



Full wwPDB NMR Structure Validation Report ⓘ

Mar 8, 2026 – 01:14 AM UTC

PDB ID : 7AFQ / pdb_00007afq
BMRB ID : 34561
Title : Ribosome binding factor A (RbfA)
Authors : Schedlbauer, A.; Iturrioz, I.; Ochoa-Lizarralde, B.; Diercks, T.; Fucini, P.;
Connell, S.
Deposited on : 2020-09-19

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

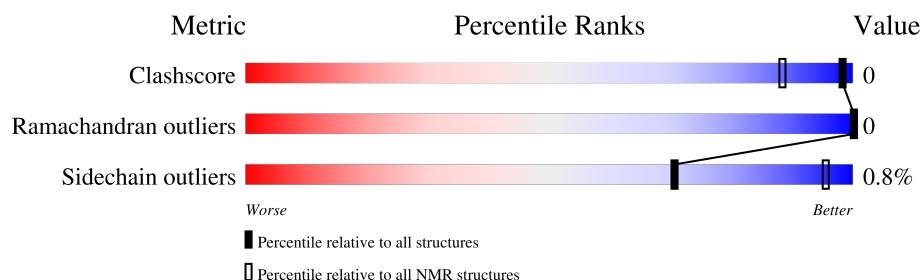
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 80%.

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	V	133	

2 Ensemble composition and analysis

This entry contains 20 models. Model 3 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	V:9-V:100 (92)	0.53	3

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 5 clusters and 2 single-model clusters were found.

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

3 Entry composition [i](#)

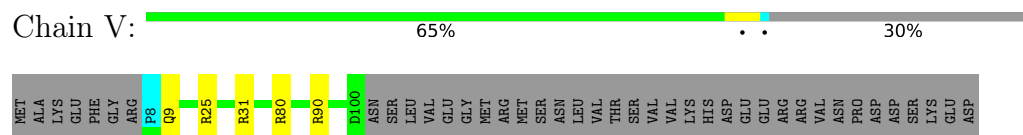
There is only 1 type of molecule in this entry. The entry contains 1509 atoms, of which 770 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Ribosome-binding factor A.

Mol	Chain	Residues	Atoms						Trace
1	V	93	Total	C	H	N	O	S	0
			1509	471	770	127	136	5	

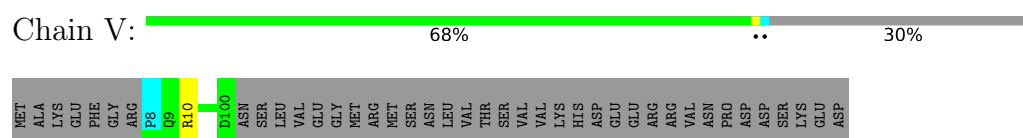
4.2.3 Score per residue for model 3 (medoid)

- Molecule 1: Ribosome-binding factor A



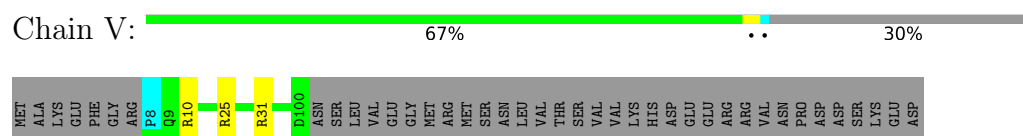
4.2.4 Score per residue for model 4

- Molecule 1: Ribosome-binding factor A



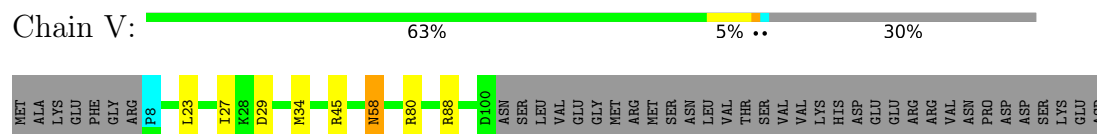
4.2.5 Score per residue for model 5

- Molecule 1: Ribosome-binding factor A



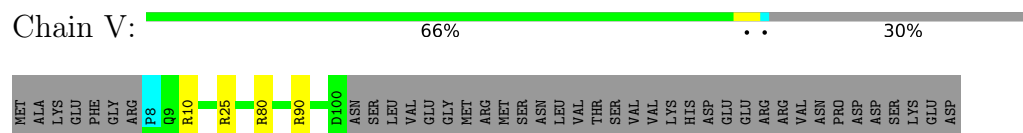
4.2.6 Score per residue for model 6

- Molecule 1: Ribosome-binding factor A



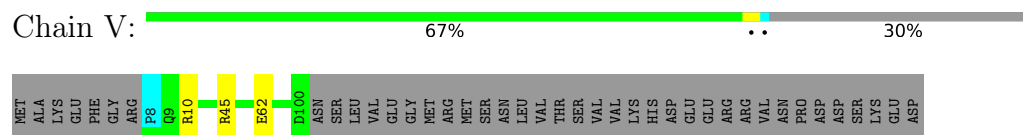
4.2.7 Score per residue for model 7

- Molecule 1: Ribosome-binding factor A



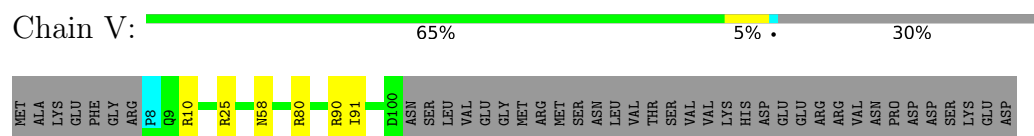
4.2.8 Score per residue for model 8

- Molecule 1: Ribosome-binding factor A



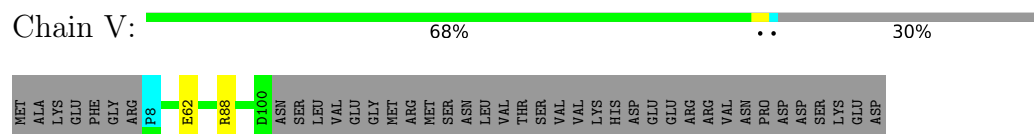
4.2.9 Score per residue for model 9

- Molecule 1: Ribosome-binding factor A



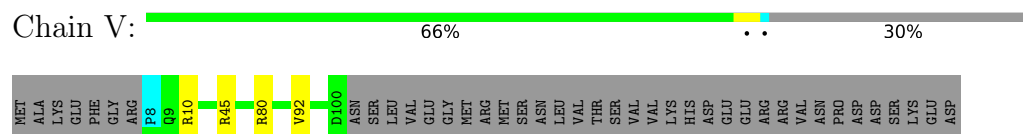
4.2.10 Score per residue for model 10

- Molecule 1: Ribosome-binding factor A



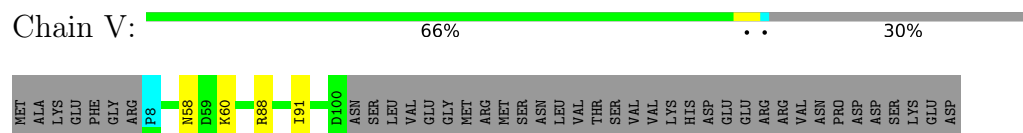
4.2.11 Score per residue for model 11

- Molecule 1: Ribosome-binding factor A



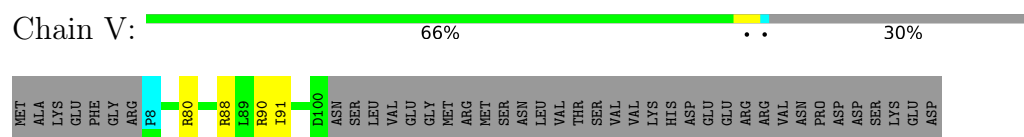
4.2.12 Score per residue for model 12

- Molecule 1: Ribosome-binding factor A



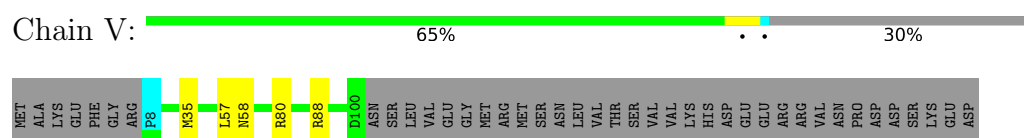
4.2.13 Score per residue for model 13

- Molecule 1: Ribosome-binding factor A



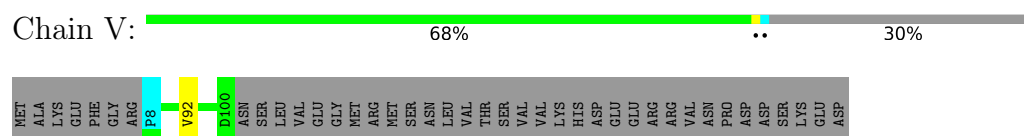
4.2.14 Score per residue for model 14

- Molecule 1: Ribosome-binding factor A



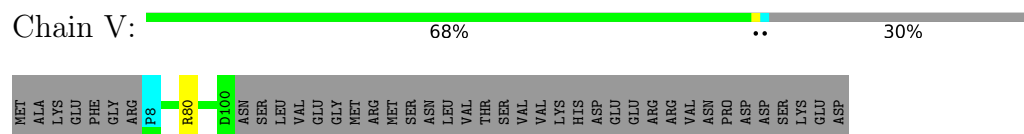
4.2.15 Score per residue for model 15

- Molecule 1: Ribosome-binding factor A



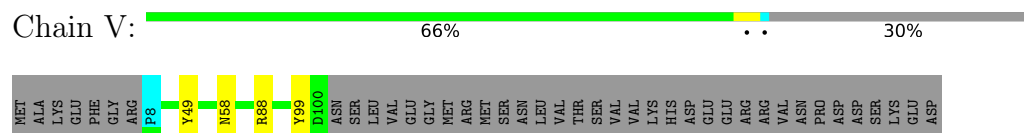
4.2.16 Score per residue for model 16

- Molecule 1: Ribosome-binding factor A



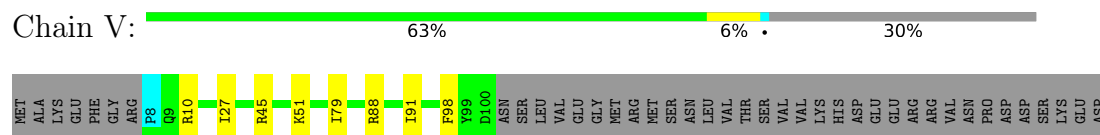
4.2.17 Score per residue for model 17

- Molecule 1: Ribosome-binding factor A



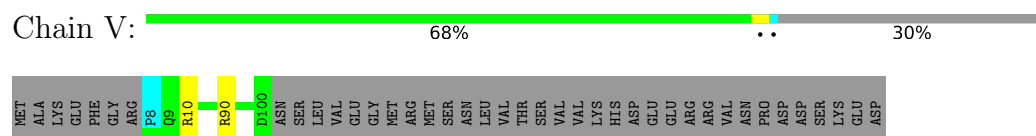
4.2.18 Score per residue for model 18

- Molecule 1: Ribosome-binding factor A



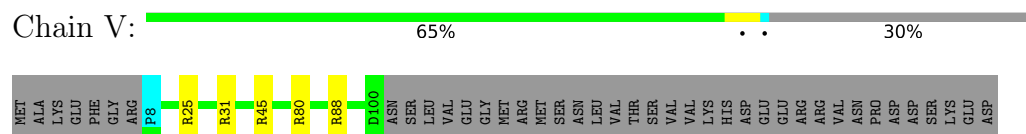
4.2.19 Score per residue for model 19

- Molecule 1: Ribosome-binding factor A



4.2.20 Score per residue for model 20

- Molecule 1: Ribosome-binding factor A



5 Refinement protocol and experimental data overview

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

Of the 60 calculated structures, 20 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
X-PLOR NIH	structure calculation	
GROMACS	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	1472
Number of shifts mapped to atoms	1060
Number of unparsed shifts	0
Number of shifts with mapping errors	412
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	80%

6 Model quality i

6.1 Standard geometry i

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	V	0.87±0.02	0±0/740 (0.0± 0.0%)	1.40±0.02	3±1/991 (0.3± 0.1%)
All	All	0.87	0/14800 (0.0%)	1.40	51/19820 (0.3%)

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

Mol	Chain	Chirality	Planarity
1	V	0.0±0.0	0.1±0.3
All	All	0	2

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	V	10	ARG	NE-CZ-NH2	7.09	125.58	119.20	4	9
1	V	90	ARG	NE-CZ-NH2	6.29	124.86	119.20	13	5
1	V	88	ARG	NE-CZ-NH2	6.21	124.79	119.20	6	8
1	V	58	ASN	CA-C-N	6.15	132.43	120.99	17	2
1	V	58	ASN	C-N-CA	6.15	132.43	120.99	17	2
1	V	80	ARG	NE-CZ-NH2	5.99	124.59	119.20	1	10
1	V	45	ARG	NE-CZ-NH2	5.97	124.57	119.20	6	6
1	V	31	ARG	NE-CZ-NH2	5.81	124.43	119.20	20	3
1	V	25	ARG	NE-CZ-NH2	5.72	124.35	119.20	20	5
1	V	9	GLN	OE1-CD-NE2	-5.12	117.48	122.60	3	1

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	V	80	ARG	Sidechain	1
1	V	49	TYR	Sidechain	1

6.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	V	732	763	763	0±1
All	All	14640	15260	15260	9

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 0.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:V:27:ILE:HD11	1:V:79:ILE:HD11	0.79	1.55	18	1
1:V:27:ILE:CD1	1:V:79:ILE:HD11	0.64	2.22	18	1
1:V:23:LEU:O	1:V:27:ILE:CG1	0.57	2.53	6	1
1:V:35:MET:HB3	1:V:57:LEU:HB2	0.46	1.87	14	1
1:V:91:ILE:O	1:V:91:ILE:HG23	0.44	2.12	12	1
1:V:29:ASP:HB3	1:V:34:MET:SD	0.42	2.55	6	1
1:V:62:GLU:H	1:V:62:GLU:CD	0.41	2.24	10	1
1:V:23:LEU:O	1:V:27:ILE:HG12	0.41	2.15	6	1
1:V:51:LYS:HE3	1:V:98:PHE:CE2	0.40	2.52	18	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	V	91/133 (68%)	88±1 (97±1%)	3±1 (3±1%)	0±0 (0±0%)	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1820/2660 (68%)	1768 (97%)	52 (3%)	0 (0%)	100	100

There are no Ramachandran outliers.

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	V	78/116 (67%)	77±1 (99±1%)	1±1 (1±1%)	70	95
All	All	1560/2320 (67%)	1548 (99%)	12 (1%)	70	95

All 6 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	V	58	ASN	4
1	V	91	ILE	3
1	V	92	VAL	2
1	V	62	GLU	1
1	V	60	LYS	1
1	V	99	TYR	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

There are no ligands in this entry.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 80% for the well-defined parts and 80% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chemical_shifts_1*

7.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1472
Number of shifts mapped to atoms	1060
Number of unparsed shifts	0
Number of shifts with mapping errors	412
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- No matching atom found in the structure. All 412 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	V	6	GLY	HA2	3.94	0.02	1
1	V	6	GLY	HA3	3.79	0.02	1
1	V	6	GLY	CA	44.9	0.3	1
1	V	101	ASN	H	7.92	0.02	1
1	V	101	ASN	HA	4.45	0.02	1
1	V	101	ASN	HB2	2.74	0.02	1
1	V	101	ASN	HB3	2.64	0.02	1
1	V	101	ASN	C	176.0	0.3	1
1	V	101	ASN	CA	52.8	0.3	1
1	V	101	ASN	CB	38.7	0.3	1
1	V	101	ASN	N	122.9	0.3	1
1	V	102	SER	H	8.23	0.02	1
1	V	102	SER	HA	4.04	0.02	1
1	V	102	SER	HB2	3.69	0.02	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	V	102	SER	HB3	3.69	0.02	1
1	V	102	SER	C	174.1	0.3	1
1	V	102	SER	CA	60.2	0.3	1
1	V	102	SER	CB	63.3	0.3	1
1	V	102	SER	N	115.8	0.3	1
1	V	103	LEU	H	7.91	0.02	1
1	V	103	LEU	HA	4.17	0.02	1
1	V	103	LEU	HB2	1.5	0.02	1
1	V	103	LEU	HB3	1.43	0.02	1
1	V	103	LEU	HD11	0.72	0.02	1
1	V	103	LEU	HD12	0.72	0.02	1
1	V	103	LEU	HD13	0.72	0.02	1
1	V	103	LEU	HD21	0.67	0.02	1
1	V	103	LEU	HD22	0.67	0.02	1
1	V	103	LEU	HD23	0.67	0.02	1
1	V	103	LEU	HG	1.48	0.02	1
1	V	103	LEU	C	177.7	0.3	1
1	V	103	LEU	CA	55.7	0.3	1
1	V	103	LEU	CB	41.9	0.3	1
1	V	103	LEU	CD1	24.8	0.3	1
1	V	103	LEU	CD2	23.5	0.3	1
1	V	103	LEU	CG	26.9	0.3	1
1	V	103	LEU	N	122.9	0.3	1
1	V	104	VAL	H	7.73	0.02	1
1	V	104	VAL	HA	3.88	0.02	1
1	V	104	VAL	HB	1.94	0.02	1
1	V	104	VAL	HG11	0.81	0.02	1
1	V	104	VAL	HG12	0.81	0.02	1
1	V	104	VAL	HG13	0.81	0.02	1
1	V	104	VAL	C	176.7	0.3	1
1	V	104	VAL	CA	63.0	0.3	1
1	V	104	VAL	CB	32.5	0.3	1
1	V	104	VAL	CG1	21.0	0.3	1
1	V	104	VAL	CG2	21.0	0.3	1
1	V	104	VAL	N	120.0	0.3	1
1	V	105	GLU	H	8.36	0.02	1
1	V	105	GLU	HA	4.01	0.02	1
1	V	105	GLU	HB2	1.89	0.02	1
1	V	105	GLU	HB3	1.82	0.02	1
1	V	105	GLU	HG2	2.12	0.02	1
1	V	105	GLU	HG3	2.12	0.02	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	V	105	GLU	C	177.4	0.3	1
1	V	105	GLU	CA	57.4	0.3	1
1	V	105	GLU	CB	29.6	0.3	1
1	V	105	GLU	CG	36.2	0.3	1
1	V	105	GLU	N	123.5	0.3	1
1	V	106	GLY	H	8.22	0.02	1
1	V	106	GLY	HA2	3.83	0.02	1
1	V	106	GLY	HA3	3.75	0.02	1
1	V	106	GLY	C	174.5	0.3	1
1	V	106	GLY	CA	45.5	0.3	1
1	V	106	GLY	N	108.7	0.3	1
1	V	107	MET	H	7.91	0.02	1
1	V	107	MET	HA	4.29	0.02	1
1	V	107	MET	HB2	1.93	0.02	1
1	V	107	MET	HB3	1.93	0.02	1
1	V	107	MET	HG2	2.45	0.02	1
1	V	107	MET	HG3	2.38	0.02	1
1	V	107	MET	C	176.3	0.3	1
1	V	107	MET	CA	55.7	0.3	1
1	V	107	MET	CB	32.8	0.3	1
1	V	107	MET	CG	32.0	0.3	1
1	V	107	MET	N	119.5	0.3	1
1	V	111	ASN	HA	4.57	0.02	1
1	V	111	ASN	C	174.9	0.3	1
1	V	111	ASN	CA	53.4	0.3	1
1	V	111	ASN	CB	38.6	0.3	1
1	V	112	LEU	H	7.94	0.02	1
1	V	112	LEU	HA	4.2	0.02	1
1	V	112	LEU	HB2	1.51	0.02	1
1	V	112	LEU	HB3	1.43	0.02	1
1	V	112	LEU	HD11	0.78	0.02	1
1	V	112	LEU	HD12	0.78	0.02	1
1	V	112	LEU	HD13	0.78	0.02	1
1	V	112	LEU	HG	1.47	0.02	1
1	V	112	LEU	C	177.2	0.3	1
1	V	112	LEU	CA	55.3	0.3	1
1	V	112	LEU	CB	42.2	0.3	1
1	V	112	LEU	CD1	24.7	0.3	1
1	V	112	LEU	CD2	24.7	0.3	1
1	V	112	LEU	CG	26.9	0.3	1
1	V	112	LEU	N	121.5	0.3	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	V	113	VAL	H	7.98	0.02	1
1	V	113	VAL	HA	4.03	0.02	1
1	V	113	VAL	HB	1.94	0.02	1
1	V	113	VAL	HG11	0.81	0.02	1
1	V	113	VAL	HG12	0.81	0.02	1
1	V	113	VAL	HG13	0.81	0.02	1
1	V	113	VAL	HG21	0.75	0.02	1
1	V	113	VAL	HG22	0.75	0.02	1
1	V	113	VAL	HG23	0.75	0.02	1
1	V	113	VAL	C	176.2	0.3	1
1	V	113	VAL	CA	62.4	0.3	1
1	V	113	VAL	CB	32.5	0.3	1
1	V	113	VAL	CG1	20.7	0.3	1
1	V	113	VAL	CG2	21.1	0.3	1
1	V	113	VAL	N	120.9	0.3	1
1	V	114	THR	H	8.08	0.02	1
1	V	114	THR	HA	4.25	0.02	1
1	V	114	THR	HB	4.08	0.02	1
1	V	114	THR	HG21	1.05	0.02	1
1	V	114	THR	HG22	1.05	0.02	1
1	V	114	THR	HG23	1.05	0.02	1
1	V	114	THR	CA	61.6	0.3	1
1	V	114	THR	CB	69.7	0.3	1
1	V	114	THR	CG2	21.4	0.3	1
1	V	114	THR	N	117.6	0.3	1
1	V	115	SER	HA	4.36	0.02	1
1	V	115	SER	HB2	3.7	0.02	1
1	V	115	SER	HB3	3.7	0.02	1
1	V	115	SER	C	174.1	0.3	1
1	V	115	SER	CA	58.1	0.3	1
1	V	115	SER	CB	63.7	0.3	1
1	V	116	VAL	H	8.02	0.02	1
1	V	116	VAL	HA	4.0	0.02	1
1	V	116	VAL	HB	1.93	0.02	1
1	V	116	VAL	HG11	0.8	0.02	1
1	V	116	VAL	HG12	0.8	0.02	1
1	V	116	VAL	HG13	0.8	0.02	1
1	V	116	VAL	C	175.9	0.3	1
1	V	116	VAL	CA	62.3	0.3	1
1	V	116	VAL	CB	32.6	0.3	1
1	V	116	VAL	CG1	20.6	0.3	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	V	116	VAL	CG2	20.6	0.3	1
1	V	116	VAL	N	122.0	0.3	1
1	V	117	VAL	H	8.08	0.02	1
1	V	117	VAL	HA	3.89	0.02	1
1	V	117	VAL	HB	1.88	0.02	1
1	V	117	VAL	HG11	0.77	0.02	1
1	V	117	VAL	HG12	0.77	0.02	1
1	V	117	VAL	HG13	0.77	0.02	1
1	V	117	VAL	C	175.7	0.3	1
1	V	117	VAL	CA	62.2	0.3	1
1	V	117	VAL	CB	32.6	0.3	1
1	V	117	VAL	CG1	20.7	0.3	1
1	V	117	VAL	CG2	20.7	0.3	1
1	V	117	VAL	N	124.7	0.3	1
1	V	118	LYS	H	8.29	0.02	1
1	V	118	LYS	HA	4.18	0.02	1
1	V	118	LYS	HB2	1.63	0.02	1
1	V	118	LYS	HB3	1.56	0.02	1
1	V	118	LYS	HD2	1.52	0.02	1
1	V	118	LYS	HD3	1.52	0.02	1
1	V	118	LYS	HE2	2.84	0.02	1
1	V	118	LYS	HE3	2.83	0.02	1
1	V	118	LYS	HG2	1.27	0.02	1
1	V	118	LYS	HG3	1.21	0.02	1
1	V	118	LYS	C	176.0	0.3	1
1	V	118	LYS	CA	55.8	0.3	1
1	V	118	LYS	CB	33.0	0.3	1
1	V	118	LYS	CD	29.0	0.3	1
1	V	118	LYS	CE	42.1	0.3	1
1	V	118	LYS	CG	24.6	0.3	1
1	V	118	LYS	N	126.0	0.3	1
1	V	120	ASP	HA	4.41	0.02	1
1	V	120	ASP	C	176.2	0.3	1
1	V	120	ASP	CA	54.4	0.3	1
1	V	120	ASP	CB	40.9	0.3	1
1	V	121	GLU	H	8.29	0.02	1
1	V	121	GLU	HA	4.07	0.02	1
1	V	121	GLU	HB2	1.84	0.02	1
1	V	121	GLU	HB3	1.84	0.02	1
1	V	121	GLU	HG2	2.12	0.02	1
1	V	121	GLU	HG3	2.12	0.02	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	V	121	GLU	C	176.6	0.3	1
1	V	121	GLU	CA	56.7	0.3	1
1	V	121	GLU	CB	30.0	0.3	1
1	V	121	GLU	CG	36.2	0.3	1
1	V	121	GLU	N	121.2	0.3	1
1	V	122	GLU	H	8.26	0.02	1
1	V	122	GLU	HA	4.07	0.02	1
1	V	122	GLU	HB2	1.84	0.02	1
1	V	122	GLU	HB3	1.84	0.02	1
1	V	122	GLU	HG2	2.12	0.02	1
1	V	122	GLU	HG3	2.12	0.02	1
1	V	122	GLU	C	176.4	0.3	1
1	V	122	GLU	CA	56.7	0.3	1
1	V	122	GLU	CB	29.9	0.3	1
1	V	122	GLU	CG	36.2	0.3	1
1	V	122	GLU	N	121.5	0.3	1
1	V	123	ARG	H	8.13	0.02	1
1	V	123	ARG	HA	4.16	0.02	1
1	V	123	ARG	HB2	1.68	0.02	1
1	V	123	ARG	HB3	1.61	0.02	1
1	V	123	ARG	HD2	3.04	0.02	1
1	V	123	ARG	HD3	3.04	0.02	1
1	V	123	ARG	HG2	1.45	0.02	1
1	V	123	ARG	HG3	1.45	0.02	1
1	V	123	ARG	C	175.9	0.3	1
1	V	123	ARG	CA	55.9	0.3	1
1	V	123	ARG	CB	30.5	0.3	1
1	V	123	ARG	CD	43.2	0.3	1
1	V	123	ARG	CG	26.9	0.3	1
1	V	123	ARG	N	122.1	0.3	1
1	V	124	ARG	H	8.21	0.02	1
1	V	124	ARG	HA	4.21	0.02	1
1	V	124	ARG	HB2	1.68	0.02	1
1	V	124	ARG	HB3	1.61	0.02	1
1	V	124	ARG	HD2	3.04	0.02	1
1	V	124	ARG	HD3	3.04	0.02	1
1	V	124	ARG	HG2	1.45	0.02	1
1	V	124	ARG	HG3	1.45	0.02	1
1	V	124	ARG	C	176.1	0.3	1
1	V	124	ARG	CA	55.9	0.3	1
1	V	124	ARG	CB	30.6	0.3	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	V	124	ARG	CD	43.0	0.3	1
1	V	124	ARG	CG	26.9	0.3	1
1	V	124	ARG	N	122.8	0.3	1
1	V	125	VAL	H	8.12	0.02	1
1	V	125	VAL	HA	3.93	0.02	1
1	V	125	VAL	HB	1.86	0.02	1
1	V	125	VAL	HG11	0.76	0.02	1
1	V	125	VAL	HG12	0.76	0.02	1
1	V	125	VAL	HG13	0.76	0.02	1
1	V	125	VAL	HG21	0.76	0.02	1
1	V	125	VAL	HG22	0.76	0.02	1
1	V	125	VAL	HG23	0.76	0.02	1
1	V	125	VAL	C	175.4	0.3	1
1	V	125	VAL	CA	62.1	0.3	1
1	V	125	VAL	CB	32.7	0.3	1
1	V	125	VAL	CG1	20.6	0.3	1
1	V	125	VAL	CG2	21.0	0.3	1
1	V	125	VAL	N	121.6	0.3	1
1	V	126	ASN	H	8.54	0.02	1
1	V	126	ASN	HA	4.86	0.02	1
1	V	126	ASN	HB2	2.78	0.02	1
1	V	126	ASN	HB3	2.56	0.02	1
1	V	126	ASN	HD21	7.56	0.02	1
1	V	126	ASN	HD22	7.56	0.02	1
1	V	126	ASN	CA	50.9	0.3	1
1	V	126	ASN	CB	38.8	0.3	1
1	V	126	ASN	N	123.9	0.3	1
1	V	126	ASN	ND2	113.3	0.3	1
1	V	127	PRO	HA	4.24	0.02	1
1	V	127	PRO	HB2	2.15	0.02	1
1	V	127	PRO	HB3	1.84	0.02	1
1	V	127	PRO	HD2	3.68	0.02	1
1	V	127	PRO	HD3	3.68	0.02	1
1	V	127	PRO	HG2	1.88	0.02	1
1	V	127	PRO	HG3	1.88	0.02	1
1	V	127	PRO	C	176.7	0.3	1
1	V	127	PRO	CA	63.7	0.3	1
1	V	127	PRO	CB	32.0	0.3	1
1	V	127	PRO	CD	50.7	0.3	1
1	V	127	PRO	CG	27.1	0.3	1
1	V	128	ASP	H	8.14	0.02	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	V	128	ASP	HA	4.44	0.02	1
1	V	128	ASP	HB2	2.58	0.02	1
1	V	128	ASP	HB3	2.46	0.02	1
1	V	128	ASP	C	176.1	0.3	1
1	V	128	ASP	CA	54.5	0.3	1
1	V	128	ASP	CB	40.7	0.3	1
1	V	128	ASP	N	118.8	0.3	1
1	V	129	ASP	H	7.94	0.02	1
1	V	129	ASP	HA	4.45	0.02	1
1	V	129	ASP	HB2	2.57	0.02	1
1	V	129	ASP	HB3	2.46	0.02	1
1	V	129	ASP	C	176.4	0.3	1
1	V	129	ASP	CA	54.4	0.3	1
1	V	129	ASP	CB	40.8	0.3	1
1	V	129	ASP	N	120.7	0.3	1
1	V	130	SER	H	8.09	0.02	1
1	V	130	SER	HA	4.26	0.02	1
1	V	130	SER	HB2	3.75	0.02	1
1	V	130	SER	HB3	3.75	0.02	1
1	V	130	SER	C	174.7	0.3	1
1	V	130	SER	CA	58.6	0.3	1
1	V	130	SER	CB	63.7	0.3	1
1	V	130	SER	N	115.9	0.3	1
1	V	131	LYS	H	8.16	0.02	1
1	V	131	LYS	HA	4.2	0.02	1
1	V	131	LYS	HB2	1.72	0.02	1
1	V	131	LYS	HB3	1.63	0.02	1
1	V	131	LYS	HD2	1.52	0.02	1
1	V	131	LYS	HD3	1.52	0.02	1
1	V	131	LYS	HE2	2.51	0.02	1
1	V	131	LYS	HE3	2.51	0.02	1
1	V	131	LYS	HG2	1.27	0.02	1
1	V	131	LYS	HG3	1.27	0.02	1
1	V	131	LYS	C	176.6	0.3	1
1	V	131	LYS	CA	56.2	0.3	1
1	V	131	LYS	CB	32.8	0.3	1
1	V	131	LYS	CD	29.0	0.3	1
1	V	131	LYS	CE	42.0	0.3	1
1	V	131	LYS	CG	24.6	0.3	1
1	V	131	LYS	N	123.0	0.3	1
1	V	132	GLU	H	8.28	0.02	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	V	132	GLU	HA	4.1	0.02	1
1	V	132	GLU	HB2	1.89	0.02	1
1	V	132	GLU	HB3	1.8	0.02	1
1	V	132	GLU	HG2	2.11	0.02	1
1	V	132	GLU	HG3	2.11	0.02	1
1	V	132	GLU	C	176.4	0.3	1
1	V	132	GLU	CA	56.6	0.3	1
1	V	132	GLU	CB	30.1	0.3	1
1	V	132	GLU	CG	36.2	0.3	1
1	V	132	GLU	N	121.6	0.3	1
1	V	133	ASP	H	8.24	0.02	1
1	V	133	ASP	HA	4.42	0.02	1
1	V	133	ASP	HB2	2.56	0.02	1
1	V	133	ASP	HB3	2.46	0.02	1
1	V	133	ASP	C	176.0	0.3	1
1	V	133	ASP	CA	54.3	0.3	1
1	V	133	ASP	CB	41.0	0.3	1
1	V	133	ASP	N	121.4	0.3	1
1	V	134	ALA	H	8.06	0.02	1
1	V	134	ALA	HA	4.16	0.02	1
1	V	134	ALA	HB1	1.25	0.02	1
1	V	134	ALA	HB2	1.25	0.02	1
1	V	134	ALA	HB3	1.25	0.02	1
1	V	134	ALA	C	177.6	0.3	1
1	V	134	ALA	CA	52.5	0.3	1
1	V	134	ALA	CB	19.1	0.3	1
1	V	134	ALA	N	124.1	0.3	1
1	V	135	LEU	H	8.05	0.02	1
1	V	135	LEU	HA	4.15	0.02	1
1	V	135	LEU	HB2	1.51	0.02	1
1	V	135	LEU	HB3	1.43	0.02	1
1	V	135	LEU	HD11	0.79	0.02	1
1	V	135	LEU	HD12	0.79	0.02	1
1	V	135	LEU	HD13	0.79	0.02	1
1	V	135	LEU	HD21	0.73	0.02	1
1	V	135	LEU	HD22	0.73	0.02	1
1	V	135	LEU	HD23	0.73	0.02	1
1	V	135	LEU	HG	1.48	0.02	1
1	V	135	LEU	C	177.4	0.3	1
1	V	135	LEU	CA	55.2	0.3	1
1	V	135	LEU	CB	42.2	0.3	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	V	135	LEU	CD1	24.9	0.3	1
1	V	135	LEU	CD2	23.4	0.3	1
1	V	135	LEU	CG	26.9	0.3	1
1	V	135	LEU	N	120.8	0.3	1
1	V	136	GLU	H	8.15	0.02	1
1	V	136	GLU	HA	4.11	0.02	1
1	V	136	GLU	HB2	1.85	0.02	1
1	V	136	GLU	HB3	1.79	0.02	1
1	V	136	GLU	HG2	2.11	0.02	1
1	V	136	GLU	HG3	2.11	0.02	1
1	V	136	GLU	C	176.2	0.3	1
1	V	136	GLU	CA	56.6	0.3	1
1	V	136	GLU	CB	30.0	0.3	1
1	V	136	GLU	CG	36.1	0.3	1
1	V	136	GLU	N	121.6	0.3	1
1	V	137	VAL	H	7.96	0.02	1
1	V	137	VAL	HA	3.88	0.02	1
1	V	137	VAL	HB	1.85	0.02	1
1	V	137	VAL	HG11	0.76	0.02	1
1	V	137	VAL	HG12	0.76	0.02	1
1	V	137	VAL	HG13	0.76	0.02	1
1	V	137	VAL	HG21	0.67	0.02	1
1	V	137	VAL	HG22	0.67	0.02	1
1	V	137	VAL	HG23	0.67	0.02	1
1	V	137	VAL	C	175.7	0.3	1
1	V	137	VAL	CA	62.2	0.3	1
1	V	137	VAL	CB	32.5	0.3	1
1	V	137	VAL	CG1	20.6	0.3	1
1	V	137	VAL	CG2	21.1	0.3	1
1	V	137	VAL	N	121.4	0.3	1
1	V	138	LEU	H	8.05	0.02	1
1	V	138	LEU	HA	4.16	0.02	1
1	V	138	LEU	HB2	1.39	0.02	1
1	V	138	LEU	HB3	1.23	0.02	1
1	V	138	LEU	HD11	0.73	0.02	1
1	V	138	LEU	HD12	0.73	0.02	1
1	V	138	LEU	HD13	0.73	0.02	1
1	V	138	LEU	HD21	0.66	0.02	1
1	V	138	LEU	HD22	0.66	0.02	1
1	V	138	LEU	HD23	0.66	0.02	1
1	V	138	LEU	HG	1.36	0.02	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	V	138	LEU	C	176.7	0.3	1
1	V	138	LEU	CA	54.9	0.3	1
1	V	138	LEU	CB	42.5	0.3	1
1	V	138	LEU	CD1	24.7	0.3	1
1	V	138	LEU	CD2	23.3	0.3	1
1	V	138	LEU	CG	26.8	0.3	1
1	V	138	LEU	N	125.3	0.3	1
1	V	139	PHE	H	8.05	0.02	1
1	V	139	PHE	HA	4.5	0.02	1
1	V	139	PHE	HB2	3.06	0.02	1
1	V	139	PHE	HB3	2.85	0.02	1
1	V	139	PHE	C	174.6	0.3	1
1	V	139	PHE	CA	57.5	0.3	1
1	V	139	PHE	CB	39.4	0.3	1
1	V	139	PHE	N	120.7	0.3	1
1	V	140	GLN	H	7.69	0.02	1
1	V	140	GLN	HA	4.0	0.02	1
1	V	140	GLN	HB2	1.94	0.02	1
1	V	140	GLN	HB3	1.76	0.02	1
1	V	140	GLN	HE21	7.41	0.02	1
1	V	140	GLN	HE22	6.7	0.02	1
1	V	140	GLN	HG2	2.1	0.02	1
1	V	140	GLN	HG3	2.1	0.02	1
1	V	140	GLN	C	180.1	0.3	1
1	V	140	GLN	CA	57.2	0.3	1
1	V	140	GLN	CB	30.5	0.3	1
1	V	140	GLN	CG	34.1	0.3	1
1	V	140	GLN	N	126.1	0.3	1
1	V	140	GLN	NE2	112.2	0.3	1

7.1.2 Chemical shift referencing ⓘ

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	126	-0.01 ± 0.09	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	119	0.14 ± 0.11	None needed (< 0.5 ppm)
$^{13}\text{C}'$	111	-0.02 ± 0.08	None needed (< 0.5 ppm)
^{15}N	109	0.69 ± 0.30	Should be applied

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 80%, i.e. 1049 atoms were assigned a chemical shift out of a possible 1314. 0 out of 17 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	412/461 (89%)	170/187 (91%)	165/184 (90%)	77/90 (86%)
Sidechain	630/786 (80%)	424/512 (83%)	203/240 (85%)	3/34 (9%)
Aromatic	7/67 (10%)	7/32 (22%)	0/35 (0%)	0/0 (—%)
Overall	1049/1314 (80%)	601/731 (82%)	368/459 (80%)	80/124 (65%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 80%, i.e. 1060 atoms were assigned a chemical shift out of a possible 1326. 0 out of 17 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	414/464 (89%)	171/188 (91%)	166/186 (89%)	77/90 (86%)
Sidechain	639/795 (80%)	430/518 (83%)	206/243 (85%)	3/34 (9%)
Aromatic	7/67 (10%)	7/32 (22%)	0/35 (0%)	0/0 (—%)
Overall	1060/1326 (80%)	608/738 (82%)	372/464 (80%)	80/124 (65%)

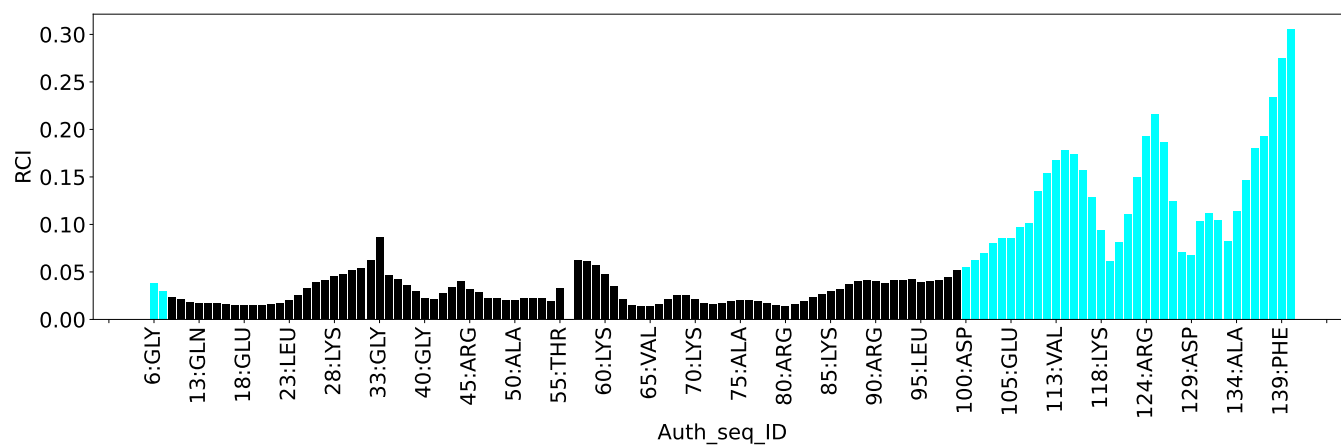
7.1.4 Statistically unusual chemical shifts [i](#)

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 V:



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	2062
Intra-residue ($ i-j =0$)	810
Sequential ($ i-j =1$)	575
Medium range ($ i-j >1$ and $ i-j <5$)	376
Long range ($ i-j \geq 5$)	191
Inter-chain	0
Hydrogen bond restraints	110
Disulfide bond restraints	0
Total dihedral-angle restraints	178
Number of unmapped restraints	159
Number of restraints per residue	16.8
Number of long range restraints per residue ¹	1.7

¹Long range hydrogen bonds and disulfide bonds are counted as long range restraints while calculating the number of long range restraints per residue

8.2 Residual restraint violations

This section provides the overview of the restraint violations analysis. The violations are binned as small, medium and large violations based on its absolute value. Average number of violations per model is calculated by dividing the total number of violations in each bin by the size of the ensemble.

8.2.1 Average number of distance violations per model

Distance violations less than 0.1 Å are not included in the calculation.

Bins (Å)	Average number of violations per model	Max (Å)
0.1-0.2 (Small)	33.3	0.2
0.2-0.5 (Medium)	43.4	0.5
>0.5 (Large)	20.1	2.36

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

Dihedral-angle violations less than 1° are not included in the calculation.

Bins (°)	Average number of violations per model	Max (°)
1.0-10.0 (Small)	5.2	9.83
10.0-20.0 (Medium)	0.3	18.83
>20.0 (Large)	0.1	54.22

9 Distance violation analysis ⓘ

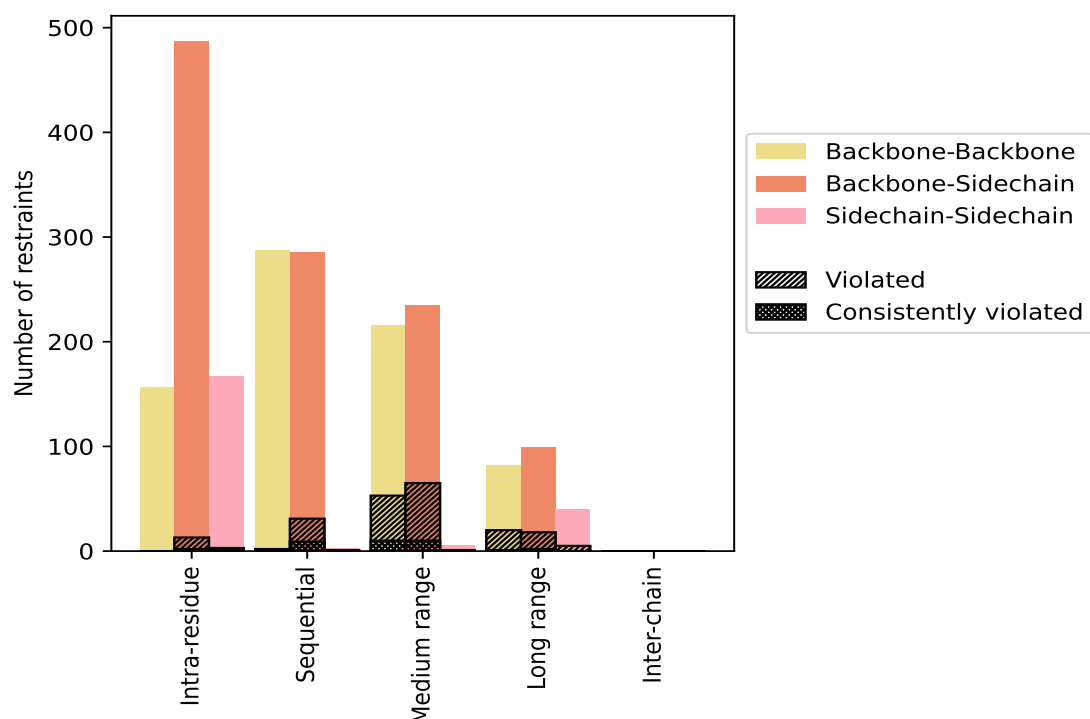
9.1 Summary of distance violations ⓘ

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 ($i-j =0$)	810	39.3	16	2.0	0.8	3	0.4	0.1
Backbone-Backbone	156	7.6	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	487	23.6	13	2.7	0.6	2	0.4	0.1
Sidechain-Sidechain	167	8.1	3	1.8	0.1	1	0.6	0.0
Sequential ($i-j =1$)	575	27.9	34	5.9	1.6	9	1.6	0.4
Backbone-Backbone	287	13.9	2	0.7	0.1	0	0.0	0.0
Backbone-Sidechain	285	13.8	31	10.9	1.5	9	3.2	0.4
Sidechain-Sidechain	3	0.1	1	33.3	0.0	0	0.0	0.0
Medium range ($i-j >1$ & $i-j <5$)	376	18.2	77	20.5	3.7	17	4.5	0.8
Backbone-Backbone	216	10.5	53	24.5	2.6	10	4.6	0.5
Backbone-Sidechain	155	7.5	23	14.8	1.1	7	4.5	0.3
Sidechain-Sidechain	5	0.2	1	20.0	0.0	0	0.0	0.0
Long range ($i-j \geq 5$)	191	9.3	39	20.4	1.9	3	1.6	0.1
Backbone-Backbone	82	4.0	20	24.4	1.0	1	1.2	0.0
Backbone-Sidechain	69	3.3	14	20.3	0.7	2	2.9	0.1
Sidechain-Sidechain	40	1.9	5	12.5	0.2	0	0.0	0.0
Inter-chain	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Hydrogen bond	110	5.3	46	41.8	2.2	3	2.7	0.1
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	2062	100.0	212	10.3	10.3	35	1.7	1.7
Backbone-Backbone	741	35.9	75	10.1	3.6	11	1.5	0.5
Backbone-Sidechain	1106	53.6	127	11.5	6.2	23	2.1	1.1
Sidechain-Sidechain	215	10.4	10	4.7	0.5	1	0.5	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 disulfide 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	10	15	65	18	0	108	0.35	1.38	0.27	0.25
2	10	15	58	19	0	102	0.36	1.58	0.27	0.27
3	9	16	69	19	0	113	0.34	1.55	0.26	0.26
4	6	16	66	12	0	100	0.37	1.39	0.29	0.26
5	9	18	54	17	0	98	0.37	1.51	0.29	0.26
6	9	16	59	16	0	100	0.38	1.4	0.31	0.27
7	9	12	55	16	0	92	0.36	1.54	0.29	0.26
8	10	14	51	17	0	92	0.36	1.64	0.31	0.26
9	7	12	54	17	0	90	0.38	1.42	0.3	0.25
10	8	18	56	12	0	94	0.37	1.38	0.28	0.26

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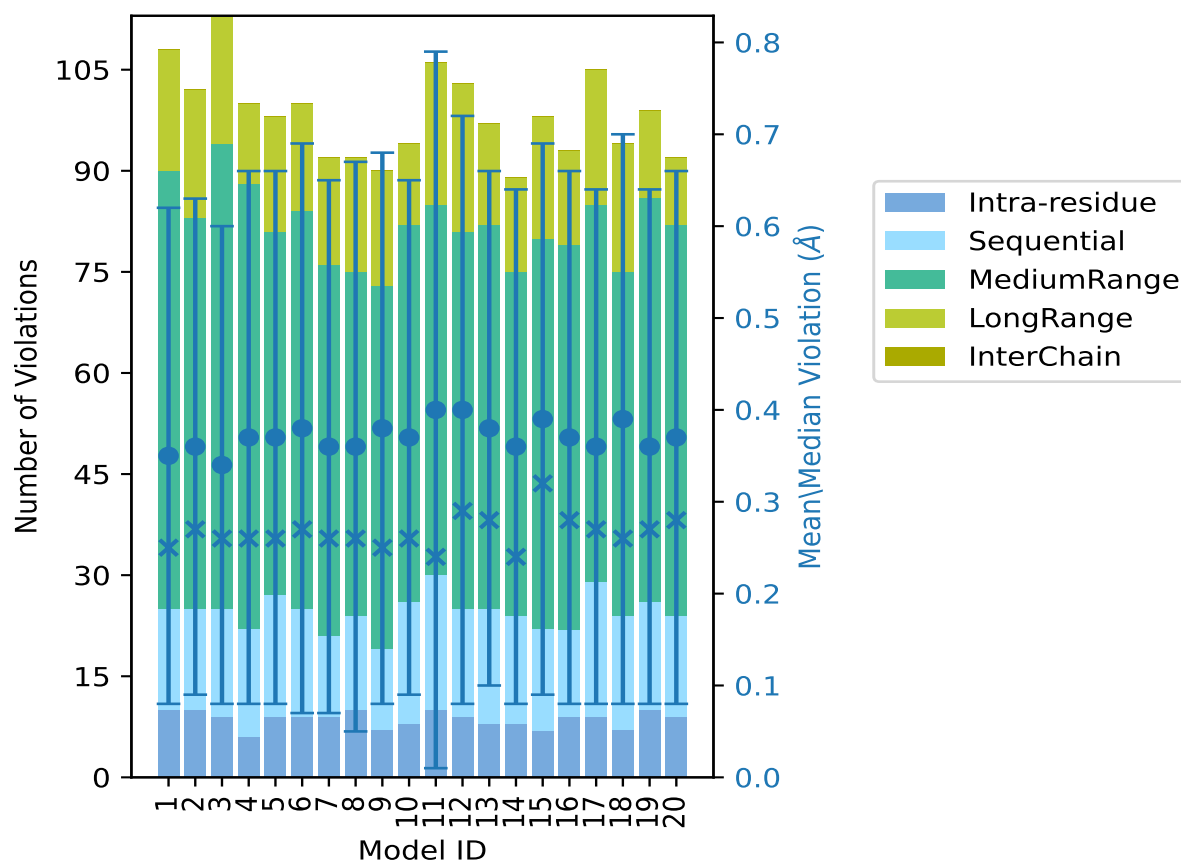
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	10	20	55	21	0	106	0.4	2.36	0.39	0.24
12	9	16	56	22	0	103	0.4	1.67	0.32	0.29
13	8	17	57	15	0	97	0.38	1.34	0.28	0.28
14	8	16	51	14	0	89	0.36	1.31	0.28	0.24
15	7	15	58	18	0	98	0.39	1.34	0.3	0.32
16	9	13	57	14	0	93	0.37	1.54	0.29	0.28
17	9	20	56	20	0	105	0.36	1.52	0.28	0.27
18	7	17	51	19	0	94	0.39	1.45	0.31	0.26
19	10	16	60	13	0	99	0.36	1.55	0.28	0.27
20	9	15	58	10	0	92	0.37	1.53	0.29	0.28

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

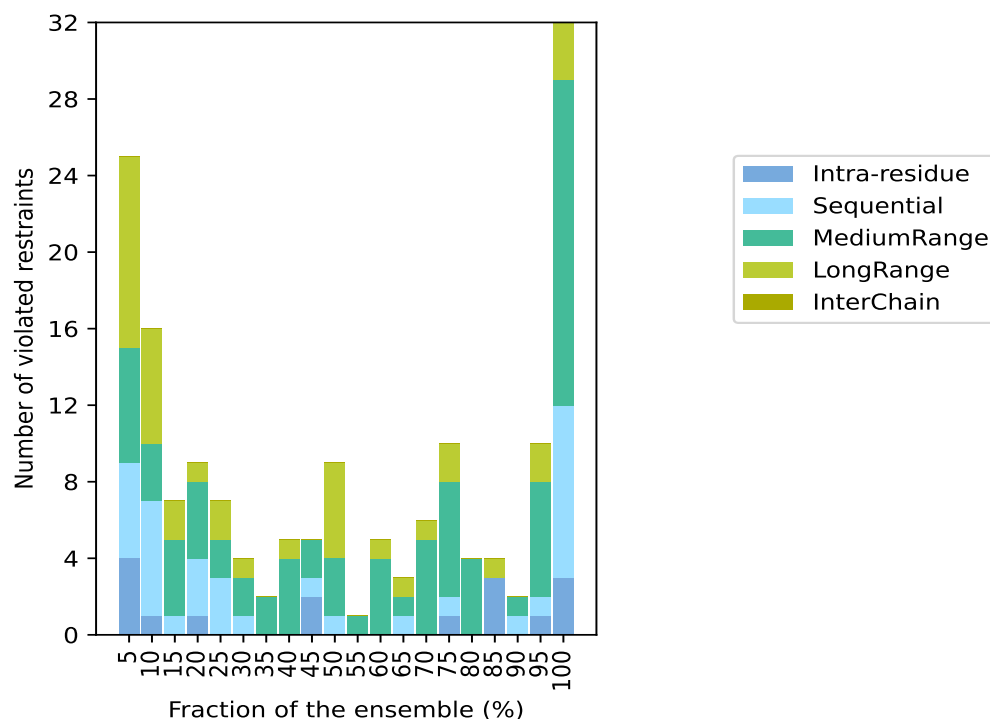
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 1786(IR:794, SQ:541, MR:299, LR:152, IC:0) restraints are not violated in the ensemble.

Number of violated restraints						Fraction of the ensemble	
IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total	Count ⁶	%
4	5	6	10	0	25	1	5.0
1	6	3	6	0	16	2	10.0
0	1	4	2	0	7	3	15.0
1	3	4	1	0	9	4	20.0
0	3	2	2	0	7	5	25.0
0	1	2	1	0	4	6	30.0
0	0	2	0	0	2	7	35.0
0	0	4	1	0	5	8	40.0
2	1	2	0	0	5	9	45.0
0	1	3	5	0	9	10	50.0
0	0	1	0	0	1	11	55.0
0	0	4	1	0	5	12	60.0
0	1	1	1	0	3	13	65.0
0	0	5	1	0	6	14	70.0
1	1	6	2	0	10	15	75.0
0	0	4	0	0	4	16	80.0
3	0	0	1	0	4	17	85.0
0	1	1	0	0	2	18	90.0
1	1	6	2	0	10	19	95.0
3	9	17	3	0	32	20	100.0

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

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

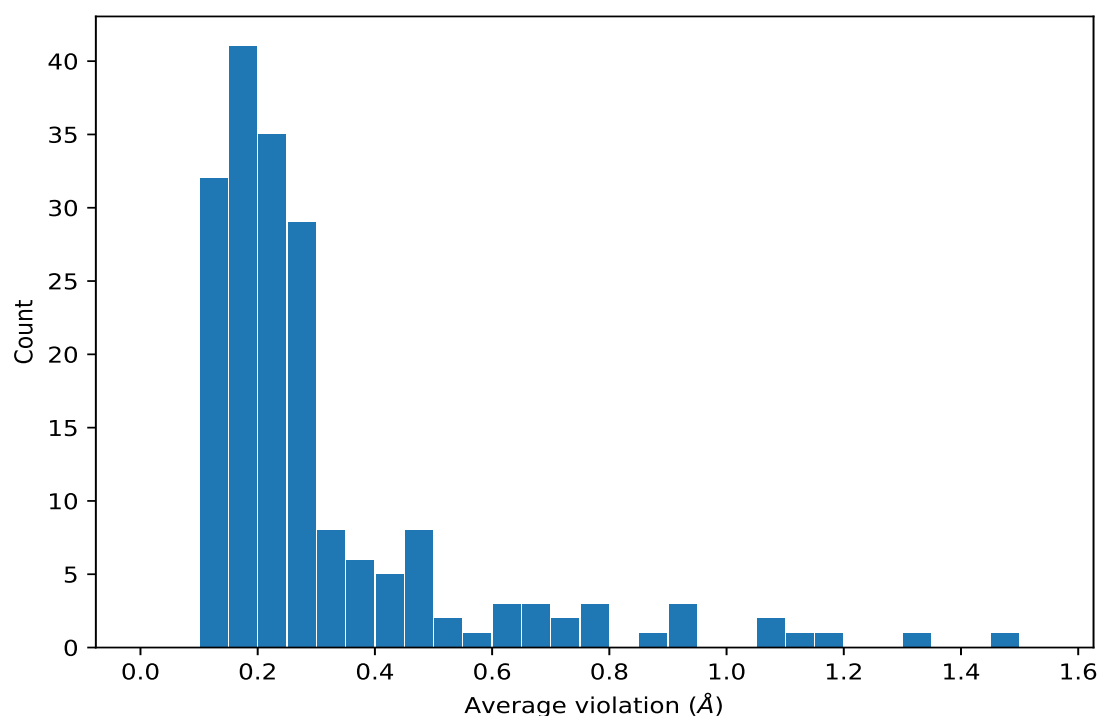
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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)
(3,442)	1:67:V:ALA:H	1:71:V:ALA:HB1	20	1.46	0.11	1.52
(3,298)	1:47:V:LEU:H	1:48:V:ALA:HB1	20	1.3	0.05	1.31
(3,473)	1:70:V:LYS:H	1:71:V:ALA:HB1	20	1.16	0.03	1.15
(3,513)	1:74:V:GLU:H	1:75:V:ALA:HB1	20	1.1	0.03	1.09
(3,5)	1:11:V:VAL:H	1:12:V:ALA:HB1	20	1.09	0.05	1.09
(3,530)	1:76:V:SER:H	1:75:V:ALA:HB1	20	0.86	0.03	0.87
(1,639)	1:100:V:ASP:H	1:55:V:THR:CG2	20	0.77	0.05	0.76
(4,47)	1:57:V:LEU:O	1:60:V:LYS:H	20	0.77	0.14	0.78
(1,176)	1:27:V:ILE:H	1:25:V:ARG:CA	20	0.76	0.2	0.68
(5,24)	1:57:V:LEU:C	1:60:V:LYS:H	20	0.69	0.13	0.68
(4,48)	1:57:V:LEU:O	1:60:V:LYS:N	20	0.66	0.13	0.68
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB2	20	0.62	0.16	0.62
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB3	20	0.62	0.16	0.62
(1,300)	1:52:V:VAL:H	1:96:V:THR:CG2	20	0.61	0.08	0.61
(4,67)	1:68:V:GLY:O	1:71:V:ALA:H	20	0.56	0.06	0.56
(3,317)	1:49:V:TYR:H	1:48:V:ALA:HB1	20	0.5	0.09	0.48

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,76)	1:18:V:GLU:H	1:18:V:GLU:CG	20	0.49	0.04	0.48
(1,94)	1:20:V:ALA:H	1:17:V:LYS:CB	20	0.47	0.09	0.48
(3,535)	1:78:V:PHE:H	1:75:V:ALA:HA	20	0.43	0.08	0.43
(1,394)	1:68:V:GLY:H	1:64:V:ALA:CB	20	0.43	0.08	0.43
(1,81)	1:19:V:ILE:H	1:17:V:LYS:CB	20	0.39	0.05	0.39
(1,107)	1:21:V:LEU:H	1:18:V:GLU:CA	20	0.39	0.08	0.38
(5,55)	1:35:V:MET:C	1:57:V:LEU:H	20	0.36	0.1	0.4
(1,175)	1:27:V:ILE:H	1:25:V:ARG:CB	20	0.36	0.19	0.32
(5,26)	1:61:V:ASP:C	1:65:V:VAL:H	20	0.34	0.08	0.34
(1,475)	1:76:V:SER:H	1:73:V:GLN:CA	20	0.32	0.07	0.3
(1,50)	1:16:V:GLN:H	1:13:V:GLN:CA	20	0.32	0.08	0.33
(5,9)	1:17:V:LYS:C	1:21:V:LEU:H	20	0.31	0.1	0.3
(5,12)	1:21:V:LEU:C	1:25:V:ARG:H	20	0.29	0.12	0.27
(1,556)	1:86:V:ALA:H	1:82:V:LEU:CB	20	0.28	0.06	0.27
(1,104)	1:20:V:ALA:H	1:21:V:LEU:CB	20	0.27	0.05	0.27
(3,325)	1:50:V:ALA:H	1:50:V:ALA:HB1	20	0.26	0.01	0.26
(3,487)	1:72:V:LEU:H	1:71:V:ALA:HB1	20	0.26	0.06	0.28
(1,477)	1:76:V:SER:H	1:74:V:GLU:CA	20	0.26	0.07	0.26
(1,342)	1:61:V:ASP:H	1:60:V:LYS:CB	20	0.18	0.05	0.18
(2,176)	1:43:V:MET:HG2	1:43:V:MET:HE1	20	0.18	0.04	0.18
(2,176)	1:43:V:MET:HG3	1:43:V:MET:HE1	20	0.18	0.04	0.18
(1,127)	1:22:V:ILE:H	1:83:V:LEU:CG	19	0.74	0.11	0.75
(3,650)	1:92:V:VAL:H	1:90:V:ARG:HA	19	0.68	0.28	0.74
(1,456)	1:74:V:GLU:H	1:70:V:LYS:CG	19	0.48	0.35	0.37
(4,109)	1:35:V:MET:O	1:57:V:LEU:H	19	0.41	0.11	0.42
(1,41)	1:15:V:MET:H	1:12:V:ALA:CB	19	0.3	0.09	0.3
(1,254)	1:47:V:LEU:H	1:45:V:ARG:CA	19	0.29	0.08	0.28
(1,108)	1:21:V:LEU:H	1:18:V:GLU:CB	19	0.27	0.06	0.25
(2,177)	1:43:V:MET:HB2	1:43:V:MET:HE1	19	0.21	0.09	0.17
(2,177)	1:43:V:MET:HB3	1:43:V:MET:HE1	19	0.21	0.09	0.17
(5,19)	1:50:V:ALA:C	1:96:V:THR:H	19	0.19	0.06	0.19
(5,39)	1:75:V:ALA:C	1:79:V:ILE:H	19	0.19	0.05	0.17
(1,466)	1:74:V:GLU:H	1:75:V:ALA:CB	19	0.15	0.02	0.14
(5,37)	1:71:V:ALA:C	1:75:V:ALA:H	18	0.26	0.1	0.26
(1,544)	1:84:V:GLY:H	1:85:V:LYS:CB	18	0.17	0.03	0.17
(2,173)	1:43:V:MET:HA	1:43:V:MET:HE1	17	1.07	0.13	1.13
(1,569)	1:87:V:MET:H	1:87:V:MET:CE	17	0.49	0.13	0.54
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD2	17	0.44	0.06	0.42
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD3	17	0.44	0.06	0.42
(5,21)	1:52:V:VAL:C	1:98:V:PHE:H	17	0.16	0.03	0.16
(5,1)	1:9:V:GLN:C	1:13:V:GLN:H	16	0.25	0.09	0.22
(4,110)	1:35:V:MET:O	1:57:V:LEU:N	16	0.24	0.09	0.22

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB2	16	0.23	0.06	0.24
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB3	16	0.23	0.06	0.24
(3,483)	1:72:V:LEU:H	1:69:V:ILE:HA	16	0.18	0.05	0.17
(1,484)	1:78:V:PHE:H	1:75:V:ALA:CB	16	0.17	0.05	0.16
(1,325)	1:60:V:LYS:H	1:57:V:LEU:CA	15	0.28	0.11	0.26
(1,238)	1:43:V:MET:H	1:42:V:GLU:CG	15	0.27	0.1	0.28
(5,25)	1:58:V:ASN:C	1:61:V:ASP:H	15	0.26	0.09	0.22
(3,265)	1:42:V:GLU:H	1:53:V:TYR:H	15	0.26	0.07	0.25
(3,356)	1:53:V:TYR:H	1:42:V:GLU:H	15	0.26	0.07	0.25
(3,495)	1:73:V:GLN:H	1:70:V:LYS:HA	15	0.25	0.07	0.27
(5,47)	1:83:V:LEU:C	1:87:V:MET:H	15	0.22	0.1	0.2
(3,194)	1:27:V:ILE:H	1:27:V:ILE:HB	15	0.2	0.05	0.2
(3,422)	1:65:V:VAL:H	1:62:V:GLU:HA	15	0.2	0.06	0.19
(3,114)	1:21:V:LEU:H	1:18:V:GLU:HA	15	0.19	0.07	0.19
(1,587)	1:92:V:VAL:H	1:89:V:LEU:CG	14	0.52	0.59	0.32
(5,5)	1:13:V:GLN:C	1:17:V:LYS:H	14	0.28	0.12	0.26
(1,18)	1:13:V:GLN:H	1:10:V:ARG:CB	14	0.26	0.1	0.29
(4,17)	1:17:V:LYS:O	1:21:V:LEU:H	14	0.23	0.1	0.22
(5,6)	1:14:V:GLU:C	1:18:V:GLU:H	14	0.22	0.12	0.16
(1,536)	1:83:V:LEU:H	1:85:V:LYS:CG	14	0.21	0.08	0.2
(1,612)	1:96:V:THR:H	1:50:V:ALA:CB	14	0.2	0.07	0.18
(1,386)	1:67:V:ALA:H	1:66:V:LYS:CD	13	0.27	0.09	0.26
(5,10)	1:18:V:GLU:C	1:22:V:ILE:H	13	0.25	0.06	0.23
(5,14)	1:37:V:THR:H	1:55:V:THR:C	13	0.15	0.03	0.15
(2,65)	1:19:V:ILE:HG13	1:87:V:MET:HE1	12	0.73	0.49	0.59
(3,177)	1:26:V:GLU:H	1:22:V:ILE:HA	12	0.32	0.2	0.26
(5,2)	1:10:V:ARG:C	1:14:V:GLU:H	12	0.26	0.14	0.22
(3,403)	1:61:V:ASP:H	1:64:V:ALA:HB1	12	0.25	0.11	0.2
(5,45)	1:81:V:SER:C	1:85:V:LYS:H	12	0.22	0.12	0.19
(4,68)	1:68:V:GLY:O	1:71:V:ALA:N	12	0.15	0.03	0.16
(4,73)	1:71:V:ALA:O	1:75:V:ALA:H	11	0.28	0.11	0.27
(4,49)	1:58:V:ASN:O	1:61:V:ASP:H	11	0.23	0.09	0.21
(3,42)	1:15:V:MET:H	1:12:V:ALA:HA	11	0.2	0.06	0.2
(5,48)	1:84:V:GLY:C	1:89:V:LEU:H	10	0.24	0.13	0.2
(3,280)	1:44:V:SER:H	1:51:V:LYS:H	10	0.23	0.08	0.23
(3,338)	1:51:V:LYS:H	1:44:V:SER:H	10	0.23	0.08	0.23
(1,287)	1:51:V:LYS:H	1:42:V:GLU:CG	10	0.21	0.1	0.17
(3,17)	1:13:V:GLN:H	1:10:V:ARG:HA	10	0.19	0.08	0.17
(5,31)	1:66:V:LYS:C	1:70:V:LYS:H	10	0.18	0.05	0.16
(1,216)	1:40:V:GLY:H	1:39:V:SER:CB	10	0.18	0.05	0.16
(5,49)	1:49:V:TYR:C	1:44:V:SER:H	10	0.16	0.05	0.14
(1,327)	1:60:V:LYS:H	1:58:V:ASN:CA	10	0.15	0.05	0.13

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,465)	1:74:V:GLU:H	1:74:V:GLU:CG	9	0.48	0.03	0.49
(3,512)	1:74:V:GLU:H	1:74:V:GLU:HG2	9	0.38	0.05	0.39
(3,512)	1:74:V:GLU:H	1:74:V:GLU:HG3	9	0.38	0.05	0.39
(4,23)	1:21:V:LEU:O	1:25:V:ARG:H	9	0.23	0.07	0.25
(5,41)	1:77:V:GLY:C	1:81:V:SER:H	9	0.19	0.1	0.16
(5,27)	1:62:V:GLU:C	1:66:V:LYS:H	9	0.15	0.03	0.14
(1,90)	1:19:V:ILE:H	1:20:V:ALA:CB	9	0.13	0.02	0.13
(3,334)	1:51:V:LYS:H	1:41:V:VAL:HA	8	0.22	0.07	0.21
(5,36)	1:70:V:LYS:C	1:74:V:GLU:H	8	0.17	0.05	0.16
(1,476)	1:76:V:SER:H	1:74:V:GLU:CB	8	0.16	0.05	0.14
(4,51)	1:61:V:ASP:O	1:65:V:VAL:H	8	0.16	0.06	0.14
(5,44)	1:80:V:ARG:C	1:84:V:GLY:H	8	0.16	0.04	0.15
(5,42)	1:78:V:PHE:C	1:82:V:LEU:H	8	0.14	0.03	0.14
(3,100)	1:20:V:ALA:H	1:16:V:GLN:HB2	7	0.31	0.07	0.34
(3,100)	1:20:V:ALA:H	1:16:V:GLN:HB3	7	0.31	0.07	0.34
(4,50)	1:58:V:ASN:O	1:61:V:ASP:N	7	0.24	0.07	0.22
(4,18)	1:17:V:LYS:O	1:21:V:LEU:N	7	0.2	0.07	0.2
(4,1)	1:9:V:GLN:O	1:13:V:GLN:H	7	0.19	0.09	0.17
(3,32)	1:14:V:GLU:H	1:11:V:VAL:HA	7	0.18	0.04	0.18
(4,9)	1:13:V:GLN:O	1:17:V:LYS:H	6	0.22	0.05	0.21
(1,278)	1:50:V:ALA:H	1:93:V:PRO:CG	6	0.19	0.08	0.17
(1,471)	1:75:V:ALA:H	1:74:V:GLU:CB	6	0.18	0.03	0.18
(5,32)	1:67:V:ALA:C	1:71:V:ALA:H	6	0.18	0.05	0.15
(3,54)	1:16:V:GLN:H	1:13:V:GLN:HA	6	0.15	0.05	0.14
(4,3)	1:10:V:ARG:O	1:14:V:GLU:H	5	0.27	0.12	0.2
(5,28)	1:63:V:ASP:C	1:67:V:ALA:H	5	0.24	0.05	0.24
(1,339)	1:61:V:ASP:H	1:60:V:LYS:CE	5	0.21	0.07	0.21
(5,11)	1:19:V:ILE:C	1:23:V:LEU:H	5	0.2	0.06	0.2
(4,75)	1:73:V:GLN:O	1:76:V:SER:H	5	0.2	0.09	0.17
(4,10)	1:13:V:GLN:O	1:17:V:LYS:N	5	0.17	0.05	0.14
(3,355)	1:53:V:TYR:H	1:41:V:VAL:HA	5	0.16	0.04	0.15
(4,19)	1:18:V:GLU:O	1:22:V:ILE:H	5	0.16	0.04	0.15
(1,525)	1:82:V:LEU:H	1:83:V:LEU:CB	5	0.14	0.02	0.15
(5,22)	1:54:V:VAL:H	1:98:V:PHE:C	5	0.13	0.02	0.12
(3,303)	1:48:V:ALA:H	1:47:V:LEU:HG	5	0.12	0.03	0.11
(2,252)	1:66:V:LYS:HD2	1:66:V:LYS:HA	4	0.49	0.06	0.49
(2,252)	1:66:V:LYS:HD3	1:66:V:LYS:HA	4	0.49	0.06	0.49
(4,107)	1:30:V:PRO:O	1:33:V:GLY:H	4	0.23	0.11	0.18
(4,89)	1:81:V:SER:O	1:85:V:LYS:H	4	0.2	0.1	0.18
(1,580)	1:91:V:ILE:H	1:90:V:ARG:CB	4	0.2	0.07	0.22
(1,174)	1:27:V:ILE:H	1:24:V:GLN:CA	4	0.2	0.07	0.19
(5,4)	1:12:V:ALA:C	1:16:V:GLN:H	4	0.19	0.05	0.19

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,221)	1:41:V:VAL:H	1:38:V:VAL:CB	4	0.18	0.06	0.16
(5,7)	1:15:V:MET:C	1:19:V:ILE:H	4	0.17	0.06	0.15
(1,157)	1:25:V:ARG:H	1:24:V:GLN:CB	4	0.17	0.05	0.18
(1,272)	1:49:V:TYR:H	1:48:V:ALA:CB	4	0.14	0.02	0.14
(5,18)	1:50:V:ALA:H	1:94:V:GLU:C	4	0.12	0.01	0.12
(4,81)	1:77:V:GLY:O	1:81:V:SER:H	3	0.26	0.07	0.3
(1,269)	1:49:V:TYR:H	1:44:V:SER:CB	3	0.25	0.08	0.31
(4,93)	1:83:V:LEU:O	1:87:V:MET:H	3	0.21	0.01	0.21
(4,76)	1:73:V:GLN:O	1:76:V:SER:N	3	0.19	0.06	0.2
(3,165)	1:25:V:ARG:H	1:21:V:LEU:HG	3	0.18	0.07	0.15
(5,8)	1:16:V:GLN:C	1:20:V:ALA:H	3	0.17	0.04	0.17
(1,604)	1:95:V:LEU:H	1:80:V:ARG:CB	3	0.16	0.03	0.16
(4,7)	1:12:V:ALA:O	1:16:V:GLN:H	3	0.15	0.02	0.16
(4,55)	1:63:V:ASP:O	1:67:V:ALA:H	3	0.15	0.03	0.13
(1,319)	1:58:V:ASN:H	1:57:V:LEU:CB	3	0.14	0.03	0.14
(4,52)	1:61:V:ASP:O	1:65:V:VAL:N	3	0.14	0.01	0.14
(5,30)	1:65:V:VAL:C	1:69:V:ILE:H	3	0.13	0.01	0.13
(5,33)	1:68:V:GLY:C	1:72:V:LEU:H	3	0.1	0.0	0.1
(2,36)	1:15:V:MET:HE1	1:91:V:ILE:HD11	2	0.92	0.75	0.92
(2,36)	1:15:V:MET:HE1	1:91:V:ILE:HD12	2	0.92	0.75	0.92
(2,36)	1:15:V:MET:HE1	1:91:V:ILE:HD13	2	0.92	0.75	0.92
(3,286)	1:46:V:ASP:H	1:47:V:LEU:HG	2	0.45	0.1	0.45
(4,95)	1:84:V:GLY:O	1:89:V:LEU:H	2	0.34	0.12	0.34
(4,4)	1:10:V:ARG:O	1:14:V:GLU:N	2	0.28	0.1	0.28
(4,108)	1:30:V:PRO:O	1:33:V:GLY:N	2	0.26	0.08	0.26
(4,90)	1:81:V:SER:O	1:85:V:LYS:N	2	0.22	0.07	0.22
(4,82)	1:77:V:GLY:O	1:81:V:SER:N	2	0.22	0.02	0.22
(3,370)	1:55:V:THR:H	1:37:V:THR:HB	2	0.19	0.06	0.19
(3,278)	1:44:V:SER:H	1:50:V:ALA:HA	2	0.18	0.06	0.18
(4,74)	1:71:V:ALA:O	1:75:V:ALA:N	2	0.18	0.02	0.18
(4,15)	1:16:V:GLN:O	1:20:V:ALA:H	2	0.16	0.04	0.16
(1,606)	1:95:V:LEU:H	1:94:V:GLU:CG	2	0.16	0.04	0.16
(5,29)	1:64:V:ALA:C	1:68:V:GLY:H	2	0.16	0.05	0.16
(1,586)	1:91:V:ILE:H	1:92:V:VAL:CA	2	0.15	0.01	0.15
(3,126)	1:22:V:ILE:H	1:19:V:ILE:HA	2	0.15	0.03	0.15
(4,96)	1:84:V:GLY:O	1:89:V:LEU:N	2	0.14	0.03	0.14
(1,281)	1:50:V:ALA:H	1:94:V:GLU:CB	2	0.14	0.03	0.14
(5,50)	1:40:V:GLY:C	1:53:V:TYR:H	2	0.14	0.01	0.14
(1,128)	1:23:V:LEU:H	1:18:V:GLU:CA	2	0.13	0.02	0.13
(2,332)	1:87:V:MET:HE1	1:87:V:MET:HG2	2	0.13	0.0	0.13
(2,332)	1:87:V:MET:HE1	1:87:V:MET:HG3	2	0.13	0.0	0.13
(1,243)	1:44:V:SER:H	1:43:V:MET:CB	2	0.12	0.01	0.12

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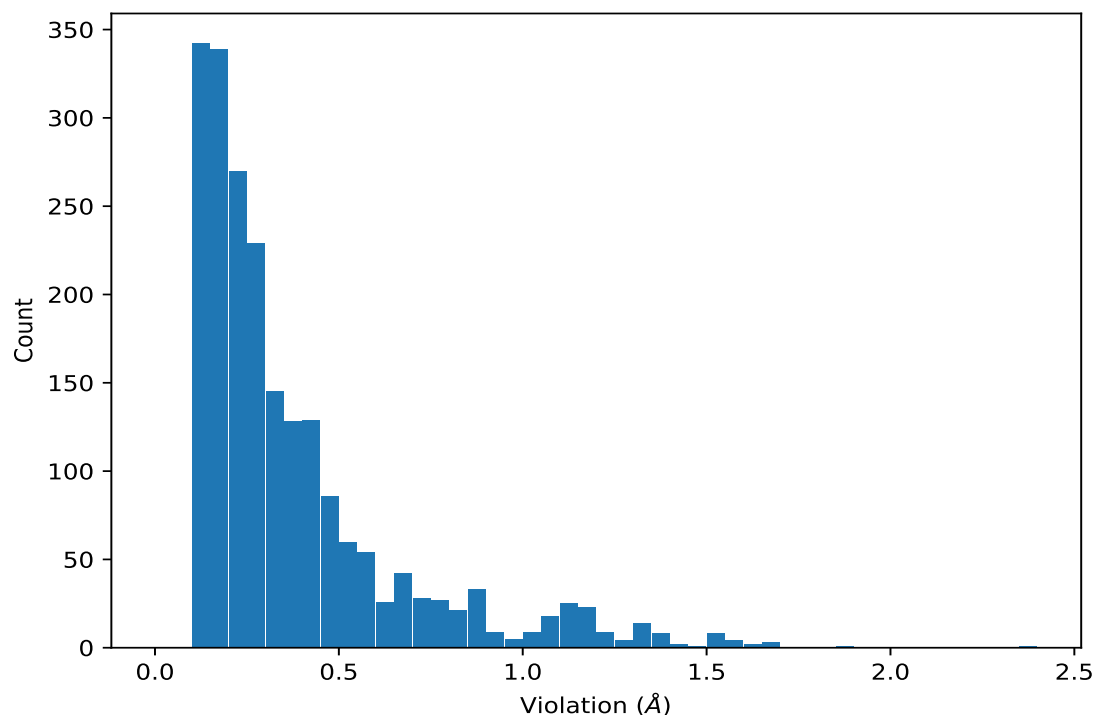
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(3,193)	1:27:V:ILE:H	1:26:V:GLU:HA	2	0.12	0.0	0.12
(4,20)	1:18:V:GLU:O	1:22:V:ILE:N	2	0.12	0.0	0.12
(3,189)	1:27:V:ILE:H	1:25:V:ARG:HA	2	0.12	0.0	0.12
(1,474)	1:75:V:ALA:H	1:76:V:SER:CB	2	0.11	0.0	0.11

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)
(1,587)	1:92:V:VAL:H	1:89:V:LEU:CG	11	2.36
(2,65)	1:19:V:ILE:HG13	1:87:V:MET:HE1	11	1.89
(2,36)	1:15:V:MET:HE1	1:91:V:ILE:HD11	12	1.67
(2,36)	1:15:V:MET:HE1	1:91:V:ILE:HD12	12	1.67
(2,36)	1:15:V:MET:HE1	1:91:V:ILE:HD13	12	1.67
(3,442)	1:67:V:ALA:H	1:71:V:ALA:HB1	8	1.64
(3,442)	1:67:V:ALA:H	1:71:V:ALA:HB1	11	1.63
(3,442)	1:67:V:ALA:H	1:71:V:ALA:HB1	2	1.58
(3,442)	1:67:V:ALA:H	1:71:V:ALA:HB1	3	1.55
(3,442)	1:67:V:ALA:H	1:71:V:ALA:HB1	12	1.55
(3,442)	1:67:V:ALA:H	1:71:V:ALA:HB1	19	1.55
(3,442)	1:67:V:ALA:H	1:71:V:ALA:HB1	7	1.54
(3,442)	1:67:V:ALA:H	1:71:V:ALA:HB1	16	1.54
(3,442)	1:67:V:ALA:H	1:71:V:ALA:HB1	20	1.53
(2,88)	1:22:V:ILE:HD11	1:87:V:MET:HE1	11	1.53
(2,88)	1:22:V:ILE:HD12	1:87:V:MET:HE1	11	1.53
(2,88)	1:22:V:ILE:HD13	1:87:V:MET:HE1	11	1.53
(3,442)	1:67:V:ALA:H	1:71:V:ALA:HB1	17	1.52
(3,442)	1:67:V:ALA:H	1:71:V:ALA:HB1	5	1.51
(1,456)	1:74:V:GLU:H	1:70:V:LYS:CG	18	1.45
(3,442)	1:67:V:ALA:H	1:71:V:ALA:HB1	9	1.42
(3,442)	1:67:V:ALA:H	1:71:V:ALA:HB1	6	1.4
(3,442)	1:67:V:ALA:H	1:71:V:ALA:HB1	4	1.39
(3,442)	1:67:V:ALA:H	1:71:V:ALA:HB1	1	1.38
(3,442)	1:67:V:ALA:H	1:71:V:ALA:HB1	10	1.38
(3,298)	1:47:V:LEU:H	1:48:V:ALA:HB1	20	1.38
(3,298)	1:47:V:LEU:H	1:48:V:ALA:HB1	9	1.37
(3,298)	1:47:V:LEU:H	1:48:V:ALA:HB1	5	1.36
(3,298)	1:47:V:LEU:H	1:48:V:ALA:HB1	7	1.36
(1,456)	1:74:V:GLU:H	1:70:V:LYS:CG	4	1.35
(3,442)	1:67:V:ALA:H	1:71:V:ALA:HB1	13	1.34
(3,298)	1:47:V:LEU:H	1:48:V:ALA:HB1	15	1.34
(3,298)	1:47:V:LEU:H	1:48:V:ALA:HB1	19	1.34
(3,298)	1:47:V:LEU:H	1:48:V:ALA:HB1	17	1.32
(3,442)	1:67:V:ALA:H	1:71:V:ALA:HB1	14	1.31
(3,442)	1:67:V:ALA:H	1:71:V:ALA:HB1	15	1.31
(3,298)	1:47:V:LEU:H	1:48:V:ALA:HB1	6	1.31
(3,298)	1:47:V:LEU:H	1:48:V:ALA:HB1	11	1.31
(3,298)	1:47:V:LEU:H	1:48:V:ALA:HB1	12	1.31
(3,298)	1:47:V:LEU:H	1:48:V:ALA:HB1	16	1.31
(3,298)	1:47:V:LEU:H	1:48:V:ALA:HB1	18	1.31
(3,298)	1:47:V:LEU:H	1:48:V:ALA:HB1	1	1.3
(1,587)	1:92:V:VAL:H	1:89:V:LEU:CG	15	1.3

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,176)	1:27:V:ILE:H	1:25:V:ARG:CA	6	1.3
(3,298)	1:47:V:LEU:H	1:48:V:ALA:HB1	8	1.29
(3,298)	1:47:V:LEU:H	1:48:V:ALA:HB1	4	1.27
(3,298)	1:47:V:LEU:H	1:48:V:ALA:HB1	13	1.27
(3,298)	1:47:V:LEU:H	1:48:V:ALA:HB1	3	1.25
(3,298)	1:47:V:LEU:H	1:48:V:ALA:HB1	2	1.24
(3,442)	1:67:V:ALA:H	1:71:V:ALA:HB1	18	1.23
(3,650)	1:92:V:VAL:H	1:90:V:ARG:HA	1	1.22
(2,65)	1:19:V:ILE:HG13	1:87:V:MET:HE1	8	1.22
(3,473)	1:70:V:LYS:H	1:71:V:ALA:HB1	5	1.21
(3,473)	1:70:V:LYS:H	1:71:V:ALA:HB1	12	1.21
(3,473)	1:70:V:LYS:H	1:71:V:ALA:HB1	20	1.21
(3,298)	1:47:V:LEU:H	1:48:V:ALA:HB1	10	1.21
(3,473)	1:70:V:LYS:H	1:71:V:ALA:HB1	19	1.2
(3,473)	1:70:V:LYS:H	1:71:V:ALA:HB1	17	1.19
(1,176)	1:27:V:ILE:H	1:25:V:ARG:CA	18	1.19
(3,473)	1:70:V:LYS:H	1:71:V:ALA:HB1	4	1.18
(3,473)	1:70:V:LYS:H	1:71:V:ALA:HB1	11	1.18
(3,473)	1:70:V:LYS:H	1:71:V:ALA:HB1	16	1.18
(3,298)	1:47:V:LEU:H	1:48:V:ALA:HB1	14	1.18
(3,5)	1:11:V:VAL:H	1:12:V:ALA:HB1	10	1.18
(2,173)	1:43:V:MET:HA	1:43:V:MET:HE1	18	1.18
(2,173)	1:43:V:MET:HA	1:43:V:MET:HE1	2	1.17
(2,173)	1:43:V:MET:HA	1:43:V:MET:HE1	6	1.17
(3,473)	1:70:V:LYS:H	1:71:V:ALA:HB1	9	1.16
(3,5)	1:11:V:VAL:H	1:12:V:ALA:HB1	5	1.16
(3,5)	1:11:V:VAL:H	1:12:V:ALA:HB1	20	1.16
(2,173)	1:43:V:MET:HA	1:43:V:MET:HE1	9	1.16
(2,173)	1:43:V:MET:HA	1:43:V:MET:HE1	15	1.16
(3,513)	1:74:V:GLU:H	1:75:V:ALA:HB1	3	1.15
(3,473)	1:70:V:LYS:H	1:71:V:ALA:HB1	1	1.15
(3,473)	1:70:V:LYS:H	1:71:V:ALA:HB1	3	1.15
(3,473)	1:70:V:LYS:H	1:71:V:ALA:HB1	8	1.15
(3,473)	1:70:V:LYS:H	1:71:V:ALA:HB1	10	1.15
(3,5)	1:11:V:VAL:H	1:12:V:ALA:HB1	19	1.15
(2,173)	1:43:V:MET:HA	1:43:V:MET:HE1	7	1.15
(2,173)	1:43:V:MET:HA	1:43:V:MET:HE1	20	1.15
(3,513)	1:74:V:GLU:H	1:75:V:ALA:HB1	1	1.14
(3,513)	1:74:V:GLU:H	1:75:V:ALA:HB1	14	1.14
(3,513)	1:74:V:GLU:H	1:75:V:ALA:HB1	15	1.14
(3,473)	1:70:V:LYS:H	1:71:V:ALA:HB1	2	1.14
(3,473)	1:70:V:LYS:H	1:71:V:ALA:HB1	6	1.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,473)	1:70:V:LYS:H	1:71:V:ALA:HB1	7	1.14
(3,473)	1:70:V:LYS:H	1:71:V:ALA:HB1	15	1.14
(2,173)	1:43:V:MET:HA	1:43:V:MET:HE1	8	1.13
(2,173)	1:43:V:MET:HA	1:43:V:MET:HE1	13	1.13
(3,513)	1:74:V:GLU:H	1:75:V:ALA:HB1	13	1.12
(3,473)	1:70:V:LYS:H	1:71:V:ALA:HB1	14	1.12
(3,5)	1:11:V:VAL:H	1:12:V:ALA:HB1	16	1.12
(3,5)	1:11:V:VAL:H	1:12:V:ALA:HB1	17	1.12
(2,173)	1:43:V:MET:HA	1:43:V:MET:HE1	5	1.12
(2,173)	1:43:V:MET:HA	1:43:V:MET:HE1	12	1.12
(3,513)	1:74:V:GLU:H	1:75:V:ALA:HB1	7	1.11
(3,513)	1:74:V:GLU:H	1:75:V:ALA:HB1	16	1.11
(3,473)	1:70:V:LYS:H	1:71:V:ALA:HB1	18	1.11
(3,5)	1:11:V:VAL:H	1:12:V:ALA:HB1	2	1.11
(3,5)	1:11:V:VAL:H	1:12:V:ALA:HB1	8	1.11
(2,173)	1:43:V:MET:HA	1:43:V:MET:HE1	19	1.11
(2,65)	1:19:V:ILE:HG13	1:87:V:MET:HE1	12	1.11
(3,513)	1:74:V:GLU:H	1:75:V:ALA:HB1	17	1.1
(3,5)	1:11:V:VAL:H	1:12:V:ALA:HB1	1	1.1
(3,5)	1:11:V:VAL:H	1:12:V:ALA:HB1	7	1.1
(3,513)	1:74:V:GLU:H	1:75:V:ALA:HB1	2	1.09
(3,513)	1:74:V:GLU:H	1:75:V:ALA:HB1	11	1.09
(3,513)	1:74:V:GLU:H	1:75:V:ALA:HB1	18	1.09
(3,473)	1:70:V:LYS:H	1:71:V:ALA:HB1	13	1.09
(3,513)	1:74:V:GLU:H	1:75:V:ALA:HB1	4	1.08
(3,513)	1:74:V:GLU:H	1:75:V:ALA:HB1	9	1.08
(3,513)	1:74:V:GLU:H	1:75:V:ALA:HB1	12	1.08
(3,513)	1:74:V:GLU:H	1:75:V:ALA:HB1	19	1.08
(3,513)	1:74:V:GLU:H	1:75:V:ALA:HB1	20	1.08
(3,5)	1:11:V:VAL:H	1:12:V:ALA:HB1	6	1.08
(3,513)	1:74:V:GLU:H	1:75:V:ALA:HB1	5	1.07
(3,513)	1:74:V:GLU:H	1:75:V:ALA:HB1	6	1.07
(3,513)	1:74:V:GLU:H	1:75:V:ALA:HB1	10	1.07
(3,5)	1:11:V:VAL:H	1:12:V:ALA:HB1	4	1.07
(2,173)	1:43:V:MET:HA	1:43:V:MET:HE1	10	1.07
(3,5)	1:11:V:VAL:H	1:12:V:ALA:HB1	9	1.06
(3,5)	1:11:V:VAL:H	1:12:V:ALA:HB1	3	1.05
(3,5)	1:11:V:VAL:H	1:12:V:ALA:HB1	18	1.05
(4,47)	1:57:V:LEU:O	1:60:V:LYS:H	6	1.04
(3,5)	1:11:V:VAL:H	1:12:V:ALA:HB1	12	1.04
(3,5)	1:11:V:VAL:H	1:12:V:ALA:HB1	15	1.04
(3,513)	1:74:V:GLU:H	1:75:V:ALA:HB1	8	1.02

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,5)	1:11:V:VAL:H	1:12:V:ALA:HB1	13	1.01
(2,173)	1:43:V:MET:HA	1:43:V:MET:HE1	3	1.01
(5,24)	1:57:V:LEU:C	1:60:V:LYS:H	6	1.0
(3,5)	1:11:V:VAL:H	1:12:V:ALA:HB1	11	1.0
(3,5)	1:11:V:VAL:H	1:12:V:ALA:HB1	14	1.0
(2,65)	1:19:V:ILE:HG13	1:87:V:MET:HE1	9	0.98
(4,47)	1:57:V:LEU:O	1:60:V:LYS:H	15	0.96
(3,650)	1:92:V:VAL:H	1:90:V:ARG:HA	6	0.96
(3,650)	1:92:V:VAL:H	1:90:V:ARG:HA	15	0.95
(1,127)	1:22:V:ILE:H	1:83:V:LEU:CG	10	0.95
(3,650)	1:92:V:VAL:H	1:90:V:ARG:HA	9	0.94
(4,48)	1:57:V:LEU:O	1:60:V:LYS:N	6	0.92
(3,530)	1:76:V:SER:H	1:75:V:ALA:HB1	4	0.92
(1,175)	1:27:V:ILE:H	1:25:V:ARG:CB	6	0.92
(4,47)	1:57:V:LEU:O	1:60:V:LYS:H	12	0.91
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB2	14	0.91
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB3	14	0.91
(2,65)	1:19:V:ILE:HG13	1:87:V:MET:HE1	5	0.91
(3,530)	1:76:V:SER:H	1:75:V:ALA:HB1	3	0.9
(3,650)	1:92:V:VAL:H	1:90:V:ARG:HA	4	0.89
(3,650)	1:92:V:VAL:H	1:90:V:ARG:HA	11	0.89
(3,530)	1:76:V:SER:H	1:75:V:ALA:HB1	1	0.89
(3,530)	1:76:V:SER:H	1:75:V:ALA:HB1	11	0.89
(3,530)	1:76:V:SER:H	1:75:V:ALA:HB1	20	0.89
(1,176)	1:27:V:ILE:H	1:25:V:ARG:CA	4	0.89
(1,176)	1:27:V:ILE:H	1:25:V:ARG:CA	11	0.89
(1,127)	1:22:V:ILE:H	1:83:V:LEU:CG	9	0.89
(4,47)	1:57:V:LEU:O	1:60:V:LYS:H	13	0.88
(4,47)	1:57:V:LEU:O	1:60:V:LYS:H	16	0.88
(3,530)	1:76:V:SER:H	1:75:V:ALA:HB1	13	0.88
(3,530)	1:76:V:SER:H	1:75:V:ALA:HB1	16	0.88
(3,530)	1:76:V:SER:H	1:75:V:ALA:HB1	2	0.87
(3,530)	1:76:V:SER:H	1:75:V:ALA:HB1	6	0.87
(3,530)	1:76:V:SER:H	1:75:V:ALA:HB1	10	0.87
(3,530)	1:76:V:SER:H	1:75:V:ALA:HB1	12	0.87
(3,530)	1:76:V:SER:H	1:75:V:ALA:HB1	17	0.87
(1,639)	1:100:V:ASP:H	1:55:V:THR:CG2	13	0.87
(1,176)	1:27:V:ILE:H	1:25:V:ARG:CA	10	0.87
(5,24)	1:57:V:LEU:C	1:60:V:LYS:H	15	0.86
(1,639)	1:100:V:ASP:H	1:55:V:THR:CG2	5	0.86
(1,127)	1:22:V:ILE:H	1:83:V:LEU:CG	12	0.86
(3,650)	1:92:V:VAL:H	1:90:V:ARG:HA	18	0.85

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,530)	1:76:V:SER:H	1:75:V:ALA:HB1	5	0.85
(3,530)	1:76:V:SER:H	1:75:V:ALA:HB1	14	0.85
(3,530)	1:76:V:SER:H	1:75:V:ALA:HB1	15	0.85
(3,530)	1:76:V:SER:H	1:75:V:ALA:HB1	18	0.85
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB2	20	0.85
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB3	20	0.85
(2,173)	1:43:V:MET:HA	1:43:V:MET:HE1	16	0.85
(1,639)	1:100:V:ASP:H	1:55:V:THR:CG2	3	0.85
(1,176)	1:27:V:ILE:H	1:25:V:ARG:CA	7	0.85
(1,127)	1:22:V:ILE:H	1:83:V:LEU:CG	13	0.85
(4,47)	1:57:V:LEU:O	1:60:V:LYS:H	17	0.84
(3,530)	1:76:V:SER:H	1:75:V:ALA:HB1	19	0.84
(4,48)	1:57:V:LEU:O	1:60:V:LYS:N	15	0.83
(4,47)	1:57:V:LEU:O	1:60:V:LYS:H	11	0.83
(4,47)	1:57:V:LEU:O	1:60:V:LYS:H	19	0.83
(3,530)	1:76:V:SER:H	1:75:V:ALA:HB1	7	0.83
(2,173)	1:43:V:MET:HA	1:43:V:MET:HE1	14	0.83
(1,639)	1:100:V:ASP:H	1:55:V:THR:CG2	20	0.83
(1,176)	1:27:V:ILE:H	1:25:V:ARG:CA	8	0.83
(3,650)	1:92:V:VAL:H	1:90:V:ARG:HA	16	0.82
(3,530)	1:76:V:SER:H	1:75:V:ALA:HB1	9	0.82
(1,127)	1:22:V:ILE:H	1:83:V:LEU:CG	7	0.82
(5,24)	1:57:V:LEU:C	1:60:V:LYS:H	12	0.8
(5,24)	1:57:V:LEU:C	1:60:V:LYS:H	13	0.8
(5,24)	1:57:V:LEU:C	1:60:V:LYS:H	17	0.8
(4,47)	1:57:V:LEU:O	1:60:V:LYS:H	5	0.8
(4,47)	1:57:V:LEU:O	1:60:V:LYS:H	18	0.8
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB2	13	0.8
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB3	13	0.8
(1,639)	1:100:V:ASP:H	1:55:V:THR:CG2	11	0.8
(1,639)	1:100:V:ASP:H	1:55:V:THR:CG2	12	0.8
(4,48)	1:57:V:LEU:O	1:60:V:LYS:N	13	0.79
(3,649)	1:91:V:ILE:H	1:91:V:ILE:HG12	12	0.79
(3,649)	1:91:V:ILE:H	1:91:V:ILE:HG13	12	0.79
(3,530)	1:76:V:SER:H	1:75:V:ALA:HB1	8	0.79
(1,639)	1:100:V:ASP:H	1:55:V:THR:CG2	9	0.79
(5,24)	1:57:V:LEU:C	1:60:V:LYS:H	16	0.78
(4,48)	1:57:V:LEU:O	1:60:V:LYS:N	16	0.78
(1,639)	1:100:V:ASP:H	1:55:V:THR:CG2	1	0.78
(1,639)	1:100:V:ASP:H	1:55:V:THR:CG2	18	0.78
(1,176)	1:27:V:ILE:H	1:25:V:ARG:CA	12	0.78
(1,127)	1:22:V:ILE:H	1:83:V:LEU:CG	2	0.78

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,127)	1:22:V:ILE:H	1:83:V:LEU:CG	14	0.78
(1,127)	1:22:V:ILE:H	1:83:V:LEU:CG	17	0.78
(3,650)	1:92:V:VAL:H	1:90:V:ARG:HA	14	0.77
(1,639)	1:100:V:ASP:H	1:55:V:THR:CG2	14	0.77
(1,127)	1:22:V:ILE:H	1:83:V:LEU:CG	1	0.77
(4,48)	1:57:V:LEU:O	1:60:V:LYS:N	12	0.76
(4,47)	1:57:V:LEU:O	1:60:V:LYS:H	8	0.76
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB2	11	0.76
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB3	11	0.76
(2,173)	1:43:V:MET:HA	1:43:V:MET:HE1	1	0.76
(1,639)	1:100:V:ASP:H	1:55:V:THR:CG2	7	0.76
(1,639)	1:100:V:ASP:H	1:55:V:THR:CG2	6	0.75
(1,639)	1:100:V:ASP:H	1:55:V:THR:CG2	8	0.75
(1,639)	1:100:V:ASP:H	1:55:V:THR:CG2	17	0.75
(1,176)	1:27:V:ILE:H	1:25:V:ARG:CA	2	0.75
(1,127)	1:22:V:ILE:H	1:83:V:LEU:CG	15	0.75
(5,24)	1:57:V:LEU:C	1:60:V:LYS:H	11	0.74
(4,47)	1:57:V:LEU:O	1:60:V:LYS:H	4	0.74
(4,47)	1:57:V:LEU:O	1:60:V:LYS:H	9	0.74
(3,650)	1:92:V:VAL:H	1:90:V:ARG:HA	3	0.74
(3,650)	1:92:V:VAL:H	1:90:V:ARG:HA	17	0.74
(1,639)	1:100:V:ASP:H	1:55:V:THR:CG2	19	0.74
(1,127)	1:22:V:ILE:H	1:83:V:LEU:CG	5	0.74
(4,47)	1:57:V:LEU:O	1:60:V:LYS:H	10	0.73
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB2	4	0.73
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB3	4	0.73
(1,175)	1:27:V:ILE:H	1:25:V:ARG:CB	18	0.73
(1,127)	1:22:V:ILE:H	1:83:V:LEU:CG	3	0.73
(1,127)	1:22:V:ILE:H	1:83:V:LEU:CG	18	0.73
(1,639)	1:100:V:ASP:H	1:55:V:THR:CG2	4	0.72
(1,639)	1:100:V:ASP:H	1:55:V:THR:CG2	10	0.72
(5,24)	1:57:V:LEU:C	1:60:V:LYS:H	5	0.71
(5,24)	1:57:V:LEU:C	1:60:V:LYS:H	18	0.71
(4,48)	1:57:V:LEU:O	1:60:V:LYS:N	19	0.71
(1,639)	1:100:V:ASP:H	1:55:V:THR:CG2	16	0.71
(1,300)	1:52:V:VAL:H	1:96:V:THR:CG2	15	0.71
(4,48)	1:57:V:LEU:O	1:60:V:LYS:N	11	0.7
(4,48)	1:57:V:LEU:O	1:60:V:LYS:N	17	0.7
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB2	1	0.7
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB3	1	0.7
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB2	7	0.7
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB3	7	0.7

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,456)	1:74:V:GLU:H	1:70:V:LYS:CG	1	0.7
(1,300)	1:52:V:VAL:H	1:96:V:THR:CG2	13	0.7
(5,24)	1:57:V:LEU:C	1:60:V:LYS:H	19	0.69
(4,48)	1:57:V:LEU:O	1:60:V:LYS:N	5	0.69
(4,47)	1:57:V:LEU:O	1:60:V:LYS:H	1	0.69
(1,569)	1:87:V:MET:H	1:87:V:MET:CE	15	0.69
(1,300)	1:52:V:VAL:H	1:96:V:THR:CG2	2	0.69
(1,300)	1:52:V:VAL:H	1:96:V:THR:CG2	4	0.69
(1,176)	1:27:V:ILE:H	1:25:V:ARG:CA	13	0.69
(5,24)	1:57:V:LEU:C	1:60:V:LYS:H	8	0.68
(5,24)	1:57:V:LEU:C	1:60:V:LYS:H	10	0.68
(4,67)	1:68:V:GLY:O	1:71:V:ALA:H	4	0.68
(4,48)	1:57:V:LEU:O	1:60:V:LYS:N	8	0.68
(4,48)	1:57:V:LEU:O	1:60:V:LYS:N	18	0.68
(4,47)	1:57:V:LEU:O	1:60:V:LYS:H	3	0.68
(3,317)	1:49:V:TYR:H	1:48:V:ALA:HB1	11	0.68
(3,200)	1:29:V:ASP:H	1:25:V:ARG:HA	11	0.68
(1,639)	1:100:V:ASP:H	1:55:V:THR:CG2	2	0.68
(1,300)	1:52:V:VAL:H	1:96:V:THR:CG2	14	0.68
(1,176)	1:27:V:ILE:H	1:25:V:ARG:CA	16	0.68
(3,317)	1:49:V:TYR:H	1:48:V:ALA:HB1	17	0.67
(3,177)	1:26:V:GLU:H	1:22:V:ILE:HA	11	0.67
(3,177)	1:26:V:GLU:H	1:22:V:ILE:HA	12	0.67
(1,639)	1:100:V:ASP:H	1:55:V:THR:CG2	15	0.67
(1,176)	1:27:V:ILE:H	1:25:V:ARG:CA	9	0.67
(1,176)	1:27:V:ILE:H	1:25:V:ARG:CA	19	0.67
(5,24)	1:57:V:LEU:C	1:60:V:LYS:H	4	0.66
(5,24)	1:57:V:LEU:C	1:60:V:LYS:H	9	0.66
(4,67)	1:68:V:GLY:O	1:71:V:ALA:H	14	0.66
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB2	18	0.66
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB3	18	0.66
(1,300)	1:52:V:VAL:H	1:96:V:THR:CG2	1	0.66
(1,300)	1:52:V:VAL:H	1:96:V:THR:CG2	10	0.66
(1,176)	1:27:V:ILE:H	1:25:V:ARG:CA	3	0.66
(1,159)	1:25:V:ARG:H	1:25:V:ARG:CG	16	0.66
(1,127)	1:22:V:ILE:H	1:83:V:LEU:CG	4	0.66
(1,127)	1:22:V:ILE:H	1:83:V:LEU:CG	16	0.66
(4,67)	1:68:V:GLY:O	1:71:V:ALA:H	19	0.65
(3,650)	1:92:V:VAL:H	1:90:V:ARG:HA	13	0.65
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB2	12	0.65
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB3	12	0.65
(2,65)	1:19:V:ILE:HG13	1:87:V:MET:HE1	18	0.65

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,300)	1:52:V:VAL:H	1:96:V:THR:CG2	18	0.65
(1,176)	1:27:V:ILE:H	1:25:V:ARG:CA	17	0.65
(4,67)	1:68:V:GLY:O	1:71:V:ALA:H	9	0.64
(4,48)	1:57:V:LEU:O	1:60:V:LYS:N	4	0.64
(3,317)	1:49:V:TYR:H	1:48:V:ALA:HB1	19	0.64
(4,48)	1:57:V:LEU:O	1:60:V:LYS:N	10	0.63
(4,47)	1:57:V:LEU:O	1:60:V:LYS:H	14	0.63
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB2	16	0.63
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB3	16	0.63
(3,317)	1:49:V:TYR:H	1:48:V:ALA:HB1	12	0.63
(1,569)	1:87:V:MET:H	1:87:V:MET:CE	3	0.63
(1,394)	1:68:V:GLY:H	1:64:V:ALA:CB	3	0.63
(1,300)	1:52:V:VAL:H	1:96:V:THR:CG2	19	0.63
(1,127)	1:22:V:ILE:H	1:83:V:LEU:CG	8	0.63
(5,24)	1:57:V:LEU:C	1:60:V:LYS:H	3	0.62
(4,48)	1:57:V:LEU:O	1:60:V:LYS:N	9	0.62
(4,47)	1:57:V:LEU:O	1:60:V:LYS:H	2	0.62
(1,456)	1:74:V:GLU:H	1:70:V:LYS:CG	16	0.62
(1,300)	1:52:V:VAL:H	1:96:V:THR:CG2	11	0.62
(1,94)	1:20:V:ALA:H	1:17:V:LYS:CB	4	0.62
(4,67)	1:68:V:GLY:O	1:71:V:ALA:H	18	0.61
(3,650)	1:92:V:VAL:H	1:90:V:ARG:HA	20	0.61
(1,569)	1:87:V:MET:H	1:87:V:MET:CE	17	0.61
(5,24)	1:57:V:LEU:C	1:60:V:LYS:H	1	0.6
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB2	17	0.6
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB3	17	0.6
(1,569)	1:87:V:MET:H	1:87:V:MET:CE	4	0.6
(1,300)	1:52:V:VAL:H	1:96:V:THR:CG2	20	0.6
(4,109)	1:35:V:MET:O	1:57:V:LEU:H	9	0.59
(4,67)	1:68:V:GLY:O	1:71:V:ALA:H	3	0.59
(4,67)	1:68:V:GLY:O	1:71:V:ALA:H	6	0.59
(4,48)	1:57:V:LEU:O	1:60:V:LYS:N	1	0.59
(4,47)	1:57:V:LEU:O	1:60:V:LYS:H	20	0.59
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB2	2	0.59
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB3	2	0.59
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB2	5	0.59
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB3	5	0.59
(1,587)	1:92:V:VAL:H	1:89:V:LEU:CG	5	0.59
(1,300)	1:52:V:VAL:H	1:96:V:THR:CG2	5	0.59
(1,300)	1:52:V:VAL:H	1:96:V:THR:CG2	12	0.59
(1,127)	1:22:V:ILE:H	1:83:V:LEU:CG	19	0.59
(4,67)	1:68:V:GLY:O	1:71:V:ALA:H	8	0.58

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,569)	1:87:V:MET:H	1:87:V:MET:CE	1	0.58
(1,569)	1:87:V:MET:H	1:87:V:MET:CE	20	0.58
(1,176)	1:27:V:ILE:H	1:25:V:ARG:CA	14	0.58
(1,94)	1:20:V:ALA:H	1:17:V:LYS:CB	11	0.58
(5,45)	1:81:V:SER:C	1:85:V:LYS:H	6	0.57
(5,24)	1:57:V:LEU:C	1:60:V:LYS:H	2	0.57
(4,67)	1:68:V:GLY:O	1:71:V:ALA:H	1	0.57
(3,713)	1:100:V:ASP:H	1:55:V:THR:HG1	17	0.57
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB2	10	0.57
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB3	10	0.57
(2,252)	1:66:V:LYS:HD2	1:66:V:LYS:HA	9	0.57
(2,252)	1:66:V:LYS:HD3	1:66:V:LYS:HA	9	0.57
(1,325)	1:60:V:LYS:H	1:57:V:LEU:CA	6	0.57
(1,300)	1:52:V:VAL:H	1:96:V:THR:CG2	8	0.57
(1,127)	1:22:V:ILE:H	1:83:V:LEU:CG	20	0.57
(1,94)	1:20:V:ALA:H	1:17:V:LYS:CB	6	0.57
(5,2)	1:10:V:ARG:C	1:14:V:GLU:H	17	0.56
(4,109)	1:35:V:MET:O	1:57:V:LEU:H	5	0.56
(4,67)	1:68:V:GLY:O	1:71:V:ALA:H	5	0.56
(4,67)	1:68:V:GLY:O	1:71:V:ALA:H	13	0.56
(4,67)	1:68:V:GLY:O	1:71:V:ALA:H	15	0.56
(4,48)	1:57:V:LEU:O	1:60:V:LYS:N	14	0.56
(1,300)	1:52:V:VAL:H	1:96:V:THR:CG2	6	0.56
(1,300)	1:52:V:VAL:H	1:96:V:THR:CG2	7	0.56
(1,176)	1:27:V:ILE:H	1:25:V:ARG:CA	15	0.56
(5,6)	1:14:V:GLU:C	1:18:V:GLU:H	12	0.55
(4,109)	1:35:V:MET:O	1:57:V:LEU:H	20	0.55
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB2	9	0.55
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB3	9	0.55
(3,317)	1:49:V:TYR:H	1:48:V:ALA:HB1	13	0.55
(3,286)	1:46:V:ASP:H	1:47:V:LEU:HG	17	0.55
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD2	16	0.55
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD3	16	0.55
(1,587)	1:92:V:VAL:H	1:89:V:LEU:CG	20	0.55
(1,300)	1:52:V:VAL:H	1:96:V:THR:CG2	16	0.55
(1,300)	1:52:V:VAL:H	1:96:V:THR:CG2	17	0.55
(1,176)	1:27:V:ILE:H	1:25:V:ARG:CA	1	0.55
(1,94)	1:20:V:ALA:H	1:17:V:LYS:CB	14	0.55
(1,76)	1:18:V:GLU:H	1:18:V:GLU:CG	8	0.55
(1,76)	1:18:V:GLU:H	1:18:V:GLU:CG	13	0.55
(5,48)	1:84:V:GLY:C	1:89:V:LEU:H	11	0.54
(4,109)	1:35:V:MET:O	1:57:V:LEU:H	18	0.54

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,67)	1:68:V:GLY:O	1:71:V:ALA:H	10	0.54
(4,67)	1:68:V:GLY:O	1:71:V:ALA:H	17	0.54
(3,535)	1:78:V:PHE:H	1:75:V:ALA:HA	14	0.54
(3,535)	1:78:V:PHE:H	1:75:V:ALA:HA	17	0.54
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB2	15	0.54
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB3	15	0.54
(2,252)	1:66:V:LYS:HD2	1:66:V:LYS:HA	7	0.54
(2,252)	1:66:V:LYS:HD3	1:66:V:LYS:HA	7	0.54
(1,569)	1:87:V:MET:H	1:87:V:MET:CE	7	0.54
(1,569)	1:87:V:MET:H	1:87:V:MET:CE	14	0.54
(1,569)	1:87:V:MET:H	1:87:V:MET:CE	19	0.54
(1,176)	1:27:V:ILE:H	1:25:V:ARG:CA	20	0.54
(1,94)	1:20:V:ALA:H	1:17:V:LYS:CB	9	0.54
(5,24)	1:57:V:LEU:C	1:60:V:LYS:H	14	0.53
(5,24)	1:57:V:LEU:C	1:60:V:LYS:H	20	0.53
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB2	8	0.53
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB3	8	0.53
(3,317)	1:49:V:TYR:H	1:48:V:ALA:HB1	7	0.53
(3,177)	1:26:V:GLU:H	1:22:V:ILE:HA	7	0.53
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD2	10	0.53
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD3	10	0.53
(2,65)	1:19:V:ILE:HG13	1:87:V:MET:HE1	7	0.53
(1,456)	1:74:V:GLU:H	1:70:V:LYS:CG	2	0.53
(1,456)	1:74:V:GLU:H	1:70:V:LYS:CG	8	0.53
(1,394)	1:68:V:GLY:H	1:64:V:ALA:CB	2	0.53
(1,76)	1:18:V:GLU:H	1:18:V:GLU:CG	1	0.53
(4,109)	1:35:V:MET:O	1:57:V:LEU:H	6	0.52
(4,67)	1:68:V:GLY:O	1:71:V:ALA:H	16	0.52
(4,48)	1:57:V:LEU:O	1:60:V:LYS:N	3	0.52
(4,48)	1:57:V:LEU:O	1:60:V:LYS:N	20	0.52
(3,535)	1:78:V:PHE:H	1:75:V:ALA:HA	3	0.52
(3,535)	1:78:V:PHE:H	1:75:V:ALA:HA	15	0.52
(3,317)	1:49:V:TYR:H	1:48:V:ALA:HB1	10	0.52
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD2	7	0.52
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD3	7	0.52
(1,465)	1:74:V:GLU:H	1:74:V:GLU:CG	19	0.52
(1,76)	1:18:V:GLU:H	1:18:V:GLU:CG	10	0.52
(1,76)	1:18:V:GLU:H	1:18:V:GLU:CG	12	0.52
(1,76)	1:18:V:GLU:H	1:18:V:GLU:CG	18	0.52
(5,5)	1:13:V:GLN:C	1:17:V:LYS:H	4	0.51
(4,67)	1:68:V:GLY:O	1:71:V:ALA:H	12	0.51
(4,48)	1:57:V:LEU:O	1:60:V:LYS:N	2	0.51

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,535)	1:78:V:PHE:H	1:75:V:ALA:HA	13	0.51
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD2	5	0.51
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD3	5	0.51
(1,465)	1:74:V:GLU:H	1:74:V:GLU:CG	8	0.51
(1,465)	1:74:V:GLU:H	1:74:V:GLU:CG	11	0.51
(1,175)	1:27:V:ILE:H	1:25:V:ARG:CB	7	0.51
(1,127)	1:22:V:ILE:H	1:83:V:LEU:CG	6	0.51
(1,94)	1:20:V:ALA:H	1:17:V:LYS:CB	2	0.51
(1,94)	1:20:V:ALA:H	1:17:V:LYS:CB	13	0.51
(5,55)	1:35:V:MET:C	1:57:V:LEU:H	5	0.5
(4,3)	1:10:V:ARG:O	1:14:V:GLU:H	17	0.5
(3,317)	1:49:V:TYR:H	1:48:V:ALA:HB1	16	0.5
(1,394)	1:68:V:GLY:H	1:64:V:ALA:CB	12	0.5
(1,176)	1:27:V:ILE:H	1:25:V:ARG:CA	5	0.5
(1,94)	1:20:V:ALA:H	1:17:V:LYS:CB	1	0.5
(1,76)	1:18:V:GLU:H	1:18:V:GLU:CG	17	0.5
(5,47)	1:83:V:LEU:C	1:87:V:MET:H	6	0.49
(5,26)	1:61:V:ASP:C	1:65:V:VAL:H	3	0.49
(5,12)	1:21:V:LEU:C	1:25:V:ARG:H	15	0.49
(4,73)	1:71:V:ALA:O	1:75:V:ALA:H	13	0.49
(3,535)	1:78:V:PHE:H	1:75:V:ALA:HA	5	0.49
(3,535)	1:78:V:PHE:H	1:75:V:ALA:HA	12	0.49
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD2	20	0.49
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD3	20	0.49
(1,465)	1:74:V:GLU:H	1:74:V:GLU:CG	2	0.49
(1,465)	1:74:V:GLU:H	1:74:V:GLU:CG	6	0.49
(1,465)	1:74:V:GLU:H	1:74:V:GLU:CG	20	0.49
(1,394)	1:68:V:GLY:H	1:64:V:ALA:CB	10	0.49
(1,394)	1:68:V:GLY:H	1:64:V:ALA:CB	16	0.49
(1,238)	1:43:V:MET:H	1:42:V:GLU:CG	8	0.49
(1,107)	1:21:V:LEU:H	1:18:V:GLU:CA	4	0.49
(1,94)	1:20:V:ALA:H	1:17:V:LYS:CB	19	0.49
(1,76)	1:18:V:GLU:H	1:18:V:GLU:CG	4	0.49
(1,76)	1:18:V:GLU:H	1:18:V:GLU:CG	20	0.49
(5,55)	1:35:V:MET:C	1:57:V:LEU:H	10	0.48
(5,26)	1:61:V:ASP:C	1:65:V:VAL:H	16	0.48
(5,26)	1:61:V:ASP:C	1:65:V:VAL:H	19	0.48
(5,9)	1:17:V:LYS:C	1:21:V:LEU:H	2	0.48
(4,67)	1:68:V:GLY:O	1:71:V:ALA:H	20	0.48
(3,535)	1:78:V:PHE:H	1:75:V:ALA:HA	1	0.48
(3,317)	1:49:V:TYR:H	1:48:V:ALA:HB1	2	0.48
(3,317)	1:49:V:TYR:H	1:48:V:ALA:HB1	3	0.48

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,394)	1:68:V:GLY:H	1:64:V:ALA:CB	6	0.48
(1,107)	1:21:V:LEU:H	1:18:V:GLU:CA	20	0.48
(1,94)	1:20:V:ALA:H	1:17:V:LYS:CB	7	0.48
(1,94)	1:20:V:ALA:H	1:17:V:LYS:CB	10	0.48
(1,76)	1:18:V:GLU:H	1:18:V:GLU:CG	2	0.48
(1,76)	1:18:V:GLU:H	1:18:V:GLU:CG	11	0.48
(1,76)	1:18:V:GLU:H	1:18:V:GLU:CG	14	0.48
(5,55)	1:35:V:MET:C	1:57:V:LEU:H	6	0.47
(5,55)	1:35:V:MET:C	1:57:V:LEU:H	13	0.47
(4,109)	1:35:V:MET:O	1:57:V:LEU:H	1	0.47
(4,109)	1:35:V:MET:O	1:57:V:LEU:H	3	0.47
(4,67)	1:68:V:GLY:O	1:71:V:ALA:H	7	0.47
(4,67)	1:68:V:GLY:O	1:71:V:ALA:H	11	0.47
(3,317)	1:49:V:TYR:H	1:48:V:ALA:HB1	1	0.47
(3,317)	1:49:V:TYR:H	1:48:V:ALA:HB1	9	0.47
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD2	14	0.47
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD3	14	0.47
(1,569)	1:87:V:MET:H	1:87:V:MET:CE	2	0.47
(1,107)	1:21:V:LEU:H	1:18:V:GLU:CA	5	0.47
(1,107)	1:21:V:LEU:H	1:18:V:GLU:CA	15	0.47
(1,81)	1:19:V:ILE:H	1:17:V:LYS:CB	4	0.47
(1,81)	1:19:V:ILE:H	1:17:V:LYS:CB	5	0.47
(1,76)	1:18:V:GLU:H	1:18:V:GLU:CG	16	0.47
(1,76)	1:18:V:GLU:H	1:18:V:GLU:CG	19	0.47
(5,9)	1:17:V:LYS:C	1:21:V:LEU:H	15	0.46
(4,95)	1:84:V:GLY:O	1:89:V:LEU:H	11	0.46
(4,67)	1:68:V:GLY:O	1:71:V:ALA:H	2	0.46
(3,650)	1:92:V:VAL:H	1:90:V:ARG:HA	19	0.46
(1,569)	1:87:V:MET:H	1:87:V:MET:CE	18	0.46
(1,475)	1:76:V:SER:H	1:73:V:GLN:CA	9	0.46
(1,456)	1:74:V:GLU:H	1:70:V:LYS:CG	9	0.46
(1,300)	1:52:V:VAL:H	1:96:V:THR:CG2	3	0.46
(1,175)	1:27:V:ILE:H	1:25:V:ARG:CB	12	0.46
(1,81)	1:19:V:ILE:H	1:17:V:LYS:CB	14	0.46
(1,76)	1:18:V:GLU:H	1:18:V:GLU:CG	3	0.46
(1,76)	1:18:V:GLU:H	1:18:V:GLU:CG	9	0.46
(1,50)	1:16:V:GLN:H	1:13:V:GLN:CA	13	0.46
(5,55)	1:35:V:MET:C	1:57:V:LEU:H	11	0.45
(5,12)	1:21:V:LEU:C	1:25:V:ARG:H	19	0.45
(5,9)	1:17:V:LYS:C	1:21:V:LEU:H	10	0.45
(5,9)	1:17:V:LYS:C	1:21:V:LEU:H	12	0.45
(4,109)	1:35:V:MET:O	1:57:V:LEU:H	11	0.45

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,11)	1:14:V:GLU:O	1:18:V:GLU:H	12	0.45
(3,535)	1:78:V:PHE:H	1:75:V:ALA:HA	19	0.45
(3,317)	1:49:V:TYR:H	1:48:V:ALA:HB1	8	0.45
(3,317)	1:49:V:TYR:H	1:48:V:ALA:HB1	14	0.45
(2,65)	1:19:V:ILE:HG13	1:87:V:MET:HE1	15	0.45
(1,587)	1:92:V:VAL:H	1:89:V:LEU:CG	12	0.45
(1,569)	1:87:V:MET:H	1:87:V:MET:CE	11	0.45
(1,465)	1:74:V:GLU:H	1:74:V:GLU:CG	1	0.45
(1,394)	1:68:V:GLY:H	1:64:V:ALA:CB	5	0.45
(1,107)	1:21:V:LEU:H	1:18:V:GLU:CA	3	0.45
(1,107)	1:21:V:LEU:H	1:18:V:GLU:CA	9	0.45
(1,107)	1:21:V:LEU:H	1:18:V:GLU:CA	17	0.45
(1,94)	1:20:V:ALA:H	1:17:V:LYS:CB	3	0.45
(1,94)	1:20:V:ALA:H	1:17:V:LYS:CB	12	0.45
(1,94)	1:20:V:ALA:H	1:17:V:LYS:CB	15	0.45
(1,94)	1:20:V:ALA:H	1:17:V:LYS:CB	17	0.45
(1,41)	1:15:V:MET:H	1:12:V:ALA:CB	2	0.45
(1,18)	1:13:V:GLN:H	1:10:V:ARG:CB	4	0.45
(5,37)	1:71:V:ALA:C	1:75:V:ALA:H	1	0.44
(5,5)	1:13:V:GLN:C	1:17:V:LYS:H	16	0.44
(5,2)	1:10:V:ARG:C	1:14:V:GLU:H	6	0.44
(5,1)	1:9:V:GLN:C	1:13:V:GLN:H	13	0.44
(4,109)	1:35:V:MET:O	1:57:V:LEU:H	17	0.44
(3,535)	1:78:V:PHE:H	1:75:V:ALA:HA	7	0.44
(3,317)	1:49:V:TYR:H	1:48:V:ALA:HB1	4	0.44
(3,317)	1:49:V:TYR:H	1:48:V:ALA:HB1	6	0.44
(3,317)	1:49:V:TYR:H	1:48:V:ALA:HB1	20	0.44
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD2	1	0.44
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD3	1	0.44
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD2	17	0.44
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD3	17	0.44
(2,252)	1:66:V:LYS:HD2	1:66:V:LYS:HA	10	0.44
(2,252)	1:66:V:LYS:HD3	1:66:V:LYS:HA	10	0.44
(1,569)	1:87:V:MET:H	1:87:V:MET:CE	13	0.44
(1,394)	1:68:V:GLY:H	1:64:V:ALA:CB	4	0.44
(1,394)	1:68:V:GLY:H	1:64:V:ALA:CB	13	0.44
(1,394)	1:68:V:GLY:H	1:64:V:ALA:CB	18	0.44
(1,175)	1:27:V:ILE:H	1:25:V:ARG:CB	13	0.44
(1,76)	1:18:V:GLU:H	1:18:V:GLU:CG	6	0.44
(1,76)	1:18:V:GLU:H	1:18:V:GLU:CG	7	0.44
(1,50)	1:16:V:GLN:H	1:13:V:GLN:CA	3	0.44
(1,41)	1:15:V:MET:H	1:12:V:ALA:CB	20	0.44

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(5,55)	1:35:V:MET:C	1:57:V:LEU:H	9	0.43
(5,55)	1:35:V:MET:C	1:57:V:LEU:H	20	0.43
(5,37)	1:71:V:ALA:C	1:75:V:ALA:H	13	0.43
(5,25)	1:58:V:ASN:C	1:61:V:ASP:H	12	0.43
(5,12)	1:21:V:LEU:C	1:25:V:ARG:H	5	0.43
(5,12)	1:21:V:LEU:C	1:25:V:ARG:H	12	0.43
(4,73)	1:71:V:ALA:O	1:75:V:ALA:H	4	0.43
(3,403)	1:61:V:ASP:H	1:64:V:ALA:HB1	11	0.43
(3,317)	1:49:V:TYR:H	1:48:V:ALA:HB1	18	0.43
(2,177)	1:43:V:MET:HB2	1:43:V:MET:HE1	17	0.43
(2,177)	1:43:V:MET:HB3	1:43:V:MET:HE1	17	0.43
(1,569)	1:87:V:MET:H	1:87:V:MET:CE	16	0.43
(1,475)	1:76:V:SER:H	1:73:V:GLN:CA	2	0.43
(1,465)	1:74:V:GLU:H	1:74:V:GLU:CG	17	0.43
(1,287)	1:51:V:LYS:H	1:42:V:GLU:CG	16	0.43
(1,175)	1:27:V:ILE:H	1:25:V:ARG:CB	2	0.43
(1,107)	1:21:V:LEU:H	1:18:V:GLU:CA	10	0.43
(1,81)	1:19:V:ILE:H	1:17:V:LYS:CB	8	0.43
(1,81)	1:19:V:ILE:H	1:17:V:LYS:CB	16	0.43
(1,81)	1:19:V:ILE:H	1:17:V:LYS:CB	17	0.43
(1,76)	1:18:V:GLU:H	1:18:V:GLU:CG	5	0.43
(1,76)	1:18:V:GLU:H	1:18:V:GLU:CG	15	0.43
(1,50)	1:16:V:GLN:H	1:13:V:GLN:CA	4	0.43
(5,55)	1:35:V:MET:C	1:57:V:LEU:H	8	0.42
(5,55)	1:35:V:MET:C	1:57:V:LEU:H	15	0.42
(5,48)	1:84:V:GLY:C	1:89:V:LEU:H	12	0.42
(5,41)	1:77:V:GLY:C	1:81:V:SER:H	14	0.42
(4,109)	1:35:V:MET:O	1:57:V:LEU:H	10	0.42
(4,49)	1:58:V:ASN:O	1:61:V:ASP:H	12	0.42
(4,47)	1:57:V:LEU:O	1:60:V:LYS:H	7	0.42
(3,535)	1:78:V:PHE:H	1:75:V:ALA:HA	9	0.42
(3,535)	1:78:V:PHE:H	1:75:V:ALA:HA	18	0.42
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB2	6	0.42
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB3	6	0.42
(3,403)	1:61:V:ASP:H	1:64:V:ALA:HB1	13	0.42
(3,403)	1:61:V:ASP:H	1:64:V:ALA:HB1	14	0.42
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD2	13	0.42
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD3	13	0.42
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD2	19	0.42
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD3	19	0.42
(2,252)	1:66:V:LYS:HD2	1:66:V:LYS:HA	3	0.42
(2,252)	1:66:V:LYS:HD3	1:66:V:LYS:HA	3	0.42

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,536)	1:83:V:LEU:H	1:85:V:LYS:CG	6	0.42
(1,475)	1:76:V:SER:H	1:73:V:GLN:CA	8	0.42
(1,465)	1:74:V:GLU:H	1:74:V:GLU:CG	5	0.42
(1,394)	1:68:V:GLY:H	1:64:V:ALA:CB	15	0.42
(1,386)	1:67:V:ALA:H	1:66:V:LYS:CD	5	0.42
(1,238)	1:43:V:MET:H	1:42:V:GLU:CG	10	0.42
(1,94)	1:20:V:ALA:H	1:17:V:LYS:CB	20	0.42
(1,81)	1:19:V:ILE:H	1:17:V:LYS:CB	13	0.42
(1,50)	1:16:V:GLN:H	1:13:V:GLN:CA	1	0.42
(1,41)	1:15:V:MET:H	1:12:V:ALA:CB	4	0.42
(5,24)	1:57:V:LEU:C	1:60:V:LYS:H	7	0.41
(5,5)	1:13:V:GLN:C	1:17:V:LYS:H	13	0.41
(4,107)	1:30:V:PRO:O	1:33:V:GLY:H	10	0.41
(4,17)	1:17:V:LYS:O	1:21:V:LEU:H	12	0.41
(3,535)	1:78:V:PHE:H	1:75:V:ALA:HA	10	0.41
(3,535)	1:78:V:PHE:H	1:75:V:ALA:HA	11	0.41
(3,512)	1:74:V:GLU:H	1:74:V:GLU:HG2	11	0.41
(3,512)	1:74:V:GLU:H	1:74:V:GLU:HG3	11	0.41
(3,512)	1:74:V:GLU:H	1:74:V:GLU:HG2	19	0.41
(3,512)	1:74:V:GLU:H	1:74:V:GLU:HG3	19	0.41
(3,391)	1:60:V:LYS:H	1:59:V:ASP:HB2	20	0.41
(3,391)	1:60:V:LYS:H	1:59:V:ASP:HB3	20	0.41
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD2	11	0.41
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD3	11	0.41
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD2	18	0.41
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD3	18	0.41
(2,177)	1:43:V:MET:HB2	1:43:V:MET:HE1	11	0.41
(2,177)	1:43:V:MET:HB3	1:43:V:MET:HE1	11	0.41
(2,128)	1:27:V:ILE:HD11	1:71:V:ALA:HB1	6	0.41
(2,128)	1:27:V:ILE:HD12	1:71:V:ALA:HB1	6	0.41
(2,128)	1:27:V:ILE:HD13	1:71:V:ALA:HB1	6	0.41
(1,556)	1:86:V:ALA:H	1:82:V:LEU:CB	6	0.41
(1,477)	1:76:V:SER:H	1:74:V:GLU:CA	3	0.41
(1,300)	1:52:V:VAL:H	1:96:V:THR:CG2	9	0.41
(1,175)	1:27:V:ILE:H	1:25:V:ARG:CB	10	0.41
(1,81)	1:19:V:ILE:H	1:17:V:LYS:CB	1	0.41
(1,81)	1:19:V:ILE:H	1:17:V:LYS:CB	18	0.41
(5,55)	1:35:V:MET:C	1:57:V:LEU:H	18	0.4
(5,37)	1:71:V:ALA:C	1:75:V:ALA:H	3	0.4
(5,37)	1:71:V:ALA:C	1:75:V:ALA:H	4	0.4
(5,25)	1:58:V:ASN:C	1:61:V:ASP:H	15	0.4
(5,12)	1:21:V:LEU:C	1:25:V:ARG:H	7	0.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(5,9)	1:17:V:LYS:C	1:21:V:LEU:H	4	0.4
(4,1)	1:9:V:GLN:O	1:13:V:GLN:H	13	0.4
(3,512)	1:74:V:GLU:H	1:74:V:GLU:HG2	6	0.4
(3,512)	1:74:V:GLU:H	1:74:V:GLU:HG3	6	0.4
(3,512)	1:74:V:GLU:H	1:74:V:GLU:HG2	20	0.4
(3,512)	1:74:V:GLU:H	1:74:V:GLU:HG3	20	0.4
(3,401)	1:61:V:ASP:H	1:60:V:LYS:HB2	15	0.4
(3,401)	1:61:V:ASP:H	1:60:V:LYS:HB3	15	0.4
(3,338)	1:51:V:LYS:H	1:44:V:SER:H	2	0.4
(3,317)	1:49:V:TYR:H	1:48:V:ALA:HB1	15	0.4
(3,280)	1:44:V:SER:H	1:51:V:LYS:H	2	0.4
(3,100)	1:20:V:ALA:H	1:16:V:GLN:HB2	8	0.4
(3,100)	1:20:V:ALA:H	1:16:V:GLN:HB3	8	0.4
(1,475)	1:76:V:SER:H	1:73:V:GLN:CA	18	0.4
(1,394)	1:68:V:GLY:H	1:64:V:ALA:CB	11	0.4
(1,386)	1:67:V:ALA:H	1:66:V:LYS:CD	17	0.4
(1,254)	1:47:V:LEU:H	1:45:V:ARG:CA	1	0.4
(1,175)	1:27:V:ILE:H	1:25:V:ARG:CB	11	0.4
(1,107)	1:21:V:LEU:H	1:18:V:GLU:CA	2	0.4
(1,81)	1:19:V:ILE:H	1:17:V:LYS:CB	11	0.4
(1,50)	1:16:V:GLN:H	1:13:V:GLN:CA	16	0.4
(5,55)	1:35:V:MET:C	1:57:V:LEU:H	2	0.39
(5,26)	1:61:V:ASP:C	1:65:V:VAL:H	7	0.39
(5,26)	1:61:V:ASP:C	1:65:V:VAL:H	15	0.39
(5,25)	1:58:V:ASN:C	1:61:V:ASP:H	3	0.39
(5,12)	1:21:V:LEU:C	1:25:V:ARG:H	16	0.39
(4,110)	1:35:V:MET:O	1:57:V:LEU:N	6	0.39
(4,17)	1:17:V:LYS:O	1:21:V:LEU:H	2	0.39
(3,512)	1:74:V:GLU:H	1:74:V:GLU:HG2	2	0.39
(3,512)	1:74:V:GLU:H	1:74:V:GLU:HG3	2	0.39
(3,512)	1:74:V:GLU:H	1:74:V:GLU:HG2	8	0.39
(3,512)	1:74:V:GLU:H	1:74:V:GLU:HG3	8	0.39
(3,356)	1:53:V:TYR:H	1:42:V:GLU:H	15	0.39
(3,265)	1:42:V:GLU:H	1:53:V:TYR:H	15	0.39
(3,17)	1:13:V:GLN:H	1:10:V:ARG:HA	4	0.39
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD2	3	0.39
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD3	3	0.39
(1,394)	1:68:V:GLY:H	1:64:V:ALA:CB	7	0.39
(1,394)	1:68:V:GLY:H	1:64:V:ALA:CB	8	0.39
(1,394)	1:68:V:GLY:H	1:64:V:ALA:CB	17	0.39
(1,325)	1:60:V:LYS:H	1:57:V:LEU:CA	15	0.39
(1,254)	1:47:V:LEU:H	1:45:V:ARG:CA	2	0.39

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,254)	1:47:V:LEU:H	1:45:V:ARG:CA	14	0.39
(1,254)	1:47:V:LEU:H	1:45:V:ARG:CA	19	0.39
(1,107)	1:21:V:LEU:H	1:18:V:GLU:CA	16	0.39
(1,41)	1:15:V:MET:H	1:12:V:ALA:CB	7	0.39
(5,9)	1:17:V:LYS:C	1:21:V:LEU:H	1	0.38
(5,1)	1:9:V:GLN:C	1:13:V:GLN:H	3	0.38
(4,109)	1:35:V:MET:O	1:57:V:LEU:H	13	0.38
(4,109)	1:35:V:MET:O	1:57:V:LEU:H	16	0.38
(4,73)	1:71:V:ALA:O	1:75:V:ALA:H	1	0.38
(3,535)	1:78:V:PHE:H	1:75:V:ALA:HA	6	0.38
(3,177)	1:26:V:GLU:H	1:22:V:ILE:HA	19	0.38
(3,100)	1:20:V:ALA:H	1:16:V:GLN:HB2	20	0.38
(3,100)	1:20:V:ALA:H	1:16:V:GLN:HB3	20	0.38
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD2	12	0.38
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD3	12	0.38
(1,587)	1:92:V:VAL:H	1:89:V:LEU:CG	10	0.38
(1,569)	1:87:V:MET:H	1:87:V:MET:CE	10	0.38
(1,475)	1:76:V:SER:H	1:73:V:GLN:CA	4	0.38
(1,456)	1:74:V:GLU:H	1:70:V:LYS:CG	19	0.38
(1,108)	1:21:V:LEU:H	1:18:V:GLU:CB	20	0.38
(1,107)	1:21:V:LEU:H	1:18:V:GLU:CA	12	0.38
(1,81)	1:19:V:ILE:H	1:17:V:LYS:CB	6	0.38
(1,81)	1:19:V:ILE:H	1:17:V:LYS:CB	9	0.38
(1,18)	1:13:V:GLN:H	1:10:V:ARG:CB	17	0.38
(5,47)	1:83:V:LEU:C	1:87:V:MET:H	1	0.37
(5,9)	1:17:V:LYS:C	1:21:V:LEU:H	9	0.37
(5,2)	1:10:V:ARG:C	1:14:V:GLU:H	13	0.37
(4,110)	1:35:V:MET:O	1:57:V:LEU:N	18	0.37
(4,109)	1:35:V:MET:O	1:57:V:LEU:H	12	0.37
(4,50)	1:58:V:ASN:O	1:61:V:ASP:N	12	0.37
(4,4)	1:10:V:ARG:O	1:14:V:GLU:N	17	0.37
(3,512)	1:74:V:GLU:H	1:74:V:GLU:HG2	1	0.37
(3,512)	1:74:V:GLU:H	1:74:V:GLU:HG3	1	0.37
(3,512)	1:74:V:GLU:H	1:74:V:GLU:HG2	17	0.37
(3,512)	1:74:V:GLU:H	1:74:V:GLU:HG3	17	0.37
(3,495)	1:73:V:GLN:H	1:70:V:LYS:HA	2	0.37
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB2	5	0.37
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB3	5	0.37
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD2	2	0.37
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD3	2	0.37
(2,18)	1:12:V:ALA:HB1	1:13:V:GLN:HE21	19	0.37
(2,18)	1:12:V:ALA:HB1	1:13:V:GLN:HE22	19	0.37

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,556)	1:86:V:ALA:H	1:82:V:LEU:CB	12	0.37
(1,475)	1:76:V:SER:H	1:73:V:GLN:CA	3	0.37
(1,456)	1:74:V:GLU:H	1:70:V:LYS:CG	3	0.37
(1,456)	1:74:V:GLU:H	1:70:V:LYS:CG	15	0.37
(1,456)	1:74:V:GLU:H	1:70:V:LYS:CG	17	0.37
(1,325)	1:60:V:LYS:H	1:57:V:LEU:CA	12	0.37
(1,107)	1:21:V:LEU:H	1:18:V:GLU:CA	19	0.37
(1,94)	1:20:V:ALA:H	1:17:V:LYS:CB	18	0.37
(1,81)	1:19:V:ILE:H	1:17:V:LYS:CB	2	0.37
(1,50)	1:16:V:GLN:H	1:13:V:GLN:CA	15	0.37
(1,41)	1:15:V:MET:H	1:12:V:ALA:CB	10	0.37
(1,41)	1:15:V:MET:H	1:12:V:ALA:CB	19	0.37
(5,26)	1:61:V:ASP:C	1:65:V:VAL:H	4	0.36
(5,12)	1:21:V:LEU:C	1:25:V:ARG:H	20	0.36
(5,10)	1:18:V:GLU:C	1:22:V:ILE:H	5	0.36
(5,10)	1:18:V:GLU:C	1:22:V:ILE:H	16	0.36
(5,9)	1:17:V:LYS:C	1:21:V:LEU:H	13	0.36
(5,5)	1:13:V:GLN:C	1:17:V:LYS:H	1	0.36
(5,2)	1:10:V:ARG:C	1:14:V:GLU:H	3	0.36
(4,110)	1:35:V:MET:O	1:57:V:LEU:N	9	0.36
(4,109)	1:35:V:MET:O	1:57:V:LEU:H	15	0.36
(4,89)	1:81:V:SER:O	1:85:V:LYS:H	6	0.36
(4,12)	1:14:V:GLU:O	1:18:V:GLU:N	12	0.36
(3,650)	1:92:V:VAL:H	1:90:V:ARG:HA	7	0.36
(3,356)	1:53:V:TYR:H	1:42:V:GLU:H	12	0.36
(3,317)	1:49:V:TYR:H	1:48:V:ALA:HB1	5	0.36
(3,265)	1:42:V:GLU:H	1:53:V:TYR:H	12	0.36
(3,100)	1:20:V:ALA:H	1:16:V:GLN:HB2	5	0.36
(3,100)	1:20:V:ALA:H	1:16:V:GLN:HB3	5	0.36
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD2	6	0.36
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD3	6	0.36
(1,587)	1:92:V:VAL:H	1:89:V:LEU:CG	1	0.36
(1,394)	1:68:V:GLY:H	1:64:V:ALA:CB	9	0.36
(1,394)	1:68:V:GLY:H	1:64:V:ALA:CB	20	0.36
(1,386)	1:67:V:ALA:H	1:66:V:LYS:CD	10	0.36
(1,278)	1:50:V:ALA:H	1:93:V:PRO:CG	9	0.36
(1,108)	1:21:V:LEU:H	1:18:V:GLU:CB	4	0.36
(1,104)	1:20:V:ALA:H	1:21:V:LEU:CB	5	0.36
(1,50)	1:16:V:GLN:H	1:13:V:GLN:CA	7	0.36
(1,50)	1:16:V:GLN:H	1:13:V:GLN:CA	18	0.36
(5,26)	1:61:V:ASP:C	1:65:V:VAL:H	12	0.35
(5,26)	1:61:V:ASP:C	1:65:V:VAL:H	13	0.35

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(5,26)	1:61:V:ASP:C	1:65:V:VAL:H	14	0.35
(5,9)	1:17:V:LYS:C	1:21:V:LEU:H	11	0.35
(4,110)	1:35:V:MET:O	1:57:V:LEU:N	5	0.35
(4,109)	1:35:V:MET:O	1:57:V:LEU:H	2	0.35
(3,495)	1:73:V:GLN:H	1:70:V:LYS:HA	20	0.35
(3,286)	1:46:V:ASP:H	1:47:V:LEU:HG	5	0.35
(3,177)	1:26:V:GLU:H	1:22:V:ILE:HA	20	0.35
(1,612)	1:96:V:THR:H	1:50:V:ALA:CB	15	0.35
(1,475)	1:76:V:SER:H	1:73:V:GLN:CA	16	0.35
(1,456)	1:74:V:GLU:H	1:70:V:LYS:CG	6	0.35
(1,386)	1:67:V:ALA:H	1:66:V:LYS:CD	15	0.35
(1,238)	1:43:V:MET:H	1:42:V:GLU:CG	3	0.35
(1,175)	1:27:V:ILE:H	1:25:V:ARG:CB	4	0.35
(1,108)	1:21:V:LEU:H	1:18:V:GLU:CB	3	0.35
(1,108)	1:21:V:LEU:H	1:18:V:GLU:CB	17	0.35
(1,107)	1:21:V:LEU:H	1:18:V:GLU:CA	11	0.35
(1,107)	1:21:V:LEU:H	1:18:V:GLU:CA	13	0.35
(1,107)	1:21:V:LEU:H	1:18:V:GLU:CA	14	0.35
(1,104)	1:20:V:ALA:H	1:21:V:LEU:CB	2	0.35
(1,81)	1:19:V:ILE:H	1:17:V:LYS:CB	12	0.35
(1,81)	1:19:V:ILE:H	1:17:V:LYS:CB	15	0.35
(1,50)	1:16:V:GLN:H	1:13:V:GLN:CA	2	0.35
(1,41)	1:15:V:MET:H	1:12:V:ALA:CB	8	0.35
(5,26)	1:61:V:ASP:C	1:65:V:VAL:H	9	0.34
(5,25)	1:58:V:ASN:C	1:61:V:ASP:H	19	0.34
(5,6)	1:14:V:GLU:C	1:18:V:GLU:H	10	0.34
(4,108)	1:30:V:PRO:O	1:33:V:GLY:N	10	0.34
(4,73)	1:71:V:ALA:O	1:75:V:ALA:H	3	0.34
(4,23)	1:21:V:LEU:O	1:25:V:ARG:H	15	0.34
(3,535)	1:78:V:PHE:H	1:75:V:ALA:HA	20	0.34
(3,495)	1:73:V:GLN:H	1:70:V:LYS:HA	3	0.34
(3,487)	1:72:V:LEU:H	1:71:V:ALA:HB1	4	0.34
(3,487)	1:72:V:LEU:H	1:71:V:ALA:HB1	17	0.34
(3,356)	1:53:V:TYR:H	1:42:V:GLU:H	8	0.34
(3,265)	1:42:V:GLU:H	1:53:V:TYR:H	8	0.34
(3,100)	1:20:V:ALA:H	1:16:V:GLN:HB2	2	0.34
(3,100)	1:20:V:ALA:H	1:16:V:GLN:HB3	2	0.34
(3,42)	1:15:V:MET:H	1:12:V:ALA:HA	2	0.34
(2,177)	1:43:V:MET:HB2	1:43:V:MET:HE1	16	0.34
(2,177)	1:43:V:MET:HB3	1:43:V:MET:HE1	16	0.34
(1,556)	1:86:V:ALA:H	1:82:V:LEU:CB	19	0.34
(1,477)	1:76:V:SER:H	1:74:V:GLU:CA	10	0.34

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,475)	1:76:V:SER:H	1:73:V:GLN:CA	14	0.34
(1,394)	1:68:V:GLY:H	1:64:V:ALA:CB	1	0.34
(1,325)	1:60:V:LYS:H	1:57:V:LEU:CA	13	0.34
(1,254)	1:47:V:LEU:H	1:45:V:ARG:CA	3	0.34
(1,238)	1:43:V:MET:H	1:42:V:GLU:CG	20	0.34
(1,108)	1:21:V:LEU:H	1:18:V:GLU:CB	5	0.34
(1,108)	1:21:V:LEU:H	1:18:V:GLU:CB	15	0.34
(1,107)	1:21:V:LEU:H	1:18:V:GLU:CA	6	0.34
(1,104)	1:20:V:ALA:H	1:21:V:LEU:CB	13	0.34
(1,94)	1:20:V:ALA:H	1:17:V:LYS:CB	5	0.34
(1,81)	1:19:V:ILE:H	1:17:V:LYS:CB	7	0.34
(1,81)	1:19:V:ILE:H	1:17:V:LYS:CB	19	0.34
(1,81)	1:19:V:ILE:H	1:17:V:LYS:CB	20	0.34
(1,41)	1:15:V:MET:H	1:12:V:ALA:CB	13	0.34
(1,18)	1:13:V:GLN:H	1:10:V:ARG:CB	8	0.34
(5,55)	1:35:V:MET:C	1:57:V:LEU:H	19	0.33
(5,47)	1:83:V:LEU:C	1:87:V:MET:H	15	0.33
(5,39)	1:75:V:ALA:C	1:79:V:ILE:H	1	0.33
(5,26)	1:61:V:ASP:C	1:65:V:VAL:H	6	0.33
(5,6)	1:14:V:GLU:C	1:18:V:GLU:H	4	0.33
(5,1)	1:9:V:GLN:C	1:13:V:GLN:H	7	0.33
(4,75)	1:73:V:GLN:O	1:76:V:SER:H	8	0.33
(4,49)	1:58:V:ASN:O	1:61:V:ASP:H	15	0.33
(4,17)	1:17:V:LYS:O	1:21:V:LEU:H	15	0.33
(3,535)	1:78:V:PHE:H	1:75:V:ALA:HA	4	0.33
(3,535)	1:78:V:PHE:H	1:75:V:ALA:HA	8	0.33
(3,487)	1:72:V:LEU:H	1:71:V:ALA:HB1	9	0.33
(2,65)	1:19:V:ILE:HG13	1:87:V:MET:HE1	17	0.33
(1,556)	1:86:V:ALA:H	1:82:V:LEU:CB	20	0.33
(1,536)	1:83:V:LEU:H	1:85:V:LYS:CG	18	0.33
(1,475)	1:76:V:SER:H	1:73:V:GLN:CA	1	0.33
(1,456)	1:74:V:GLU:H	1:70:V:LYS:CG	7	0.33
(1,325)	1:60:V:LYS:H	1:57:V:LEU:CA	17	0.33
(1,254)	1:47:V:LEU:H	1:45:V:ARG:CA	7	0.33
(1,238)	1:43:V:MET:H	1:42:V:GLU:CG	5	0.33
(1,175)	1:27:V:ILE:H	1:25:V:ARG:CB	8	0.33
(1,107)	1:21:V:LEU:H	1:18:V:GLU:CA	1	0.33
(1,107)	1:21:V:LEU:H	1:18:V:GLU:CA	7	0.33
(1,50)	1:16:V:GLN:H	1:13:V:GLN:CA	6	0.33
(1,50)	1:16:V:GLN:H	1:13:V:GLN:CA	10	0.33
(5,55)	1:35:V:MET:C	1:57:V:LEU:H	3	0.32
(5,55)	1:35:V:MET:C	1:57:V:LEU:H	7	0.32

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(5,45)	1:81:V:SER:C	1:85:V:LYS:H	18	0.32
(5,37)	1:71:V:ALA:C	1:75:V:ALA:H	15	0.32
(5,28)	1:63:V:ASP:C	1:67:V:ALA:H	3	0.32
(5,26)	1:61:V:ASP:C	1:65:V:VAL:H	2	0.32
(5,12)	1:21:V:LEU:C	1:25:V:ARG:H	9	0.32
(5,1)	1:9:V:GLN:C	1:13:V:GLN:H	4	0.32
(4,49)	1:58:V:ASN:O	1:61:V:ASP:H	3	0.32
(4,48)	1:57:V:LEU:O	1:60:V:LYS:N	7	0.32
(3,650)	1:92:V:VAL:H	1:90:V:ARG:HA	2	0.32
(3,650)	1:92:V:VAL:H	1:90:V:ARG:HA	5	0.32
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB2	19	0.32
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB3	19	0.32
(3,403)	1:61:V:ASP:H	1:64:V:ALA:HB1	16	0.32
(3,356)	1:53:V:TYR:H	1:42:V:GLU:H	9	0.32
(3,338)	1:51:V:LYS:H	1:44:V:SER:H	1	0.32
(3,334)	1:51:V:LYS:H	1:41:V:VAL:HA	6	0.32
(3,334)	1:51:V:LYS:H	1:41:V:VAL:HA	17	0.32
(3,280)	1:44:V:SER:H	1:51:V:LYS:H	1	0.32
(3,265)	1:42:V:GLU:H	1:53:V:TYR:H	9	0.32
(3,114)	1:21:V:LEU:H	1:18:V:GLU:HA	4	0.32
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD2	8	0.32
(2,324)	1:85:V:LYS:HA	1:85:V:LYS:HD3	8	0.32
(2,177)	1:43:V:MET:HB2	1:43:V:MET:HE1	14	0.32
(2,177)	1:43:V:MET:HB3	1:43:V:MET:HE1	14	0.32
(1,556)	1:86:V:ALA:H	1:82:V:LEU:CB	2	0.32
(1,556)	1:86:V:ALA:H	1:82:V:LEU:CB	18	0.32
(1,477)	1:76:V:SER:H	1:74:V:GLU:CA	4	0.32
(1,287)	1:51:V:LYS:H	1:42:V:GLU:CG	15	0.32
(1,287)	1:51:V:LYS:H	1:42:V:GLU:CG	17	0.32
(1,254)	1:47:V:LEU:H	1:45:V:ARG:CA	5	0.32
(1,254)	1:47:V:LEU:H	1:45:V:ARG:CA	8	0.32
(1,108)	1:21:V:LEU:H	1:18:V:GLU:CB	9	0.32
(1,41)	1:15:V:MET:H	1:12:V:ALA:CB	15	0.32
(5,55)	1:35:V:MET:C	1:57:V:LEU:H	17	0.31
(5,26)	1:61:V:ASP:C	1:65:V:VAL:H	18	0.31
(5,12)	1:21:V:LEU:C	1:25:V:ARG:H	2	0.31
(5,10)	1:18:V:GLU:C	1:22:V:ILE:H	20	0.31
(5,9)	1:17:V:LYS:C	1:21:V:LEU:H	5	0.31
(5,5)	1:13:V:GLN:C	1:17:V:LYS:H	17	0.31
(5,1)	1:9:V:GLN:C	1:13:V:GLN:H	1	0.31
(5,1)	1:9:V:GLN:C	1:13:V:GLN:H	10	0.31
(4,81)	1:77:V:GLY:O	1:81:V:SER:H	14	0.31

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,23)	1:21:V:LEU:O	1:25:V:ARG:H	19	0.31
(3,535)	1:78:V:PHE:H	1:75:V:ALA:HA	16	0.31
(3,487)	1:72:V:LEU:H	1:71:V:ALA:HB1	5	0.31
(2,65)	1:19:V:ILE:HG13	1:87:V:MET:HE1	2	0.31
(1,556)	1:86:V:ALA:H	1:82:V:LEU:CB	7	0.31
(1,556)	1:86:V:ALA:H	1:82:V:LEU:CB	15	0.31
(1,477)	1:76:V:SER:H	1:74:V:GLU:CA	20	0.31
(1,475)	1:76:V:SER:H	1:73:V:GLN:CA	19	0.31
(1,394)	1:68:V:GLY:H	1:64:V:ALA:CB	19	0.31
(1,325)	1:60:V:LYS:H	1:57:V:LEU:CA	16	0.31
(1,269)	1:49:V:TYR:H	1:44:V:SER:CB	10	0.31
(1,269)	1:49:V:TYR:H	1:44:V:SER:CB	13	0.31
(1,175)	1:27:V:ILE:H	1:25:V:ARG:CB	19	0.31
(1,104)	1:20:V:ALA:H	1:21:V:LEU:CB	16	0.31
(1,94)	1:20:V:ALA:H	1:17:V:LYS:CB	8	0.31
(1,81)	1:19:V:ILE:H	1:17:V:LYS:CB	10	0.31
(1,50)	1:16:V:GLN:H	1:13:V:GLN:CA	20	0.31
(1,18)	1:13:V:GLN:H	1:10:V:ARG:CB	12	0.31
(5,37)	1:71:V:ALA:C	1:75:V:ALA:H	7	0.3
(5,9)	1:17:V:LYS:C	1:21:V:LEU:H	19	0.3
(5,5)	1:13:V:GLN:C	1:17:V:LYS:H	12	0.3
(4,81)	1:77:V:GLY:O	1:81:V:SER:H	8	0.3
(4,18)	1:17:V:LYS:O	1:21:V:LEU:N	12	0.3
(4,17)	1:17:V:LYS:O	1:21:V:LEU:H	4	0.3
(4,17)	1:17:V:LYS:O	1:21:V:LEU:H	10	0.3
(4,9)	1:13:V:GLN:O	1:17:V:LYS:H	16	0.3
(3,487)	1:72:V:LEU:H	1:71:V:ALA:HB1	12	0.3
(3,487)	1:72:V:LEU:H	1:71:V:ALA:HB1	13	0.3
(3,422)	1:65:V:VAL:H	1:62:V:GLU:HA	16	0.3
(1,612)	1:96:V:THR:H	1:50:V:ALA:CB	14	0.3
(1,484)	1:78:V:PHE:H	1:75:V:ALA:CB	17	0.3
(1,475)	1:76:V:SER:H	1:73:V:GLN:CA	11	0.3
(1,475)	1:76:V:SER:H	1:73:V:GLN:CA	12	0.3
(1,475)	1:76:V:SER:H	1:73:V:GLN:CA	13	0.3
(1,394)	1:68:V:GLY:H	1:64:V:ALA:CB	14	0.3
(1,386)	1:67:V:ALA:H	1:66:V:LYS:CD	13	0.3
(1,174)	1:27:V:ILE:H	1:24:V:GLN:CA	18	0.3
(1,108)	1:21:V:LEU:H	1:18:V:GLU:CB	10	0.3
(1,104)	1:20:V:ALA:H	1:21:V:LEU:CB	1	0.3
(1,104)	1:20:V:ALA:H	1:21:V:LEU:CB	11	0.3
(1,41)	1:15:V:MET:H	1:12:V:ALA:CB	9	0.3
(1,18)	1:13:V:GLN:H	1:10:V:ARG:CB	2	0.3

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(5,31)	1:66:V:LYS:C	1:70:V:LYS:H	13	0.29
(5,25)	1:58:V:ASN:C	1:61:V:ASP:H	4	0.29
(5,25)	1:58:V:ASN:C	1:61:V:ASP:H	5	0.29
(5,9)	1:17:V:LYS:C	1:21:V:LEU:H	3	0.29
(5,2)	1:10:V:ARG:C	1:14:V:GLU:H	11	0.29
(4,109)	1:35:V:MET:O	1:57:V:LEU:H	8	0.29
(4,109)	1:35:V:MET:O	1:57:V:LEU:H	19	0.29
(4,90)	1:81:V:SER:O	1:85:V:LYS:N	6	0.29
(4,73)	1:71:V:ALA:O	1:75:V:ALA:H	15	0.29
(3,650)	1:92:V:VAL:H	1:90:V:ARG:HA	12	0.29
(3,495)	1:73:V:GLN:H	1:70:V:LYS:HA	5	0.29
(3,495)	1:73:V:GLN:H	1:70:V:LYS:HA	16	0.29
(3,487)	1:72:V:LEU:H	1:71:V:ALA:HB1	1	0.29
(3,487)	1:72:V:LEU:H	1:71:V:ALA:HB1	14	0.29
(3,483)	1:72:V:LEU:H	1:69:V:ILE:HA	7	0.29
(3,422)	1:65:V:VAL:H	1:62:V:GLU:HA	7	0.29
(3,356)	1:53:V:TYR:H	1:42:V:GLU:H	18	0.29
(3,325)	1:50:V:ALA:H	1:50:V:ALA:HB1	17	0.29
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB2	20	0.29
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB3	20	0.29
(3,265)	1:42:V:GLU:H	1:53:V:TYR:H	18	0.29
(1,612)	1:96:V:THR:H	1:50:V:ALA:CB	18	0.29
(1,587)	1:92:V:VAL:H	1:89:V:LEU:CG	16	0.29
(1,477)	1:76:V:SER:H	1:74:V:GLU:CA	15	0.29
(1,477)	1:76:V:SER:H	1:74:V:GLU:CA	19	0.29
(1,386)	1:67:V:ALA:H	1:66:V:LYS:CD	19	0.29
(1,339)	1:61:V:ASP:H	1:60:V:LYS:CE	11	0.29
(1,327)	1:60:V:LYS:H	1:58:V:ASN:CA	6	0.29
(1,254)	1:47:V:LEU:H	1:45:V:ARG:CA	9	0.29
(1,238)	1:43:V:MET:H	1:42:V:GLU:CG	6	0.29
(1,175)	1:27:V:ILE:H	1:25:V:ARG:CB	3	0.29
(1,107)	1:21:V:LEU:H	1:18:V:GLU:CA	18	0.29
(1,104)	1:20:V:ALA:H	1:21:V:LEU:CB	4	0.29
(1,104)	1:20:V:ALA:H	1:21:V:LEU:CB	10	0.29
(1,94)	1:20:V:ALA:H	1:17:V:LYS:CB	16	0.29
(1,81)	1:19:V:ILE:H	1:17:V:LYS:CB	3	0.29
(1,50)	1:16:V:GLN:H	1:13:V:GLN:CA	17	0.29
(1,18)	1:13:V:GLN:H	1:10:V:ARG:CB	6	0.29
(1,18)	1:13:V:GLN:H	1:10:V:ARG:CB	18	0.29
(5,37)	1:71:V:ALA:C	1:75:V:ALA:H	12	0.28
(5,37)	1:71:V:ALA:C	1:75:V:ALA:H	19	0.28
(5,36)	1:70:V:LYS:C	1:74:V:GLU:H	1	0.28

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(5,32)	1:67:V:ALA:C	1:71:V:ALA:H	2	0.28
(5,26)	1:61:V:ASP:C	1:65:V:VAL:H	10	0.28
(5,26)	1:61:V:ASP:C	1:65:V:VAL:H	11	0.28
(5,26)	1:61:V:ASP:C	1:65:V:VAL:H	20	0.28
(5,25)	1:58:V:ASN:C	1:61:V:ASP:H	2	0.28
(5,11)	1:19:V:ILE:C	1:23:V:LEU:H	5	0.28
(5,9)	1:17:V:LYS:C	1:21:V:LEU:H	20	0.28
(5,6)	1:14:V:GLU:C	1:18:V:GLU:H	13	0.28
(4,110)	1:35:V:MET:O	1:57:V:LEU:N	20	0.28
(4,9)	1:13:V:GLN:O	1:17:V:LYS:H	4	0.28
(4,3)	1:10:V:ARG:O	1:14:V:GLU:H	6	0.28
(3,495)	1:73:V:GLN:H	1:70:V:LYS:HA	1	0.28
(3,487)	1:72:V:LEU:H	1:71:V:ALA:HB1	15	0.28
(3,487)	1:72:V:LEU:H	1:71:V:ALA:HB1	18	0.28
(3,483)	1:72:V:LEU:H	1:69:V:ILE:HA	13	0.28
(3,356)	1:53:V:TYR:H	1:42:V:GLU:H	16	0.28
(3,338)	1:51:V:LYS:H	1:44:V:SER:H	19	0.28
(3,325)	1:50:V:ALA:H	1:50:V:ALA:HB1	15	0.28
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB2	18	0.28
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB3	18	0.28
(3,280)	1:44:V:SER:H	1:51:V:LYS:H	19	0.28
(3,265)	1:42:V:GLU:H	1:53:V:TYR:H	16	0.28
(3,194)	1:27:V:ILE:H	1:27:V:ILE:HB	12	0.28
(3,100)	1:20:V:ALA:H	1:16:V:GLN:HB2	17	0.28
(3,100)	1:20:V:ALA:H	1:16:V:GLN:HB3	17	0.28
(3,42)	1:15:V:MET:H	1:12:V:ALA:HA	20	0.28
(1,556)	1:86:V:ALA:H	1:82:V:LEU:CB	3	0.28
(1,477)	1:76:V:SER:H	1:74:V:GLU:CA	1	0.28
(1,325)	1:60:V:LYS:H	1:57:V:LEU:CA	18	0.28
(1,254)	1:47:V:LEU:H	1:45:V:ARG:CA	11	0.28
(1,254)	1:47:V:LEU:H	1:45:V:ARG:CA	16	0.28
(1,238)	1:43:V:MET:H	1:42:V:GLU:CG	13	0.28
(1,238)	1:43:V:MET:H	1:42:V:GLU:CG	14	0.28
(1,221)	1:41:V:VAL:H	1:38:V:VAL:CB	9	0.28
(1,216)	1:40:V:GLY:H	1:39:V:SER:CB	19	0.28
(1,108)	1:21:V:LEU:H	1:18:V:GLU:CB	16	0.28
(1,104)	1:20:V:ALA:H	1:21:V:LEU:CB	8	0.28
(1,41)	1:15:V:MET:H	1:12:V:ALA:CB	12	0.28
(1,18)	1:13:V:GLN:H	1:10:V:ARG:CB	20	0.28
(5,55)	1:35:V:MET:C	1:57:V:LEU:H	4	0.27
(5,37)	1:71:V:ALA:C	1:75:V:ALA:H	14	0.27
(5,19)	1:50:V:ALA:C	1:96:V:THR:H	2	0.27

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(5,12)	1:21:V:LEU:C	1:25:V:ARG:H	1	0.27
(5,12)	1:21:V:LEU:C	1:25:V:ARG:H	17	0.27
(5,10)	1:18:V:GLU:C	1:22:V:ILE:H	9	0.27
(5,10)	1:18:V:GLU:C	1:22:V:ILE:H	17	0.27
(5,9)	1:17:V:LYS:C	1:21:V:LEU:H	17	0.27
(5,5)	1:13:V:GLN:C	1:17:V:LYS:H	3	0.27
(4,110)	1:35:V:MET:O	1:57:V:LEU:N	3	0.27
(4,110)	1:35:V:MET:O	1:57:V:LEU:N	10	0.27
(4,75)	1:73:V:GLN:O	1:76:V:SER:H	9	0.27
(4,73)	1:71:V:ALA:O	1:75:V:ALA:H	12	0.27
(4,50)	1:58:V:ASN:O	1:61:V:ASP:N	3	0.27
(4,49)	1:58:V:ASN:O	1:61:V:ASP:H	19	0.27
(4,23)	1:21:V:LEU:O	1:25:V:ARG:H	5	0.27
(4,18)	1:17:V:LYS:O	1:21:V:LEU:N	2	0.27
(3,495)	1:73:V:GLN:H	1:70:V:LYS:HA	6	0.27
(3,495)	1:73:V:GLN:H	1:70:V:LYS:HA	19	0.27
(3,487)	1:72:V:LEU:H	1:71:V:ALA:HB1	16	0.27
(3,487)	1:72:V:LEU:H	1:71:V:ALA:HB1	19	0.27
(3,403)	1:61:V:ASP:H	1:64:V:ALA:HB1	20	0.27
(3,325)	1:50:V:ALA:H	1:50:V:ALA:HB1	4	0.27
(3,325)	1:50:V:ALA:H	1:50:V:ALA:HB1	11	0.27
(3,325)	1:50:V:ALA:H	1:50:V:ALA:HB1	19	0.27
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB2	2	0.27
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB3	2	0.27
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB2	6	0.27
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB3	6	0.27
(3,165)	1:25:V:ARG:H	1:21:V:LEU:HG	15	0.27
(3,114)	1:21:V:LEU:H	1:18:V:GLU:HA	17	0.27
(3,54)	1:16:V:GLN:H	1:13:V:GLN:HA	13	0.27
(2,177)	1:43:V:MET:HB2	1:43:V:MET:HE1	4	0.27
(2,177)	1:43:V:MET:HB3	1:43:V:MET:HE1	4	0.27
(1,580)	1:91:V:ILE:H	1:90:V:ARG:CB	12	0.27
(1,556)	1:86:V:ALA:H	1:82:V:LEU:CB	14	0.27
(1,556)	1:86:V:ALA:H	1:82:V:LEU:CB	16	0.27
(1,477)	1:76:V:SER:H	1:74:V:GLU:CA	7	0.27
(1,477)	1:76:V:SER:H	1:74:V:GLU:CA	12	0.27
(1,476)	1:76:V:SER:H	1:74:V:GLU:CB	3	0.27
(1,475)	1:76:V:SER:H	1:73:V:GLN:CA	6	0.27
(1,475)	1:76:V:SER:H	1:73:V:GLN:CA	7	0.27
(1,456)	1:74:V:GLU:H	1:70:V:LYS:CG	5	0.27
(1,342)	1:61:V:ASP:H	1:60:V:LYS:CB	8	0.27
(1,342)	1:61:V:ASP:H	1:60:V:LYS:CB	14	0.27

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,339)	1:61:V:ASP:H	1:60:V:LYS:CE	8	0.27
(1,254)	1:47:V:LEU:H	1:45:V:ARG:CA	10	0.27
(1,175)	1:27:V:ILE:H	1:25:V:ARG:CB	16	0.27
(1,104)	1:20:V:ALA:H	1:21:V:LEU:CB	14	0.27
(1,104)	1:20:V:ALA:H	1:21:V:LEU:CB	17	0.27
(1,50)	1:16:V:GLN:H	1:13:V:GLN:CA	19	0.27
(5,55)	1:35:V:MET:C	1:57:V:LEU:H	16	0.26
(5,45)	1:81:V:SER:C	1:85:V:LYS:H	8	0.26
(5,39)	1:75:V:ALA:C	1:79:V:ILE:H	3	0.26
(5,39)	1:75:V:ALA:C	1:79:V:ILE:H	13	0.26
(5,39)	1:75:V:ALA:C	1:79:V:ILE:H	19	0.26
(5,26)	1:61:V:ASP:C	1:65:V:VAL:H	5	0.26
(5,26)	1:61:V:ASP:C	1:65:V:VAL:H	8	0.26
(5,19)	1:50:V:ALA:C	1:96:V:THR:H	15	0.26
(5,19)	1:50:V:ALA:C	1:96:V:THR:H	18	0.26
(5,7)	1:15:V:MET:C	1:19:V:ILE:H	3	0.26
(5,1)	1:9:V:GLN:C	1:13:V:GLN:H	20	0.26
(4,50)	1:58:V:ASN:O	1:61:V:ASP:N	15	0.26
(4,23)	1:21:V:LEU:O	1:25:V:ARG:H	7	0.26
(3,535)	1:78:V:PHE:H	1:75:V:ALA:HA	2	0.26
(3,487)	1:72:V:LEU:H	1:71:V:ALA:HB1	3	0.26
(3,422)	1:65:V:VAL:H	1:62:V:GLU:HA	8	0.26
(3,356)	1:53:V:TYR:H	1:42:V:GLU:H	3	0.26
(3,338)	1:51:V:LYS:H	1:44:V:SER:H	3	0.26
(3,338)	1:51:V:LYS:H	1:44:V:SER:H	18	0.26
(3,325)	1:50:V:ALA:H	1:50:V:ALA:HB1	5	0.26
(3,325)	1:50:V:ALA:H	1:50:V:ALA:HB1	8	0.26
(3,325)	1:50:V:ALA:H	1:50:V:ALA:HB1	10	0.26
(3,325)	1:50:V:ALA:H	1:50:V:ALA:HB1	12	0.26
(3,325)	1:50:V:ALA:H	1:50:V:ALA:HB1	13	0.26
(3,325)	1:50:V:ALA:H	1:50:V:ALA:HB1	16	0.26
(3,325)	1:50:V:ALA:H	1:50:V:ALA:HB1	20	0.26
(3,280)	1:44:V:SER:H	1:51:V:LYS:H	3	0.26
(3,280)	1:44:V:SER:H	1:51:V:LYS:H	18	0.26
(3,265)	1:42:V:GLU:H	1:53:V:TYR:H	3	0.26
(3,194)	1:27:V:ILE:H	1:27:V:ILE:HB	13	0.26
(3,177)	1:26:V:GLU:H	1:22:V:ILE:HA	15	0.26
(3,114)	1:21:V:LEU:H	1:18:V:GLU:HA	5	0.26
(3,114)	1:21:V:LEU:H	1:18:V:GLU:HA	20	0.26
(1,612)	1:96:V:THR:H	1:50:V:ALA:CB	7	0.26
(1,587)	1:92:V:VAL:H	1:89:V:LEU:CG	7	0.26
(1,580)	1:91:V:ILE:H	1:90:V:ARG:CB	10	0.26

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,556)	1:86:V:ALA:H	1:82:V:LEU:CB	1	0.26
(1,477)	1:76:V:SER:H	1:74:V:GLU:CA	2	0.26
(1,477)	1:76:V:SER:H	1:74:V:GLU:CA	14	0.26
(1,477)	1:76:V:SER:H	1:74:V:GLU:CA	17	0.26
(1,475)	1:76:V:SER:H	1:73:V:GLN:CA	10	0.26
(1,386)	1:67:V:ALA:H	1:66:V:LYS:CD	1	0.26
(1,386)	1:67:V:ALA:H	1:66:V:LYS:CD	3	0.26
(1,342)	1:61:V:ASP:H	1:60:V:LYS:CB	4	0.26
(1,325)	1:60:V:LYS:H	1:57:V:LEU:CA	11	0.26
(1,254)	1:47:V:LEU:H	1:45:V:ARG:CA	15	0.26
(1,104)	1:20:V:ALA:H	1:21:V:LEU:CB	12	0.26
(1,50)	1:16:V:GLN:H	1:13:V:GLN:CA	9	0.26
(1,41)	1:15:V:MET:H	1:12:V:ALA:CB	1	0.26
(1,41)	1:15:V:MET:H	1:12:V:ALA:CB	5	0.26
(5,55)	1:35:V:MET:C	1:57:V:LEU:H	1	0.25
(5,55)	1:35:V:MET:C	1:57:V:LEU:H	12	0.25
(5,49)	1:49:V:TYR:C	1:44:V:SER:H	1	0.25
(5,47)	1:83:V:LEU:C	1:87:V:MET:H	14	0.25
(5,44)	1:80:V:ARG:C	1:84:V:GLY:H	6	0.25
(5,41)	1:77:V:GLY:C	1:81:V:SER:H	8	0.25
(5,19)	1:50:V:ALA:C	1:96:V:THR:H	1	0.25
(5,12)	1:21:V:LEU:C	1:25:V:ARG:H	4	0.25
(5,11)	1:19:V:ILE:C	1:23:V:LEU:H	17	0.25
(5,5)	1:13:V:GLN:C	1:17:V:LYS:H	14	0.25
(4,76)	1:73:V:GLN:O	1:76:V:SER:N	8	0.25
(4,51)	1:61:V:ASP:O	1:65:V:VAL:H	3	0.25
(4,49)	1:58:V:ASN:O	1:61:V:ASP:H	2	0.25
(4,23)	1:21:V:LEU:O	1:25:V:ARG:H	12	0.25
(4,10)	1:13:V:GLN:O	1:17:V:LYS:N	16	0.25
(3,422)	1:65:V:VAL:H	1:62:V:GLU:HA	5	0.25
(3,370)	1:55:V:THR:H	1:37:V:THR:HB	19	0.25
(3,356)	1:53:V:TYR:H	1:42:V:GLU:H	7	0.25
(3,334)	1:51:V:LYS:H	1:41:V:VAL:HA	13	0.25
(3,325)	1:50:V:ALA:H	1:50:V:ALA:HB1	1	0.25
(3,325)	1:50:V:ALA:H	1:50:V:ALA:HB1	2	0.25
(3,325)	1:50:V:ALA:H	1:50:V:ALA:HB1	3	0.25
(3,325)	1:50:V:ALA:H	1:50:V:ALA:HB1	6	0.25
(3,325)	1:50:V:ALA:H	1:50:V:ALA:HB1	7	0.25
(3,325)	1:50:V:ALA:H	1:50:V:ALA:HB1	14	0.25
(3,325)	1:50:V:ALA:H	1:50:V:ALA:HB1	18	0.25
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB2	11	0.25
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB3	11	0.25

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,278)	1:44:V:SER:H	1:50:V:ALA:HA	2	0.25
(3,265)	1:42:V:GLU:H	1:53:V:TYR:H	7	0.25
(3,194)	1:27:V:ILE:H	1:27:V:ILE:HB	3	0.25
(3,177)	1:26:V:GLU:H	1:22:V:ILE:HA	5	0.25
(3,42)	1:15:V:MET:H	1:12:V:ALA:HA	4	0.25
(1,556)	1:86:V:ALA:H	1:82:V:LEU:CB	5	0.25
(1,556)	1:86:V:ALA:H	1:82:V:LEU:CB	13	0.25
(1,536)	1:83:V:LEU:H	1:85:V:LYS:CG	7	0.25
(1,475)	1:76:V:SER:H	1:73:V:GLN:CA	15	0.25
(1,475)	1:76:V:SER:H	1:73:V:GLN:CA	20	0.25
(1,342)	1:61:V:ASP:H	1:60:V:LYS:CB	15	0.25
(1,254)	1:47:V:LEU:H	1:45:V:ARG:CA	12	0.25
(1,108)	1:21:V:LEU:H	1:18:V:GLU:CB	2	0.25
(1,108)	1:21:V:LEU:H	1:18:V:GLU:CB	12	0.25
(1,108)	1:21:V:LEU:H	1:18:V:GLU:CB	19	0.25
(1,104)	1:20:V:ALA:H	1:21:V:LEU:CB	15	0.25
(1,104)	1:20:V:ALA:H	1:21:V:LEU:CB	20	0.25
(1,50)	1:16:V:GLN:H	1:13:V:GLN:CA	11	0.25
(1,41)	1:15:V:MET:H	1:12:V:ALA:CB	6	0.25
(5,48)	1:84:V:GLY:C	1:89:V:LEU:H	5	0.24
(5,37)	1:71:V:ALA:C	1:75:V:ALA:H	11	0.24
(5,28)	1:63:V:ASP:C	1:67:V:ALA:H	9	0.24
(5,28)	1:63:V:ASP:C	1:67:V:ALA:H	13	0.24
(5,19)	1:50:V:ALA:C	1:96:V:THR:H	7	0.24
(5,19)	1:50:V:ALA:C	1:96:V:THR:H	14	0.24
(5,19)	1:50:V:ALA:C	1:96:V:THR:H	20	0.24
(5,12)	1:21:V:LEU:C	1:25:V:ARG:H	14	0.24
(5,4)	1:12:V:ALA:C	1:16:V:GLN:H	4	0.24
(4,107)	1:30:V:PRO:O	1:33:V:GLY:H	3	0.24
(4,82)	1:77:V:GLY:O	1:81:V:SER:N	14	0.24
(4,51)	1:61:V:ASP:O	1:65:V:VAL:H	19	0.24
(3,512)	1:74:V:GLU:H	1:74:V:GLU:HG2	5	0.24
(3,512)	1:74:V:GLU:H	1:74:V:GLU:HG3	5	0.24
(3,495)	1:73:V:GLN:H	1:70:V:LYS:HA	17	0.24
(3,487)	1:72:V:LEU:H	1:71:V:ALA:HB1	20	0.24
(3,483)	1:72:V:LEU:H	1:69:V:ILE:HA	16	0.24
(3,422)	1:65:V:VAL:H	1:62:V:GLU:HA	17	0.24
(3,356)	1:53:V:TYR:H	1:42:V:GLU:H	2	0.24
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB2	1	0.24
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB3	1	0.24
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB2	4	0.24
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB3	4	0.24

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB2	12	0.24
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB3	12	0.24
(3,265)	1:42:V:GLU:H	1:53:V:TYR:H	2	0.24
(2,176)	1:43:V:MET:HG2	1:43:V:MET:HE1	10	0.24
(2,176)	1:43:V:MET:HG3	1:43:V:MET:HE1	10	0.24
(2,65)	1:19:V:ILE:HG13	1:87:V:MET:HE1	10	0.24
(1,569)	1:87:V:MET:H	1:87:V:MET:CE	5	0.24
(1,484)	1:78:V:PHE:H	1:75:V:ALA:CB	3	0.24
(1,477)	1:76:V:SER:H	1:74:V:GLU:CA	6	0.24
(1,475)	1:76:V:SER:H	1:73:V:GLN:CA	5	0.24
(1,456)	1:74:V:GLU:H	1:70:V:LYS:CG	11	0.24
(1,456)	1:74:V:GLU:H	1:70:V:LYS:CG	20	0.24
(1,386)	1:67:V:ALA:H	1:66:V:LYS:CD	4	0.24
(1,342)	1:61:V:ASP:H	1:60:V:LYS:CB	6	0.24
(1,216)	1:40:V:GLY:H	1:39:V:SER:CB	5	0.24
(1,104)	1:20:V:ALA:H	1:21:V:LEU:CB	9	0.24
(1,50)	1:16:V:GLN:H	1:13:V:GLN:CA	8	0.24
(1,41)	1:15:V:MET:H	1:12:V:ALA:CB	11	0.24
(1,41)	1:15:V:MET:H	1:12:V:ALA:CB	18	0.24
(1,18)	1:13:V:GLN:H	1:10:V:ARG:CB	11	0.24
(5,49)	1:49:V:TYR:C	1:44:V:SER:H	2	0.23
(5,47)	1:83:V:LEU:C	1:87:V:MET:H	20	0.23
(5,45)	1:81:V:SER:C	1:85:V:LYS:H	20	0.23
(5,19)	1:50:V:ALA:C	1:96:V:THR:H	12	0.23
(5,12)	1:21:V:LEU:C	1:25:V:ARG:H	10	0.23
(5,10)	1:18:V:GLU:C	1:22:V:ILE:H	15	0.23
(5,10)	1:18:V:GLU:C	1:22:V:ILE:H	18	0.23
(5,9)	1:17:V:LYS:C	1:21:V:LEU:H	7	0.23
(5,4)	1:12:V:ALA:C	1:16:V:GLN:H	10	0.23
(5,2)	1:10:V:ARG:C	1:14:V:GLU:H	18	0.23
(5,1)	1:9:V:GLN:C	1:13:V:GLN:H	15	0.23
(4,110)	1:35:V:MET:O	1:57:V:LEU:N	16	0.23
(4,109)	1:35:V:MET:O	1:57:V:LEU:H	4	0.23
(4,93)	1:83:V:LEU:O	1:87:V:MET:H	6	0.23
(4,89)	1:81:V:SER:O	1:85:V:LYS:H	18	0.23
(4,73)	1:71:V:ALA:O	1:75:V:ALA:H	14	0.23
(4,23)	1:21:V:LEU:O	1:25:V:ARG:H	16	0.23
(4,17)	1:17:V:LYS:O	1:21:V:LEU:H	1	0.23
(4,17)	1:17:V:LYS:O	1:21:V:LEU:H	9	0.23
(3,487)	1:72:V:LEU:H	1:71:V:ALA:HB1	11	0.23
(3,483)	1:72:V:LEU:H	1:69:V:ILE:HA	18	0.23
(3,356)	1:53:V:TYR:H	1:42:V:GLU:H	1	0.23

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,356)	1:53:V:TYR:H	1:42:V:GLU:H	17	0.23
(3,355)	1:53:V:TYR:H	1:41:V:VAL:HA	2	0.23
(3,325)	1:50:V:ALA:H	1:50:V:ALA:HB1	9	0.23
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB2	7	0.23
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB3	7	0.23
(3,265)	1:42:V:GLU:H	1:53:V:TYR:H	1	0.23
(3,265)	1:42:V:GLU:H	1:53:V:TYR:H	17	0.23
(3,194)	1:27:V:ILE:H	1:27:V:ILE:HB	7	0.23
(3,194)	1:27:V:ILE:H	1:27:V:ILE:HB	14	0.23
(3,114)	1:21:V:LEU:H	1:18:V:GLU:HA	3	0.23
(3,114)	1:21:V:LEU:H	1:18:V:GLU:HA	9	0.23
(3,114)	1:21:V:LEU:H	1:18:V:GLU:HA	15	0.23
(3,32)	1:14:V:GLU:H	1:11:V:VAL:HA	10	0.23
(3,17)	1:13:V:GLN:H	1:10:V:ARG:HA	8	0.23
(2,176)	1:43:V:MET:HG2	1:43:V:MET:HE1	18	0.23
(2,176)	1:43:V:MET:HG3	1:43:V:MET:HE1	18	0.23
(1,556)	1:86:V:ALA:H	1:82:V:LEU:CB	8	0.23
(1,556)	1:86:V:ALA:H	1:82:V:LEU:CB	9	0.23
(1,536)	1:83:V:LEU:H	1:85:V:LYS:CG	12	0.23
(1,536)	1:83:V:LEU:H	1:85:V:LYS:CG	17	0.23
(1,536)	1:83:V:LEU:H	1:85:V:LYS:CG	20	0.23
(1,484)	1:78:V:PHE:H	1:75:V:ALA:CB	12	0.23
(1,477)	1:76:V:SER:H	1:74:V:GLU:CA	11	0.23
(1,477)	1:76:V:SER:H	1:74:V:GLU:CA	13	0.23
(1,475)	1:76:V:SER:H	1:73:V:GLN:CA	17	0.23
(1,342)	1:61:V:ASP:H	1:60:V:LYS:CB	17	0.23
(1,335)	1:60:V:LYS:H	1:64:V:ALA:CB	14	0.23
(1,254)	1:47:V:LEU:H	1:45:V:ARG:CA	13	0.23
(1,238)	1:43:V:MET:H	1:42:V:GLU:CG	4	0.23
(1,175)	1:27:V:ILE:H	1:25:V:ARG:CB	9	0.23
(1,175)	1:27:V:ILE:H	1:25:V:ARG:CB	15	0.23
(1,108)	1:21:V:LEU:H	1:18:V:GLU:CB	14	0.23
(1,104)	1:20:V:ALA:H	1:21:V:LEU:CB	19	0.23
(1,50)	1:16:V:GLN:H	1:13:V:GLN:CA	12	0.23
(5,49)	1:49:V:TYR:C	1:44:V:SER:H	11	0.22
(5,47)	1:83:V:LEU:C	1:87:V:MET:H	10	0.22
(5,39)	1:75:V:ALA:C	1:79:V:ILE:H	4	0.22
(5,37)	1:71:V:ALA:C	1:75:V:ALA:H	10	0.22
(5,31)	1:66:V:LYS:C	1:70:V:LYS:H	10	0.22
(5,25)	1:58:V:ASN:C	1:61:V:ASP:H	11	0.22
(5,14)	1:37:V:THR:H	1:55:V:THR:C	5	0.22
(5,1)	1:9:V:GLN:C	1:13:V:GLN:H	2	0.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(5,1)	1:9:V:GLN:C	1:13:V:GLN:H	11	0.22
(4,95)	1:84:V:GLY:O	1:89:V:LEU:H	12	0.22
(4,68)	1:68:V:GLY:O	1:71:V:ALA:N	19	0.22
(4,51)	1:61:V:ASP:O	1:65:V:VAL:H	16	0.22
(4,50)	1:58:V:ASN:O	1:61:V:ASP:N	19	0.22
(4,19)	1:18:V:GLU:O	1:22:V:ILE:H	5	0.22
(4,10)	1:13:V:GLN:O	1:17:V:LYS:N	4	0.22
(3,650)	1:92:V:VAL:H	1:90:V:ARG:HA	10	0.22
(3,334)	1:51:V:LYS:H	1:41:V:VAL:HA	10	0.22
(3,194)	1:27:V:ILE:H	1:27:V:ILE:HB	11	0.22
(3,100)	1:20:V:ALA:H	1:16:V:GLN:HB2	7	0.22
(3,100)	1:20:V:ALA:H	1:16:V:GLN:HB3	7	0.22
(3,32)	1:14:V:GLU:H	1:11:V:VAL:HA	4	0.22
(3,17)	1:13:V:GLN:H	1:10:V:ARG:HA	6	0.22
(2,176)	1:43:V:MET:HG2	1:43:V:MET:HE1	9	0.22
(2,176)	1:43:V:MET:HG3	1:43:V:MET:HE1	9	0.22
(2,176)	1:43:V:MET:HG2	1:43:V:MET:HE1	12	0.22
(2,176)	1:43:V:MET:HG3	1:43:V:MET:HE1	12	0.22
(2,151)	1:36:V:THR:HG21	1:27:V:ILE:HD13	18	0.22
(1,556)	1:86:V:ALA:H	1:82:V:LEU:CB	4	0.22
(1,556)	1:86:V:ALA:H	1:82:V:LEU:CB	11	0.22
(1,544)	1:84:V:GLY:H	1:85:V:LYS:CB	11	0.22
(1,544)	1:84:V:GLY:H	1:85:V:LYS:CB	19	0.22
(1,484)	1:78:V:PHE:H	1:75:V:ALA:CB	13	0.22
(1,477)	1:76:V:SER:H	1:74:V:GLU:CA	16	0.22
(1,471)	1:75:V:ALA:H	1:74:V:GLU:CB	4	0.22
(1,456)	1:74:V:GLU:H	1:70:V:LYS:CG	14	0.22
(1,342)	1:61:V:ASP:H	1:60:V:LYS:CB	11	0.22
(1,325)	1:60:V:LYS:H	1:57:V:LEU:CA	10	0.22
(1,238)	1:43:V:MET:H	1:42:V:GLU:CG	2	0.22
(1,216)	1:40:V:GLY:H	1:39:V:SER:CB	18	0.22
(1,175)	1:27:V:ILE:H	1:25:V:ARG:CB	1	0.22
(1,175)	1:27:V:ILE:H	1:25:V:ARG:CB	17	0.22
(1,174)	1:27:V:ILE:H	1:24:V:GLN:CA	10	0.22
(1,157)	1:25:V:ARG:H	1:24:V:GLN:CB	15	0.22
(1,108)	1:21:V:LEU:H	1:18:V:GLU:CB	6	0.22
(1,104)	1:20:V:ALA:H	1:21:V:LEU:CB	18	0.22
(1,50)	1:16:V:GLN:H	1:13:V:GLN:CA	14	0.22
(1,18)	1:13:V:GLN:H	1:10:V:ARG:CB	5	0.22
(5,48)	1:84:V:GLY:C	1:89:V:LEU:H	8	0.21
(5,48)	1:84:V:GLY:C	1:89:V:LEU:H	18	0.21
(5,45)	1:81:V:SER:C	1:85:V:LYS:H	1	0.21

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(5,45)	1:81:V:SER:C	1:85:V:LYS:H	16	0.21
(5,37)	1:71:V:ALA:C	1:75:V:ALA:H	16	0.21
(5,31)	1:66:V:LYS:C	1:70:V:LYS:H	7	0.21
(5,28)	1:63:V:ASP:C	1:67:V:ALA:H	12	0.21
(5,26)	1:61:V:ASP:C	1:65:V:VAL:H	1	0.21
(5,26)	1:61:V:ASP:C	1:65:V:VAL:H	17	0.21
(5,25)	1:58:V:ASN:C	1:61:V:ASP:H	1	0.21
(5,25)	1:58:V:ASN:C	1:61:V:ASP:H	17	0.21
(5,14)	1:37:V:THR:H	1:55:V:THR:C	10	0.21
(5,12)	1:21:V:LEU:C	1:25:V:ARG:H	18	0.21
(5,10)	1:18:V:GLU:C	1:22:V:ILE:H	4	0.21
(5,10)	1:18:V:GLU:C	1:22:V:ILE:H	10	0.21
(5,9)	1:17:V:LYS:C	1:21:V:LEU:H	14	0.21
(5,8)	1:16:V:GLN:C	1:20:V:ALA:H	14	0.21
(5,5)	1:13:V:GLN:C	1:17:V:LYS:H	18	0.21
(4,110)	1:35:V:MET:O	1:57:V:LEU:N	1	0.21
(4,93)	1:83:V:LEU:O	1:87:V:MET:H	1	0.21
(4,63)	1:67:V:ALA:O	1:71:V:ALA:H	2	0.21
(4,49)	1:58:V:ASN:O	1:61:V:ASP:H	5	0.21
(4,18)	1:17:V:LYS:O	1:21:V:LEU:N	15	0.21
(4,17)	1:17:V:LYS:O	1:21:V:LEU:H	11	0.21
(4,9)	1:13:V:GLN:O	1:17:V:LYS:H	1	0.21
(4,9)	1:13:V:GLN:O	1:17:V:LYS:H	17	0.21
(4,1)	1:9:V:GLN:O	1:13:V:GLN:H	1	0.21
(3,495)	1:73:V:GLN:H	1:70:V:LYS:HA	7	0.21
(3,495)	1:73:V:GLN:H	1:70:V:LYS:HA	11	0.21
(3,422)	1:65:V:VAL:H	1:62:V:GLU:HA	1	0.21
(3,422)	1:65:V:VAL:H	1:62:V:GLU:HA	2	0.21
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB2	3	0.21
(3,405)	1:63:V:ASP:H	1:61:V:ASP:HB3	3	0.21
(3,194)	1:27:V:ILE:H	1:27:V:ILE:HB	19	0.21
(3,100)	1:20:V:ALA:H	1:16:V:GLN:HB2	12	0.21
(3,100)	1:20:V:ALA:H	1:16:V:GLN:HB3	12	0.21
(3,42)	1:15:V:MET:H	1:12:V:ALA:HA	19	0.21
(3,17)	1:13:V:GLN:H	1:10:V:ARG:HA	17	0.21
(2,177)	1:43:V:MET:HB2	1:43:V:MET:HE1	1	0.21
(2,177)	1:43:V:MET:HB3	1:43:V:MET:HE1	1	0.21
(2,176)	1:43:V:MET:HG2	1:43:V:MET:HE1	3	0.21
(2,176)	1:43:V:MET:HG3	1:43:V:MET:HE1	3	0.21
(2,176)	1:43:V:MET:HG2	1:43:V:MET:HE1	7	0.21
(2,176)	1:43:V:MET:HG3	1:43:V:MET:HE1	7	0.21
(2,176)	1:43:V:MET:HG2	1:43:V:MET:HE1	15	0.21

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,176)	1:43:V:MET:HG3	1:43:V:MET:HE1	15	0.21
(2,176)	1:43:V:MET:HG2	1:43:V:MET:HE1	20	0.21
(2,176)	1:43:V:MET:HG3	1:43:V:MET:HE1	20	0.21
(1,544)	1:84:V:GLY:H	1:85:V:LYS:CB	20	0.21
(1,536)	1:83:V:LEU:H	1:85:V:LYS:CG	2	0.21
(1,484)	1:78:V:PHE:H	1:75:V:ALA:CB	15	0.21
(1,476)	1:76:V:SER:H	1:74:V:GLU:CB	4	0.21
(1,471)	1:75:V:ALA:H	1:74:V:GLU:CB	5	0.21
(1,386)	1:67:V:ALA:H	1:66:V:LYS:CD	18	0.21
(1,339)	1:61:V:ASP:H	1:60:V:LYS:CE	4	0.21
(1,278)	1:50:V:ALA:H	1:93:V:PRO:CG	16	0.21
(1,175)	1:27:V:ILE:H	1:25:V:ARG:CB	14	0.21
(1,108)	1:21:V:LEU:H	1:18:V:GLU:CB	7	0.21
(1,108)	1:21:V:LEU:H	1:18:V:GLU:CB	11	0.21
(1,18)	1:13:V:GLN:H	1:10:V:ARG:CB	3	0.21
(5,47)	1:83:V:LEU:C	1:87:V:MET:H	4	0.2
(5,47)	1:83:V:LEU:C	1:87:V:MET:H	7	0.2
(5,42)	1:78:V:PHE:C	1:82:V:LEU:H	20	0.2
(5,41)	1:77:V:GLY:C	1:81:V:SER:H	19	0.2
(5,39)	1:75:V:ALA:C	1:79:V:ILE:H	2	0.2
(5,36)	1:70:V:LYS:C	1:74:V:GLU:H	8	0.2
(5,31)	1:66:V:LYS:C	1:70:V:LYS:H	19	0.2
(5,29)	1:64:V:ALA:C	1:68:V:GLY:H	3	0.2
(5,25)	1:58:V:ASN:C	1:61:V:ASP:H	6	0.2
(5,25)	1:58:V:ASN:C	1:61:V:ASP:H	18	0.2
(5,21)	1:52:V:VAL:C	1:98:V:PHE:H	1	0.2
(5,21)	1:52:V:VAL:C	1:98:V:PHE:H	10	0.2
(5,21)	1:52:V:VAL:C	1:98:V:PHE:H	15	0.2
(5,19)	1:50:V:ALA:C	1:96:V:THR:H	13	0.2
(5,12)	1:21:V:LEU:C	1:25:V:ARG:H	11	0.2
(5,11)	1:19:V:ILE:C	1:23:V:LEU:H	9	0.2
(5,10)	1:18:V:GLU:C	1:22:V:ILE:H	2	0.2
(5,10)	1:18:V:GLU:C	1:22:V:ILE:H	3	0.2
(5,10)	1:18:V:GLU:C	1:22:V:ILE:H	14	0.2
(5,6)	1:14:V:GLU:C	1:18:V:GLU:H	19	0.2
(5,2)	1:10:V:ARG:C	1:14:V:GLU:H	19	0.2
(4,110)	1:35:V:MET:O	1:57:V:LEU:N	11	0.2
(4,109)	1:35:V:MET:O	1:57:V:LEU:H	7	0.2
(4,93)	1:83:V:LEU:O	1:87:V:MET:H	15	0.2
(4,76)	1:73:V:GLN:O	1:76:V:SER:N	9	0.2
(4,74)	1:71:V:ALA:O	1:75:V:ALA:N	13	0.2
(4,73)	1:71:V:ALA:O	1:75:V:ALA:H	19	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,68)	1:68:V:GLY:O	1:71:V:ALA:N	14	0.2
(4,50)	1:58:V:ASN:O	1:61:V:ASP:N	2	0.2
(4,49)	1:58:V:ASN:O	1:61:V:ASP:H	4	0.2
(4,18)	1:17:V:LYS:O	1:21:V:LEU:N	10	0.2
(4,15)	1:16:V:GLN:O	1:20:V:ALA:H	14	0.2
(4,3)	1:10:V:ARG:O	1:14:V:GLU:H	11	0.2
(3,487)	1:72:V:LEU:H	1:71:V:ALA:HB1	6	0.2
(3,483)	1:72:V:LEU:H	1:69:V:ILE:HA	6	0.2
(3,403)	1:61:V:ASP:H	1:64:V:ALA:HB1	9	0.2
(3,356)	1:53:V:TYR:H	1:42:V:GLU:H	13	0.2
(3,338)	1:51:V:LYS:H	1:44:V:SER:H	9	0.2
(3,334)	1:51:V:LYS:H	1:41:V:VAL:HA	5	0.2
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB2	17	0.2
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB3	17	0.2
(3,280)	1:44:V:SER:H	1:51:V:LYS:H	9	0.2
(3,265)	1:42:V:GLU:H	1:53:V:TYR:H	13	0.2
(3,194)	1:27:V:ILE:H	1:27:V:ILE:HB	1	0.2
(3,194)	1:27:V:ILE:H	1:27:V:ILE:HB	9	0.2
(3,194)	1:27:V:ILE:H	1:27:V:ILE:HB	15	0.2
(3,149)	1:24:V:GLN:H	1:20:V:ALA:HA	5	0.2
(3,42)	1:15:V:MET:H	1:12:V:ALA:HA	7	0.2
(3,42)	1:15:V:MET:H	1:12:V:ALA:HA	8	0.2
(3,32)	1:14:V:GLU:H	1:11:V:VAL:HA	2	0.2
(2,176)	1:43:V:MET:HG2	1:43:V:MET:HE1	5	0.2
(2,176)	1:43:V:MET:HG3	1:43:V:MET:HE1	5	0.2
(1,612)	1:96:V:THR:H	1:50:V:ALA:CB	13	0.2
(1,606)	1:95:V:LEU:H	1:94:V:GLU:CG	11	0.2
(1,484)	1:78:V:PHE:H	1:75:V:ALA:CB	14	0.2
(1,476)	1:76:V:SER:H	1:74:V:GLU:CB	10	0.2
(1,325)	1:60:V:LYS:H	1:57:V:LEU:CA	8	0.2
(1,325)	1:60:V:LYS:H	1:57:V:LEU:CA	9	0.2
(1,325)	1:60:V:LYS:H	1:57:V:LEU:CA	19	0.2
(1,287)	1:51:V:LYS:H	1:42:V:GLU:CG	3	0.2
(1,238)	1:43:V:MET:H	1:42:V:GLU:CG	1	0.2
(1,216)	1:40:V:GLY:H	1:39:V:SER:CB	3	0.2
(1,157)	1:25:V:ARG:H	1:24:V:GLN:CB	16	0.2
(1,108)	1:21:V:LEU:H	1:18:V:GLU:CB	13	0.2
(5,47)	1:83:V:LEU:C	1:87:V:MET:H	3	0.19
(5,44)	1:80:V:ARG:C	1:84:V:GLY:H	1	0.19
(5,41)	1:77:V:GLY:C	1:81:V:SER:H	7	0.19
(5,39)	1:75:V:ALA:C	1:79:V:ILE:H	10	0.19
(5,32)	1:67:V:ALA:C	1:71:V:ALA:H	3	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(5,27)	1:62:V:GLU:C	1:66:V:LYS:H	1	0.19
(5,21)	1:52:V:VAL:C	1:98:V:PHE:H	9	0.19
(5,21)	1:52:V:VAL:C	1:98:V:PHE:H	18	0.19
(5,19)	1:50:V:ALA:C	1:96:V:THR:H	9	0.19
(5,14)	1:37:V:THR:H	1:55:V:THR:C	20	0.19
(5,9)	1:17:V:LYS:C	1:21:V:LEU:H	6	0.19
(5,6)	1:14:V:GLU:C	1:18:V:GLU:H	18	0.19
(5,5)	1:13:V:GLN:C	1:17:V:LYS:H	5	0.19
(5,2)	1:10:V:ARG:C	1:14:V:GLU:H	4	0.19
(4,82)	1:77:V:GLY:O	1:81:V:SER:N	8	0.19
(4,55)	1:63:V:ASP:O	1:67:V:ALA:H	3	0.19
(4,19)	1:18:V:GLU:O	1:22:V:ILE:H	16	0.19
(4,17)	1:17:V:LYS:O	1:21:V:LEU:H	13	0.19
(4,3)	1:10:V:ARG:O	1:14:V:GLU:H	3	0.19
(3,495)	1:73:V:GLN:H	1:70:V:LYS:HA	8	0.19
(3,483)	1:72:V:LEU:H	1:69:V:ILE:HA	14	0.19
(3,422)	1:65:V:VAL:H	1:62:V:GLU:HA	4	0.19
(3,403)	1:61:V:ASP:H	1:64:V:ALA:HB1	7	0.19
(3,356)	1:53:V:TYR:H	1:42:V:GLU:H	14	0.19
(3,338)	1:51:V:LYS:H	1:44:V:SER:H	12	0.19
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB2	3	0.19
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB3	3	0.19
(3,280)	1:44:V:SER:H	1:51:V:LYS:H	12	0.19
(3,265)	1:42:V:GLU:H	1:53:V:TYR:H	14	0.19
(3,114)	1:21:V:LEU:H	1:18:V:GLU:HA	16	0.19
(2,177)	1:43:V:MET:HB2	1:43:V:MET:HE1	19	0.19
(2,177)	1:43:V:MET:HB3	1:43:V:MET:HE1	19	0.19
(2,176)	1:43:V:MET:HG2	1:43:V:MET:HE1	4	0.19
(2,176)	1:43:V:MET:HG3	1:43:V:MET:HE1	4	0.19
(1,612)	1:96:V:THR:H	1:50:V:ALA:CB	11	0.19
(1,604)	1:95:V:LEU:H	1:80:V:ARG:CB	12	0.19
(1,556)	1:86:V:ALA:H	1:82:V:LEU:CB	17	0.19
(1,544)	1:84:V:GLY:H	1:85:V:LYS:CB	1	0.19
(1,544)	1:84:V:GLY:H	1:85:V:LYS:CB	6	0.19
(1,544)	1:84:V:GLY:H	1:85:V:LYS:CB	8	0.19
(1,471)	1:75:V:ALA:H	1:74:V:GLU:CB	13	0.19
(1,466)	1:74:V:GLU:H	1:75:V:ALA:CB	1	0.19
(1,466)	1:74:V:GLU:H	1:75:V:ALA:CB	3	0.19
(1,466)	1:74:V:GLU:H	1:75:V:ALA:CB	14	0.19
(1,456)	1:74:V:GLU:H	1:70:V:LYS:CG	10	0.19
(1,342)	1:61:V:ASP:H	1:60:V:LYS:CB	10	0.19
(1,325)	1:60:V:LYS:H	1:57:V:LEU:CA	4	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,278)	1:50:V:ALA:H	1:93:V:PRO:CG	5	0.19
(1,254)	1:47:V:LEU:H	1:45:V:ARG:CA	20	0.19
(1,104)	1:20:V:ALA:H	1:21:V:LEU:CB	6	0.19
(1,104)	1:20:V:ALA:H	1:21:V:LEU:CB	7	0.19
(1,41)	1:15:V:MET:H	1:12:V:ALA:CB	14	0.19
(5,48)	1:84:V:GLY:C	1:89:V:LEU:H	1	0.18
(5,48)	1:84:V:GLY:C	1:89:V:LEU:H	15	0.18
(5,42)	1:78:V:PHE:C	1:82:V:LEU:H	19	0.18
(5,39)	1:75:V:ALA:C	1:79:V:ILE:H	12	0.18
(5,39)	1:75:V:ALA:C	1:79:V:ILE:H	18	0.18
(5,28)	1:63:V:ASP:C	1:67:V:ALA:H	1	0.18
(5,27)	1:62:V:GLU:C	1:66:V:LYS:H	3	0.18
(5,27)	1:62:V:GLU:C	1:66:V:LYS:H	14	0.18
(5,25)	1:58:V:ASN:C	1:61:V:ASP:H	16	0.18
(5,21)	1:52:V:VAL:C	1:98:V:PHE:H	20	0.18
(5,19)	1:50:V:ALA:C	1:96:V:THR:H	11	0.18
(5,9)	1:17:V:LYS:C	1:21:V:LEU:H	8	0.18
(5,9)	1:17:V:LYS:C	1:21:V:LEU:H	16	0.18
(5,7)	1:15:V:MET:C	1:19:V:ILE:H	10	0.18
(5,5)	1:13:V:GLN:C	1:17:V:LYS:H	6	0.18
(5,5)	1:13:V:GLN:C	1:17:V:LYS:H	10	0.18
(5,1)	1:9:V:GLN:C	1:13:V:GLN:H	5	0.18
(5,1)	1:9:V:GLN:C	1:13:V:GLN:H	19	0.18
(4,110)	1:35:V:MET:O	1:57:V:LEU:N	12	0.18
(4,110)	1:35:V:MET:O	1:57:V:LEU:N	13	0.18
(4,96)	1:84:V:GLY:O	1:89:V:LEU:N	11	0.18
(4,73)	1:71:V:ALA:O	1:75:V:ALA:H	7	0.18
(4,68)	1:68:V:GLY:O	1:71:V:ALA:N	9	0.18
(4,18)	1:17:V:LYS:O	1:21:V:LEU:N	4	0.18
(4,9)	1:13:V:GLN:O	1:17:V:LYS:H	13	0.18
(4,4)	1:10:V:ARG:O	1:14:V:GLU:N	6	0.18
(4,2)	1:9:V:GLN:O	1:13:V:GLN:N	13	0.18
(4,1)	1:9:V:GLN:O	1:13:V:GLN:H	3	0.18
(3,495)	1:73:V:GLN:H	1:70:V:LYS:HA	10	0.18
(3,487)	1:72:V:LEU:H	1:71:V:ALA:HB1	10	0.18
(3,483)	1:72:V:LEU:H	1:69:V:ILE:HA	3	0.18
(3,403)	1:61:V:ASP:H	1:64:V:ALA:HB1	10	0.18
(3,403)	1:61:V:ASP:H	1:64:V:ALA:HB1	15	0.18
(3,355)	1:53:V:TYR:H	1:41:V:VAL:HA	8	0.18
(3,32)	1:14:V:GLU:H	1:11:V:VAL:HA	12	0.18
(2,177)	1:43:V:MET:HB2	1:43:V:MET:HE1	6	0.18
(2,177)	1:43:V:MET:HB3	1:43:V:MET:HE1	6	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,176)	1:43:V:MET:HG2	1:43:V:MET:HE1	2	0.18
(2,176)	1:43:V:MET:HG3	1:43:V:MET:HE1	2	0.18
(2,176)	1:43:V:MET:HG2	1:43:V:MET:HE1	8	0.18
(2,176)	1:43:V:MET:HG3	1:43:V:MET:HE1	8	0.18
(2,176)	1:43:V:MET:HG2	1:43:V:MET:HE1	13	0.18
(2,176)	1:43:V:MET:HG3	1:43:V:MET:HE1	13	0.18
(1,612)	1:96:V:THR:H	1:50:V:ALA:CB	12	0.18
(1,612)	1:96:V:THR:H	1:50:V:ALA:CB	20	0.18
(1,587)	1:92:V:VAL:H	1:89:V:LEU:CG	17	0.18
(1,580)	1:91:V:ILE:H	1:90:V:ARG:CB	5	0.18
(1,569)	1:87:V:MET:H	1:87:V:MET:CE	8	0.18
(1,544)	1:84:V:GLY:H	1:85:V:LYS:CB	12	0.18
(1,544)	1:84:V:GLY:H	1:85:V:LYS:CB	18	0.18
(1,536)	1:83:V:LEU:H	1:85:V:LYS:CG	1	0.18
(1,471)	1:75:V:ALA:H	1:74:V:GLU:CB	3	0.18
(1,466)	1:74:V:GLU:H	1:75:V:ALA:CB	15	0.18
(1,342)	1:61:V:ASP:H	1:60:V:LYS:CB	2	0.18
(1,342)	1:61:V:ASP:H	1:60:V:LYS:CB	16	0.18
(1,319)	1:58:V:ASN:H	1:57:V:LEU:CB	20	0.18
(1,238)	1:43:V:MET:H	1:42:V:GLU:CG	19	0.18
(1,221)	1:41:V:VAL:H	1:38:V:VAL:CB	2	0.18
(1,108)	1:21:V:LEU:H	1:18:V:GLU:CB	1	0.18
(1,108)	1:21:V:LEU:H	1:18:V:GLU:CB	18	0.18
(1,104)	1:20:V:ALA:H	1:21:V:LEU:CB	3	0.18
(1,90)	1:19:V:ILE:H	1:20:V:ALA:CB	10	0.18
(5,49)	1:49:V:TYR:C	1:44:V:SER:H	4	0.17
(5,47)	1:83:V:LEU:C	1:87:V:MET:H	2	0.17
(5,47)	1:83:V:LEU:C	1:87:V:MET:H	13	0.17
(5,45)	1:81:V:SER:C	1:85:V:LYS:H	3	0.17
(5,44)	1:80:V:ARG:C	1:84:V:GLY:H	4	0.17
(5,39)	1:75:V:ALA:C	1:79:V:ILE:H	5	0.17
(5,39)	1:75:V:ALA:C	1:79:V:ILE:H	8	0.17
(5,39)	1:75:V:ALA:C	1:79:V:ILE:H	14	0.17
(5,39)	1:75:V:ALA:C	1:79:V:ILE:H	17	0.17
(5,37)	1:71:V:ALA:C	1:75:V:ALA:H	18	0.17
(5,37)	1:71:V:ALA:C	1:75:V:ALA:H	20	0.17
(5,36)	1:70:V:LYS:C	1:74:V:GLU:H	9	0.17
(5,36)	1:70:V:LYS:C	1:74:V:GLU:H	16	0.17
(5,31)	1:66:V:LYS:C	1:70:V:LYS:H	1	0.17
(5,27)	1:62:V:GLU:C	1:66:V:LYS:H	8	0.17
(5,21)	1:52:V:VAL:C	1:98:V:PHE:H	13	0.17
(5,14)	1:37:V:THR:H	1:55:V:THR:C	7	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(5,11)	1:19:V:ILE:C	1:23:V:LEU:H	4	0.17
(5,8)	1:16:V:GLN:C	1:20:V:ALA:H	1	0.17
(5,6)	1:14:V:GLU:C	1:18:V:GLU:H	9	0.17
(4,110)	1:35:V:MET:O	1:57:V:LEU:N	15	0.17
(4,108)	1:30:V:PRO:O	1:33:V:GLY:N	3	0.17
(4,75)	1:73:V:GLN:O	1:76:V:SER:H	2	0.17
(4,74)	1:71:V:ALA:O	1:75:V:ALA:N	1	0.17
(4,68)	1:68:V:GLY:O	1:71:V:ALA:N	18	0.17
(4,50)	1:58:V:ASN:O	1:61:V:ASP:N	5	0.17
(4,23)	1:21:V:LEU:O	1:25:V:ARG:H	20	0.17
(4,7)	1:12:V:ALA:O	1:16:V:GLN:H	10	0.17
(4,3)	1:10:V:ARG:O	1:14:V:GLU:H	13	0.17
(4,1)	1:9:V:GLN:O	1:13:V:GLN:H	10	0.17
(4,1)	1:9:V:GLN:O	1:13:V:GLN:H	20	0.17
(3,487)	1:72:V:LEU:H	1:71:V:ALA:HB1	2	0.17
(3,483)	1:72:V:LEU:H	1:69:V:ILE:HA	4	0.17
(3,483)	1:72:V:LEU:H	1:69:V:ILE:HA	11	0.17
(3,422)	1:65:V:VAL:H	1:62:V:GLU:HA	20	0.17
(3,356)	1:53:V:TYR:H	1:42:V:GLU:H	19	0.17
(3,334)	1:51:V:LYS:H	1:41:V:VAL:HA	14	0.17
(3,303)	1:48:V:ALA:H	1:47:V:LEU:HG	17	0.17
(3,265)	1:42:V:GLU:H	1:53:V:TYR:H	19	0.17
(3,177)	1:26:V:GLU:H	1:22:V:ILE:HA	4	0.17
(3,126)	1:22:V:ILE:H	1:19:V:ILE:HA	18	0.17
(3,42)	1:15:V:MET:H	1:12:V:ALA:HA	10	0.17
(3,17)	1:13:V:GLN:H	1:10:V:ARG:HA	2	0.17
(3,17)	1:13:V:GLN:H	1:10:V:ARG:HA	11	0.17
(2,177)	1:43:V:MET:HB2	1:43:V:MET:HE1	2	0.17
(2,177)	1:43:V:MET:HB3	1:43:V:MET:HE1	2	0.17
(2,177)	1:43:V:MET:HB2	1:43:V:MET:HE1	5	0.17
(2,177)	1:43:V:MET:HB3	1:43:V:MET:HE1	5	0.17
(2,177)	1:43:V:MET:HB2	1:43:V:MET:HE1	9	0.17
(2,177)	1:43:V:MET:HB3	1:43:V:MET:HE1	9	0.17
(2,177)	1:43:V:MET:HB2	1:43:V:MET:HE1	13	0.17
(2,177)	1:43:V:MET:HB3	1:43:V:MET:HE1	13	0.17
(2,176)	1:43:V:MET:HG2	1:43:V:MET:HE1	6	0.17
(2,176)	1:43:V:MET:HG3	1:43:V:MET:HE1	6	0.17
(2,65)	1:19:V:ILE:HG13	1:87:V:MET:HE1	3	0.17
(2,36)	1:15:V:MET:HE1	1:91:V:ILE:HD11	15	0.17
(2,36)	1:15:V:MET:HE1	1:91:V:ILE:HD12	15	0.17
(2,36)	1:15:V:MET:HE1	1:91:V:ILE:HD13	15	0.17
(1,587)	1:92:V:VAL:H	1:89:V:LEU:CG	9	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,544)	1:84:V:GLY:H	1:85:V:LYS:CB	3	0.17
(1,544)	1:84:V:GLY:H	1:85:V:LYS:CB	7	0.17
(1,536)	1:83:V:LEU:H	1:85:V:LYS:CG	8	0.17
(1,536)	1:83:V:LEU:H	1:85:V:LYS:CG	9	0.17
(1,536)	1:83:V:LEU:H	1:85:V:LYS:CG	11	0.17
(1,484)	1:78:V:PHE:H	1:75:V:ALA:CB	10	0.17
(1,471)	1:75:V:ALA:H	1:74:V:GLU:CB	14	0.17
(1,466)	1:74:V:GLU:H	1:75:V:ALA:CB	13	0.17
(1,386)	1:67:V:ALA:H	1:66:V:LYS:CD	11	0.17
(1,342)	1:61:V:ASP:H	1:60:V:LYS:CB	9	0.17
(1,327)	1:60:V:LYS:H	1:58:V:ASN:CA	5	0.17
(1,325)	1:60:V:LYS:H	1:57:V:LEU:CA	3	0.17
(1,325)	1:60:V:LYS:H	1:57:V:LEU:CA	5	0.17
(1,287)	1:51:V:LYS:H	1:42:V:GLU:CG	4	0.17
(1,287)	1:51:V:LYS:H	1:42:V:GLU:CG	6	0.17
(1,281)	1:50:V:ALA:H	1:94:V:GLU:CB	17	0.17
(1,254)	1:47:V:LEU:H	1:45:V:ARG:CA	17	0.17
(1,216)	1:40:V:GLY:H	1:39:V:SER:CB	2	0.17
(5,47)	1:83:V:LEU:C	1:87:V:MET:H	17	0.16
(5,45)	1:81:V:SER:C	1:85:V:LYS:H	9	0.16
(5,44)	1:80:V:ARG:C	1:84:V:GLY:H	14	0.16
(5,42)	1:78:V:PHE:C	1:82:V:LEU:H	9	0.16
(5,41)	1:77:V:GLY:C	1:81:V:SER:H	3	0.16
(5,37)	1:71:V:ALA:C	1:75:V:ALA:H	2	0.16
(5,36)	1:70:V:LYS:C	1:74:V:GLU:H	2	0.16
(5,31)	1:66:V:LYS:C	1:70:V:LYS:H	9	0.16
(5,22)	1:54:V:VAL:H	1:98:V:PHE:C	11	0.16
(5,21)	1:52:V:VAL:C	1:98:V:PHE:H	3	0.16
(5,21)	1:52:V:VAL:C	1:98:V:PHE:H	5	0.16
(5,21)	1:52:V:VAL:C	1:98:V:PHE:H	11	0.16
(5,19)	1:50:V:ALA:C	1:96:V:THR:H	16	0.16
(5,19)	1:50:V:ALA:C	1:96:V:THR:H	19	0.16
(5,6)	1:14:V:GLU:C	1:18:V:GLU:H	6	0.16
(5,6)	1:14:V:GLU:C	1:18:V:GLU:H	15	0.16
(5,2)	1:10:V:ARG:C	1:14:V:GLU:H	1	0.16
(5,1)	1:9:V:GLN:C	1:13:V:GLN:H	18	0.16
(4,110)	1:35:V:MET:O	1:57:V:LEU:N	2	0.16
(4,81)	1:77:V:GLY:O	1:81:V:SER:H	7	0.16
(4,73)	1:71:V:ALA:O	1:75:V:ALA:H	11	0.16
(4,68)	1:68:V:GLY:O	1:71:V:ALA:N	4	0.16
(4,68)	1:68:V:GLY:O	1:71:V:ALA:N	8	0.16
(4,50)	1:58:V:ASN:O	1:61:V:ASP:N	4	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,9)	1:13:V:GLN:O	1:17:V:LYS:H	3	0.16
(4,7)	1:12:V:ALA:O	1:16:V:GLN:H	4	0.16
(3,487)	1:72:V:LEU:H	1:71:V:ALA:HB1	7	0.16
(3,483)	1:72:V:LEU:H	1:69:V:ILE:HA	15	0.16
(3,422)	1:65:V:VAL:H	1:62:V:GLU:HA	3	0.16
(3,334)	1:51:V:LYS:H	1:41:V:VAL:HA	11	0.16
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB2	16	0.16
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB3	16	0.16
(3,194)	1:27:V:ILE:H	1:27:V:ILE:HB	4	0.16
(3,32)	1:14:V:GLU:H	1:11:V:VAL:HA	16	0.16
(2,211)	1:54:V:VAL:HG11	1:56:V:PHE:HD1	8	0.16
(2,211)	1:54:V:VAL:HG11	1:56:V:PHE:HD2	8	0.16
(2,211)	1:54:V:VAL:HG12	1:56:V:PHE:HD1	8	0.16
(2,211)	1:54:V:VAL:HG12	1:56:V:PHE:HD2	8	0.16
(2,211)	1:54:V:VAL:HG13	1:56:V:PHE:HD1	8	0.16
(2,211)	1:54:V:VAL:HG13	1:56:V:PHE:HD2	8	0.16
(2,211)	1:54:V:VAL:HG21	1:56:V:PHE:HD1	8	0.16
(2,211)	1:54:V:VAL:HG21	1:56:V:PHE:HD2	8	0.16
(2,211)	1:54:V:VAL:HG22	1:56:V:PHE:HD1	8	0.16
(2,211)	1:54:V:VAL:HG22	1:56:V:PHE:HD2	8	0.16
(2,211)	1:54:V:VAL:HG23	1:56:V:PHE:HD1	8	0.16
(2,211)	1:54:V:VAL:HG23	1:56:V:PHE:HD2	8	0.16
(2,177)	1:43:V:MET:HB2	1:43:V:MET:HE1	12	0.16
(2,177)	1:43:V:MET:HB3	1:43:V:MET:HE1	12	0.16
(2,176)	1:43:V:MET:HG2	1:43:V:MET:HE1	1	0.16
(2,176)	1:43:V:MET:HG3	1:43:V:MET:HE1	1	0.16
(1,612)	1:96:V:THR:H	1:50:V:ALA:CB	2	0.16
(1,604)	1:95:V:LEU:H	1:80:V:ARG:CB	18	0.16
(1,586)	1:91:V:ILE:H	1:92:V:VAL:CA	15	0.16
(1,544)	1:84:V:GLY:H	1:85:V:LYS:CB	2	0.16
(1,536)	1:83:V:LEU:H	1:85:V:LYS:CG	3	0.16
(1,525)	1:82:V:LEU:H	1:83:V:LEU:CB	11	0.16
(1,484)	1:78:V:PHE:H	1:75:V:ALA:CB	5	0.16
(1,484)	1:78:V:PHE:H	1:75:V:ALA:CB	18	0.16
(1,477)	1:76:V:SER:H	1:74:V:GLU:CA	8	0.16
(1,477)	1:76:V:SER:H	1:74:V:GLU:CA	18	0.16
(1,466)	1:74:V:GLU:H	1:75:V:ALA:CB	16	0.16
(1,466)	1:74:V:GLU:H	1:75:V:ALA:CB	17	0.16
(1,386)	1:67:V:ALA:H	1:66:V:LYS:CD	14	0.16
(1,342)	1:61:V:ASP:H	1:60:V:LYS:CB	12	0.16
(1,339)	1:61:V:ASP:H	1:60:V:LYS:CE	17	0.16
(1,254)	1:47:V:LEU:H	1:45:V:ARG:CA	6	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,254)	1:47:V:LEU:H	1:45:V:ARG:CA	18	0.16
(1,238)	1:43:V:MET:H	1:42:V:GLU:CG	11	0.16
(1,216)	1:40:V:GLY:H	1:39:V:SER:CB	11	0.16
(1,174)	1:27:V:ILE:H	1:24:V:GLN:CA	6	0.16
(1,107)	1:21:V:LEU:H	1:18:V:GLU:CA	8	0.16
(1,41)	1:15:V:MET:H	1:12:V:ALA:CB	3	0.16
(5,48)	1:84:V:GLY:C	1:89:V:LEU:H	7	0.15
(5,45)	1:81:V:SER:C	1:85:V:LYS:H	4	0.15
(5,37)	1:71:V:ALA:C	1:75:V:ALA:H	5	0.15
(5,32)	1:67:V:ALA:C	1:71:V:ALA:H	8	0.15
(5,32)	1:67:V:ALA:C	1:71:V:ALA:H	16	0.15
(5,31)	1:66:V:LYS:C	1:70:V:LYS:H	15	0.15
(5,30)	1:65:V:VAL:C	1:69:V:ILE:H	13	0.15
(5,14)	1:37:V:THR:H	1:55:V:THR:C	2	0.15
(5,14)	1:37:V:THR:H	1:55:V:THR:C	18	0.15
(5,14)	1:37:V:THR:H	1:55:V:THR:C	19	0.15
(5,12)	1:21:V:LEU:C	1:25:V:ARG:H	13	0.15
(5,10)	1:18:V:GLU:C	1:22:V:ILE:H	8	0.15
(5,9)	1:17:V:LYS:C	1:21:V:LEU:H	18	0.15
(5,6)	1:14:V:GLU:C	1:18:V:GLU:H	1	0.15
(5,6)	1:14:V:GLU:C	1:18:V:GLU:H	7	0.15
(5,4)	1:12:V:ALA:C	1:16:V:GLN:H	20	0.15
(5,1)	1:9:V:GLN:C	1:13:V:GLN:H	14	0.15
(4,94)	1:83:V:LEU:O	1:87:V:MET:N	6	0.15
(4,90)	1:81:V:SER:O	1:85:V:LYS:N	18	0.15
(4,73)	1:71:V:ALA:O	1:75:V:ALA:H	10	0.15
(4,68)	1:68:V:GLY:O	1:71:V:ALA:N	1	0.15
(4,68)	1:68:V:GLY:O	1:71:V:ALA:N	3	0.15
(4,52)	1:61:V:ASP:O	1:65:V:VAL:N	3	0.15
(4,49)	1:58:V:ASN:O	1:61:V:ASP:H	11	0.15
(4,49)	1:58:V:ASN:O	1:61:V:ASP:H	18	0.15
(4,19)	1:18:V:GLU:O	1:22:V:ILE:H	20	0.15
(4,17)	1:17:V:LYS:O	1:21:V:LEU:H	3	0.15
(4,17)	1:17:V:LYS:O	1:21:V:LEU:H	5	0.15
(3,495)	1:73:V:GLN:H	1:70:V:LYS:HA	9	0.15
(3,422)	1:65:V:VAL:H	1:62:V:GLU:HA	10	0.15
(3,422)	1:65:V:VAL:H	1:62:V:GLU:HA	11	0.15
(3,422)	1:65:V:VAL:H	1:62:V:GLU:HA	18	0.15
(3,403)	1:61:V:ASP:H	1:64:V:ALA:HB1	1	0.15
(3,403)	1:61:V:ASP:H	1:64:V:ALA:HB1	8	0.15
(3,355)	1:53:V:TYR:H	1:41:V:VAL:HA	12	0.15
(3,338)	1:51:V:LYS:H	1:44:V:SER:H	14	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB2	13	0.15
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB3	13	0.15
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB2	19	0.15
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB3	19	0.15
(3,280)	1:44:V:SER:H	1:51:V:LYS:H	14	0.15
(3,165)	1:25:V:ARG:H	1:21:V:LEU:HG	7	0.15
(3,42)	1:15:V:MET:H	1:12:V:ALA:HA	9	0.15
(3,42)	1:15:V:MET:H	1:12:V:ALA:HA	12	0.15
(2,177)	1:43:V:MET:HB2	1:43:V:MET:HE1	7	0.15
(2,177)	1:43:V:MET:HB3	1:43:V:MET:HE1	7	0.15
(2,177)	1:43:V:MET:HB2	1:43:V:MET:HE1	15	0.15
(2,177)	1:43:V:MET:HB3	1:43:V:MET:HE1	15	0.15
(2,176)	1:43:V:MET:HG2	1:43:V:MET:HE1	19	0.15
(2,176)	1:43:V:MET:HG3	1:43:V:MET:HE1	19	0.15
(1,612)	1:96:V:THR:H	1:50:V:ALA:CB	3	0.15
(1,612)	1:96:V:THR:H	1:50:V:ALA:CB	8	0.15
(1,582)	1:91:V:ILE:H	1:91:V:ILE:CD1	12	0.15
(1,556)	1:86:V:ALA:H	1:82:V:LEU:CB	10	0.15
(1,544)	1:84:V:GLY:H	1:85:V:LYS:CB	4	0.15
(1,544)	1:84:V:GLY:H	1:85:V:LYS:CB	5	0.15
(1,544)	1:84:V:GLY:H	1:85:V:LYS:CB	17	0.15
(1,525)	1:82:V:LEU:H	1:83:V:LEU:CB	14	0.15
(1,525)	1:82:V:LEU:H	1:83:V:LEU:CB	17	0.15
(1,477)	1:76:V:SER:H	1:74:V:GLU:CA	5	0.15
(1,477)	1:76:V:SER:H	1:74:V:GLU:CA	9	0.15
(1,476)	1:76:V:SER:H	1:74:V:GLU:CB	20	0.15
(1,466)	1:74:V:GLU:H	1:75:V:ALA:CB	7	0.15
(1,342)	1:61:V:ASP:H	1:60:V:LYS:CB	5	0.15
(1,342)	1:61:V:ASP:H	1:60:V:LYS:CB	13	0.15
(1,327)	1:60:V:LYS:H	1:58:V:ASN:CA	17	0.15
(1,278)	1:50:V:ALA:H	1:93:V:PRO:CG	7	0.15
(1,272)	1:49:V:TYR:H	1:48:V:ALA:CB	11	0.15
(1,272)	1:49:V:TYR:H	1:48:V:ALA:CB	17	0.15
(1,238)	1:43:V:MET:H	1:42:V:GLU:CG	18	0.15
(1,236)	1:43:V:MET:H	1:12:V:ALA:CB	14	0.15
(1,221)	1:41:V:VAL:H	1:38:V:VAL:CB	19	0.15
(1,157)	1:25:V:ARG:H	1:24:V:GLN:CB	10	0.15
(1,128)	1:23:V:LEU:H	1:18:V:GLU:CA	5	0.15
(1,90)	1:19:V:ILE:H	1:20:V:ALA:CB	11	0.15
(1,90)	1:19:V:ILE:H	1:20:V:ALA:CB	13	0.15
(5,50)	1:40:V:GLY:C	1:53:V:TYR:H	8	0.14
(5,49)	1:49:V:TYR:C	1:44:V:SER:H	8	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(5,47)	1:83:V:LEU:C	1:87:V:MET:H	19	0.14
(5,42)	1:78:V:PHE:C	1:82:V:LEU:H	4	0.14
(5,39)	1:75:V:ALA:C	1:79:V:ILE:H	7	0.14
(5,39)	1:75:V:ALA:C	1:79:V:ILE:H	11	0.14
(5,39)	1:75:V:ALA:C	1:79:V:ILE:H	15	0.14
(5,39)	1:75:V:ALA:C	1:79:V:ILE:H	20	0.14
(5,37)	1:71:V:ALA:C	1:75:V:ALA:H	6	0.14
(5,36)	1:70:V:LYS:C	1:74:V:GLU:H	3	0.14
(5,36)	1:70:V:LYS:C	1:74:V:GLU:H	19	0.14
(5,32)	1:67:V:ALA:C	1:71:V:ALA:H	11	0.14
(5,32)	1:67:V:ALA:C	1:71:V:ALA:H	20	0.14
(5,31)	1:66:V:LYS:C	1:70:V:LYS:H	5	0.14
(5,31)	1:66:V:LYS:C	1:70:V:LYS:H	8	0.14
(5,27)	1:62:V:GLU:C	1:66:V:LYS:H	7	0.14
(5,25)	1:58:V:ASN:C	1:61:V:ASP:H	10	0.14
(5,22)	1:54:V:VAL:H	1:98:V:PHE:C	1	0.14
(5,21)	1:52:V:VAL:C	1:98:V:PHE:H	6	0.14
(5,21)	1:52:V:VAL:C	1:98:V:PHE:H	8	0.14
(5,21)	1:52:V:VAL:C	1:98:V:PHE:H	14	0.14
(5,19)	1:50:V:ALA:C	1:96:V:THR:H	3	0.14
(5,19)	1:50:V:ALA:C	1:96:V:THR:H	4	0.14
(5,14)	1:37:V:THR:H	1:55:V:THR:C	6	0.14
(5,14)	1:37:V:THR:H	1:55:V:THR:C	16	0.14
(5,1)	1:9:V:GLN:C	1:13:V:GLN:H	6	0.14
(4,68)	1:68:V:GLY:O	1:71:V:ALA:N	6	0.14
(4,52)	1:61:V:ASP:O	1:65:V:VAL:N	19	0.14
(4,51)	1:61:V:ASP:O	1:65:V:VAL:H	15	0.14
(4,49)	1:58:V:ASN:O	1:61:V:ASP:H	17	0.14
(4,23)	1:21:V:LEU:O	1:25:V:ARG:H	9	0.14
(4,10)	1:13:V:GLN:O	1:17:V:LYS:N	17	0.14
(3,588)	1:83:V:LEU:H	1:81:V:SER:HB2	11	0.14
(3,588)	1:83:V:LEU:H	1:81:V:SER:HB3	11	0.14
(3,495)	1:73:V:GLN:H	1:70:V:LYS:HA	4	0.14
(3,483)	1:72:V:LEU:H	1:69:V:ILE:HA	8	0.14
(3,483)	1:72:V:LEU:H	1:69:V:ILE:HA	12	0.14
(3,483)	1:72:V:LEU:H	1:69:V:ILE:HA	19	0.14
(3,483)	1:72:V:LEU:H	1:69:V:ILE:HA	20	0.14
(3,338)	1:51:V:LYS:H	1:44:V:SER:H	6	0.14
(3,281)	1:44:V:SER:H	1:93:V:PRO:HG2	17	0.14
(3,281)	1:44:V:SER:H	1:93:V:PRO:HG3	17	0.14
(3,280)	1:44:V:SER:H	1:51:V:LYS:H	6	0.14
(3,194)	1:27:V:ILE:H	1:27:V:ILE:HB	16	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,177)	1:26:V:GLU:H	1:22:V:ILE:HA	2	0.14
(3,177)	1:26:V:GLU:H	1:22:V:ILE:HA	13	0.14
(3,177)	1:26:V:GLU:H	1:22:V:ILE:HA	17	0.14
(3,54)	1:16:V:GLN:H	1:13:V:GLN:HA	7	0.14
(3,54)	1:16:V:GLN:H	1:13:V:GLN:HA	15	0.14
(3,42)	1:15:V:MET:H	1:12:V:ALA:HA	13	0.14
(3,17)	1:13:V:GLN:H	1:10:V:ARG:HA	5	0.14
(3,17)	1:13:V:GLN:H	1:10:V:ARG:HA	12	0.14
(2,177)	1:43:V:MET:HB2	1:43:V:MET:HE1	20	0.14
(2,177)	1:43:V:MET:HB3	1:43:V:MET:HE1	20	0.14
(1,586)	1:91:V:ILE:H	1:92:V:VAL:CA	11	0.14
(1,544)	1:84:V:GLY:H	1:85:V:LYS:CB	9	0.14
(1,544)	1:84:V:GLY:H	1:85:V:LYS:CB	10	0.14
(1,484)	1:78:V:PHE:H	1:75:V:ALA:CB	1	0.14
(1,484)	1:78:V:PHE:H	1:75:V:ALA:CB	9	0.14
(1,466)	1:74:V:GLU:H	1:75:V:ALA:CB	2	0.14
(1,466)	1:74:V:GLU:H	1:75:V:ALA:CB	11	0.14
(1,466)	1:74:V:GLU:H	1:75:V:ALA:CB	18	0.14
(1,456)	1:74:V:GLU:H	1:70:V:LYS:CG	12	0.14
(1,342)	1:61:V:ASP:H	1:60:V:LYS:CB	19	0.14
(1,327)	1:60:V:LYS:H	1:58:V:ASN:CA	10	0.14
(1,319)	1:58:V:ASN:H	1:57:V:LEU:CB	17	0.14
(1,287)	1:51:V:LYS:H	1:42:V:GLU:CG	13	0.14
(1,287)	1:51:V:LYS:H	1:42:V:GLU:CG	18	0.14
(1,269)	1:49:V:TYR:H	1:44:V:SER:CB	5	0.14
(1,258)	1:47:V:LEU:H	1:47:V:LEU:CG	17	0.14
(1,216)	1:40:V:GLY:H	1:39:V:SER:CB	17	0.14
(1,175)	1:27:V:ILE:H	1:25:V:ARG:CB	20	0.14
(1,18)	1:13:V:GLN:H	1:10:V:ARG:CB	19	0.14
(5,50)	1:40:V:GLY:C	1:53:V:TYR:H	7	0.13
(5,49)	1:49:V:TYR:C	1:44:V:SER:H	5	0.13
(5,48)	1:84:V:GLY:C	1:89:V:LEU:H	4	0.13
(5,47)	1:83:V:LEU:C	1:87:V:MET:H	18	0.13
(5,44)	1:80:V:ARG:C	1:84:V:GLY:H	13	0.13
(5,44)	1:80:V:ARG:C	1:84:V:GLY:H	16	0.13
(5,42)	1:78:V:PHE:C	1:82:V:LEU:H	12	0.13
(5,39)	1:75:V:ALA:C	1:79:V:ILE:H	6	0.13
(5,39)	1:75:V:ALA:C	1:79:V:ILE:H	9	0.13
(5,30)	1:65:V:VAL:C	1:69:V:ILE:H	15	0.13
(5,27)	1:62:V:GLU:C	1:66:V:LYS:H	16	0.13
(5,21)	1:52:V:VAL:C	1:98:V:PHE:H	17	0.13
(5,18)	1:50:V:ALA:H	1:94:V:GLU:C	1	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(5,14)	1:37:V:THR:H	1:55:V:THR:C	3	0.13
(5,14)	1:37:V:THR:H	1:55:V:THR:C	11	0.13
(5,14)	1:37:V:THR:H	1:55:V:THR:C	17	0.13
(5,12)	1:21:V:LEU:C	1:25:V:ARG:H	3	0.13
(5,6)	1:14:V:GLU:C	1:18:V:GLU:H	3	0.13
(5,5)	1:13:V:GLN:C	1:17:V:LYS:H	7	0.13
(5,4)	1:12:V:ALA:C	1:16:V:GLN:H	11	0.13
(5,1)	1:9:V:GLN:C	1:13:V:GLN:H	17	0.13
(4,110)	1:35:V:MET:O	1:57:V:LEU:N	17	0.13
(4,107)	1:30:V:PRO:O	1:33:V:GLY:H	11	0.13
(4,107)	1:30:V:PRO:O	1:33:V:GLY:H	14	0.13
(4,71)	1:70:V:LYS:O	1:74:V:GLU:H	1	0.13
(4,55)	1:63:V:ASP:O	1:67:V:ALA:H	13	0.13
(4,52)	1:61:V:ASP:O	1:65:V:VAL:N	16	0.13
(4,51)	1:61:V:ASP:O	1:65:V:VAL:H	7	0.13
(4,23)	1:21:V:LEU:O	1:25:V:ARG:H	2	0.13
(4,17)	1:17:V:LYS:O	1:21:V:LEU:H	19	0.13
(4,15)	1:16:V:GLN:O	1:20:V:ALA:H	1	0.13
(3,576)	1:82:V:LEU:H	1:80:V:ARG:HB2	6	0.13
(3,576)	1:82:V:LEU:H	1:80:V:ARG:HB3	6	0.13
(3,370)	1:55:V:THR:H	1:37:V:THR:HB	3	0.13
(3,355)	1:53:V:TYR:H	1:41:V:VAL:HA	15	0.13
(3,338)	1:51:V:LYS:H	1:44:V:SER:H	15	0.13
(3,334)	1:51:V:LYS:H	1:41:V:VAL:HA	4	0.13
(3,330)	1:50:V:ALA:H	1:94:V:GLU:HA	6	0.13
(3,280)	1:44:V:SER:H	1:51:V:LYS:H	15	0.13
(3,245)	1:40:V:GLY:H	1:54:V:VAL:HA	3	0.13
(3,194)	1:27:V:ILE:H	1:27:V:ILE:HB	2	0.13
(3,194)	1:27:V:ILE:H	1:27:V:ILE:HB	8	0.13
(3,114)	1:21:V:LEU:H	1:18:V:GLU:HA	2	0.13
(3,54)	1:16:V:GLN:H	1:13:V:GLN:HA	1	0.13
(3,54)	1:16:V:GLN:H	1:13:V:GLN:HA	4	0.13
(2,332)	1:87:V:MET:HE1	1:87:V:MET:HG2	6	0.13
(2,332)	1:87:V:MET:HE1	1:87:V:MET:HG3	6	0.13
(2,332)	1:87:V:MET:HE1	1:87:V:MET:HG2	11	0.13
(2,332)	1:87:V:MET:HE1	1:87:V:MET:HG3	11	0.13
(2,177)	1:43:V:MET:HB2	1:43:V:MET:HE1	3	0.13
(2,177)	1:43:V:MET:HB3	1:43:V:MET:HE1	3	0.13
(2,177)	1:43:V:MET:HB2	1:43:V:MET:HE1	8	0.13
(2,177)	1:43:V:MET:HB3	1:43:V:MET:HE1	8	0.13
(2,176)	1:43:V:MET:HG2	1:43:V:MET:HE1	17	0.13
(2,176)	1:43:V:MET:HG3	1:43:V:MET:HE1	17	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,612)	1:96:V:THR:H	1:50:V:ALA:CB	1	0.13
(1,587)	1:92:V:VAL:H	1:89:V:LEU:CG	19	0.13
(1,544)	1:84:V:GLY:H	1:85:V:LYS:CB	14	0.13
(1,536)	1:83:V:LEU:H	1:85:V:LYS:CG	5	0.13
(1,484)	1:78:V:PHE:H	1:75:V:ALA:CB	6	0.13
(1,484)	1:78:V:PHE:H	1:75:V:ALA:CB	7	0.13
(1,476)	1:76:V:SER:H	1:74:V:GLU:CB	19	0.13
(1,471)	1:75:V:ALA:H	1:74:V:GLU:CB	10	0.13
(1,466)	1:74:V:GLU:H	1:75:V:ALA:CB	4	0.13
(1,466)	1:74:V:GLU:H	1:75:V:ALA:CB	12	0.13
(1,466)	1:74:V:GLU:H	1:75:V:ALA:CB	19	0.13
(1,466)	1:74:V:GLU:H	1:75:V:ALA:CB	20	0.13
(1,342)	1:61:V:ASP:H	1:60:V:LYS:CB	1	0.13
(1,327)	1:60:V:LYS:H	1:58:V:ASN:CA	1	0.13
(1,327)	1:60:V:LYS:H	1:58:V:ASN:CA	4	0.13
(1,327)	1:60:V:LYS:H	1:58:V:ASN:CA	15	0.13
(1,278)	1:50:V:ALA:H	1:93:V:PRO:CG	12	0.13
(1,243)	1:44:V:SER:H	1:43:V:MET:CB	4	0.13
(1,238)	1:43:V:MET:H	1:42:V:GLU:CG	7	0.13
(1,175)	1:27:V:ILE:H	1:25:V:ARG:CB	5	0.13
(1,168)	1:26:V:GLU:H	1:25:V:ARG:CB	13	0.13
(1,90)	1:19:V:ILE:H	1:20:V:ALA:CB	6	0.13
(1,90)	1:19:V:ILE:H	1:20:V:ALA:CB	8	0.13
(1,50)	1:16:V:GLN:H	1:13:V:GLN:CA	5	0.13
(1,41)	1:15:V:MET:H	1:12:V:ALA:CB	16	0.13
(5,49)	1:49:V:TYR:C	1:44:V:SER:H	6	0.12
(5,49)	1:49:V:TYR:C	1:44:V:SER:H	9	0.12
(5,49)	1:49:V:TYR:C	1:44:V:SER:H	14	0.12
(5,49)	1:49:V:TYR:C	1:44:V:SER:H	17	0.12
(5,48)	1:84:V:GLY:C	1:89:V:LEU:H	13	0.12
(5,47)	1:83:V:LEU:C	1:87:V:MET:H	16	0.12
(5,45)	1:81:V:SER:C	1:85:V:LYS:H	2	0.12
(5,45)	1:81:V:SER:C	1:85:V:LYS:H	12	0.12
(5,45)	1:81:V:SER:C	1:85:V:LYS:H	15	0.12
(5,44)	1:80:V:ARG:C	1:84:V:GLY:H	9	0.12
(5,41)	1:77:V:GLY:C	1:81:V:SER:H	11	0.12
(5,30)	1:65:V:VAL:C	1:69:V:ILE:H	1	0.12
(5,27)	1:62:V:GLU:C	1:66:V:LYS:H	17	0.12
(5,27)	1:62:V:GLU:C	1:66:V:LYS:H	20	0.12
(5,22)	1:54:V:VAL:H	1:98:V:PHE:C	9	0.12
(5,21)	1:52:V:VAL:C	1:98:V:PHE:H	2	0.12
(5,21)	1:52:V:VAL:C	1:98:V:PHE:H	12	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(5,18)	1:50:V:ALA:H	1:94:V:GLU:C	2	0.12
(5,8)	1:16:V:GLN:C	1:20:V:ALA:H	13	0.12
(5,7)	1:15:V:MET:C	1:19:V:ILE:H	18	0.12
(5,6)	1:14:V:GLU:C	1:18:V:GLU:H	11	0.12
(5,6)	1:14:V:GLU:C	1:18:V:GLU:H	16	0.12
(5,2)	1:10:V:ARG:C	1:14:V:GLU:H	2	0.12
(5,2)	1:10:V:ARG:C	1:14:V:GLU:H	8	0.12
(4,89)	1:81:V:SER:O	1:85:V:LYS:H	8	0.12
(4,55)	1:63:V:ASP:O	1:67:V:ALA:H	9	0.12
(4,51)	1:61:V:ASP:O	1:65:V:VAL:H	12	0.12
(4,49)	1:58:V:ASN:O	1:61:V:ASP:H	1	0.12
(4,20)	1:18:V:GLU:O	1:22:V:ILE:N	5	0.12
(4,20)	1:18:V:GLU:O	1:22:V:ILE:N	16	0.12
(4,19)	1:18:V:GLU:O	1:22:V:ILE:H	17	0.12
(4,17)	1:17:V:LYS:O	1:21:V:LEU:H	7	0.12
(4,17)	1:17:V:LYS:O	1:21:V:LEU:H	17	0.12
(4,10)	1:13:V:GLN:O	1:17:V:LYS:N	1	0.12
(4,10)	1:13:V:GLN:O	1:17:V:LYS:N	13	0.12
(4,7)	1:12:V:ALA:O	1:16:V:GLN:H	20	0.12
(4,1)	1:9:V:GLN:O	1:13:V:GLN:H	15	0.12
(3,487)	1:72:V:LEU:H	1:71:V:ALA:HB1	8	0.12
(3,483)	1:72:V:LEU:H	1:69:V:ILE:HA	10	0.12
(3,356)	1:53:V:TYR:H	1:42:V:GLU:H	11	0.12
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB2	15	0.12
(3,311)	1:49:V:TYR:H	1:45:V:ARG:HB3	15	0.12
(3,278)	1:44:V:SER:H	1:50:V:ALA:HA	1	0.12
(3,265)	1:42:V:GLU:H	1:53:V:TYR:H	11	0.12
(3,194)	1:27:V:ILE:H	1:27:V:ILE:HB	10	0.12
(3,193)	1:27:V:ILE:H	1:26:V:GLU:HA	6	0.12
(3,193)	1:27:V:ILE:H	1:26:V:GLU:HA	18	0.12
(3,189)	1:27:V:ILE:H	1:25:V:ARG:HA	18	0.12
(3,176)	1:26:V:GLU:H	1:21:V:LEU:HG	7	0.12
(3,126)	1:22:V:ILE:H	1:19:V:ILE:HA	16	0.12
(3,114)	1:21:V:LEU:H	1:18:V:GLU:HA	10	0.12
(3,114)	1:21:V:LEU:H	1:18:V:GLU:HA	11	0.12
(3,114)	1:21:V:LEU:H	1:18:V:GLU:HA	14	0.12
(3,114)	1:21:V:LEU:H	1:18:V:GLU:HA	19	0.12
(3,42)	1:15:V:MET:H	1:12:V:ALA:HA	15	0.12
(3,32)	1:14:V:GLU:H	1:11:V:VAL:HA	6	0.12
(3,32)	1:14:V:GLU:H	1:11:V:VAL:HA	19	0.12
(2,177)	1:43:V:MET:HB2	1:43:V:MET:HE1	18	0.12
(2,177)	1:43:V:MET:HB3	1:43:V:MET:HE1	18	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,176)	1:43:V:MET:HG2	1:43:V:MET:HE1	14	0.12
(2,176)	1:43:V:MET:HG3	1:43:V:MET:HE1	14	0.12
(1,612)	1:96:V:THR:H	1:50:V:ALA:CB	16	0.12
(1,606)	1:95:V:LEU:H	1:94:V:GLU:CG	17	0.12
(1,604)	1:95:V:LEU:H	1:80:V:ARG:CB	9	0.12
(1,525)	1:82:V:LEU:H	1:83:V:LEU:CB	13	0.12
(1,484)	1:78:V:PHE:H	1:75:V:ALA:CB	11	0.12
(1,484)	1:78:V:PHE:H	1:75:V:ALA:CB	19	0.12
(1,484)	1:78:V:PHE:H	1:75:V:ALA:CB	20	0.12
(1,476)	1:76:V:SER:H	1:74:V:GLU:CB	12	0.12
(1,476)	1:76:V:SER:H	1:74:V:GLU:CB	13	0.12
(1,476)	1:76:V:SER:H	1:74:V:GLU:CB	14	0.12
(1,466)	1:74:V:GLU:H	1:75:V:ALA:CB	5	0.12
(1,466)	1:74:V:GLU:H	1:75:V:ALA:CB	6	0.12
(1,466)	1:74:V:GLU:H	1:75:V:ALA:CB	9	0.12
(1,466)	1:74:V:GLU:H	1:75:V:ALA:CB	10	0.12
(1,386)	1:67:V:ALA:H	1:66:V:LYS:CD	6	0.12
(1,342)	1:61:V:ASP:H	1:60:V:LYS:CB	7	0.12
(1,272)	1:49:V:TYR:H	1:48:V:ALA:CB	12	0.12
(1,272)	1:49:V:TYR:H	1:48:V:ALA:CB	19	0.12
(1,221)	1:41:V:VAL:H	1:38:V:VAL:CB	4	0.12
(1,216)	1:40:V:GLY:H	1:39:V:SER:CB	12	0.12
(1,216)	1:40:V:GLY:H	1:39:V:SER:CB	16	0.12
(1,90)	1:19:V:ILE:H	1:20:V:ALA:CB	1	0.12
(1,90)	1:19:V:ILE:H	1:20:V:ALA:CB	20	0.12
(1,18)	1:13:V:GLN:H	1:10:V:ARG:CB	16	0.12
(5,55)	1:35:V:MET:C	1:57:V:LEU:H	14	0.11
(5,44)	1:80:V:ARG:C	1:84:V:GLY:H	19	0.11
(5,42)	1:78:V:PHE:C	1:82:V:LEU:H	2	0.11
(5,42)	1:78:V:PHE:C	1:82:V:LEU:H	6	0.11
(5,41)	1:77:V:GLY:C	1:81:V:SER:H	1	0.11
(5,41)	1:77:V:GLY:C	1:81:V:SER:H	4	0.11
(5,41)	1:77:V:GLY:C	1:81:V:SER:H	5	0.11
(5,37)	1:71:V:ALA:C	1:75:V:ALA:H	17	0.11
(5,36)	1:70:V:LYS:C	1:74:V:GLU:H	7	0.11
(5,33)	1:68:V:GLY:C	1:72:V:LEU:H	19	0.11
(5,31)	1:66:V:LYS:C	1:70:V:LYS:H	3	0.11
(5,29)	1:64:V:ALA:C	1:68:V:GLY:H	2	0.11
(5,27)	1:62:V:GLU:C	1:66:V:LYS:H	19	0.11
(5,25)	1:58:V:ASN:C	1:61:V:ASP:H	9	0.11
(5,22)	1:54:V:VAL:H	1:98:V:PHE:C	5	0.11
(5,19)	1:50:V:ALA:C	1:96:V:THR:H	6	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(5,19)	1:50:V:ALA:C	1:96:V:THR:H	8	0.11
(5,19)	1:50:V:ALA:C	1:96:V:THR:H	10	0.11
(5,19)	1:50:V:ALA:C	1:96:V:THR:H	17	0.11
(5,18)	1:50:V:ALA:H	1:94:V:GLU:C	12	0.11
(5,18)	1:50:V:ALA:H	1:94:V:GLU:C	17	0.11
(5,16)	1:42:V:GLU:C	1:51:V:LYS:H	11	0.11
(5,12)	1:21:V:LEU:C	1:25:V:ARG:H	6	0.11
(5,12)	1:21:V:LEU:C	1:25:V:ARG:H	8	0.11
(5,11)	1:19:V:ILE:C	1:23:V:LEU:H	11	0.11
(5,7)	1:15:V:MET:C	1:19:V:ILE:H	4	0.11
(5,5)	1:13:V:GLN:C	1:17:V:LYS:H	20	0.11
(5,2)	1:10:V:ARG:C	1:14:V:GLU:H	14	0.11
(4,96)	1:84:V:GLY:O	1:89:V:LEU:N	12	0.11
(4,89)	1:81:V:SER:O	1:85:V:LYS:H	20	0.11
(4,76)	1:73:V:GLN:O	1:76:V:SER:N	2	0.11
(4,75)	1:73:V:GLN:O	1:76:V:SER:H	3	0.11
(4,75)	1:73:V:GLN:O	1:76:V:SER:H	4	0.11
(4,68)	1:68:V:GLY:O	1:71:V:ALA:N	15	0.11
(4,68)	1:68:V:GLY:O	1:71:V:ALA:N	17	0.11
(4,56)	1:63:V:ASP:O	1:67:V:ALA:N	3	0.11
(4,19)	1:18:V:GLU:O	1:22:V:ILE:H	9	0.11
(4,18)	1:17:V:LYS:O	1:21:V:LEU:N	1	0.11
(4,18)	1:17:V:LYS:O	1:21:V:LEU:N	9	0.11
(4,16)	1:16:V:GLN:O	1:20:V:ALA:N	14	0.11
(4,1)	1:9:V:GLN:O	1:13:V:GLN:H	7	0.11
(3,483)	1:72:V:LEU:H	1:69:V:ILE:HA	1	0.11
(3,422)	1:65:V:VAL:H	1:62:V:GLU:HA	14	0.11
(3,403)	1:61:V:ASP:H	1:64:V:ALA:HB1	17	0.11
(3,355)	1:53:V:TYR:H	1:41:V:VAL:HA	3	0.11
(3,303)	1:48:V:ALA:H	1:47:V:LEU:HG	5	0.11
(3,303)	1:48:V:ALA:H	1:47:V:LEU:HG	9	0.11
(3,189)	1:27:V:ILE:H	1:25:V:ARG:HA	6	0.11
(3,177)	1:26:V:GLU:H	1:22:V:ILE:HA	16	0.11
(3,165)	1:25:V:ARG:H	1:21:V:LEU:HG	20	0.11
(3,54)	1:16:V:GLN:H	1:13:V:GLN:HA	2	0.11
(3,17)	1:13:V:GLN:H	1:10:V:ARG:HA	20	0.11
(2,176)	1:43:V:MET:HG2	1:43:V:MET:HE1	16	0.11
(2,176)	1:43:V:MET:HG3	1:43:V:MET:HE1	16	0.11
(1,587)	1:92:V:VAL:H	1:89:V:LEU:CG	3	0.11
(1,536)	1:83:V:LEU:H	1:85:V:LYS:CG	14	0.11
(1,525)	1:82:V:LEU:H	1:83:V:LEU:CB	3	0.11
(1,474)	1:75:V:ALA:H	1:76:V:SER:CB	2	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,474)	1:75:V:ALA:H	1:76:V:SER:CB	8	0.11
(1,342)	1:61:V:ASP:H	1:60:V:LYS:CB	3	0.11
(1,342)	1:61:V:ASP:H	1:60:V:LYS:CB	18	0.11
(1,342)	1:61:V:ASP:H	1:60:V:LYS:CB	20	0.11
(1,339)	1:61:V:ASP:H	1:60:V:LYS:CE	18	0.11
(1,327)	1:60:V:LYS:H	1:58:V:ASN:CA	13	0.11
(1,327)	1:60:V:LYS:H	1:58:V:ASN:CA	20	0.11
(1,287)	1:51:V:LYS:H	1:42:V:GLU:CG	5	0.11
(1,281)	1:50:V:ALA:H	1:94:V:GLU:CB	4	0.11
(1,278)	1:50:V:ALA:H	1:93:V:PRO:CG	4	0.11
(1,243)	1:44:V:SER:H	1:43:V:MET:CB	10	0.11
(1,216)	1:40:V:GLY:H	1:39:V:SER:CB	13	0.11
(1,174)	1:27:V:ILE:H	1:24:V:GLN:CA	15	0.11
(1,128)	1:23:V:LEU:H	1:18:V:GLU:CA	17	0.11
(1,90)	1:19:V:ILE:H	1:20:V:ALA:CB	14	0.11
(5,42)	1:78:V:PHE:C	1:82:V:LEU:H	8	0.1
(5,33)	1:68:V:GLY:C	1:72:V:LEU:H	12	0.1
(5,33)	1:68:V:GLY:C	1:72:V:LEU:H	13	0.1
(5,22)	1:54:V:VAL:H	1:98:V:PHE:C	16	0.1
(5,21)	1:52:V:VAL:C	1:98:V:PHE:H	7	0.1
(5,14)	1:37:V:THR:H	1:55:V:THR:C	8	0.1
(4,110)	1:35:V:MET:O	1:57:V:LEU:N	8	0.1
(4,77)	1:75:V:ALA:O	1:79:V:ILE:H	1	0.1
(4,68)	1:68:V:GLY:O	1:71:V:ALA:N	16	0.1
(4,53)	1:62:V:GLU:O	1:66:V:LYS:H	8	0.1
(4,51)	1:61:V:ASP:O	1:65:V:VAL:H	4	0.1
(4,51)	1:61:V:ASP:O	1:65:V:VAL:H	13	0.1
(3,422)	1:65:V:VAL:H	1:62:V:GLU:HA	6	0.1
(3,303)	1:48:V:ALA:H	1:47:V:LEU:HG	6	0.1
(3,303)	1:48:V:ALA:H	1:47:V:LEU:HG	15	0.1
(3,114)	1:21:V:LEU:H	1:18:V:GLU:HA	6	0.1
(3,114)	1:21:V:LEU:H	1:18:V:GLU:HA	7	0.1
(3,17)	1:13:V:GLN:H	1:10:V:ARG:HA	18	0.1
(2,176)	1:43:V:MET:HG2	1:43:V:MET:HE1	11	0.1
(2,176)	1:43:V:MET:HG3	1:43:V:MET:HE1	11	0.1
(1,612)	1:96:V:THR:H	1:50:V:ALA:CB	19	0.1
(1,587)	1:92:V:VAL:H	1:89:V:LEU:CG	6	0.1
(1,580)	1:91:V:ILE:H	1:90:V:ARG:CB	2	0.1
(1,544)	1:84:V:GLY:H	1:85:V:LYS:CB	16	0.1
(1,327)	1:60:V:LYS:H	1:58:V:ASN:CA	16	0.1
(1,319)	1:58:V:ASN:H	1:57:V:LEU:CB	1	0.1
(1,287)	1:51:V:LYS:H	1:42:V:GLU:CG	11	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,157)	1:25:V:ARG:H	1:24:V:GLN:CB	12	0.1
(1,150)	1:24:V:GLN:H	1:25:V:ARG:CB	12	0.1
(1,90)	1:19:V:ILE:H	1:20:V:ALA:CB	18	0.1
(1,18)	1:13:V:GLN:H	1:10:V:ARG:CB	9	0.1

10 Dihedral-angle violation analysis [i](#)

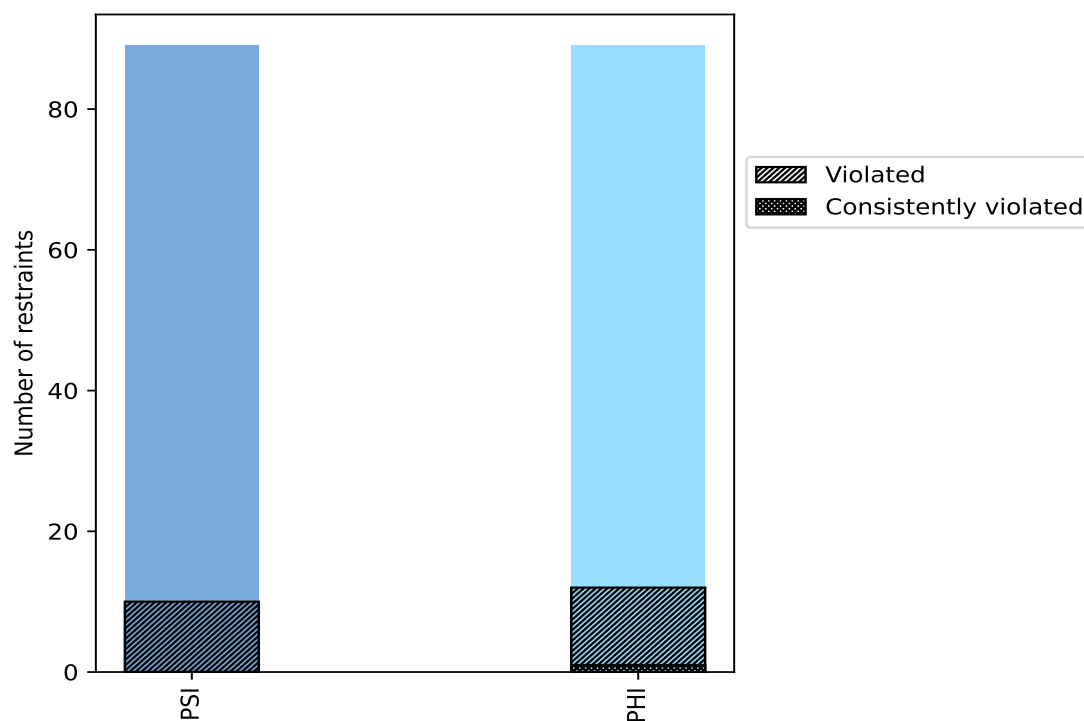
10.1 Summary of dihedral-angle violations [i](#)

The following table provides the summary of dihedral-angle violations in different dihedral-angle types. Violations less than 1° are not included in the calculation.

Angle type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
PSI	89	50.0	10	11.2	5.6	0	0.0	0.0
PHI	89	50.0	12	13.5	6.7	1	1.1	0.6
Total	178	100.0	22	12.4	12.4	1	0.6	0.6

¹ percentage calculated with respect to total number of dihedral-angle restraints, ² percentage calculated with respect to number of restraints in a particular dihedral-angle type, ³ violated in at least one model, ⁴ violated in all the models

10.1.1 Bar chart : Distribution of dihedral-angles and violations [i](#)



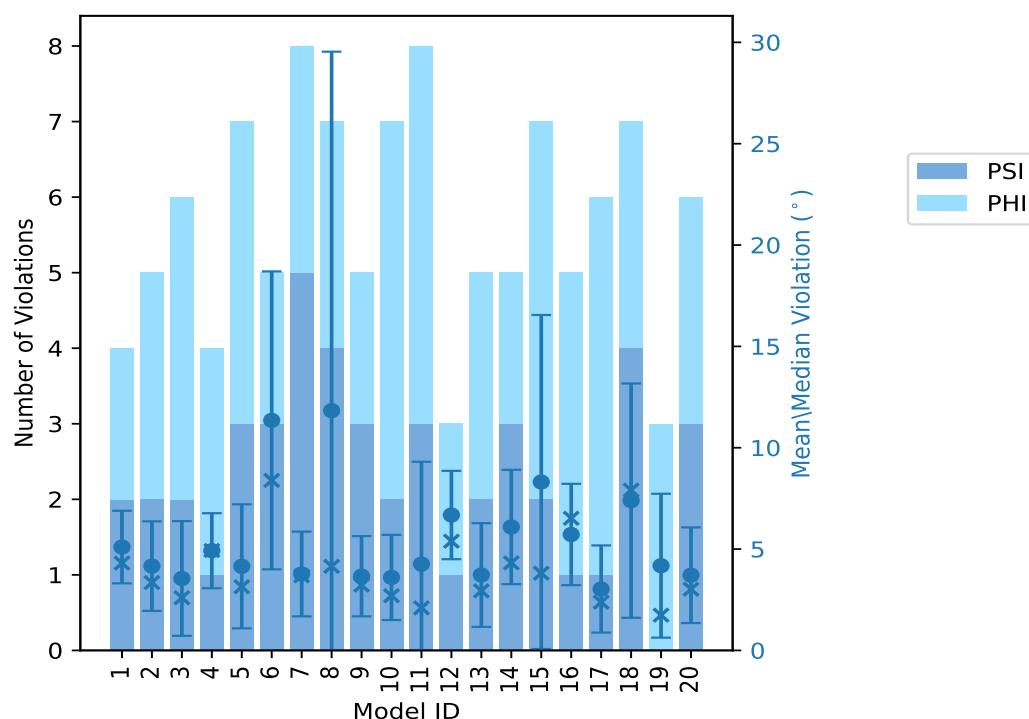
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

10.2 Dihedral-angle violation statistics for each model

The following table provides the dihedral-angle violation statistics for each model in the ensemble. Violations less than 1° are not included in the statistics.

Model ID	Number of violations			Mean (°)	Max (°)	SD (°)	Median (°)
	PSI	PHI	Total				
1	2	2	4	5.1	8.14	1.79	4.31
2	2	3	5	4.16	8.43	2.21	3.35
3	2	4	6	3.55	9.71	2.83	2.6
4	1	3	4	4.92	7.49	1.85	4.93
5	3	4	7	4.15	10.11	3.06	3.14
6	3	2	5	11.35	21.95	7.35	8.39
7	5	3	8	3.77	8.19	2.09	3.68
8	4	3	7	11.83	54.22	17.71	4.15
9	3	2	5	3.66	7.33	1.98	3.22
10	2	5	7	3.6	6.78	2.1	2.7
11	3	5	8	4.26	17.17	5.05	2.1
12	1	2	3	6.68	9.76	2.18	5.39
13	2	3	5	3.72	8.1	2.56	2.94
14	3	2	5	6.09	9.83	2.82	4.32
15	2	5	7	8.31	26.12	8.24	3.81
16	1	4	5	5.72	8.98	2.5	6.52
17	1	5	6	3.03	7.25	2.15	2.38
18	4	3	7	7.39	18.83	5.78	7.91
19	0	3	3	4.18	9.2	3.55	1.74
20	3	3	6	3.71	8.43	2.36	3.02

10.2.1 Bar graph : Dihedral 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

10.3 Dihedral-angle violation statistics for the ensemble [i](#)

Violation analysis may find that some restraints are violated in very 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 ensemble.

Number of violated restraints			Fraction of the ensemble	
PSI	PHI	Total	Count ¹	%
2	4	6	1	5.0
1	1	2	2	10.0
2	2	4	3	15.0
0	1	1	4	20.0
1	1	2	5	25.0
1	0	1	6	30.0
2	0	2	7	35.0
0	0	0	8	40.0
0	0	0	9	45.0
0	1	1	10	50.0
0	0	0	11	55.0

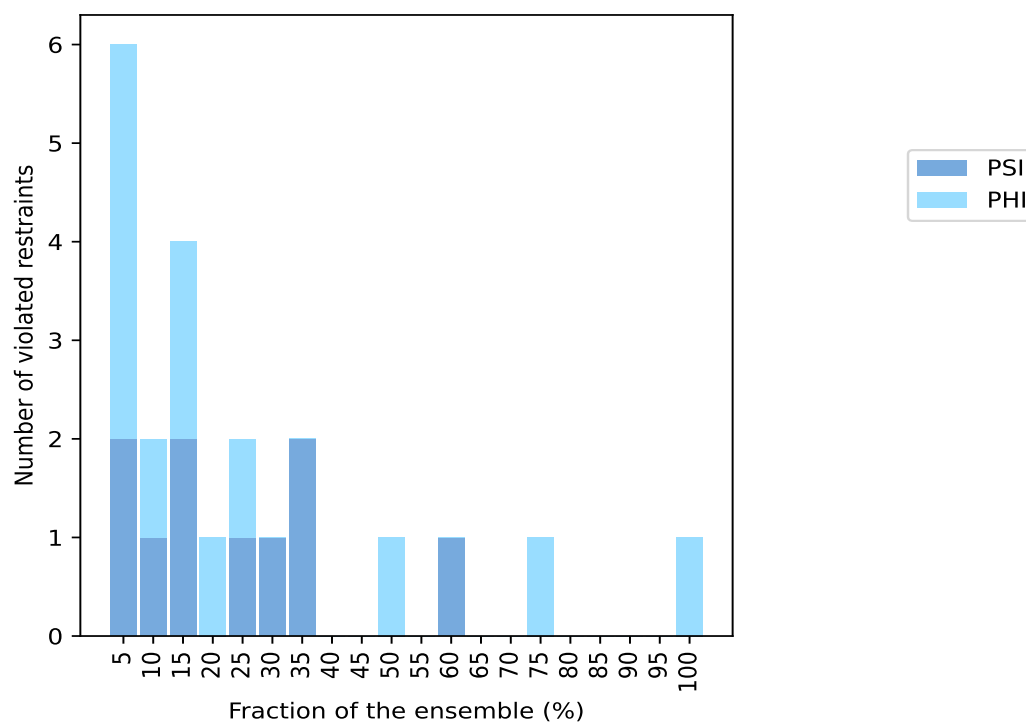
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Number of violated restraints			Fraction of the ensemble	
PSI	PHI	Total	Count ¹	%
1	0	1	12	60.0
0	0	0	13	65.0
0	0	0	14	70.0
0	1	1	15	75.0
0	0	0	16	80.0
0	0	0	17	85.0
0	0	0	18	90.0
0	0	0	19	95.0
0	1	1	20	100.0

¹ Number of models with violations

10.3.1 Bar graph : Dihedral-angle Violation statistics for the ensemble ⓘ

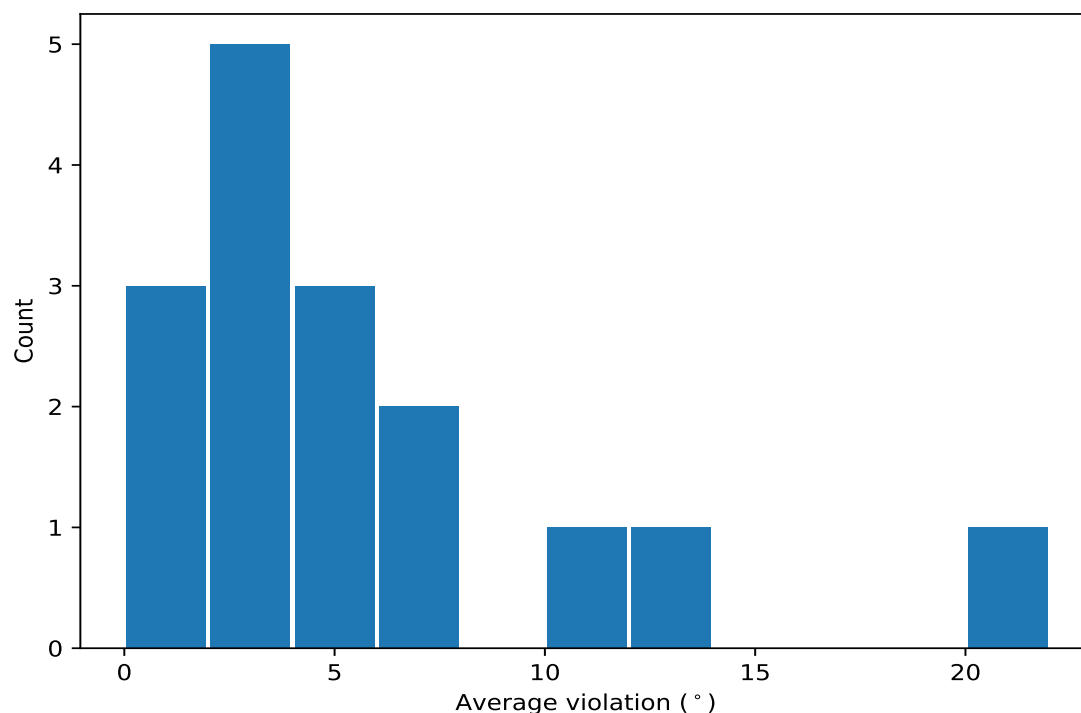


10.4 Most violated dihedral-angle restraints in the ensemble ⓘ

10.4.1 Histogram : Distribution of mean dihedral-angle violations ⓘ

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

in the ensemble



10.4.2 Table: Most violated dihedral-angle 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.

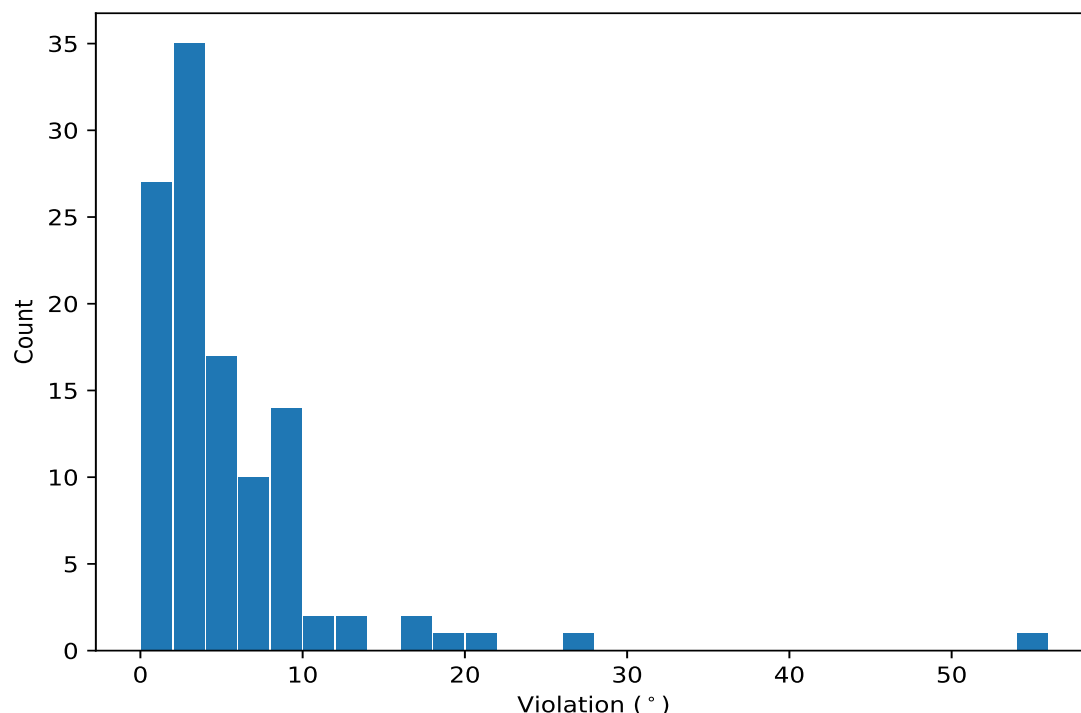
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,93)	1:59:V:ASP:C	1:60:V:LYS:N	1:60:V:LYS:CA	1:60:V:LYS:C	20	7.55	1.87	8.12
(1,85)	1:55:V:THR:C	1:56:V:PHE:N	1:56:V:PHE:CA	1:56:V:PHE:C	15	3.58	1.32	3.31
(1,40)	1:28:V:LYS:N	1:28:V:LYS:CA	1:28:V:LYS:C	1:29:V:ASP:N	12	5.72	4.23	4.7
(1,89)	1:57:V:LEU:C	1:58:V:ASN:N	1:58:V:ASN:CA	1:58:V:ASN:C	10	2.53	1.05	2.59
(1,38)	1:27:V:ILE:N	1:27:V:ILE:CA	1:27:V:ILE:C	1:28:V:LYS:N	7	4.28	2.53	3.15
(1,82)	1:54:V:VAL:N	1:54:V:VAL:CA	1:54:V:VAL:C	1:55:V:THR:N	7	2.43	1.05	2.73
(1,156)	1:91:V:ILE:N	1:91:V:ILE:CA	1:91:V:ILE:C	1:92:V:VAL:N	6	12.73	18.75	3.78
(1,157)	1:91:V:ILE:C	1:92:V:VAL:N	1:92:V:VAL:CA	1:92:V:VAL:C	5	10.99	9.22	6.01
(1,92)	1:59:V:ASP:N	1:59:V:ASP:CA	1:59:V:ASP:C	1:60:V:LYS:N	5	1.95	1.36	1.36
(1,173)	1:99:V:TYR:C	1:100:V:ASP:N	1:100:V:ASP:CA	1:100:V:ASP:C	4	1.66	0.47	1.62
(1,152)	1:89:V:LEU:N	1:89:V:LEU:CA	1:89:V:LEU:C	1:90:V:ARG:N	3	6.49	4.87	3.81
(1,150)	1:88:V:ARG:N	1:88:V:ARG:CA	1:88:V:ARG:C	1:89:V:LEU:N	3	2.79	1.56	2.33
(1,153)	1:89:V:LEU:C	1:90:V:ARG:N	1:90:V:ARG:CA	1:90:V:ARG:C	3	2.12	0.74	1.87
(1,91)	1:58:V:ASN:C	1:59:V:ASP:N	1:59:V:ASP:CA	1:59:V:ASP:C	3	1.31	0.23	1.25
(1,36)	1:26:V:GLU:N	1:26:V:GLU:CA	1:26:V:GLU:C	1:27:V:ILE:N	2	20.39	1.56	20.39
(1,147)	1:86:V:ALA:C	1:87:V:MET:N	1:87:V:MET:CA	1:87:V:MET:C	2	4.93	0.06	4.93

¹ Number of violated models, ²Standard deviation, All angle values are in degree (°)

10.5 All violated dihedral-angle restraints [i](#)

10.5.1 Histogram : Distribution of violations [i](#)

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



10.5.2 Table: All violated dihedral-angle restraints [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.

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,156)	1:91:V:ILE:N	1:91:V:ILE:CA	1:91:V:ILE:C	1:92:V:VAL:N	8	54.22
(1,157)	1:91:V:ILE:C	1:92:V:VAL:N	1:92:V:VAL:CA	1:92:V:VAL:C	15	26.12
(1,36)	1:26:V:GLU:N	1:26:V:GLU:CA	1:26:V:GLU:C	1:27:V:ILE:N	6	21.95
(1,36)	1:26:V:GLU:N	1:26:V:GLU:CA	1:26:V:GLU:C	1:27:V:ILE:N	18	18.83
(1,40)	1:28:V:LYS:N	1:28:V:LYS:CA	1:28:V:LYS:C	1:29:V:ASP:N	6	17.54
(1,157)	1:91:V:ILE:C	1:92:V:VAL:N	1:92:V:VAL:CA	1:92:V:VAL:C	11	17.17
(1,152)	1:89:V:LEU:N	1:89:V:LEU:CA	1:89:V:LEU:C	1:90:V:ARG:N	8	13.32
(1,33)	1:24:V:GLN:C	1:25:V:ARG:N	1:25:V:ARG:CA	1:25:V:ARG:C	15	13.05
(1,93)	1:59:V:ASP:C	1:60:V:LYS:N	1:60:V:LYS:CA	1:60:V:LYS:C	18	10.34
(1,156)	1:91:V:ILE:N	1:91:V:ILE:CA	1:91:V:ILE:C	1:92:V:VAL:N	5	10.11
(1,51)	1:37:V:THR:C	1:38:V:VAL:N	1:38:V:VAL:CA	1:38:V:VAL:C	14	9.83
(1,93)	1:59:V:ASP:C	1:60:V:LYS:N	1:60:V:LYS:CA	1:60:V:LYS:C	12	9.76
(1,93)	1:59:V:ASP:C	1:60:V:LYS:N	1:60:V:LYS:CA	1:60:V:LYS:C	3	9.71
(1,93)	1:59:V:ASP:C	1:60:V:LYS:N	1:60:V:LYS:CA	1:60:V:LYS:C	19	9.2

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,46)	1:32:V:LEU:N	1:32:V:LEU:CA	1:32:V:LEU:C	1:33:V:GLY:N	14	9.19
(1,93)	1:59:V:ASP:C	1:60:V:LYS:N	1:60:V:LYS:CA	1:60:V:LYS:C	16	8.98
(1,40)	1:28:V:LYS:N	1:28:V:LYS:CA	1:28:V:LYS:C	1:29:V:ASP:N	18	8.9
(1,93)	1:59:V:ASP:C	1:60:V:LYS:N	1:60:V:LYS:CA	1:60:V:LYS:C	15	8.76
(1,93)	1:59:V:ASP:C	1:60:V:LYS:N	1:60:V:LYS:CA	1:60:V:LYS:C	2	8.43
(1,93)	1:59:V:ASP:C	1:60:V:LYS:N	1:60:V:LYS:CA	1:60:V:LYS:C	20	8.43
(1,38)	1:27:V:ILE:N	1:27:V:ILE:CA	1:27:V:ILE:C	1:28:V:LYS:N	6	8.39
(1,93)	1:59:V:ASP:C	1:60:V:LYS:N	1:60:V:LYS:CA	1:60:V:LYS:C	7	8.19
(1,93)	1:59:V:ASP:C	1:60:V:LYS:N	1:60:V:LYS:CA	1:60:V:LYS:C	1	8.14
(1,93)	1:59:V:ASP:C	1:60:V:LYS:N	1:60:V:LYS:CA	1:60:V:LYS:C	13	8.1
(1,38)	1:27:V:ILE:N	1:27:V:ILE:CA	1:27:V:ILE:C	1:28:V:LYS:N	18	7.91
(1,40)	1:28:V:LYS:N	1:28:V:LYS:CA	1:28:V:LYS:C	1:29:V:ASP:N	4	7.49
(1,40)	1:28:V:LYS:N	1:28:V:LYS:CA	1:28:V:LYS:C	1:29:V:ASP:N	16	7.44
(1,93)	1:59:V:ASP:C	1:60:V:LYS:N	1:60:V:LYS:CA	1:60:V:LYS:C	9	7.33
(1,93)	1:59:V:ASP:C	1:60:V:LYS:N	1:60:V:LYS:CA	1:60:V:LYS:C	17	7.25
(1,93)	1:59:V:ASP:C	1:60:V:LYS:N	1:60:V:LYS:CA	1:60:V:LYS:C	6	7.17
(1,93)	1:59:V:ASP:C	1:60:V:LYS:N	1:60:V:LYS:CA	1:60:V:LYS:C	5	6.93
(1,93)	1:59:V:ASP:C	1:60:V:LYS:N	1:60:V:LYS:CA	1:60:V:LYS:C	10	6.78
(1,85)	1:55:V:THR:C	1:56:V:PHE:N	1:56:V:PHE:CA	1:56:V:PHE:C	16	6.52
(1,157)	1:91:V:ILE:C	1:92:V:VAL:N	1:92:V:VAL:CA	1:92:V:VAL:C	10	6.01
(1,85)	1:55:V:THR:C	1:56:V:PHE:N	1:56:V:PHE:CA	1:56:V:PHE:C	12	5.39
(1,93)	1:59:V:ASP:C	1:60:V:LYS:N	1:60:V:LYS:CA	1:60:V:LYS:C	4	5.36
(1,147)	1:86:V:ALA:C	1:87:V:MET:N	1:87:V:MET:CA	1:87:V:MET:C	11	4.99
(1,85)	1:55:V:THR:C	1:56:V:PHE:N	1:56:V:PHE:CA	1:56:V:PHE:C	13	4.92
(1,40)	1:28:V:LYS:N	1:28:V:LYS:CA	1:28:V:LYS:C	1:29:V:ASP:N	12	4.9
(1,150)	1:88:V:ARG:N	1:88:V:ARG:CA	1:88:V:ARG:C	1:89:V:LEU:N	7	4.88
(1,147)	1:86:V:ALA:C	1:87:V:MET:N	1:87:V:MET:CA	1:87:V:MET:C	8	4.87
(1,40)	1:28:V:LYS:N	1:28:V:LYS:CA	1:28:V:LYS:C	1:29:V:ASP:N	10	4.8
(1,92)	1:59:V:ASP:N	1:59:V:ASP:CA	1:59:V:ASP:C	1:60:V:LYS:N	20	4.65
(1,40)	1:28:V:LYS:N	1:28:V:LYS:CA	1:28:V:LYS:C	1:29:V:ASP:N	1	4.59
(1,85)	1:55:V:THR:C	1:56:V:PHE:N	1:56:V:PHE:CA	1:56:V:PHE:C	4	4.5
(1,85)	1:55:V:THR:C	1:56:V:PHE:N	1:56:V:PHE:CA	1:56:V:PHE:C	7	4.43
(1,40)	1:28:V:LYS:N	1:28:V:LYS:CA	1:28:V:LYS:C	1:29:V:ASP:N	14	4.32
(1,82)	1:54:V:VAL:N	1:54:V:VAL:CA	1:54:V:VAL:C	1:55:V:THR:N	5	4.24
(1,93)	1:59:V:ASP:C	1:60:V:LYS:N	1:60:V:LYS:CA	1:60:V:LYS:C	8	4.15
(1,89)	1:57:V:LEU:C	1:58:V:ASN:N	1:58:V:ASN:CA	1:58:V:ASN:C	1	4.04
(1,156)	1:91:V:ILE:N	1:91:V:ILE:CA	1:91:V:ILE:C	1:92:V:VAL:N	2	4.01
(1,93)	1:59:V:ASP:C	1:60:V:LYS:N	1:60:V:LYS:CA	1:60:V:LYS:C	14	3.98
(1,93)	1:59:V:ASP:C	1:60:V:LYS:N	1:60:V:LYS:CA	1:60:V:LYS:C	11	3.93
(1,152)	1:89:V:LEU:N	1:89:V:LEU:CA	1:89:V:LEU:C	1:90:V:ARG:N	15	3.81
(1,89)	1:57:V:LEU:C	1:58:V:ASN:N	1:58:V:ASN:CA	1:58:V:ASN:C	7	3.81
(1,85)	1:55:V:THR:C	1:56:V:PHE:N	1:56:V:PHE:CA	1:56:V:PHE:C	17	3.76
(1,85)	1:55:V:THR:C	1:56:V:PHE:N	1:56:V:PHE:CA	1:56:V:PHE:C	8	3.67
(1,38)	1:27:V:ILE:N	1:27:V:ILE:CA	1:27:V:ILE:C	1:28:V:LYS:N	1	3.61
(1,156)	1:91:V:ILE:N	1:91:V:ILE:CA	1:91:V:ILE:C	1:92:V:VAL:N	7	3.56
(1,40)	1:28:V:LYS:N	1:28:V:LYS:CA	1:28:V:LYS:C	1:29:V:ASP:N	9	3.5
(1,89)	1:57:V:LEU:C	1:58:V:ASN:N	1:58:V:ASN:CA	1:58:V:ASN:C	17	3.4
(1,89)	1:57:V:LEU:C	1:58:V:ASN:N	1:58:V:ASN:CA	1:58:V:ASN:C	2	3.35
(1,85)	1:55:V:THR:C	1:56:V:PHE:N	1:56:V:PHE:CA	1:56:V:PHE:C	20	3.31
(1,85)	1:55:V:THR:C	1:56:V:PHE:N	1:56:V:PHE:CA	1:56:V:PHE:C	9	3.22
(1,38)	1:27:V:ILE:N	1:27:V:ILE:CA	1:27:V:ILE:C	1:28:V:LYS:N	14	3.15

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,157)	1:91:V:ILE:C	1:92:V:VAL:N	1:92:V:VAL:CA	1:92:V:VAL:C	5	3.14
(1,153)	1:89:V:LEU:C	1:90:V:ARG:N	1:90:V:ARG:CA	1:90:V:ARG:C	16	3.12
(1,82)	1:54:V:VAL:N	1:54:V:VAL:CA	1:54:V:VAL:C	1:55:V:THR:N	3	3.08
(1,38)	1:27:V:ILE:N	1:27:V:ILE:CA	1:27:V:ILE:C	1:28:V:LYS:N	13	2.94
(1,82)	1:54:V:VAL:N	1:54:V:VAL:CA	1:54:V:VAL:C	1:55:V:THR:N	9	2.86
(1,89)	1:57:V:LEU:C	1:58:V:ASN:N	1:58:V:ASN:CA	1:58:V:ASN:C	3	2.85
(1,40)	1:28:V:LYS:N	1:28:V:LYS:CA	1:28:V:LYS:C	1:29:V:ASP:N	7	2.81
(1,85)	1:55:V:THR:C	1:56:V:PHE:N	1:56:V:PHE:CA	1:56:V:PHE:C	18	2.79
(1,82)	1:54:V:VAL:N	1:54:V:VAL:CA	1:54:V:VAL:C	1:55:V:THR:N	20	2.73
(1,156)	1:91:V:ILE:N	1:91:V:ILE:CA	1:91:V:ILE:C	1:92:V:VAL:N	10	2.7
(1,85)	1:55:V:THR:C	1:56:V:PHE:N	1:56:V:PHE:CA	1:56:V:PHE:C	2	2.69
(1,38)	1:27:V:ILE:N	1:27:V:ILE:CA	1:27:V:ILE:C	1:28:V:LYS:N	15	2.59
(1,157)	1:91:V:ILE:C	1:92:V:VAL:N	1:92:V:VAL:CA	1:92:V:VAL:C	16	2.52
(1,85)	1:55:V:THR:C	1:56:V:PHE:N	1:56:V:PHE:CA	1:56:V:PHE:C	15	2.48
(1,85)	1:55:V:THR:C	1:56:V:PHE:N	1:56:V:PHE:CA	1:56:V:PHE:C	10	2.46
(1,173)	1:99:V:TYR:C	1:100:V:ASP:N	1:100:V:ASP:CA	1:100:V:ASP:C	3	2.35
(1,152)	1:89:V:LEU:N	1:89:V:LEU:CA	1:89:V:LEU:C	1:90:V:ARG:N	11	2.33
(1,151)	1:88:V:ARG:C	1:89:V:LEU:N	1:89:V:LEU:CA	1:89:V:LEU:C	5	2.33
(1,150)	1:88:V:ARG:N	1:88:V:ARG:CA	1:88:V:ARG:C	1:89:V:LEU:N	2	2.33
(1,89)	1:57:V:LEU:C	1:58:V:ASN:N	1:58:V:ASN:CA	1:58:V:ASN:C	4	2.33
(1,85)	1:55:V:THR:C	1:56:V:PHE:N	1:56:V:PHE:CA	1:56:V:PHE:C	3	2.32
(1,82)	1:54:V:VAL:N	1:54:V:VAL:CA	1:54:V:VAL:C	1:55:V:THR:N	18	1.89
(1,153)	1:89:V:LEU:C	1:90:V:ARG:N	1:90:V:ARG:CA	1:90:V:ARG:C	11	1.87
(1,156)	1:91:V:ILE:N	1:91:V:ILE:CA	1:91:V:ILE:C	1:92:V:VAL:N	20	1.77
(1,173)	1:99:V:TYR:C	1:100:V:ASP:N	1:100:V:ASP:CA	1:100:V:ASP:C	19	1.74
(1,89)	1:57:V:LEU:C	1:58:V:ASN:N	1:58:V:ASN:CA	1:58:V:ASN:C	6	1.7
(1,91)	1:58:V:ASN:C	1:59:V:ASP:N	1:59:V:ASP:CA	1:59:V:ASP:C	19	1.61
(1,173)	1:99:V:TYR:C	1:100:V:ASP:N	1:100:V:ASP:CA	1:100:V:ASP:C	13	1.51
(1,34)	1:25:V:ARG:N	1:25:V:ARG:CA	1:25:V:ARG:C	1:26:V:GLU:N	8	1.48
(1,89)	1:57:V:LEU:C	1:58:V:ASN:N	1:58:V:ASN:CA	1:58:V:ASN:C	10	1.39
(1,38)	1:27:V:ILE:N	1:27:V:ILE:CA	1:27:V:ILE:C	1:28:V:LYS:N	11	1.38
(1,153)	1:89:V:LEU:C	1:90:V:ARG:N	1:90:V:ARG:CA	1:90:V:ARG:C	15	1.37
(1,92)	1:59:V:ASP:N	1:59:V:ASP:CA	1:59:V:ASP:C	1:60:V:LYS:N	9	1.37
(1,89)	1:57:V:LEU:C	1:58:V:ASN:N	1:58:V:ASN:CA	1:58:V:ASN:C	20	1.37
(1,92)	1:59:V:ASP:N	1:59:V:ASP:CA	1:59:V:ASP:C	1:60:V:LYS:N	7	1.36
(1,92)	1:59:V:ASP:N	1:59:V:ASP:CA	1:59:V:ASP:C	1:60:V:LYS:N	17	1.35
(1,85)	1:55:V:THR:C	1:56:V:PHE:N	1:56:V:PHE:CA	1:56:V:PHE:C	11	1.31
(1,40)	1:28:V:LYS:N	1:28:V:LYS:CA	1:28:V:LYS:C	1:29:V:ASP:N	5	1.29
(1,91)	1:58:V:ASN:C	1:59:V:ASP:N	1:59:V:ASP:CA	1:59:V:ASP:C	17	1.25
(1,73)	1:49:V:TYR:C	1:50:V:ALA:N	1:50:V:ALA:CA	1:50:V:ALA:C	17	1.19
(1,150)	1:88:V:ARG:N	1:88:V:ARG:CA	1:88:V:ARG:C	1:89:V:LEU:N	13	1.15
(1,82)	1:54:V:VAL:N	1:54:V:VAL:CA	1:54:V:VAL:C	1:55:V:THR:N	7	1.14
(1,40)	1:28:V:LYS:N	1:28:V:LYS:CA	1:28:V:LYS:C	1:29:V:ASP:N	8	1.09
(1,82)	1:54:V:VAL:N	1:54:V:VAL:CA	1:54:V:VAL:C	1:55:V:THR:N	11	1.08
(1,91)	1:58:V:ASN:C	1:59:V:ASP:N	1:59:V:ASP:CA	1:59:V:ASP:C	10	1.06
(1,173)	1:99:V:TYR:C	1:100:V:ASP:N	1:100:V:ASP:CA	1:100:V:ASP:C	18	1.04
(1,89)	1:57:V:LEU:C	1:58:V:ASN:N	1:58:V:ASN:CA	1:58:V:ASN:C	5	1.04
(1,92)	1:59:V:ASP:N	1:59:V:ASP:CA	1:59:V:ASP:C	1:60:V:LYS:N	3	1.01