



Full wwPDB NMR Structure Validation Report ⓘ

Mar 26, 2026 – 09:42 AM UTC

PDB ID : 2LRE / pdb_00002lre
BMRB ID : 18358
Title : The solution structure of the dimeric Acanthaporin
Authors : Michalek, M.; Soennichsen, F.D.; Wechselberger, R.; Dingley, A.J.; Wienk, H.; Simanski, M.; Herbst, R.; Lorenzen, I.; Marciano-Cabral, F.; Gelhaus, C.; Groetzinger, J.; Leippe, M.
Deposited on : 2012-03-28

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

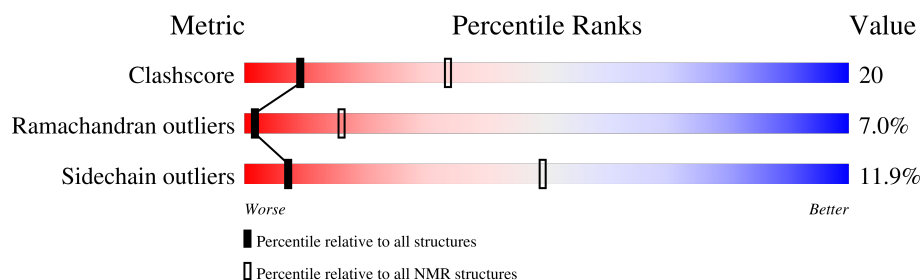
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

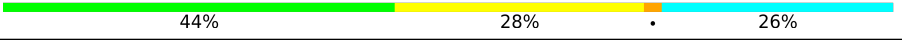
The overall completeness of chemical shifts assignment is 22%.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	61	
1	B	61	

2 Ensemble composition and analysis

This entry contains 17 models. Model 16 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:13-A:61, B:74-B:98, B:103-B:122 (94)	1.98	16

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 4 clusters and 2 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1634 atoms, of which 816 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Acanthaporin.

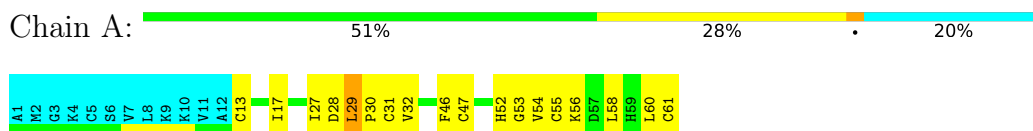
Mol	Chain	Residues	Atoms						Trace
1	A	61	Total	C	H	N	O	S	0
			817	252	408	72	74	11	
1	B	61	Total	C	H	N	O	S	0
			817	252	408	72	74	11	

4 Residue-property plots

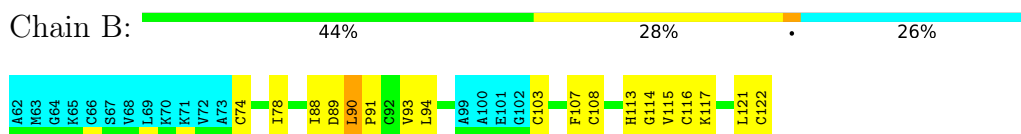
4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

• Molecule 1: Acanthaporin



• Molecule 1: Acanthaporin

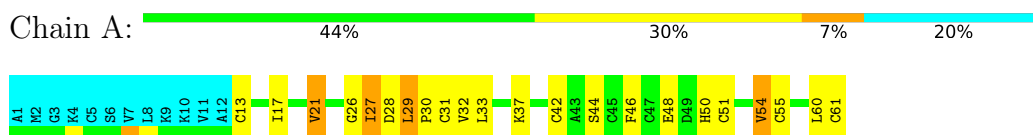


4.2 Scores per residue for each member of the ensemble

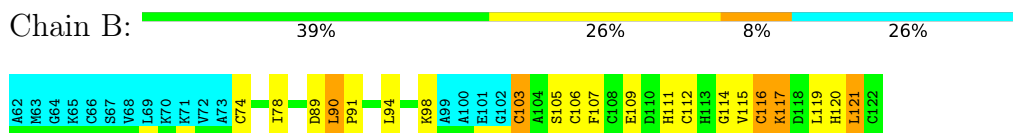
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: Acanthaporin

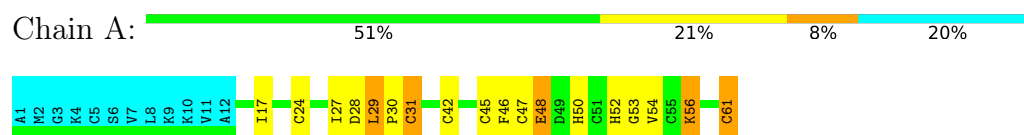


• Molecule 1: Acanthaporin

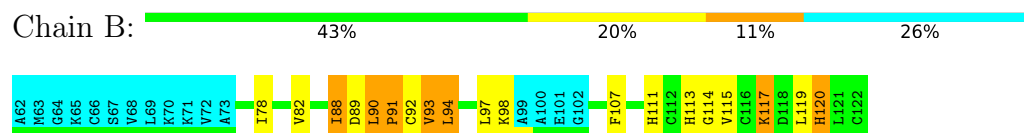


4.2.2 Score per residue for model 2

• Molecule 1: Acanthaporin

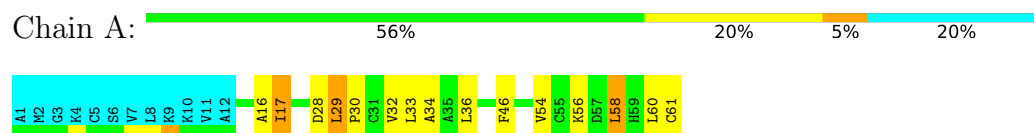


• Molecule 1: Acanthaporin

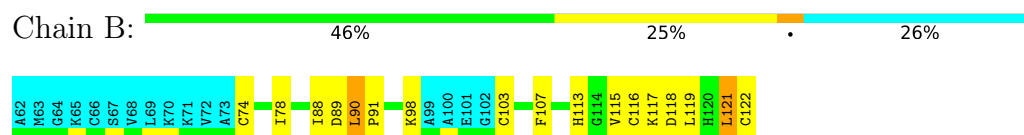


4.2.3 Score per residue for model 3

• Molecule 1: Acanthaporin

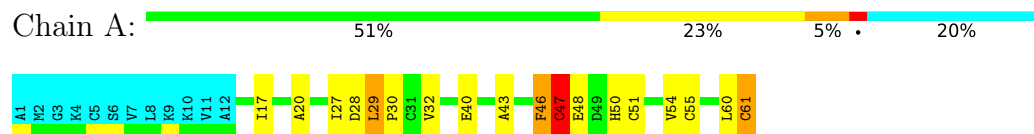


• Molecule 1: Acanthaporin

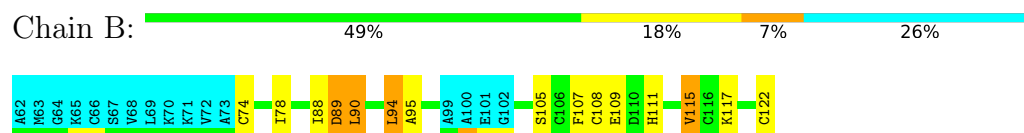


4.2.4 Score per residue for model 4

• Molecule 1: Acanthaporin



• Molecule 1: Acanthaporin



4.2.5 Score per residue for model 5

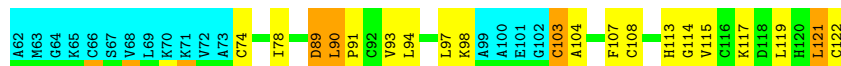
• Molecule 1: Acanthaporin

Chain A: 



• Molecule 1: Acanthaporin

Chain B: 



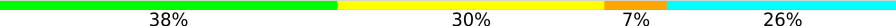
4.2.6 Score per residue for model 6

• Molecule 1: Acanthaporin

Chain A: 



• Molecule 1: Acanthaporin

Chain B: 



4.2.7 Score per residue for model 7

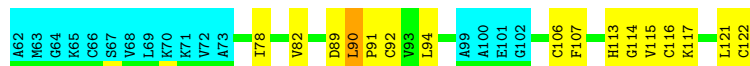
• Molecule 1: Acanthaporin

Chain A: 



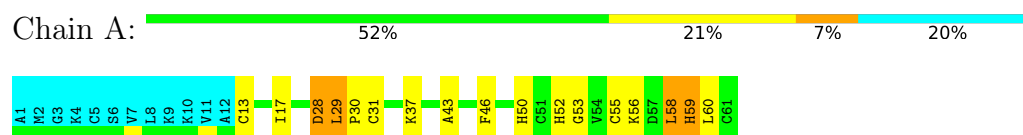
• Molecule 1: Acanthaporin

Chain B: 

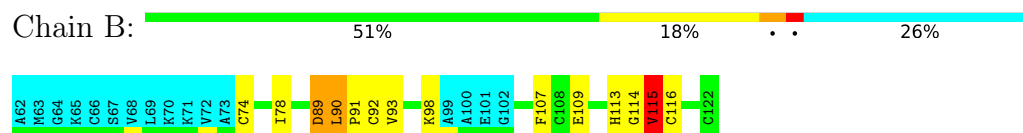


4.2.8 Score per residue for model 8

• Molecule 1: Acanthaporin

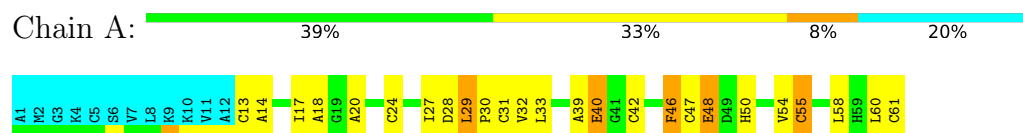


• Molecule 1: Acanthaporin

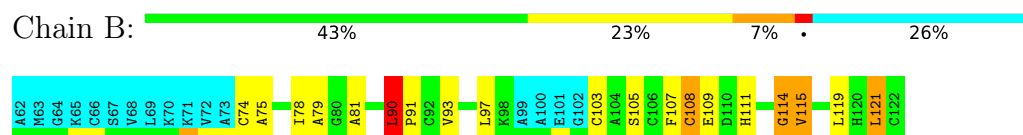


4.2.9 Score per residue for model 9

• Molecule 1: Acanthaporin

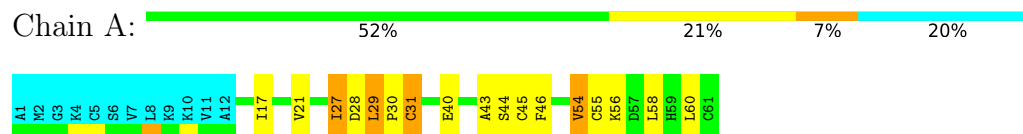


• Molecule 1: Acanthaporin

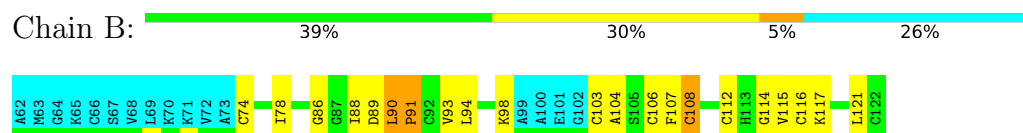


4.2.10 Score per residue for model 10

• Molecule 1: Acanthaporin

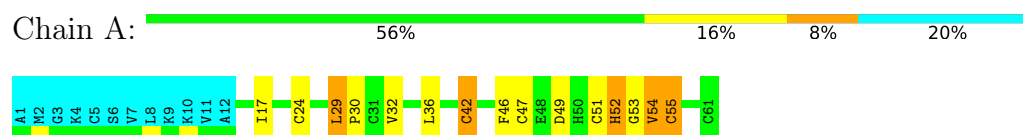


• Molecule 1: Acanthaporin

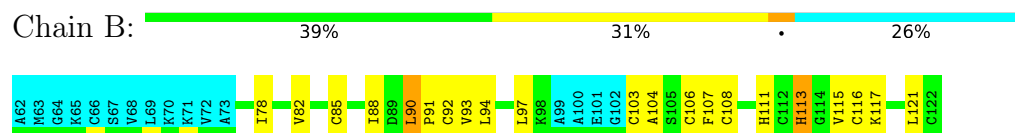


4.2.11 Score per residue for model 11

• Molecule 1: Acanthaporin

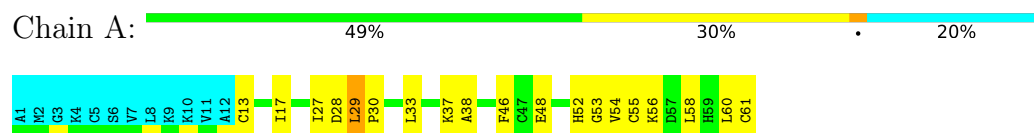


• Molecule 1: Acanthaporin

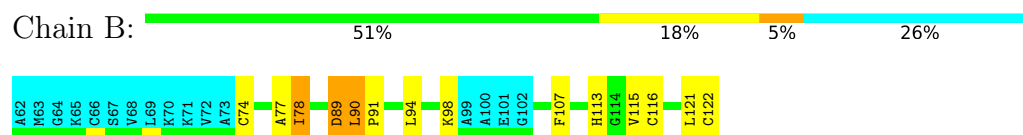


4.2.12 Score per residue for model 12

• Molecule 1: Acanthaporin

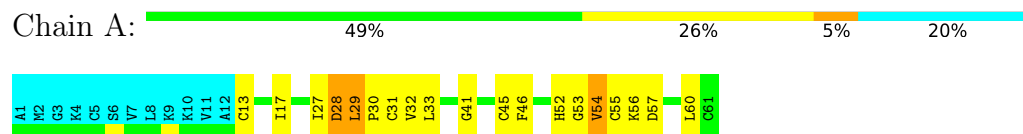


• Molecule 1: Acanthaporin

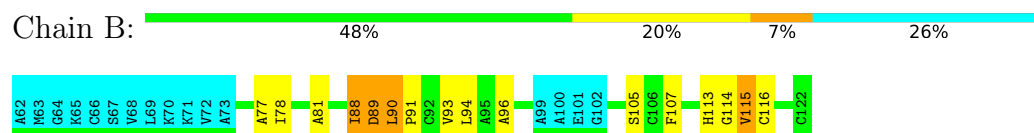


4.2.13 Score per residue for model 13

• Molecule 1: Acanthaporin

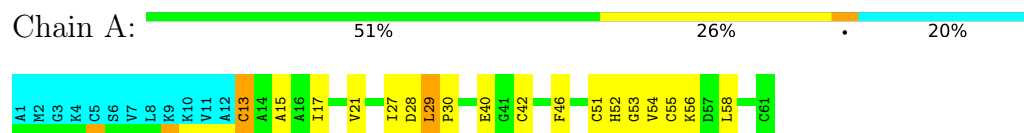


• Molecule 1: Acanthaporin

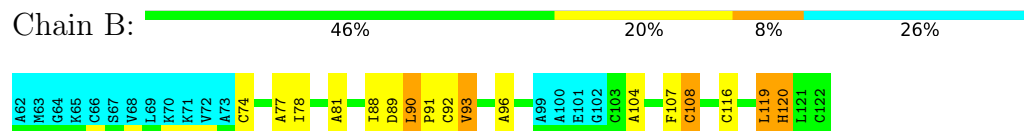


4.2.14 Score per residue for model 14

• Molecule 1: Acanthaporin

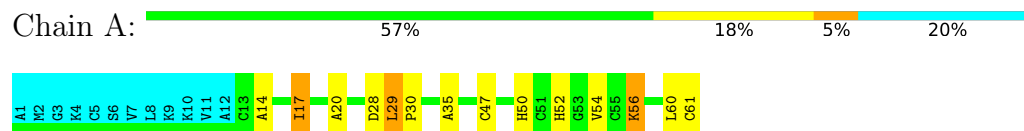


• Molecule 1: Acanthaporin

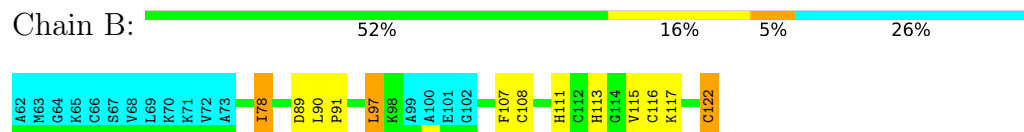


4.2.15 Score per residue for model 15

• Molecule 1: Acanthaporin

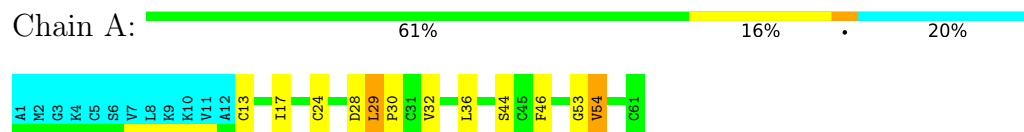


• Molecule 1: Acanthaporin

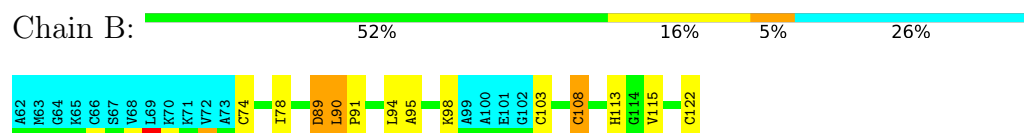


4.2.16 Score per residue for model 16 (medoid)

• Molecule 1: Acanthaporin

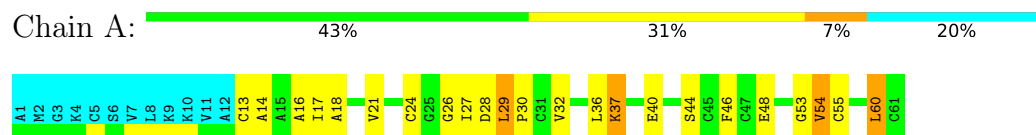


• Molecule 1: Acanthaporin

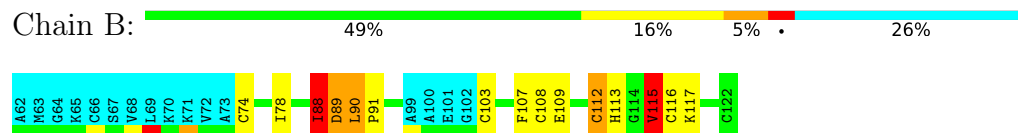


4.2.17 Score per residue for model 17

• Molecule 1: Acanthaporin



• Molecule 1: Acanthaporin



5 Refinement protocol and experimental data overview

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

Of the 400 calculated structures, 17 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
CYANA	structure solution	
X-PLOR NIH	refinement	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	263
Number of shifts mapped to atoms	262
Number of unparsed shifts	0
Number of shifts with mapping errors	1
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	22%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.47±0.03	0±0/330 (0.0± 0.0%)	0.84±0.05	0±0/445 (0.1± 0.1%)
1	B	0.46±0.03	0±0/307 (0.0± 0.0%)	0.84±0.04	0±0/414 (0.0± 0.1%)
All	All	0.46	0/10829 (0.0%)	0.84	6/14603 (0.0%)

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	A	38	ALA	N-CA-C	-6.71	106.03	114.56	5	1
1	B	106	CYS	N-CA-C	-5.80	106.74	113.88	1	1
1	A	57	ASP	N-CA-C	-5.22	105.65	112.23	13	1
1	A	40	GLU	CB-CA-C	-5.15	110.66	116.63	6	1
1	A	45	CYS	N-CA-C	-5.13	108.29	114.75	10	1
1	B	119	LEU	N-CA-C	-5.07	105.93	112.68	14	1

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	326	307	307	15±4
1	B	303	288	288	13±5
All	All	10693	10115	10115	425

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 20.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:74:CYS:HB2	1:B:78:ILE:HD12	0.89	1.44	1	2
1:A:13:CYS:HB2	1:A:17:ILE:HD12	0.84	1.47	6	3
1:A:30:PRO:HA	1:A:54:VAL:HG11	0.82	1.49	6	8
1:B:91:PRO:HA	1:B:115:VAL:HG11	0.82	1.50	17	4
1:B:94:LEU:HD22	1:B:115:VAL:HB	0.82	1.50	6	3
1:B:78:ILE:HD13	1:B:97:LEU:HD13	0.80	1.54	11	1
1:A:52:HIS:HA	1:A:56:LYS:HB3	0.79	1.54	15	1
1:B:91:PRO:HB3	1:B:115:VAL:HG11	0.78	1.55	9	1
1:B:75:ALA:HA	1:B:79:ALA:HB3	0.77	1.56	9	2
1:A:53:GLY:HA3	1:B:91:PRO:HB2	0.74	1.59	14	3
1:A:30:PRO:HB3	1:A:54:VAL:HG13	0.74	1.60	9	1
1:B:74:CYS:HB3	1:B:78:ILE:HD12	0.72	1.60	16	5
1:A:17:ILE:HG12	1:A:46:PHE:CD2	0.70	2.21	8	10
1:A:17:ILE:HD13	1:A:36:LEU:HD13	0.70	1.60	11	1
1:A:30:PRO:HB2	1:B:115:VAL:HG13	0.69	1.65	6	1
1:B:90:LEU:HD11	1:B:116:CYS:SG	0.69	2.27	17	1
1:B:78:ILE:HD13	1:B:107:PHE:HB2	0.68	1.65	17	8
1:A:29:LEU:HD21	1:A:55:CYS:HB2	0.68	1.64	4	3
1:A:29:LEU:HD11	1:A:55:CYS:SG	0.68	2.28	12	2
1:A:13:CYS:HB3	1:A:17:ILE:HD12	0.68	1.64	12	2
1:B:113:HIS:HA	1:B:117:LYS:HG2	0.68	1.65	2	1
1:A:28:ASP:C	1:A:30:PRO:HD2	0.67	2.15	16	1
1:B:90:LEU:HD11	1:B:116:CYS:HB2	0.67	1.65	12	6
1:A:47:CYS:HB3	1:A:61:CYS:SG	0.67	2.29	9	1
1:A:30:PRO:HA	1:A:54:VAL:HG21	0.67	1.66	3	5
1:A:17:ILE:HD13	1:A:46:PHE:HB2	0.66	1.67	1	7
1:B:91:PRO:HA	1:B:115:VAL:HG21	0.66	1.66	15	4
1:A:30:PRO:HB3	1:B:115:VAL:HG13	0.66	1.67	1	1
1:A:30:PRO:HB2	1:B:91:PRO:HB2	0.65	1.67	9	1
1:B:108:CYS:O	1:B:122:CYS:HB3	0.65	1.92	15	2
1:A:53:GLY:HA2	1:B:91:PRO:HB2	0.64	1.69	8	1
1:B:103:CYS:HB2	1:B:121:LEU:HD21	0.64	1.70	1	1
1:B:81:ALA:HB2	1:B:96:ALA:HB3	0.63	1.68	14	2
1:A:29:LEU:HD21	1:A:55:CYS:HB3	0.63	1.70	9	1
1:A:29:LEU:HD11	1:A:55:CYS:HB2	0.63	1.70	17	5
1:A:20:ALA:HB1	1:A:32:VAL:HG13	0.63	1.70	4	1
1:B:90:LEU:HD11	1:B:108:CYS:SG	0.62	2.34	9	1
1:A:17:ILE:CD1	1:A:46:PHE:HB2	0.62	2.24	12	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:74:CYS:O	1:B:78:ILE:HB	0.62	1.94	12	3
1:B:119:LEU:O	1:B:120:HIS:HB2	0.61	1.94	2	3
1:A:13:CYS:CB	1:A:17:ILE:HD12	0.60	2.26	14	1
1:A:29:LEU:HG	1:A:54:VAL:HG22	0.60	1.71	15	1
1:A:29:LEU:HB3	1:A:30:PRO:HD3	0.60	1.74	10	5
1:A:40:GLU:HG2	1:A:42:CYS:H	0.60	1.56	9	1
1:A:30:PRO:CA	1:A:54:VAL:HG11	0.60	2.26	10	1
1:A:33:LEU:HD13	1:A:54:VAL:HB	0.60	1.73	13	1
1:B:108:CYS:HA	1:B:111:HIS:HB2	0.60	1.71	4	2
1:A:28:ASP:OD2	1:A:31:CYS:HB3	0.60	1.96	1	1
1:B:78:ILE:HD13	1:B:97:LEU:HD12	0.59	1.75	5	1
1:A:28:ASP:O	1:A:29:LEU:HB3	0.59	1.98	16	1
1:A:58:LEU:O	1:A:59:HIS:HB2	0.59	1.96	8	2
1:A:17:ILE:HG12	1:A:46:PHE:CD1	0.59	2.32	7	2
1:A:51:CYS:HB2	1:A:55:CYS:SG	0.59	2.37	4	1
1:B:78:ILE:HG12	1:B:107:PHE:CD2	0.59	2.33	11	5
1:B:108:CYS:HB3	1:B:111:HIS:O	0.59	1.95	15	1
1:A:52:HIS:O	1:B:92:CYS:HB3	0.59	1.98	11	1
1:A:20:ALA:HB2	1:A:35:ALA:HB3	0.59	1.75	15	1
1:B:90:LEU:N	1:B:91:PRO:HD2	0.58	2.13	10	9
1:A:30:PRO:HG2	1:B:91:PRO:HB2	0.58	1.75	9	1
1:A:52:HIS:ND1	1:B:92:CYS:HB3	0.58	2.13	14	2
1:B:94:LEU:HD13	1:B:115:VAL:HB	0.58	1.75	13	1
1:B:104:ALA:HB1	1:B:121:LEU:HB3	0.58	1.75	11	1
1:A:13:CYS:HA	1:A:17:ILE:HD12	0.58	1.75	17	1
1:A:33:LEU:HD22	1:A:54:VAL:HB	0.57	1.75	1	1
1:B:94:LEU:HD22	1:B:115:VAL:HG23	0.57	1.75	5	1
1:A:30:PRO:CB	1:B:91:PRO:HB2	0.57	2.28	9	1
1:A:13:CYS:O	1:A:17:ILE:HB	0.57	1.98	1	3
1:B:90:LEU:HD12	1:B:94:LEU:HB2	0.57	1.76	7	1
1:A:33:LEU:HD23	1:A:54:VAL:HB	0.57	1.76	3	1
1:B:90:LEU:HB3	1:B:91:PRO:HD3	0.57	1.77	17	4
1:A:30:PRO:CG	1:B:91:PRO:HB2	0.57	2.29	9	1
1:A:31:CYS:HB3	1:B:114:GLY:HA2	0.57	1.77	6	1
1:A:28:ASP:HB3	1:A:32:VAL:HG23	0.56	1.75	7	3
1:A:29:LEU:HG	1:A:54:VAL:CG2	0.56	2.30	11	5
1:A:53:GLY:HA3	1:B:91:PRO:HG2	0.56	1.77	5	1
1:B:91:PRO:HA	1:B:115:VAL:CG2	0.56	2.30	5	2
1:A:28:ASP:OD1	1:A:30:PRO:HD2	0.56	2.01	1	2
1:B:90:LEU:O	1:B:94:LEU:HB2	0.56	2.01	2	1
1:B:103:CYS:SG	1:B:106:CYS:HB2	0.56	2.40	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:29:LEU:HG	1:A:54:VAL:HG21	0.55	1.79	6	1
1:A:24:CYS:SG	1:B:113:HIS:CD2	0.55	2.99	11	1
1:B:78:ILE:CD1	1:B:107:PHE:HB2	0.55	2.31	4	5
1:A:28:ASP:HB2	1:B:113:HIS:CE1	0.55	2.36	2	2
1:A:51:CYS:CB	1:A:56:LYS:HG2	0.55	2.32	6	1
1:A:30:PRO:HA	1:A:54:VAL:CG2	0.55	2.32	9	1
1:A:51:CYS:HB3	1:A:56:LYS:HG2	0.55	1.78	6	1
1:B:108:CYS:HB3	1:B:122:CYS:SG	0.55	2.41	6	1
1:A:29:LEU:N	1:A:30:PRO:HD2	0.55	2.17	11	4
1:B:113:HIS:HA	1:B:117:LYS:HB3	0.55	1.79	15	1
1:A:30:PRO:HA	1:A:54:VAL:CG1	0.55	2.31	10	2
1:A:30:PRO:HG3	1:B:91:PRO:HD3	0.54	1.79	5	1
1:A:13:CYS:HB2	1:A:17:ILE:CD1	0.54	2.28	6	1
1:A:30:PRO:HB2	1:B:114:GLY:HA3	0.54	1.78	8	1
1:B:113:HIS:HA	1:B:117:LYS:HD2	0.54	1.79	5	1
1:B:90:LEU:HD21	1:B:116:CYS:CB	0.54	2.32	14	1
1:A:17:ILE:HG12	1:A:46:PHE:HD2	0.54	1.63	6	4
1:A:30:PRO:HA	1:A:54:VAL:HG22	0.54	1.78	9	1
1:B:98:LYS:HA	1:B:119:LEU:HD11	0.54	1.78	3	1
1:B:89:ASP:CG	1:B:91:PRO:HD2	0.54	2.26	13	3
1:B:94:LEU:HD12	1:B:95:ALA:N	0.54	2.18	16	2
1:A:28:ASP:OD2	1:B:114:GLY:HA2	0.54	2.02	7	1
1:A:21:VAL:HG13	1:A:26:GLY:HA2	0.54	1.79	1	2
1:B:74:CYS:HB3	1:B:103:CYS:SG	0.54	2.43	5	1
1:A:52:HIS:CE1	1:B:92:CYS:HB3	0.54	2.38	8	2
1:A:52:HIS:HB2	1:B:89:ASP:OD2	0.54	2.03	13	1
1:B:78:ILE:O	1:B:82:VAL:HG23	0.54	2.03	2	3
1:A:52:HIS:O	1:B:91:PRO:HB2	0.54	2.02	6	1
1:B:74:CYS:HB3	1:B:78:ILE:CD1	0.54	2.32	6	1
1:A:43:ALA:CB	1:A:60:LEU:HB3	0.53	2.33	10	2
1:B:94:LEU:HG	1:B:98:LYS:HG3	0.53	1.80	5	1
1:A:28:ASP:CG	1:A:31:CYS:HB3	0.53	2.28	10	1
1:B:105:SER:O	1:B:109:GLU:HG2	0.53	2.04	4	1
1:A:28:ASP:OD1	1:A:31:CYS:HB3	0.53	2.04	9	2
1:A:17:ILE:HD13	1:A:46:PHE:HB3	0.53	1.81	4	1
1:A:47:CYS:SG	1:A:60:LEU:HB2	0.53	2.43	9	1
1:A:30:PRO:HD3	1:B:91:PRO:HG3	0.53	1.80	16	2
1:B:81:ALA:HB3	1:B:93:VAL:HG13	0.52	1.81	9	2
1:A:41:GLY:HA2	1:A:60:LEU:HD22	0.52	1.80	13	1
1:B:104:ALA:HB1	1:B:108:CYS:HB2	0.52	1.80	14	1
1:A:33:LEU:HA	1:A:36:LEU:HB3	0.52	1.79	6	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:31:CYS:HB3	1:B:113:HIS:CE1	0.52	2.40	8	1
1:A:29:LEU:H	1:A:30:PRO:HD2	0.51	1.65	13	1
1:A:30:PRO:HB2	1:B:91:PRO:CB	0.51	2.35	9	1
1:B:108:CYS:SG	1:B:122:CYS:HB3	0.51	2.45	16	1
1:A:30:PRO:HG3	1:B:91:PRO:HG3	0.51	1.81	17	1
1:A:33:LEU:O	1:A:37:LYS:HD3	0.51	2.06	6	1
1:B:90:LEU:HG	1:B:115:VAL:HB	0.51	1.83	10	1
1:A:21:VAL:HG13	1:A:27:ILE:H	0.51	1.65	1	1
1:A:48:GLU:HA	1:A:48:GLU:OE1	0.51	2.06	1	2
1:A:51:CYS:HB2	1:A:55:CYS:HB3	0.51	1.81	4	1
1:B:78:ILE:HD13	1:B:97:LEU:HD22	0.51	1.82	2	1
1:B:78:ILE:HB	1:B:97:LEU:HD13	0.51	1.82	2	1
1:A:53:GLY:O	1:A:56:LYS:HG3	0.51	2.06	2	3
1:A:27:ILE:HG12	1:A:28:ASP:N	0.50	2.21	7	2
1:B:78:ILE:HG12	1:B:107:PHE:CD1	0.50	2.42	8	1
1:A:20:ALA:HB3	1:A:32:VAL:HG13	0.50	1.83	9	1
1:B:90:LEU:HD21	1:B:116:CYS:HB2	0.50	1.83	1	2
1:B:112:CYS:HB3	1:B:117:LYS:HG2	0.50	1.84	17	1
1:A:47:CYS:O	1:A:61:CYS:HB3	0.50	2.06	15	2
1:A:52:HIS:CD2	1:B:89:ASP:HB2	0.50	2.42	12	1
1:A:45:CYS:O	1:A:48:GLU:HG2	0.49	2.07	2	1
1:A:29:LEU:HG	1:A:54:VAL:HG23	0.49	1.84	11	3
1:B:90:LEU:HG	1:B:115:VAL:HG22	0.49	1.82	16	1
1:A:17:ILE:HD11	1:A:46:PHE:HB2	0.49	1.84	12	1
1:A:31:CYS:HB2	1:B:113:HIS:O	0.49	2.08	2	2
1:A:31:CYS:HB2	1:B:115:VAL:HG13	0.49	1.84	9	1
1:A:30:PRO:HG2	1:B:114:GLY:HA2	0.49	1.83	7	1
1:A:53:GLY:O	1:A:56:LYS:HD3	0.49	2.07	5	1
1:A:14:ALA:HA	1:A:17:ILE:HG22	0.48	1.84	15	1
1:B:114:GLY:O	1:B:117:LYS:HG3	0.48	2.08	2	2
1:A:28:ASP:OD1	1:A:32:VAL:HG23	0.48	2.08	16	2
1:B:89:ASP:CG	1:B:90:LEU:H	0.48	2.14	12	2
1:B:107:PHE:C	1:B:109:GLU:H	0.48	2.16	6	1
1:A:29:LEU:O	1:A:33:LEU:HB2	0.48	2.08	7	1
1:A:53:GLY:O	1:A:55:CYS:N	0.48	2.47	13	3
1:B:94:LEU:HG	1:B:115:VAL:HG12	0.48	1.86	10	1
1:A:14:ALA:HA	1:A:18:ALA:HB3	0.48	1.86	9	2
1:A:24:CYS:SG	1:B:114:GLY:HA3	0.48	2.48	9	1
1:A:28:ASP:CG	1:A:29:LEU:H	0.48	2.17	3	2
1:B:121:LEU:N	1:B:121:LEU:HD23	0.48	2.24	5	1
1:B:90:LEU:HD22	1:B:107:PHE:CE1	0.48	2.44	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:56:LYS:C	1:A:58:LEU:H	0.48	2.16	3	1
1:A:50:HIS:HA	1:B:89:ASP:OD2	0.47	2.09	15	1
1:A:47:CYS:O	1:A:51:CYS:HB3	0.47	2.09	4	1
1:B:90:LEU:HG	1:B:115:VAL:HG21	0.47	1.86	17	1
1:A:52:HIS:CE1	1:B:89:ASP:HB2	0.47	2.44	15	3
1:B:78:ILE:HG12	1:B:107:PHE:HD2	0.47	1.70	6	2
1:A:24:CYS:SG	1:B:113:HIS:HB2	0.47	2.49	5	2
1:B:107:PHE:C	1:B:107:PHE:CD1	0.47	2.92	6	2
1:A:28:ASP:CG	1:A:30:PRO:HD2	0.47	2.35	17	1
1:A:60:LEU:HD23	1:A:60:LEU:N	0.47	2.24	17	1
1:B:117:LYS:C	1:B:117:LYS:HD3	0.47	2.35	2	1
1:B:104:ALA:CB	1:B:121:LEU:HB3	0.46	2.39	10	1
1:B:90:LEU:HG	1:B:115:VAL:CG2	0.46	2.39	13	2
1:B:119:LEU:HB3	1:B:121:LEU:CD2	0.46	2.40	9	1
1:A:47:CYS:O	1:A:51:CYS:HB2	0.46	2.11	11	1
1:A:51:CYS:HB2	1:A:55:CYS:CB	0.46	2.40	4	1
1:B:114:GLY:O	1:B:117:LYS:HG2	0.46	2.10	7	2
1:A:44:SER:O	1:A:48:GLU:HG2	0.46	2.11	17	1
1:A:46:PHE:C	1:A:48:GLU:H	0.46	2.19	4	1
1:A:43:ALA:CB	1:A:60:LEU:HG	0.46	2.39	4	1
1:A:33:LEU:HD22	1:A:54:VAL:CG2	0.46	2.41	9	1
1:A:30:PRO:CG	1:B:91:PRO:HD3	0.45	2.40	5	1
1:A:30:PRO:HB3	1:A:54:VAL:CG1	0.45	2.36	9	1
1:B:113:HIS:O	1:B:117:LYS:HE2	0.45	2.12	3	1
1:B:97:LEU:HD21	1:B:103:CYS:HB2	0.45	1.88	9	1
1:A:29:LEU:HD13	1:A:46:PHE:CE2	0.45	2.46	7	1
1:A:52:HIS:O	1:B:92:CYS:HB2	0.45	2.12	8	1
1:B:97:LEU:O	1:B:97:LEU:HG	0.45	2.12	15	1
1:A:37:LYS:H	1:A:37:LYS:HD3	0.45	1.71	17	1
1:B:89:ASP:OD2	1:B:91:PRO:HG2	0.45	2.11	3	1
1:B:94:LEU:HD23	1:B:115:VAL:HG11	0.45	1.86	4	1
1:A:28:ASP:HB2	1:B:113:HIS:HE1	0.45	1.70	5	1
1:B:94:LEU:HD23	1:B:115:VAL:HG21	0.45	1.88	16	1
1:B:82:VAL:HG22	1:B:88:ILE:HB	0.45	1.89	6	2
1:A:24:CYS:HB3	1:B:113:HIS:CG	0.44	2.47	2	1
1:A:29:LEU:HD21	1:A:55:CYS:CB	0.44	2.41	9	1
1:B:78:ILE:HG13	1:B:107:PHE:CD2	0.44	2.46	15	1
1:A:47:CYS:HA	1:A:50:HIS:HB2	0.44	1.88	7	2
1:A:47:CYS:HA	1:A:50:HIS:O	0.44	2.12	9	1
1:A:30:PRO:CA	1:A:54:VAL:HG21	0.44	2.41	11	1
1:B:89:ASP:H	1:B:93:VAL:HG21	0.44	1.72	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:30:PRO:CB	1:B:115:VAL:HG13	0.44	2.42	1	1
1:B:107:PHE:O	1:B:111:HIS:HD2	0.44	1.95	2	1
1:A:17:ILE:O	1:A:21:VAL:HG23	0.44	2.13	14	1
1:A:55:CYS:SG	1:A:60:LEU:HB2	0.43	2.52	7	2
1:B:119:LEU:HB2	1:B:121:LEU:HD22	0.43	1.89	5	1
1:A:52:HIS:CE1	1:B:89:ASP:HB3	0.43	2.48	8	1
1:B:121:LEU:H	1:B:121:LEU:HD13	0.43	1.73	3	1
1:A:13:CYS:HB3	1:A:41:GLY:O	0.43	2.13	6	1
1:B:89:ASP:HB3	1:B:93:VAL:HG23	0.43	1.90	13	1
1:A:16:ALA:HB1	1:A:36:LEU:HA	0.43	1.89	17	1
1:A:47:CYS:CB	1:A:61:CYS:SG	0.43	3.06	2	1
1:B:88:ILE:HD11	1:B:107:PHE:CE2	0.43	2.48	11	1
1:B:106:CYS:SG	1:B:107:PHE:N	0.43	2.92	7	1
1:A:46:PHE:O	1:A:47:CYS:HB2	0.43	2.14	9	1
1:B:91:PRO:CA	1:B:115:VAL:HG21	0.43	2.43	13	1
1:B:119:LEU:O	1:B:120:HIS:CB	0.43	2.66	6	1
1:B:94:LEU:HG	1:B:115:VAL:HG22	0.43	1.90	12	1
1:B:88:ILE:HG12	1:B:89:ASP:N	0.42	2.29	13	1
1:A:46:PHE:O	1:A:50:HIS:HD2	0.42	1.98	1	1
1:A:28:ASP:O	1:A:29:LEU:HB2	0.42	2.13	4	2
1:A:28:ASP:O	1:A:29:LEU:CB	0.42	2.67	16	1
1:A:20:ALA:CB	1:A:32:VAL:HG13	0.42	2.41	4	1
1:A:28:ASP:OD2	1:A:30:PRO:HD2	0.42	2.14	8	1
1:B:77:ALA:HB1	1:B:96:ALA:O	0.42	2.14	13	1
1:B:81:ALA:CB	1:B:93:VAL:HG13	0.42	2.45	13	1
1:A:33:LEU:HD12	1:A:34:ALA:N	0.42	2.30	3	1
1:B:103:CYS:SG	1:B:104:ALA:N	0.42	2.93	5	1
1:A:46:PHE:HD1	1:A:50:HIS:CE1	0.42	2.33	9	1
1:B:98:LYS:HE3	1:B:119:LEU:HD11	0.42	1.91	1	1
1:A:30:PRO:HG3	1:B:91:PRO:CB	0.42	2.44	3	1
1:B:89:ASP:O	1:B:90:LEU:HB2	0.41	2.15	4	2
1:B:82:VAL:CG2	1:B:88:ILE:HB	0.41	2.45	6	1
1:B:107:PHE:CD1	1:B:107:PHE:C	0.41	2.98	17	2
1:A:33:LEU:HG	1:A:54:VAL:HG22	0.41	1.91	12	1
1:B:89:ASP:OD1	1:B:91:PRO:HD2	0.41	2.15	5	1
1:B:105:SER:O	1:B:109:GLU:HB2	0.41	2.15	9	1
1:A:53:GLY:O	1:A:56:LYS:HB3	0.41	2.16	12	1
1:A:29:LEU:N	1:A:30:PRO:CD	0.41	2.83	3	1
1:B:74:CYS:HA	1:B:78:ILE:HD12	0.41	1.93	17	1
1:B:89:ASP:O	1:B:90:LEU:CB	0.41	2.67	3	1
1:A:53:GLY:CA	1:B:91:PRO:HB2	0.41	2.46	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:58:LEU:HD23	1:A:58:LEU:O	0.41	2.16	12	1
1:A:29:LEU:HD13	1:A:46:PHE:HE1	0.41	1.76	8	1
1:A:58:LEU:O	1:A:58:LEU:HD23	0.41	2.16	9	1
1:A:53:GLY:O	1:A:54:VAL:HG22	0.41	2.16	16	1
1:B:91:PRO:CB	1:B:115:VAL:HG11	0.41	2.36	9	1
1:A:29:LEU:H	1:A:30:PRO:CD	0.41	2.29	1	1
1:B:78:ILE:HD12	1:B:93:VAL:HG12	0.41	1.91	2	1
1:B:82:VAL:HG13	1:B:88:ILE:HB	0.41	1.92	2	1
1:B:94:LEU:HB3	1:B:115:VAL:CG2	0.41	2.46	7	1
1:A:30:PRO:HB2	1:B:114:GLY:HA2	0.40	1.93	5	1
1:B:112:CYS:SG	1:B:117:LYS:HG3	0.40	2.56	10	1
1:A:52:HIS:HB2	1:B:91:PRO:HG2	0.40	1.93	6	1
1:B:94:LEU:HB3	1:B:115:VAL:HG23	0.40	1.93	7	1
1:A:46:PHE:CD1	1:A:46:PHE:C	0.40	2.98	10	1
1:A:51:CYS:O	1:A:56:LYS:HB3	0.40	2.16	14	1
1:A:54:VAL:HG23	1:A:55:CYS:H	0.40	1.77	1	1
1:B:114:GLY:O	1:B:116:CYS:N	0.40	2.49	13	1
1:B:121:LEU:C	1:B:121:LEU:HD22	0.40	2.41	3	1
1:B:90:LEU:H	1:B:91:PRO:HD2	0.40	1.76	16	1
1:B:88:ILE:O	1:B:89:ASP:HB2	0.40	2.16	17	1

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	48/61 (79%)	35±3 (72±6%)	10±3 (22±6%)	3±1 (6±2%)	2	18
1	B	44/61 (72%)	32±2 (73±5%)	8±2 (19±5%)	3±1 (8±3%)	1	14
All	All	1564/2074 (75%)	1137 (73%)	318 (20%)	109 (7%)	2	16

All 35 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	29	LEU	17

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Mol	Chain	Res	Type	Models (Total)
1	B	90	LEU	17
1	B	89	ASP	10
1	A	54	VAL	6
1	B	115	VAL	6
1	A	28	ASP	6
1	B	120	HIS	4
1	B	108	CYS	4
1	B	109	GLU	3
1	A	48	GLU	3
1	A	27	ILE	2
1	B	91	PRO	2
1	B	98	LYS	2
1	A	58	LEU	2
1	A	40	GLU	2
1	A	13	CYS	2
1	B	114	GLY	2
1	B	77	ALA	2
1	A	44	SER	1
1	A	31	CYS	1
1	A	16	ALA	1
1	A	47	CYS	1
1	B	103	CYS	1
1	A	52	HIS	1
1	B	76	ALA	1
1	B	80	GLY	1
1	A	14	ALA	1
1	A	37	LYS	1
1	A	59	HIS	1
1	B	74	CYS	1
1	B	86	GLY	1
1	A	42	CYS	1
1	A	38	ALA	1
1	A	60	LEU	1
1	B	88	ILE	1

6.3.2 Protein sidechains ⓘ

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	32/41 (78%)	28±1 (89±4%)	4±1 (11±4%)	8	51
1	B	31/41 (76%)	27±2 (87±6%)	4±2 (13±6%)	7	48
All	All	1071/1394 (77%)	944 (88%)	127 (12%)	7	49

All 48 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	27	ILE	9
1	B	88	ILE	7
1	B	121	LEU	6
1	A	56	LYS	6
1	B	93	VAL	6
1	A	61	CYS	5
1	B	122	CYS	5
1	A	37	LYS	4
1	A	42	CYS	4
1	B	116	CYS	4
1	B	117	LYS	4
1	B	113	HIS	4
1	B	111	HIS	3
1	A	50	HIS	3
1	A	60	LEU	3
1	A	55	CYS	3
1	B	98	LYS	3
1	B	108	CYS	3
1	A	21	VAL	2
1	B	103	CYS	2
1	B	105	SER	2
1	B	107	PHE	2
1	B	112	CYS	2
1	B	94	LEU	2
1	A	17	ILE	2
1	A	46	PHE	2
1	A	47	CYS	2
1	B	85	CYS	2
1	A	31	CYS	2
1	B	115	VAL	2
1	A	58	LEU	2
1	A	32	VAL	2
1	B	78	ILE	2
1	A	51	CYS	1

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Mol	Chain	Res	Type	Models (Total)
1	B	118	ASP	1
1	B	74	CYS	1
1	A	13	CYS	1
1	A	54	VAL	1
1	A	33	LEU	1
1	B	90	LEU	1
1	A	49	ASP	1
1	A	52	HIS	1
1	B	106	CYS	1
1	A	45	CYS	1
1	B	97	LEU	1
1	A	36	LEU	1
1	A	44	SER	1
1	A	24	CYS	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 22% for the well-defined parts and 19% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping

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

Total number of shifts	263
Number of shifts mapped to atoms	262
Number of unparsed shifts	0
Number of shifts with mapping errors	1
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 1 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	50	HIS	HD1	12.833	.	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
$^{13}\text{C}_\alpha$	0	—	None (insufficient data)
$^{13}\text{C}_\beta$	0	—	None (insufficient data)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	43	0.27 ± 0.42	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 22%, i.e. 235 atoms were assigned a chemical shift out of a possible 1066. 0 out of 16 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	119/475 (25%)	81/195 (42%)	0/188 (0%)	38/92 (41%)
Sidechain	112/529 (21%)	112/358 (31%)	0/167 (0%)	0/4 (0%)
Aromatic	4/62 (6%)	4/34 (12%)	0/22 (0%)	0/6 (0%)
Overall	235/1066 (22%)	197/587 (34%)	0/377 (0%)	38/102 (37%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 19%, i.e. 263 atoms were assigned a chemical shift out of a possible 1416. 0 out of 22 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	134/618 (22%)	91/254 (36%)	0/244 (0%)	43/120 (36%)
Sidechain	125/736 (17%)	125/496 (25%)	0/230 (0%)	0/10 (0%)
Aromatic	4/62 (6%)	4/34 (12%)	0/22 (0%)	0/6 (0%)
Overall	263/1416 (19%)	220/784 (28%)	0/496 (0%)	43/136 (32%)

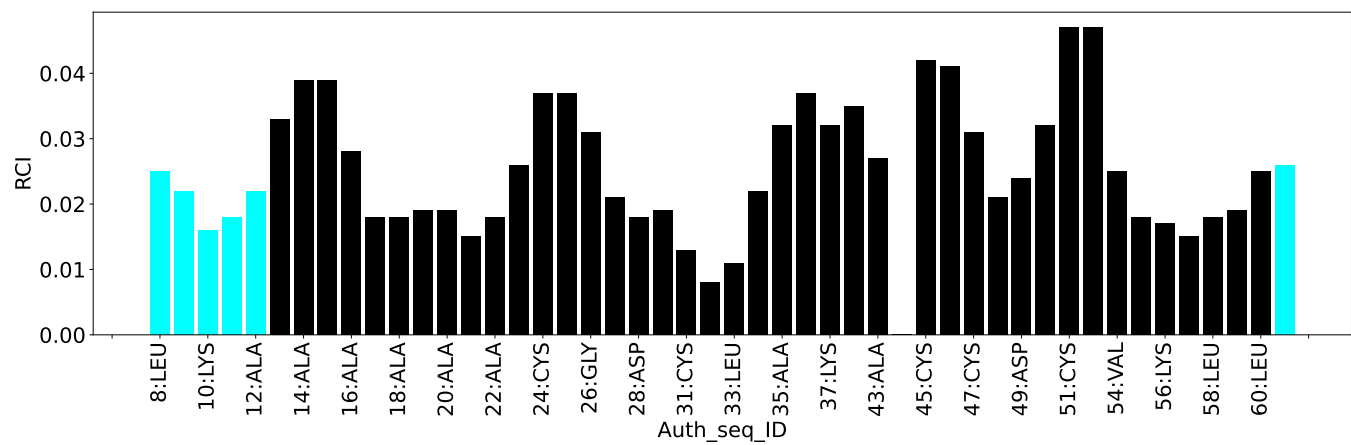
7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

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

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:



8 NMR restraints analysis

8.1 Conformationally restricting restraints

The following table provides the summary of experimentally observed NMR restraints in different categories. Restraints are classified into different categories based on the sequence separation of the atoms involved.

Description	Value
Total distance restraints	646
Intra-residue ($ i-j =0$)	242
Sequential ($ i-j =1$)	222
Medium range ($ i-j >1$ and $ i-j <5$)	92
Long range ($ i-j \geq 5$)	76
Inter-chain	14
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	5.3
Number of long range restraints per residue ¹	0.6

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)	21.8	0.2
0.2-0.5 (Medium)	12.8	0.49
>0.5 (Large)	2.5	2.02

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

Dihedral-angle violations less than 1° are not included in the calculation. There are no dihedral-angle violations

9 Distance violation analysis ⓘ

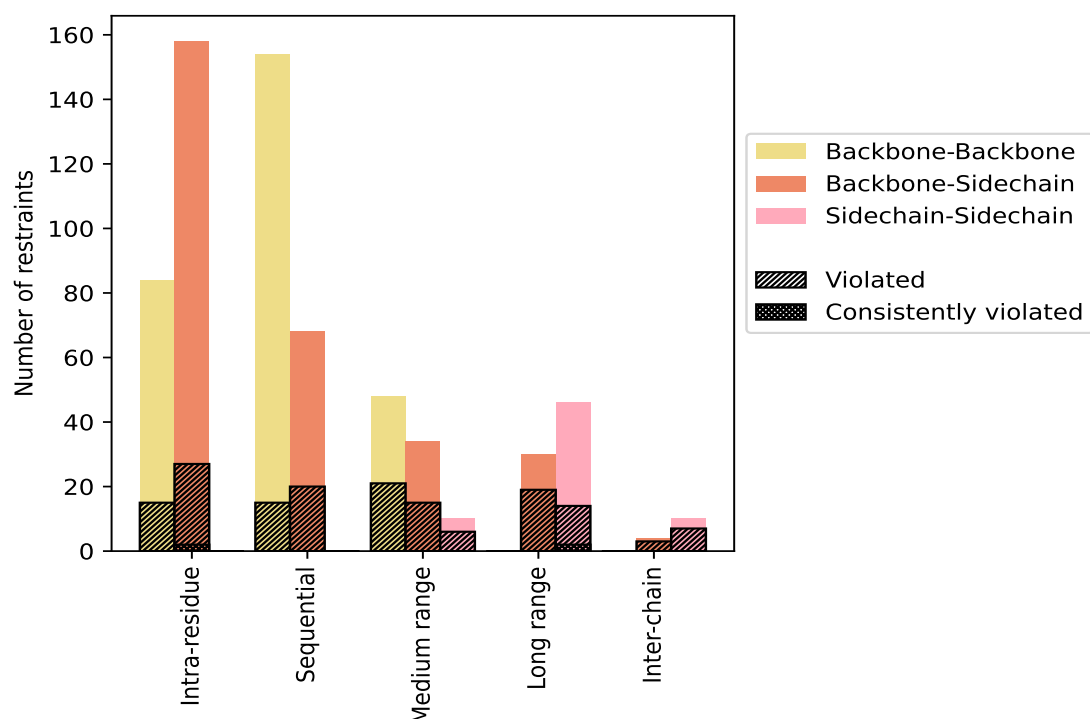
9.1 Summary of distance violations ⓘ

The following table shows the summary of distance violations in different restraint categories based on the sequence separation of the atoms involved. Each category is further sub-divided into three sub-categories based on the atoms involved. Violations less than 0.1 Å are not included in the statistics.

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue ($i-j =0$)	242	37.5	42	17.4	6.5	2	0.8	0.3
Backbone-Backbone	84	13.0	15	17.9	2.3	0	0.0	0.0
Backbone-Sidechain	158	24.5	27	17.1	4.2	2	1.3	0.3
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sequential ($i-j =1$)	222	34.4	35	15.8	5.4	0	0.0	0.0
Backbone-Backbone	154	23.8	15	9.7	2.3	0	0.0	0.0
Backbone-Sidechain	68	10.5	20	29.4	3.1	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Medium range ($i-j >1$ & $i-j <5$)	92	14.2	42	45.7	6.5	0	0.0	0.0
Backbone-Backbone	48	7.4	21	43.8	3.3	0	0.0	0.0
Backbone-Sidechain	34	5.3	15	44.1	2.3	0	0.0	0.0
Sidechain-Sidechain	10	1.5	6	60.0	0.9	0	0.0	0.0
Long range ($i-j \geq 5$)	76	11.8	33	43.4	5.1	2	2.6	0.3
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	30	4.6	19	63.3	2.9	0	0.0	0.0
Sidechain-Sidechain	46	7.1	14	30.4	2.2	2	4.3	0.3
Inter-chain	14	2.2	10	71.4	1.5	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	4	0.6	3	75.0	0.5	0	0.0	0.0
Sidechain-Sidechain	10	1.5	7	70.0	1.1	0	0.0	0.0
Hydrogen bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	646	100.0	162	25.1	25.1	4	0.6	0.6
Backbone-Backbone	286	44.3	51	17.8	7.9	0	0.0	0.0
Backbone-Sidechain	294	45.5	84	28.6	13.0	2	0.7	0.3
Sidechain-Sidechain	66	10.2	27	40.9	4.2	2	3.0	0.3

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

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



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

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

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

Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
1	13	5	11	6	3	38	0.2	0.98	0.15	0.16
2	16	2	6	10	4	38	0.25	1.32	0.24	0.18
3	16	3	7	11	4	41	0.2	0.57	0.11	0.15
4	13	3	15	10	1	42	0.19	0.39	0.07	0.2
5	10	8	11	11	4	44	0.24	0.89	0.19	0.16
6	13	1	14	12	4	44	0.23	0.9	0.17	0.18
7	12	6	11	9	6	44	0.23	0.97	0.16	0.19
8	13	5	8	8	5	39	0.21	0.98	0.18	0.16
9	13	9	11	8	7	48	0.23	0.79	0.15	0.2
10	14	4	7	9	4	38	0.23	1.16	0.19	0.19

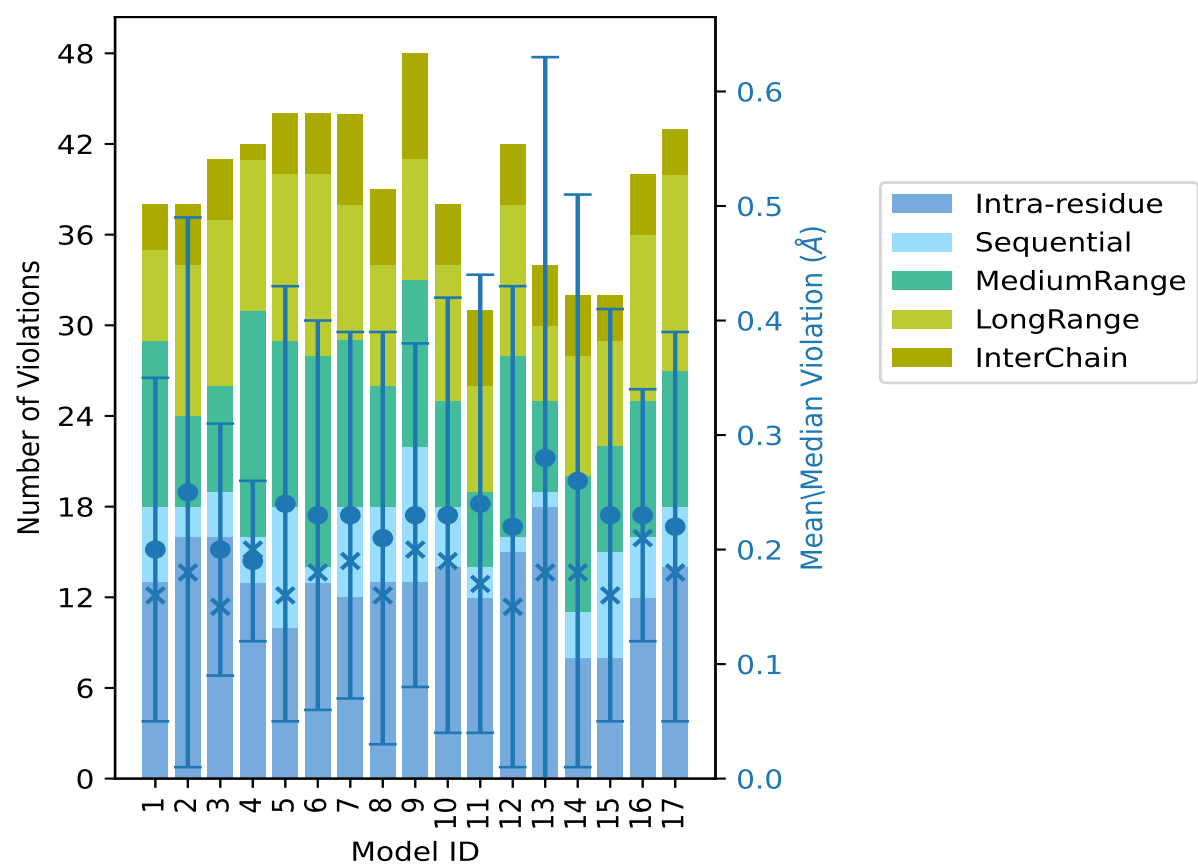
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	12	2	5	7	5	31	0.24	1.01	0.2	0.17
12	15	1	12	10	4	42	0.22	1.23	0.21	0.15
13	18	1	6	5	4	34	0.28	2.02	0.35	0.18
14	8	3	9	8	4	32	0.26	1.31	0.25	0.18
15	8	7	7	7	3	32	0.23	0.88	0.18	0.16
16	12	4	9	11	4	40	0.23	0.56	0.11	0.21
17	14	4	9	13	3	43	0.22	1.06	0.17	0.18

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

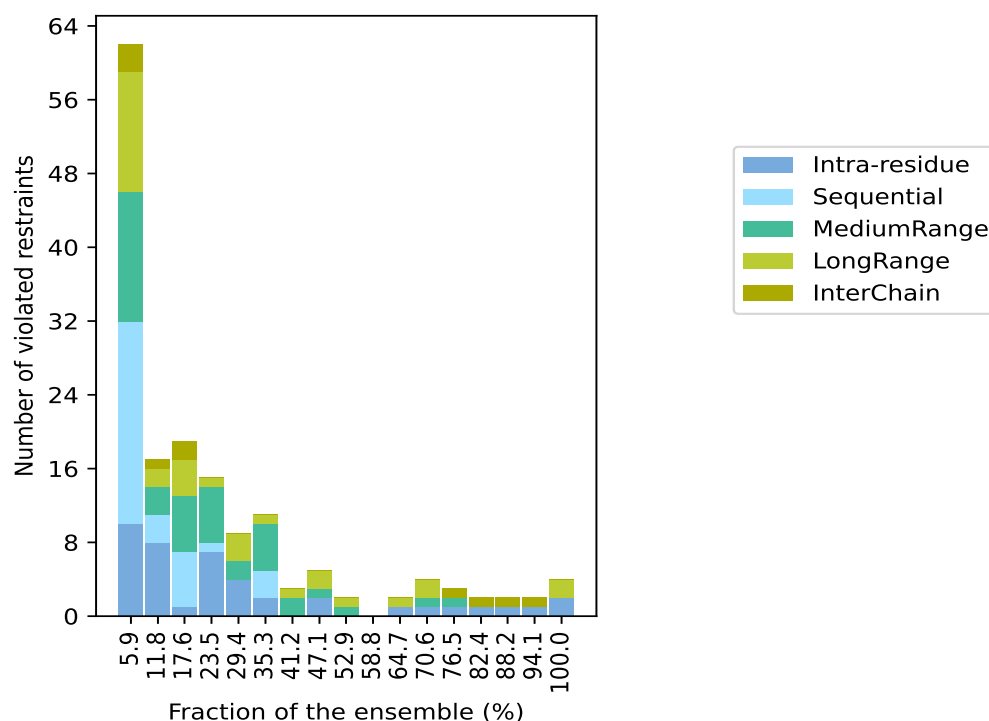
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 484(IR:200, SQ:187, MR:50, LR:43, IC:4) restraints are not 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	%
10	22	14	13	3	62	1	5.9
8	3	3	2	1	17	2	11.8
1	6	6	4	2	19	3	17.6
7	1	6	1	0	15	4	23.5
4	0	2	3	0	9	5	29.4
2	3	5	1	0	11	6	35.3
0	0	2	1	0	3	7	41.2
2	0	1	2	0	5	8	47.1
0	0	1	1	0	2	9	52.9
0	0	0	0	0	0	10	58.8
1	0	0	1	0	2	11	64.7
1	0	1	2	0	4	12	70.6
1	0	1	0	1	3	13	76.5
1	0	0	0	1	2	14	82.4
1	0	0	0	1	2	15	88.2
1	0	0	0	1	2	16	94.1
2	0	0	2	0	4	17	100.0

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

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

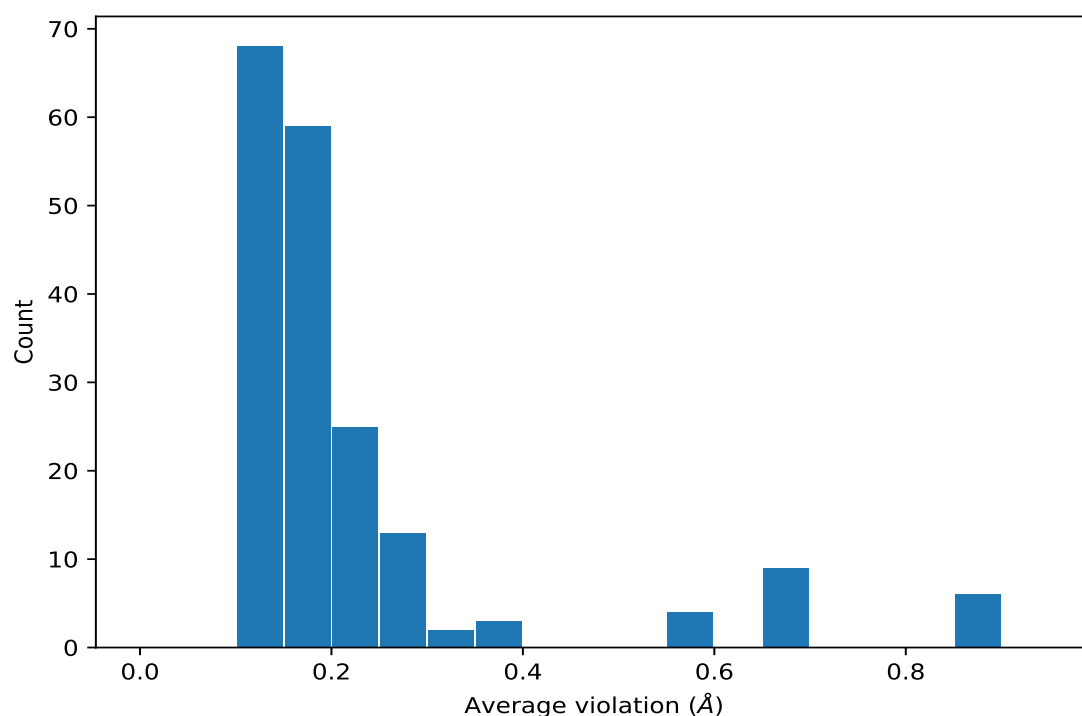
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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

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

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



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

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

Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG11	17	0.28	0.03	0.3
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG12	17	0.28	0.03	0.3
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG13	17	0.28	0.03	0.3
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG11	17	0.26	0.04	0.28
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG12	17	0.26	0.04	0.28
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG13	17	0.26	0.04	0.28
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE1	17	0.2	0.05	0.22
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE2	17	0.2	0.05	0.22
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE1	17	0.19	0.04	0.2
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE2	17	0.19	0.04	0.2
(1,13)	1:52:A:HIS:HE2	1:88:B:ILE:HD11	16	0.69	0.33	0.6
(1,13)	1:52:A:HIS:HE2	1:88:B:ILE:HD12	16	0.69	0.33	0.6
(1,13)	1:52:A:HIS:HE2	1:88:B:ILE:HD13	16	0.69	0.33	0.6
(1,13)	1:52:A:HIS:HE1	1:88:B:ILE:HD11	16	0.69	0.33	0.6
(1,13)	1:52:A:HIS:HE1	1:88:B:ILE:HD13	16	0.69	0.33	0.6
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG11	16	0.29	0.03	0.3

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG12	16	0.29	0.03	0.3
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG13	16	0.29	0.03	0.3
(1,8)	1:113:B:HIS:HE1	1:27:A:ILE:HD11	15	0.86	0.43	0.88
(1,8)	1:113:B:HIS:HE1	1:27:A:ILE:HD13	15	0.86	0.43	0.88
(1,8)	1:113:B:HIS:HE2	1:27:A:ILE:HD12	15	0.86	0.43	0.88
(1,8)	1:113:B:HIS:HE1	1:27:A:ILE:HD12	15	0.86	0.43	0.88
(1,8)	1:113:B:HIS:HE2	1:27:A:ILE:HD13	15	0.86	0.43	0.88
(1,8)	1:113:B:HIS:HE2	1:27:A:ILE:HD11	15	0.86	0.43	0.88
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG11	15	0.29	0.04	0.3
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG12	15	0.29	0.04	0.3
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG13	15	0.29	0.04	0.3
(1,14)	1:52:A:HIS:HE1	1:88:B:ILE:HG13	14	0.65	0.18	0.66
(1,14)	1:52:A:HIS:HE2	1:88:B:ILE:HG12	14	0.65	0.18	0.66
(1,14)	1:52:A:HIS:HE2	1:88:B:ILE:HG13	14	0.65	0.18	0.66
(1,14)	1:52:A:HIS:HE1	1:88:B:ILE:HG12	14	0.65	0.18	0.66
(1,336)	1:70:B:LYS:H	1:70:B:LYS:HB3	14	0.19	0.02	0.18
(1,9)	1:113:B:HIS:HE1	1:27:A:ILE:HG12	13	0.56	0.22	0.52
(1,9)	1:113:B:HIS:HE2	1:27:A:ILE:HG13	13	0.56	0.22	0.52
(1,9)	1:113:B:HIS:HE2	1:27:A:ILE:HG12	13	0.56	0.22	0.52
(1,9)	1:113:B:HIS:HE1	1:27:A:ILE:HG13	13	0.56	0.22	0.52
(1,635)	1:109:B:GLU:HB2	1:111:B:HIS:HD2	13	0.18	0.06	0.17
(1,587)	1:121:B:LEU:H	1:121:B:LEU:HA	13	0.12	0.01	0.12
(1,320)	1:48:A:GLU:HB2	1:50:A:HIS:HD2	12	0.2	0.07	0.2
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG11	12	0.2	0.06	0.18
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG12	12	0.2	0.06	0.18
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG13	12	0.2	0.06	0.18
(1,329)	1:48:A:GLU:HA	1:61:A:CYS:HB3	12	0.17	0.06	0.15
(1,234)	1:52:A:HIS:H	1:52:A:HIS:HA	12	0.12	0.01	0.12
(1,644)	1:109:B:GLU:HA	1:122:B:CYS:HB3	11	0.2	0.05	0.19
(1,272)	1:60:A:LEU:H	1:60:A:LEU:HA	11	0.12	0.01	0.12
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD11	9	0.19	0.08	0.17
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD12	9	0.19	0.08	0.17
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD13	9	0.19	0.08	0.17
(1,293)	1:29:A:LEU:HD11	1:33:A:LEU:HA	9	0.16	0.04	0.15
(1,293)	1:29:A:LEU:HD12	1:33:A:LEU:HA	9	0.16	0.04	0.15
(1,293)	1:29:A:LEU:HD13	1:33:A:LEU:HA	9	0.16	0.04	0.15
(1,21)	1:9:A:LYS:H	1:9:A:LYS:HB3	8	0.19	0.03	0.2
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD11	8	0.19	0.04	0.2
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD12	8	0.19	0.04	0.2
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD13	8	0.19	0.04	0.2
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG11	8	0.15	0.05	0.14
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG12	8	0.15	0.05	0.14

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG13	8	0.15	0.05	0.14
(1,319)	1:50:A:HIS:HD2	1:46:A:PHE:HZ	8	0.13	0.04	0.12
(1,549)	1:113:B:HIS:H	1:113:B:HIS:HA	8	0.12	0.01	0.12
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG21	7	0.19	0.06	0.19
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG22	7	0.19	0.06	0.19
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG23	7	0.19	0.06	0.19
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG21	7	0.19	0.06	0.19
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG22	7	0.19	0.06	0.19
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG23	7	0.19	0.06	0.19
(1,345)	1:72:B:VAL:H	1:69:B:LEU:HA	7	0.19	0.06	0.22
(1,634)	1:111:B:HIS:HD2	1:107:B:PHE:HZ	7	0.17	0.08	0.15
(1,73)	1:18:A:ALA:H	1:17:A:ILE:HB	6	0.35	0.05	0.32
(1,388)	1:79:B:ALA:H	1:78:B:ILE:HB	6	0.3	0.06	0.3
(1,588)	1:121:B:LEU:H	1:121:B:LEU:HB2	6	0.29	0.1	0.33
(1,134)	1:29:A:LEU:H	1:27:A:ILE:HA	6	0.23	0.13	0.17
(1,30)	1:11:A:VAL:H	1:8:A:LEU:HA	6	0.22	0.06	0.22
(1,608)	1:90:B:LEU:HD11	1:94:B:LEU:HA	6	0.18	0.04	0.2
(1,608)	1:90:B:LEU:HD12	1:94:B:LEU:HA	6	0.18	0.04	0.2
(1,608)	1:90:B:LEU:HD13	1:94:B:LEU:HA	6	0.18	0.04	0.2
(1,284)	1:13:A:CYS:HB2	1:17:A:ILE:HG21	6	0.14	0.02	0.14
(1,284)	1:13:A:CYS:HB2	1:17:A:ILE:HG22	6	0.14	0.02	0.14
(1,284)	1:13:A:CYS:HB2	1:17:A:ILE:HG23	6	0.14	0.02	0.14
(1,284)	1:13:A:CYS:HB3	1:17:A:ILE:HG21	6	0.14	0.02	0.14
(1,284)	1:13:A:CYS:HB3	1:17:A:ILE:HG22	6	0.14	0.02	0.14
(1,284)	1:13:A:CYS:HB3	1:17:A:ILE:HG23	6	0.14	0.02	0.14
(1,639)	1:118:B:ASP:HB3	1:115:B:VAL:HA	6	0.14	0.02	0.14
(1,71)	1:17:A:ILE:H	1:18:A:ALA:HA	6	0.13	0.02	0.12
(1,454)	1:92:B:CYS:H	1:92:B:CYS:HA	6	0.12	0.01	0.12
(1,195)	1:46:A:PHE:H	1:17:A:ILE:HG21	6	0.12	0.01	0.12
(1,195)	1:46:A:PHE:H	1:17:A:ILE:HG22	6	0.12	0.01	0.12
(1,195)	1:46:A:PHE:H	1:17:A:ILE:HG23	6	0.12	0.01	0.12
(1,566)	1:117:B:LYS:H	1:117:B:LYS:HG2	5	0.36	0.05	0.38
(1,566)	1:117:B:LYS:H	1:117:B:LYS:HG3	5	0.36	0.05	0.38
(1,350)	1:72:B:VAL:H	1:72:B:VAL:HB	5	0.23	0.01	0.23
(1,35)	1:11:A:VAL:H	1:11:A:VAL:HB	5	0.2	0.01	0.2
(1,187)	1:37:A:LYS:H	1:37:A:LYS:HB2	5	0.19	0.04	0.19
(1,643)	1:109:B:GLU:HA	1:122:B:CYS:HB2	5	0.18	0.07	0.16
(1,305)	1:45:A:CYS:HB2	1:17:A:ILE:HG21	5	0.15	0.02	0.16
(1,305)	1:45:A:CYS:HB2	1:17:A:ILE:HG22	5	0.15	0.02	0.16
(1,305)	1:45:A:CYS:HB2	1:17:A:ILE:HG23	5	0.15	0.02	0.16
(1,305)	1:45:A:CYS:HB3	1:17:A:ILE:HG21	5	0.15	0.02	0.16
(1,305)	1:45:A:CYS:HB3	1:17:A:ILE:HG22	5	0.15	0.02	0.16

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,305)	1:45:A:CYS:HB3	1:17:A:ILE:HG23	5	0.15	0.02	0.16
(2,2)	1:90:B:LEU:H	1:92:B:CYS:HA	5	0.15	0.04	0.13
(1,597)	1:68:B:VAL:HA	1:71:B:LYS:HB2	5	0.13	0.04	0.11
(1,597)	1:68:B:VAL:HA	1:71:B:LYS:HB3	5	0.13	0.04	0.11
(1,510)	1:107:B:PHE:H	1:78:B:ILE:HG21	5	0.13	0.02	0.12
(1,510)	1:107:B:PHE:H	1:78:B:ILE:HG22	5	0.13	0.02	0.12
(1,510)	1:107:B:PHE:H	1:78:B:ILE:HG23	5	0.13	0.02	0.12
(1,273)	1:60:A:LEU:H	1:60:A:LEU:HB2	4	0.3	0.13	0.33
(1,251)	1:56:A:LYS:H	1:56:A:LYS:HG2	4	0.24	0.1	0.26
(1,251)	1:56:A:LYS:H	1:56:A:LYS:HG3	4	0.24	0.1	0.26
(1,449)	1:90:B:LEU:H	1:88:B:ILE:HA	4	0.2	0.07	0.19
(1,328)	1:48:A:GLU:HA	1:61:A:CYS:HB2	4	0.2	0.05	0.21
(1,20)	1:9:A:LYS:H	1:9:A:LYS:HB2	4	0.19	0.05	0.18
(1,600)	1:75:B:ALA:HA	1:78:B:ILE:HB	4	0.18	0.03	0.18
(2,1)	1:29:A:LEU:H	1:31:A:CYS:HA	4	0.16	0.03	0.17
(1,550)	1:113:B:HIS:H	1:113:B:HIS:HB2	4	0.16	0.02	0.15
(1,285)	1:14:A:ALA:HA	1:17:A:ILE:HB	4	0.15	0.03	0.16
(1,599)	1:74:B:CYS:HB2	1:78:B:ILE:HG21	4	0.13	0.03	0.13
(1,599)	1:74:B:CYS:HB2	1:78:B:ILE:HG22	4	0.13	0.03	0.13
(1,599)	1:74:B:CYS:HB2	1:78:B:ILE:HG23	4	0.13	0.03	0.13
(1,599)	1:74:B:CYS:HB3	1:78:B:ILE:HG21	4	0.13	0.03	0.13
(1,599)	1:74:B:CYS:HB3	1:78:B:ILE:HG22	4	0.13	0.03	0.13
(1,599)	1:74:B:CYS:HB3	1:78:B:ILE:HG23	4	0.13	0.03	0.13
(1,139)	1:31:A:CYS:H	1:31:A:CYS:HA	4	0.12	0.01	0.12
(1,374)	1:75:B:ALA:H	1:75:B:ALA:HA	4	0.12	0.01	0.12
(1,460)	1:93:B:VAL:H	1:92:B:CYS:HB2	4	0.12	0.01	0.12
(1,460)	1:93:B:VAL:H	1:92:B:CYS:HB3	4	0.12	0.01	0.12
(1,59)	1:14:A:ALA:H	1:14:A:ALA:HA	4	0.12	0.01	0.12
(1,324)	1:57:A:ASP:HB3	1:54:A:VAL:HA	4	0.11	0.01	0.11
(1,47)	1:13:A:CYS:H	1:10:A:LYS:HA	3	0.23	0.02	0.23
(1,539)	1:111:B:HIS:H	1:109:B:GLU:HG2	3	0.21	0.07	0.22
(1,539)	1:111:B:HIS:H	1:109:B:GLU:HG3	3	0.21	0.07	0.22
(1,224)	1:50:A:HIS:H	1:48:A:GLU:HG2	3	0.2	0.06	0.2
(1,224)	1:50:A:HIS:H	1:48:A:GLU:HG3	3	0.2	0.06	0.2
(1,353)	1:73:B:ALA:H	1:70:B:LYS:HA	3	0.2	0.02	0.19
(1,327)	1:61:A:CYS:HB3	1:47:A:CYS:HB3	3	0.19	0.08	0.17
(1,526)	1:109:B:GLU:H	1:106:B:CYS:HA	3	0.18	0.05	0.16
(1,642)	1:122:B:CYS:HB3	1:108:B:CYS:HB3	3	0.18	0.05	0.18
(1,1)	1:91:B:PRO:HD2	1:54:A:VAL:HG11	3	0.17	0.03	0.17
(1,1)	1:91:B:PRO:HD2	1:54:A:VAL:HG12	3	0.17	0.03	0.17
(1,1)	1:91:B:PRO:HD2	1:54:A:VAL:HG13	3	0.17	0.03	0.17
(1,1)	1:91:B:PRO:HD3	1:54:A:VAL:HG11	3	0.17	0.03	0.17

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,1)	1:91:B:PRO:HD3	1:54:A:VAL:HG12	3	0.17	0.03	0.17
(1,1)	1:91:B:PRO:HD3	1:54:A:VAL:HG13	3	0.17	0.03	0.17
(1,211)	1:48:A:GLU:H	1:45:A:CYS:HA	3	0.17	0.01	0.17
(1,5)	1:113:B:HIS:HD2	1:24:A:CYS:HA	3	0.16	0.02	0.17
(1,358)	1:73:B:ALA:H	1:72:B:VAL:H	3	0.14	0.03	0.12
(1,43)	1:12:A:ALA:H	1:11:A:VAL:H	3	0.13	0.01	0.13
(1,586)	1:120:B:HIS:H	1:121:B:LEU:HD11	3	0.13	0.01	0.13
(1,586)	1:120:B:HIS:H	1:121:B:LEU:HD12	3	0.13	0.01	0.13
(1,586)	1:120:B:HIS:H	1:121:B:LEU:HD13	3	0.13	0.01	0.13
(1,74)	1:18:A:ALA:H	1:17:A:ILE:HG12	3	0.13	0.02	0.12
(1,314)	1:29:A:LEU:HD11	1:46:A:PHE:HZ	3	0.13	0.02	0.12
(1,314)	1:29:A:LEU:HD12	1:46:A:PHE:HZ	3	0.13	0.02	0.12
(1,314)	1:29:A:LEU:HD13	1:46:A:PHE:HZ	3	0.13	0.02	0.12
(1,386)	1:78:B:ILE:H	1:79:B:ALA:HA	3	0.13	0.01	0.12
(1,422)	1:84:B:ALA:H	1:84:B:ALA:HA	3	0.12	0.0	0.12
(1,623)	1:78:B:ILE:HG12	1:107:B:PHE:HZ	3	0.11	0.01	0.11
(1,145)	1:32:A:VAL:H	1:31:A:CYS:HB2	3	0.1	0.0	0.1
(1,145)	1:32:A:VAL:H	1:31:A:CYS:HB3	3	0.1	0.0	0.1
(1,335)	1:70:B:LYS:H	1:70:B:LYS:HB2	2	0.24	0.04	0.24
(1,362)	1:74:B:CYS:H	1:71:B:LYS:HA	2	0.24	0.02	0.24
(1,22)	1:9:A:LYS:H	1:9:A:LYS:HG2	2	0.24	0.12	0.24
(1,22)	1:9:A:LYS:H	1:9:A:LYS:HG3	2	0.24	0.12	0.24
(1,617)	1:97:B:LEU:HD11	1:98:B:LYS:HA	2	0.19	0.08	0.19
(1,617)	1:97:B:LEU:HD12	1:98:B:LYS:HA	2	0.19	0.08	0.19
(1,617)	1:97:B:LEU:HD13	1:98:B:LYS:HA	2	0.19	0.08	0.19
(1,548)	1:112:B:CYS:H	1:113:B:HIS:HA	2	0.16	0.01	0.16
(1,6)	1:113:B:HIS:HD2	1:24:A:CYS:HB2	2	0.16	0.04	0.16
(1,464)	1:93:B:VAL:H	1:93:B:VAL:HB	2	0.14	0.04	0.14
(1,524)	1:108:B:CYS:H	1:108:B:CYS:HB2	2	0.14	0.02	0.14
(1,38)	1:12:A:ALA:H	1:9:A:LYS:HA	2	0.14	0.01	0.14
(1,235)	1:52:A:HIS:H	1:52:A:HIS:HB2	2	0.14	0.02	0.14
(1,309)	1:27:A:ILE:HD11	1:46:A:PHE:HD1	2	0.12	0.01	0.12
(1,309)	1:27:A:ILE:HD11	1:46:A:PHE:HD2	2	0.12	0.01	0.12
(1,309)	1:27:A:ILE:HD12	1:46:A:PHE:HD1	2	0.12	0.01	0.12
(1,309)	1:27:A:ILE:HD12	1:46:A:PHE:HD2	2	0.12	0.01	0.12
(1,309)	1:27:A:ILE:HD13	1:46:A:PHE:HD1	2	0.12	0.01	0.12
(1,309)	1:27:A:ILE:HD13	1:46:A:PHE:HD2	2	0.12	0.01	0.12
(1,77)	1:18:A:ALA:H	1:18:A:ALA:HA	2	0.12	0.01	0.12
(1,271)	1:59:A:HIS:H	1:60:A:LEU:HD11	2	0.12	0.01	0.12
(1,271)	1:59:A:HIS:H	1:60:A:LEU:HD12	2	0.12	0.01	0.12
(1,271)	1:59:A:HIS:H	1:60:A:LEU:HD13	2	0.12	0.01	0.12
(1,282)	1:7:A:VAL:HA	1:10:A:LYS:HB2	2	0.12	0.01	0.12

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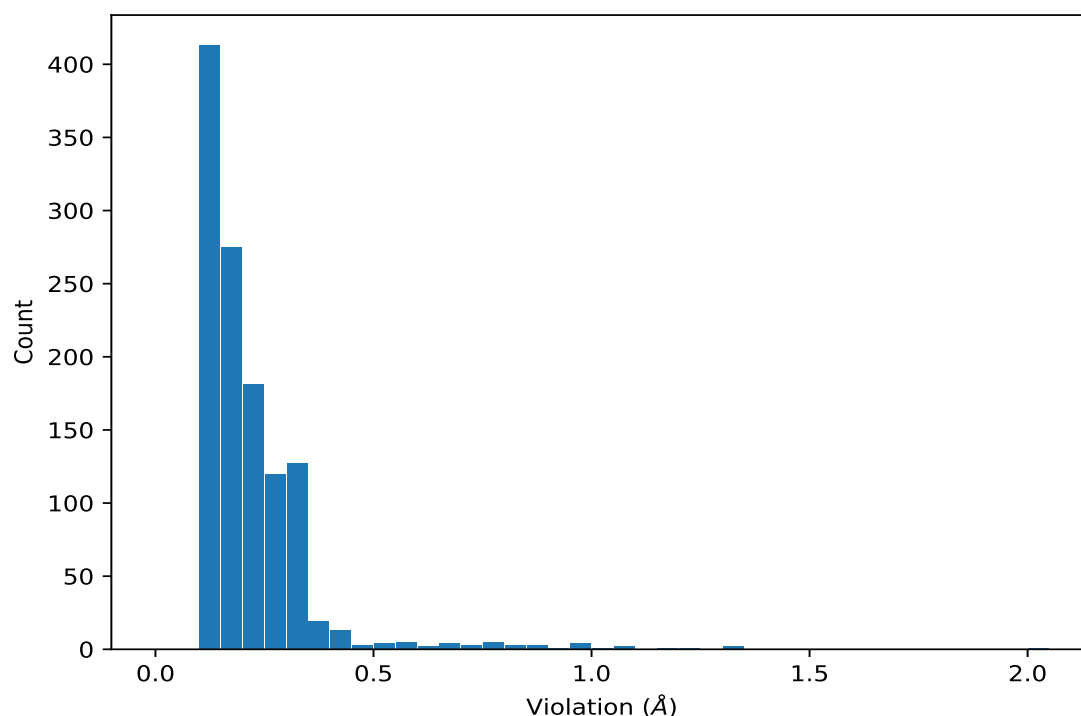
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,282)	1:7:A:VAL:HA	1:10:A:LYS:HB3	2	0.12	0.01	0.12
(1,308)	1:17:A:ILE:HG12	1:46:A:PHE:HZ	2	0.12	0.01	0.12
(1,584)	1:120:B:HIS:H	1:120:B:HIS:HA	2	0.12	0.0	0.12
(1,140)	1:31:A:CYS:H	1:31:A:CYS:HB2	2	0.1	0.0	0.1
(1,140)	1:31:A:CYS:H	1:31:A:CYS:HB3	2	0.1	0.0	0.1

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)
(1,8)	1:113:B:HIS:HE2	1:27:A:ILE:HD12	13	2.02
(1,13)	1:52:A:HIS:HE2	1:88:B:ILE:HD11	2	1.32
(1,13)	1:52:A:HIS:HE1	1:88:B:ILE:HD11	14	1.31
(1,8)	1:113:B:HIS:HE2	1:27:A:ILE:HD11	12	1.23
(1,8)	1:113:B:HIS:HE2	1:27:A:ILE:HD11	10	1.16
(1,8)	1:113:B:HIS:HE2	1:27:A:ILE:HD13	17	1.06
(1,13)	1:52:A:HIS:HE1	1:88:B:ILE:HD13	13	1.05
(1,13)	1:52:A:HIS:HE2	1:88:B:ILE:HD13	11	1.01
(1,9)	1:113:B:HIS:HE2	1:27:A:ILE:HG13	8	0.98
(1,8)	1:113:B:HIS:HE1	1:27:A:ILE:HD11	1	0.98
(1,14)	1:52:A:HIS:HE2	1:88:B:ILE:HG13	7	0.97
(1,8)	1:113:B:HIS:HE1	1:27:A:ILE:HD13	2	0.96
(1,8)	1:113:B:HIS:HE2	1:27:A:ILE:HD13	6	0.9
(1,14)	1:52:A:HIS:HE2	1:88:B:ILE:HG13	5	0.89
(1,14)	1:52:A:HIS:HE2	1:88:B:ILE:HG13	15	0.88
(1,8)	1:113:B:HIS:HE2	1:27:A:ILE:HD13	14	0.88
(1,9)	1:113:B:HIS:HE1	1:27:A:ILE:HG12	5	0.83
(1,8)	1:113:B:HIS:HE2	1:27:A:ILE:HD12	7	0.82
(1,8)	1:113:B:HIS:HE1	1:27:A:ILE:HD12	5	0.81
(1,9)	1:113:B:HIS:HE1	1:27:A:ILE:HG12	9	0.79
(1,14)	1:52:A:HIS:HE2	1:88:B:ILE:HG13	8	0.77
(1,13)	1:52:A:HIS:HE2	1:88:B:ILE:HD13	12	0.76
(1,13)	1:52:A:HIS:HE2	1:88:B:ILE:HD13	17	0.76
(1,13)	1:52:A:HIS:HE2	1:88:B:ILE:HD12	15	0.75
(1,9)	1:113:B:HIS:HE2	1:27:A:ILE:HG12	6	0.73
(1,14)	1:52:A:HIS:HE1	1:88:B:ILE:HG12	13	0.71
(1,14)	1:52:A:HIS:HE2	1:88:B:ILE:HG12	2	0.7
(1,8)	1:113:B:HIS:HE1	1:27:A:ILE:HD13	9	0.69
(1,14)	1:52:A:HIS:HE1	1:88:B:ILE:HG12	14	0.67
(1,14)	1:52:A:HIS:HE2	1:88:B:ILE:HG13	11	0.66
(1,9)	1:113:B:HIS:HE2	1:27:A:ILE:HG12	12	0.65
(1,13)	1:52:A:HIS:HE2	1:88:B:ILE:HD13	10	0.62
(1,14)	1:52:A:HIS:HE2	1:88:B:ILE:HG13	6	0.61
(1,13)	1:52:A:HIS:HE2	1:88:B:ILE:HD11	9	0.59
(1,13)	1:52:A:HIS:HE2	1:88:B:ILE:HD11	3	0.57
(1,14)	1:52:A:HIS:HE2	1:88:B:ILE:HG13	16	0.56
(1,9)	1:113:B:HIS:HE2	1:27:A:ILE:HG12	14	0.56
(1,8)	1:113:B:HIS:HE2	1:27:A:ILE:HD11	11	0.56
(1,13)	1:52:A:HIS:HE2	1:88:B:ILE:HD12	16	0.54
(1,13)	1:52:A:HIS:HE2	1:88:B:ILE:HD13	6	0.52
(1,9)	1:113:B:HIS:HE1	1:27:A:ILE:HG13	15	0.52
(1,9)	1:113:B:HIS:HE2	1:27:A:ILE:HG13	3	0.51
(1,9)	1:113:B:HIS:HE2	1:27:A:ILE:HG13	11	0.49

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,134)	1:29:A:LEU:H	1:27:A:ILE:HA	1	0.46
(1,13)	1:52:A:HIS:HE2	1:88:B:ILE:HD12	5	0.46
(1,73)	1:18:A:ALA:H	1:17:A:ILE:HB	5	0.44
(1,273)	1:60:A:LEU:H	1:60:A:LEU:HB2	5	0.43
(1,14)	1:52:A:HIS:HE1	1:88:B:ILE:HG13	1	0.42
(1,566)	1:117:B:LYS:H	1:117:B:LYS:HG2	8	0.41
(1,566)	1:117:B:LYS:H	1:117:B:LYS:HG3	8	0.41
(1,566)	1:117:B:LYS:H	1:117:B:LYS:HG2	9	0.41
(1,566)	1:117:B:LYS:H	1:117:B:LYS:HG3	9	0.41
(1,520)	1:108:B:CYS:H	1:107:B:PHE:HB2	10	0.41
(1,520)	1:108:B:CYS:H	1:107:B:PHE:HB3	10	0.41
(1,14)	1:52:A:HIS:HE2	1:88:B:ILE:HG12	3	0.41
(1,14)	1:52:A:HIS:HE1	1:88:B:ILE:HG12	9	0.41
(1,320)	1:48:A:GLU:HB2	1:50:A:HIS:HD2	9	0.4
(1,14)	1:52:A:HIS:HE2	1:88:B:ILE:HG12	10	0.4
(1,588)	1:121:B:LEU:H	1:121:B:LEU:HB2	3	0.39
(1,388)	1:79:B:ALA:H	1:78:B:ILE:HB	8	0.39
(1,273)	1:60:A:LEU:H	1:60:A:LEU:HB2	17	0.39
(1,205)	1:47:A:CYS:H	1:46:A:PHE:HB2	4	0.39
(1,205)	1:47:A:CYS:H	1:46:A:PHE:HB3	4	0.39
(1,73)	1:18:A:ALA:H	1:17:A:ILE:HB	11	0.39
(1,13)	1:52:A:HIS:HE1	1:88:B:ILE:HD11	7	0.39
(1,566)	1:117:B:LYS:H	1:117:B:LYS:HG2	16	0.38
(1,566)	1:117:B:LYS:H	1:117:B:LYS:HG3	16	0.38
(1,588)	1:121:B:LEU:H	1:121:B:LEU:HB2	5	0.37
(1,588)	1:121:B:LEU:H	1:121:B:LEU:HB2	17	0.37
(1,9)	1:113:B:HIS:HE1	1:27:A:ILE:HG12	2	0.37
(1,22)	1:9:A:LYS:H	1:9:A:LYS:HG2	5	0.36
(1,22)	1:9:A:LYS:H	1:9:A:LYS:HG3	5	0.36
(1,634)	1:111:B:HIS:HD2	1:107:B:PHE:HZ	6	0.35
(1,388)	1:79:B:ALA:H	1:78:B:ILE:HB	15	0.35
(1,251)	1:56:A:LYS:H	1:56:A:LYS:HG2	16	0.35
(1,251)	1:56:A:LYS:H	1:56:A:LYS:HG3	16	0.35
(1,9)	1:113:B:HIS:HE2	1:27:A:ILE:HG12	7	0.35
(1,635)	1:109:B:GLU:HB2	1:111:B:HIS:HD2	6	0.34
(1,566)	1:117:B:LYS:H	1:117:B:LYS:HG2	12	0.34
(1,566)	1:117:B:LYS:H	1:117:B:LYS:HG3	12	0.34
(1,413)	1:83:B:ALA:H	1:82:B:VAL:HB	9	0.33
(1,251)	1:56:A:LYS:H	1:56:A:LYS:HG2	12	0.33
(1,251)	1:56:A:LYS:H	1:56:A:LYS:HG3	12	0.33
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD11	16	0.33
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD12	16	0.33

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD13	16	0.33
(1,134)	1:29:A:LEU:H	1:27:A:ILE:HA	10	0.33
(1,9)	1:113:B:HIS:HE2	1:27:A:ILE:HG13	17	0.33
(1,8)	1:113:B:HIS:HE2	1:27:A:ILE:HD11	16	0.33
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG11	10	0.32
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG12	10	0.32
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG13	10	0.32
(1,388)	1:79:B:ALA:H	1:78:B:ILE:HB	11	0.32
(1,329)	1:48:A:GLU:HA	1:61:A:CYS:HB3	17	0.32
(1,302)	1:36:A:LEU:HD11	1:37:A:LYS:HA	7	0.32
(1,302)	1:36:A:LEU:HD12	1:37:A:LYS:HA	7	0.32
(1,302)	1:36:A:LEU:HD13	1:37:A:LYS:HA	7	0.32
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD11	6	0.32
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD12	6	0.32
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD13	6	0.32
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG11	10	0.32
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG12	10	0.32
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG13	10	0.32
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG11	7	0.32
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG12	7	0.32
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG13	7	0.32
(1,73)	1:18:A:ALA:H	1:17:A:ILE:HB	7	0.32
(1,73)	1:18:A:ALA:H	1:17:A:ILE:HB	15	0.32
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG21	6	0.31
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG22	6	0.31
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG23	6	0.31
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG21	6	0.31
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG22	6	0.31
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG23	6	0.31
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG11	1	0.31
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG12	1	0.31
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG13	1	0.31
(1,449)	1:90:B:LEU:H	1:88:B:ILE:HA	12	0.31
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG11	2	0.31
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG12	2	0.31
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG13	2	0.31
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG11	7	0.31
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG12	7	0.31
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG13	7	0.31
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG11	8	0.31
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG12	8	0.31
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG13	8	0.31

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG11	10	0.31
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG12	10	0.31
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG13	10	0.31
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG11	1	0.31
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG12	1	0.31
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG13	1	0.31
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG11	9	0.31
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG12	9	0.31
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG13	9	0.31
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG11	17	0.31
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG12	17	0.31
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG13	17	0.31
(1,98)	1:22:A:ALA:H	1:21:A:VAL:HB	9	0.31
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG11	5	0.31
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG12	5	0.31
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG13	5	0.31
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG11	11	0.31
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG12	11	0.31
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG13	11	0.31
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG11	12	0.31
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG12	12	0.31
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG13	12	0.31
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG11	15	0.31
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG12	15	0.31
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG13	15	0.31
(1,73)	1:18:A:ALA:H	1:17:A:ILE:HB	2	0.31
(1,644)	1:109:B:GLU:HA	1:122:B:CYS:HB3	16	0.3
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG11	12	0.3
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG12	12	0.3
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG13	12	0.3
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG11	16	0.3
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG12	16	0.3
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG13	16	0.3
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG11	17	0.3
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG12	17	0.3
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG13	17	0.3
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG11	3	0.3
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG12	3	0.3
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG13	3	0.3
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG11	11	0.3
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG12	11	0.3
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG13	11	0.3

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG11	13	0.3
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG12	13	0.3
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG13	13	0.3
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG11	14	0.3
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG12	14	0.3
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG13	14	0.3
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG11	15	0.3
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG12	15	0.3
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG13	15	0.3
(1,327)	1:61:A:CYS:HB3	1:47:A:CYS:HB3	7	0.3
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG11	2	0.3
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG12	2	0.3
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG13	2	0.3
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG11	6	0.3
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG12	6	0.3
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG13	6	0.3
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG11	7	0.3
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG12	7	0.3
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG13	7	0.3
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG11	12	0.3
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG12	12	0.3
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG13	12	0.3
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG11	16	0.3
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG12	16	0.3
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG13	16	0.3
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG11	3	0.3
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG12	3	0.3
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG13	3	0.3
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG11	8	0.3
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG12	8	0.3
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG13	8	0.3
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG11	13	0.3
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG12	13	0.3
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG13	13	0.3
(1,73)	1:18:A:ALA:H	1:17:A:ILE:HB	8	0.3
(1,588)	1:121:B:LEU:H	1:121:B:LEU:HB2	9	0.29
(1,539)	1:111:B:HIS:H	1:109:B:GLU:HG2	14	0.29
(1,539)	1:111:B:HIS:H	1:109:B:GLU:HG3	14	0.29
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG11	4	0.29
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG12	4	0.29
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG13	4	0.29
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG11	7	0.29

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG12	7	0.29
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG13	7	0.29
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG11	13	0.29
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG12	13	0.29
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG13	13	0.29
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG11	1	0.29
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG12	1	0.29
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG13	1	0.29
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG11	12	0.29
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG12	12	0.29
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG13	12	0.29
(1,388)	1:79:B:ALA:H	1:78:B:ILE:HB	2	0.29
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG11	16	0.29
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG12	16	0.29
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG13	16	0.29
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE1	16	0.29
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE2	16	0.29
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG11	3	0.29
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG12	3	0.29
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG13	3	0.29
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG11	8	0.29
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG12	8	0.29
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG13	8	0.29
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG11	2	0.29
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG12	2	0.29
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG13	2	0.29
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG11	14	0.29
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG12	14	0.29
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG13	14	0.29
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG11	16	0.29
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG12	16	0.29
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG13	16	0.29
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG11	17	0.29
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG12	17	0.29
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG13	17	0.29
(1,30)	1:11:A:VAL:H	1:8:A:LEU:HA	9	0.29
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE1	6	0.28
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE2	6	0.28
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG11	3	0.28
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG12	3	0.28
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG13	3	0.28
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG11	9	0.28

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG12	9	0.28
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG13	9	0.28
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG11	5	0.28
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG12	5	0.28
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG13	5	0.28
(1,335)	1:70:B:LYS:H	1:70:B:LYS:HB2	4	0.28
(1,224)	1:50:A:HIS:H	1:48:A:GLU:HG2	17	0.28
(1,224)	1:50:A:HIS:H	1:48:A:GLU:HG3	17	0.28
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG11	14	0.28
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG12	14	0.28
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG13	14	0.28
(1,644)	1:109:B:GLU:HA	1:122:B:CYS:HB3	11	0.27
(1,617)	1:97:B:LEU:HD11	1:98:B:LYS:HA	5	0.27
(1,617)	1:97:B:LEU:HD12	1:98:B:LYS:HA	5	0.27
(1,617)	1:97:B:LEU:HD13	1:98:B:LYS:HA	5	0.27
(1,566)	1:117:B:LYS:H	1:117:B:LYS:HG2	13	0.27
(1,566)	1:117:B:LYS:H	1:117:B:LYS:HG3	13	0.27
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG11	6	0.27
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG12	6	0.27
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG13	6	0.27
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG11	15	0.27
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG12	15	0.27
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG13	15	0.27
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG11	16	0.27
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG12	16	0.27
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG13	16	0.27
(1,345)	1:72:B:VAL:H	1:69:B:LEU:HA	4	0.27
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE1	10	0.27
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE2	10	0.27
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE1	12	0.27
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE2	12	0.27
(1,273)	1:60:A:LEU:H	1:60:A:LEU:HB2	3	0.27
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG11	5	0.27
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG12	5	0.27
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG13	5	0.27
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG11	15	0.27
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG12	15	0.27
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG13	15	0.27
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG11	4	0.27
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG12	4	0.27
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG13	4	0.27
(1,20)	1:9:A:LYS:H	1:9:A:LYS:HB2	17	0.27

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,643)	1:109:B:GLU:HA	1:122:B:CYS:HB2	5	0.26
(1,643)	1:109:B:GLU:HA	1:122:B:CYS:HB2	9	0.26
(1,388)	1:79:B:ALA:H	1:78:B:ILE:HB	5	0.26
(1,362)	1:74:B:CYS:H	1:71:B:LYS:HA	16	0.26
(1,328)	1:48:A:GLU:HA	1:61:A:CYS:HB2	9	0.26
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG11	3	0.26
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG12	3	0.26
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG13	3	0.26
(1,187)	1:37:A:LYS:H	1:37:A:LYS:HB2	12	0.26
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG11	4	0.26
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG12	4	0.26
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG13	4	0.26
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG11	13	0.26
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG12	13	0.26
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG13	13	0.26
(1,47)	1:13:A:CYS:H	1:10:A:LYS:HA	14	0.26
(1,30)	1:11:A:VAL:H	1:8:A:LEU:HA	14	0.26
(1,635)	1:109:B:GLU:HB2	1:111:B:HIS:HD2	5	0.25
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE1	13	0.25
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE2	13	0.25
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE1	17	0.25
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE2	17	0.25
(1,526)	1:109:B:GLU:H	1:106:B:CYS:HA	1	0.25
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG11	6	0.25
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG12	6	0.25
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG13	6	0.25
(1,350)	1:72:B:VAL:H	1:72:B:VAL:HB	4	0.25
(1,233)	1:51:A:CYS:H	1:52:A:HIS:HA	9	0.25
(1,8)	1:113:B:HIS:HE2	1:27:A:ILE:HD12	3	0.25
(1,642)	1:122:B:CYS:HB3	1:108:B:CYS:HB3	16	0.24
(1,608)	1:90:B:LEU:HD11	1:94:B:LEU:HA	9	0.24
(1,608)	1:90:B:LEU:HD12	1:94:B:LEU:HA	9	0.24
(1,608)	1:90:B:LEU:HD13	1:94:B:LEU:HA	9	0.24
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD11	10	0.24
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD12	10	0.24
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD13	10	0.24
(1,519)	1:108:B:CYS:H	1:90:B:LEU:HD11	10	0.24
(1,519)	1:108:B:CYS:H	1:90:B:LEU:HD12	10	0.24
(1,519)	1:108:B:CYS:H	1:90:B:LEU:HD13	10	0.24
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG11	5	0.24
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG12	5	0.24
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG13	5	0.24

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG11	14	0.24
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG12	14	0.24
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG13	14	0.24
(1,453)	1:90:B:LEU:H	1:90:B:LEU:HG	9	0.24
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG11	17	0.24
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG12	17	0.24
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG13	17	0.24
(1,350)	1:72:B:VAL:H	1:72:B:VAL:HB	3	0.24
(1,345)	1:72:B:VAL:H	1:69:B:LEU:HA	9	0.24
(1,336)	1:70:B:LYS:H	1:70:B:LYS:HB3	7	0.24
(1,329)	1:48:A:GLU:HA	1:61:A:CYS:HB3	13	0.24
(1,329)	1:48:A:GLU:HA	1:61:A:CYS:HB3	16	0.24
(1,320)	1:48:A:GLU:HB2	1:50:A:HIS:HD2	8	0.24
(1,320)	1:48:A:GLU:HB2	1:50:A:HIS:HD2	11	0.24
(1,318)	1:36:A:LEU:HD11	1:46:A:PHE:HB2	4	0.24
(1,318)	1:36:A:LEU:HD12	1:46:A:PHE:HB2	4	0.24
(1,318)	1:36:A:LEU:HD13	1:46:A:PHE:HB2	4	0.24
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE1	2	0.24
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE2	2	0.24
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE1	7	0.24
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE2	7	0.24
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE1	17	0.24
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE2	17	0.24
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG11	6	0.24
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG12	6	0.24
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG13	6	0.24
(1,30)	1:11:A:VAL:H	1:8:A:LEU:HA	4	0.24
(1,21)	1:9:A:LYS:H	1:9:A:LYS:HB3	4	0.24
(1,13)	1:52:A:HIS:HE2	1:88:B:ILE:HD12	4	0.24
(2,2)	1:90:B:LEU:H	1:92:B:CYS:HA	10	0.23
(1,644)	1:109:B:GLU:HA	1:122:B:CYS:HB3	17	0.23
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG11	4	0.23
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG12	4	0.23
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG13	4	0.23
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG11	5	0.23
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG12	5	0.23
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG13	5	0.23
(1,635)	1:109:B:GLU:HB2	1:111:B:HIS:HD2	13	0.23
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE1	4	0.23
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE2	4	0.23
(1,362)	1:74:B:CYS:H	1:71:B:LYS:HA	17	0.23
(1,353)	1:73:B:ALA:H	1:70:B:LYS:HA	7	0.23

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,350)	1:72:B:VAL:H	1:72:B:VAL:HB	13	0.23
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE1	4	0.23
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE2	4	0.23
(1,293)	1:29:A:LEU:HD11	1:33:A:LEU:HA	7	0.23
(1,293)	1:29:A:LEU:HD12	1:33:A:LEU:HA	7	0.23
(1,293)	1:29:A:LEU:HD13	1:33:A:LEU:HA	7	0.23
(1,278)	1:60:A:LEU:H	1:61:A:CYS:H	15	0.23
(1,245)	1:56:A:LYS:H	1:55:A:CYS:HB2	9	0.23
(1,47)	1:13:A:CYS:H	1:10:A:LYS:HA	16	0.23
(1,8)	1:113:B:HIS:HE2	1:27:A:ILE:HD11	8	0.23
(1,3)	1:30:A:PRO:HD3	1:115:B:VAL:HG11	9	0.23
(1,3)	1:30:A:PRO:HD3	1:115:B:VAL:HG12	9	0.23
(1,3)	1:30:A:PRO:HD3	1:115:B:VAL:HG13	9	0.23
(1,644)	1:109:B:GLU:HA	1:122:B:CYS:HB3	13	0.22
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG21	2	0.22
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG22	2	0.22
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG23	2	0.22
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG21	2	0.22
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG22	2	0.22
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG23	2	0.22
(1,608)	1:90:B:LEU:HD11	1:94:B:LEU:HA	17	0.22
(1,608)	1:90:B:LEU:HD12	1:94:B:LEU:HA	17	0.22
(1,608)	1:90:B:LEU:HD13	1:94:B:LEU:HA	17	0.22
(1,560)	1:117:B:LYS:H	1:116:B:CYS:HB2	15	0.22
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD11	16	0.22
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD12	16	0.22
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD13	16	0.22
(1,539)	1:111:B:HIS:H	1:109:B:GLU:HG2	4	0.22
(1,539)	1:111:B:HIS:H	1:109:B:GLU:HG3	4	0.22
(1,506)	1:106:B:CYS:H	1:103:B:CYS:HA	9	0.22
(1,350)	1:72:B:VAL:H	1:72:B:VAL:HB	10	0.22
(1,345)	1:72:B:VAL:H	1:69:B:LEU:HA	12	0.22
(1,345)	1:72:B:VAL:H	1:69:B:LEU:HA	15	0.22
(1,328)	1:48:A:GLU:HA	1:61:A:CYS:HB2	2	0.22
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG11	11	0.22
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG12	11	0.22
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG13	11	0.22
(1,320)	1:48:A:GLU:HB2	1:50:A:HIS:HD2	1	0.22
(1,319)	1:50:A:HIS:HD2	1:46:A:PHE:HZ	4	0.22
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE1	1	0.22
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE2	1	0.22
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE1	3	0.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE2	3	0.22
(1,293)	1:29:A:LEU:HD11	1:33:A:LEU:HA	9	0.22
(1,293)	1:29:A:LEU:HD12	1:33:A:LEU:HA	9	0.22
(1,293)	1:29:A:LEU:HD13	1:33:A:LEU:HA	9	0.22
(1,196)	1:46:A:PHE:H	1:36:A:LEU:HD11	17	0.22
(1,196)	1:46:A:PHE:H	1:36:A:LEU:HD12	17	0.22
(1,196)	1:46:A:PHE:H	1:36:A:LEU:HD13	17	0.22
(1,644)	1:109:B:GLU:HA	1:122:B:CYS:HB3	6	0.21
(1,635)	1:109:B:GLU:HB2	1:111:B:HIS:HD2	9	0.21
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE1	1	0.21
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE2	1	0.21
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE1	16	0.21
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE2	16	0.21
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG21	4	0.21
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG22	4	0.21
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG23	4	0.21
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG21	4	0.21
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG22	4	0.21
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG23	4	0.21
(1,600)	1:75:B:ALA:HA	1:78:B:ILE:HB	7	0.21
(1,598)	1:75:B:ALA:HB1	1:72:B:VAL:HA	6	0.21
(1,598)	1:75:B:ALA:HB2	1:72:B:VAL:HA	6	0.21
(1,598)	1:75:B:ALA:HB3	1:72:B:VAL:HA	6	0.21
(1,597)	1:68:B:VAL:HA	1:71:B:LYS:HB2	16	0.21
(1,597)	1:68:B:VAL:HA	1:71:B:LYS:HB3	16	0.21
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD11	15	0.21
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD12	15	0.21
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD13	15	0.21
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD11	17	0.21
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD12	17	0.21
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD13	17	0.21
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG11	10	0.21
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG12	10	0.21
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG13	10	0.21
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG11	11	0.21
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG12	11	0.21
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG13	11	0.21
(1,449)	1:90:B:LEU:H	1:88:B:ILE:HA	4	0.21
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG11	4	0.21
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG12	4	0.21
(1,409)	1:82:B:VAL:H	1:82:B:VAL:HG13	4	0.21
(1,350)	1:72:B:VAL:H	1:72:B:VAL:HB	2	0.21

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,336)	1:70:B:LYS:H	1:70:B:LYS:HB3	6	0.21
(1,336)	1:70:B:LYS:H	1:70:B:LYS:HB3	14	0.21
(1,335)	1:70:B:LYS:H	1:70:B:LYS:HB2	3	0.21
(1,204)	1:47:A:CYS:H	1:29:A:LEU:HD11	4	0.21
(1,204)	1:47:A:CYS:H	1:29:A:LEU:HD12	4	0.21
(1,204)	1:47:A:CYS:H	1:29:A:LEU:HD13	4	0.21
(1,197)	1:46:A:PHE:H	1:43:A:ALA:HA	1	0.21
(1,134)	1:29:A:LEU:H	1:27:A:ILE:HA	4	0.21
(1,35)	1:11:A:VAL:H	1:11:A:VAL:HB	2	0.21
(1,35)	1:11:A:VAL:H	1:11:A:VAL:HB	3	0.21
(1,21)	1:9:A:LYS:H	1:9:A:LYS:HB3	16	0.21
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE1	2	0.2
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE2	2	0.2
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE1	3	0.2
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE2	3	0.2
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE1	9	0.2
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE2	9	0.2
(1,608)	1:90:B:LEU:HD11	1:94:B:LEU:HA	16	0.2
(1,608)	1:90:B:LEU:HD12	1:94:B:LEU:HA	16	0.2
(1,608)	1:90:B:LEU:HD13	1:94:B:LEU:HA	16	0.2
(1,388)	1:79:B:ALA:H	1:78:B:ILE:HB	7	0.2
(1,336)	1:70:B:LYS:H	1:70:B:LYS:HB3	13	0.2
(1,336)	1:70:B:LYS:H	1:70:B:LYS:HB3	15	0.2
(1,328)	1:48:A:GLU:HA	1:61:A:CYS:HB2	5	0.2
(1,320)	1:48:A:GLU:HB2	1:50:A:HIS:HD2	5	0.2
(1,320)	1:48:A:GLU:HB2	1:50:A:HIS:HD2	10	0.2
(1,224)	1:50:A:HIS:H	1:48:A:GLU:HG2	6	0.2
(1,224)	1:50:A:HIS:H	1:48:A:GLU:HG3	6	0.2
(1,47)	1:13:A:CYS:H	1:10:A:LYS:HA	7	0.2
(1,35)	1:11:A:VAL:H	1:11:A:VAL:HB	4	0.2
(1,35)	1:11:A:VAL:H	1:11:A:VAL:HB	10	0.2
(1,21)	1:9:A:LYS:H	1:9:A:LYS:HB3	6	0.2
(1,21)	1:9:A:LYS:H	1:9:A:LYS:HB3	9	0.2
(1,21)	1:9:A:LYS:H	1:9:A:LYS:HB3	10	0.2
(1,20)	1:9:A:LYS:H	1:9:A:LYS:HB2	1	0.2
(1,9)	1:113:B:HIS:HE2	1:27:A:ILE:HG13	16	0.2
(1,1)	1:91:B:PRO:HD2	1:54:A:VAL:HG11	7	0.2
(1,1)	1:91:B:PRO:HD2	1:54:A:VAL:HG12	7	0.2
(1,1)	1:91:B:PRO:HD2	1:54:A:VAL:HG13	7	0.2
(1,1)	1:91:B:PRO:HD3	1:54:A:VAL:HG11	7	0.2
(1,1)	1:91:B:PRO:HD3	1:54:A:VAL:HG12	7	0.2
(1,1)	1:91:B:PRO:HD3	1:54:A:VAL:HG13	7	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,1)	1:29:A:LEU:H	1:31:A:CYS:HA	1	0.19
(2,1)	1:29:A:LEU:H	1:31:A:CYS:HA	10	0.19
(1,644)	1:109:B:GLU:HA	1:122:B:CYS:HB3	8	0.19
(1,635)	1:109:B:GLU:HB2	1:111:B:HIS:HD2	1	0.19
(1,633)	1:97:B:LEU:HD11	1:107:B:PHE:HB2	10	0.19
(1,633)	1:97:B:LEU:HD12	1:107:B:PHE:HB2	10	0.19
(1,633)	1:97:B:LEU:HD13	1:107:B:PHE:HB2	10	0.19
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE1	14	0.19
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE2	14	0.19
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG21	16	0.19
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG22	16	0.19
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG23	16	0.19
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG21	16	0.19
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG22	16	0.19
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG23	16	0.19
(1,608)	1:90:B:LEU:HD11	1:94:B:LEU:HA	7	0.19
(1,608)	1:90:B:LEU:HD12	1:94:B:LEU:HA	7	0.19
(1,608)	1:90:B:LEU:HD13	1:94:B:LEU:HA	7	0.19
(1,600)	1:75:B:ALA:HA	1:78:B:ILE:HB	6	0.19
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD11	2	0.19
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD12	2	0.19
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD13	2	0.19
(1,550)	1:113:B:HIS:H	1:113:B:HIS:HB2	14	0.19
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG11	2	0.19
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG12	2	0.19
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG13	2	0.19
(1,358)	1:73:B:ALA:H	1:72:B:VAL:H	8	0.19
(1,353)	1:73:B:ALA:H	1:70:B:LYS:HA	13	0.19
(1,353)	1:73:B:ALA:H	1:70:B:LYS:HA	14	0.19
(1,336)	1:70:B:LYS:H	1:70:B:LYS:HB3	9	0.19
(1,336)	1:70:B:LYS:H	1:70:B:LYS:HB3	10	0.19
(1,329)	1:48:A:GLU:HA	1:61:A:CYS:HB3	7	0.19
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG11	9	0.19
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG12	9	0.19
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG13	9	0.19
(1,320)	1:48:A:GLU:HB2	1:50:A:HIS:HD2	3	0.19
(1,320)	1:48:A:GLU:HB2	1:50:A:HIS:HD2	4	0.19
(1,320)	1:48:A:GLU:HB2	1:50:A:HIS:HD2	13	0.19
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE1	8	0.19
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE2	8	0.19
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE1	14	0.19
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE2	14	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,293)	1:29:A:LEU:HD11	1:33:A:LEU:HA	6	0.19
(1,293)	1:29:A:LEU:HD12	1:33:A:LEU:HA	6	0.19
(1,293)	1:29:A:LEU:HD13	1:33:A:LEU:HA	6	0.19
(1,285)	1:14:A:ALA:HA	1:17:A:ILE:HB	7	0.19
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD11	5	0.19
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD12	5	0.19
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD13	5	0.19
(1,187)	1:37:A:LYS:H	1:37:A:LYS:HB2	2	0.19
(1,187)	1:37:A:LYS:H	1:37:A:LYS:HB2	6	0.19
(1,35)	1:11:A:VAL:H	1:11:A:VAL:HB	13	0.19
(1,30)	1:11:A:VAL:H	1:8:A:LEU:HA	7	0.19
(1,30)	1:11:A:VAL:H	1:8:A:LEU:HA	15	0.19
(1,6)	1:113:B:HIS:HD2	1:24:A:CYS:HB2	1	0.19
(1,642)	1:122:B:CYS:HB3	1:108:B:CYS:HB3	17	0.18
(1,634)	1:111:B:HIS:HD2	1:107:B:PHE:HZ	13	0.18
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE1	5	0.18
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE2	5	0.18
(1,464)	1:93:B:VAL:H	1:93:B:VAL:HB	8	0.18
(1,336)	1:70:B:LYS:H	1:70:B:LYS:HB3	8	0.18
(1,336)	1:70:B:LYS:H	1:70:B:LYS:HB3	11	0.18
(1,336)	1:70:B:LYS:H	1:70:B:LYS:HB3	17	0.18
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG11	6	0.18
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG12	6	0.18
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG13	6	0.18
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG11	15	0.18
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG12	15	0.18
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG13	15	0.18
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE1	6	0.18
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE2	6	0.18
(1,305)	1:45:A:CYS:HB2	1:17:A:ILE:HG21	16	0.18
(1,305)	1:45:A:CYS:HB2	1:17:A:ILE:HG22	16	0.18
(1,305)	1:45:A:CYS:HB2	1:17:A:ILE:HG23	16	0.18
(1,305)	1:45:A:CYS:HB3	1:17:A:ILE:HG21	16	0.18
(1,305)	1:45:A:CYS:HB3	1:17:A:ILE:HG22	16	0.18
(1,305)	1:45:A:CYS:HB3	1:17:A:ILE:HG23	16	0.18
(1,293)	1:29:A:LEU:HD11	1:33:A:LEU:HA	16	0.18
(1,293)	1:29:A:LEU:HD12	1:33:A:LEU:HA	16	0.18
(1,293)	1:29:A:LEU:HD13	1:33:A:LEU:HA	16	0.18
(1,285)	1:14:A:ALA:HA	1:17:A:ILE:HB	2	0.18
(1,283)	1:14:A:ALA:HB1	1:11:A:VAL:HA	6	0.18
(1,283)	1:14:A:ALA:HB2	1:11:A:VAL:HA	6	0.18
(1,283)	1:14:A:ALA:HB3	1:11:A:VAL:HA	6	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,251)	1:56:A:LYS:H	1:56:A:LYS:HG2	1	0.18
(1,251)	1:56:A:LYS:H	1:56:A:LYS:HG3	1	0.18
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD11	11	0.18
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD12	11	0.18
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD13	11	0.18
(1,211)	1:48:A:GLU:H	1:45:A:CYS:HA	9	0.18
(1,209)	1:47:A:CYS:H	1:47:A:CYS:HB2	9	0.18
(1,187)	1:37:A:LYS:H	1:37:A:LYS:HB2	17	0.18
(1,61)	1:16:A:ALA:H	1:13:A:CYS:HA	6	0.18
(1,5)	1:113:B:HIS:HD2	1:24:A:CYS:HA	8	0.18
(1,644)	1:109:B:GLU:HA	1:122:B:CYS:HB3	2	0.17
(1,644)	1:109:B:GLU:HA	1:122:B:CYS:HB3	14	0.17
(1,635)	1:109:B:GLU:HB2	1:111:B:HIS:HD2	2	0.17
(1,635)	1:109:B:GLU:HB2	1:111:B:HIS:HD2	16	0.17
(1,634)	1:111:B:HIS:HD2	1:107:B:PHE:HZ	9	0.17
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE1	12	0.17
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE2	12	0.17
(1,600)	1:75:B:ALA:HA	1:78:B:ILE:HB	2	0.17
(1,548)	1:112:B:CYS:H	1:113:B:HIS:HA	14	0.17
(1,510)	1:107:B:PHE:H	1:78:B:ILE:HG21	1	0.17
(1,510)	1:107:B:PHE:H	1:78:B:ILE:HG22	1	0.17
(1,510)	1:107:B:PHE:H	1:78:B:ILE:HG23	1	0.17
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG11	8	0.17
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG12	8	0.17
(1,465)	1:93:B:VAL:H	1:93:B:VAL:HG13	8	0.17
(1,449)	1:90:B:LEU:H	1:88:B:ILE:HA	13	0.17
(1,361)	1:73:B:ALA:H	1:73:B:ALA:HB1	7	0.17
(1,361)	1:73:B:ALA:H	1:73:B:ALA:HB2	7	0.17
(1,361)	1:73:B:ALA:H	1:73:B:ALA:HB3	7	0.17
(1,336)	1:70:B:LYS:H	1:70:B:LYS:HB3	1	0.17
(1,336)	1:70:B:LYS:H	1:70:B:LYS:HB3	12	0.17
(1,327)	1:61:A:CYS:HB3	1:47:A:CYS:HB3	2	0.17
(1,320)	1:48:A:GLU:HB2	1:50:A:HIS:HD2	12	0.17
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE1	13	0.17
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE2	13	0.17
(1,284)	1:13:A:CYS:HB2	1:17:A:ILE:HG21	7	0.17
(1,284)	1:13:A:CYS:HB2	1:17:A:ILE:HG22	7	0.17
(1,284)	1:13:A:CYS:HB2	1:17:A:ILE:HG23	7	0.17
(1,284)	1:13:A:CYS:HB3	1:17:A:ILE:HG21	7	0.17
(1,284)	1:13:A:CYS:HB3	1:17:A:ILE:HG22	7	0.17
(1,284)	1:13:A:CYS:HB3	1:17:A:ILE:HG23	7	0.17
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD11	14	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD12	14	0.17
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD13	14	0.17
(1,213)	1:47:A:CYS:H	1:48:A:GLU:H	5	0.17
(1,211)	1:48:A:GLU:H	1:45:A:CYS:HA	6	0.17
(1,191)	1:45:A:CYS:H	1:42:A:CYS:HA	17	0.17
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG11	11	0.17
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG12	11	0.17
(1,150)	1:32:A:VAL:H	1:32:A:VAL:HG13	11	0.17
(1,21)	1:9:A:LYS:H	1:9:A:LYS:HB3	13	0.17
(1,5)	1:113:B:HIS:HD2	1:24:A:CYS:HA	11	0.17
(1,1)	1:91:B:PRO:HD2	1:54:A:VAL:HG11	9	0.17
(1,1)	1:91:B:PRO:HD2	1:54:A:VAL:HG12	9	0.17
(1,1)	1:91:B:PRO:HD2	1:54:A:VAL:HG13	9	0.17
(1,1)	1:91:B:PRO:HD3	1:54:A:VAL:HG11	9	0.17
(1,1)	1:91:B:PRO:HD3	1:54:A:VAL:HG12	9	0.17
(1,1)	1:91:B:PRO:HD3	1:54:A:VAL:HG13	9	0.17
(1,643)	1:109:B:GLU:HA	1:122:B:CYS:HB2	6	0.16
(1,639)	1:118:B:ASP:HB3	1:115:B:VAL:HA	5	0.16
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG11	12	0.16
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG12	12	0.16
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG13	12	0.16
(1,635)	1:109:B:GLU:HB2	1:111:B:HIS:HD2	3	0.16
(1,624)	1:88:B:ILE:HD11	1:107:B:PHE:HD1	17	0.16
(1,624)	1:88:B:ILE:HD11	1:107:B:PHE:HD2	17	0.16
(1,624)	1:88:B:ILE:HD12	1:107:B:PHE:HD1	17	0.16
(1,624)	1:88:B:ILE:HD12	1:107:B:PHE:HD2	17	0.16
(1,624)	1:88:B:ILE:HD13	1:107:B:PHE:HD1	17	0.16
(1,624)	1:88:B:ILE:HD13	1:107:B:PHE:HD2	17	0.16
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE1	7	0.16
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE2	7	0.16
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE1	10	0.16
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE2	10	0.16
(1,599)	1:74:B:CYS:HB2	1:78:B:ILE:HG21	13	0.16
(1,599)	1:74:B:CYS:HB2	1:78:B:ILE:HG22	13	0.16
(1,599)	1:74:B:CYS:HB2	1:78:B:ILE:HG23	13	0.16
(1,599)	1:74:B:CYS:HB3	1:78:B:ILE:HG21	13	0.16
(1,599)	1:74:B:CYS:HB3	1:78:B:ILE:HG22	13	0.16
(1,599)	1:74:B:CYS:HB3	1:78:B:ILE:HG23	13	0.16
(1,588)	1:121:B:LEU:H	1:121:B:LEU:HB2	7	0.16
(1,588)	1:121:B:LEU:H	1:121:B:LEU:HB2	12	0.16
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD11	5	0.16
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD12	5	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD13	5	0.16
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD11	7	0.16
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD12	7	0.16
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD13	7	0.16
(1,548)	1:112:B:CYS:H	1:113:B:HIS:HA	16	0.16
(1,526)	1:109:B:GLU:H	1:106:B:CYS:HA	10	0.16
(1,524)	1:108:B:CYS:H	1:108:B:CYS:HB2	1	0.16
(1,336)	1:70:B:LYS:H	1:70:B:LYS:HB3	2	0.16
(1,336)	1:70:B:LYS:H	1:70:B:LYS:HB3	5	0.16
(1,329)	1:48:A:GLU:HA	1:61:A:CYS:HB3	10	0.16
(1,329)	1:48:A:GLU:HA	1:61:A:CYS:HB3	11	0.16
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG11	4	0.16
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG12	4	0.16
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG13	4	0.16
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG11	8	0.16
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG12	8	0.16
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG13	8	0.16
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG11	14	0.16
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG12	14	0.16
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG13	14	0.16
(1,314)	1:29:A:LEU:HD11	1:46:A:PHE:HZ	7	0.16
(1,314)	1:29:A:LEU:HD12	1:46:A:PHE:HZ	7	0.16
(1,314)	1:29:A:LEU:HD13	1:46:A:PHE:HZ	7	0.16
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE1	5	0.16
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE2	5	0.16
(1,305)	1:45:A:CYS:HB2	1:17:A:ILE:HG21	2	0.16
(1,305)	1:45:A:CYS:HB2	1:17:A:ILE:HG22	2	0.16
(1,305)	1:45:A:CYS:HB2	1:17:A:ILE:HG23	2	0.16
(1,305)	1:45:A:CYS:HB3	1:17:A:ILE:HG21	2	0.16
(1,305)	1:45:A:CYS:HB3	1:17:A:ILE:HG22	2	0.16
(1,305)	1:45:A:CYS:HB3	1:17:A:ILE:HG23	2	0.16
(1,305)	1:45:A:CYS:HB2	1:17:A:ILE:HG21	3	0.16
(1,305)	1:45:A:CYS:HB2	1:17:A:ILE:HG22	3	0.16
(1,305)	1:45:A:CYS:HB2	1:17:A:ILE:HG23	3	0.16
(1,305)	1:45:A:CYS:HB3	1:17:A:ILE:HG21	3	0.16
(1,305)	1:45:A:CYS:HB3	1:17:A:ILE:HG22	3	0.16
(1,305)	1:45:A:CYS:HB3	1:17:A:ILE:HG23	3	0.16
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG11	10	0.16
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG12	10	0.16
(1,94)	1:21:A:VAL:H	1:21:A:VAL:HG13	10	0.16
(1,74)	1:18:A:ALA:H	1:17:A:ILE:HG12	6	0.16
(1,71)	1:17:A:ILE:H	1:18:A:ALA:HA	9	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,71)	1:17:A:ILE:H	1:18:A:ALA:HA	13	0.16
(1,21)	1:9:A:LYS:H	1:9:A:LYS:HB3	8	0.16
(1,13)	1:52:A:HIS:HE2	1:88:B:ILE:HD11	8	0.16
(1,10)	1:52:A:HIS:HD2	1:85:B:CYS:HA	7	0.16
(2,2)	1:90:B:LEU:H	1:92:B:CYS:HA	2	0.15
(2,1)	1:29:A:LEU:H	1:31:A:CYS:HA	5	0.15
(1,644)	1:109:B:GLU:HA	1:122:B:CYS:HB3	3	0.15
(1,639)	1:118:B:ASP:HB3	1:115:B:VAL:HA	4	0.15
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG11	3	0.15
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG12	3	0.15
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG13	3	0.15
(1,635)	1:109:B:GLU:HB2	1:111:B:HIS:HD2	7	0.15
(1,635)	1:109:B:GLU:HB2	1:111:B:HIS:HD2	12	0.15
(1,634)	1:111:B:HIS:HD2	1:107:B:PHE:HZ	17	0.15
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE1	15	0.15
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE2	15	0.15
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG21	12	0.15
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG22	12	0.15
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG23	12	0.15
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG21	12	0.15
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG22	12	0.15
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG23	12	0.15
(1,599)	1:74:B:CYS:HB2	1:78:B:ILE:HG21	12	0.15
(1,599)	1:74:B:CYS:HB2	1:78:B:ILE:HG22	12	0.15
(1,599)	1:74:B:CYS:HB2	1:78:B:ILE:HG23	12	0.15
(1,599)	1:74:B:CYS:HB3	1:78:B:ILE:HG21	12	0.15
(1,599)	1:74:B:CYS:HB3	1:78:B:ILE:HG22	12	0.15
(1,599)	1:74:B:CYS:HB3	1:78:B:ILE:HG23	12	0.15
(1,586)	1:120:B:HIS:H	1:121:B:LEU:HD11	5	0.15
(1,586)	1:120:B:HIS:H	1:121:B:LEU:HD12	5	0.15
(1,586)	1:120:B:HIS:H	1:121:B:LEU:HD13	5	0.15
(1,550)	1:113:B:HIS:H	1:113:B:HIS:HB2	2	0.15
(1,550)	1:113:B:HIS:H	1:113:B:HIS:HB2	6	0.15
(1,550)	1:113:B:HIS:H	1:113:B:HIS:HB2	13	0.15
(1,512)	1:107:B:PHE:H	1:104:B:ALA:HA	1	0.15
(1,345)	1:72:B:VAL:H	1:69:B:LEU:HA	1	0.15
(1,325)	1:55:A:CYS:HA	1:60:A:LEU:HD11	15	0.15
(1,325)	1:55:A:CYS:HA	1:60:A:LEU:HD12	15	0.15
(1,325)	1:55:A:CYS:HA	1:60:A:LEU:HD13	15	0.15
(1,305)	1:45:A:CYS:HB2	1:17:A:ILE:HG21	12	0.15
(1,305)	1:45:A:CYS:HB2	1:17:A:ILE:HG22	12	0.15
(1,305)	1:45:A:CYS:HB2	1:17:A:ILE:HG23	12	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,305)	1:45:A:CYS:HB3	1:17:A:ILE:HG21	12	0.15
(1,305)	1:45:A:CYS:HB3	1:17:A:ILE:HG22	12	0.15
(1,305)	1:45:A:CYS:HB3	1:17:A:ILE:HG23	12	0.15
(1,293)	1:29:A:LEU:HD11	1:33:A:LEU:HA	3	0.15
(1,293)	1:29:A:LEU:HD12	1:33:A:LEU:HA	3	0.15
(1,293)	1:29:A:LEU:HD13	1:33:A:LEU:HA	3	0.15
(1,293)	1:29:A:LEU:HD11	1:33:A:LEU:HA	14	0.15
(1,293)	1:29:A:LEU:HD12	1:33:A:LEU:HA	14	0.15
(1,293)	1:29:A:LEU:HD13	1:33:A:LEU:HA	14	0.15
(1,284)	1:13:A:CYS:HB2	1:17:A:ILE:HG21	2	0.15
(1,284)	1:13:A:CYS:HB2	1:17:A:ILE:HG22	2	0.15
(1,284)	1:13:A:CYS:HB2	1:17:A:ILE:HG23	2	0.15
(1,284)	1:13:A:CYS:HB3	1:17:A:ILE:HG21	2	0.15
(1,284)	1:13:A:CYS:HB3	1:17:A:ILE:HG22	2	0.15
(1,284)	1:13:A:CYS:HB3	1:17:A:ILE:HG23	2	0.15
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD11	12	0.15
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD12	12	0.15
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD13	12	0.15
(1,235)	1:52:A:HIS:H	1:52:A:HIS:HB2	11	0.15
(1,211)	1:48:A:GLU:H	1:45:A:CYS:HA	4	0.15
(1,43)	1:12:A:ALA:H	1:11:A:VAL:H	9	0.15
(1,21)	1:9:A:LYS:H	1:9:A:LYS:HB3	2	0.15
(1,20)	1:9:A:LYS:H	1:9:A:LYS:HB2	3	0.15
(1,644)	1:109:B:GLU:HA	1:122:B:CYS:HB3	5	0.14
(1,644)	1:109:B:GLU:HA	1:122:B:CYS:HB3	12	0.14
(1,639)	1:118:B:ASP:HB3	1:115:B:VAL:HA	1	0.14
(1,639)	1:118:B:ASP:HB3	1:115:B:VAL:HA	2	0.14
(1,635)	1:109:B:GLU:HB2	1:111:B:HIS:HD2	10	0.14
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE1	8	0.14
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE2	8	0.14
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG21	13	0.14
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG22	13	0.14
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG23	13	0.14
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG21	13	0.14
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG22	13	0.14
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG23	13	0.14
(1,600)	1:75:B:ALA:HA	1:78:B:ILE:HB	5	0.14
(1,386)	1:78:B:ILE:H	1:79:B:ALA:HA	1	0.14
(1,329)	1:48:A:GLU:HA	1:61:A:CYS:HB3	3	0.14
(1,329)	1:48:A:GLU:HA	1:61:A:CYS:HB3	9	0.14
(1,329)	1:48:A:GLU:HA	1:61:A:CYS:HB3	14	0.14
(1,293)	1:29:A:LEU:HD11	1:33:A:LEU:HA	15	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,293)	1:29:A:LEU:HD12	1:33:A:LEU:HA	15	0.14
(1,293)	1:29:A:LEU:HD13	1:33:A:LEU:HA	15	0.14
(1,284)	1:13:A:CYS:HB2	1:17:A:ILE:HG21	5	0.14
(1,284)	1:13:A:CYS:HB2	1:17:A:ILE:HG22	5	0.14
(1,284)	1:13:A:CYS:HB2	1:17:A:ILE:HG23	5	0.14
(1,284)	1:13:A:CYS:HB3	1:17:A:ILE:HG21	5	0.14
(1,284)	1:13:A:CYS:HB3	1:17:A:ILE:HG22	5	0.14
(1,284)	1:13:A:CYS:HB3	1:17:A:ILE:HG23	5	0.14
(1,272)	1:60:A:LEU:H	1:60:A:LEU:HA	2	0.14
(1,234)	1:52:A:HIS:H	1:52:A:HIS:HA	13	0.14
(1,195)	1:46:A:PHE:H	1:17:A:ILE:HG21	12	0.14
(1,195)	1:46:A:PHE:H	1:17:A:ILE:HG22	12	0.14
(1,195)	1:46:A:PHE:H	1:17:A:ILE:HG23	12	0.14
(1,187)	1:37:A:LYS:H	1:37:A:LYS:HB2	1	0.14
(1,38)	1:12:A:ALA:H	1:9:A:LYS:HA	4	0.14
(1,20)	1:9:A:LYS:H	1:9:A:LYS:HB2	7	0.14
(2,2)	1:90:B:LEU:H	1:92:B:CYS:HA	11	0.13
(2,2)	1:90:B:LEU:H	1:92:B:CYS:HA	14	0.13
(1,640)	1:116:B:CYS:HA	1:121:B:LEU:HD11	15	0.13
(1,640)	1:116:B:CYS:HA	1:121:B:LEU:HD12	15	0.13
(1,640)	1:116:B:CYS:HA	1:121:B:LEU:HD13	15	0.13
(1,634)	1:111:B:HIS:HD2	1:107:B:PHE:HZ	16	0.13
(1,608)	1:90:B:LEU:HD11	1:94:B:LEU:HA	1	0.13
(1,608)	1:90:B:LEU:HD12	1:94:B:LEU:HA	1	0.13
(1,608)	1:90:B:LEU:HD13	1:94:B:LEU:HA	1	0.13
(1,608)	1:90:B:LEU:HD11	1:94:B:LEU:HA	5	0.13
(1,608)	1:90:B:LEU:HD12	1:94:B:LEU:HA	5	0.13
(1,608)	1:90:B:LEU:HD13	1:94:B:LEU:HA	5	0.13
(1,602)	1:79:B:ALA:HA	1:82:B:VAL:HB	6	0.13
(1,597)	1:68:B:VAL:HA	1:71:B:LYS:HB2	5	0.13
(1,597)	1:68:B:VAL:HA	1:71:B:LYS:HB3	5	0.13
(1,587)	1:121:B:LEU:H	1:121:B:LEU:HA	4	0.13
(1,587)	1:121:B:LEU:H	1:121:B:LEU:HA	6	0.13
(1,587)	1:121:B:LEU:H	1:121:B:LEU:HA	13	0.13
(1,586)	1:120:B:HIS:H	1:121:B:LEU:HD11	9	0.13
(1,586)	1:120:B:HIS:H	1:121:B:LEU:HD12	9	0.13
(1,586)	1:120:B:HIS:H	1:121:B:LEU:HD13	9	0.13
(1,549)	1:113:B:HIS:H	1:113:B:HIS:HA	1	0.13
(1,549)	1:113:B:HIS:H	1:113:B:HIS:HA	4	0.13
(1,526)	1:109:B:GLU:H	1:106:B:CYS:HA	5	0.13
(1,510)	1:107:B:PHE:H	1:78:B:ILE:HG21	17	0.13
(1,510)	1:107:B:PHE:H	1:78:B:ILE:HG22	17	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,510)	1:107:B:PHE:H	1:78:B:ILE:HG23	17	0.13
(1,502)	1:98:B:LYS:H	1:98:B:LYS:HB2	12	0.13
(1,460)	1:93:B:VAL:H	1:92:B:CYS:HB2	16	0.13
(1,460)	1:93:B:VAL:H	1:92:B:CYS:HB3	16	0.13
(1,454)	1:92:B:CYS:H	1:92:B:CYS:HA	1	0.13
(1,454)	1:92:B:CYS:H	1:92:B:CYS:HA	16	0.13
(1,449)	1:90:B:LEU:H	1:88:B:ILE:HA	17	0.13
(1,374)	1:75:B:ALA:H	1:75:B:ALA:HA	13	0.13
(1,374)	1:75:B:ALA:H	1:75:B:ALA:HA	17	0.13
(1,329)	1:48:A:GLU:HA	1:61:A:CYS:HB3	5	0.13
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG11	12	0.13
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG12	12	0.13
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG13	12	0.13
(1,319)	1:50:A:HIS:HD2	1:46:A:PHE:HZ	3	0.13
(1,319)	1:50:A:HIS:HD2	1:46:A:PHE:HZ	10	0.13
(1,309)	1:27:A:ILE:HD11	1:46:A:PHE:HD1	7	0.13
(1,309)	1:27:A:ILE:HD11	1:46:A:PHE:HD2	7	0.13
(1,309)	1:27:A:ILE:HD12	1:46:A:PHE:HD1	7	0.13
(1,309)	1:27:A:ILE:HD12	1:46:A:PHE:HD2	7	0.13
(1,309)	1:27:A:ILE:HD13	1:46:A:PHE:HD1	7	0.13
(1,309)	1:27:A:ILE:HD13	1:46:A:PHE:HD2	7	0.13
(1,308)	1:17:A:ILE:HG12	1:46:A:PHE:HZ	4	0.13
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE1	11	0.13
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE2	11	0.13
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE1	15	0.13
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE2	15	0.13
(1,285)	1:14:A:ALA:HA	1:17:A:ILE:HB	8	0.13
(1,284)	1:13:A:CYS:HB2	1:17:A:ILE:HG21	8	0.13
(1,284)	1:13:A:CYS:HB2	1:17:A:ILE:HG22	8	0.13
(1,284)	1:13:A:CYS:HB2	1:17:A:ILE:HG23	8	0.13
(1,284)	1:13:A:CYS:HB3	1:17:A:ILE:HG21	8	0.13
(1,284)	1:13:A:CYS:HB3	1:17:A:ILE:HG22	8	0.13
(1,284)	1:13:A:CYS:HB3	1:17:A:ILE:HG23	8	0.13
(1,282)	1:7:A:VAL:HA	1:10:A:LYS:HB2	4	0.13
(1,282)	1:7:A:VAL:HA	1:10:A:LYS:HB3	4	0.13
(1,272)	1:60:A:LEU:H	1:60:A:LEU:HA	11	0.13
(1,272)	1:60:A:LEU:H	1:60:A:LEU:HA	16	0.13
(1,271)	1:59:A:HIS:H	1:60:A:LEU:HD11	5	0.13
(1,271)	1:59:A:HIS:H	1:60:A:LEU:HD12	5	0.13
(1,271)	1:59:A:HIS:H	1:60:A:LEU:HD13	5	0.13
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD11	15	0.13
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD12	15	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD13	15	0.13
(1,234)	1:52:A:HIS:H	1:52:A:HIS:HA	1	0.13
(1,224)	1:50:A:HIS:H	1:48:A:GLU:HG2	14	0.13
(1,224)	1:50:A:HIS:H	1:48:A:GLU:HG3	14	0.13
(1,149)	1:32:A:VAL:H	1:32:A:VAL:HB	11	0.13
(1,139)	1:31:A:CYS:H	1:31:A:CYS:HA	13	0.13
(1,134)	1:29:A:LEU:H	1:27:A:ILE:HA	7	0.13
(1,86)	1:20:A:ALA:H	1:20:A:ALA:HA	17	0.13
(1,77)	1:18:A:ALA:H	1:18:A:ALA:HA	6	0.13
(1,71)	1:17:A:ILE:H	1:18:A:ALA:HA	4	0.13
(1,59)	1:14:A:ALA:H	1:14:A:ALA:HA	13	0.13
(1,43)	1:12:A:ALA:H	1:11:A:VAL:H	8	0.13
(1,38)	1:12:A:ALA:H	1:9:A:LYS:HA	6	0.13
(1,5)	1:113:B:HIS:HD2	1:24:A:CYS:HA	13	0.13
(1,2)	1:91:B:PRO:HA	1:54:A:VAL:HG11	12	0.13
(1,2)	1:91:B:PRO:HA	1:54:A:VAL:HG12	12	0.13
(1,2)	1:91:B:PRO:HA	1:54:A:VAL:HG13	12	0.13
(1,1)	1:91:B:PRO:HD2	1:54:A:VAL:HG11	10	0.13
(1,1)	1:91:B:PRO:HD2	1:54:A:VAL:HG12	10	0.13
(1,1)	1:91:B:PRO:HD2	1:54:A:VAL:HG13	10	0.13
(1,1)	1:91:B:PRO:HD3	1:54:A:VAL:HG11	10	0.13
(1,1)	1:91:B:PRO:HD3	1:54:A:VAL:HG12	10	0.13
(1,1)	1:91:B:PRO:HD3	1:54:A:VAL:HG13	10	0.13
(2,1)	1:29:A:LEU:H	1:31:A:CYS:HA	12	0.12
(1,639)	1:118:B:ASP:HB3	1:115:B:VAL:HA	3	0.12
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG11	17	0.12
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG12	17	0.12
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG13	17	0.12
(1,635)	1:109:B:GLU:HB2	1:111:B:HIS:HD2	15	0.12
(1,634)	1:111:B:HIS:HD2	1:107:B:PHE:HZ	15	0.12
(1,623)	1:78:B:ILE:HG12	1:107:B:PHE:HZ	6	0.12
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE1	11	0.12
(1,622)	1:78:B:ILE:HG12	1:107:B:PHE:HE2	11	0.12
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG21	3	0.12
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG22	3	0.12
(1,620)	1:106:B:CYS:HB2	1:78:B:ILE:HG23	3	0.12
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG21	3	0.12
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG22	3	0.12
(1,620)	1:106:B:CYS:HB3	1:78:B:ILE:HG23	3	0.12
(1,610)	1:97:B:LEU:HD11	1:78:B:ILE:HA	14	0.12
(1,610)	1:97:B:LEU:HD12	1:78:B:ILE:HA	14	0.12
(1,610)	1:97:B:LEU:HD13	1:78:B:ILE:HA	14	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,587)	1:121:B:LEU:H	1:121:B:LEU:HA	2	0.12
(1,587)	1:121:B:LEU:H	1:121:B:LEU:HA	10	0.12
(1,587)	1:121:B:LEU:H	1:121:B:LEU:HA	11	0.12
(1,587)	1:121:B:LEU:H	1:121:B:LEU:HA	12	0.12
(1,587)	1:121:B:LEU:H	1:121:B:LEU:HA	16	0.12
(1,586)	1:120:B:HIS:H	1:121:B:LEU:HD11	17	0.12
(1,586)	1:120:B:HIS:H	1:121:B:LEU:HD12	17	0.12
(1,586)	1:120:B:HIS:H	1:121:B:LEU:HD13	17	0.12
(1,584)	1:120:B:HIS:H	1:120:B:HIS:HA	8	0.12
(1,584)	1:120:B:HIS:H	1:120:B:HIS:HA	15	0.12
(1,549)	1:113:B:HIS:H	1:113:B:HIS:HA	8	0.12
(1,549)	1:113:B:HIS:H	1:113:B:HIS:HA	12	0.12
(1,539)	1:111:B:HIS:H	1:109:B:GLU:HG2	6	0.12
(1,539)	1:111:B:HIS:H	1:109:B:GLU:HG3	6	0.12
(1,524)	1:108:B:CYS:H	1:108:B:CYS:HB2	16	0.12
(1,514)	1:107:B:PHE:H	1:106:B:CYS:HB2	12	0.12
(1,514)	1:107:B:PHE:H	1:106:B:CYS:HB3	12	0.12
(1,510)	1:107:B:PHE:H	1:78:B:ILE:HG21	2	0.12
(1,510)	1:107:B:PHE:H	1:78:B:ILE:HG22	2	0.12
(1,510)	1:107:B:PHE:H	1:78:B:ILE:HG23	2	0.12
(1,460)	1:93:B:VAL:H	1:92:B:CYS:HB2	10	0.12
(1,460)	1:93:B:VAL:H	1:92:B:CYS:HB3	10	0.12
(1,460)	1:93:B:VAL:H	1:92:B:CYS:HB2	15	0.12
(1,460)	1:93:B:VAL:H	1:92:B:CYS:HB3	15	0.12
(1,454)	1:92:B:CYS:H	1:92:B:CYS:HA	3	0.12
(1,454)	1:92:B:CYS:H	1:92:B:CYS:HA	4	0.12
(1,454)	1:92:B:CYS:H	1:92:B:CYS:HA	13	0.12
(1,422)	1:84:B:ALA:H	1:84:B:ALA:HA	6	0.12
(1,422)	1:84:B:ALA:H	1:84:B:ALA:HA	8	0.12
(1,422)	1:84:B:ALA:H	1:84:B:ALA:HA	13	0.12
(1,386)	1:78:B:ILE:H	1:79:B:ALA:HA	9	0.12
(1,386)	1:78:B:ILE:H	1:79:B:ALA:HA	17	0.12
(1,374)	1:75:B:ALA:H	1:75:B:ALA:HA	3	0.12
(1,358)	1:73:B:ALA:H	1:72:B:VAL:H	9	0.12
(1,358)	1:73:B:ALA:H	1:72:B:VAL:H	16	0.12
(1,345)	1:72:B:VAL:H	1:69:B:LEU:HA	8	0.12
(1,329)	1:48:A:GLU:HA	1:61:A:CYS:HB3	2	0.12
(1,328)	1:48:A:GLU:HA	1:61:A:CYS:HB2	16	0.12
(1,324)	1:57:A:ASP:HB3	1:54:A:VAL:HA	4	0.12
(1,319)	1:50:A:HIS:HD2	1:46:A:PHE:HZ	1	0.12
(1,314)	1:29:A:LEU:HD11	1:46:A:PHE:HZ	6	0.12
(1,314)	1:29:A:LEU:HD12	1:46:A:PHE:HZ	6	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,314)	1:29:A:LEU:HD13	1:46:A:PHE:HZ	6	0.12
(1,309)	1:27:A:ILE:HD11	1:46:A:PHE:HD1	6	0.12
(1,309)	1:27:A:ILE:HD11	1:46:A:PHE:HD2	6	0.12
(1,309)	1:27:A:ILE:HD12	1:46:A:PHE:HD1	6	0.12
(1,309)	1:27:A:ILE:HD12	1:46:A:PHE:HD2	6	0.12
(1,309)	1:27:A:ILE:HD13	1:46:A:PHE:HD1	6	0.12
(1,309)	1:27:A:ILE:HD13	1:46:A:PHE:HD2	6	0.12
(1,305)	1:45:A:CYS:HB2	1:17:A:ILE:HG21	17	0.12
(1,305)	1:45:A:CYS:HB2	1:17:A:ILE:HG22	17	0.12
(1,305)	1:45:A:CYS:HB2	1:17:A:ILE:HG23	17	0.12
(1,305)	1:45:A:CYS:HB3	1:17:A:ILE:HG21	17	0.12
(1,305)	1:45:A:CYS:HB3	1:17:A:ILE:HG22	17	0.12
(1,305)	1:45:A:CYS:HB3	1:17:A:ILE:HG23	17	0.12
(1,295)	1:36:A:LEU:HD11	1:17:A:ILE:HA	7	0.12
(1,295)	1:36:A:LEU:HD12	1:17:A:ILE:HA	7	0.12
(1,295)	1:36:A:LEU:HD13	1:17:A:ILE:HA	7	0.12
(1,284)	1:13:A:CYS:HB2	1:17:A:ILE:HG21	4	0.12
(1,284)	1:13:A:CYS:HB2	1:17:A:ILE:HG22	4	0.12
(1,284)	1:13:A:CYS:HB2	1:17:A:ILE:HG23	4	0.12
(1,284)	1:13:A:CYS:HB3	1:17:A:ILE:HG21	4	0.12
(1,284)	1:13:A:CYS:HB3	1:17:A:ILE:HG22	4	0.12
(1,284)	1:13:A:CYS:HB3	1:17:A:ILE:HG23	4	0.12
(1,272)	1:60:A:LEU:H	1:60:A:LEU:HA	1	0.12
(1,272)	1:60:A:LEU:H	1:60:A:LEU:HA	6	0.12
(1,272)	1:60:A:LEU:H	1:60:A:LEU:HA	9	0.12
(1,272)	1:60:A:LEU:H	1:60:A:LEU:HA	13	0.12
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD11	3	0.12
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD12	3	0.12
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD13	3	0.12
(1,235)	1:52:A:HIS:H	1:52:A:HIS:HB2	5	0.12
(1,234)	1:52:A:HIS:H	1:52:A:HIS:HA	2	0.12
(1,234)	1:52:A:HIS:H	1:52:A:HIS:HA	7	0.12
(1,234)	1:52:A:HIS:H	1:52:A:HIS:HA	8	0.12
(1,234)	1:52:A:HIS:H	1:52:A:HIS:HA	10	0.12
(1,234)	1:52:A:HIS:H	1:52:A:HIS:HA	12	0.12
(1,234)	1:52:A:HIS:H	1:52:A:HIS:HA	16	0.12
(1,234)	1:52:A:HIS:H	1:52:A:HIS:HA	17	0.12
(1,199)	1:46:A:PHE:H	1:45:A:CYS:HB2	17	0.12
(1,199)	1:46:A:PHE:H	1:45:A:CYS:HB3	17	0.12
(1,195)	1:46:A:PHE:H	1:17:A:ILE:HG21	7	0.12
(1,195)	1:46:A:PHE:H	1:17:A:ILE:HG22	7	0.12
(1,195)	1:46:A:PHE:H	1:17:A:ILE:HG23	7	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,195)	1:46:A:PHE:H	1:17:A:ILE:HG21	14	0.12
(1,195)	1:46:A:PHE:H	1:17:A:ILE:HG22	14	0.12
(1,195)	1:46:A:PHE:H	1:17:A:ILE:HG23	14	0.12
(1,139)	1:31:A:CYS:H	1:31:A:CYS:HA	4	0.12
(1,139)	1:31:A:CYS:H	1:31:A:CYS:HA	9	0.12
(1,134)	1:29:A:LEU:H	1:27:A:ILE:HA	6	0.12
(1,134)	1:29:A:LEU:H	1:27:A:ILE:HA	17	0.12
(1,124)	1:26:A:GLY:H	1:25:A:GLY:H	1	0.12
(1,74)	1:18:A:ALA:H	1:17:A:ILE:HG12	1	0.12
(1,71)	1:17:A:ILE:H	1:18:A:ALA:HA	3	0.12
(1,71)	1:17:A:ILE:H	1:18:A:ALA:HA	14	0.12
(1,59)	1:14:A:ALA:H	1:14:A:ALA:HA	17	0.12
(1,53)	1:14:A:ALA:H	1:12:A:ALA:HA	14	0.12
(1,52)	1:14:A:ALA:H	1:12:A:ALA:HA	14	0.12
(1,46)	1:12:A:ALA:H	1:12:A:ALA:HB1	14	0.12
(1,46)	1:12:A:ALA:H	1:12:A:ALA:HB2	14	0.12
(1,46)	1:12:A:ALA:H	1:12:A:ALA:HB3	14	0.12
(1,43)	1:12:A:ALA:H	1:11:A:VAL:H	16	0.12
(1,30)	1:11:A:VAL:H	1:8:A:LEU:HA	12	0.12
(1,6)	1:113:B:HIS:HD2	1:24:A:CYS:HB2	9	0.12
(2,2)	1:90:B:LEU:H	1:92:B:CYS:HA	15	0.11
(1,643)	1:109:B:GLU:HA	1:122:B:CYS:HB2	4	0.11
(1,643)	1:109:B:GLU:HA	1:122:B:CYS:HB2	8	0.11
(1,642)	1:122:B:CYS:HB3	1:108:B:CYS:HB3	3	0.11
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG11	1	0.11
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG12	1	0.11
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG13	1	0.11
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG11	10	0.11
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG12	10	0.11
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG13	10	0.11
(1,634)	1:111:B:HIS:HD2	1:107:B:PHE:HZ	3	0.11
(1,629)	1:90:B:LEU:HD11	1:107:B:PHE:HZ	17	0.11
(1,629)	1:90:B:LEU:HD12	1:107:B:PHE:HZ	17	0.11
(1,629)	1:90:B:LEU:HD13	1:107:B:PHE:HZ	17	0.11
(1,623)	1:78:B:ILE:HG12	1:107:B:PHE:HZ	12	0.11
(1,617)	1:97:B:LEU:HD11	1:98:B:LYS:HA	7	0.11
(1,617)	1:97:B:LEU:HD12	1:98:B:LYS:HA	7	0.11
(1,617)	1:97:B:LEU:HD13	1:98:B:LYS:HA	7	0.11
(1,599)	1:74:B:CYS:HB2	1:78:B:ILE:HG21	8	0.11
(1,599)	1:74:B:CYS:HB2	1:78:B:ILE:HG22	8	0.11
(1,599)	1:74:B:CYS:HB2	1:78:B:ILE:HG23	8	0.11
(1,599)	1:74:B:CYS:HB3	1:78:B:ILE:HG21	8	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,599)	1:74:B:CYS:HB3	1:78:B:ILE:HG22	8	0.11
(1,599)	1:74:B:CYS:HB3	1:78:B:ILE:HG23	8	0.11
(1,597)	1:68:B:VAL:HA	1:71:B:LYS:HB2	8	0.11
(1,597)	1:68:B:VAL:HA	1:71:B:LYS:HB3	8	0.11
(1,597)	1:68:B:VAL:HA	1:71:B:LYS:HB2	12	0.11
(1,597)	1:68:B:VAL:HA	1:71:B:LYS:HB3	12	0.11
(1,587)	1:121:B:LEU:H	1:121:B:LEU:HA	1	0.11
(1,587)	1:121:B:LEU:H	1:121:B:LEU:HA	7	0.11
(1,587)	1:121:B:LEU:H	1:121:B:LEU:HA	8	0.11
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD11	3	0.11
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD12	3	0.11
(1,558)	1:117:B:LYS:H	1:90:B:LEU:HD13	3	0.11
(1,549)	1:113:B:HIS:H	1:113:B:HIS:HA	7	0.11
(1,549)	1:113:B:HIS:H	1:113:B:HIS:HA	10	0.11
(1,549)	1:113:B:HIS:H	1:113:B:HIS:HA	11	0.11
(1,528)	1:108:B:CYS:H	1:109:B:GLU:H	5	0.11
(1,511)	1:107:B:PHE:H	1:97:B:LEU:HD11	9	0.11
(1,511)	1:107:B:PHE:H	1:97:B:LEU:HD12	9	0.11
(1,511)	1:107:B:PHE:H	1:97:B:LEU:HD13	9	0.11
(1,510)	1:107:B:PHE:H	1:78:B:ILE:HG21	5	0.11
(1,510)	1:107:B:PHE:H	1:78:B:ILE:HG22	5	0.11
(1,510)	1:107:B:PHE:H	1:78:B:ILE:HG23	5	0.11
(1,480)	1:95:B:ALA:H	1:94:B:LEU:HG	7	0.11
(1,460)	1:93:B:VAL:H	1:92:B:CYS:HB2	3	0.11
(1,460)	1:93:B:VAL:H	1:92:B:CYS:HB3	3	0.11
(1,454)	1:92:B:CYS:H	1:92:B:CYS:HA	9	0.11
(1,418)	1:83:B:ALA:H	1:83:B:ALA:HA	11	0.11
(1,389)	1:79:B:ALA:H	1:78:B:ILE:HG12	17	0.11
(1,345)	1:72:B:VAL:H	1:69:B:LEU:HA	7	0.11
(1,338)	1:71:B:LYS:H	1:69:B:LEU:HG	5	0.11
(1,327)	1:61:A:CYS:HB3	1:47:A:CYS:HB3	8	0.11
(1,324)	1:57:A:ASP:HB3	1:54:A:VAL:HA	3	0.11
(1,324)	1:57:A:ASP:HB3	1:54:A:VAL:HA	8	0.11
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG11	1	0.11
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG12	1	0.11
(1,321)	1:31:A:CYS:HA	1:54:A:VAL:HG13	1	0.11
(1,320)	1:48:A:GLU:HB2	1:50:A:HIS:HD2	15	0.11
(1,319)	1:50:A:HIS:HD2	1:46:A:PHE:HZ	8	0.11
(1,319)	1:50:A:HIS:HD2	1:46:A:PHE:HZ	9	0.11
(1,319)	1:50:A:HIS:HD2	1:46:A:PHE:HZ	12	0.11
(1,308)	1:17:A:ILE:HG12	1:46:A:PHE:HZ	6	0.11
(1,293)	1:29:A:LEU:HD11	1:33:A:LEU:HA	11	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,293)	1:29:A:LEU:HD12	1:33:A:LEU:HA	11	0.11
(1,293)	1:29:A:LEU:HD13	1:33:A:LEU:HA	11	0.11
(1,293)	1:29:A:LEU:HD11	1:33:A:LEU:HA	12	0.11
(1,293)	1:29:A:LEU:HD12	1:33:A:LEU:HA	12	0.11
(1,293)	1:29:A:LEU:HD13	1:33:A:LEU:HA	12	0.11
(1,285)	1:14:A:ALA:HA	1:17:A:ILE:HB	11	0.11
(1,282)	1:7:A:VAL:HA	1:10:A:LYS:HB2	6	0.11
(1,282)	1:7:A:VAL:HA	1:10:A:LYS:HB3	6	0.11
(1,272)	1:60:A:LEU:H	1:60:A:LEU:HA	10	0.11
(1,272)	1:60:A:LEU:H	1:60:A:LEU:HA	12	0.11
(1,271)	1:59:A:HIS:H	1:60:A:LEU:HD11	14	0.11
(1,271)	1:59:A:HIS:H	1:60:A:LEU:HD12	14	0.11
(1,271)	1:59:A:HIS:H	1:60:A:LEU:HD13	14	0.11
(1,268)	1:59:A:HIS:H	1:58:A:LEU:H	8	0.11
(1,251)	1:56:A:LYS:H	1:56:A:LYS:HG2	5	0.11
(1,251)	1:56:A:LYS:H	1:56:A:LYS:HG3	5	0.11
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD11	9	0.11
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD12	9	0.11
(1,243)	1:56:A:LYS:H	1:29:A:LEU:HD13	9	0.11
(1,234)	1:52:A:HIS:H	1:52:A:HIS:HA	14	0.11
(1,234)	1:52:A:HIS:H	1:52:A:HIS:HA	15	0.11
(1,195)	1:46:A:PHE:H	1:17:A:ILE:HG21	1	0.11
(1,195)	1:46:A:PHE:H	1:17:A:ILE:HG22	1	0.11
(1,195)	1:46:A:PHE:H	1:17:A:ILE:HG23	1	0.11
(1,145)	1:32:A:VAL:H	1:31:A:CYS:HB2	5	0.11
(1,145)	1:32:A:VAL:H	1:31:A:CYS:HB3	5	0.11
(1,139)	1:31:A:CYS:H	1:31:A:CYS:HA	3	0.11
(1,83)	1:19:A:GLY:H	1:20:A:ALA:HA	15	0.11
(1,77)	1:18:A:ALA:H	1:18:A:ALA:HA	9	0.11
(1,74)	1:18:A:ALA:H	1:17:A:ILE:HG12	3	0.11
(1,71)	1:17:A:ILE:H	1:18:A:ALA:HA	1	0.11
(1,59)	1:14:A:ALA:H	1:14:A:ALA:HA	10	0.11
(1,22)	1:9:A:LYS:H	1:9:A:LYS:HG2	11	0.11
(1,22)	1:9:A:LYS:H	1:9:A:LYS:HG3	11	0.11
(1,639)	1:118:B:ASP:HB3	1:115:B:VAL:HA	12	0.1
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG11	8	0.1
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG12	8	0.1
(1,636)	1:92:B:CYS:HA	1:115:B:VAL:HG13	8	0.1
(1,635)	1:109:B:GLU:HB2	1:111:B:HIS:HD2	17	0.1
(1,628)	1:90:B:LEU:HA	1:107:B:PHE:HZ	4	0.1
(1,623)	1:78:B:ILE:HG12	1:107:B:PHE:HZ	17	0.1
(1,599)	1:74:B:CYS:HB2	1:78:B:ILE:HG21	5	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,599)	1:74:B:CYS:HB2	1:78:B:ILE:HG22	5	0.1
(1,599)	1:74:B:CYS:HB2	1:78:B:ILE:HG23	5	0.1
(1,599)	1:74:B:CYS:HB3	1:78:B:ILE:HG21	5	0.1
(1,599)	1:74:B:CYS:HB3	1:78:B:ILE:HG22	5	0.1
(1,599)	1:74:B:CYS:HB3	1:78:B:ILE:HG23	5	0.1
(1,597)	1:68:B:VAL:HA	1:71:B:LYS:HB2	9	0.1
(1,597)	1:68:B:VAL:HA	1:71:B:LYS:HB3	9	0.1
(1,587)	1:121:B:LEU:H	1:121:B:LEU:HA	9	0.1
(1,587)	1:121:B:LEU:H	1:121:B:LEU:HA	17	0.1
(1,549)	1:113:B:HIS:H	1:113:B:HIS:HA	3	0.1
(1,510)	1:107:B:PHE:H	1:78:B:ILE:HG21	6	0.1
(1,510)	1:107:B:PHE:H	1:78:B:ILE:HG22	6	0.1
(1,510)	1:107:B:PHE:H	1:78:B:ILE:HG23	6	0.1
(1,464)	1:93:B:VAL:H	1:93:B:VAL:HB	10	0.1
(1,439)	1:87:B:GLY:H	1:86:B:GLY:H	1	0.1
(1,432)	1:86:B:GLY:H	1:85:B:CYS:H	10	0.1
(1,431)	1:85:B:CYS:H	1:86:B:GLY:H	10	0.1
(1,392)	1:79:B:ALA:H	1:79:B:ALA:HA	6	0.1
(1,374)	1:75:B:ALA:H	1:75:B:ALA:HA	2	0.1
(1,329)	1:48:A:GLU:HA	1:61:A:CYS:HB3	8	0.1
(1,324)	1:57:A:ASP:HB3	1:54:A:VAL:HA	12	0.1
(1,320)	1:48:A:GLU:HB2	1:50:A:HIS:HD2	16	0.1
(1,319)	1:50:A:HIS:HD2	1:46:A:PHE:HZ	16	0.1
(1,314)	1:29:A:LEU:HD11	1:46:A:PHE:HZ	5	0.1
(1,314)	1:29:A:LEU:HD12	1:46:A:PHE:HZ	5	0.1
(1,314)	1:29:A:LEU:HD13	1:46:A:PHE:HZ	5	0.1
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE1	9	0.1
(1,307)	1:17:A:ILE:HG12	1:46:A:PHE:HE2	9	0.1
(1,287)	1:18:A:ALA:HA	1:21:A:VAL:HB	17	0.1
(1,284)	1:13:A:CYS:HB2	1:17:A:ILE:HG21	11	0.1
(1,284)	1:13:A:CYS:HB2	1:17:A:ILE:HG22	11	0.1
(1,284)	1:13:A:CYS:HB2	1:17:A:ILE:HG23	11	0.1
(1,284)	1:13:A:CYS:HB3	1:17:A:ILE:HG21	11	0.1
(1,284)	1:13:A:CYS:HB3	1:17:A:ILE:HG22	11	0.1
(1,284)	1:13:A:CYS:HB3	1:17:A:ILE:HG23	11	0.1
(1,273)	1:60:A:LEU:H	1:60:A:LEU:HB2	12	0.1
(1,272)	1:60:A:LEU:H	1:60:A:LEU:HA	3	0.1
(1,272)	1:60:A:LEU:H	1:60:A:LEU:HA	7	0.1
(1,269)	1:59:A:HIS:H	1:59:A:HIS:HA	15	0.1
(1,239)	1:55:A:CYS:H	1:52:A:HIS:H	4	0.1
(1,238)	1:52:A:HIS:H	1:55:A:CYS:H	4	0.1
(1,234)	1:52:A:HIS:H	1:52:A:HIS:HA	3	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,195)	1:46:A:PHE:H	1:17:A:ILE:HG21	10	0.1
(1,195)	1:46:A:PHE:H	1:17:A:ILE:HG22	10	0.1
(1,195)	1:46:A:PHE:H	1:17:A:ILE:HG23	10	0.1
(1,195)	1:46:A:PHE:H	1:17:A:ILE:HG21	11	0.1
(1,195)	1:46:A:PHE:H	1:17:A:ILE:HG22	11	0.1
(1,195)	1:46:A:PHE:H	1:17:A:ILE:HG23	11	0.1
(1,165)	1:34:A:ALA:H	1:33:A:LEU:HG	7	0.1
(1,145)	1:32:A:VAL:H	1:31:A:CYS:HB2	4	0.1
(1,145)	1:32:A:VAL:H	1:31:A:CYS:HB3	4	0.1
(1,145)	1:32:A:VAL:H	1:31:A:CYS:HB2	15	0.1
(1,145)	1:32:A:VAL:H	1:31:A:CYS:HB3	15	0.1
(1,140)	1:31:A:CYS:H	1:31:A:CYS:HB2	2	0.1
(1,140)	1:31:A:CYS:H	1:31:A:CYS:HB3	2	0.1
(1,140)	1:31:A:CYS:H	1:31:A:CYS:HB2	4	0.1
(1,140)	1:31:A:CYS:H	1:31:A:CYS:HB3	4	0.1
(1,59)	1:14:A:ALA:H	1:14:A:ALA:HA	2	0.1

10 Dihedral-angle violation analysis ⓘ

No dihedral-angle restraints found