



Full wwPDB NMR Structure Validation Report ⓘ

Mar 8, 2026 – 11:27 AM UTC

PDB ID : 9LBR / pdb_00009lbr
BMRB ID : 36723
Title : Response regulator RR468 mutant M56A
Authors : Liu, X.; Wang, D.; Liu, Y.; Jiang, L.
Deposited on : 2025-01-03

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
BMRB Restraints Analysis : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

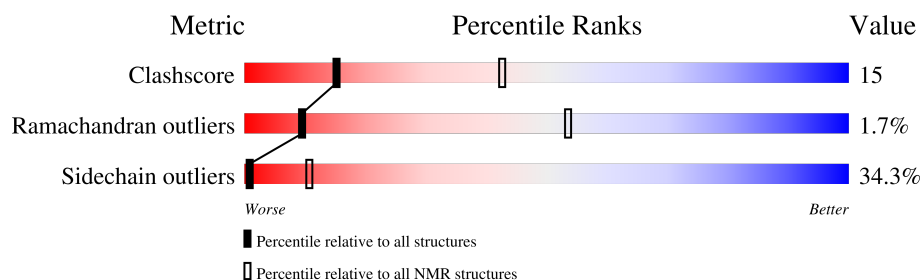
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 80%.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	122	<div> <div>46%</div> <div>40%</div> <div>7%</div> <div>7%</div> </div>

2 Ensemble composition and analysis

This entry contains 20 models. Model 13 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *target function*.

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:3-A:54, A:60-A:120 (113)	0.45	13

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

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

The models can be grouped into 3 clusters and 2 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1984 atoms, of which 1018 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Response regulator.

Mol	Chain	Residues	Atoms						Trace
1	A	122	Total	C	H	N	O	S	0
			1984	623	1018	157	182	4	

There is a discrepancy between the modelled and reference sequences:

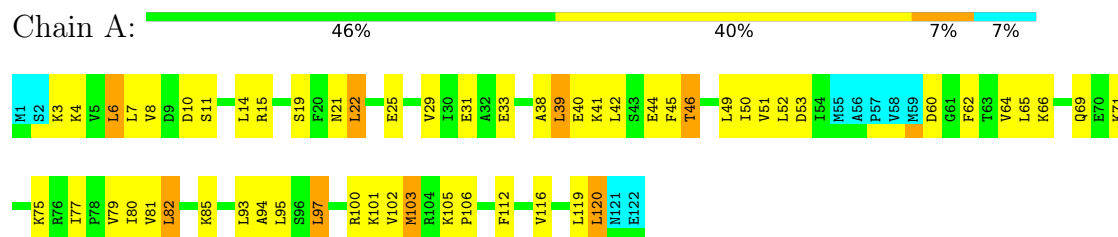
Chain	Residue	Modelled	Actual	Comment	Reference
A	56	ALA	MET	engineered mutation	UNP Q9WYT9

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: Response regulator

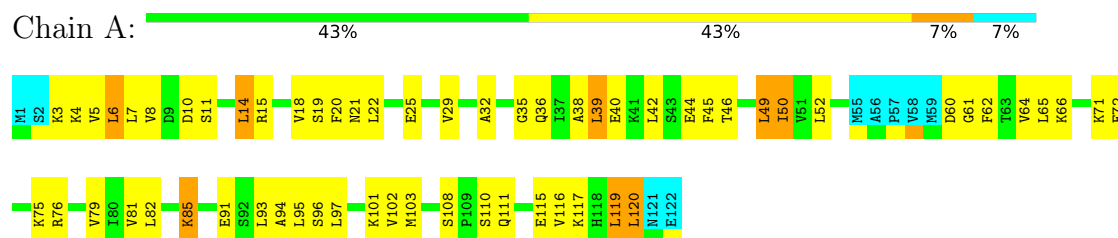


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

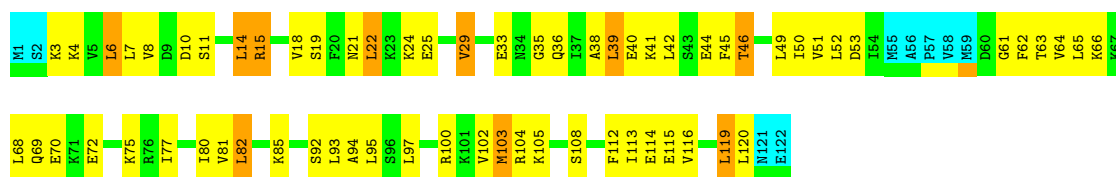
- Molecule 1: Response regulator



4.2.2 Score per residue for model 2

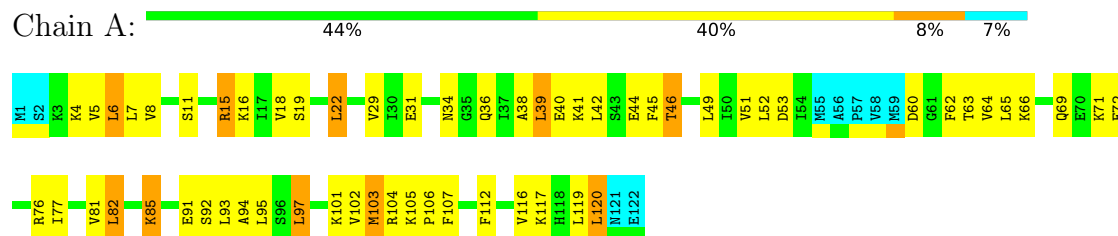
- Molecule 1: Response regulator





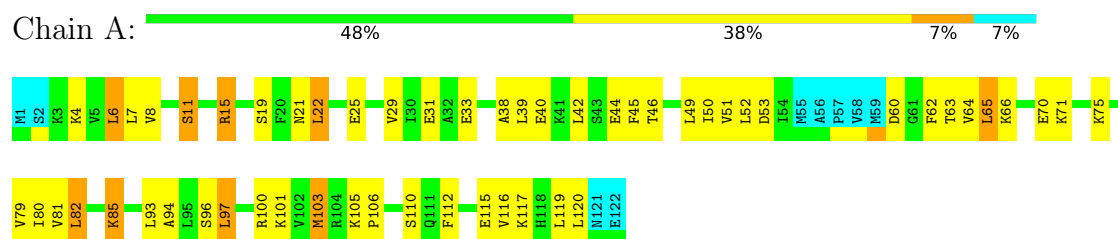
4.2.3 Score per residue for model 3

- Molecule 1: Response regulator



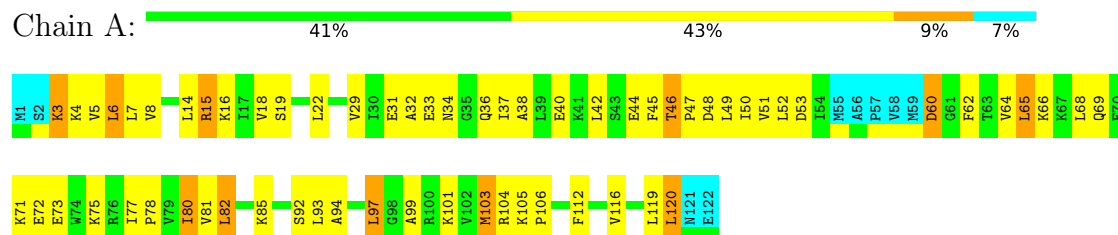
4.2.4 Score per residue for model 4

- Molecule 1: Response regulator



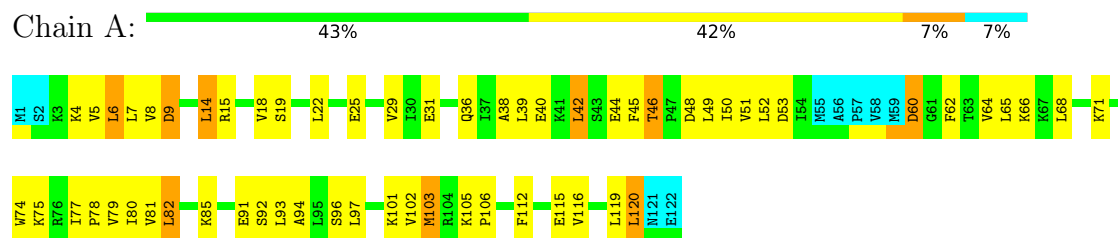
4.2.5 Score per residue for model 5

- Molecule 1: Response regulator



4.2.6 Score per residue for model 6

- Molecule 1: Response regulator



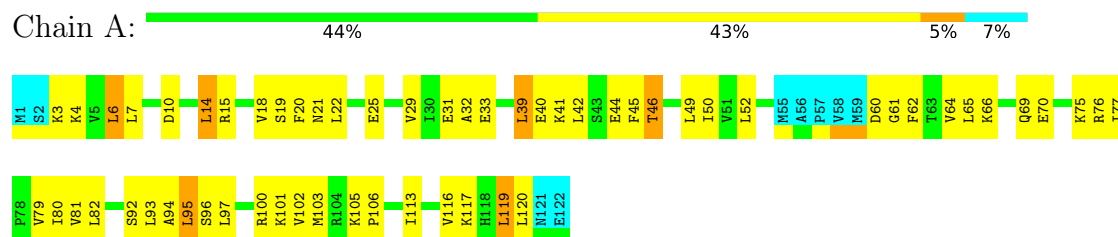
4.2.7 Score per residue for model 7

- Molecule 1: Response regulator



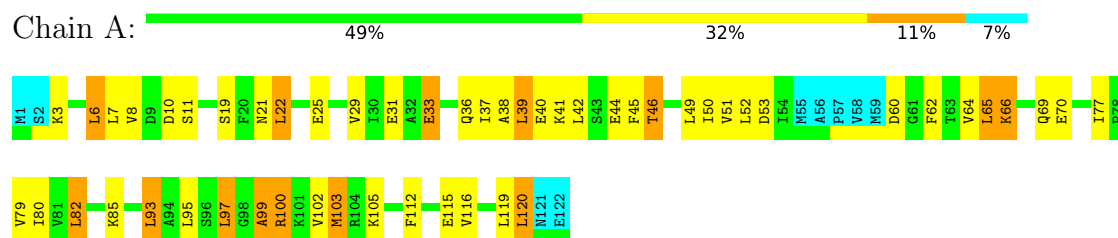
4.2.8 Score per residue for model 8

- Molecule 1: Response regulator



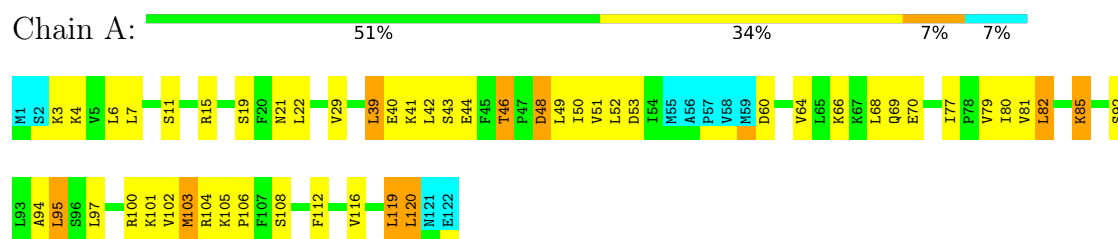
4.2.9 Score per residue for model 9

- Molecule 1: Response regulator



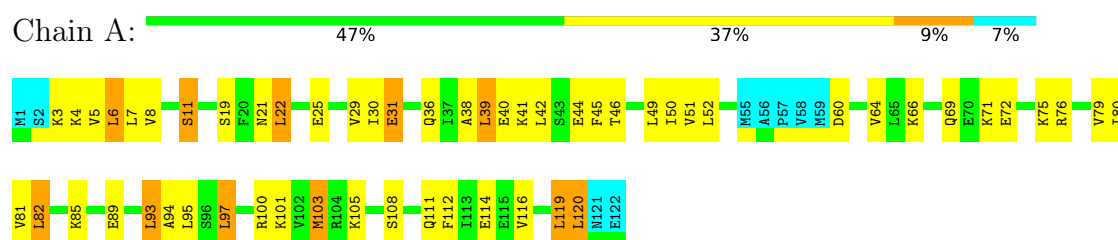
4.2.10 Score per residue for model 10

- Molecule 1: Response regulator



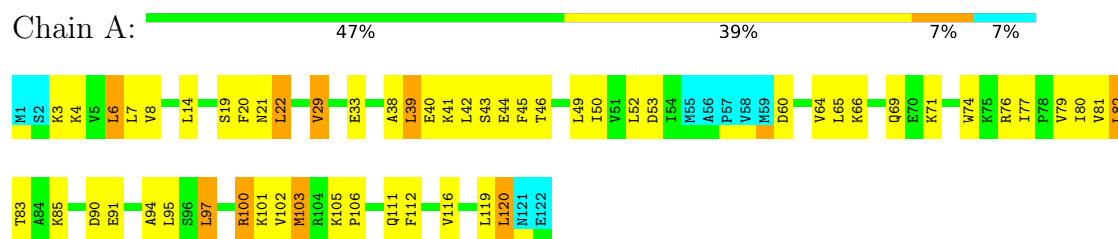
4.2.11 Score per residue for model 11

- Molecule 1: Response regulator



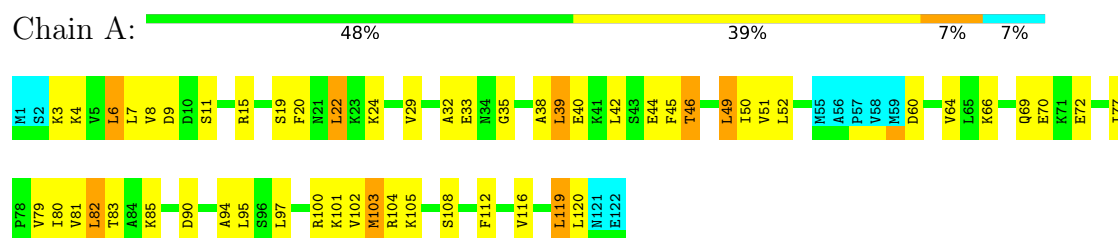
4.2.12 Score per residue for model 12

- Molecule 1: Response regulator



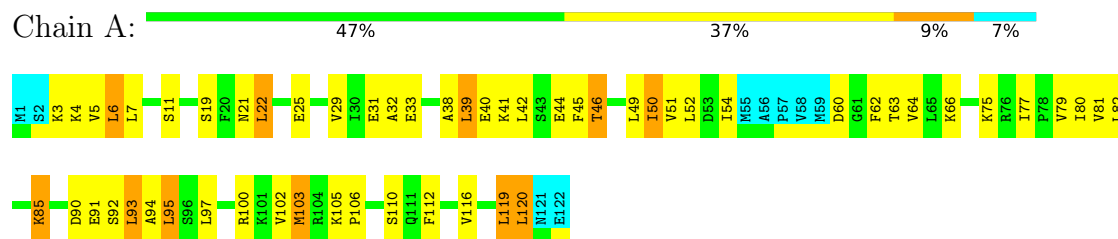
4.2.13 Score per residue for model 13 (medoid)

- Molecule 1: Response regulator



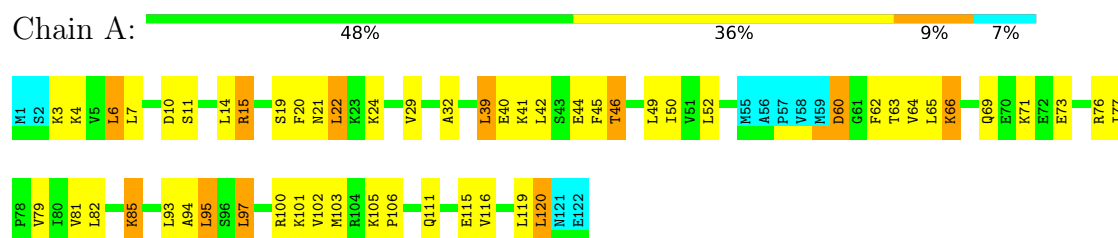
4.2.14 Score per residue for model 14

- Molecule 1: Response regulator



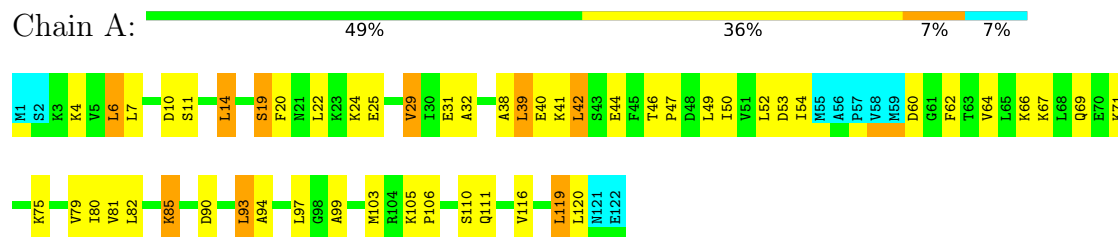
4.2.15 Score per residue for model 15

- Molecule 1: Response regulator



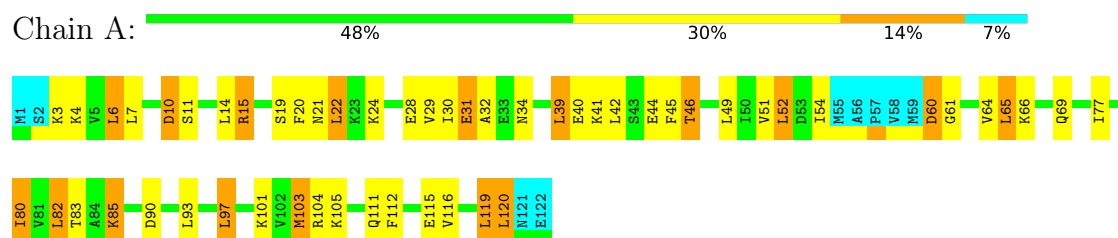
4.2.16 Score per residue for model 16

- Molecule 1: Response regulator



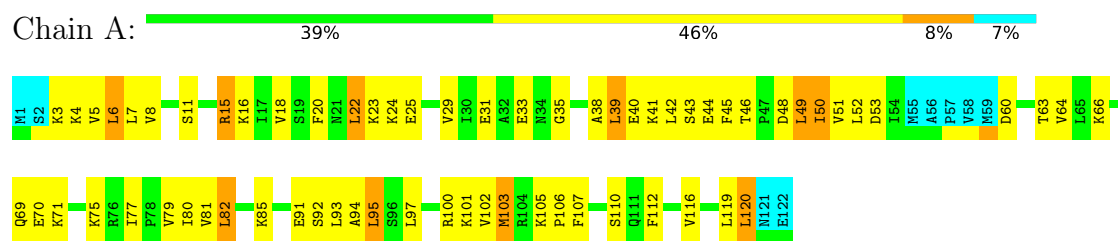
4.2.17 Score per residue for model 17

- Molecule 1: Response regulator



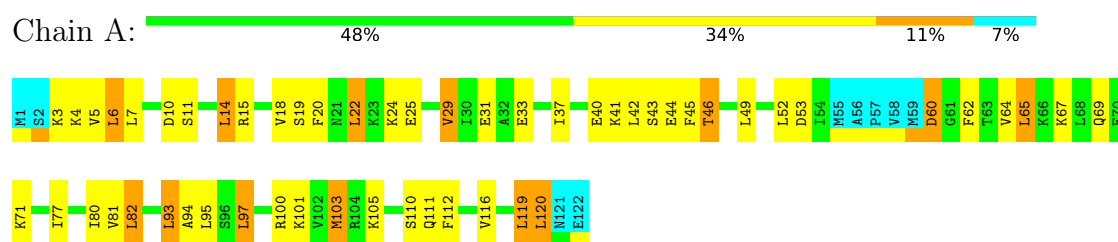
4.2.18 Score per residue for model 18

- Molecule 1: Response regulator



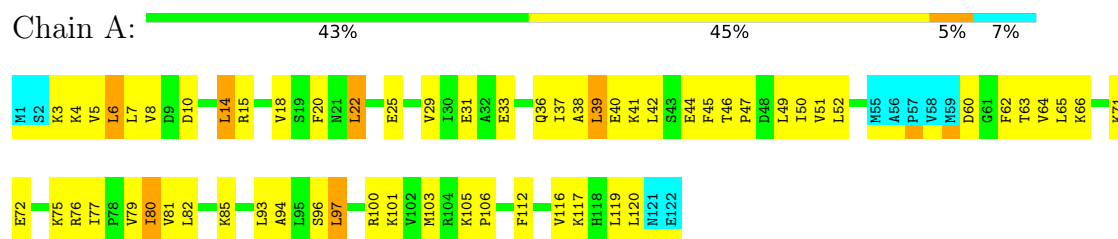
4.2.19 Score per residue for model 19

- Molecule 1: Response regulator



4.2.20 Score per residue for model 20

- Molecule 1: Response regulator



5 Refinement protocol and experimental data overview

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

Of the 200 calculated structures, 20 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
CNS	refinement	
CYANA	structure calculation	

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	1351
Number of shifts mapped to atoms	1351
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	80%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts [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	900	953	953	28±4
All	All	18000	19060	19060	552

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 15.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:46:THR:HG22	1:A:77:ILE:HD11	1.01	1.32	2	12
1:A:80:ILE:HD11	1:A:119:LEU:HD22	0.86	1.47	8	7
1:A:49:LEU:HD11	1:A:80:ILE:HD11	0.85	1.49	9	1
1:A:81:VAL:HG21	1:A:94:ALA:HB1	0.84	1.49	3	17
1:A:39:LEU:HD12	1:A:64:VAL:HG22	0.79	1.54	20	11
1:A:22:LEU:HD11	1:A:116:VAL:HG11	0.76	1.58	9	17
1:A:49:LEU:HD22	1:A:120:LEU:HD12	0.76	1.55	9	9
1:A:7:LEU:HD12	1:A:7:LEU:O	0.69	1.87	17	5
1:A:7:LEU:HD13	1:A:15:ARG:HD3	0.68	1.66	19	4
1:A:5:VAL:HG21	1:A:22:LEU:HD12	0.68	1.66	6	1
1:A:80:ILE:HD11	1:A:119:LEU:HD13	0.66	1.65	13	6
1:A:6:LEU:HD12	1:A:45:PHE:CZ	0.66	2.26	4	18
1:A:49:LEU:HD22	1:A:116:VAL:HG13	0.66	1.66	17	7
1:A:62:PHE:CZ	1:A:93:LEU:HD23	0.64	2.27	15	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:39:LEU:CD1	1:A:64:VAL:HG22	0.64	2.22	1	16
1:A:39:LEU:HD12	1:A:64:VAL:HG13	0.64	1.67	13	4
1:A:7:LEU:HD13	1:A:9:ASP:OD2	0.63	1.93	7	1
1:A:49:LEU:CD2	1:A:116:VAL:HG13	0.62	2.24	12	15
1:A:49:LEU:HD11	1:A:119:LEU:CD2	0.62	2.24	13	1
1:A:95:LEU:HD13	1:A:102:VAL:HB	0.61	1.71	13	4
1:A:49:LEU:HD12	1:A:78:PRO:O	0.61	1.94	5	2
1:A:5:VAL:HG22	1:A:120:LEU:HD11	0.61	1.71	1	2
1:A:50:ILE:CG2	1:A:79:VAL:HG22	0.61	2.25	9	9
1:A:50:ILE:HG23	1:A:79:VAL:HG13	0.61	1.72	6	7
1:A:39:LEU:HD13	1:A:64:VAL:HG22	0.61	1.71	17	4
1:A:65:LEU:CB	1:A:97:LEU:HD22	0.61	2.25	12	2
1:A:19:SER:HA	1:A:29:VAL:HG11	0.60	1.71	12	17
1:A:47:PRO:O	1:A:77:ILE:HD12	0.60	1.96	20	1
1:A:49:LEU:HD11	1:A:119:LEU:HD13	0.60	1.72	1	1
1:A:46:THR:HG22	1:A:77:ILE:CD1	0.60	2.26	15	12
1:A:48:ASP:C	1:A:77:ILE:HG23	0.60	2.21	18	2
1:A:54:ILE:HG21	1:A:90:ASP:CG	0.60	2.21	16	3
1:A:62:PHE:CD1	1:A:93:LEU:HD12	0.60	2.31	9	1
1:A:33:GLU:HB2	1:A:37:ILE:HD12	0.59	1.74	5	4
1:A:7:LEU:HD13	1:A:15:ARG:CD	0.59	2.28	17	5
1:A:80:ILE:CD1	1:A:119:LEU:HD13	0.59	2.28	14	6
1:A:49:LEU:HD11	1:A:80:ILE:HG13	0.59	1.75	5	6
1:A:95:LEU:HD22	1:A:102:VAL:CG1	0.58	2.29	3	4
1:A:53:ASP:OD1	1:A:82:LEU:HD21	0.58	1.97	9	6
1:A:51:VAL:HG11	1:A:112:PHE:CZ	0.58	2.33	2	8
1:A:3:LYS:NZ	1:A:120:LEU:HD22	0.58	2.13	5	1
1:A:48:ASP:OD1	1:A:120:LEU:HD11	0.58	1.99	5	1
1:A:82:LEU:HB2	1:A:103:MET:HE3	0.57	1.75	5	10
1:A:54:ILE:HG21	1:A:90:ASP:CB	0.57	2.30	17	3
1:A:7:LEU:HD23	1:A:29:VAL:CG1	0.56	2.31	4	7
1:A:48:ASP:HB3	1:A:120:LEU:HD21	0.56	1.76	7	2
1:A:21:ASN:CG	1:A:113:ILE:HD11	0.56	2.25	8	2
1:A:7:LEU:HD22	1:A:18:VAL:CG1	0.56	2.31	5	2
1:A:6:LEU:HG	1:A:30:ILE:HG23	0.56	1.76	11	1
1:A:5:VAL:CG2	1:A:120:LEU:HD11	0.55	2.30	18	4
1:A:65:LEU:HB3	1:A:97:LEU:HD22	0.55	1.78	19	3
1:A:81:VAL:HG21	1:A:94:ALA:CB	0.55	2.29	3	1
1:A:46:THR:CG2	1:A:77:ILE:HD11	0.55	2.31	19	3
1:A:5:VAL:HG11	1:A:49:LEU:HD23	0.55	1.79	3	2
1:A:49:LEU:HD11	1:A:80:ILE:CG1	0.55	2.32	5	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:74:TRP:O	1:A:77:ILE:HD12	0.54	2.01	12	1
1:A:49:LEU:HD11	1:A:119:LEU:HD22	0.54	1.78	13	1
1:A:80:ILE:CD1	1:A:119:LEU:HD22	0.54	2.33	17	2
1:A:49:LEU:HD11	1:A:119:LEU:HD23	0.54	1.79	18	1
1:A:3:LYS:HZ2	1:A:120:LEU:HD22	0.53	1.61	5	1
1:A:14:LEU:HD22	1:A:53:ASP:CG	0.53	2.28	16	1
1:A:48:ASP:O	1:A:77:ILE:HG23	0.53	2.02	18	1
1:A:7:LEU:O	1:A:32:ALA:HB3	0.53	2.02	17	8
1:A:48:ASP:OD1	1:A:120:LEU:HD21	0.53	2.04	5	1
1:A:65:LEU:HD21	1:A:99:ALA:CB	0.52	2.35	9	1
1:A:82:LEU:CB	1:A:103:MET:HE3	0.52	2.35	5	5
1:A:49:LEU:HD13	1:A:119:LEU:HD23	0.52	1.82	6	1
1:A:5:VAL:HG21	1:A:22:LEU:CD1	0.52	2.34	6	2
1:A:60:ASP:O	1:A:64:VAL:HG23	0.52	2.05	9	8
1:A:8:VAL:CG2	1:A:38:ALA:HB2	0.51	2.35	1	6
1:A:8:VAL:HG22	1:A:38:ALA:HB2	0.51	1.81	12	10
1:A:53:ASP:OD1	1:A:82:LEU:HD11	0.51	2.05	19	1
1:A:22:LEU:HD21	1:A:116:VAL:HG21	0.51	1.81	9	4
1:A:103:MET:HE1	1:A:112:PHE:CD1	0.51	2.41	12	3
1:A:80:ILE:CG1	1:A:119:LEU:HD22	0.51	2.36	4	1
1:A:7:LEU:HD13	1:A:15:ARG:NE	0.50	2.21	17	1
1:A:33:GLU:CB	1:A:37:ILE:HD12	0.50	2.36	9	2
1:A:7:LEU:HD21	1:A:19:SER:OG	0.50	2.06	4	2
1:A:32:ALA:HB1	1:A:38:ALA:HB2	0.50	1.82	16	3
1:A:5:VAL:CG1	1:A:49:LEU:HD23	0.49	2.37	3	2
1:A:22:LEU:CD1	1:A:116:VAL:HG11	0.49	2.33	12	4
1:A:14:LEU:HD22	1:A:53:ASP:OD1	0.49	2.07	2	1
1:A:52:LEU:HD21	1:A:61:GLY:HA2	0.49	1.85	17	1
1:A:80:ILE:HG12	1:A:119:LEU:HD22	0.49	1.83	12	2
1:A:91:GLU:HG2	1:A:102:VAL:HG21	0.49	1.84	6	2
1:A:14:LEU:HD22	1:A:15:ARG:NH2	0.49	2.22	8	1
1:A:6:LEU:HD13	1:A:42:LEU:HD12	0.49	1.83	16	1
1:A:74:TRP:HA	1:A:77:ILE:HD12	0.49	1.83	6	1
1:A:35:GLY:CA	1:A:64:VAL:HG21	0.48	2.38	13	4
1:A:6:LEU:HD12	1:A:47:PRO:HG3	0.48	1.84	16	1
1:A:65:LEU:HB3	1:A:97:LEU:HD23	0.48	1.85	17	2
1:A:62:PHE:CE1	1:A:93:LEU:HD12	0.48	2.44	9	2
1:A:7:LEU:HD23	1:A:29:VAL:HG12	0.48	1.84	12	2
1:A:95:LEU:HD22	1:A:102:VAL:HG12	0.48	1.85	2	4
1:A:32:ALA:CB	1:A:38:ALA:HB2	0.48	2.38	5	2
1:A:7:LEU:HD11	1:A:31:GLU:CG	0.48	2.38	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:19:SER:O	1:A:29:VAL:HG21	0.48	2.08	2	4
1:A:65:LEU:HD12	1:A:97:LEU:O	0.48	2.09	4	1
1:A:93:LEU:HD12	1:A:97:LEU:CD1	0.48	2.39	11	1
1:A:65:LEU:HD11	1:A:99:ALA:HA	0.47	1.87	7	2
1:A:14:LEU:HD22	1:A:15:ARG:HH21	0.47	1.69	19	4
1:A:61:GLY:C	1:A:65:LEU:HD12	0.47	2.35	1	3
1:A:7:LEU:HD11	1:A:15:ARG:HG3	0.47	1.87	4	6
1:A:49:LEU:HD23	1:A:116:VAL:HG13	0.47	1.86	6	1
1:A:50:ILE:CG2	1:A:79:VAL:HG13	0.47	2.38	6	1
1:A:22:LEU:HB3	1:A:29:VAL:HG22	0.47	1.87	10	4
1:A:54:ILE:HG21	1:A:90:ASP:HB3	0.46	1.85	14	1
1:A:7:LEU:HD11	1:A:31:GLU:HA	0.46	1.85	17	1
1:A:49:LEU:CD1	1:A:80:ILE:HD11	0.46	2.31	9	1
1:A:14:LEU:O	1:A:18:VAL:HG23	0.46	2.09	5	5
1:A:95:LEU:HD22	1:A:102:VAL:HG22	0.46	1.87	9	1
1:A:65:LEU:HD21	1:A:99:ALA:HA	0.46	1.87	7	1
1:A:49:LEU:CD1	1:A:119:LEU:HD22	0.46	2.40	14	2
1:A:91:GLU:HG3	1:A:102:VAL:HG21	0.46	1.86	1	1
1:A:66:LYS:HB3	1:A:97:LEU:HD21	0.45	1.89	15	3
1:A:7:LEU:HD13	1:A:15:ARG:HE	0.45	1.71	17	1
1:A:91:GLU:HA	1:A:102:VAL:HG21	0.45	1.87	18	1
1:A:54:ILE:HG13	1:A:83:THR:HG22	0.45	1.86	7	1
1:A:100:ARG:HB3	1:A:119:LEU:HD21	0.45	1.87	12	1
1:A:80:ILE:HD11	1:A:119:LEU:CD1	0.45	2.37	13	2
1:A:95:LEU:HD13	1:A:102:VAL:CB	0.45	2.42	2	4
1:A:62:PHE:CE2	1:A:93:LEU:HD23	0.45	2.47	4	2
1:A:93:LEU:HD12	1:A:97:LEU:HD12	0.45	1.87	19	2
1:A:18:VAL:HG22	1:A:107:PHE:CE2	0.44	2.47	3	2
1:A:7:LEU:HD11	1:A:31:GLU:CB	0.44	2.43	11	1
1:A:6:LEU:HD12	1:A:45:PHE:HZ	0.44	1.70	15	14
1:A:80:ILE:HD11	1:A:119:LEU:CD2	0.44	2.36	2	4
1:A:62:PHE:HA	1:A:97:LEU:HD13	0.44	1.90	4	4
1:A:68:LEU:C	1:A:68:LEU:HD23	0.44	2.38	6	3
1:A:51:VAL:HG11	1:A:112:PHE:HZ	0.44	1.73	9	10
1:A:65:LEU:HB2	1:A:97:LEU:HD22	0.44	1.89	15	2
1:A:62:PHE:CE1	1:A:93:LEU:HD23	0.44	2.48	8	1
1:A:39:LEU:CD1	1:A:64:VAL:HG13	0.43	2.40	13	2
1:A:7:LEU:C	1:A:7:LEU:HD12	0.43	2.38	15	5
1:A:49:LEU:HD22	1:A:120:LEU:CD1	0.43	2.44	4	1
1:A:4:LYS:H	1:A:48:ASP:CG	0.43	2.22	10	1
1:A:95:LEU:HD23	1:A:102:VAL:HB	0.43	1.91	18	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:50:ILE:HD12	1:A:51:VAL:H	0.43	1.74	7	2
1:A:5:VAL:HG13	1:A:49:LEU:O	0.43	2.13	11	1
1:A:14:LEU:HD23	1:A:18:VAL:HG23	0.43	1.90	19	2
1:A:8:VAL:HG22	1:A:38:ALA:CB	0.43	2.44	5	1
1:A:65:LEU:CD2	1:A:79:VAL:HG11	0.42	2.43	7	1
1:A:6:LEU:HD13	1:A:42:LEU:CD1	0.42	2.44	16	1
1:A:14:LEU:HD23	1:A:18:VAL:CG2	0.42	2.44	20	3
1:A:49:LEU:CD1	1:A:119:LEU:HD23	0.42	2.45	4	1
1:A:53:ASP:OD2	1:A:82:LEU:HD21	0.42	2.14	5	1
1:A:7:LEU:HD22	1:A:18:VAL:HG12	0.42	1.90	6	1
1:A:95:LEU:HD11	1:A:102:VAL:CG1	0.42	2.44	1	1
1:A:50:ILE:HG21	1:A:68:LEU:CD1	0.42	2.45	5	1
1:A:53:ASP:OD2	1:A:82:LEU:HD11	0.42	2.15	6	1
1:A:95:LEU:HG	1:A:102:VAL:HG13	0.42	1.91	8	3
1:A:6:LEU:O	1:A:50:ILE:HD12	0.41	2.15	5	1
1:A:91:GLU:CG	1:A:102:VAL:HG21	0.41	2.45	14	1
1:A:28:GLU:O	1:A:30:ILE:HD12	0.41	2.14	17	1
1:A:50:ILE:HD12	1:A:51:VAL:N	0.41	2.30	7	1
1:A:39:LEU:HD11	1:A:64:VAL:HG22	0.41	1.92	1	1
1:A:47:PRO:O	1:A:77:ILE:HD13	0.41	2.16	5	1
1:A:53:ASP:CG	1:A:82:LEU:HD21	0.41	2.41	2	1
1:A:65:LEU:HD21	1:A:99:ALA:HB2	0.41	1.92	5	1
1:A:7:LEU:HD13	1:A:9:ASP:OD1	0.41	2.15	6	1
1:A:54:ILE:CG1	1:A:83:THR:HG22	0.41	2.45	17	1
1:A:6:LEU:HD13	1:A:42:LEU:CD2	0.40	2.45	6	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	113/122 (93%)	103±2 (91±1%)	8±2 (7±2%)	2±1 (2±1%)	9	53
All	All	2260/2440 (93%)	2057 (91%)	165 (7%)	38 (2%)	9	53

All 6 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	85	LYS	15
1	A	106	PRO	13
1	A	11	SER	4
1	A	99	ALA	3
1	A	100	ARG	2
1	A	60	ASP	1

6.3.2 Protein sidechains [i](#)

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	101/109 (93%)	66±3 (66±3%)	35±3 (34±3%)	1	11
All	All	2020/2180 (93%)	1327 (66%)	693 (34%)	1	11

All 69 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	6	LEU	20
1	A	40	GLU	20
1	A	42	LEU	20
1	A	44	GLU	20
1	A	46	THR	20
1	A	82	LEU	20
1	A	97	LEU	20
1	A	103	MET	20
1	A	52	LEU	19
1	A	66	LYS	19
1	A	120	LEU	19
1	A	105	LYS	19
1	A	4	LYS	18
1	A	3	LYS	16
1	A	39	LEU	16
1	A	101	LYS	16
1	A	60	ASP	15
1	A	69	GLN	15
1	A	119	LEU	14
1	A	22	LEU	14

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Mol	Chain	Res	Type	Models (Total)
1	A	41	LYS	14
1	A	100	ARG	14
1	A	31	GLU	14
1	A	11	SER	13
1	A	25	GLU	13
1	A	71	LYS	13
1	A	85	LYS	12
1	A	14	LEU	11
1	A	75	LYS	11
1	A	10	ASP	10
1	A	20	PHE	10
1	A	93	LEU	10
1	A	15	ARG	10
1	A	21	ASN	9
1	A	36	GLN	9
1	A	33	GLU	9
1	A	76	ARG	8
1	A	70	GLU	8
1	A	92	SER	8
1	A	65	LEU	8
1	A	72	GLU	7
1	A	110	SER	7
1	A	111	GLN	7
1	A	115	GLU	7
1	A	24	LYS	7
1	A	63	THR	7
1	A	104	ARG	7
1	A	95	LEU	7
1	A	96	SER	5
1	A	108	SER	5
1	A	117	LYS	5
1	A	29	VAL	5
1	A	50	ILE	4
1	A	16	LYS	4
1	A	80	ILE	4
1	A	43	SER	4
1	A	49	LEU	3
1	A	34	ASN	3
1	A	9	ASP	3
1	A	114	GLU	2
1	A	91	GLU	2
1	A	73	GLU	2

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Mol	Chain	Res	Type	Models (Total)
1	A	19	SER	2
1	A	48	ASP	2
1	A	83	THR	2
1	A	90	ASP	2
1	A	67	LYS	2
1	A	89	GLU	1
1	A	23	LYS	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 80% for the well-defined parts and 78% for the entire structure.

7.1 Chemical shift list 1

File name: `working_cs.cif`

Chemical shift list name: *starch_output*

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	1351
Number of shifts mapped to atoms	1351
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	118	2.31 ± 0.08	Should be checked
$^{13}\text{C}_\beta$	112	2.59 ± 0.10	Should be checked
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	106	0.59 ± 0.29	Should be applied

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 80%, i.e. 1293 atoms were assigned a chemical shift out of a possible 1616. 0 out of 27 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	435/563 (77%)	221/228 (97%)	111/226 (49%)	103/109 (94%)
Sidechain	844/975 (87%)	577/634 (91%)	267/310 (86%)	0/31 (0%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	14/78 (18%)	14/39 (36%)	0/37 (0%)	0/2 (0%)
Overall	1293/1616 (80%)	812/901 (90%)	378/573 (66%)	103/142 (73%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 78%, i.e. 1351 atoms were assigned a chemical shift out of a possible 1729. 0 out of 28 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	455/606 (75%)	231/245 (94%)	118/244 (48%)	106/117 (91%)
Sidechain	882/1045 (84%)	603/681 (89%)	279/332 (84%)	0/32 (0%)
Aromatic	14/78 (18%)	14/39 (36%)	0/37 (0%)	0/2 (0%)
Overall	1351/1729 (78%)	848/965 (88%)	397/613 (65%)	106/151 (70%)

7.1.4 Statistically unusual chemical shifts [i](#)

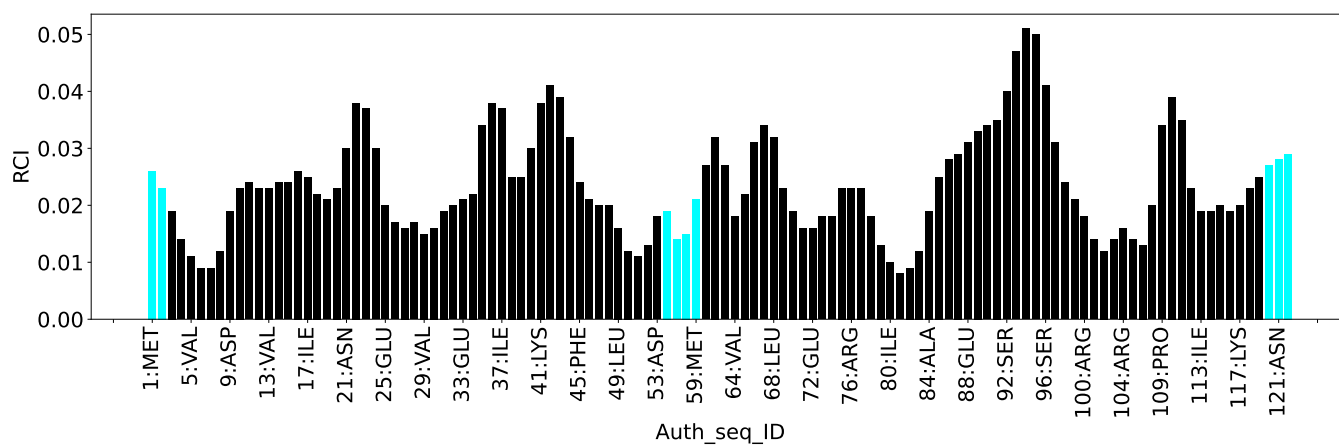
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	71	LYS	HD3	0.07	0.54 – 2.65	-7.2
1	A	71	LYS	HD2	0.22	0.58 – 2.64	-6.8

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	2086
Intra-residue ($ i-j =0$)	1076
Sequential ($ i-j =1$)	452
Medium range ($ i-j >1$ and $ i-j <5$)	183
Long range ($ i-j \geq 5$)	249
Inter-chain	0
Hydrogen bond restraints	126
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	17.1
Number of long range restraints per residue ¹	2.4

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)	31.0	0.2
0.2-0.5 (Medium)	2.2	0.35
>0.5 (Large)	None	None

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

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

9 Distance violation analysis ⓘ

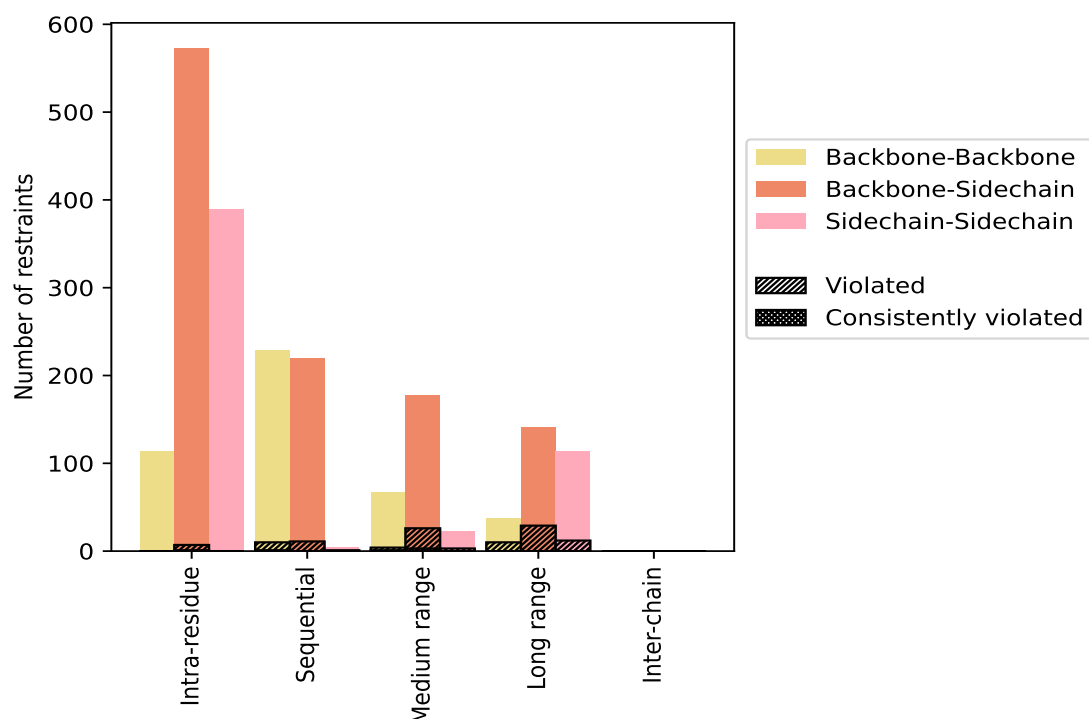
9.1 Summary of distance violations ⓘ

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

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue ($i-j =0$)	1076	51.6	7	0.7	0.3	1	0.1	0.0
Backbone-Backbone	114	5.5	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	573	27.5	7	1.2	0.3	1	0.2	0.0
Sidechain-Sidechain	389	18.6	0	0.0	0.0	0	0.0	0.0
Sequential ($i-j =1$)	452	21.7	22	4.9	1.1	1	0.2	0.0
Backbone-Backbone	229	11.0	10	4.4	0.5	1	0.4	0.0
Backbone-Sidechain	219	10.5	11	5.0	0.5	0	0.0	0.0
Sidechain-Sidechain	4	0.2	1	25.0	0.0	0	0.0	0.0
Medium range ($i-j >1$ & $i-j <5$)	183	8.8	21	11.5	1.0	2	1.1	0.1
Backbone-Backbone	67	3.2	4	6.0	0.2	1	1.5	0.0
Backbone-Sidechain	93	4.5	14	15.1	0.7	1	1.1	0.0
Sidechain-Sidechain	23	1.1	3	13.0	0.1	0	0.0	0.0
Long range ($i-j \geq 5$)	249	11.9	38	15.3	1.8	0	0.0	0.0
Backbone-Backbone	37	1.8	10	27.0	0.5	0	0.0	0.0
Backbone-Sidechain	99	4.7	16	16.2	0.8	0	0.0	0.0
Sidechain-Sidechain	113	5.4	12	10.6	0.6	0	0.0	0.0
Inter-chain	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Hydrogen bond	126	6.0	25	19.8	1.2	2	1.6	0.1
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	2086	100.0	113	5.4	5.4	6	0.3	0.3
Backbone-Backbone	447	21.4	24	5.4	1.2	2	0.4	0.1
Backbone-Sidechain	1110	53.2	73	6.6	3.5	4	0.4	0.2
Sidechain-Sidechain	529	25.4	16	3.0	0.8	0	0.0	0.0

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

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



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

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

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

Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
1	3	8	16	17	0	44	0.15	0.29	0.04	0.14
2	2	5	10	12	0	29	0.14	0.25	0.03	0.13
3	3	6	14	10	0	33	0.14	0.29	0.04	0.12
4	3	5	16	15	0	39	0.13	0.25	0.03	0.12
5	2	6	12	10	0	30	0.14	0.29	0.04	0.12
6	1	5	9	8	0	23	0.14	0.29	0.05	0.14
7	3	5	13	13	0	34	0.14	0.34	0.05	0.13
8	6	8	13	18	0	45	0.14	0.23	0.03	0.13
9	3	6	16	15	0	40	0.14	0.31	0.04	0.13
10	2	5	10	8	0	25	0.15	0.27	0.04	0.14

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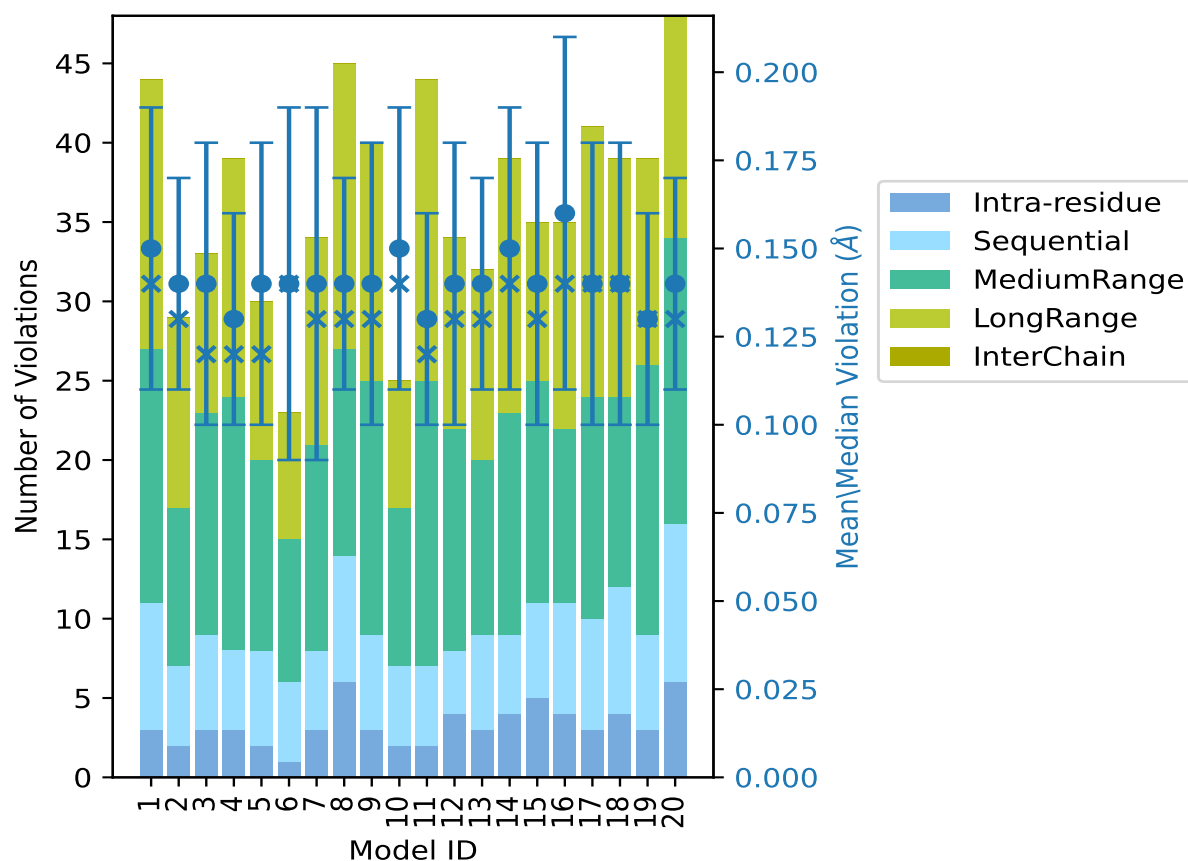
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	2	5	18	19	0	44	0.13	0.26	0.03	0.12
12	4	4	14	12	0	34	0.14	0.28	0.04	0.13
13	3	6	11	12	0	32	0.14	0.28	0.03	0.13
14	4	5	14	16	0	39	0.15	0.35	0.04	0.14
15	5	6	14	10	0	35	0.14	0.27	0.04	0.13
16	4	7	11	13	0	35	0.16	0.29	0.05	0.14
17	3	7	14	17	0	41	0.14	0.31	0.04	0.14
18	4	8	12	15	0	39	0.14	0.24	0.04	0.14
19	3	6	17	13	0	39	0.13	0.24	0.03	0.13
20	6	10	18	14	0	48	0.14	0.21	0.03	0.13

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

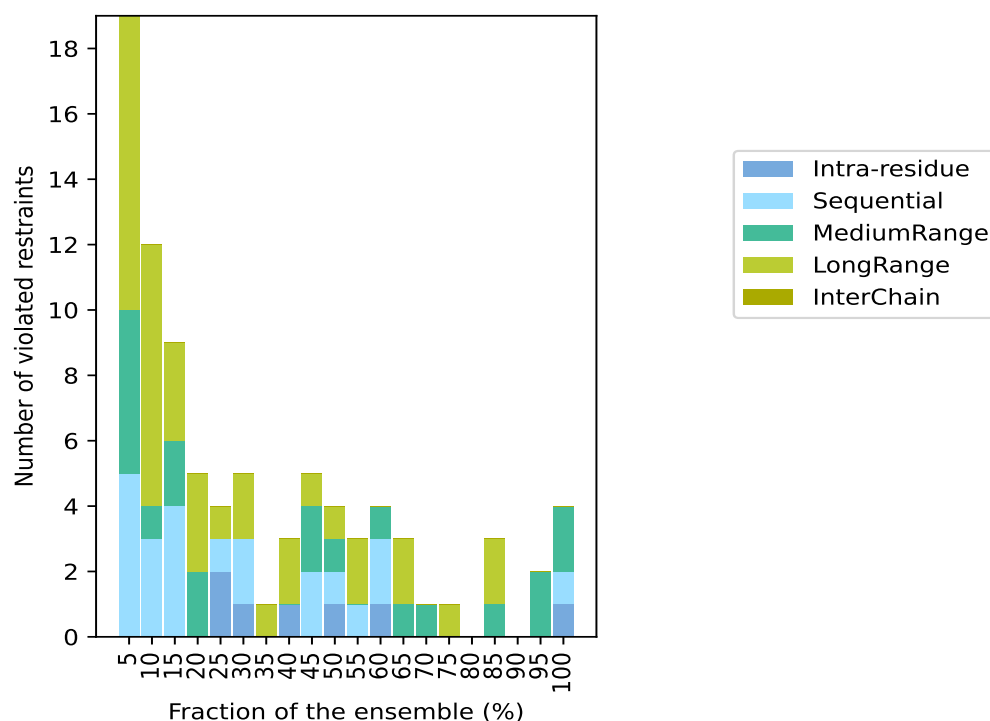
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 1872(IR:1069, SQ:430, MR:162, LR:211, IC:0) restraints are not violated in the ensemble.

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

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

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

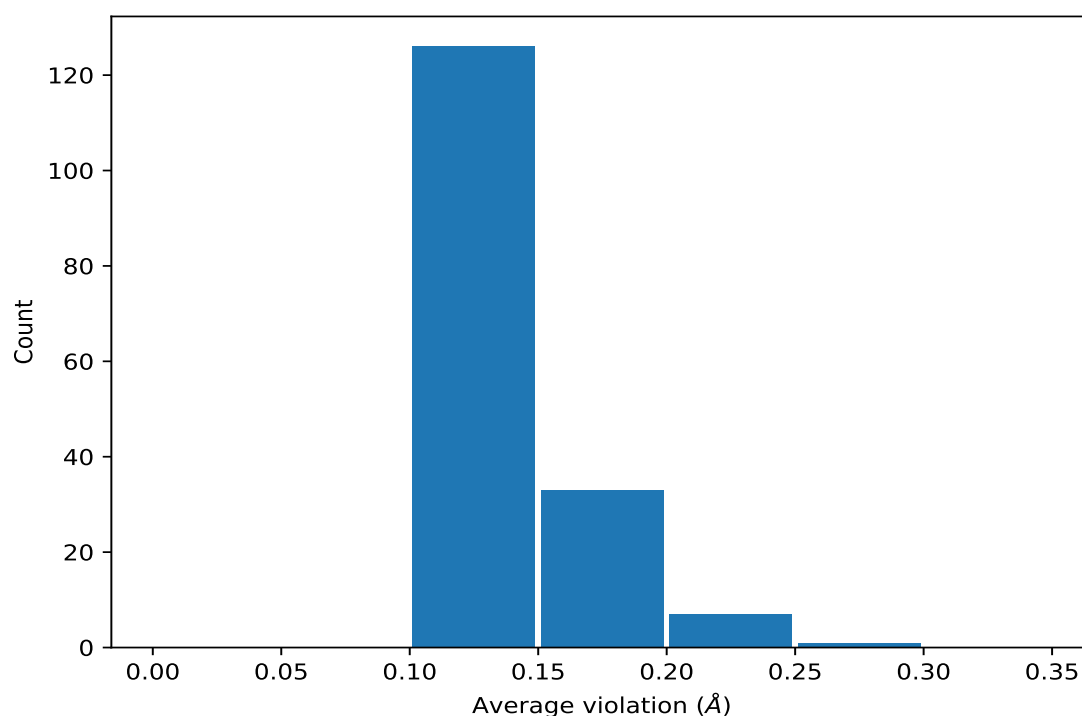
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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

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

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



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

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

Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,1554)	1:42:A:LEU:HB3	1:45:A:PHE:H	20	0.17	0.01	0.17
(1,825)	1:84:A:ALA:HA	1:87:A:GLY:H	20	0.15	0.02	0.15
(1,801)	1:62:A:PHE:H	1:62:A:PHE:HZ	20	0.15	0.02	0.15
(2,81)	1:63:A:THR:O	1:67:A:LYS:H	20	0.15	0.02	0.15
(1,157)	1:84:A:ALA:HA	1:85:A:LYS:H	20	0.13	0.01	0.13
(2,67)	1:36:A:GLN:O	1:40:A:GLU:H	20	0.12	0.01	0.12
(1,1535)	1:42:A:LEU:HD21	1:45:A:PHE:H	19	0.16	0.01	0.15
(1,1535)	1:42:A:LEU:HD22	1:45:A:PHE:H	19	0.16	0.01	0.15
(1,1535)	1:42:A:LEU:HD23	1:45:A:PHE:H	19	0.16	0.01	0.15
(1,592)	1:41:A:LYS:HA	1:44:A:GLU:HB2	19	0.12	0.01	0.12
(2,87)	1:71:A:LYS:O	1:74:A:TRP:H	19	0.12	0.01	0.11
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB1	17	0.18	0.04	0.18
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB2	17	0.18	0.04	0.18
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB3	17	0.18	0.04	0.18
(1,611)	1:82:A:LEU:HD11	1:103:A:MET:HG3	17	0.15	0.04	0.13
(1,611)	1:82:A:LEU:HD12	1:103:A:MET:HG3	17	0.15	0.04	0.13

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,611)	1:82:A:LEU:HD13	1:103:A:MET:HG3	17	0.15	0.04	0.13
(2,107)	1:94:A:ALA:O	1:99:A:ALA:H	17	0.13	0.02	0.13
(1,591)	1:41:A:LYS:HA	1:44:A:GLU:HB3	17	0.12	0.02	0.11
(1,427)	1:4:A:LYS:H	1:49:A:LEU:H	15	0.16	0.03	0.15
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD11	14	0.14	0.02	0.13
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD12	14	0.14	0.02	0.13
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD13	14	0.14	0.02	0.13
(1,552)	1:81:A:VAL:H	1:103:A:MET:H	13	0.17	0.04	0.16
(1,434)	1:50:A:ILE:H	1:79:A:VAL:HA	13	0.15	0.03	0.14
(1,1257)	1:71:A:LYS:HD3	1:74:A:TRP:H	13	0.11	0.01	0.11
(1,500)	1:80:A:ILE:HD11	1:81:A:VAL:H	12	0.24	0.06	0.24
(1,500)	1:80:A:ILE:HD12	1:81:A:VAL:H	12	0.24	0.06	0.24
(1,500)	1:80:A:ILE:HD13	1:81:A:VAL:H	12	0.24	0.06	0.24
(1,267)	1:6:A:LEU:HB3	1:7:A:LEU:H	12	0.13	0.02	0.13
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE1	12	0.12	0.02	0.12
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE2	12	0.12	0.02	0.12
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE1	12	0.12	0.02	0.12
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE2	12	0.12	0.02	0.12
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE1	12	0.12	0.02	0.12
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE2	12	0.12	0.02	0.12
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD11	12	0.11	0.01	0.11
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD12	12	0.11	0.01	0.11
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD13	12	0.11	0.01	0.11
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG11	11	0.21	0.05	0.21
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG12	11	0.21	0.05	0.21
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG13	11	0.21	0.05	0.21
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB1	11	0.19	0.08	0.17
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB2	11	0.19	0.08	0.17
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB3	11	0.19	0.08	0.17
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB1	11	0.19	0.08	0.17
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB2	11	0.19	0.08	0.17
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB3	11	0.19	0.08	0.17
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB1	11	0.19	0.08	0.17
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB2	11	0.19	0.08	0.17
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB3	11	0.19	0.08	0.17
(2,1)	1:3:A:LYS:O	1:28:A:GLU:H	11	0.19	0.01	0.19
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD11	11	0.13	0.02	0.13
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD12	11	0.13	0.02	0.13
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD13	11	0.13	0.02	0.13
(1,372)	1:5:A:VAL:H	1:28:A:GLU:H	10	0.13	0.02	0.13
(1,67)	1:34:A:ASN:HA	1:35:A:GLY:H	10	0.13	0.02	0.12
(1,1091)	1:113:A:ILE:H	1:116:A:VAL:HB	10	0.12	0.02	0.12

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,753)	1:67:A:LYS:H	1:67:A:LYS:HG2	10	0.12	0.01	0.12
(1,51)	1:26:A:GLY:HA3	1:27:A:TYR:H	9	0.26	0.02	0.25
(1,255)	1:5:A:VAL:H	1:27:A:TYR:HB2	9	0.16	0.02	0.16
(1,376)	1:27:A:TYR:HD1	1:28:A:GLU:H	9	0.15	0.03	0.16
(1,376)	1:27:A:TYR:HD2	1:28:A:GLU:H	9	0.15	0.03	0.16
(1,361)	1:24:A:LYS:HA	1:26:A:GLY:H	9	0.13	0.02	0.13
(1,357)	1:23:A:LYS:HB2	1:26:A:GLY:H	9	0.13	0.01	0.13
(1,357)	1:23:A:LYS:HB3	1:26:A:GLY:H	9	0.13	0.01	0.13
(2,31)	1:79:A:VAL:O	1:101:A:LYS:H	9	0.12	0.02	0.12
(2,45)	1:13:A:VAL:O	1:17:A:ILE:H	8	0.16	0.04	0.16
(1,870)	1:20:A:PHE:H	1:20:A:PHE:HD1	8	0.14	0.02	0.15
(1,870)	1:20:A:PHE:H	1:20:A:PHE:HD2	8	0.14	0.02	0.15
(1,1861)	1:82:A:LEU:HB2	1:104:A:ARG:HA	8	0.12	0.02	0.12
(1,1349)	1:68:A:LEU:HD21	1:74:A:TRP:H	8	0.12	0.01	0.12
(1,1349)	1:68:A:LEU:HD22	1:74:A:TRP:H	8	0.12	0.01	0.12
(1,1349)	1:68:A:LEU:HD23	1:74:A:TRP:H	8	0.12	0.01	0.12
(2,13)	1:7:A:LEU:O	1:32:A:ALA:H	7	0.15	0.07	0.12
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD11	7	0.12	0.01	0.12
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD12	7	0.12	0.01	0.12
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD13	7	0.12	0.01	0.12
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD11	7	0.12	0.01	0.12
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD12	7	0.12	0.01	0.12
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD13	7	0.12	0.01	0.12
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD11	7	0.12	0.01	0.12
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD12	7	0.12	0.01	0.12
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD13	7	0.12	0.01	0.12
(1,272)	1:7:A:LEU:HB3	1:8:A:VAL:H	6	0.14	0.02	0.15
(1,508)	1:52:A:LEU:HB2	1:82:A:LEU:H	6	0.14	0.02	0.15
(1,1328)	1:22:A:LEU:HA	1:27:A:TYR:H	6	0.14	0.01	0.15
(1,24)	1:13:A:VAL:H	1:14:A:LEU:H	6	0.12	0.02	0.11
(1,709)	1:74:A:TRP:H	1:74:A:TRP:HE3	6	0.12	0.01	0.12
(2,75)	1:60:A:ASP:O	1:64:A:VAL:H	6	0.11	0.01	0.11
(2,46)	1:13:A:VAL:O	1:17:A:ILE:N	5	0.16	0.03	0.16
(1,261)	1:6:A:LEU:H	1:47:A:PRO:HG3	5	0.13	0.03	0.11
(2,51)	1:16:A:LYS:O	1:20:A:PHE:H	5	0.12	0.02	0.12
(1,880)	1:50:A:ILE:H	1:50:A:ILE:HD11	5	0.12	0.01	0.12
(1,880)	1:50:A:ILE:H	1:50:A:ILE:HD12	5	0.12	0.01	0.12
(1,880)	1:50:A:ILE:H	1:50:A:ILE:HD13	5	0.12	0.01	0.12
(1,744)	1:80:A:ILE:H	1:80:A:ILE:HD11	5	0.12	0.01	0.11
(1,744)	1:80:A:ILE:H	1:80:A:ILE:HD12	5	0.12	0.01	0.11
(1,744)	1:80:A:ILE:H	1:80:A:ILE:HD13	5	0.12	0.01	0.11
(1,161)	1:86:A:GLY:HA2	1:87:A:GLY:H	5	0.11	0.01	0.11

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,283)	1:9:A:ASP:H	1:15:A:ARG:HD3	4	0.2	0.01	0.2
(2,39)	1:83:A:THR:O	1:105:A:LYS:H	4	0.14	0.03	0.14
(1,553)	1:83:A:THR:H	1:103:A:MET:H	4	0.14	0.02	0.14
(1,1721)	1:21:A:ASN:HB3	1:107:A:PHE:HE1	4	0.14	0.02	0.13
(1,1721)	1:21:A:ASN:HB3	1:107:A:PHE:HE2	4	0.14	0.02	0.13
(1,1194)	1:3:A:LYS:HG2	1:5:A:VAL:H	4	0.13	0.02	0.12
(1,1194)	1:3:A:LYS:HG3	1:5:A:VAL:H	4	0.13	0.02	0.12
(1,1609)	1:67:A:LYS:HA	1:71:A:LYS:HE3	4	0.11	0.0	0.11
(1,1491)	1:113:A:ILE:HG13	1:114:A:GLU:H	3	0.13	0.0	0.13
(1,256)	1:5:A:VAL:H	1:27:A:TYR:HB3	3	0.13	0.02	0.13
(1,15)	1:9:A:ASP:HA	1:10:A:ASP:H	3	0.12	0.0	0.12
(1,351)	1:24:A:LYS:HB2	1:25:A:GLU:H	3	0.12	0.0	0.12
(1,430)	1:47:A:PRO:HA	1:49:A:LEU:H	3	0.12	0.0	0.12
(2,19)	1:9:A:ASP:H	1:32:A:ALA:O	3	0.12	0.01	0.12
(2,7)	1:6:A:LEU:H	1:49:A:LEU:O	3	0.12	0.0	0.12
(2,21)	1:50:A:ILE:H	1:78:A:PRO:O	3	0.12	0.0	0.12
(2,27)	1:52:A:LEU:O	1:82:A:LEU:H	3	0.12	0.01	0.11
(1,572)	1:18:A:VAL:HG11	1:51:A:VAL:HG11	3	0.11	0.01	0.11
(1,572)	1:18:A:VAL:HG11	1:51:A:VAL:HG12	3	0.11	0.01	0.11
(1,572)	1:18:A:VAL:HG11	1:51:A:VAL:HG13	3	0.11	0.01	0.11
(1,572)	1:18:A:VAL:HG12	1:51:A:VAL:HG11	3	0.11	0.01	0.11
(1,572)	1:18:A:VAL:HG12	1:51:A:VAL:HG12	3	0.11	0.01	0.11
(1,572)	1:18:A:VAL:HG12	1:51:A:VAL:HG13	3	0.11	0.01	0.11
(1,572)	1:18:A:VAL:HG13	1:51:A:VAL:HG11	3	0.11	0.01	0.11
(1,572)	1:18:A:VAL:HG13	1:51:A:VAL:HG12	3	0.11	0.01	0.11
(1,572)	1:18:A:VAL:HG13	1:51:A:VAL:HG13	3	0.11	0.01	0.11
(1,474)	1:71:A:LYS:CD	1:74:A:TRP:CZ2	3	0.11	0.0	0.11
(1,3)	1:3:A:LYS:HA	1:4:A:LYS:H	3	0.11	0.01	0.1
(1,542)	1:80:A:ILE:HA	1:101:A:LYS:H	3	0.1	0.0	0.1
(1,284)	1:9:A:ASP:H	1:15:A:ARG:HD2	2	0.16	0.01	0.16
(1,1802)	1:56:A:ALA:HB1	1:59:A:MET:HA	2	0.14	0.02	0.14
(1,1802)	1:56:A:ALA:HB2	1:59:A:MET:HA	2	0.14	0.02	0.14
(1,1802)	1:56:A:ALA:HB3	1:59:A:MET:HA	2	0.14	0.02	0.14
(1,765)	1:81:A:VAL:HG21	1:82:A:LEU:H	2	0.13	0.02	0.13
(1,765)	1:81:A:VAL:HG22	1:82:A:LEU:H	2	0.13	0.02	0.13
(1,765)	1:81:A:VAL:HG23	1:82:A:LEU:H	2	0.13	0.02	0.13
(1,1722)	1:14:A:LEU:HD21	1:82:A:LEU:HD11	2	0.12	0.0	0.12
(1,1722)	1:14:A:LEU:HD21	1:82:A:LEU:HD12	2	0.12	0.0	0.12
(1,1722)	1:14:A:LEU:HD21	1:82:A:LEU:HD13	2	0.12	0.0	0.12
(1,1722)	1:14:A:LEU:HD22	1:82:A:LEU:HD11	2	0.12	0.0	0.12
(1,1722)	1:14:A:LEU:HD22	1:82:A:LEU:HD12	2	0.12	0.0	0.12
(1,1722)	1:14:A:LEU:HD22	1:82:A:LEU:HD13	2	0.12	0.0	0.12

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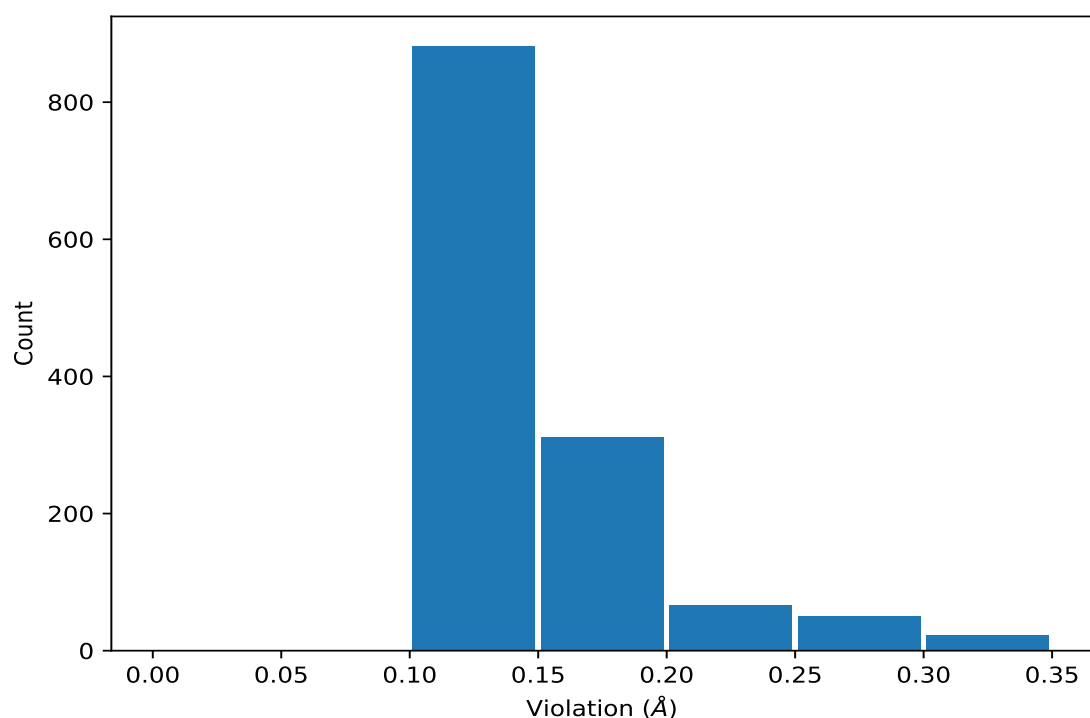
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,1722)	1:14:A:LEU:HD23	1:82:A:LEU:HD11	2	0.12	0.0	0.12
(1,1722)	1:14:A:LEU:HD23	1:82:A:LEU:HD12	2	0.12	0.0	0.12
(1,1722)	1:14:A:LEU:HD23	1:82:A:LEU:HD13	2	0.12	0.0	0.12
(2,11)	1:7:A:LEU:H	1:30:A:ILE:O	2	0.12	0.01	0.12
(1,114)	1:61:A:GLY:H	1:62:A:PHE:H	2	0.12	0.02	0.12
(1,274)	1:8:A:VAL:H	1:51:A:VAL:HB	2	0.12	0.02	0.12
(1,540)	1:80:A:ILE:HG21	1:101:A:LYS:H	2	0.12	0.02	0.12
(1,540)	1:80:A:ILE:HG22	1:101:A:LYS:H	2	0.12	0.02	0.12
(1,540)	1:80:A:ILE:HG23	1:101:A:LYS:H	2	0.12	0.02	0.12
(1,1484)	1:80:A:ILE:HD11	1:116:A:VAL:H	2	0.12	0.02	0.12
(1,1484)	1:80:A:ILE:HD12	1:116:A:VAL:H	2	0.12	0.02	0.12
(1,1484)	1:80:A:ILE:HD13	1:116:A:VAL:H	2	0.12	0.02	0.12
(1,251)	1:4:A:LYS:HB2	1:5:A:VAL:H	2	0.12	0.0	0.12
(1,1506)	1:95:A:LEU:HD21	1:102:A:VAL:HG21	2	0.12	0.0	0.12
(1,1506)	1:95:A:LEU:HD21	1:102:A:VAL:HG22	2	0.12	0.0	0.12
(1,1506)	1:95:A:LEU:HD21	1:102:A:VAL:HG23	2	0.12	0.0	0.12
(1,1506)	1:95:A:LEU:HD22	1:102:A:VAL:HG21	2	0.12	0.0	0.12
(1,1506)	1:95:A:LEU:HD22	1:102:A:VAL:HG22	2	0.12	0.0	0.12
(1,1506)	1:95:A:LEU:HD22	1:102:A:VAL:HG23	2	0.12	0.0	0.12
(1,1506)	1:95:A:LEU:HD23	1:102:A:VAL:HG21	2	0.12	0.0	0.12
(1,1506)	1:95:A:LEU:HD23	1:102:A:VAL:HG22	2	0.12	0.0	0.12
(1,1506)	1:95:A:LEU:HD23	1:102:A:VAL:HG23	2	0.12	0.0	0.12
(1,371)	1:4:A:LYS:HA	1:28:A:GLU:H	2	0.11	0.0	0.11
(1,1888)	1:82:A:LEU:HA	1:103:A:MET:HB3	2	0.11	0.0	0.11
(2,49)	1:15:A:ARG:O	1:19:A:SER:H	2	0.11	0.0	0.11

¹Number of violated models, ²Standard deviation

9.5 All violated distance restraints [i](#)

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

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



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

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

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,500)	1:80:A:ILE:HD11	1:81:A:VAL:H	14	0.35
(1,500)	1:80:A:ILE:HD12	1:81:A:VAL:H	14	0.35
(1,500)	1:80:A:ILE:HD13	1:81:A:VAL:H	14	0.35
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB1	7	0.34
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB2	7	0.34
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB3	7	0.34
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB1	7	0.34
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB2	7	0.34
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB3	7	0.34
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB1	7	0.34
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB2	7	0.34
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB3	7	0.34
(2,13)	1:7:A:LEU:O	1:32:A:ALA:H	17	0.31
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB1	9	0.31
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB2	9	0.31
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB3	9	0.31

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB1	9	0.31
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB2	9	0.31
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB3	9	0.31
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB1	9	0.31
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB2	9	0.31
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB3	9	0.31
(1,611)	1:82:A:LEU:HD11	1:103:A:MET:HG3	16	0.29
(1,611)	1:82:A:LEU:HD12	1:103:A:MET:HG3	16	0.29
(1,611)	1:82:A:LEU:HD13	1:103:A:MET:HG3	16	0.29
(1,500)	1:80:A:ILE:HD11	1:81:A:VAL:H	1	0.29
(1,500)	1:80:A:ILE:HD12	1:81:A:VAL:H	1	0.29
(1,500)	1:80:A:ILE:HD13	1:81:A:VAL:H	1	0.29
(1,500)	1:80:A:ILE:HD11	1:81:A:VAL:H	3	0.29
(1,500)	1:80:A:ILE:HD12	1:81:A:VAL:H	3	0.29
(1,500)	1:80:A:ILE:HD13	1:81:A:VAL:H	3	0.29
(1,51)	1:26:A:GLY:HA3	1:27:A:TYR:H	5	0.29
(1,51)	1:26:A:GLY:HA3	1:27:A:TYR:H	6	0.29
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB1	16	0.28
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB2	16	0.28
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB3	16	0.28
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB1	16	0.28
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB2	16	0.28
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB3	16	0.28
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB1	16	0.28
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB2	16	0.28
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB3	16	0.28
(1,500)	1:80:A:ILE:HD11	1:81:A:VAL:H	12	0.28
(1,500)	1:80:A:ILE:HD12	1:81:A:VAL:H	12	0.28
(1,500)	1:80:A:ILE:HD13	1:81:A:VAL:H	12	0.28
(1,500)	1:80:A:ILE:HD11	1:81:A:VAL:H	16	0.28
(1,500)	1:80:A:ILE:HD12	1:81:A:VAL:H	16	0.28
(1,500)	1:80:A:ILE:HD13	1:81:A:VAL:H	16	0.28
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG11	13	0.28
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG12	13	0.28
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG13	13	0.28
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB1	16	0.27
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB2	16	0.27
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB3	16	0.27
(1,500)	1:80:A:ILE:HD11	1:81:A:VAL:H	9	0.27
(1,500)	1:80:A:ILE:HD12	1:81:A:VAL:H	9	0.27
(1,500)	1:80:A:ILE:HD13	1:81:A:VAL:H	9	0.27
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG11	15	0.27

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG12	15	0.27
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG13	15	0.27
(1,51)	1:26:A:GLY:HA3	1:27:A:TYR:H	10	0.27
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG11	11	0.26
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG12	11	0.26
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG13	11	0.26
(1,51)	1:26:A:GLY:HA3	1:27:A:TYR:H	7	0.26
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB1	1	0.25
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB2	1	0.25
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB3	1	0.25
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG11	4	0.25
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG12	4	0.25
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG13	4	0.25
(1,51)	1:26:A:GLY:HA3	1:27:A:TYR:H	1	0.25
(1,51)	1:26:A:GLY:HA3	1:27:A:TYR:H	2	0.25
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB1	6	0.24
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB2	6	0.24
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB3	6	0.24
(1,552)	1:81:A:VAL:H	1:103:A:MET:H	19	0.24
(1,434)	1:50:A:ILE:H	1:79:A:VAL:HA	18	0.24
(1,51)	1:26:A:GLY:HA3	1:27:A:TYR:H	16	0.24
(1,552)	1:81:A:VAL:H	1:103:A:MET:H	2	0.23
(1,51)	1:26:A:GLY:HA3	1:27:A:TYR:H	8	0.23
(1,1803)	1:49:A:LEU:HB3	1:120:A:LEU:HB2	5	0.22
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB1	18	0.22
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB2	18	0.22
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB3	18	0.22
(1,500)	1:80:A:ILE:HD11	1:81:A:VAL:H	15	0.22
(1,500)	1:80:A:ILE:HD12	1:81:A:VAL:H	15	0.22
(1,500)	1:80:A:ILE:HD13	1:81:A:VAL:H	15	0.22
(1,427)	1:4:A:LYS:H	1:49:A:LEU:H	12	0.22
(1,51)	1:26:A:GLY:HA3	1:27:A:TYR:H	17	0.22
(2,45)	1:13:A:VAL:O	1:17:A:ILE:H	1	0.21
(2,1)	1:3:A:LYS:O	1:28:A:GLU:H	11	0.21
(1,552)	1:81:A:VAL:H	1:103:A:MET:H	13	0.21
(1,500)	1:80:A:ILE:HD11	1:81:A:VAL:H	4	0.21
(1,500)	1:80:A:ILE:HD12	1:81:A:VAL:H	4	0.21
(1,500)	1:80:A:ILE:HD13	1:81:A:VAL:H	4	0.21
(1,500)	1:80:A:ILE:HD11	1:81:A:VAL:H	20	0.21
(1,500)	1:80:A:ILE:HD12	1:81:A:VAL:H	20	0.21
(1,500)	1:80:A:ILE:HD13	1:81:A:VAL:H	20	0.21
(1,434)	1:50:A:ILE:H	1:79:A:VAL:HA	5	0.21

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,427)	1:4:A:LYS:H	1:49:A:LEU:H	11	0.21
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG11	9	0.21
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG12	9	0.21
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG13	9	0.21
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG11	18	0.21
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG12	18	0.21
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG13	18	0.21
(1,283)	1:9:A:ASP:H	1:15:A:ARG:HD3	8	0.21
(1,283)	1:9:A:ASP:H	1:15:A:ARG:HD3	20	0.21
(2,45)	1:13:A:VAL:O	1:17:A:ILE:H	8	0.2
(2,1)	1:3:A:LYS:O	1:28:A:GLU:H	4	0.2
(2,1)	1:3:A:LYS:O	1:28:A:GLU:H	18	0.2
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB1	14	0.2
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB2	14	0.2
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB3	14	0.2
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB1	14	0.2
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB2	14	0.2
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB3	14	0.2
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB1	14	0.2
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB2	14	0.2
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB3	14	0.2
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB1	18	0.2
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB2	18	0.2
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB3	18	0.2
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB1	18	0.2
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB2	18	0.2
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB3	18	0.2
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB1	18	0.2
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB2	18	0.2
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB3	18	0.2
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB1	15	0.2
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB2	15	0.2
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB3	15	0.2
(1,611)	1:82:A:LEU:HD11	1:103:A:MET:HG3	8	0.2
(1,611)	1:82:A:LEU:HD12	1:103:A:MET:HG3	8	0.2
(1,611)	1:82:A:LEU:HD13	1:103:A:MET:HG3	8	0.2
(1,500)	1:80:A:ILE:HD11	1:81:A:VAL:H	17	0.2
(1,500)	1:80:A:ILE:HD12	1:81:A:VAL:H	17	0.2
(1,500)	1:80:A:ILE:HD13	1:81:A:VAL:H	17	0.2
(2,46)	1:13:A:VAL:O	1:17:A:ILE:N	1	0.19
(2,1)	1:3:A:LYS:O	1:28:A:GLU:H	9	0.19
(2,1)	1:3:A:LYS:O	1:28:A:GLU:H	14	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,1)	1:3:A:LYS:O	1:28:A:GLU:H	15	0.19
(1,1554)	1:42:A:LEU:HB3	1:45:A:PHE:H	7	0.19
(1,1554)	1:42:A:LEU:HB3	1:45:A:PHE:H	17	0.19
(1,801)	1:62:A:PHE:H	1:62:A:PHE:HZ	6	0.19
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB1	12	0.19
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB2	12	0.19
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB3	12	0.19
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB1	17	0.19
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB2	17	0.19
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB3	17	0.19
(1,611)	1:82:A:LEU:HD11	1:103:A:MET:HG3	9	0.19
(1,611)	1:82:A:LEU:HD12	1:103:A:MET:HG3	9	0.19
(1,611)	1:82:A:LEU:HD13	1:103:A:MET:HG3	9	0.19
(1,500)	1:80:A:ILE:HD11	1:81:A:VAL:H	18	0.19
(1,500)	1:80:A:ILE:HD12	1:81:A:VAL:H	18	0.19
(1,500)	1:80:A:ILE:HD13	1:81:A:VAL:H	18	0.19
(1,427)	1:4:A:LYS:H	1:49:A:LEU:H	20	0.19
(1,376)	1:27:A:TYR:HD1	1:28:A:GLU:H	7	0.19
(1,376)	1:27:A:TYR:HD2	1:28:A:GLU:H	7	0.19
(1,376)	1:27:A:TYR:HD1	1:28:A:GLU:H	10	0.19
(1,376)	1:27:A:TYR:HD2	1:28:A:GLU:H	10	0.19
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG11	3	0.19
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG12	3	0.19
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG13	3	0.19
(1,283)	1:9:A:ASP:H	1:15:A:ARG:HD3	1	0.19
(1,283)	1:9:A:ASP:H	1:15:A:ARG:HD3	19	0.19
(1,255)	1:5:A:VAL:H	1:27:A:TYR:HB2	10	0.19
(2,81)	1:63:A:THR:O	1:67:A:LYS:H	13	0.18
(2,46)	1:13:A:VAL:O	1:17:A:ILE:N	8	0.18
(2,45)	1:13:A:VAL:O	1:17:A:ILE:H	19	0.18
(2,45)	1:13:A:VAL:O	1:17:A:ILE:H	20	0.18
(2,39)	1:83:A:THR:O	1:105:A:LYS:H	7	0.18
(2,13)	1:7:A:LEU:O	1:32:A:ALA:H	1	0.18
(2,1)	1:3:A:LYS:O	1:28:A:GLU:H	3	0.18
(2,1)	1:3:A:LYS:O	1:28:A:GLU:H	13	0.18
(2,1)	1:3:A:LYS:O	1:28:A:GLU:H	19	0.18
(1,1554)	1:42:A:LEU:HB3	1:45:A:PHE:H	5	0.18
(1,1554)	1:42:A:LEU:HB3	1:45:A:PHE:H	9	0.18
(1,1554)	1:42:A:LEU:HB3	1:45:A:PHE:H	10	0.18
(1,1554)	1:42:A:LEU:HB3	1:45:A:PHE:H	11	0.18
(1,1554)	1:42:A:LEU:HB3	1:45:A:PHE:H	12	0.18
(1,1554)	1:42:A:LEU:HB3	1:45:A:PHE:H	15	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1554)	1:42:A:LEU:HB3	1:45:A:PHE:H	18	0.18
(1,1535)	1:42:A:LEU:HD21	1:45:A:PHE:H	5	0.18
(1,1535)	1:42:A:LEU:HD22	1:45:A:PHE:H	5	0.18
(1,1535)	1:42:A:LEU:HD23	1:45:A:PHE:H	5	0.18
(1,825)	1:84:A:ALA:HA	1:87:A:GLY:H	1	0.18
(1,825)	1:84:A:ALA:HA	1:87:A:GLY:H	18	0.18
(1,801)	1:62:A:PHE:H	1:62:A:PHE:HZ	17	0.18
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE1	16	0.18
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE2	16	0.18
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE1	16	0.18
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE2	16	0.18
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE1	16	0.18
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE2	16	0.18
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB1	4	0.18
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB2	4	0.18
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB3	4	0.18
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB1	14	0.18
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB2	14	0.18
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB3	14	0.18
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD11	16	0.18
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD12	16	0.18
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD13	16	0.18
(1,434)	1:50:A:ILE:H	1:79:A:VAL:HA	16	0.18
(1,427)	1:4:A:LYS:H	1:49:A:LEU:H	3	0.18
(1,427)	1:4:A:LYS:H	1:49:A:LEU:H	18	0.18
(1,376)	1:27:A:TYR:HD1	1:28:A:GLU:H	16	0.18
(1,376)	1:27:A:TYR:HD2	1:28:A:GLU:H	16	0.18
(1,361)	1:24:A:LYS:HA	1:26:A:GLY:H	20	0.18
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG11	14	0.18
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG12	14	0.18
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG13	14	0.18
(1,272)	1:7:A:LEU:HB3	1:8:A:VAL:H	15	0.18
(2,107)	1:94:A:ALA:O	1:99:A:ALA:H	12	0.17
(2,81)	1:63:A:THR:O	1:67:A:LYS:H	7	0.17
(2,81)	1:63:A:THR:O	1:67:A:LYS:H	10	0.17
(2,67)	1:36:A:GLN:O	1:40:A:GLU:H	6	0.17
(2,39)	1:83:A:THR:O	1:105:A:LYS:H	16	0.17
(2,31)	1:79:A:VAL:O	1:101:A:LYS:H	14	0.17
(2,1)	1:3:A:LYS:O	1:28:A:GLU:H	12	0.17
(1,1891)	1:82:A:LEU:HA	1:104:A:ARG:HA	16	0.17
(1,1721)	1:21:A:ASN:HB3	1:107:A:PHE:HE1	17	0.17
(1,1721)	1:21:A:ASN:HB3	1:107:A:PHE:HE2	17	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1554)	1:42:A:LEU:HB3	1:45:A:PHE:H	2	0.17
(1,1554)	1:42:A:LEU:HB3	1:45:A:PHE:H	3	0.17
(1,1554)	1:42:A:LEU:HB3	1:45:A:PHE:H	4	0.17
(1,1554)	1:42:A:LEU:HB3	1:45:A:PHE:H	14	0.17
(1,1554)	1:42:A:LEU:HB3	1:45:A:PHE:H	16	0.17
(1,1554)	1:42:A:LEU:HB3	1:45:A:PHE:H	19	0.17
(1,1554)	1:42:A:LEU:HB3	1:45:A:PHE:H	20	0.17
(1,1535)	1:42:A:LEU:HD21	1:45:A:PHE:H	10	0.17
(1,1535)	1:42:A:LEU:HD22	1:45:A:PHE:H	10	0.17
(1,1535)	1:42:A:LEU:HD23	1:45:A:PHE:H	10	0.17
(1,1535)	1:42:A:LEU:HD21	1:45:A:PHE:H	11	0.17
(1,1535)	1:42:A:LEU:HD22	1:45:A:PHE:H	11	0.17
(1,1535)	1:42:A:LEU:HD23	1:45:A:PHE:H	11	0.17
(1,870)	1:20:A:PHE:H	1:20:A:PHE:HD1	12	0.17
(1,870)	1:20:A:PHE:H	1:20:A:PHE:HD2	12	0.17
(1,825)	1:84:A:ALA:HA	1:87:A:GLY:H	3	0.17
(1,825)	1:84:A:ALA:HA	1:87:A:GLY:H	6	0.17
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB1	1	0.17
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB2	1	0.17
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB3	1	0.17
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB1	1	0.17
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB2	1	0.17
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB3	1	0.17
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB1	1	0.17
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB2	1	0.17
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB3	1	0.17
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB1	3	0.17
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB2	3	0.17
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB3	3	0.17
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB1	5	0.17
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB2	5	0.17
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB3	5	0.17
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD11	15	0.17
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD12	15	0.17
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD13	15	0.17
(1,552)	1:81:A:VAL:H	1:103:A:MET:H	10	0.17
(1,552)	1:81:A:VAL:H	1:103:A:MET:H	17	0.17
(1,427)	1:4:A:LYS:H	1:49:A:LEU:H	10	0.17
(1,427)	1:4:A:LYS:H	1:49:A:LEU:H	15	0.17
(1,376)	1:27:A:TYR:HD1	1:28:A:GLU:H	17	0.17
(1,376)	1:27:A:TYR:HD2	1:28:A:GLU:H	17	0.17
(1,372)	1:5:A:VAL:H	1:28:A:GLU:H	11	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,361)	1:24:A:LYS:HA	1:26:A:GLY:H	14	0.17
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG11	17	0.17
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG12	17	0.17
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG13	17	0.17
(1,284)	1:9:A:ASP:H	1:15:A:ARG:HD2	14	0.17
(1,267)	1:6:A:LEU:HB3	1:7:A:LEU:H	17	0.17
(1,261)	1:6:A:LEU:H	1:47:A:PRO:HG3	10	0.17
(1,255)	1:5:A:VAL:H	1:27:A:TYR:HB2	5	0.17
(1,255)	1:5:A:VAL:H	1:27:A:TYR:HB2	16	0.17
(1,24)	1:13:A:VAL:H	1:14:A:LEU:H	14	0.17
(2,107)	1:94:A:ALA:O	1:99:A:ALA:H	6	0.16
(2,81)	1:63:A:THR:O	1:67:A:LYS:H	1	0.16
(2,81)	1:63:A:THR:O	1:67:A:LYS:H	6	0.16
(2,81)	1:63:A:THR:O	1:67:A:LYS:H	11	0.16
(2,81)	1:63:A:THR:O	1:67:A:LYS:H	12	0.16
(2,81)	1:63:A:THR:O	1:67:A:LYS:H	14	0.16
(2,81)	1:63:A:THR:O	1:67:A:LYS:H	19	0.16
(2,46)	1:13:A:VAL:O	1:17:A:ILE:N	19	0.16
(2,46)	1:13:A:VAL:O	1:17:A:ILE:N	20	0.16
(2,1)	1:3:A:LYS:O	1:28:A:GLU:H	20	0.16
(1,1802)	1:56:A:ALA:HB1	1:59:A:MET:HA	20	0.16
(1,1802)	1:56:A:ALA:HB2	1:59:A:MET:HA	20	0.16
(1,1802)	1:56:A:ALA:HB3	1:59:A:MET:HA	20	0.16
(1,1554)	1:42:A:LEU:HB3	1:45:A:PHE:H	8	0.16
(1,1535)	1:42:A:LEU:HD21	1:45:A:PHE:H	1	0.16
(1,1535)	1:42:A:LEU:HD22	1:45:A:PHE:H	1	0.16
(1,1535)	1:42:A:LEU:HD23	1:45:A:PHE:H	1	0.16
(1,1535)	1:42:A:LEU:HD21	1:45:A:PHE:H	8	0.16
(1,1535)	1:42:A:LEU:HD22	1:45:A:PHE:H	8	0.16
(1,1535)	1:42:A:LEU:HD23	1:45:A:PHE:H	8	0.16
(1,1535)	1:42:A:LEU:HD21	1:45:A:PHE:H	9	0.16
(1,1535)	1:42:A:LEU:HD22	1:45:A:PHE:H	9	0.16
(1,1535)	1:42:A:LEU:HD23	1:45:A:PHE:H	9	0.16
(1,1535)	1:42:A:LEU:HD21	1:45:A:PHE:H	12	0.16
(1,1535)	1:42:A:LEU:HD22	1:45:A:PHE:H	12	0.16
(1,1535)	1:42:A:LEU:HD23	1:45:A:PHE:H	12	0.16
(1,1535)	1:42:A:LEU:HD21	1:45:A:PHE:H	19	0.16
(1,1535)	1:42:A:LEU:HD22	1:45:A:PHE:H	19	0.16
(1,1535)	1:42:A:LEU:HD23	1:45:A:PHE:H	19	0.16
(1,1328)	1:22:A:LEU:HA	1:27:A:TYR:H	8	0.16
(1,870)	1:20:A:PHE:H	1:20:A:PHE:HD1	15	0.16
(1,870)	1:20:A:PHE:H	1:20:A:PHE:HD2	15	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,870)	1:20:A:PHE:H	1:20:A:PHE:HD1	19	0.16
(1,870)	1:20:A:PHE:H	1:20:A:PHE:HD2	19	0.16
(1,825)	1:84:A:ALA:HA	1:87:A:GLY:H	14	0.16
(1,825)	1:84:A:ALA:HA	1:87:A:GLY:H	15	0.16
(1,825)	1:84:A:ALA:HA	1:87:A:GLY:H	17	0.16
(1,801)	1:62:A:PHE:H	1:62:A:PHE:HZ	1	0.16
(1,801)	1:62:A:PHE:H	1:62:A:PHE:HZ	10	0.16
(1,801)	1:62:A:PHE:H	1:62:A:PHE:HZ	14	0.16
(1,801)	1:62:A:PHE:H	1:62:A:PHE:HZ	19	0.16
(1,801)	1:62:A:PHE:H	1:62:A:PHE:HZ	20	0.16
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB1	6	0.16
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB2	6	0.16
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB3	6	0.16
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB1	6	0.16
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB2	6	0.16
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB3	6	0.16
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB1	6	0.16
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB2	6	0.16
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB3	6	0.16
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB1	8	0.16
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB2	8	0.16
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB3	8	0.16
(1,611)	1:82:A:LEU:HD11	1:103:A:MET:HG3	2	0.16
(1,611)	1:82:A:LEU:HD12	1:103:A:MET:HG3	2	0.16
(1,611)	1:82:A:LEU:HD13	1:103:A:MET:HG3	2	0.16
(1,591)	1:41:A:LYS:HA	1:44:A:GLU:HB3	10	0.16
(1,552)	1:81:A:VAL:H	1:103:A:MET:H	8	0.16
(1,552)	1:81:A:VAL:H	1:103:A:MET:H	9	0.16
(1,552)	1:81:A:VAL:H	1:103:A:MET:H	11	0.16
(1,508)	1:52:A:LEU:HB2	1:82:A:LEU:H	19	0.16
(1,376)	1:27:A:TYR:HD1	1:28:A:GLU:H	5	0.16
(1,376)	1:27:A:TYR:HD2	1:28:A:GLU:H	5	0.16
(1,255)	1:5:A:VAL:H	1:27:A:TYR:HB2	7	0.16
(1,255)	1:5:A:VAL:H	1:27:A:TYR:HB2	17	0.16
(2,107)	1:94:A:ALA:O	1:99:A:ALA:H	3	0.15
(2,107)	1:94:A:ALA:O	1:99:A:ALA:H	13	0.15
(2,87)	1:71:A:LYS:O	1:74:A:TRP:H	20	0.15
(2,81)	1:63:A:THR:O	1:67:A:LYS:H	18	0.15
(2,51)	1:16:A:LYS:O	1:20:A:PHE:H	1	0.15
(1,1861)	1:82:A:LEU:HB2	1:104:A:ARG:HA	8	0.15
(1,1861)	1:82:A:LEU:HB2	1:104:A:ARG:HA	14	0.15
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD11	9	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD12	9	0.15
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD13	9	0.15
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD11	20	0.15
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD12	20	0.15
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD13	20	0.15
(1,1554)	1:42:A:LEU:HB3	1:45:A:PHE:H	1	0.15
(1,1554)	1:42:A:LEU:HB3	1:45:A:PHE:H	13	0.15
(1,1535)	1:42:A:LEU:HD21	1:45:A:PHE:H	2	0.15
(1,1535)	1:42:A:LEU:HD22	1:45:A:PHE:H	2	0.15
(1,1535)	1:42:A:LEU:HD23	1:45:A:PHE:H	2	0.15
(1,1535)	1:42:A:LEU:HD21	1:45:A:PHE:H	3	0.15
(1,1535)	1:42:A:LEU:HD22	1:45:A:PHE:H	3	0.15
(1,1535)	1:42:A:LEU:HD23	1:45:A:PHE:H	3	0.15
(1,1535)	1:42:A:LEU:HD21	1:45:A:PHE:H	4	0.15
(1,1535)	1:42:A:LEU:HD22	1:45:A:PHE:H	4	0.15
(1,1535)	1:42:A:LEU:HD23	1:45:A:PHE:H	4	0.15
(1,1535)	1:42:A:LEU:HD21	1:45:A:PHE:H	7	0.15
(1,1535)	1:42:A:LEU:HD22	1:45:A:PHE:H	7	0.15
(1,1535)	1:42:A:LEU:HD23	1:45:A:PHE:H	7	0.15
(1,1535)	1:42:A:LEU:HD21	1:45:A:PHE:H	13	0.15
(1,1535)	1:42:A:LEU:HD22	1:45:A:PHE:H	13	0.15
(1,1535)	1:42:A:LEU:HD23	1:45:A:PHE:H	13	0.15
(1,1535)	1:42:A:LEU:HD21	1:45:A:PHE:H	14	0.15
(1,1535)	1:42:A:LEU:HD22	1:45:A:PHE:H	14	0.15
(1,1535)	1:42:A:LEU:HD23	1:45:A:PHE:H	14	0.15
(1,1535)	1:42:A:LEU:HD21	1:45:A:PHE:H	15	0.15
(1,1535)	1:42:A:LEU:HD22	1:45:A:PHE:H	15	0.15
(1,1535)	1:42:A:LEU:HD23	1:45:A:PHE:H	15	0.15
(1,1535)	1:42:A:LEU:HD21	1:45:A:PHE:H	17	0.15
(1,1535)	1:42:A:LEU:HD22	1:45:A:PHE:H	17	0.15
(1,1535)	1:42:A:LEU:HD23	1:45:A:PHE:H	17	0.15
(1,1535)	1:42:A:LEU:HD21	1:45:A:PHE:H	18	0.15
(1,1535)	1:42:A:LEU:HD22	1:45:A:PHE:H	18	0.15
(1,1535)	1:42:A:LEU:HD23	1:45:A:PHE:H	18	0.15
(1,1535)	1:42:A:LEU:HD21	1:45:A:PHE:H	20	0.15
(1,1535)	1:42:A:LEU:HD22	1:45:A:PHE:H	20	0.15
(1,1535)	1:42:A:LEU:HD23	1:45:A:PHE:H	20	0.15
(1,1328)	1:22:A:LEU:HA	1:27:A:TYR:H	1	0.15
(1,1328)	1:22:A:LEU:HA	1:27:A:TYR:H	16	0.15
(1,1194)	1:3:A:LYS:HG2	1:5:A:VAL:H	12	0.15
(1,1194)	1:3:A:LYS:HG3	1:5:A:VAL:H	12	0.15
(1,1091)	1:113:A:ILE:H	1:116:A:VAL:HB	9	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,870)	1:20:A:PHE:H	1:20:A:PHE:HD1	13	0.15
(1,870)	1:20:A:PHE:H	1:20:A:PHE:HD2	13	0.15
(1,870)	1:20:A:PHE:H	1:20:A:PHE:HD1	20	0.15
(1,870)	1:20:A:PHE:H	1:20:A:PHE:HD2	20	0.15
(1,825)	1:84:A:ALA:HA	1:87:A:GLY:H	4	0.15
(1,825)	1:84:A:ALA:HA	1:87:A:GLY:H	7	0.15
(1,825)	1:84:A:ALA:HA	1:87:A:GLY:H	8	0.15
(1,825)	1:84:A:ALA:HA	1:87:A:GLY:H	20	0.15
(1,801)	1:62:A:PHE:H	1:62:A:PHE:HZ	4	0.15
(1,801)	1:62:A:PHE:H	1:62:A:PHE:HZ	5	0.15
(1,801)	1:62:A:PHE:H	1:62:A:PHE:HZ	16	0.15
(1,801)	1:62:A:PHE:H	1:62:A:PHE:HZ	18	0.15
(1,765)	1:81:A:VAL:HG21	1:82:A:LEU:H	8	0.15
(1,765)	1:81:A:VAL:HG22	1:82:A:LEU:H	8	0.15
(1,765)	1:81:A:VAL:HG23	1:82:A:LEU:H	8	0.15
(1,611)	1:82:A:LEU:HD11	1:103:A:MET:HG3	15	0.15
(1,611)	1:82:A:LEU:HD12	1:103:A:MET:HG3	15	0.15
(1,611)	1:82:A:LEU:HD13	1:103:A:MET:HG3	15	0.15
(1,605)	1:52:A:LEU:HD21	1:61:A:GLY:HA3	7	0.15
(1,605)	1:52:A:LEU:HD22	1:61:A:GLY:HA3	7	0.15
(1,605)	1:52:A:LEU:HD23	1:61:A:GLY:HA3	7	0.15
(1,592)	1:41:A:LYS:HA	1:44:A:GLU:HB2	10	0.15
(1,592)	1:41:A:LYS:HA	1:44:A:GLU:HB2	15	0.15
(1,591)	1:41:A:LYS:HA	1:44:A:GLU:HB3	9	0.15
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD11	13	0.15
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD12	13	0.15
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD13	13	0.15
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD11	14	0.15
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD12	14	0.15
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD13	14	0.15
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD11	18	0.15
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD12	18	0.15
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD13	18	0.15
(1,553)	1:83:A:THR:H	1:103:A:MET:H	8	0.15
(1,553)	1:83:A:THR:H	1:103:A:MET:H	20	0.15
(1,552)	1:81:A:VAL:H	1:103:A:MET:H	18	0.15
(1,508)	1:52:A:LEU:HB2	1:82:A:LEU:H	1	0.15
(1,508)	1:52:A:LEU:HB2	1:82:A:LEU:H	17	0.15
(1,434)	1:50:A:ILE:H	1:79:A:VAL:HA	4	0.15
(1,434)	1:50:A:ILE:H	1:79:A:VAL:HA	12	0.15
(1,434)	1:50:A:ILE:H	1:79:A:VAL:HA	15	0.15
(1,427)	1:4:A:LYS:H	1:49:A:LEU:H	14	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,376)	1:27:A:TYR:HD1	1:28:A:GLU:H	8	0.15
(1,376)	1:27:A:TYR:HD2	1:28:A:GLU:H	8	0.15
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG11	1	0.15
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG12	1	0.15
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG13	1	0.15
(1,284)	1:9:A:ASP:H	1:15:A:ARG:HD2	17	0.15
(1,272)	1:7:A:LEU:HB3	1:8:A:VAL:H	4	0.15
(1,272)	1:7:A:LEU:HB3	1:8:A:VAL:H	16	0.15
(1,272)	1:7:A:LEU:HB3	1:8:A:VAL:H	18	0.15
(1,256)	1:5:A:VAL:H	1:27:A:TYR:HB3	11	0.15
(1,157)	1:84:A:ALA:HA	1:85:A:LYS:H	12	0.15
(1,157)	1:84:A:ALA:HA	1:85:A:LYS:H	13	0.15
(1,157)	1:84:A:ALA:HA	1:85:A:LYS:H	14	0.15
(1,67)	1:34:A:ASN:HA	1:35:A:GLY:H	1	0.15
(1,67)	1:34:A:ASN:HA	1:35:A:GLY:H	11	0.15
(2,107)	1:94:A:ALA:O	1:99:A:ALA:H	1	0.14
(2,107)	1:94:A:ALA:O	1:99:A:ALA:H	2	0.14
(2,81)	1:63:A:THR:O	1:67:A:LYS:H	2	0.14
(2,81)	1:63:A:THR:O	1:67:A:LYS:H	3	0.14
(2,81)	1:63:A:THR:O	1:67:A:LYS:H	4	0.14
(2,81)	1:63:A:THR:O	1:67:A:LYS:H	16	0.14
(2,67)	1:36:A:GLN:O	1:40:A:GLU:H	15	0.14
(2,67)	1:36:A:GLN:O	1:40:A:GLU:H	20	0.14
(2,51)	1:16:A:LYS:O	1:20:A:PHE:H	17	0.14
(1,1861)	1:82:A:LEU:HB2	1:104:A:ARG:HA	2	0.14
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD11	14	0.14
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD12	14	0.14
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD13	14	0.14
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD11	18	0.14
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD12	18	0.14
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD13	18	0.14
(1,1721)	1:21:A:ASN:HB3	1:107:A:PHE:HE1	8	0.14
(1,1721)	1:21:A:ASN:HB3	1:107:A:PHE:HE2	8	0.14
(1,1554)	1:42:A:LEU:HB3	1:45:A:PHE:H	6	0.14
(1,1535)	1:42:A:LEU:HD21	1:45:A:PHE:H	16	0.14
(1,1535)	1:42:A:LEU:HD22	1:45:A:PHE:H	16	0.14
(1,1535)	1:42:A:LEU:HD23	1:45:A:PHE:H	16	0.14
(1,1491)	1:113:A:ILE:HG13	1:114:A:GLU:H	18	0.14
(1,1328)	1:22:A:LEU:HA	1:27:A:TYR:H	17	0.14
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD11	18	0.14
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD12	18	0.14
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD13	18	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD11	18	0.14
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD12	18	0.14
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD13	18	0.14
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD11	18	0.14
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD12	18	0.14
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD13	18	0.14
(1,1194)	1:3:A:LYS:HG2	1:5:A:VAL:H	19	0.14
(1,1194)	1:3:A:LYS:HG3	1:5:A:VAL:H	19	0.14
(1,1091)	1:113:A:ILE:H	1:116:A:VAL:HB	13	0.14
(1,1006)	1:103:A:MET:HG3	1:104:A:ARG:H	16	0.14
(1,870)	1:20:A:PHE:H	1:20:A:PHE:HD1	18	0.14
(1,870)	1:20:A:PHE:H	1:20:A:PHE:HD2	18	0.14
(1,825)	1:84:A:ALA:HA	1:87:A:GLY:H	9	0.14
(1,825)	1:84:A:ALA:HA	1:87:A:GLY:H	11	0.14
(1,825)	1:84:A:ALA:HA	1:87:A:GLY:H	13	0.14
(1,825)	1:84:A:ALA:HA	1:87:A:GLY:H	16	0.14
(1,825)	1:84:A:ALA:HA	1:87:A:GLY:H	19	0.14
(1,801)	1:62:A:PHE:H	1:62:A:PHE:HZ	2	0.14
(1,801)	1:62:A:PHE:H	1:62:A:PHE:HZ	3	0.14
(1,801)	1:62:A:PHE:H	1:62:A:PHE:HZ	12	0.14
(1,801)	1:62:A:PHE:H	1:62:A:PHE:HZ	13	0.14
(1,753)	1:67:A:LYS:H	1:67:A:LYS:HG2	17	0.14
(1,744)	1:80:A:ILE:H	1:80:A:ILE:HD11	20	0.14
(1,744)	1:80:A:ILE:H	1:80:A:ILE:HD12	20	0.14
(1,744)	1:80:A:ILE:H	1:80:A:ILE:HD13	20	0.14
(1,709)	1:74:A:TRP:H	1:74:A:TRP:HE3	7	0.14
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE1	17	0.14
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE2	17	0.14
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE1	17	0.14
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE2	17	0.14
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE1	17	0.14
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE2	17	0.14
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB1	2	0.14
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB2	2	0.14
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB3	2	0.14
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB1	10	0.14
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB2	10	0.14
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB3	10	0.14
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB1	20	0.14
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB2	20	0.14
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB3	20	0.14
(1,611)	1:82:A:LEU:HD11	1:103:A:MET:HG3	1	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,611)	1:82:A:LEU:HD12	1:103:A:MET:HG3	1	0.14
(1,611)	1:82:A:LEU:HD13	1:103:A:MET:HG3	1	0.14
(1,611)	1:82:A:LEU:HD11	1:103:A:MET:HG3	17	0.14
(1,611)	1:82:A:LEU:HD12	1:103:A:MET:HG3	17	0.14
(1,611)	1:82:A:LEU:HD13	1:103:A:MET:HG3	17	0.14
(1,611)	1:82:A:LEU:HD11	1:103:A:MET:HG3	18	0.14
(1,611)	1:82:A:LEU:HD12	1:103:A:MET:HG3	18	0.14
(1,611)	1:82:A:LEU:HD13	1:103:A:MET:HG3	18	0.14
(1,592)	1:41:A:LYS:HA	1:44:A:GLU:HB2	7	0.14
(1,592)	1:41:A:LYS:HA	1:44:A:GLU:HB2	9	0.14
(1,592)	1:41:A:LYS:HA	1:44:A:GLU:HB2	14	0.14
(1,591)	1:41:A:LYS:HA	1:44:A:GLU:HB3	5	0.14
(1,591)	1:41:A:LYS:HA	1:44:A:GLU:HB3	11	0.14
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD11	11	0.14
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD12	11	0.14
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD13	11	0.14
(1,552)	1:81:A:VAL:H	1:103:A:MET:H	1	0.14
(1,508)	1:52:A:LEU:HB2	1:82:A:LEU:H	8	0.14
(1,508)	1:52:A:LEU:HB2	1:82:A:LEU:H	20	0.14
(1,434)	1:50:A:ILE:H	1:79:A:VAL:HA	6	0.14
(1,434)	1:50:A:ILE:H	1:79:A:VAL:HA	9	0.14
(1,434)	1:50:A:ILE:H	1:79:A:VAL:HA	10	0.14
(1,434)	1:50:A:ILE:H	1:79:A:VAL:HA	11	0.14
(1,434)	1:50:A:ILE:H	1:79:A:VAL:HA	14	0.14
(1,372)	1:5:A:VAL:H	1:28:A:GLU:H	4	0.14
(1,372)	1:5:A:VAL:H	1:28:A:GLU:H	14	0.14
(1,372)	1:5:A:VAL:H	1:28:A:GLU:H	18	0.14
(1,357)	1:23:A:LYS:HB2	1:26:A:GLY:H	3	0.14
(1,357)	1:23:A:LYS:HB3	1:26:A:GLY:H	3	0.14
(1,357)	1:23:A:LYS:HB2	1:26:A:GLY:H	18	0.14
(1,357)	1:23:A:LYS:HB3	1:26:A:GLY:H	18	0.14
(1,267)	1:6:A:LEU:HB3	1:7:A:LEU:H	3	0.14
(1,261)	1:6:A:LEU:H	1:47:A:PRO:HG3	5	0.14
(1,255)	1:5:A:VAL:H	1:27:A:TYR:HB2	1	0.14
(1,255)	1:5:A:VAL:H	1:27:A:TYR:HB2	2	0.14
(1,255)	1:5:A:VAL:H	1:27:A:TYR:HB2	6	0.14
(1,255)	1:5:A:VAL:H	1:27:A:TYR:HB2	8	0.14
(1,243)	1:3:A:LYS:HD2	1:4:A:LYS:H	20	0.14
(1,243)	1:3:A:LYS:HD3	1:4:A:LYS:H	20	0.14
(1,157)	1:84:A:ALA:HA	1:85:A:LYS:H	6	0.14
(1,157)	1:84:A:ALA:HA	1:85:A:LYS:H	8	0.14
(1,157)	1:84:A:ALA:HA	1:85:A:LYS:H	18	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,67)	1:34:A:ASN:HA	1:35:A:GLY:H	3	0.14
(1,67)	1:34:A:ASN:HA	1:35:A:GLY:H	13	0.14
(1,24)	1:13:A:VAL:H	1:14:A:LEU:H	11	0.14
(2,107)	1:94:A:ALA:O	1:99:A:ALA:H	4	0.13
(2,107)	1:94:A:ALA:O	1:99:A:ALA:H	9	0.13
(2,107)	1:94:A:ALA:O	1:99:A:ALA:H	17	0.13
(2,87)	1:71:A:LYS:O	1:74:A:TRP:H	8	0.13
(2,87)	1:71:A:LYS:O	1:74:A:TRP:H	19	0.13
(2,81)	1:63:A:THR:O	1:67:A:LYS:H	8	0.13
(2,81)	1:63:A:THR:O	1:67:A:LYS:H	9	0.13
(2,81)	1:63:A:THR:O	1:67:A:LYS:H	15	0.13
(2,81)	1:63:A:THR:O	1:67:A:LYS:H	20	0.13
(2,67)	1:36:A:GLN:O	1:40:A:GLU:H	9	0.13
(2,67)	1:36:A:GLN:O	1:40:A:GLU:H	10	0.13
(2,67)	1:36:A:GLN:O	1:40:A:GLU:H	17	0.13
(2,67)	1:36:A:GLN:O	1:40:A:GLU:H	19	0.13
(2,45)	1:13:A:VAL:O	1:17:A:ILE:H	11	0.13
(2,31)	1:79:A:VAL:O	1:101:A:LYS:H	13	0.13
(2,31)	1:79:A:VAL:O	1:101:A:LYS:H	18	0.13
(2,27)	1:52:A:LEU:O	1:82:A:LEU:H	7	0.13
(2,19)	1:9:A:ASP:H	1:32:A:ALA:O	7	0.13
(2,17)	1:8:A:VAL:O	1:53:A:ASP:H	19	0.13
(2,13)	1:7:A:LEU:O	1:32:A:ALA:H	20	0.13
(2,11)	1:7:A:LEU:H	1:30:A:ILE:O	17	0.13
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD11	13	0.13
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD12	13	0.13
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD13	13	0.13
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD11	15	0.13
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD12	15	0.13
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD13	15	0.13
(1,1491)	1:113:A:ILE:HG13	1:114:A:GLU:H	14	0.13
(1,1491)	1:113:A:ILE:HG13	1:114:A:GLU:H	15	0.13
(1,1484)	1:80:A:ILE:HD11	1:116:A:VAL:H	9	0.13
(1,1484)	1:80:A:ILE:HD12	1:116:A:VAL:H	9	0.13
(1,1484)	1:80:A:ILE:HD13	1:116:A:VAL:H	9	0.13
(1,1349)	1:68:A:LEU:HD21	1:74:A:TRP:H	2	0.13
(1,1349)	1:68:A:LEU:HD22	1:74:A:TRP:H	2	0.13
(1,1349)	1:68:A:LEU:HD23	1:74:A:TRP:H	2	0.13
(1,1349)	1:68:A:LEU:HD21	1:74:A:TRP:H	14	0.13
(1,1349)	1:68:A:LEU:HD22	1:74:A:TRP:H	14	0.13
(1,1349)	1:68:A:LEU:HD23	1:74:A:TRP:H	14	0.13
(1,1328)	1:22:A:LEU:HA	1:27:A:TYR:H	2	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1257)	1:71:A:LYS:HD3	1:74:A:TRP:H	19	0.13
(1,880)	1:50:A:ILE:H	1:50:A:ILE:HD11	9	0.13
(1,880)	1:50:A:ILE:H	1:50:A:ILE:HD12	9	0.13
(1,880)	1:50:A:ILE:H	1:50:A:ILE:HD13	9	0.13
(1,825)	1:84:A:ALA:HA	1:87:A:GLY:H	2	0.13
(1,825)	1:84:A:ALA:HA	1:87:A:GLY:H	5	0.13
(1,825)	1:84:A:ALA:HA	1:87:A:GLY:H	10	0.13
(1,825)	1:84:A:ALA:HA	1:87:A:GLY:H	12	0.13
(1,801)	1:62:A:PHE:H	1:62:A:PHE:HZ	8	0.13
(1,801)	1:62:A:PHE:H	1:62:A:PHE:HZ	11	0.13
(1,801)	1:62:A:PHE:H	1:62:A:PHE:HZ	15	0.13
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD11	8	0.13
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD12	8	0.13
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD13	8	0.13
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD11	16	0.13
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD12	16	0.13
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD13	16	0.13
(1,753)	1:67:A:LYS:H	1:67:A:LYS:HG2	16	0.13
(1,709)	1:74:A:TRP:H	1:74:A:TRP:HE3	4	0.13
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE1	2	0.13
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE2	2	0.13
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE1	2	0.13
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE2	2	0.13
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE1	2	0.13
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE2	2	0.13
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE1	12	0.13
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE2	12	0.13
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE1	12	0.13
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE2	12	0.13
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE1	12	0.13
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE2	12	0.13
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB1	11	0.13
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB2	11	0.13
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB3	11	0.13
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB1	13	0.13
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB2	13	0.13
(1,624)	1:79:A:VAL:HB	1:99:A:ALA:HB3	13	0.13
(1,611)	1:82:A:LEU:HD11	1:103:A:MET:HG3	7	0.13
(1,611)	1:82:A:LEU:HD12	1:103:A:MET:HG3	7	0.13
(1,611)	1:82:A:LEU:HD13	1:103:A:MET:HG3	7	0.13
(1,611)	1:82:A:LEU:HD11	1:103:A:MET:HG3	12	0.13
(1,611)	1:82:A:LEU:HD12	1:103:A:MET:HG3	12	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,611)	1:82:A:LEU:HD13	1:103:A:MET:HG3	12	0.13
(1,611)	1:82:A:LEU:HD11	1:103:A:MET:HG3	14	0.13
(1,611)	1:82:A:LEU:HD12	1:103:A:MET:HG3	14	0.13
(1,611)	1:82:A:LEU:HD13	1:103:A:MET:HG3	14	0.13
(1,611)	1:82:A:LEU:HD11	1:103:A:MET:HG3	20	0.13
(1,611)	1:82:A:LEU:HD12	1:103:A:MET:HG3	20	0.13
(1,611)	1:82:A:LEU:HD13	1:103:A:MET:HG3	20	0.13
(1,592)	1:41:A:LYS:HA	1:44:A:GLU:HB2	1	0.13
(1,592)	1:41:A:LYS:HA	1:44:A:GLU:HB2	8	0.13
(1,592)	1:41:A:LYS:HA	1:44:A:GLU:HB2	13	0.13
(1,592)	1:41:A:LYS:HA	1:44:A:GLU:HB2	20	0.13
(1,591)	1:41:A:LYS:HA	1:44:A:GLU:HB3	7	0.13
(1,572)	1:18:A:VAL:HG11	1:51:A:VAL:HG11	1	0.13
(1,572)	1:18:A:VAL:HG11	1:51:A:VAL:HG12	1	0.13
(1,572)	1:18:A:VAL:HG11	1:51:A:VAL:HG13	1	0.13
(1,572)	1:18:A:VAL:HG12	1:51:A:VAL:HG11	1	0.13
(1,572)	1:18:A:VAL:HG12	1:51:A:VAL:HG12	1	0.13
(1,572)	1:18:A:VAL:HG12	1:51:A:VAL:HG13	1	0.13
(1,572)	1:18:A:VAL:HG13	1:51:A:VAL:HG11	1	0.13
(1,572)	1:18:A:VAL:HG13	1:51:A:VAL:HG12	1	0.13
(1,572)	1:18:A:VAL:HG13	1:51:A:VAL:HG13	1	0.13
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD11	2	0.13
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD12	2	0.13
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD13	2	0.13
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD11	3	0.13
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD12	3	0.13
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD13	3	0.13
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD11	4	0.13
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD12	4	0.13
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD13	4	0.13
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD11	9	0.13
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD12	9	0.13
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD13	9	0.13
(1,553)	1:83:A:THR:H	1:103:A:MET:H	19	0.13
(1,552)	1:81:A:VAL:H	1:103:A:MET:H	5	0.13
(1,552)	1:81:A:VAL:H	1:103:A:MET:H	14	0.13
(1,552)	1:81:A:VAL:H	1:103:A:MET:H	20	0.13
(1,540)	1:80:A:ILE:HG21	1:101:A:LYS:H	16	0.13
(1,540)	1:80:A:ILE:HG22	1:101:A:LYS:H	16	0.13
(1,540)	1:80:A:ILE:HG23	1:101:A:LYS:H	16	0.13
(1,430)	1:47:A:PRO:HA	1:49:A:LEU:H	5	0.13
(1,427)	1:4:A:LYS:H	1:49:A:LEU:H	2	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,427)	1:4:A:LYS:H	1:49:A:LEU:H	4	0.13
(1,427)	1:4:A:LYS:H	1:49:A:LEU:H	13	0.13
(1,427)	1:4:A:LYS:H	1:49:A:LEU:H	19	0.13
(1,372)	1:5:A:VAL:H	1:28:A:GLU:H	9	0.13
(1,372)	1:5:A:VAL:H	1:28:A:GLU:H	12	0.13
(1,372)	1:5:A:VAL:H	1:28:A:GLU:H	15	0.13
(1,361)	1:24:A:LYS:HA	1:26:A:GLY:H	3	0.13
(1,361)	1:24:A:LYS:HA	1:26:A:GLY:H	4	0.13
(1,361)	1:24:A:LYS:HA	1:26:A:GLY:H	19	0.13
(1,357)	1:23:A:LYS:HB2	1:26:A:GLY:H	9	0.13
(1,357)	1:23:A:LYS:HB3	1:26:A:GLY:H	9	0.13
(1,357)	1:23:A:LYS:HB2	1:26:A:GLY:H	13	0.13
(1,357)	1:23:A:LYS:HB3	1:26:A:GLY:H	13	0.13
(1,357)	1:23:A:LYS:HB2	1:26:A:GLY:H	14	0.13
(1,357)	1:23:A:LYS:HB3	1:26:A:GLY:H	14	0.13
(1,357)	1:23:A:LYS:HB2	1:26:A:GLY:H	15	0.13
(1,357)	1:23:A:LYS:HB3	1:26:A:GLY:H	15	0.13
(1,351)	1:24:A:LYS:HB2	1:25:A:GLU:H	13	0.13
(1,274)	1:8:A:VAL:H	1:51:A:VAL:HB	16	0.13
(1,267)	1:6:A:LEU:HB3	1:7:A:LEU:H	1	0.13
(1,267)	1:6:A:LEU:HB3	1:7:A:LEU:H	2	0.13
(1,267)	1:6:A:LEU:HB3	1:7:A:LEU:H	7	0.13
(1,267)	1:6:A:LEU:HB3	1:7:A:LEU:H	8	0.13
(1,267)	1:6:A:LEU:HB3	1:7:A:LEU:H	10	0.13
(1,267)	1:6:A:LEU:HB3	1:7:A:LEU:H	19	0.13
(1,256)	1:5:A:VAL:H	1:27:A:TYR:HB3	20	0.13
(1,157)	1:84:A:ALA:HA	1:85:A:LYS:H	1	0.13
(1,157)	1:84:A:ALA:HA	1:85:A:LYS:H	4	0.13
(1,157)	1:84:A:ALA:HA	1:85:A:LYS:H	7	0.13
(1,157)	1:84:A:ALA:HA	1:85:A:LYS:H	9	0.13
(1,157)	1:84:A:ALA:HA	1:85:A:LYS:H	15	0.13
(1,157)	1:84:A:ALA:HA	1:85:A:LYS:H	16	0.13
(1,157)	1:84:A:ALA:HA	1:85:A:LYS:H	19	0.13
(1,157)	1:84:A:ALA:HA	1:85:A:LYS:H	20	0.13
(1,114)	1:61:A:GLY:H	1:62:A:PHE:H	17	0.13
(1,67)	1:34:A:ASN:HA	1:35:A:GLY:H	12	0.13
(1,15)	1:9:A:ASP:HA	1:10:A:ASP:H	19	0.13
(1,3)	1:3:A:LYS:HA	1:4:A:LYS:H	20	0.13
(2,107)	1:94:A:ALA:O	1:99:A:ALA:H	5	0.12
(2,107)	1:94:A:ALA:O	1:99:A:ALA:H	7	0.12
(2,107)	1:94:A:ALA:O	1:99:A:ALA:H	10	0.12
(2,107)	1:94:A:ALA:O	1:99:A:ALA:H	15	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,87)	1:71:A:LYS:O	1:74:A:TRP:H	4	0.12
(2,87)	1:71:A:LYS:O	1:74:A:TRP:H	6	0.12
(2,87)	1:71:A:LYS:O	1:74:A:TRP:H	9	0.12
(2,87)	1:71:A:LYS:O	1:74:A:TRP:H	11	0.12
(2,87)	1:71:A:LYS:O	1:74:A:TRP:H	12	0.12
(2,81)	1:63:A:THR:O	1:67:A:LYS:H	5	0.12
(2,81)	1:63:A:THR:O	1:67:A:LYS:H	17	0.12
(2,75)	1:60:A:ASP:O	1:64:A:VAL:H	3	0.12
(2,75)	1:60:A:ASP:O	1:64:A:VAL:H	7	0.12
(2,73)	1:40:A:GLU:O	1:43:A:SER:H	6	0.12
(2,67)	1:36:A:GLN:O	1:40:A:GLU:H	1	0.12
(2,67)	1:36:A:GLN:O	1:40:A:GLU:H	2	0.12
(2,67)	1:36:A:GLN:O	1:40:A:GLU:H	3	0.12
(2,67)	1:36:A:GLN:O	1:40:A:GLU:H	4	0.12
(2,67)	1:36:A:GLN:O	1:40:A:GLU:H	7	0.12
(2,67)	1:36:A:GLN:O	1:40:A:GLU:H	8	0.12
(2,67)	1:36:A:GLN:O	1:40:A:GLU:H	12	0.12
(2,67)	1:36:A:GLN:O	1:40:A:GLU:H	13	0.12
(2,51)	1:16:A:LYS:O	1:20:A:PHE:H	2	0.12
(2,45)	1:13:A:VAL:O	1:17:A:ILE:H	17	0.12
(2,31)	1:79:A:VAL:O	1:101:A:LYS:H	3	0.12
(2,31)	1:79:A:VAL:O	1:101:A:LYS:H	7	0.12
(2,31)	1:79:A:VAL:O	1:101:A:LYS:H	12	0.12
(2,21)	1:50:A:ILE:H	1:78:A:PRO:O	5	0.12
(2,21)	1:50:A:ILE:H	1:78:A:PRO:O	7	0.12
(2,19)	1:9:A:ASP:H	1:32:A:ALA:O	1	0.12
(2,13)	1:7:A:LEU:O	1:32:A:ALA:H	8	0.12
(2,13)	1:7:A:LEU:O	1:32:A:ALA:H	19	0.12
(2,7)	1:6:A:LEU:H	1:49:A:LEU:O	1	0.12
(2,7)	1:6:A:LEU:H	1:49:A:LEU:O	11	0.12
(1,1861)	1:82:A:LEU:HB2	1:104:A:ARG:HA	16	0.12
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD11	4	0.12
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD12	4	0.12
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD13	4	0.12
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD11	19	0.12
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD12	19	0.12
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD13	19	0.12
(1,1802)	1:56:A:ALA:HB1	1:59:A:MET:HA	17	0.12
(1,1802)	1:56:A:ALA:HB2	1:59:A:MET:HA	17	0.12
(1,1802)	1:56:A:ALA:HB3	1:59:A:MET:HA	17	0.12
(1,1722)	1:14:A:LEU:HD21	1:82:A:LEU:HD11	1	0.12
(1,1722)	1:14:A:LEU:HD21	1:82:A:LEU:HD12	1	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1722)	1:14:A:LEU:HD21	1:82:A:LEU:HD13	1	0.12
(1,1722)	1:14:A:LEU:HD22	1:82:A:LEU:HD11	1	0.12
(1,1722)	1:14:A:LEU:HD22	1:82:A:LEU:HD12	1	0.12
(1,1722)	1:14:A:LEU:HD22	1:82:A:LEU:HD13	1	0.12
(1,1722)	1:14:A:LEU:HD23	1:82:A:LEU:HD11	1	0.12
(1,1722)	1:14:A:LEU:HD23	1:82:A:LEU:HD12	1	0.12
(1,1722)	1:14:A:LEU:HD23	1:82:A:LEU:HD13	1	0.12
(1,1722)	1:14:A:LEU:HD21	1:82:A:LEU:HD11	8	0.12
(1,1722)	1:14:A:LEU:HD21	1:82:A:LEU:HD12	8	0.12
(1,1722)	1:14:A:LEU:HD21	1:82:A:LEU:HD13	8	0.12
(1,1722)	1:14:A:LEU:HD22	1:82:A:LEU:HD11	8	0.12
(1,1722)	1:14:A:LEU:HD22	1:82:A:LEU:HD12	8	0.12
(1,1722)	1:14:A:LEU:HD22	1:82:A:LEU:HD13	8	0.12
(1,1722)	1:14:A:LEU:HD23	1:82:A:LEU:HD11	8	0.12
(1,1722)	1:14:A:LEU:HD23	1:82:A:LEU:HD12	8	0.12
(1,1722)	1:14:A:LEU:HD23	1:82:A:LEU:HD13	8	0.12
(1,1721)	1:21:A:ASN:HB3	1:107:A:PHE:HE1	2	0.12
(1,1721)	1:21:A:ASN:HB3	1:107:A:PHE:HE2	2	0.12
(1,1506)	1:95:A:LEU:HD21	1:102:A:VAL:HG21	2	0.12
(1,1506)	1:95:A:LEU:HD21	1:102:A:VAL:HG22	2	0.12
(1,1506)	1:95:A:LEU:HD21	1:102:A:VAL:HG23	2	0.12
(1,1506)	1:95:A:LEU:HD22	1:102:A:VAL:HG21	2	0.12
(1,1506)	1:95:A:LEU:HD22	1:102:A:VAL:HG22	2	0.12
(1,1506)	1:95:A:LEU:HD22	1:102:A:VAL:HG23	2	0.12
(1,1506)	1:95:A:LEU:HD23	1:102:A:VAL:HG21	2	0.12
(1,1506)	1:95:A:LEU:HD23	1:102:A:VAL:HG22	2	0.12
(1,1506)	1:95:A:LEU:HD23	1:102:A:VAL:HG23	2	0.12
(1,1349)	1:68:A:LEU:HD21	1:74:A:TRP:H	8	0.12
(1,1349)	1:68:A:LEU:HD22	1:74:A:TRP:H	8	0.12
(1,1349)	1:68:A:LEU:HD23	1:74:A:TRP:H	8	0.12
(1,1349)	1:68:A:LEU:HD21	1:74:A:TRP:H	9	0.12
(1,1349)	1:68:A:LEU:HD22	1:74:A:TRP:H	9	0.12
(1,1349)	1:68:A:LEU:HD23	1:74:A:TRP:H	9	0.12
(1,1328)	1:22:A:LEU:HA	1:27:A:TYR:H	6	0.12
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD11	3	0.12
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD12	3	0.12
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD13	3	0.12
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD11	3	0.12
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD12	3	0.12
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD13	3	0.12
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD11	3	0.12
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD12	3	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD13	3	0.12
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD11	4	0.12
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD12	4	0.12
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD13	4	0.12
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD11	4	0.12
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD12	4	0.12
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD13	4	0.12
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD11	4	0.12
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD12	4	0.12
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD13	4	0.12
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD11	11	0.12
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD12	11	0.12
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD13	11	0.12
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD11	11	0.12
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD12	11	0.12
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD13	11	0.12
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD11	11	0.12
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD12	11	0.12
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD13	11	0.12
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD11	16	0.12
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD12	16	0.12
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD13	16	0.12
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD11	16	0.12
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD12	16	0.12
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD13	16	0.12
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD11	16	0.12
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD12	16	0.12
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD13	16	0.12
(1,1257)	1:71:A:LYS:HD3	1:74:A:TRP:H	8	0.12
(1,1257)	1:71:A:LYS:HD3	1:74:A:TRP:H	9	0.12
(1,1257)	1:71:A:LYS:HD3	1:74:A:TRP:H	14	0.12
(1,1257)	1:71:A:LYS:HD3	1:74:A:TRP:H	20	0.12
(1,1091)	1:113:A:ILE:H	1:116:A:VAL:HB	1	0.12
(1,1091)	1:113:A:ILE:H	1:116:A:VAL:HB	3	0.12
(1,1091)	1:113:A:ILE:H	1:116:A:VAL:HB	5	0.12
(1,1091)	1:113:A:ILE:H	1:116:A:VAL:HB	18	0.12
(1,880)	1:50:A:ILE:H	1:50:A:ILE:HD11	8	0.12
(1,880)	1:50:A:ILE:H	1:50:A:ILE:HD12	8	0.12
(1,880)	1:50:A:ILE:H	1:50:A:ILE:HD13	8	0.12
(1,880)	1:50:A:ILE:H	1:50:A:ILE:HD11	14	0.12
(1,880)	1:50:A:ILE:H	1:50:A:ILE:HD12	14	0.12
(1,880)	1:50:A:ILE:H	1:50:A:ILE:HD13	14	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,880)	1:50:A:ILE:H	1:50:A:ILE:HD11	20	0.12
(1,880)	1:50:A:ILE:H	1:50:A:ILE:HD12	20	0.12
(1,880)	1:50:A:ILE:H	1:50:A:ILE:HD13	20	0.12
(1,801)	1:62:A:PHE:H	1:62:A:PHE:HZ	7	0.12
(1,753)	1:67:A:LYS:H	1:67:A:LYS:HG2	1	0.12
(1,753)	1:67:A:LYS:H	1:67:A:LYS:HG2	8	0.12
(1,753)	1:67:A:LYS:H	1:67:A:LYS:HG2	11	0.12
(1,753)	1:67:A:LYS:H	1:67:A:LYS:HG2	20	0.12
(1,744)	1:80:A:ILE:H	1:80:A:ILE:HD11	17	0.12
(1,744)	1:80:A:ILE:H	1:80:A:ILE:HD12	17	0.12
(1,744)	1:80:A:ILE:H	1:80:A:ILE:HD13	17	0.12
(1,709)	1:74:A:TRP:H	1:74:A:TRP:HE3	8	0.12
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE1	1	0.12
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE2	1	0.12
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE1	1	0.12
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE2	1	0.12
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE1	1	0.12
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE2	1	0.12
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE1	14	0.12
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE2	14	0.12
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE1	14	0.12
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE2	14	0.12
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE1	14	0.12
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE2	14	0.12
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE1	20	0.12
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE2	20	0.12
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE1	20	0.12
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE2	20	0.12
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE1	20	0.12
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE2	20	0.12
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB1	15	0.12
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB2	15	0.12
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB3	15	0.12
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB1	15	0.12
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB2	15	0.12
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB3	15	0.12
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB1	15	0.12
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB2	15	0.12
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB3	15	0.12
(1,611)	1:82:A:LEU:HD11	1:103:A:MET:HG3	4	0.12
(1,611)	1:82:A:LEU:HD12	1:103:A:MET:HG3	4	0.12
(1,611)	1:82:A:LEU:HD13	1:103:A:MET:HG3	4	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,611)	1:82:A:LEU:HD11	1:103:A:MET:HG3	11	0.12
(1,611)	1:82:A:LEU:HD12	1:103:A:MET:HG3	11	0.12
(1,611)	1:82:A:LEU:HD13	1:103:A:MET:HG3	11	0.12
(1,592)	1:41:A:LYS:HA	1:44:A:GLU:HB2	2	0.12
(1,592)	1:41:A:LYS:HA	1:44:A:GLU:HB2	4	0.12
(1,592)	1:41:A:LYS:HA	1:44:A:GLU:HB2	17	0.12
(1,592)	1:41:A:LYS:HA	1:44:A:GLU:HB2	19	0.12
(1,591)	1:41:A:LYS:HA	1:44:A:GLU:HB3	1	0.12
(1,591)	1:41:A:LYS:HA	1:44:A:GLU:HB3	14	0.12
(1,591)	1:41:A:LYS:HA	1:44:A:GLU:HB3	15	0.12
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD11	12	0.12
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD12	12	0.12
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD13	12	0.12
(1,500)	1:80:A:ILE:HD11	1:81:A:VAL:H	5	0.12
(1,500)	1:80:A:ILE:HD12	1:81:A:VAL:H	5	0.12
(1,500)	1:80:A:ILE:HD13	1:81:A:VAL:H	5	0.12
(1,474)	1:71:A:LYS:CD	1:74:A:TRP:CZ2	7	0.12
(1,434)	1:50:A:ILE:H	1:79:A:VAL:HA	8	0.12
(1,430)	1:47:A:PRO:HA	1:49:A:LEU:H	10	0.12
(1,430)	1:47:A:PRO:HA	1:49:A:LEU:H	20	0.12
(1,427)	1:4:A:LYS:H	1:49:A:LEU:H	5	0.12
(1,427)	1:4:A:LYS:H	1:49:A:LEU:H	9	0.12
(1,427)	1:4:A:LYS:H	1:49:A:LEU:H	17	0.12
(1,389)	1:9:A:ASP:H	1:32:A:ALA:H	17	0.12
(1,376)	1:27:A:TYR:HD1	1:28:A:GLU:H	1	0.12
(1,376)	1:27:A:TYR:HD2	1:28:A:GLU:H	1	0.12
(1,376)	1:27:A:TYR:HD1	1:28:A:GLU:H	2	0.12
(1,376)	1:27:A:TYR:HD2	1:28:A:GLU:H	2	0.12
(1,372)	1:5:A:VAL:H	1:28:A:GLU:H	20	0.12
(1,361)	1:24:A:LYS:HA	1:26:A:GLY:H	9	0.12
(1,361)	1:24:A:LYS:HA	1:26:A:GLY:H	12	0.12
(1,361)	1:24:A:LYS:HA	1:26:A:GLY:H	15	0.12
(1,357)	1:23:A:LYS:HB2	1:26:A:GLY:H	4	0.12
(1,357)	1:23:A:LYS:HB3	1:26:A:GLY:H	4	0.12
(1,351)	1:24:A:LYS:HB2	1:25:A:GLU:H	15	0.12
(1,351)	1:24:A:LYS:HB2	1:25:A:GLU:H	18	0.12
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG11	19	0.12
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG12	19	0.12
(1,348)	1:23:A:LYS:H	1:29:A:VAL:HG13	19	0.12
(1,267)	1:6:A:LEU:HB3	1:7:A:LEU:H	13	0.12
(1,267)	1:6:A:LEU:HB3	1:7:A:LEU:H	20	0.12
(1,251)	1:4:A:LYS:HB2	1:5:A:VAL:H	18	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,161)	1:86:A:GLY:HA2	1:87:A:GLY:H	19	0.12
(1,157)	1:84:A:ALA:HA	1:85:A:LYS:H	2	0.12
(1,157)	1:84:A:ALA:HA	1:85:A:LYS:H	5	0.12
(1,157)	1:84:A:ALA:HA	1:85:A:LYS:H	10	0.12
(1,157)	1:84:A:ALA:HA	1:85:A:LYS:H	11	0.12
(1,157)	1:84:A:ALA:HA	1:85:A:LYS:H	17	0.12
(1,67)	1:34:A:ASN:HA	1:35:A:GLY:H	4	0.12
(1,67)	1:34:A:ASN:HA	1:35:A:GLY:H	6	0.12
(1,67)	1:34:A:ASN:HA	1:35:A:GLY:H	18	0.12
(1,15)	1:9:A:ASP:HA	1:10:A:ASP:H	8	0.12
(1,15)	1:9:A:ASP:HA	1:10:A:ASP:H	20	0.12
(2,107)	1:94:A:ALA:O	1:99:A:ALA:H	8	0.11
(2,107)	1:94:A:ALA:O	1:99:A:ALA:H	20	0.11
(2,87)	1:71:A:LYS:O	1:74:A:TRP:H	1	0.11
(2,87)	1:71:A:LYS:O	1:74:A:TRP:H	3	0.11
(2,87)	1:71:A:LYS:O	1:74:A:TRP:H	5	0.11
(2,87)	1:71:A:LYS:O	1:74:A:TRP:H	13	0.11
(2,87)	1:71:A:LYS:O	1:74:A:TRP:H	14	0.11
(2,87)	1:71:A:LYS:O	1:74:A:TRP:H	15	0.11
(2,87)	1:71:A:LYS:O	1:74:A:TRP:H	16	0.11
(2,87)	1:71:A:LYS:O	1:74:A:TRP:H	17	0.11
(2,75)	1:60:A:ASP:O	1:64:A:VAL:H	6	0.11
(2,75)	1:60:A:ASP:O	1:64:A:VAL:H	19	0.11
(2,69)	1:37:A:ILE:O	1:41:A:LYS:H	6	0.11
(2,67)	1:36:A:GLN:O	1:40:A:GLU:H	5	0.11
(2,67)	1:36:A:GLN:O	1:40:A:GLU:H	11	0.11
(2,67)	1:36:A:GLN:O	1:40:A:GLU:H	14	0.11
(2,67)	1:36:A:GLN:O	1:40:A:GLU:H	16	0.11
(2,67)	1:36:A:GLN:O	1:40:A:GLU:H	18	0.11
(2,51)	1:16:A:LYS:O	1:20:A:PHE:H	20	0.11
(2,49)	1:15:A:ARG:O	1:19:A:SER:H	16	0.11
(2,45)	1:13:A:VAL:O	1:17:A:ILE:H	7	0.11
(2,45)	1:13:A:VAL:O	1:17:A:ILE:H	9	0.11
(2,39)	1:83:A:THR:O	1:105:A:LYS:H	9	0.11
(2,39)	1:83:A:THR:O	1:105:A:LYS:H	14	0.11
(2,31)	1:79:A:VAL:O	1:101:A:LYS:H	1	0.11
(2,31)	1:79:A:VAL:O	1:101:A:LYS:H	4	0.11
(2,31)	1:79:A:VAL:O	1:101:A:LYS:H	9	0.11
(2,28)	1:52:A:LEU:O	1:82:A:LEU:N	7	0.11
(2,27)	1:52:A:LEU:O	1:82:A:LEU:H	4	0.11
(2,27)	1:52:A:LEU:O	1:82:A:LEU:H	12	0.11
(2,21)	1:50:A:ILE:H	1:78:A:PRO:O	9	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,19)	1:9:A:ASP:H	1:32:A:ALA:O	11	0.11
(2,13)	1:7:A:LEU:O	1:32:A:ALA:H	6	0.11
(2,13)	1:7:A:LEU:O	1:32:A:ALA:H	15	0.11
(2,11)	1:7:A:LEU:H	1:30:A:ILE:O	11	0.11
(2,7)	1:6:A:LEU:H	1:49:A:LEU:O	8	0.11
(1,1888)	1:82:A:LEU:HA	1:103:A:MET:HB3	18	0.11
(1,1861)	1:82:A:LEU:HB2	1:104:A:ARG:HA	11	0.11
(1,1861)	1:82:A:LEU:HB2	1:104:A:ARG:HA	17	0.11
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD11	3	0.11
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD12	3	0.11
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD13	3	0.11
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD11	11	0.11
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD12	11	0.11
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD13	11	0.11
(1,1721)	1:21:A:ASN:HB3	1:107:A:PHE:HE1	1	0.11
(1,1721)	1:21:A:ASN:HB3	1:107:A:PHE:HE2	1	0.11
(1,1609)	1:67:A:LYS:HA	1:71:A:LYS:HE3	8	0.11
(1,1609)	1:67:A:LYS:HA	1:71:A:LYS:HE3	14	0.11
(1,1609)	1:67:A:LYS:HA	1:71:A:LYS:HE3	15	0.11
(1,1609)	1:67:A:LYS:HA	1:71:A:LYS:HE3	18	0.11
(1,1506)	1:95:A:LEU:HD21	1:102:A:VAL:HG21	13	0.11
(1,1506)	1:95:A:LEU:HD21	1:102:A:VAL:HG22	13	0.11
(1,1506)	1:95:A:LEU:HD21	1:102:A:VAL:HG23	13	0.11
(1,1506)	1:95:A:LEU:HD22	1:102:A:VAL:HG21	13	0.11
(1,1506)	1:95:A:LEU:HD22	1:102:A:VAL:HG22	13	0.11
(1,1506)	1:95:A:LEU:HD22	1:102:A:VAL:HG23	13	0.11
(1,1506)	1:95:A:LEU:HD23	1:102:A:VAL:HG21	13	0.11
(1,1506)	1:95:A:LEU:HD23	1:102:A:VAL:HG22	13	0.11
(1,1506)	1:95:A:LEU:HD23	1:102:A:VAL:HG23	13	0.11
(1,1477)	1:54:A:ILE:HG21	1:81:A:VAL:HG21	4	0.11
(1,1477)	1:54:A:ILE:HG21	1:81:A:VAL:HG22	4	0.11
(1,1477)	1:54:A:ILE:HG21	1:81:A:VAL:HG23	4	0.11
(1,1477)	1:54:A:ILE:HG22	1:81:A:VAL:HG21	4	0.11
(1,1477)	1:54:A:ILE:HG22	1:81:A:VAL:HG22	4	0.11
(1,1477)	1:54:A:ILE:HG22	1:81:A:VAL:HG23	4	0.11
(1,1477)	1:54:A:ILE:HG23	1:81:A:VAL:HG21	4	0.11
(1,1477)	1:54:A:ILE:HG23	1:81:A:VAL:HG22	4	0.11
(1,1477)	1:54:A:ILE:HG23	1:81:A:VAL:HG23	4	0.11
(1,1349)	1:68:A:LEU:HD21	1:74:A:TRP:H	3	0.11
(1,1349)	1:68:A:LEU:HD22	1:74:A:TRP:H	3	0.11
(1,1349)	1:68:A:LEU:HD23	1:74:A:TRP:H	3	0.11
(1,1349)	1:68:A:LEU:HD21	1:74:A:TRP:H	13	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1349)	1:68:A:LEU:HD22	1:74:A:TRP:H	13	0.11
(1,1349)	1:68:A:LEU:HD23	1:74:A:TRP:H	13	0.11
(1,1338)	1:29:A:VAL:HG21	1:31:A:GLU:HG3	17	0.11
(1,1338)	1:29:A:VAL:HG22	1:31:A:GLU:HG3	17	0.11
(1,1338)	1:29:A:VAL:HG23	1:31:A:GLU:HG3	17	0.11
(1,1335)	1:42:A:LEU:HG	1:68:A:LEU:HD11	12	0.11
(1,1335)	1:42:A:LEU:HG	1:68:A:LEU:HD12	12	0.11
(1,1335)	1:42:A:LEU:HG	1:68:A:LEU:HD13	12	0.11
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD11	9	0.11
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD12	9	0.11
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD13	9	0.11
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD11	9	0.11
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD12	9	0.11
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD13	9	0.11
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD11	9	0.11
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD12	9	0.11
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD13	9	0.11
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD11	20	0.11
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD12	20	0.11
(1,1307)	1:14:A:LEU:HD11	1:82:A:LEU:HD13	20	0.11
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD11	20	0.11
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD12	20	0.11
(1,1307)	1:14:A:LEU:HD12	1:82:A:LEU:HD13	20	0.11
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD11	20	0.11
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD12	20	0.11
(1,1307)	1:14:A:LEU:HD13	1:82:A:LEU:HD13	20	0.11
(1,1257)	1:71:A:LYS:HD3	1:74:A:TRP:H	3	0.11
(1,1257)	1:71:A:LYS:HD3	1:74:A:TRP:H	4	0.11
(1,1257)	1:71:A:LYS:HD3	1:74:A:TRP:H	7	0.11
(1,1257)	1:71:A:LYS:HD3	1:74:A:TRP:H	12	0.11
(1,1257)	1:71:A:LYS:HD3	1:74:A:TRP:H	15	0.11
(1,1194)	1:3:A:LYS:HG2	1:5:A:VAL:H	5	0.11
(1,1194)	1:3:A:LYS:HG3	1:5:A:VAL:H	5	0.11
(1,1194)	1:3:A:LYS:HG2	1:5:A:VAL:H	11	0.11
(1,1194)	1:3:A:LYS:HG3	1:5:A:VAL:H	11	0.11
(1,1091)	1:113:A:ILE:H	1:116:A:VAL:HB	4	0.11
(1,1091)	1:113:A:ILE:H	1:116:A:VAL:HB	11	0.11
(1,870)	1:20:A:PHE:H	1:20:A:PHE:HD1	8	0.11
(1,870)	1:20:A:PHE:H	1:20:A:PHE:HD2	8	0.11
(1,870)	1:20:A:PHE:H	1:20:A:PHE:HD1	16	0.11
(1,870)	1:20:A:PHE:H	1:20:A:PHE:HD2	16	0.11
(1,801)	1:62:A:PHE:H	1:62:A:PHE:HZ	9	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,765)	1:81:A:VAL:HG21	1:82:A:LEU:H	20	0.11
(1,765)	1:81:A:VAL:HG22	1:82:A:LEU:H	20	0.11
(1,765)	1:81:A:VAL:HG23	1:82:A:LEU:H	20	0.11
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD11	1	0.11
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD12	1	0.11
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD13	1	0.11
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD11	3	0.11
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD12	3	0.11
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD13	3	0.11
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD11	4	0.11
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD12	4	0.11
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD13	4	0.11
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD11	13	0.11
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD12	13	0.11
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD13	13	0.11
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD11	14	0.11
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD12	14	0.11
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD13	14	0.11
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD11	19	0.11
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD12	19	0.11
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD13	19	0.11
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD11	20	0.11
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD12	20	0.11
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD13	20	0.11
(1,753)	1:67:A:LYS:H	1:67:A:LYS:HG2	2	0.11
(1,753)	1:67:A:LYS:H	1:67:A:LYS:HG2	10	0.11
(1,753)	1:67:A:LYS:H	1:67:A:LYS:HG2	18	0.11
(1,744)	1:80:A:ILE:H	1:80:A:ILE:HD11	14	0.11
(1,744)	1:80:A:ILE:H	1:80:A:ILE:HD12	14	0.11
(1,744)	1:80:A:ILE:H	1:80:A:ILE:HD13	14	0.11
(1,744)	1:80:A:ILE:H	1:80:A:ILE:HD11	18	0.11
(1,744)	1:80:A:ILE:H	1:80:A:ILE:HD12	18	0.11
(1,744)	1:80:A:ILE:H	1:80:A:ILE:HD13	18	0.11
(1,741)	1:51:A:VAL:HG21	1:80:A:ILE:H	14	0.11
(1,741)	1:51:A:VAL:HG22	1:80:A:ILE:H	14	0.11
(1,741)	1:51:A:VAL:HG23	1:80:A:ILE:H	14	0.11
(1,709)	1:74:A:TRP:H	1:74:A:TRP:HE3	3	0.11
(1,709)	1:74:A:TRP:H	1:74:A:TRP:HE3	12	0.11
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE1	11	0.11
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE2	11	0.11
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE1	11	0.11
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE2	11	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE1	11	0.11
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE2	11	0.11
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE1	15	0.11
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE2	15	0.11
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE1	15	0.11
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE2	15	0.11
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE1	15	0.11
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE2	15	0.11
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE1	19	0.11
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE2	19	0.11
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE1	19	0.11
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE2	19	0.11
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE1	19	0.11
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE2	19	0.11
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB1	4	0.11
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB2	4	0.11
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB3	4	0.11
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB1	4	0.11
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB2	4	0.11
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB3	4	0.11
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB1	4	0.11
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB2	4	0.11
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB3	4	0.11
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB1	11	0.11
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB2	11	0.11
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB3	11	0.11
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB1	11	0.11
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB2	11	0.11
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB3	11	0.11
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB1	11	0.11
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB2	11	0.11
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB3	11	0.11
(1,611)	1:82:A:LEU:HD11	1:103:A:MET:HG3	6	0.11
(1,611)	1:82:A:LEU:HD12	1:103:A:MET:HG3	6	0.11
(1,611)	1:82:A:LEU:HD13	1:103:A:MET:HG3	6	0.11
(1,611)	1:82:A:LEU:HD11	1:103:A:MET:HG3	10	0.11
(1,611)	1:82:A:LEU:HD12	1:103:A:MET:HG3	10	0.11
(1,611)	1:82:A:LEU:HD13	1:103:A:MET:HG3	10	0.11
(1,592)	1:41:A:LYS:HA	1:44:A:GLU:HB2	3	0.11
(1,592)	1:41:A:LYS:HA	1:44:A:GLU:HB2	11	0.11
(1,592)	1:41:A:LYS:HA	1:44:A:GLU:HB2	12	0.11
(1,592)	1:41:A:LYS:HA	1:44:A:GLU:HB2	16	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,592)	1:41:A:LYS:HA	1:44:A:GLU:HB2	18	0.11
(1,591)	1:41:A:LYS:HA	1:44:A:GLU:HB3	4	0.11
(1,591)	1:41:A:LYS:HA	1:44:A:GLU:HB3	8	0.11
(1,591)	1:41:A:LYS:HA	1:44:A:GLU:HB3	12	0.11
(1,591)	1:41:A:LYS:HA	1:44:A:GLU:HB3	13	0.11
(1,591)	1:41:A:LYS:HA	1:44:A:GLU:HB3	16	0.11
(1,591)	1:41:A:LYS:HA	1:44:A:GLU:HB3	17	0.11
(1,572)	1:18:A:VAL:HG11	1:51:A:VAL:HG11	17	0.11
(1,572)	1:18:A:VAL:HG11	1:51:A:VAL:HG12	17	0.11
(1,572)	1:18:A:VAL:HG11	1:51:A:VAL:HG13	17	0.11
(1,572)	1:18:A:VAL:HG12	1:51:A:VAL:HG11	17	0.11
(1,572)	1:18:A:VAL:HG12	1:51:A:VAL:HG12	17	0.11
(1,572)	1:18:A:VAL:HG12	1:51:A:VAL:HG13	17	0.11
(1,572)	1:18:A:VAL:HG13	1:51:A:VAL:HG11	17	0.11
(1,572)	1:18:A:VAL:HG13	1:51:A:VAL:HG12	17	0.11
(1,572)	1:18:A:VAL:HG13	1:51:A:VAL:HG13	17	0.11
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD11	19	0.11
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD12	19	0.11
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD13	19	0.11
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD11	20	0.11
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD12	20	0.11
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD13	20	0.11
(1,553)	1:83:A:THR:H	1:103:A:MET:H	11	0.11
(1,542)	1:80:A:ILE:HA	1:101:A:LYS:H	18	0.11
(1,508)	1:52:A:LEU:HB2	1:82:A:LEU:H	4	0.11
(1,495)	1:51:A:VAL:HG11	1:80:A:ILE:H	14	0.11
(1,495)	1:51:A:VAL:HG12	1:80:A:ILE:H	14	0.11
(1,495)	1:51:A:VAL:HG13	1:80:A:ILE:H	14	0.11
(1,474)	1:71:A:LYS:CD	1:74:A:TRP:CZ2	4	0.11
(1,474)	1:71:A:LYS:CD	1:74:A:TRP:CZ2	18	0.11
(1,434)	1:50:A:ILE:H	1:79:A:VAL:HA	13	0.11
(1,376)	1:27:A:TYR:HD1	1:28:A:GLU:H	6	0.11
(1,376)	1:27:A:TYR:HD2	1:28:A:GLU:H	6	0.11
(1,372)	1:5:A:VAL:H	1:28:A:GLU:H	13	0.11
(1,371)	1:4:A:LYS:HA	1:28:A:GLU:H	11	0.11
(1,371)	1:4:A:LYS:HA	1:28:A:GLU:H	12	0.11
(1,361)	1:24:A:LYS:HA	1:26:A:GLY:H	11	0.11
(1,357)	1:23:A:LYS:HB2	1:26:A:GLY:H	20	0.11
(1,357)	1:23:A:LYS:HB3	1:26:A:GLY:H	20	0.11
(1,296)	1:11:A:SER:HA	1:13:A:VAL:H	5	0.11
(1,272)	1:7:A:LEU:HB3	1:8:A:VAL:H	3	0.11
(1,272)	1:7:A:LEU:HB3	1:8:A:VAL:H	9	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,267)	1:6:A:LEU:HB3	1:7:A:LEU:H	5	0.11
(1,261)	1:6:A:LEU:H	1:47:A:PRO:HG3	7	0.11
(1,261)	1:6:A:LEU:H	1:47:A:PRO:HG3	13	0.11
(1,251)	1:4:A:LYS:HB2	1:5:A:VAL:H	1	0.11
(1,202)	1:106:A:PRO:HA	1:107:A:PHE:H	16	0.11
(1,161)	1:86:A:GLY:HA2	1:87:A:GLY:H	8	0.11
(1,161)	1:86:A:GLY:HA2	1:87:A:GLY:H	9	0.11
(1,161)	1:86:A:GLY:HA2	1:87:A:GLY:H	10	0.11
(1,157)	1:84:A:ALA:HA	1:85:A:LYS:H	3	0.11
(1,67)	1:34:A:ASN:HA	1:35:A:GLY:H	2	0.11
(1,24)	1:13:A:VAL:H	1:14:A:LEU:H	1	0.11
(1,24)	1:13:A:VAL:H	1:14:A:LEU:H	8	0.11
(1,24)	1:13:A:VAL:H	1:14:A:LEU:H	19	0.11
(2,107)	1:94:A:ALA:O	1:99:A:ALA:H	16	0.1
(2,107)	1:94:A:ALA:O	1:99:A:ALA:H	19	0.1
(2,87)	1:71:A:LYS:O	1:74:A:TRP:H	2	0.1
(2,87)	1:71:A:LYS:O	1:74:A:TRP:H	7	0.1
(2,87)	1:71:A:LYS:O	1:74:A:TRP:H	10	0.1
(2,83)	1:64:A:VAL:O	1:68:A:LEU:H	11	0.1
(2,75)	1:60:A:ASP:O	1:64:A:VAL:H	4	0.1
(2,75)	1:60:A:ASP:O	1:64:A:VAL:H	9	0.1
(2,59)	1:20:A:PHE:O	1:24:A:LYS:H	17	0.1
(2,51)	1:16:A:LYS:O	1:20:A:PHE:H	19	0.1
(2,49)	1:15:A:ARG:O	1:19:A:SER:H	7	0.1
(2,46)	1:13:A:VAL:O	1:17:A:ILE:N	11	0.1
(2,12)	1:7:A:LEU:N	1:30:A:ILE:O	17	0.1
(1,1888)	1:82:A:LEU:HA	1:103:A:MET:HB3	4	0.1
(1,1861)	1:82:A:LEU:HB2	1:104:A:ARG:HA	18	0.1
(1,1861)	1:82:A:LEU:HB2	1:104:A:ARG:HA	19	0.1
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD11	12	0.1
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD12	12	0.1
(1,1837)	1:21:A:ASN:HB3	1:22:A:LEU:HD13	12	0.1
(1,1574)	1:71:A:LYS:HG3	1:73:A:GLU:H	12	0.1
(1,1484)	1:80:A:ILE:HD11	1:116:A:VAL:H	8	0.1
(1,1484)	1:80:A:ILE:HD12	1:116:A:VAL:H	8	0.1
(1,1484)	1:80:A:ILE:HD13	1:116:A:VAL:H	8	0.1
(1,1349)	1:68:A:LEU:HD21	1:74:A:TRP:H	18	0.1
(1,1349)	1:68:A:LEU:HD22	1:74:A:TRP:H	18	0.1
(1,1349)	1:68:A:LEU:HD23	1:74:A:TRP:H	18	0.1
(1,1349)	1:68:A:LEU:HD21	1:74:A:TRP:H	20	0.1
(1,1349)	1:68:A:LEU:HD22	1:74:A:TRP:H	20	0.1
(1,1349)	1:68:A:LEU:HD23	1:74:A:TRP:H	20	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1257)	1:71:A:LYS:HD3	1:74:A:TRP:H	1	0.1
(1,1257)	1:71:A:LYS:HD3	1:74:A:TRP:H	6	0.1
(1,1257)	1:71:A:LYS:HD3	1:74:A:TRP:H	11	0.1
(1,1127)	1:22:A:LEU:HD21	1:116:A:VAL:HG11	19	0.1
(1,1127)	1:22:A:LEU:HD21	1:116:A:VAL:HG12	19	0.1
(1,1127)	1:22:A:LEU:HD21	1:116:A:VAL:HG13	19	0.1
(1,1127)	1:22:A:LEU:HD22	1:116:A:VAL:HG11	19	0.1
(1,1127)	1:22:A:LEU:HD22	1:116:A:VAL:HG12	19	0.1
(1,1127)	1:22:A:LEU:HD22	1:116:A:VAL:HG13	19	0.1
(1,1127)	1:22:A:LEU:HD23	1:116:A:VAL:HG11	19	0.1
(1,1127)	1:22:A:LEU:HD23	1:116:A:VAL:HG12	19	0.1
(1,1127)	1:22:A:LEU:HD23	1:116:A:VAL:HG13	19	0.1
(1,1091)	1:113:A:ILE:H	1:116:A:VAL:HB	8	0.1
(1,1091)	1:113:A:ILE:H	1:116:A:VAL:HB	10	0.1
(1,880)	1:50:A:ILE:H	1:50:A:ILE:HD11	15	0.1
(1,880)	1:50:A:ILE:H	1:50:A:ILE:HD12	15	0.1
(1,880)	1:50:A:ILE:H	1:50:A:ILE:HD13	15	0.1
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD11	7	0.1
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD12	7	0.1
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD13	7	0.1
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD11	9	0.1
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD12	9	0.1
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD13	9	0.1
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD11	15	0.1
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD12	15	0.1
(1,764)	1:82:A:LEU:H	1:82:A:LEU:HD13	15	0.1
(1,753)	1:67:A:LYS:H	1:67:A:LYS:HG2	15	0.1
(1,744)	1:80:A:ILE:H	1:80:A:ILE:HD11	12	0.1
(1,744)	1:80:A:ILE:H	1:80:A:ILE:HD12	12	0.1
(1,744)	1:80:A:ILE:H	1:80:A:ILE:HD13	12	0.1
(1,709)	1:74:A:TRP:H	1:74:A:TRP:HE3	5	0.1
(1,648)	1:116:A:VAL:HA	1:120:A:LEU:HD11	4	0.1
(1,648)	1:116:A:VAL:HA	1:120:A:LEU:HD12	4	0.1
(1,648)	1:116:A:VAL:HA	1:120:A:LEU:HD13	4	0.1
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE1	3	0.1
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE2	3	0.1
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE1	3	0.1
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE2	3	0.1
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE1	3	0.1
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE2	3	0.1
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE1	9	0.1
(1,630)	1:103:A:MET:HE1	1:107:A:PHE:HE2	9	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE1	9	0.1
(1,630)	1:103:A:MET:HE2	1:107:A:PHE:HE2	9	0.1
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE1	9	0.1
(1,630)	1:103:A:MET:HE3	1:107:A:PHE:HE2	9	0.1
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB1	5	0.1
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB2	5	0.1
(1,625)	1:81:A:VAL:HG11	1:99:A:ALA:HB3	5	0.1
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB1	5	0.1
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB2	5	0.1
(1,625)	1:81:A:VAL:HG12	1:99:A:ALA:HB3	5	0.1
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB1	5	0.1
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB2	5	0.1
(1,625)	1:81:A:VAL:HG13	1:99:A:ALA:HB3	5	0.1
(1,611)	1:82:A:LEU:HD11	1:103:A:MET:HG3	3	0.1
(1,611)	1:82:A:LEU:HD12	1:103:A:MET:HG3	3	0.1
(1,611)	1:82:A:LEU:HD13	1:103:A:MET:HG3	3	0.1
(1,606)	1:61:A:GLY:HA2	1:64:A:VAL:HB	1	0.1
(1,606)	1:61:A:GLY:HA3	1:64:A:VAL:HB	1	0.1
(1,592)	1:41:A:LYS:HA	1:44:A:GLU:HB2	5	0.1
(1,591)	1:41:A:LYS:HA	1:44:A:GLU:HB3	18	0.1
(1,591)	1:41:A:LYS:HA	1:44:A:GLU:HB3	19	0.1
(1,591)	1:41:A:LYS:HA	1:44:A:GLU:HB3	20	0.1
(1,572)	1:18:A:VAL:HG11	1:51:A:VAL:HG11	11	0.1
(1,572)	1:18:A:VAL:HG11	1:51:A:VAL:HG12	11	0.1
(1,572)	1:18:A:VAL:HG11	1:51:A:VAL:HG13	11	0.1
(1,572)	1:18:A:VAL:HG12	1:51:A:VAL:HG11	11	0.1
(1,572)	1:18:A:VAL:HG12	1:51:A:VAL:HG12	11	0.1
(1,572)	1:18:A:VAL:HG12	1:51:A:VAL:HG13	11	0.1
(1,572)	1:18:A:VAL:HG13	1:51:A:VAL:HG11	11	0.1
(1,572)	1:18:A:VAL:HG13	1:51:A:VAL:HG12	11	0.1
(1,572)	1:18:A:VAL:HG13	1:51:A:VAL:HG13	11	0.1
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD11	1	0.1
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD12	1	0.1
(1,571)	1:14:A:LEU:HA	1:17:A:ILE:HD13	1	0.1
(1,542)	1:80:A:ILE:HA	1:101:A:LYS:H	2	0.1
(1,542)	1:80:A:ILE:HA	1:101:A:LYS:H	8	0.1
(1,540)	1:80:A:ILE:HG21	1:101:A:LYS:H	11	0.1
(1,540)	1:80:A:ILE:HG22	1:101:A:LYS:H	11	0.1
(1,540)	1:80:A:ILE:HG23	1:101:A:LYS:H	11	0.1
(1,372)	1:5:A:VAL:H	1:28:A:GLU:H	3	0.1
(1,357)	1:23:A:LYS:HB2	1:26:A:GLY:H	11	0.1
(1,357)	1:23:A:LYS:HB3	1:26:A:GLY:H	11	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,274)	1:8:A:VAL:H	1:51:A:VAL:HB	7	0.1
(1,271)	1:7:A:LEU:HD11	1:8:A:VAL:H	17	0.1
(1,271)	1:7:A:LEU:HD12	1:8:A:VAL:H	17	0.1
(1,271)	1:7:A:LEU:HD13	1:8:A:VAL:H	17	0.1
(1,267)	1:6:A:LEU:HB3	1:7:A:LEU:H	11	0.1
(1,261)	1:6:A:LEU:H	1:47:A:PRO:HG3	19	0.1
(1,256)	1:5:A:VAL:H	1:27:A:TYR:HB3	12	0.1
(1,161)	1:86:A:GLY:HA2	1:87:A:GLY:H	20	0.1
(1,114)	1:61:A:GLY:H	1:62:A:PHE:H	6	0.1
(1,110)	1:59:A:MET:H	1:60:A:ASP:H	7	0.1
(1,67)	1:34:A:ASN:HA	1:35:A:GLY:H	5	0.1
(1,24)	1:13:A:VAL:H	1:14:A:LEU:H	20	0.1
(1,3)	1:3:A:LYS:HA	1:4:A:LYS:H	9	0.1
(1,3)	1:3:A:LYS:HA	1:4:A:LYS:H	13	0.1

10 Dihedral-angle violation analysis

No dihedral-angle restraints found