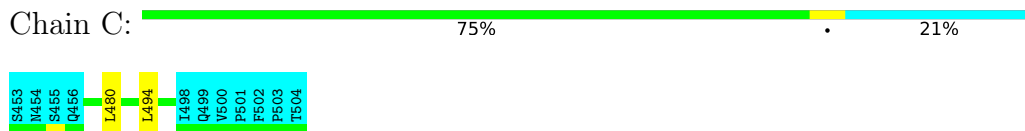
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Ubiquitin



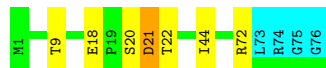
- Molecule 2: E3 ubiquitin-protein ligase AMFR



4.2.2 Score per residue for model 2

- Molecule 1: Ubiquitin

Chain A:  86% 8% 5%



- Molecule 2: E3 ubiquitin-protein ligase AMFR

Chain C:  63% 13% 21%



4.2.3 Score per residue for model 3

- Molecule 1: Ubiquitin

Chain A:  79% 14% 5%



- Molecule 2: E3 ubiquitin-protein ligase AMFR

Chain C:  65% 13% 21%



4.2.4 Score per residue for model 4

- Molecule 1: Ubiquitin

Chain A:  84% 11% 5%



- Molecule 2: E3 ubiquitin-protein ligase AMFR

Chain C:  71% 8% 21%



4.2.5 Score per residue for model 5

- Molecule 1: Ubiquitin

Chain A:  79% 14% 5%



- Molecule 2: E3 ubiquitin-protein ligase AMFR

Chain C:  69% 10% 21%



4.2.6 Score per residue for model 6

- Molecule 1: Ubiquitin

Chain A:  84% 11% 5%



- Molecule 2: E3 ubiquitin-protein ligase AMFR

Chain C:  69% 10% 21%



4.2.7 Score per residue for model 7

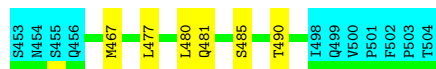
- Molecule 1: Ubiquitin

Chain A:  83% 12% 5%



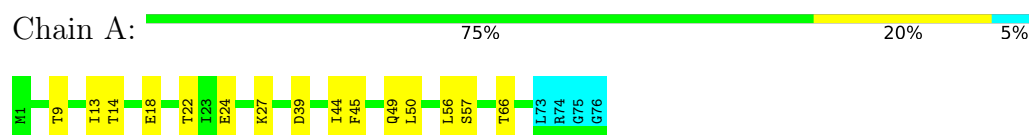
- Molecule 2: E3 ubiquitin-protein ligase AMFR

Chain C:  67% 12% 21%

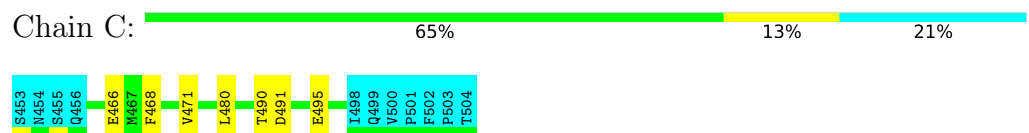


4.2.8 Score per residue for model 8

- Molecule 1: Ubiquitin

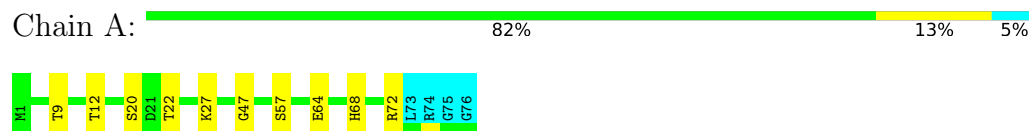


- Molecule 2: E3 ubiquitin-protein ligase AMFR



4.2.9 Score per residue for model 9 (medoid)

- Molecule 1: Ubiquitin

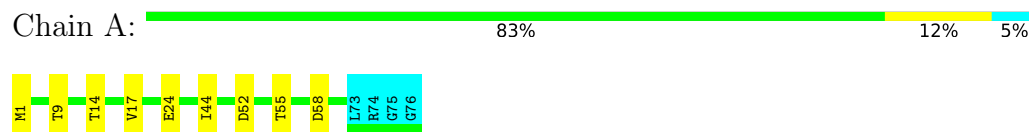


- Molecule 2: E3 ubiquitin-protein ligase AMFR

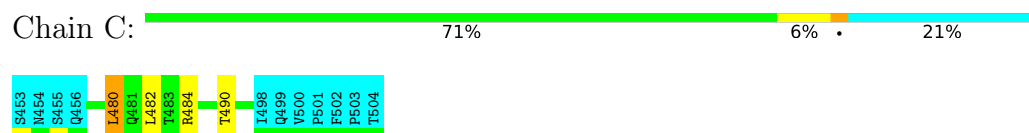


4.2.10 Score per residue for model 10

- Molecule 1: Ubiquitin

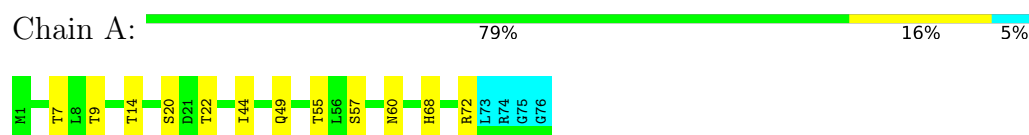


- Molecule 2: E3 ubiquitin-protein ligase AMFR

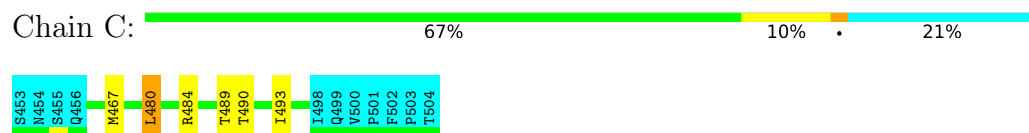


4.2.11 Score per residue for model 11

- Molecule 1: Ubiquitin

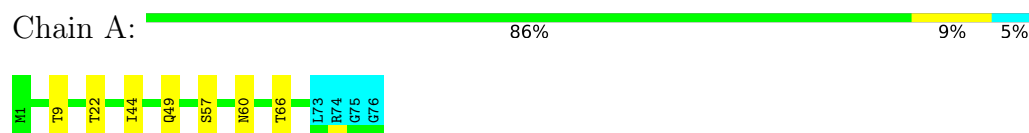


- Molecule 2: E3 ubiquitin-protein ligase AMFR

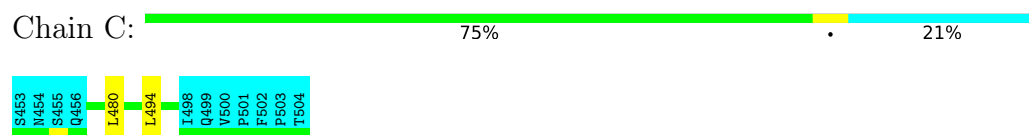


4.2.12 Score per residue for model 12

- Molecule 1: Ubiquitin

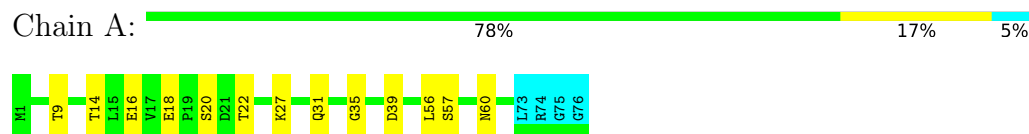


- Molecule 2: E3 ubiquitin-protein ligase AMFR

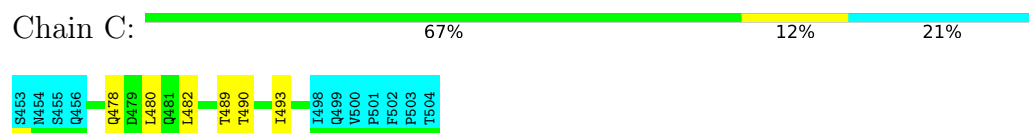


4.2.13 Score per residue for model 13

- Molecule 1: Ubiquitin



- Molecule 2: E3 ubiquitin-protein ligase AMFR



4.2.14 Score per residue for model 14

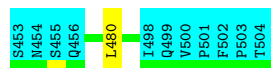
- Molecule 1: Ubiquitin

Chain A:  86% 9% 5%



- Molecule 2: E3 ubiquitin-protein ligase AMFR

Chain C:  77% 21%



4.2.15 Score per residue for model 15

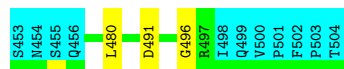
- Molecule 1: Ubiquitin

Chain A:  83% 11% 5%



- Molecule 2: E3 ubiquitin-protein ligase AMFR

Chain C:  73% 6% 21%



4.2.16 Score per residue for model 16

- Molecule 1: Ubiquitin

Chain A:  79% 14% 5%



- Molecule 2: E3 ubiquitin-protein ligase AMFR

Chain C:  69% 10% 21%



4.2.17 Score per residue for model 17

- Molecule 1: Ubiquitin

Chain A:  88% 7% 5%



- Molecule 2: E3 ubiquitin-protein ligase AMFR

Chain C:  69% 10% 21%



4.2.18 Score per residue for model 18

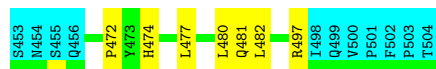
- Molecule 1: Ubiquitin

Chain A:  87% 8% 5%



- Molecule 2: E3 ubiquitin-protein ligase AMFR

Chain C:  65% 13% 21%



4.2.19 Score per residue for model 19

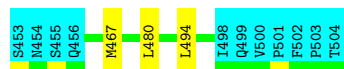
- Molecule 1: Ubiquitin

Chain A:  76% 18% 5%



- Molecule 2: E3 ubiquitin-protein ligase AMFR

Chain C:  73% 6% 21%



4.2.20 Score per residue for model 20

- Molecule 1: Ubiquitin

Chain A:  84% 9% • 5%



- Molecule 2: E3 ubiquitin-protein ligase AMFR

Chain C:  71% 8% 21%



5 Refinement protocol and experimental data overview

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

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
CNS	structure solution	
X-PLOR NIH	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	792
Number of shifts mapped to atoms	792
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	42%

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	574	599	599	2±1
2	C	333	333	333	1±1
All	All	18140	18640	18640	50

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:45:PHE:HB3	1:A:50:LEU:HD21	0.64	1.68	18	6
2:C:479:ASP:HB3	2:C:489:THR:HG23	0.60	1.73	2	3
2:C:480:LEU:HD22	2:C:489:THR:HG21	0.52	1.81	2	1
1:A:18:GLU:O	1:A:21:ASP:HB2	0.51	2.05	16	3
1:A:72:ARG:HB2	2:C:491:ASP:OD1	0.50	2.06	15	2
2:C:491:ASP:O	2:C:495:GLU:HG2	0.50	2.05	8	1
1:A:68:HIS:CD2	2:C:467:MET:HA	0.47	2.45	9	6
1:A:1:MET:HG2	1:A:17:VAL:O	0.47	2.10	10	3
1:A:41:GLN:HG2	1:A:69:LEU:HD11	0.47	1.86	3	1
2:C:489:THR:O	2:C:493:ILE:HG13	0.46	2.11	13	4
1:A:51:GLU:HB2	1:A:54:ARG:CG	0.46	2.41	7	1
2:C:463:GLN:O	2:C:467:MET:HG2	0.46	2.10	2	1
1:A:47:GLY:HA3	2:C:470:GLN:OE1	0.45	2.11	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:31:GLN:O	1:A:35:GLY:HA2	0.45	2.12	13	1
1:A:70:VAL:HG13	2:C:490:THR:HB	0.45	1.89	16	1
2:C:468:PHE:O	2:C:471:VAL:HG12	0.44	2.13	8	1
1:A:55:THR:O	1:A:58:ASP:HB2	0.44	2.13	4	2
2:C:480:LEU:O	2:C:484:ARG:HG3	0.43	2.13	10	1
2:C:477:LEU:O	2:C:481:GLN:HG3	0.43	2.14	18	2
1:A:72:ARG:HG3	2:C:491:ASP:OD1	0.42	2.15	5	1
1:A:72:ARG:HA	2:C:491:ASP:CG	0.42	2.40	9	1
1:A:40:GLN:HG2	1:A:72:ARG:O	0.41	2.14	19	1
1:A:18:GLU:O	1:A:56:LEU:HD12	0.41	2.16	14	3
1:A:72:ARG:HG3	2:C:491:ASP:OD2	0.41	2.15	2	1
2:C:472:PRO:HB3	2:C:474:HIS:CE1	0.40	2.51	18	1
2:C:480:LEU:O	2:C:484:ARG:HD2	0.40	2.16	11	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	71/76 (93%)	70±1 (98±1%)	1±1 (2±1%)	0±0 (0±0%)	49	83
2	C	41/52 (79%)	39±1 (96±2%)	2±1 (4±2%)	0±0 (0±1%)	49	83
All	All	2240/2560 (88%)	2181 (97%)	57 (3%)	2 (0%)	49	83

All 2 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	47	GLY	1
2	C	496	GLY	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	66/68 (97%)	59±2 (90±3%)	7±2 (10±3%)	9	53
2	C	38/49 (78%)	35±1 (93±3%)	3±1 (7±3%)	15	64
All	All	2080/2340 (89%)	1890 (91%)	190 (9%)	11	57

All 36 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	9	THR	20
2	C	480	LEU	20
1	A	20	SER	13
1	A	22	THR	13
1	A	57	SER	13
1	A	14	THR	10
1	A	44	ILE	10
2	C	490	THR	9
1	A	39	ASP	6
1	A	24	GLU	6
1	A	49	GLN	6
2	C	494	LEU	5
1	A	27	LYS	5
2	C	482	LEU	5
2	C	485	SER	5
1	A	60	ASN	5
1	A	72	ARG	5
1	A	21	ASP	4
2	C	478	GLN	3
1	A	52	ASP	3
1	A	64	GLU	3
1	A	7	THR	3
1	A	55	THR	2
1	A	66	THR	2
2	C	497	ARG	2
1	A	16	GLU	2
2	C	458	ASN	1
1	A	41	GLN	1
1	A	48	LYS	1
2	C	468	PHE	1
1	A	13	ILE	1
2	C	466	GLU	1

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Mol	Chain	Res	Type	Models (Total)
1	A	12	THR	1
1	A	62	GLN	1
2	C	484	ARG	1
2	C	462	HIS	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 oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 42% for the well-defined parts and 44% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *gp78CUE_shifts_in_gp78CUE_Ub*

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	792
Number of shifts mapped to atoms	792
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

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	49	-0.37 ± 0.33	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	47	0.30 ± 0.12	None needed (< 0.5 ppm)
$^{13}\text{C}'$	46	-0.25 ± 0.11	None needed (< 0.5 ppm)
^{15}N	113	0.68 ± 0.50	None needed (imprecise)

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 42%, i.e. 674 atoms were assigned a chemical shift out of a possible 1608. 0 out of 21 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	331/560 (59%)	146/226 (65%)	81/226 (36%)	104/108 (96%)
Sidechain	317/979 (32%)	216/635 (34%)	95/307 (31%)	6/37 (16%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	26/69 (38%)	13/35 (37%)	13/31 (42%)	0/3 (0%)
Overall	674/1608 (42%)	375/896 (42%)	189/564 (34%)	110/148 (74%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 44%, i.e. 792 atoms were assigned a chemical shift out of a possible 1805. 0 out of 23 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	371/633 (59%)	163/256 (64%)	95/256 (37%)	113/121 (93%)
Sidechain	385/1093 (35%)	262/709 (37%)	115/341 (34%)	8/43 (19%)
Aromatic	36/79 (46%)	18/40 (45%)	18/36 (50%)	0/3 (0%)
Overall	792/1805 (44%)	443/1005 (44%)	228/633 (36%)	121/167 (72%)

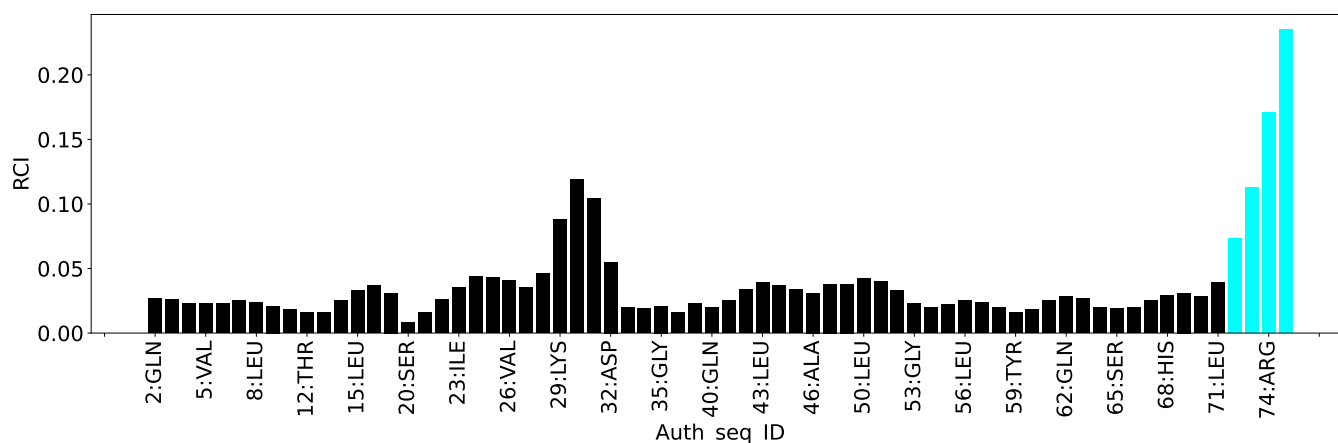
7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

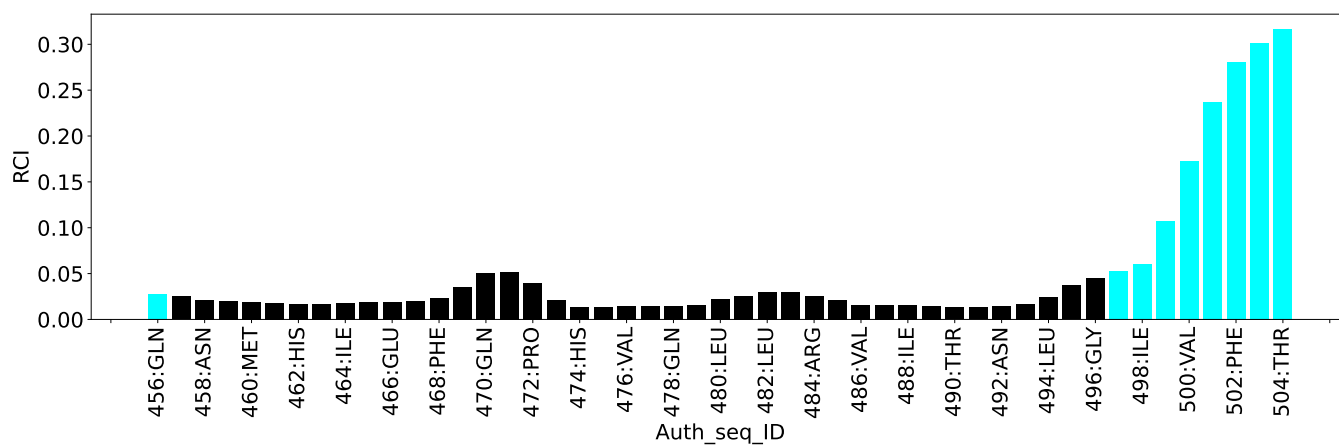
7.1.5 Random Coil Index (RCI) plots [i](#)

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:



Random coil index (RCI) for chain C:



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	63
Intra-residue ($ i-j =0$)	0
Sequential ($ i-j =1$)	0
Medium range ($ i-j >1$ and $ i-j <5$)	0
Long range ($ i-j \geq 5$)	0
Inter-chain	63
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	0.5
Number of long range restraints per residue ¹	0.0

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)	4.5	0.2
0.2-0.5 (Medium)	4.3	0.5
>0.5 (Large)	11.2	4.7

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 ⓘ

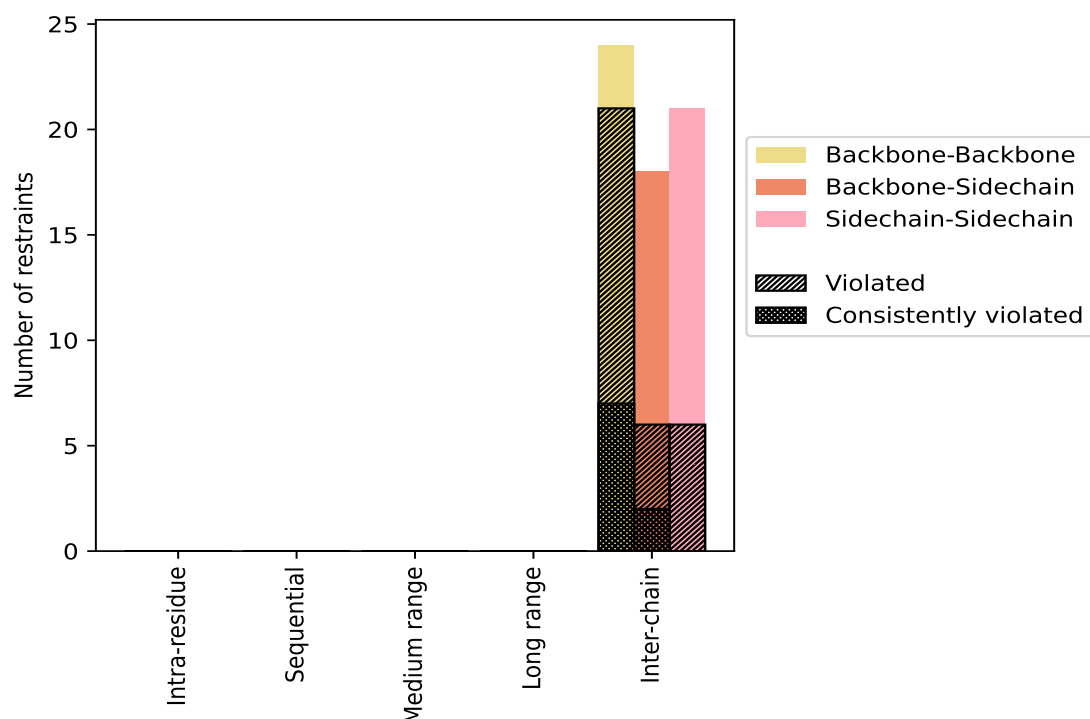
9.1 Summary of distance violations ⓘ

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)	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
Sequential (i-j =1)	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
Medium range (i-j >1 & i-j <5)	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
Long range (i-j ≥5)	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
Inter-chain	63	100.0	33	52.4	52.4	9	14.3	14.3
Backbone-Backbone	24	38.1	21	87.5	33.3	7	29.2	11.1
Backbone-Sidechain	18	28.6	6	33.3	9.5	2	11.1	3.2
Sidechain-Sidechain	21	33.3	6	28.6	9.5	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	63	100.0	33	52.4	52.4	9	14.3	14.3
Backbone-Backbone	24	38.1	21	87.5	33.3	7	29.2	11.1
Backbone-Sidechain	18	28.6	6	33.3	9.5	2	11.1	3.2
Sidechain-Sidechain	21	33.3	6	28.6	9.5	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	0	0	0	18	18	1.18	4.45	1.32	0.54
2	0	0	0	0	19	19	1.41	4.3	1.25	0.84
3	0	0	0	0	20	20	1.49	4.15	1.3	1.12
4	0	0	0	0	21	21	1.41	4.34	1.32	1.09
5	0	0	0	0	20	20	1.27	4.16	1.22	0.84
6	0	0	0	0	20	20	1.27	4.35	1.37	0.76
7	0	0	0	0	22	22	1.12	4.1	1.27	0.48
8	0	0	0	0	19	19	1.19	3.77	1.24	0.39
9	0	0	0	0	18	18	1.3	4.53	1.3	1.07
10	0	0	0	0	22	22	1.24	4.25	1.29	0.66

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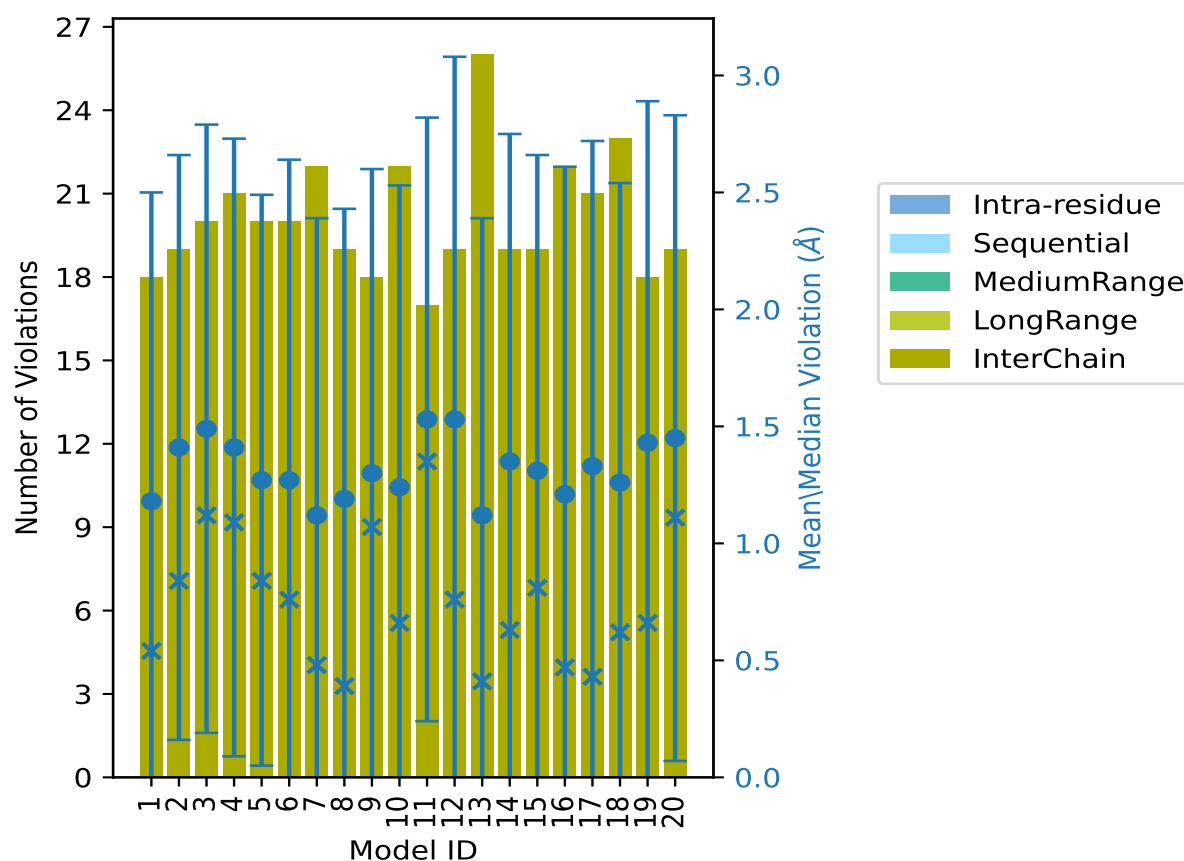
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	0	0	0	0	17	17	1.53	4.24	1.29	1.35
12	0	0	0	0	19	19	1.53	4.7	1.55	0.76
13	0	0	0	0	26	26	1.12	4.27	1.27	0.41
14	0	0	0	0	19	19	1.35	4.49	1.4	0.63
15	0	0	0	0	19	19	1.31	4.56	1.35	0.81
16	0	0	0	0	22	22	1.21	4.24	1.4	0.47
17	0	0	0	0	21	21	1.33	4.48	1.39	0.43
18	0	0	0	0	23	23	1.26	4.16	1.28	0.62
19	0	0	0	0	18	18	1.43	4.61	1.46	0.66
20	0	0	0	0	19	19	1.45	4.44	1.38	1.11

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

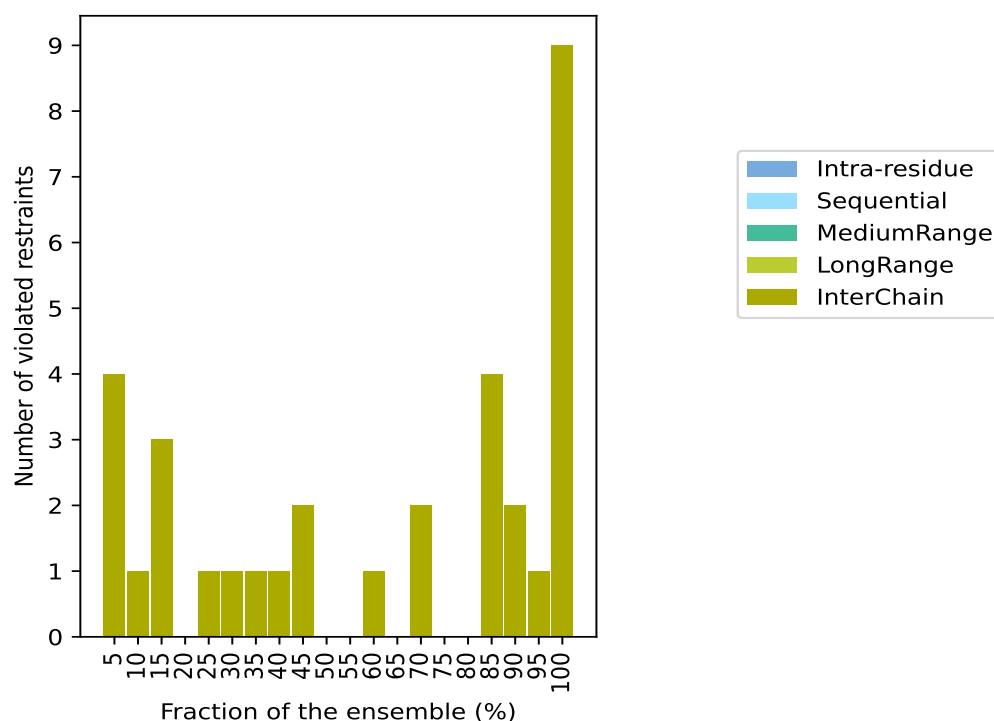
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 30(IR:0, SQ:0, MR:0, LR:0, IC:30) restraints are not violated in the ensemble.

Number of violated restraints						Fraction of the ensemble	
IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total	Count ⁶	%
0	0	0	0	4	4	1	5.0
0	0	0	0	1	1	2	10.0
0	0	0	0	3	3	3	15.0
0	0	0	0	0	0	4	20.0
0	0	0	0	1	1	5	25.0
0	0	0	0	1	1	6	30.0
0	0	0	0	1	1	7	35.0
0	0	0	0	1	1	8	40.0
0	0	0	0	2	2	9	45.0
0	0	0	0	0	0	10	50.0
0	0	0	0	0	0	11	55.0
0	0	0	0	1	1	12	60.0
0	0	0	0	0	0	13	65.0
0	0	0	0	2	2	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	4	4	17	85.0
0	0	0	0	2	2	18	90.0
0	0	0	0	1	1	19	95.0
0	0	0	0	9	9	20	100.0

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

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

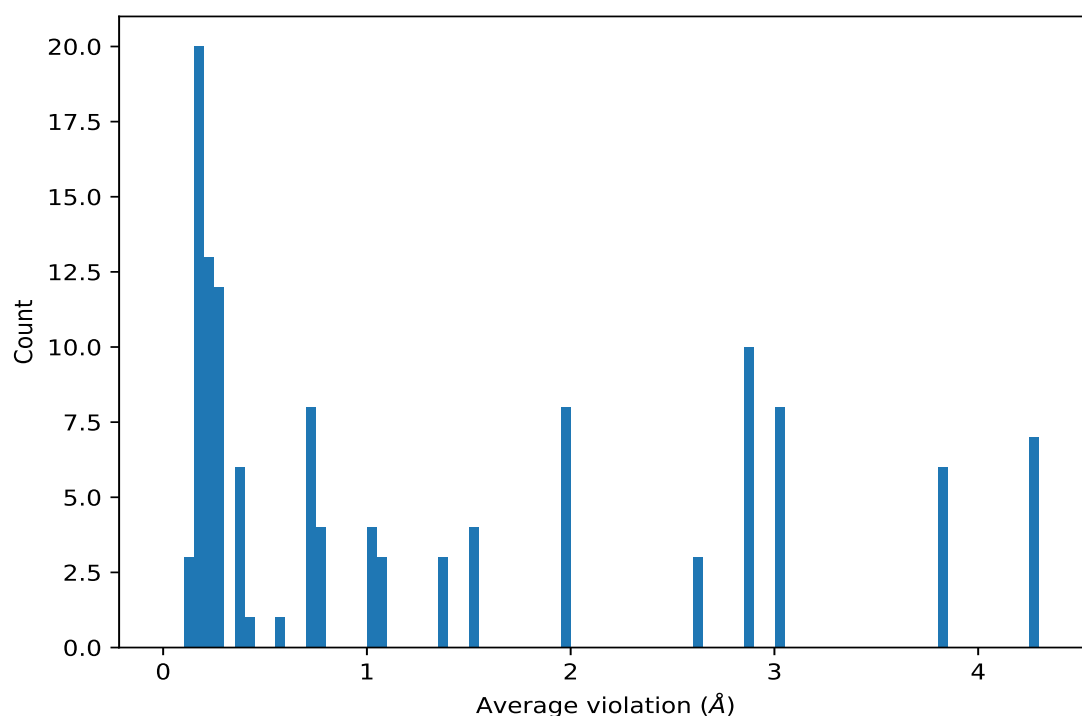
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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)
(1,5)	1:45:A:PHE:HA	2:467:C:MET:O	20	4.28	0.23	4.28
(1,5)	1:45:A:PHE:H	2:468:C:PHE:HZ	20	4.28	0.23	4.28
(1,5)	1:45:A:PHE:H	2:468:C:PHE:HE1	20	4.28	0.23	4.28
(1,5)	1:45:A:PHE:O	2:470:C:GLN:OE1	20	4.28	0.23	4.28
(1,5)	1:45:A:PHE:H	2:468:C:PHE:HE2	20	4.28	0.23	4.28
(1,5)	1:45:A:PHE:C	2:467:C:MET:O	20	4.28	0.23	4.28
(1,5)	1:45:A:PHE:O	2:470:C:GLN:HE22	20	4.28	0.23	4.28
(1,3)	1:43:A:LEU:O	2:494:C:LEU:HD22	20	3.82	0.16	3.81
(1,3)	1:43:A:LEU:C	2:494:C:LEU:HD11	20	3.82	0.16	3.81
(1,3)	1:43:A:LEU:C	2:468:C:PHE:HZ	20	3.82	0.16	3.81
(1,3)	1:43:A:LEU:O	2:494:C:LEU:HD11	20	3.82	0.16	3.81
(1,3)	1:43:A:LEU:HD22	2:467:C:MET:HE2	20	3.82	0.16	3.81
(1,3)	1:43:A:LEU:N	2:494:C:LEU:HD11	20	3.82	0.16	3.81
(1,20)	2:492:C:ASN:HD22	1:73:A:LEU:O	20	3.0	0.71	3.33
(1,20)	2:492:C:ASN:N	1:70:A:VAL:HG13	20	3.0	0.71	3.33
(1,20)	2:492:C:ASN:N	1:42:A:ARG:HH11	20	3.0	0.71	3.33

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,20)	2:492:C:ASN:HA	1:74:A:ARG:HH21	20	3.0	0.71	3.33
(1,20)	2:492:C:ASN:HA	1:74:A:ARG:HH22	20	3.0	0.71	3.33
(1,20)	2:492:C:ASN:HA	1:72:A:ARG:HH21	20	3.0	0.71	3.33
(1,20)	2:492:C:ASN:H	1:70:A:VAL:HG12	20	3.0	0.71	3.33
(1,20)	2:492:C:ASN:N	1:42:A:ARG:HH12	20	3.0	0.71	3.33
(1,26)	2:467:C:MET:HE1	1:70:A:VAL:HA	20	2.6	0.64	2.83
(1,26)	2:467:C:MET:HE2	1:70:A:VAL:HA	20	2.6	0.64	2.83
(1,26)	2:467:C:MET:HE3	1:70:A:VAL:HA	20	2.6	0.64	2.83
(1,6)	1:48:A:LYS:HA	2:470:C:GLN:HE22	20	1.99	0.47	1.98
(1,6)	1:48:A:LYS:N	2:470:C:GLN:HE22	20	1.99	0.47	1.98
(1,6)	1:48:A:LYS:HE2	2:470:C:GLN:OE1	20	1.99	0.47	1.98
(1,6)	1:48:A:LYS:HG3	2:470:C:GLN:HE22	20	1.99	0.47	1.98
(1,6)	1:48:A:LYS:N	2:468:C:PHE:HE1	20	1.99	0.47	1.98
(1,6)	1:48:A:LYS:HA	2:468:C:PHE:HE2	20	1.99	0.47	1.98
(1,6)	1:48:A:LYS:HG2	2:470:C:GLN:OE1	20	1.99	0.47	1.98
(1,6)	1:48:A:LYS:HG2	2:470:C:GLN:HE22	20	1.99	0.47	1.98
(1,18)	2:469:C:PRO:HD2	1:47:A:GLY:HA2	20	1.53	0.46	1.49
(1,18)	2:469:C:PRO:HD3	1:68:A:HIS:HE1	20	1.53	0.46	1.49
(1,18)	2:469:C:PRO:HD2	1:47:A:GLY:HA3	20	1.53	0.46	1.49
(1,18)	2:469:C:PRO:HD2	1:46:A:ALA:O	20	1.53	0.46	1.49
(1,25)	2:467:C:MET:HE1	1:8:A:LEU:HA	20	1.05	0.34	0.98
(1,25)	2:467:C:MET:HE2	1:8:A:LEU:HA	20	1.05	0.34	0.98
(1,25)	2:467:C:MET:HE3	1:8:A:LEU:HA	20	1.05	0.34	0.98
(1,7)	1:49:A:GLN:HG3	2:494:C:LEU:HD22	20	0.78	0.4	0.86
(1,7)	1:49:A:GLN:OE1	2:494:C:LEU:HD12	20	0.78	0.4	0.86
(1,7)	1:49:A:GLN:HB2	2:494:C:LEU:HD22	20	0.78	0.4	0.86
(1,7)	1:49:A:GLN:HB2	2:494:C:LEU:HD11	20	0.78	0.4	0.86
(1,19)	2:486:C:VAL:HG23	1:8:A:LEU:HB3	20	0.38	0.11	0.39
(1,19)	2:486:C:VAL:HB	1:8:A:LEU:HB3	20	0.38	0.11	0.39
(1,19)	2:486:C:VAL:HB	1:8:A:LEU:HD23	20	0.38	0.11	0.39
(1,19)	2:486:C:VAL:HG21	1:8:A:LEU:HB3	20	0.38	0.11	0.39
(1,19)	2:486:C:VAL:HG22	1:8:A:LEU:HB3	20	0.38	0.11	0.39
(1,19)	2:486:C:VAL:O	1:8:A:LEU:HD11	20	0.38	0.11	0.39
(1,9)	1:69:A:LEU:H	2:467:C:MET:HE3	19	0.7	0.7	0.51
(1,9)	1:69:A:LEU:H	2:467:C:MET:SD	19	0.7	0.7	0.51
(1,9)	1:69:A:LEU:H	2:467:C:MET:HE2	19	0.7	0.7	0.51
(1,9)	1:69:A:LEU:O	2:467:C:MET:HE3	19	0.7	0.7	0.51
(1,9)	1:69:A:LEU:H	2:467:C:MET:HE1	19	0.7	0.7	0.51
(1,24)	2:467:C:MET:HE1	1:68:A:HIS:HA	18	1.35	0.47	1.4
(1,24)	2:467:C:MET:HE2	1:68:A:HIS:HA	18	1.35	0.47	1.4
(1,24)	2:467:C:MET:HE3	1:68:A:HIS:HA	18	1.35	0.47	1.4
(1,11)	1:71:A:LEU:HB2	2:487:C:GLU:HB3	18	0.26	0.11	0.24

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,11)	1:71:A:LEU:O	2:491:C:ASP:HB2	18	0.26	0.11	0.24
(1,11)	1:71:A:LEU:HD12	2:487:C:GLU:HG2	18	0.26	0.11	0.24
(1,11)	1:71:A:LEU:HD11	2:487:C:GLU:HG2	18	0.26	0.11	0.24
(1,11)	1:71:A:LEU:O	2:487:C:GLU:HB3	18	0.26	0.11	0.24
(1,15)	2:466:C:GLU:O	1:68:A:HIS:HE2	17	1.0	0.79	0.92
(1,15)	2:466:C:GLU:HB3	1:6:A:LYS:HD3	17	1.0	0.79	0.92
(1,15)	2:466:C:GLU:HB3	1:6:A:LYS:HE2	17	1.0	0.79	0.92
(1,15)	2:466:C:GLU:HB3	1:6:A:LYS:HZ2	17	1.0	0.79	0.92
(1,33)	2:494:C:LEU:HD11	1:42:A:ARG:HB3	17	0.59	0.35	0.54
(1,31)	2:486:C:VAL:HG22	1:8:A:LEU:HB3	17	0.43	0.37	0.32
(1,8)	1:68:A:HIS:HB3	2:467:C:MET:HE1	17	0.26	0.16	0.18
(1,8)	1:68:A:HIS:HD2	2:467:C:MET:HG2	17	0.26	0.16	0.18
(1,8)	1:68:A:HIS:HB3	2:467:C:MET:HE3	17	0.26	0.16	0.18
(1,8)	1:68:A:HIS:HE2	2:466:C:GLU:O	17	0.26	0.16	0.18
(1,8)	1:68:A:HIS:HB3	2:467:C:MET:HB3	17	0.26	0.16	0.18
(1,8)	1:68:A:HIS:HD2	2:467:C:MET:HA	17	0.26	0.16	0.18
(1,8)	1:68:A:HIS:HB3	2:467:C:MET:HE2	17	0.26	0.16	0.18
(1,14)	1:74:A:ARG:H	2:488:C:ILE:HD11	14	2.86	1.19	3.23
(1,14)	1:74:A:ARG:NH2	2:495:C:GLU:OE2	14	2.86	1.19	3.23
(1,14)	1:74:A:ARG:HA	2:497:C:ARG:HH22	14	2.86	1.19	3.23
(1,14)	1:74:A:ARG:HH12	2:495:C:GLU:OE2	14	2.86	1.19	3.23
(1,14)	1:74:A:ARG:N	2:491:C:ASP:OD2	14	2.86	1.19	3.23
(1,14)	1:74:A:ARG:H	2:488:C:ILE:HG12	14	2.86	1.19	3.23
(1,14)	1:74:A:ARG:HH12	2:495:C:GLU:OE1	14	2.86	1.19	3.23
(1,14)	1:74:A:ARG:N	2:488:C:ILE:HG12	14	2.86	1.19	3.23
(1,14)	1:74:A:ARG:HG2	2:491:C:ASP:OD2	14	2.86	1.19	3.23
(1,14)	1:74:A:ARG:HH11	2:495:C:GLU:OE2	14	2.86	1.19	3.23
(1,21)	2:494:C:LEU:HD11	1:44:A:ILE:HD11	14	0.19	0.06	0.17
(1,21)	2:494:C:LEU:HD13	1:70:A:VAL:HG13	14	0.19	0.06	0.17
(1,21)	2:494:C:LEU:HD11	1:44:A:ILE:HD12	14	0.19	0.06	0.17
(1,21)	2:494:C:LEU:HD22	1:49:A:GLN:HG3	14	0.19	0.06	0.17
(1,21)	2:494:C:LEU:HD12	1:70:A:VAL:HG12	14	0.19	0.06	0.17
(1,21)	2:494:C:LEU:HD22	1:44:A:ILE:HD12	14	0.19	0.06	0.17
(1,21)	2:494:C:LEU:HD11	1:42:A:ARG:HD3	14	0.19	0.06	0.17
(1,21)	2:494:C:LEU:HD12	1:44:A:ILE:HD11	14	0.19	0.06	0.17
(1,54)	2:489:C:THR:H	1:72:A:ARG:HA	12	0.14	0.03	0.15
(1,16)	2:467:C:MET:HG2	1:68:A:HIS:HD2	9	0.2	0.08	0.17
(1,16)	2:467:C:MET:HE1	1:68:A:HIS:HB3	9	0.2	0.08	0.17
(1,16)	2:467:C:MET:HB3	1:68:A:HIS:HB3	9	0.2	0.08	0.17
(1,16)	2:467:C:MET:HG3	1:8:A:LEU:HD22	9	0.2	0.08	0.17
(1,16)	2:467:C:MET:HE2	1:8:A:LEU:HD22	9	0.2	0.08	0.17
(1,17)	2:468:C:PHE:HE1	1:70:A:VAL:HG23	9	0.2	0.07	0.18

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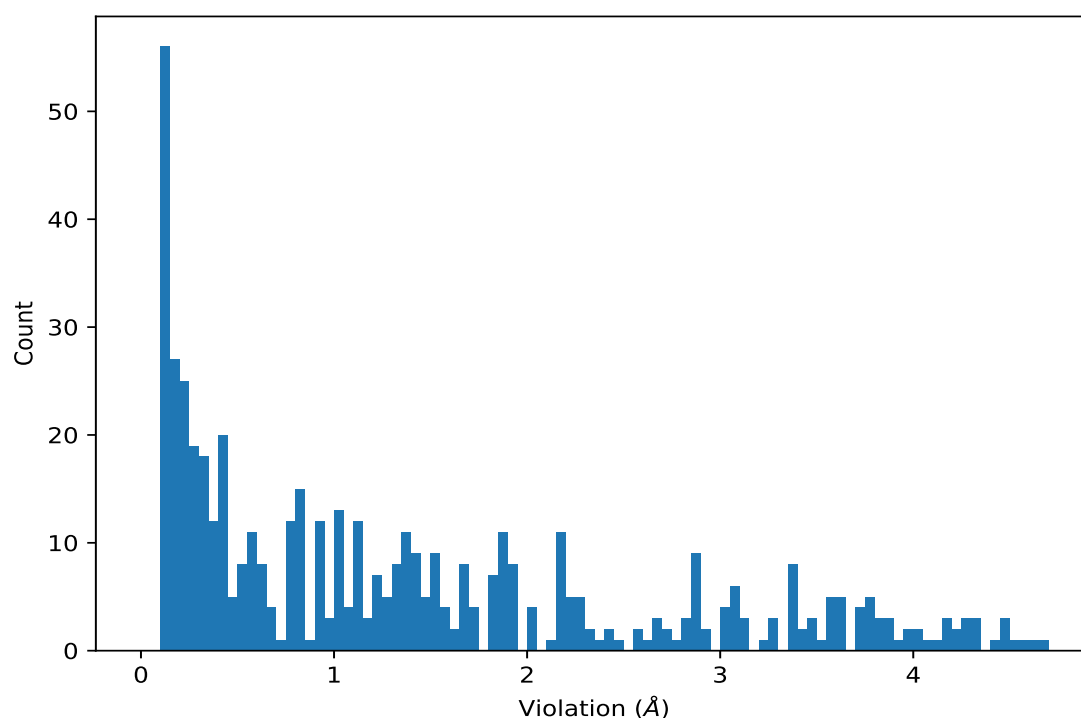
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,17)	2:468:C:PHE:HZ	1:70:A:VAL:HG23	9	0.2	0.07	0.18
(1,17)	2:468:C:PHE:HE1	1:44:A:ILE:HG12	9	0.2	0.07	0.18
(1,17)	2:468:C:PHE:HZ	1:44:A:ILE:HG12	9	0.2	0.07	0.18
(1,13)	1:73:A:LEU:HD13	2:488:C:ILE:HG12	8	0.21	0.08	0.19
(1,13)	1:73:A:LEU:HB2	2:488:C:ILE:HG12	8	0.21	0.08	0.19
(1,13)	1:73:A:LEU:HD22	2:488:C:ILE:HG12	8	0.21	0.08	0.19
(1,13)	1:73:A:LEU:HD22	2:488:C:ILE:HD13	8	0.21	0.08	0.19
(1,4)	1:44:A:ILE:HD11	2:494:C:LEU:HD11	7	0.19	0.07	0.17
(1,4)	1:44:A:ILE:HD12	2:494:C:LEU:HD11	7	0.19	0.07	0.17
(1,4)	1:44:A:ILE:HG12	2:468:C:PHE:HZ	7	0.19	0.07	0.17
(1,1)	1:8:A:LEU:HD22	2:467:C:MET:HG3	6	0.18	0.06	0.17
(1,1)	1:8:A:LEU:HD21	2:490:C:THR:HG22	6	0.18	0.06	0.17
(1,1)	1:8:A:LEU:HD23	2:486:C:VAL:HB	6	0.18	0.06	0.17
(1,1)	1:8:A:LEU:HD11	2:487:C:GLU:HA	6	0.18	0.06	0.17
(1,1)	1:8:A:LEU:HD13	2:490:C:THR:HG22	6	0.18	0.06	0.17
(1,42)	2:494:C:LEU:HD21	1:49:A:GLN:HB2	5	0.11	0.01	0.11
(1,23)	2:467:C:MET:HE1	1:44:A:ILE:HD11	3	0.7	0.12	0.77
(1,23)	2:467:C:MET:HE2	1:44:A:ILE:HD11	3	0.7	0.12	0.77
(1,23)	2:467:C:MET:HE3	1:44:A:ILE:HD11	3	0.7	0.12	0.77
(1,10)	1:70:A:VAL:HG12	2:490:C:THR:HB	3	0.19	0.08	0.17
(1,10)	1:70:A:VAL:HG11	2:490:C:THR:HB	3	0.19	0.08	0.17
(1,10)	1:70:A:VAL:HG23	2:468:C:PHE:HZ	3	0.19	0.08	0.17
(1,40)	2:494:C:LEU:HD22	1:42:A:ARG:HG3	3	0.15	0.04	0.12
(1,52)	2:494:C:LEU:HD22	1:43:A:LEU:H	2	0.11	0.01	0.11

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)
(1,14)	1:74:A:ARG:H	2:488:C:ILE:HG12	12	4.7
(1,5)	1:45:A:PHE:HA	2:467:C:MET:O	19	4.61
(1,5)	1:45:A:PHE:O	2:470:C:GLN:HE22	15	4.56
(1,5)	1:45:A:PHE:O	2:470:C:GLN:OE1	9	4.53
(1,5)	1:45:A:PHE:H	2:468:C:PHE:HZ	14	4.49
(1,5)	1:45:A:PHE:H	2:468:C:PHE:HZ	17	4.48
(1,5)	1:45:A:PHE:HA	2:467:C:MET:O	1	4.45
(1,5)	1:45:A:PHE:H	2:468:C:PHE:HZ	20	4.44
(1,5)	1:45:A:PHE:H	2:468:C:PHE:HE1	6	4.35
(1,5)	1:45:A:PHE:HA	2:467:C:MET:O	4	4.34
(1,5)	1:45:A:PHE:HA	2:467:C:MET:O	2	4.3
(1,5)	1:45:A:PHE:C	2:467:C:MET:O	12	4.27
(1,5)	1:45:A:PHE:H	2:468:C:PHE:HE2	13	4.27
(1,5)	1:45:A:PHE:H	2:468:C:PHE:HE2	10	4.25
(1,14)	1:74:A:ARG:N	2:488:C:ILE:HG12	16	4.24
(1,5)	1:45:A:PHE:H	2:468:C:PHE:HZ	11	4.24

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,5)	1:45:A:PHE:H	2:468:C:PHE:HZ	5	4.16
(1,5)	1:45:A:PHE:H	2:468:C:PHE:HZ	18	4.16
(1,5)	1:45:A:PHE:H	2:468:C:PHE:HZ	3	4.15
(1,3)	1:43:A:LEU:HD22	2:467:C:MET:HE2	6	4.14
(1,5)	1:45:A:PHE:H	2:468:C:PHE:HE1	7	4.1
(1,3)	1:43:A:LEU:O	2:494:C:LEU:HD22	14	4.03
(1,3)	1:43:A:LEU:C	2:468:C:PHE:HZ	3	4.01
(1,3)	1:43:A:LEU:O	2:494:C:LEU:HD22	13	3.99
(1,3)	1:43:A:LEU:O	2:494:C:LEU:HD22	7	3.97
(1,3)	1:43:A:LEU:O	2:494:C:LEU:HD22	17	3.94
(1,3)	1:43:A:LEU:O	2:494:C:LEU:HD22	9	3.9
(1,3)	1:43:A:LEU:N	2:494:C:LEU:HD11	10	3.89
(1,14)	1:74:A:ARG:N	2:488:C:ILE:HG12	20	3.88
(1,3)	1:43:A:LEU:O	2:494:C:LEU:HD22	16	3.82
(1,3)	1:43:A:LEU:O	2:494:C:LEU:HD22	1	3.81
(1,3)	1:43:A:LEU:O	2:494:C:LEU:HD22	18	3.81
(1,3)	1:43:A:LEU:O	2:494:C:LEU:HD22	20	3.79
(1,3)	1:43:A:LEU:C	2:494:C:LEU:HD11	2	3.78
(1,20)	2:492:C:ASN:N	1:42:A:ARG:HH11	12	3.77
(1,5)	1:45:A:PHE:H	2:468:C:PHE:HE1	8	3.77
(1,14)	1:74:A:ARG:N	2:491:C:ASP:OD2	11	3.76
(1,3)	1:43:A:LEU:C	2:468:C:PHE:HZ	5	3.74
(1,3)	1:43:A:LEU:O	2:494:C:LEU:HD22	12	3.74
(1,5)	1:45:A:PHE:H	2:468:C:PHE:HE1	16	3.72
(1,3)	1:43:A:LEU:O	2:494:C:LEU:HD22	15	3.72
(1,3)	1:43:A:LEU:O	2:494:C:LEU:HD22	19	3.64
(1,3)	1:43:A:LEU:O	2:494:C:LEU:HD11	4	3.63
(1,26)	2:467:C:MET:HE1	1:70:A:VAL:HA	15	3.62
(1,26)	2:467:C:MET:HE2	1:70:A:VAL:HA	15	3.62
(1,26)	2:467:C:MET:HE3	1:70:A:VAL:HA	15	3.62
(1,20)	2:492:C:ASN:N	1:42:A:ARG:HH11	14	3.59
(1,3)	1:43:A:LEU:O	2:494:C:LEU:HD22	11	3.59
(1,20)	2:492:C:ASN:N	1:42:A:ARG:HH11	3	3.57
(1,14)	1:74:A:ARG:N	2:491:C:ASP:OD2	17	3.57
(1,20)	2:492:C:ASN:N	1:42:A:ARG:HH12	19	3.56
(1,20)	2:492:C:ASN:N	1:42:A:ARG:HH11	4	3.55
(1,20)	2:492:C:ASN:N	1:42:A:ARG:HH11	7	3.49
(1,3)	1:43:A:LEU:O	2:494:C:LEU:HD22	8	3.46
(1,20)	2:492:C:ASN:N	1:42:A:ARG:HH11	18	3.45
(1,20)	2:492:C:ASN:N	1:42:A:ARG:HH11	6	3.42
(1,20)	2:492:C:ASN:N	1:42:A:ARG:HH11	16	3.41
(1,20)	2:492:C:ASN:H	1:70:A:VAL:HG12	13	3.38

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,26)	2:467:C:MET:HE1	1:70:A:VAL:HA	14	3.37
(1,26)	2:467:C:MET:HE2	1:70:A:VAL:HA	14	3.37
(1,26)	2:467:C:MET:HE3	1:70:A:VAL:HA	14	3.37
(1,26)	2:467:C:MET:HE1	1:70:A:VAL:HA	16	3.37
(1,26)	2:467:C:MET:HE2	1:70:A:VAL:HA	16	3.37
(1,26)	2:467:C:MET:HE3	1:70:A:VAL:HA	16	3.37
(1,14)	1:74:A:ARG:HH12	2:495:C:GLU:OE1	13	3.37
(1,20)	2:492:C:ASN:N	1:42:A:ARG:HH11	10	3.28
(1,20)	2:492:C:ASN:N	1:70:A:VAL:HG13	2	3.25
(1,14)	1:74:A:ARG:HG2	2:491:C:ASP:OD2	18	3.25
(1,14)	1:74:A:ARG:HH11	2:495:C:GLU:OE2	19	3.21
(1,26)	2:467:C:MET:HE1	1:70:A:VAL:HA	8	3.15
(1,26)	2:467:C:MET:HE2	1:70:A:VAL:HA	8	3.15
(1,26)	2:467:C:MET:HE3	1:70:A:VAL:HA	8	3.15
(1,26)	2:467:C:MET:HE1	1:70:A:VAL:HA	19	3.09
(1,26)	2:467:C:MET:HE2	1:70:A:VAL:HA	19	3.09
(1,26)	2:467:C:MET:HE3	1:70:A:VAL:HA	19	3.09
(1,26)	2:467:C:MET:HE1	1:70:A:VAL:HA	12	3.06
(1,26)	2:467:C:MET:HE2	1:70:A:VAL:HA	12	3.06
(1,26)	2:467:C:MET:HE3	1:70:A:VAL:HA	12	3.06
(1,26)	2:467:C:MET:HE1	1:70:A:VAL:HA	1	3.02
(1,26)	2:467:C:MET:HE2	1:70:A:VAL:HA	1	3.02
(1,26)	2:467:C:MET:HE3	1:70:A:VAL:HA	1	3.02
(1,14)	1:74:A:ARG:HA	2:497:C:ARG:HH22	4	3.02
(1,6)	1:48:A:LYS:N	2:470:C:GLN:HE22	4	2.92
(1,20)	2:492:C:ASN:HA	1:74:A:ARG:HH21	8	2.91
(1,26)	2:467:C:MET:HE1	1:70:A:VAL:HA	17	2.9
(1,26)	2:467:C:MET:HE2	1:70:A:VAL:HA	17	2.9
(1,26)	2:467:C:MET:HE3	1:70:A:VAL:HA	17	2.9
(1,26)	2:467:C:MET:HE1	1:70:A:VAL:HA	6	2.88
(1,26)	2:467:C:MET:HE2	1:70:A:VAL:HA	6	2.88
(1,26)	2:467:C:MET:HE3	1:70:A:VAL:HA	6	2.88
(1,26)	2:467:C:MET:HE1	1:70:A:VAL:HA	9	2.85
(1,26)	2:467:C:MET:HE2	1:70:A:VAL:HA	9	2.85
(1,26)	2:467:C:MET:HE3	1:70:A:VAL:HA	9	2.85
(1,26)	2:467:C:MET:HE1	1:70:A:VAL:HA	10	2.81
(1,26)	2:467:C:MET:HE2	1:70:A:VAL:HA	10	2.81
(1,26)	2:467:C:MET:HE3	1:70:A:VAL:HA	10	2.81
(1,9)	1:69:A:LEU:H	2:467:C:MET:SD	5	2.8
(1,20)	2:492:C:ASN:HA	1:72:A:ARG:HH21	15	2.74
(1,18)	2:469:C:PRO:HD3	1:68:A:HIS:HE1	3	2.73
(1,26)	2:467:C:MET:HE1	1:70:A:VAL:HA	7	2.66

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,26)	2:467:C:MET:HE2	1:70:A:VAL:HA	7	2.66
(1,26)	2:467:C:MET:HE3	1:70:A:VAL:HA	7	2.66
(1,6)	1:48:A:LYS:HG2	2:470:C:GLN:OE1	12	2.65
(1,20)	2:492:C:ASN:HA	1:72:A:ARG:HH21	17	2.59
(1,6)	1:48:A:LYS:HA	2:470:C:GLN:HE22	5	2.59
(1,20)	2:492:C:ASN:HA	1:74:A:ARG:HH22	9	2.45
(1,20)	2:492:C:ASN:HA	1:72:A:ARG:HH21	11	2.42
(1,15)	2:466:C:GLU:HB3	1:6:A:LYS:HZ2	18	2.42
(1,6)	1:48:A:LYS:N	2:470:C:GLN:HE22	17	2.39
(1,6)	1:48:A:LYS:N	2:470:C:GLN:HE22	20	2.33
(1,15)	2:466:C:GLU:O	1:68:A:HIS:HE2	3	2.31
(1,18)	2:469:C:PRO:HD2	1:47:A:GLY:HA2	10	2.3
(1,26)	2:467:C:MET:HE1	1:70:A:VAL:HA	20	2.27
(1,26)	2:467:C:MET:HE2	1:70:A:VAL:HA	20	2.27
(1,26)	2:467:C:MET:HE3	1:70:A:VAL:HA	20	2.27
(1,15)	2:466:C:GLU:O	1:68:A:HIS:HE2	5	2.26
(1,20)	2:492:C:ASN:HA	1:72:A:ARG:HH21	20	2.21
(1,26)	2:467:C:MET:HE1	1:70:A:VAL:HA	4	2.2
(1,26)	2:467:C:MET:HE2	1:70:A:VAL:HA	4	2.2
(1,26)	2:467:C:MET:HE3	1:70:A:VAL:HA	4	2.2
(1,6)	1:48:A:LYS:HA	2:468:C:PHE:HE2	10	2.2
(1,26)	2:467:C:MET:HE1	1:70:A:VAL:HA	11	2.18
(1,26)	2:467:C:MET:HE2	1:70:A:VAL:HA	11	2.18
(1,26)	2:467:C:MET:HE3	1:70:A:VAL:HA	11	2.18
(1,6)	1:48:A:LYS:N	2:470:C:GLN:HE22	3	2.17
(1,6)	1:48:A:LYS:N	2:470:C:GLN:HE22	2	2.16
(1,26)	2:467:C:MET:HE1	1:70:A:VAL:HA	3	2.15
(1,26)	2:467:C:MET:HE2	1:70:A:VAL:HA	3	2.15
(1,26)	2:467:C:MET:HE3	1:70:A:VAL:HA	3	2.15
(1,24)	2:467:C:MET:HE1	1:68:A:HIS:HA	2	2.15
(1,24)	2:467:C:MET:HE2	1:68:A:HIS:HA	2	2.15
(1,24)	2:467:C:MET:HE3	1:68:A:HIS:HA	2	2.15
(1,14)	1:74:A:ARG:H	2:488:C:ILE:HD11	2	2.1
(1,6)	1:48:A:LYS:HG3	2:470:C:GLN:HE22	11	2.04
(1,18)	2:469:C:PRO:HD3	1:68:A:HIS:HE1	2	2.03
(1,20)	2:492:C:ASN:HD22	1:73:A:LEU:O	1	2.01
(1,6)	1:48:A:LYS:HE2	2:470:C:GLN:OE1	6	2.01
(1,6)	1:48:A:LYS:N	2:470:C:GLN:HE22	15	1.95
(1,24)	2:467:C:MET:HE1	1:68:A:HIS:HA	20	1.93
(1,24)	2:467:C:MET:HE2	1:68:A:HIS:HA	20	1.93
(1,24)	2:467:C:MET:HE3	1:68:A:HIS:HA	20	1.93
(1,25)	2:467:C:MET:HE1	1:8:A:LEU:HA	5	1.92

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,25)	2:467:C:MET:HE2	1:8:A:LEU:HA	5	1.92
(1,25)	2:467:C:MET:HE3	1:8:A:LEU:HA	5	1.92
(1,9)	1:69:A:LEU:H	2:467:C:MET:HE3	18	1.92
(1,26)	2:467:C:MET:HE1	1:70:A:VAL:HA	13	1.9
(1,26)	2:467:C:MET:HE2	1:70:A:VAL:HA	13	1.9
(1,26)	2:467:C:MET:HE3	1:70:A:VAL:HA	13	1.9
(1,18)	2:469:C:PRO:HD2	1:47:A:GLY:HA2	6	1.89
(1,6)	1:48:A:LYS:HG3	2:470:C:GLN:HE22	7	1.89
(1,18)	2:469:C:PRO:HD2	1:47:A:GLY:HA2	20	1.88
(1,15)	2:466:C:GLU:O	1:68:A:HIS:HE2	13	1.88
(1,9)	1:69:A:LEU:H	2:467:C:MET:SD	3	1.88
(1,26)	2:467:C:MET:HE1	1:70:A:VAL:HA	18	1.87
(1,26)	2:467:C:MET:HE2	1:70:A:VAL:HA	18	1.87
(1,26)	2:467:C:MET:HE3	1:70:A:VAL:HA	18	1.87
(1,24)	2:467:C:MET:HE1	1:68:A:HIS:HA	13	1.83
(1,24)	2:467:C:MET:HE2	1:68:A:HIS:HA	13	1.83
(1,24)	2:467:C:MET:HE3	1:68:A:HIS:HA	13	1.83
(1,18)	2:469:C:PRO:HD3	1:68:A:HIS:HE1	17	1.83
(1,31)	2:486:C:VAL:HG22	1:8:A:LEU:HB3	8	1.82
(1,6)	1:48:A:LYS:HA	2:470:C:GLN:HE22	19	1.82
(1,6)	1:48:A:LYS:HA	2:470:C:GLN:HE22	1	1.81
(1,24)	2:467:C:MET:HE1	1:68:A:HIS:HA	11	1.73
(1,24)	2:467:C:MET:HE2	1:68:A:HIS:HA	11	1.73
(1,24)	2:467:C:MET:HE3	1:68:A:HIS:HA	11	1.73
(1,6)	1:48:A:LYS:HG3	2:470:C:GLN:HE22	14	1.72
(1,6)	1:48:A:LYS:HE2	2:470:C:GLN:OE1	9	1.7
(1,25)	2:467:C:MET:HE1	1:8:A:LEU:HA	3	1.69
(1,25)	2:467:C:MET:HE2	1:8:A:LEU:HA	3	1.69
(1,25)	2:467:C:MET:HE3	1:8:A:LEU:HA	3	1.69
(1,24)	2:467:C:MET:HE1	1:68:A:HIS:HA	4	1.69
(1,24)	2:467:C:MET:HE2	1:68:A:HIS:HA	4	1.69
(1,24)	2:467:C:MET:HE3	1:68:A:HIS:HA	4	1.69
(1,6)	1:48:A:LYS:N	2:468:C:PHE:HE1	8	1.68
(1,6)	1:48:A:LYS:HA	2:470:C:GLN:HE22	13	1.65
(1,18)	2:469:C:PRO:HD3	1:68:A:HIS:HE1	14	1.6
(1,35)	2:494:C:LEU:HD13	1:42:A:ARG:HG3	4	1.55
(1,24)	2:467:C:MET:HE1	1:68:A:HIS:HA	6	1.55
(1,24)	2:467:C:MET:HE2	1:68:A:HIS:HA	6	1.55
(1,24)	2:467:C:MET:HE3	1:68:A:HIS:HA	6	1.55
(1,26)	2:467:C:MET:HE1	1:70:A:VAL:HA	2	1.54
(1,26)	2:467:C:MET:HE2	1:70:A:VAL:HA	2	1.54
(1,26)	2:467:C:MET:HE3	1:70:A:VAL:HA	2	1.54

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,18)	2:469:C:PRO:HD2	1:47:A:GLY:HA3	7	1.53
(1,24)	2:467:C:MET:HE1	1:68:A:HIS:HA	17	1.5
(1,24)	2:467:C:MET:HE2	1:68:A:HIS:HA	17	1.5
(1,24)	2:467:C:MET:HE3	1:68:A:HIS:HA	17	1.5
(1,18)	2:469:C:PRO:HD2	1:47:A:GLY:HA3	5	1.5
(1,18)	2:469:C:PRO:HD2	1:47:A:GLY:HA2	9	1.5
(1,18)	2:469:C:PRO:HD2	1:47:A:GLY:HA3	18	1.48
(1,33)	2:494:C:LEU:HD11	1:42:A:ARG:HB3	10	1.47
(1,24)	2:467:C:MET:HE1	1:68:A:HIS:HA	7	1.46
(1,24)	2:467:C:MET:HE2	1:68:A:HIS:HA	7	1.46
(1,24)	2:467:C:MET:HE3	1:68:A:HIS:HA	7	1.46
(1,7)	1:49:A:GLN:HB2	2:494:C:LEU:HD22	15	1.44
(1,24)	2:467:C:MET:HE1	1:68:A:HIS:HA	19	1.43
(1,24)	2:467:C:MET:HE2	1:68:A:HIS:HA	19	1.43
(1,24)	2:467:C:MET:HE3	1:68:A:HIS:HA	19	1.43
(1,18)	2:469:C:PRO:HD2	1:47:A:GLY:HA2	8	1.42
(1,15)	2:466:C:GLU:O	1:68:A:HIS:HE2	20	1.42
(1,25)	2:467:C:MET:HE1	1:8:A:LEU:HA	4	1.41
(1,25)	2:467:C:MET:HE2	1:8:A:LEU:HA	4	1.41
(1,25)	2:467:C:MET:HE3	1:8:A:LEU:HA	4	1.41
(1,14)	1:74:A:ARG:HH12	2:495:C:GLU:OE2	15	1.4
(1,24)	2:467:C:MET:HE1	1:68:A:HIS:HA	8	1.38
(1,24)	2:467:C:MET:HE2	1:68:A:HIS:HA	8	1.38
(1,24)	2:467:C:MET:HE3	1:68:A:HIS:HA	8	1.38
(1,18)	2:469:C:PRO:HD2	1:47:A:GLY:HA3	11	1.37
(1,7)	1:49:A:GLN:HB2	2:494:C:LEU:HD22	14	1.37
(1,6)	1:48:A:LYS:HG2	2:470:C:GLN:HE22	16	1.37
(1,25)	2:467:C:MET:HE1	1:8:A:LEU:HA	11	1.35
(1,25)	2:467:C:MET:HE2	1:8:A:LEU:HA	11	1.35
(1,25)	2:467:C:MET:HE3	1:8:A:LEU:HA	11	1.35
(1,15)	2:466:C:GLU:O	1:68:A:HIS:HE2	12	1.35
(1,24)	2:467:C:MET:HE1	1:68:A:HIS:HA	1	1.34
(1,24)	2:467:C:MET:HE2	1:68:A:HIS:HA	1	1.34
(1,24)	2:467:C:MET:HE3	1:68:A:HIS:HA	1	1.34
(1,24)	2:467:C:MET:HE1	1:68:A:HIS:HA	10	1.33
(1,24)	2:467:C:MET:HE2	1:68:A:HIS:HA	10	1.33
(1,24)	2:467:C:MET:HE3	1:68:A:HIS:HA	10	1.33
(1,7)	1:49:A:GLN:HB2	2:494:C:LEU:HD22	18	1.31
(1,14)	1:74:A:ARG:NH2	2:495:C:GLU:OE2	3	1.3
(1,25)	2:467:C:MET:HE1	1:8:A:LEU:HA	10	1.29
(1,25)	2:467:C:MET:HE2	1:8:A:LEU:HA	10	1.29
(1,25)	2:467:C:MET:HE3	1:8:A:LEU:HA	10	1.29

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,18)	2:469:C:PRO:HD2	1:47:A:GLY:HA2	1	1.29
(1,14)	1:74:A:ARG:HH12	2:495:C:GLU:OE2	10	1.27
(1,24)	2:467:C:MET:HE1	1:68:A:HIS:HA	9	1.23
(1,24)	2:467:C:MET:HE2	1:68:A:HIS:HA	9	1.23
(1,24)	2:467:C:MET:HE3	1:68:A:HIS:HA	9	1.23
(1,26)	2:467:C:MET:HE1	1:70:A:VAL:HA	5	1.21
(1,26)	2:467:C:MET:HE2	1:70:A:VAL:HA	5	1.21
(1,26)	2:467:C:MET:HE3	1:70:A:VAL:HA	5	1.21
(1,7)	1:49:A:GLN:HB2	2:494:C:LEU:HD22	9	1.21
(1,33)	2:494:C:LEU:HD11	1:42:A:ARG:HB3	9	1.19
(1,18)	2:469:C:PRO:HD2	1:46:A:ALA:O	15	1.19
(1,15)	2:466:C:GLU:O	1:68:A:HIS:HE2	4	1.18
(1,24)	2:467:C:MET:HE1	1:68:A:HIS:HA	14	1.15
(1,24)	2:467:C:MET:HE2	1:68:A:HIS:HA	14	1.15
(1,24)	2:467:C:MET:HE3	1:68:A:HIS:HA	14	1.15
(1,25)	2:467:C:MET:HE1	1:8:A:LEU:HA	13	1.12
(1,25)	2:467:C:MET:HE2	1:8:A:LEU:HA	13	1.12
(1,25)	2:467:C:MET:HE3	1:8:A:LEU:HA	13	1.12
(1,25)	2:467:C:MET:HE1	1:8:A:LEU:HA	1	1.11
(1,25)	2:467:C:MET:HE2	1:8:A:LEU:HA	1	1.11
(1,25)	2:467:C:MET:HE3	1:8:A:LEU:HA	1	1.11
(1,25)	2:467:C:MET:HE1	1:8:A:LEU:HA	20	1.11
(1,25)	2:467:C:MET:HE2	1:8:A:LEU:HA	20	1.11
(1,25)	2:467:C:MET:HE3	1:8:A:LEU:HA	20	1.11
(1,24)	2:467:C:MET:HE1	1:68:A:HIS:HA	16	1.09
(1,24)	2:467:C:MET:HE2	1:68:A:HIS:HA	16	1.09
(1,24)	2:467:C:MET:HE3	1:68:A:HIS:HA	16	1.09
(1,18)	2:469:C:PRO:HD2	1:47:A:GLY:HA2	4	1.09
(1,18)	2:469:C:PRO:HD2	1:47:A:GLY:HA2	13	1.04
(1,15)	2:466:C:GLU:HB3	1:6:A:LYS:HD3	15	1.03
(1,7)	1:49:A:GLN:HB2	2:494:C:LEU:HD22	13	1.03
(1,7)	1:49:A:GLN:HG3	2:494:C:LEU:HD22	5	1.02
(1,25)	2:467:C:MET:HE1	1:8:A:LEU:HA	18	1.01
(1,25)	2:467:C:MET:HE2	1:8:A:LEU:HA	18	1.01
(1,25)	2:467:C:MET:HE3	1:8:A:LEU:HA	18	1.01
(1,18)	2:469:C:PRO:HD2	1:47:A:GLY:HA3	12	1.01
(1,18)	2:469:C:PRO:HD2	1:47:A:GLY:HA3	16	1.01
(1,25)	2:467:C:MET:HE1	1:8:A:LEU:HA	6	1.0
(1,25)	2:467:C:MET:HE2	1:8:A:LEU:HA	6	1.0
(1,25)	2:467:C:MET:HE3	1:8:A:LEU:HA	6	1.0
(1,7)	1:49:A:GLN:HG3	2:494:C:LEU:HD22	17	1.0
(1,25)	2:467:C:MET:HE1	1:8:A:LEU:HA	7	0.97

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,25)	2:467:C:MET:HE2	1:8:A:LEU:HA	7	0.97
(1,25)	2:467:C:MET:HE3	1:8:A:LEU:HA	7	0.97
(1,33)	2:494:C:LEU:HD11	1:42:A:ARG:HB3	6	0.95
(1,25)	2:467:C:MET:HE1	1:8:A:LEU:HA	9	0.95
(1,25)	2:467:C:MET:HE2	1:8:A:LEU:HA	9	0.95
(1,25)	2:467:C:MET:HE3	1:8:A:LEU:HA	9	0.95
(1,7)	1:49:A:GLN:HB2	2:494:C:LEU:HD22	3	0.95
(1,7)	1:49:A:GLN:HB2	2:494:C:LEU:HD22	6	0.95
(1,25)	2:467:C:MET:HE1	1:8:A:LEU:HA	19	0.94
(1,25)	2:467:C:MET:HE2	1:8:A:LEU:HA	19	0.94
(1,25)	2:467:C:MET:HE3	1:8:A:LEU:HA	19	0.94
(1,15)	2:466:C:GLU:O	1:68:A:HIS:HE2	2	0.92
(1,7)	1:49:A:GLN:HB2	2:494:C:LEU:HD22	7	0.92
(1,14)	1:74:A:ARG:HH12	2:495:C:GLU:OE1	14	0.91
(1,20)	2:492:C:ASN:HD22	1:73:A:LEU:O	5	0.87
(1,25)	2:467:C:MET:HE1	1:8:A:LEU:HA	8	0.85
(1,25)	2:467:C:MET:HE2	1:8:A:LEU:HA	8	0.85
(1,25)	2:467:C:MET:HE3	1:8:A:LEU:HA	8	0.85
(1,18)	2:469:C:PRO:HD2	1:47:A:GLY:HA2	19	0.85
(1,33)	2:494:C:LEU:HD11	1:42:A:ARG:HB3	2	0.84
(1,25)	2:467:C:MET:HE1	1:8:A:LEU:HA	12	0.81
(1,25)	2:467:C:MET:HE2	1:8:A:LEU:HA	12	0.81
(1,25)	2:467:C:MET:HE3	1:8:A:LEU:HA	12	0.81
(1,25)	2:467:C:MET:HE1	1:8:A:LEU:HA	15	0.81
(1,25)	2:467:C:MET:HE2	1:8:A:LEU:HA	15	0.81
(1,25)	2:467:C:MET:HE3	1:8:A:LEU:HA	15	0.81
(1,23)	2:467:C:MET:HE1	1:44:A:ILE:HD11	5	0.81
(1,23)	2:467:C:MET:HE2	1:44:A:ILE:HD11	5	0.81
(1,23)	2:467:C:MET:HE3	1:44:A:ILE:HD11	5	0.81
(1,7)	1:49:A:GLN:OE1	2:494:C:LEU:HD12	2	0.81
(1,23)	2:467:C:MET:HE1	1:44:A:ILE:HD11	3	0.77
(1,23)	2:467:C:MET:HE2	1:44:A:ILE:HD11	3	0.77
(1,23)	2:467:C:MET:HE3	1:44:A:ILE:HD11	3	0.77
(1,25)	2:467:C:MET:HE1	1:8:A:LEU:HA	17	0.76
(1,25)	2:467:C:MET:HE2	1:8:A:LEU:HA	17	0.76
(1,25)	2:467:C:MET:HE3	1:8:A:LEU:HA	17	0.76
(1,24)	2:467:C:MET:HE1	1:68:A:HIS:HA	12	0.76
(1,24)	2:467:C:MET:HE2	1:68:A:HIS:HA	12	0.76
(1,24)	2:467:C:MET:HE3	1:68:A:HIS:HA	12	0.76
(1,6)	1:48:A:LYS:HG3	2:470:C:GLN:HE22	18	0.76
(1,9)	1:69:A:LEU:H	2:467:C:MET:HE3	2	0.75
(1,7)	1:49:A:GLN:HB2	2:494:C:LEU:HD22	10	0.75

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,9)	1:69:A:LEU:H	2:467:C:MET:HE2	11	0.71
(1,33)	2:494:C:LEU:HD11	1:42:A:ARG:HB3	11	0.66
(1,9)	1:69:A:LEU:O	2:467:C:MET:HE3	12	0.66
(1,7)	1:49:A:GLN:HG3	2:494:C:LEU:HD22	16	0.66
(1,33)	2:494:C:LEU:HD11	1:42:A:ARG:HB3	13	0.65
(1,25)	2:467:C:MET:HE1	1:8:A:LEU:HA	14	0.63
(1,25)	2:467:C:MET:HE2	1:8:A:LEU:HA	14	0.63
(1,25)	2:467:C:MET:HE3	1:8:A:LEU:HA	14	0.63
(1,31)	2:486:C:VAL:HG22	1:8:A:LEU:HB3	3	0.62
(1,8)	1:68:A:HIS:HB3	2:467:C:MET:HE1	18	0.62
(1,25)	2:467:C:MET:HE1	1:8:A:LEU:HA	16	0.61
(1,25)	2:467:C:MET:HE2	1:8:A:LEU:HA	16	0.61
(1,25)	2:467:C:MET:HE3	1:8:A:LEU:HA	16	0.61
(1,33)	2:494:C:LEU:HD11	1:42:A:ARG:HB3	14	0.59
(1,7)	1:49:A:GLN:HG3	2:494:C:LEU:HD22	1	0.59
(1,25)	2:467:C:MET:HE1	1:8:A:LEU:HA	2	0.58
(1,25)	2:467:C:MET:HE2	1:8:A:LEU:HA	2	0.58
(1,25)	2:467:C:MET:HE3	1:8:A:LEU:HA	2	0.58
(1,19)	2:486:C:VAL:HB	1:8:A:LEU:HB3	20	0.58
(1,9)	1:69:A:LEU:H	2:467:C:MET:HE3	10	0.58
(1,19)	2:486:C:VAL:HB	1:8:A:LEU:HB3	6	0.57
(1,33)	2:494:C:LEU:HD11	1:42:A:ARG:HB3	18	0.56
(1,9)	1:69:A:LEU:H	2:467:C:MET:HE3	7	0.56
(1,8)	1:68:A:HIS:HD2	2:467:C:MET:HG2	5	0.55
(1,33)	2:494:C:LEU:HD11	1:42:A:ARG:HB3	7	0.54
(1,31)	2:486:C:VAL:HG22	1:8:A:LEU:HB3	18	0.53
(1,23)	2:467:C:MET:HE1	1:44:A:ILE:HD11	2	0.53
(1,23)	2:467:C:MET:HE2	1:44:A:ILE:HD11	2	0.53
(1,23)	2:467:C:MET:HE3	1:44:A:ILE:HD11	2	0.53
(1,9)	1:69:A:LEU:H	2:467:C:MET:HE3	4	0.51
(1,9)	1:69:A:LEU:H	2:467:C:MET:HE3	16	0.51
(1,19)	2:486:C:VAL:HG23	1:8:A:LEU:HB3	1	0.5
(1,33)	2:494:C:LEU:HD11	1:42:A:ARG:HB3	5	0.49
(1,33)	2:494:C:LEU:HD11	1:42:A:ARG:HB3	19	0.48
(1,19)	2:486:C:VAL:HB	1:8:A:LEU:HB3	2	0.48
(1,31)	2:486:C:VAL:HG22	1:8:A:LEU:HB3	5	0.47
(1,15)	2:466:C:GLU:O	1:68:A:HIS:HE2	11	0.45
(1,19)	2:486:C:VAL:HG23	1:8:A:LEU:HB3	4	0.44
(1,19)	2:486:C:VAL:O	1:8:A:LEU:HD11	10	0.44
(1,7)	1:49:A:GLN:HB2	2:494:C:LEU:HD11	4	0.44
(1,31)	2:486:C:VAL:HG22	1:8:A:LEU:HB3	16	0.43
(1,11)	1:71:A:LEU:HD11	2:487:C:GLU:HG2	7	0.43

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,11)	1:71:A:LEU:HB2	2:487:C:GLU:HB3	17	0.43
(1,8)	1:68:A:HIS:HD2	2:467:C:MET:HA	14	0.43
(1,19)	2:486:C:VAL:HG23	1:8:A:LEU:HB3	7	0.42
(1,9)	1:69:A:LEU:H	2:467:C:MET:HE3	14	0.42
(1,19)	2:486:C:VAL:HG21	1:8:A:LEU:HB3	11	0.41
(1,19)	2:486:C:VAL:HG23	1:8:A:LEU:HB3	13	0.41
(1,9)	1:69:A:LEU:H	2:467:C:MET:HE3	13	0.41
(1,8)	1:68:A:HIS:HB3	2:467:C:MET:HE2	17	0.41
(1,33)	2:494:C:LEU:HD11	1:42:A:ARG:HB3	15	0.4
(1,31)	2:486:C:VAL:HG22	1:8:A:LEU:HB3	11	0.4
(1,24)	2:467:C:MET:HE1	1:68:A:HIS:HA	18	0.4
(1,24)	2:467:C:MET:HE2	1:68:A:HIS:HA	18	0.4
(1,24)	2:467:C:MET:HE3	1:68:A:HIS:HA	18	0.4
(1,19)	2:486:C:VAL:HG23	1:8:A:LEU:HB3	14	0.4
(1,11)	1:71:A:LEU:HB2	2:487:C:GLU:HB3	16	0.4
(1,31)	2:486:C:VAL:HG22	1:8:A:LEU:HB3	13	0.39
(1,11)	1:71:A:LEU:O	2:491:C:ASP:HB2	8	0.39
(1,31)	2:486:C:VAL:HG22	1:8:A:LEU:HB3	7	0.38
(1,19)	2:486:C:VAL:HG22	1:8:A:LEU:HB3	8	0.38
(1,19)	2:486:C:VAL:HB	1:8:A:LEU:HD23	16	0.38
(1,19)	2:486:C:VAL:HB	1:8:A:LEU:HB3	19	0.38
(1,11)	1:71:A:LEU:O	2:487:C:GLU:HB3	11	0.38
(1,19)	2:486:C:VAL:HG23	1:8:A:LEU:HB3	17	0.37
(1,17)	2:468:C:PHE:HE1	1:70:A:VAL:HG23	19	0.37
(1,9)	1:69:A:LEU:O	2:467:C:MET:HE3	15	0.37
(1,7)	1:49:A:GLN:HG3	2:494:C:LEU:HD22	12	0.37
(1,33)	2:494:C:LEU:HD11	1:42:A:ARG:HB3	8	0.36
(1,21)	2:494:C:LEU:HD11	1:44:A:ILE:HD12	4	0.35
(1,13)	1:73:A:LEU:HD22	2:488:C:ILE:HG12	16	0.35
(1,11)	1:71:A:LEU:O	2:487:C:GLU:HB3	12	0.35
(1,4)	1:44:A:ILE:HD12	2:494:C:LEU:HD11	4	0.35
(1,24)	2:467:C:MET:HE1	1:68:A:HIS:HA	15	0.34
(1,24)	2:467:C:MET:HE2	1:68:A:HIS:HA	15	0.34
(1,24)	2:467:C:MET:HE3	1:68:A:HIS:HA	15	0.34
(1,9)	1:69:A:LEU:H	2:467:C:MET:HE3	20	0.34
(1,19)	2:486:C:VAL:HB	1:8:A:LEU:HD23	9	0.33
(1,15)	2:466:C:GLU:O	1:68:A:HIS:HE2	6	0.33
(1,15)	2:466:C:GLU:O	1:68:A:HIS:HE2	9	0.33
(1,13)	1:73:A:LEU:HB2	2:488:C:ILE:HG12	7	0.33
(1,31)	2:486:C:VAL:HG22	1:8:A:LEU:HB3	15	0.32
(1,16)	2:467:C:MET:HB3	1:68:A:HIS:HB3	12	0.32
(1,16)	2:467:C:MET:HE2	1:8:A:LEU:HD22	18	0.32

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,8)	1:68:A:HIS:HB3	2:467:C:MET:HB3	12	0.32
(1,19)	2:486:C:VAL:HG21	1:8:A:LEU:HB3	5	0.31
(1,11)	1:71:A:LEU:O	2:491:C:ASP:HB2	3	0.31
(1,31)	2:486:C:VAL:HG22	1:8:A:LEU:HB3	4	0.3
(1,15)	2:466:C:GLU:HB3	1:6:A:LYS:HE2	17	0.3
(1,10)	1:70:A:VAL:HG23	2:468:C:PHE:HZ	13	0.3
(1,7)	1:49:A:GLN:HG3	2:494:C:LEU:HD22	19	0.3
(1,33)	2:494:C:LEU:HD11	1:42:A:ARG:HB3	16	0.29
(1,31)	2:486:C:VAL:HG22	1:8:A:LEU:HB3	1	0.29
(1,31)	2:486:C:VAL:HG22	1:8:A:LEU:HB3	9	0.29
(1,31)	2:486:C:VAL:HG22	1:8:A:LEU:HB3	10	0.29
(1,19)	2:486:C:VAL:HB	1:8:A:LEU:HD23	12	0.29
(1,1)	1:8:A:LEU:HD23	2:486:C:VAL:HB	12	0.29
(1,16)	2:467:C:MET:HG2	1:68:A:HIS:HD2	3	0.28
(1,8)	1:68:A:HIS:HD2	2:467:C:MET:HG2	3	0.28
(1,8)	1:68:A:HIS:HB3	2:467:C:MET:HE1	9	0.28
(1,33)	2:494:C:LEU:HD11	1:42:A:ARG:HB3	20	0.27
(1,21)	2:494:C:LEU:HD22	1:44:A:ILE:HD12	10	0.26
(1,11)	1:71:A:LEU:HB2	2:487:C:GLU:HB3	19	0.26
(1,31)	2:486:C:VAL:HG22	1:8:A:LEU:HB3	17	0.25
(1,15)	2:466:C:GLU:O	1:68:A:HIS:HE2	16	0.25
(1,11)	1:71:A:LEU:O	2:491:C:ASP:HB2	14	0.25
(1,21)	2:494:C:LEU:HD12	1:44:A:ILE:HD11	18	0.24
(1,11)	1:71:A:LEU:O	2:487:C:GLU:HB3	13	0.24
(1,31)	2:486:C:VAL:HG22	1:8:A:LEU:HB3	14	0.23
(1,21)	2:494:C:LEU:HD22	1:49:A:GLN:HG3	20	0.23
(1,17)	2:468:C:PHE:HE1	1:44:A:ILE:HG12	6	0.23
(1,17)	2:468:C:PHE:HZ	1:44:A:ILE:HG12	13	0.23
(1,7)	1:49:A:GLN:HG3	2:494:C:LEU:HD22	20	0.23
(1,54)	2:489:C:THR:H	1:72:A:ARG:HA	19	0.22
(1,15)	2:466:C:GLU:O	1:68:A:HIS:HE2	10	0.22
(1,11)	1:71:A:LEU:O	2:487:C:GLU:HB3	15	0.22
(1,9)	1:69:A:LEU:H	2:467:C:MET:HE3	8	0.22
(1,40)	2:494:C:LEU:HD22	1:42:A:ARG:HG3	11	0.21
(1,15)	2:466:C:GLU:O	1:68:A:HIS:HE2	19	0.21
(1,12)	1:72:A:ARG:HB2	2:491:C:ASP:OD1	18	0.21
(1,8)	1:68:A:HIS:HB3	2:467:C:MET:HE1	1	0.21
(1,21)	2:494:C:LEU:HD11	1:44:A:ILE:HD11	13	0.2
(1,19)	2:486:C:VAL:HB	1:8:A:LEU:HD23	3	0.2
(1,17)	2:468:C:PHE:HE1	1:70:A:VAL:HG23	4	0.2
(1,16)	2:467:C:MET:HG3	1:8:A:LEU:HD22	17	0.2
(1,13)	1:73:A:LEU:HD22	2:488:C:ILE:HG12	17	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,13)	1:73:A:LEU:HD22	2:488:C:ILE:HD13	20	0.2
(1,11)	1:71:A:LEU:HB2	2:487:C:GLU:HB3	9	0.2
(1,9)	1:69:A:LEU:H	2:467:C:MET:HE1	17	0.2
(1,4)	1:44:A:ILE:HD11	2:494:C:LEU:HD11	13	0.2
(1,1)	1:8:A:LEU:HD22	2:467:C:MET:HG3	17	0.2
(1,31)	2:486:C:VAL:HG22	1:8:A:LEU:HB3	12	0.19
(1,21)	2:494:C:LEU:HD11	1:44:A:ILE:HD11	6	0.19
(1,19)	2:486:C:VAL:HB	1:8:A:LEU:HD23	15	0.19
(1,9)	1:69:A:LEU:H	2:467:C:MET:HE2	6	0.19
(1,4)	1:44:A:ILE:HD11	2:494:C:LEU:HD11	6	0.19
(1,17)	2:468:C:PHE:HE1	1:44:A:ILE:HG12	7	0.18
(1,13)	1:73:A:LEU:HB2	2:488:C:ILE:HG12	15	0.18
(1,8)	1:68:A:HIS:HB3	2:467:C:MET:HE1	19	0.18
(1,8)	1:68:A:HIS:HB3	2:467:C:MET:HE1	20	0.18
(1,1)	1:8:A:LEU:HD11	2:487:C:GLU:HA	15	0.18
(1,54)	2:489:C:THR:H	1:72:A:ARG:HA	17	0.17
(1,21)	2:494:C:LEU:HD13	1:70:A:VAL:HG13	14	0.17
(1,21)	2:494:C:LEU:HD11	1:42:A:ARG:HD3	15	0.17
(1,17)	2:468:C:PHE:HZ	1:44:A:ILE:HG12	16	0.17
(1,16)	2:467:C:MET:HE1	1:68:A:HIS:HB3	7	0.17
(1,13)	1:73:A:LEU:HD13	2:488:C:ILE:HG12	13	0.17
(1,11)	1:71:A:LEU:HD11	2:487:C:GLU:HG2	6	0.17
(1,10)	1:70:A:VAL:HG11	2:490:C:THR:HB	12	0.17
(1,7)	1:49:A:GLN:HG3	2:494:C:LEU:HD22	11	0.17
(1,4)	1:44:A:ILE:HG12	2:468:C:PHE:HZ	16	0.17
(1,54)	2:489:C:THR:H	1:72:A:ARG:HA	5	0.16
(1,54)	2:489:C:THR:H	1:72:A:ARG:HA	9	0.16
(1,33)	2:494:C:LEU:HD11	1:42:A:ARG:HB3	3	0.16
(1,21)	2:494:C:LEU:HD11	1:44:A:ILE:HD11	1	0.16
(1,17)	2:468:C:PHE:HZ	1:70:A:VAL:HG23	5	0.16
(1,4)	1:44:A:ILE:HD11	2:494:C:LEU:HD11	1	0.16
(1,1)	1:8:A:LEU:HD22	2:467:C:MET:HG3	8	0.16
(1,54)	2:489:C:THR:H	1:72:A:ARG:HA	1	0.15
(1,54)	2:489:C:THR:H	1:72:A:ARG:HA	14	0.15
(1,31)	2:486:C:VAL:HG22	1:8:A:LEU:HB3	19	0.15
(1,21)	2:494:C:LEU:HD13	1:70:A:VAL:HG13	3	0.15
(1,16)	2:467:C:MET:HE1	1:68:A:HIS:HB3	8	0.15
(1,11)	1:71:A:LEU:HB2	2:487:C:GLU:HB3	2	0.15
(1,11)	1:71:A:LEU:O	2:491:C:ASP:HB2	10	0.15
(1,8)	1:68:A:HIS:HB3	2:467:C:MET:HE3	6	0.15
(1,8)	1:68:A:HIS:HB3	2:467:C:MET:HE1	8	0.15
(1,54)	2:489:C:THR:H	1:72:A:ARG:HA	18	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,21)	2:494:C:LEU:HD12	1:70:A:VAL:HG12	9	0.14
(1,21)	2:494:C:LEU:HD13	1:70:A:VAL:HG13	17	0.14
(1,13)	1:73:A:LEU:HB2	2:488:C:ILE:HG12	6	0.14
(1,11)	1:71:A:LEU:HB2	2:487:C:GLU:HB3	18	0.14
(1,4)	1:44:A:ILE:HD11	2:494:C:LEU:HD11	7	0.14
(1,1)	1:8:A:LEU:HD13	2:490:C:THR:HG22	16	0.14
(1,54)	2:489:C:THR:H	1:72:A:ARG:HA	3	0.13
(1,42)	2:494:C:LEU:HD21	1:49:A:GLN:HB2	13	0.13
(1,21)	2:494:C:LEU:HD13	1:70:A:VAL:HG13	7	0.13
(1,17)	2:468:C:PHE:HZ	1:44:A:ILE:HG12	18	0.13
(1,16)	2:467:C:MET:HE1	1:68:A:HIS:HB3	10	0.13
(1,11)	1:71:A:LEU:HD12	2:487:C:GLU:HG2	4	0.13
(1,9)	1:69:A:LEU:H	2:467:C:MET:HE3	9	0.13
(1,8)	1:68:A:HIS:HB3	2:467:C:MET:HE1	10	0.13
(1,4)	1:44:A:ILE:HG12	2:468:C:PHE:HZ	18	0.13
(1,54)	2:489:C:THR:H	1:72:A:ARG:HA	2	0.12
(1,54)	2:489:C:THR:H	1:72:A:ARG:HA	4	0.12
(1,54)	2:489:C:THR:H	1:72:A:ARG:HA	8	0.12
(1,52)	2:494:C:LEU:HD22	1:43:A:LEU:H	14	0.12
(1,40)	2:494:C:LEU:HD22	1:42:A:ARG:HG3	2	0.12
(1,21)	2:494:C:LEU:HD22	1:49:A:GLN:HG3	8	0.12
(1,19)	2:486:C:VAL:HB	1:8:A:LEU:HD23	18	0.12
(1,16)	2:467:C:MET:HE1	1:68:A:HIS:HB3	13	0.12
(1,15)	2:466:C:GLU:O	1:68:A:HIS:HE2	7	0.12
(1,13)	1:73:A:LEU:HD13	2:488:C:ILE:HG12	4	0.12
(1,9)	1:69:A:LEU:H	2:467:C:MET:HE3	1	0.12
(1,8)	1:68:A:HIS:HE2	2:466:C:GLU:O	7	0.12
(1,8)	1:68:A:HIS:HB3	2:467:C:MET:HE1	13	0.12
(1,7)	1:49:A:GLN:HG3	2:494:C:LEU:HD22	8	0.12
(1,50)	2:494:C:LEU:HD22	1:70:A:VAL:H	5	0.11
(1,42)	2:494:C:LEU:HD21	1:49:A:GLN:HB2	5	0.11
(1,42)	2:494:C:LEU:HD21	1:49:A:GLN:HB2	6	0.11
(1,42)	2:494:C:LEU:HD21	1:49:A:GLN:HB2	7	0.11
(1,40)	2:494:C:LEU:HD22	1:42:A:ARG:HG3	13	0.11
(1,36)	2:494:C:LEU:HD11	1:48:A:LYS:HA	5	0.11
(1,33)	2:494:C:LEU:HD11	1:42:A:ARG:HB3	1	0.11
(1,17)	2:468:C:PHE:HE1	1:70:A:VAL:HG23	1	0.11
(1,16)	2:467:C:MET:HE1	1:68:A:HIS:HB3	16	0.11
(1,11)	1:71:A:LEU:HB2	2:487:C:GLU:HB3	20	0.11
(1,10)	1:70:A:VAL:HG12	2:490:C:THR:HB	20	0.11
(1,8)	1:68:A:HIS:HB3	2:467:C:MET:HE1	2	0.11
(1,8)	1:68:A:HIS:HB3	2:467:C:MET:HE1	16	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,54)	2:489:C:THR:H	1:72:A:ARG:HA	10	0.1
(1,52)	2:494:C:LEU:HD22	1:43:A:LEU:H	13	0.1
(1,42)	2:494:C:LEU:HD21	1:49:A:GLN:HB2	10	0.1
(1,1)	1:8:A:LEU:HD21	2:490:C:THR:HG22	10	0.1

10 Dihedral-angle violation analysis ⓘ

No dihedral-angle restraints found