



Full wwPDB NMR Structure Validation Report ⓘ

Mar 7, 2026 – 02:38 AM UTC

PDB ID : 5T82 / pdb_00005t82
BMRB ID : 30171
Title : HIV-1 reverse transcriptase thumb subdomain
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Deposited on : 2016-09-06

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

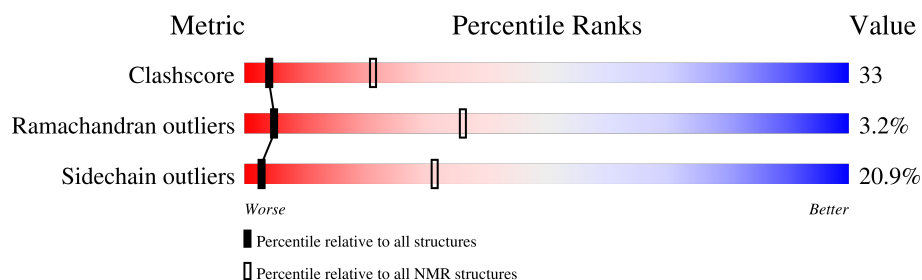
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 82%.

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



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	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	90	30% 38% . 28%

2 Ensemble composition and analysis ⓘ

This entry contains 30 models. Model 17 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:244-A:283, A:288-A:312 (65)	0.48	17

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

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

The models can be grouped into 4 clusters. No single-model clusters were found.

Cluster number	Models
1	3, 6, 7, 9, 12, 13, 16, 17, 19, 20, 21, 22, 26, 27, 28, 30
2	4, 18, 23, 25, 29
3	2, 8, 11, 14, 24
4	1, 5, 10, 15

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1491 atoms, of which 751 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Reverse transcriptase.

Mol	Chain	Residues	Atoms					Trace
1	A	90	Total	C	H	N	O	0
			1491	475	751	131	134	

There are 9 discrepancies between the modelled and reference sequences:

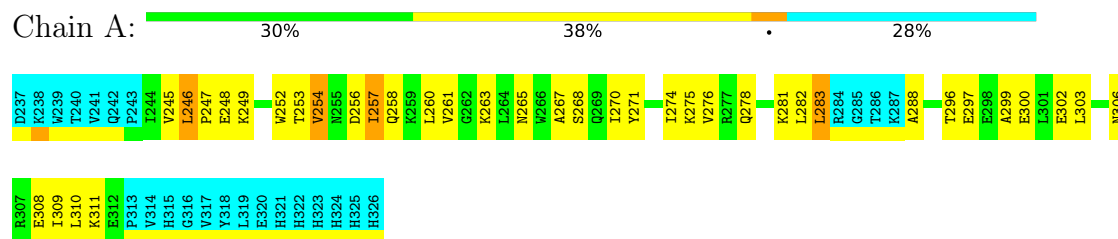
Chain	Residue	Modelled	Actual	Comment	Reference
A	280	SER	CYS	engineered mutation	UNP Q74596
A	319	LEU	-	expression tag	UNP Q74596
A	320	GLU	-	expression tag	UNP Q74596
A	321	HIS	-	expression tag	UNP Q74596
A	322	HIS	-	expression tag	UNP Q74596
A	323	HIS	-	expression tag	UNP Q74596
A	324	HIS	-	expression tag	UNP Q74596
A	325	HIS	-	expression tag	UNP Q74596
A	326	HIS	-	expression tag	UNP Q74596

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: Reverse transcriptase

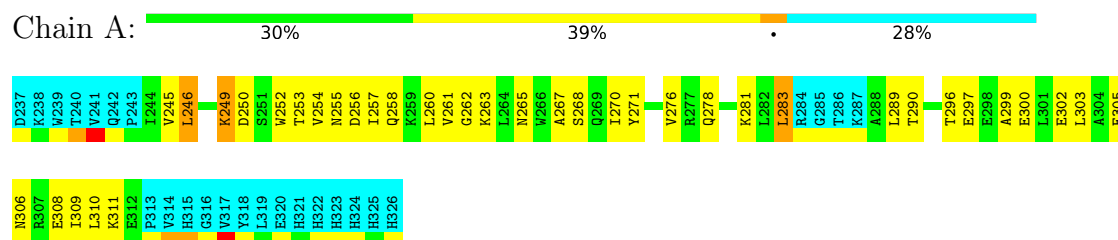


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

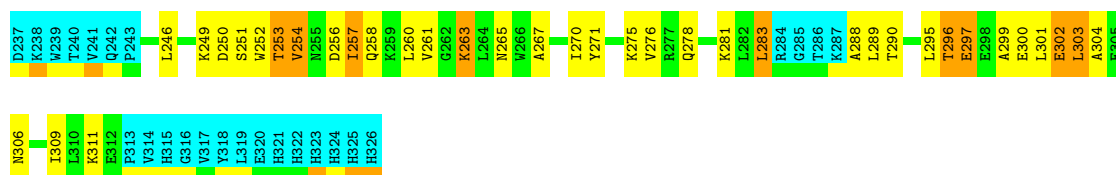
- Molecule 1: Reverse transcriptase



4.2.2 Score per residue for model 2

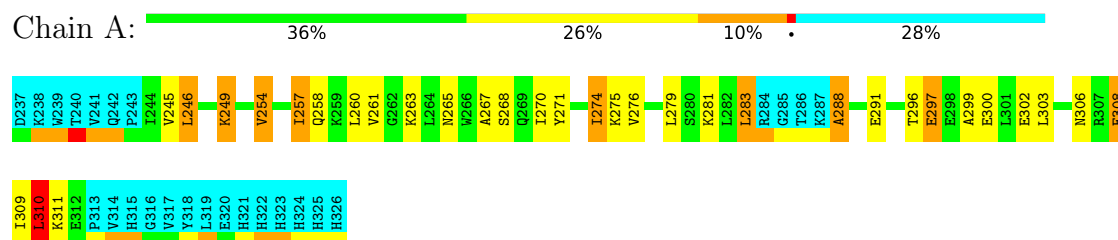
- Molecule 1: Reverse transcriptase





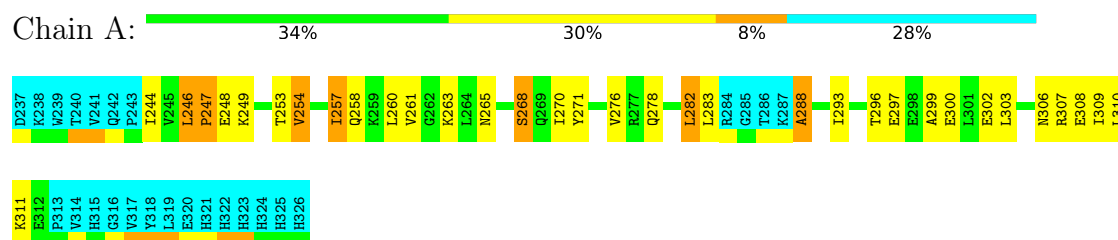
4.2.3 Score per residue for model 3

- Molecule 1: Reverse transcriptase



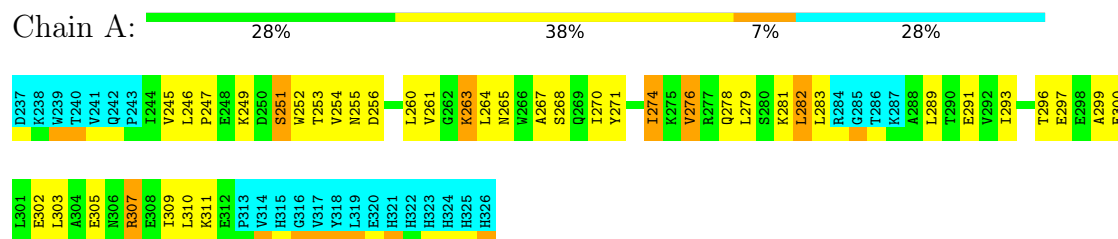
4.2.4 Score per residue for model 4

- Molecule 1: Reverse transcriptase



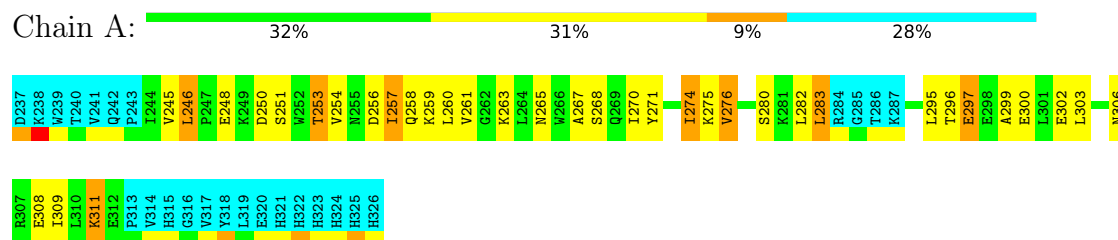
4.2.5 Score per residue for model 5

- Molecule 1: Reverse transcriptase



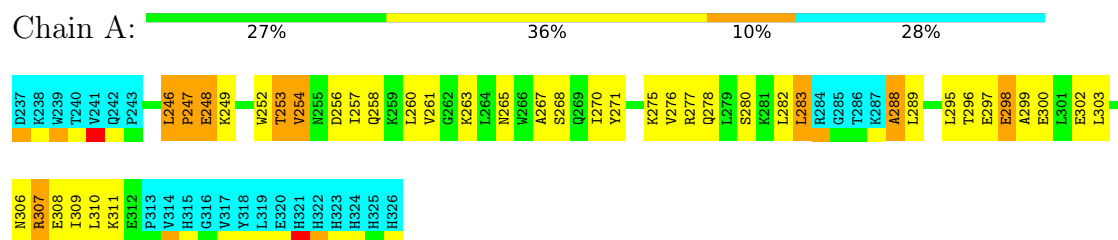
4.2.6 Score per residue for model 6

- Molecule 1: Reverse transcriptase



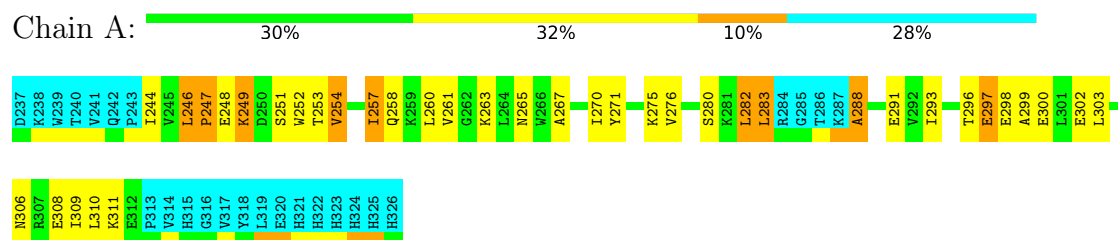
4.2.7 Score per residue for model 7

- Molecule 1: Reverse transcriptase



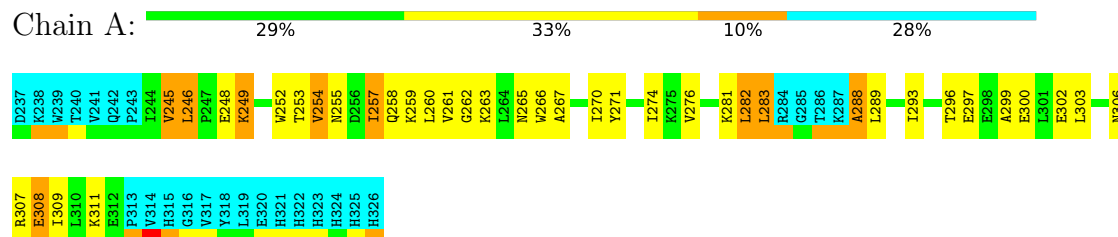
4.2.8 Score per residue for model 8

- Molecule 1: Reverse transcriptase



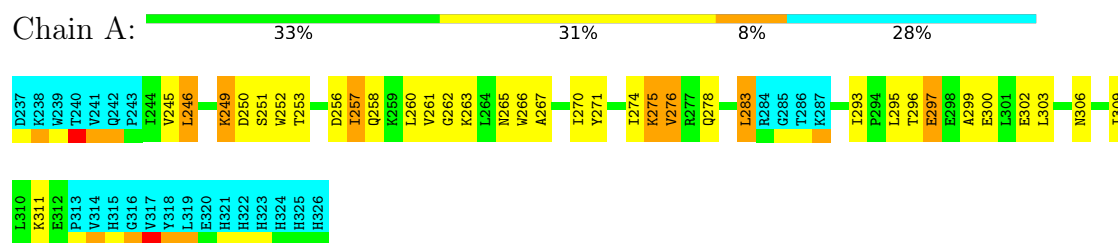
4.2.9 Score per residue for model 9

- Molecule 1: Reverse transcriptase



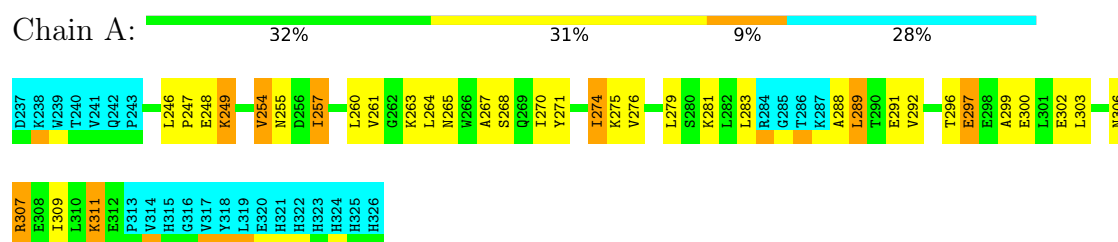
4.2.10 Score per residue for model 10

- Molecule 1: Reverse transcriptase



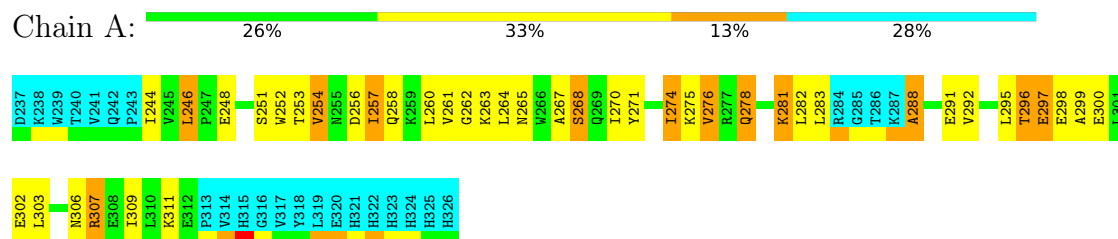
4.2.11 Score per residue for model 11

- Molecule 1: Reverse transcriptase



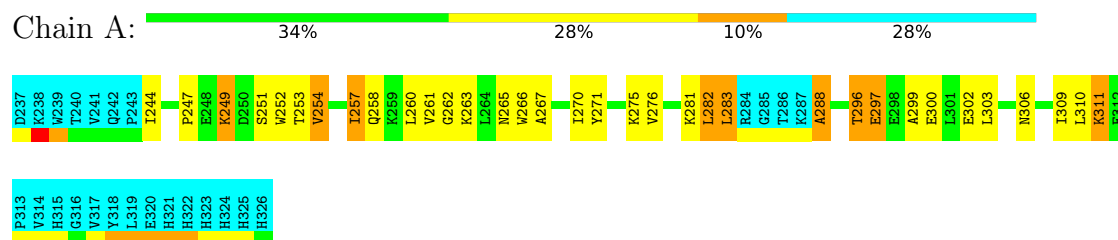
4.2.12 Score per residue for model 12

- Molecule 1: Reverse transcriptase



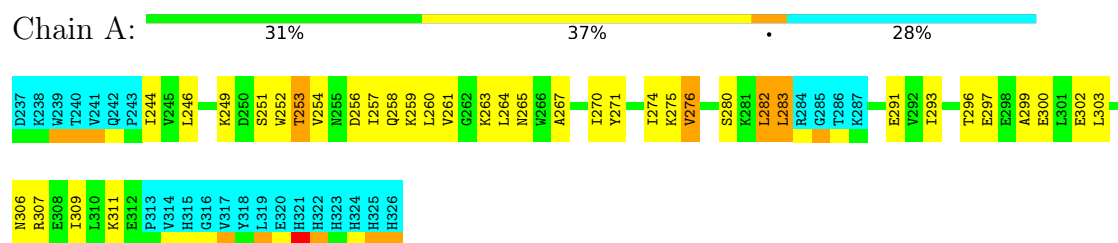
4.2.13 Score per residue for model 13

- Molecule 1: Reverse transcriptase



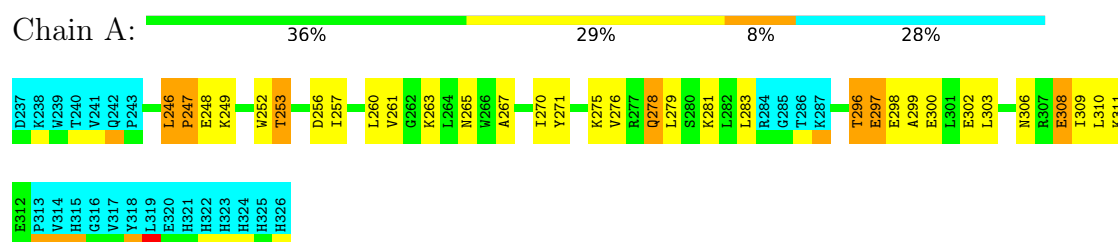
4.2.14 Score per residue for model 14

- Molecule 1: Reverse transcriptase



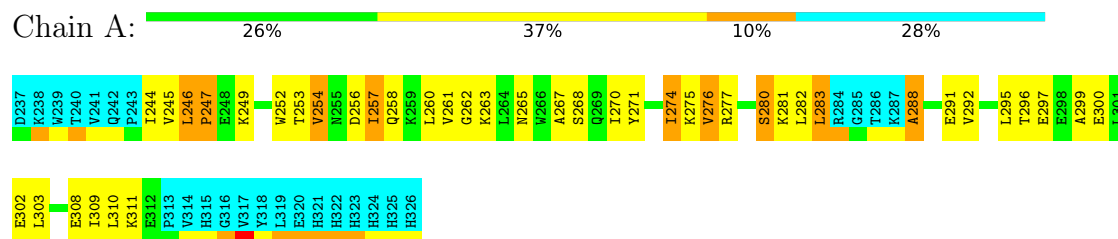
4.2.15 Score per residue for model 15

- Molecule 1: Reverse transcriptase



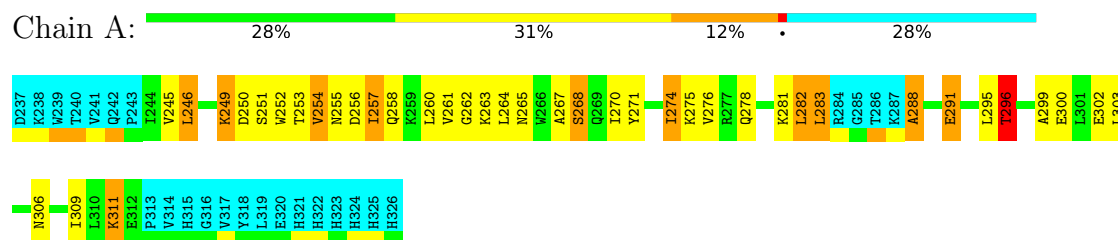
4.2.16 Score per residue for model 16

- Molecule 1: Reverse transcriptase



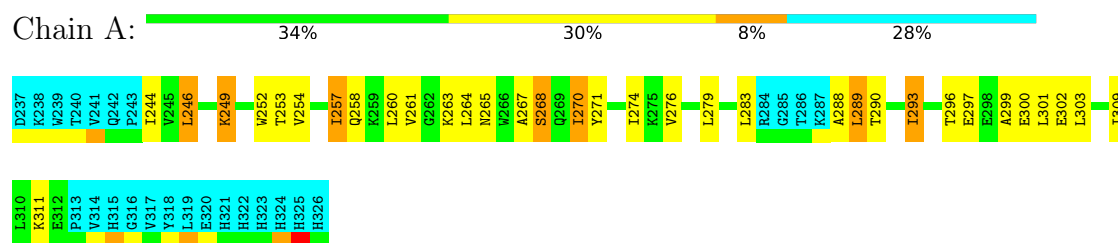
4.2.17 Score per residue for model 17 (medoid)

- Molecule 1: Reverse transcriptase



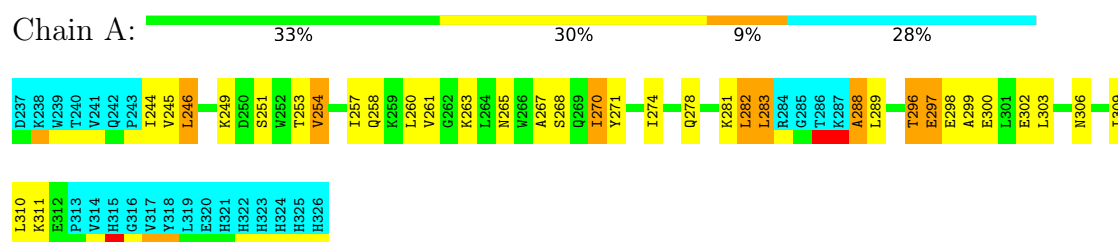
4.2.18 Score per residue for model 18

- Molecule 1: Reverse transcriptase



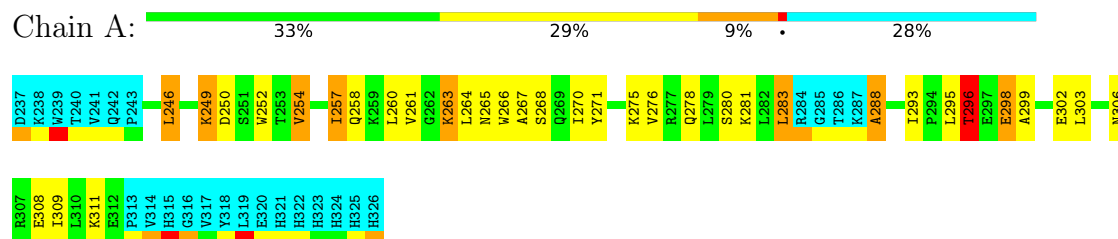
4.2.19 Score per residue for model 19

- Molecule 1: Reverse transcriptase



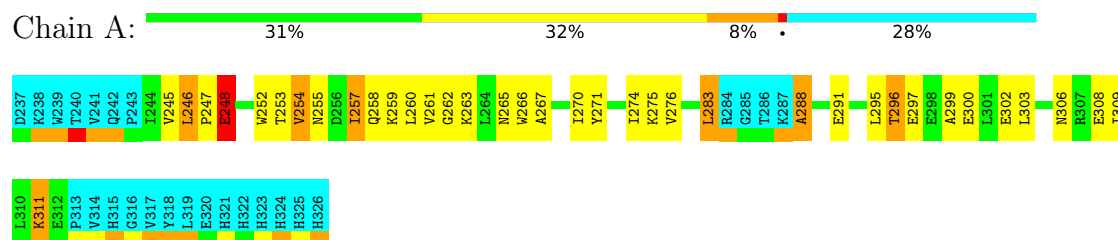
4.2.20 Score per residue for model 20

- Molecule 1: Reverse transcriptase



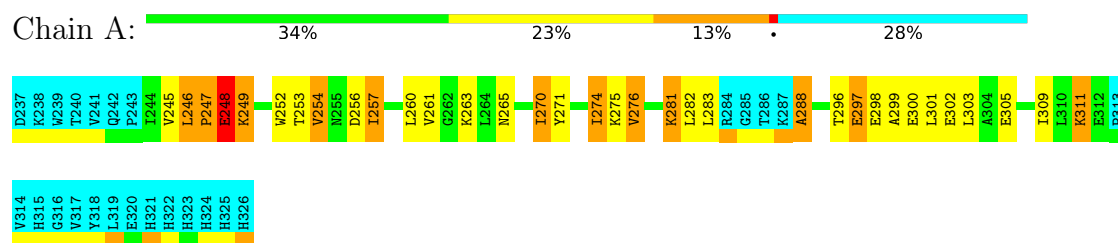
4.2.21 Score per residue for model 21

- Molecule 1: Reverse transcriptase



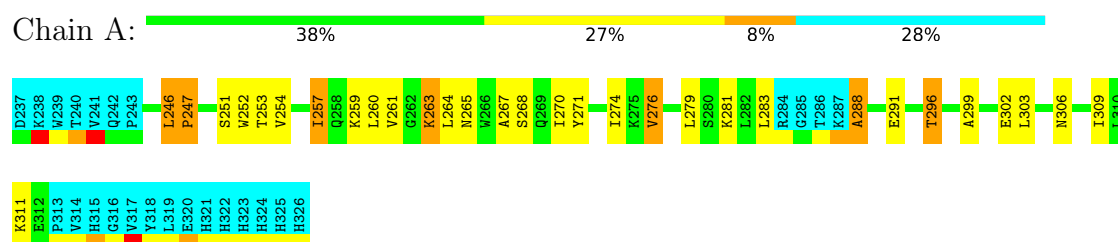
4.2.22 Score per residue for model 22

- Molecule 1: Reverse transcriptase



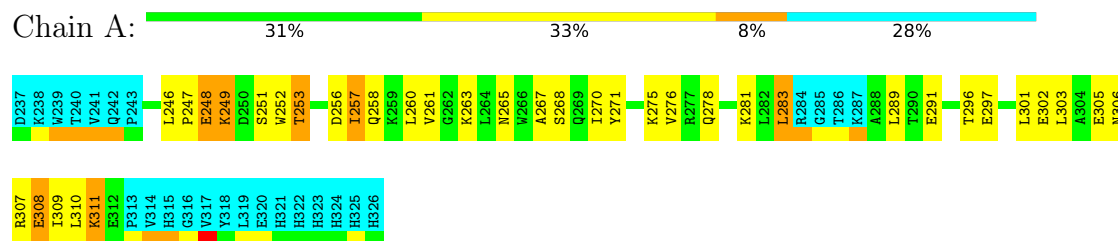
4.2.23 Score per residue for model 23

- Molecule 1: Reverse transcriptase



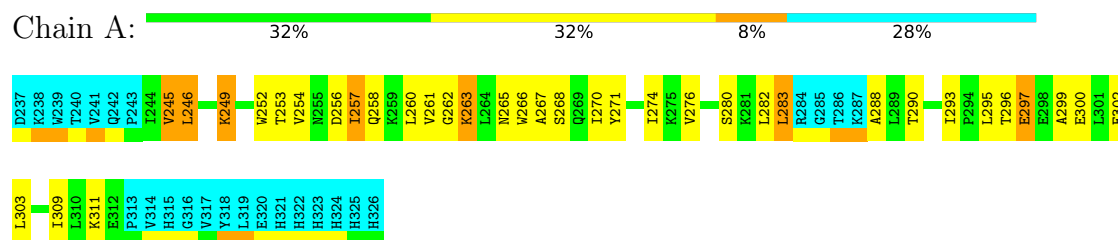
4.2.24 Score per residue for model 24

- Molecule 1: Reverse transcriptase



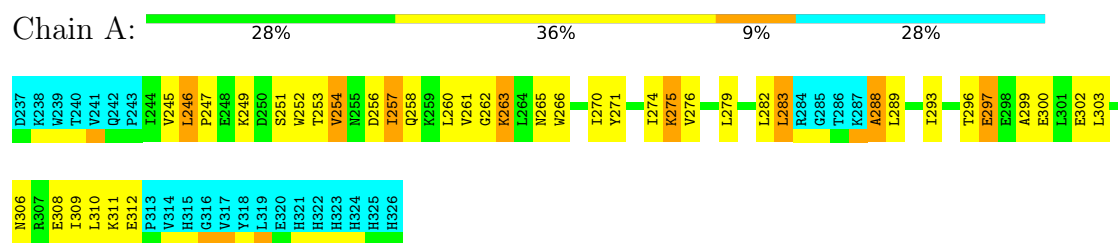
4.2.25 Score per residue for model 25

- Molecule 1: Reverse transcriptase



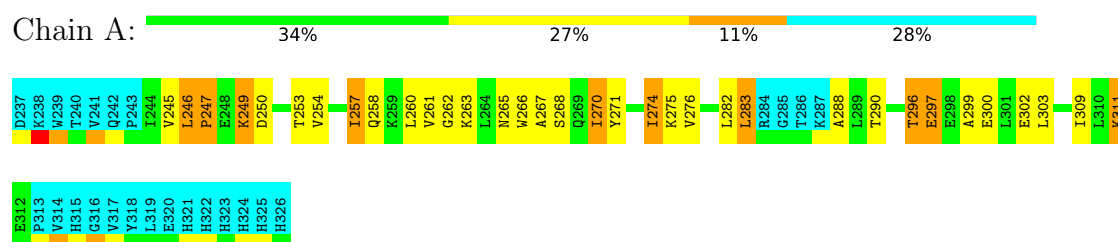
4.2.26 Score per residue for model 26

- Molecule 1: Reverse transcriptase



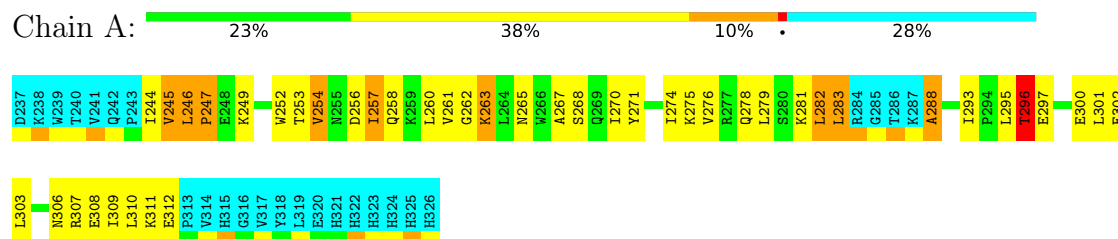
4.2.27 Score per residue for model 27

- Molecule 1: Reverse transcriptase



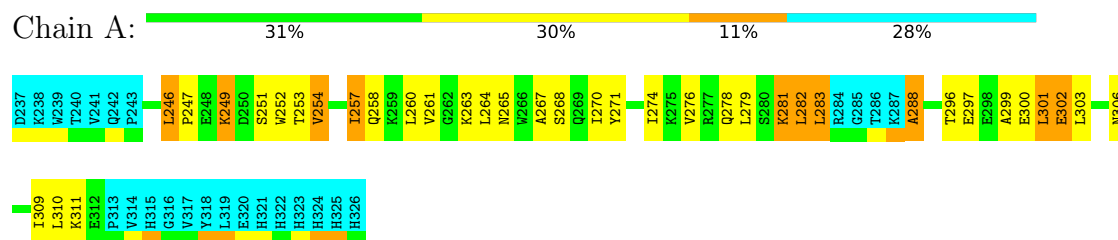
4.2.28 Score per residue for model 28

- Molecule 1: Reverse transcriptase



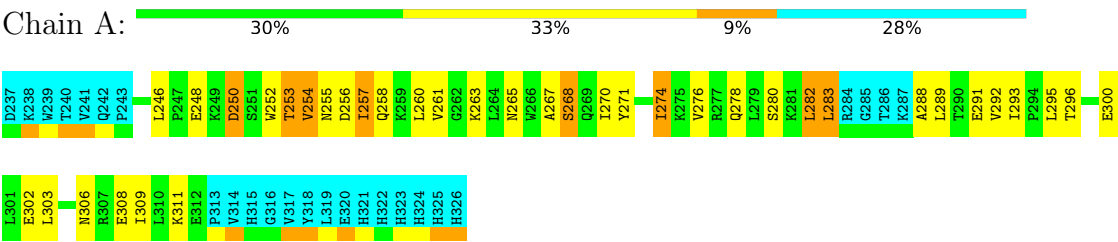
4.2.29 Score per residue for model 29

- Molecule 1: Reverse transcriptase



4.2.30 Score per residue for model 30

● Molecule 1: Reverse transcriptase



5 Refinement protocol and experimental data overview

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

Of the 256 calculated structures, 30 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
CNS	refinement	

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

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	939
Number of shifts mapped to atoms	939
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	82%

6 Model quality

6.1 Standard geometry

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

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	523	552	552	35±4
All	All	15690	16560	16560	1061

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 33.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:246:LEU:H	1:A:246:LEU:HD22	0.94	1.23	9	2
1:A:246:LEU:HD12	1:A:246:LEU:H	0.79	1.38	29	11
1:A:255:ASN:OD1	1:A:289:LEU:HD22	0.78	1.78	5	2
1:A:246:LEU:N	1:A:246:LEU:HD13	0.77	1.95	25	1
1:A:245:VAL:C	1:A:246:LEU:HD23	0.77	2.05	3	4
1:A:245:VAL:C	1:A:246:LEU:HD13	0.76	2.06	9	2
1:A:246:LEU:HD13	1:A:246:LEU:N	0.75	1.95	9	1
1:A:246:LEU:HD22	1:A:246:LEU:N	0.75	1.97	9	2
1:A:257:ILE:O	1:A:261:VAL:HG23	0.72	1.83	30	21
1:A:246:LEU:HD23	1:A:246:LEU:N	0.71	2.01	3	5
1:A:246:LEU:HD12	1:A:246:LEU:N	0.70	2.01	12	11
1:A:303:LEU:C	1:A:303:LEU:HD13	0.69	2.12	14	30
1:A:276:VAL:HG22	1:A:276:VAL:O	0.69	1.88	22	22
1:A:265:ASN:OD1	1:A:276:VAL:HG11	0.68	1.89	12	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:301:LEU:C	1:A:301:LEU:HD13	0.68	2.13	29	1
1:A:301:LEU:C	1:A:301:LEU:HD23	0.63	2.17	18	1
1:A:264:LEU:HD12	1:A:279:LEU:HD13	0.62	1.70	23	1
1:A:245:VAL:O	1:A:246:LEU:HD12	0.62	1.94	5	1
1:A:279:LEU:HD21	1:A:302:GLU:OE1	0.62	1.95	18	2
1:A:254:VAL:HG23	1:A:293:ILE:HD11	0.62	1.71	30	1
1:A:254:VAL:HG21	1:A:288:ALA:O	0.61	1.96	28	17
1:A:249:LYS:NZ	1:A:252:TRP:CD2	0.61	2.69	18	1
1:A:252:TRP:CD1	1:A:295:LEU:HD11	0.60	2.32	21	6
1:A:261:VAL:O	1:A:265:ASN:ND2	0.60	2.34	21	30
1:A:258:GLN:CG	1:A:283:LEU:HD21	0.59	2.28	2	15
1:A:282:LEU:HD11	1:A:299:ALA:CB	0.58	2.28	13	4
1:A:246:LEU:N	1:A:246:LEU:CD1	0.58	2.66	4	13
1:A:267:ALA:O	1:A:271:TYR:N	0.58	2.37	20	16
1:A:261:VAL:HG13	1:A:276:VAL:CG2	0.58	2.29	29	18
1:A:282:LEU:HD11	1:A:299:ALA:HB1	0.57	1.75	13	3
1:A:261:VAL:HG12	1:A:265:ASN:ND2	0.57	2.15	7	4
1:A:302:GLU:N	1:A:302:GLU:OE1	0.57	2.38	15	1
1:A:249:LYS:CD	1:A:249:LYS:N	0.57	2.67	11	6
1:A:302:GLU:OE1	1:A:303:LEU:N	0.57	2.37	29	1
1:A:296:THR:O	1:A:299:ALA:N	0.56	2.38	26	26
1:A:302:GLU:CD	1:A:303:LEU:N	0.56	2.63	11	7
1:A:268:SER:CA	1:A:274:ILE:HD11	0.56	2.30	18	2
1:A:246:LEU:HD12	1:A:246:LEU:O	0.56	2.01	20	1
1:A:298:GLU:CD	1:A:298:GLU:H	0.56	2.09	20	2
1:A:246:LEU:N	1:A:246:LEU:CD2	0.56	2.68	16	6
1:A:260:LEU:O	1:A:263:LYS:N	0.56	2.39	4	30
1:A:279:LEU:HD11	1:A:302:GLU:CD	0.56	2.26	11	2
1:A:253:THR:O	1:A:256:ASP:N	0.56	2.39	5	8
1:A:270:ILE:O	1:A:271:TYR:CG	0.55	2.59	27	26
1:A:278:GLN:H	1:A:278:GLN:CD	0.55	2.08	15	1
1:A:270:ILE:O	1:A:271:TYR:CD1	0.55	2.60	4	10
1:A:270:ILE:O	1:A:271:TYR:CD2	0.55	2.60	7	11
1:A:279:LEU:CD2	1:A:279:LEU:N	0.55	2.70	5	1
1:A:279:LEU:HD11	1:A:302:GLU:OE1	0.55	2.02	11	2
1:A:279:LEU:HD22	1:A:279:LEU:N	0.55	2.17	28	2
1:A:297:GLU:H	1:A:297:GLU:CD	0.54	2.10	22	4
1:A:278:GLN:OE1	1:A:278:GLN:N	0.54	2.41	28	6
1:A:309:ILE:O	1:A:311:LYS:N	0.53	2.40	28	17
1:A:288:ALA:C	1:A:290:THR:H	0.53	2.10	2	4
1:A:279:LEU:N	1:A:279:LEU:HD22	0.53	2.18	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:252:TRP:CE3	1:A:256:ASP:OD2	0.53	2.62	12	5
1:A:249:LYS:O	1:A:252:TRP:CD1	0.53	2.62	13	3
1:A:265:ASN:ND2	1:A:276:VAL:HG21	0.53	2.18	23	3
1:A:276:VAL:O	1:A:276:VAL:HG13	0.53	2.04	9	3
1:A:246:LEU:HD21	1:A:264:LEU:CD2	0.53	2.34	5	1
1:A:252:TRP:CE3	1:A:256:ASP:OD1	0.53	2.62	22	4
1:A:302:GLU:CD	1:A:303:LEU:H	0.53	2.11	15	1
1:A:303:LEU:HD13	1:A:303:LEU:O	0.53	2.04	11	28
1:A:248:GLU:OE1	1:A:307:ARG:NH2	0.53	2.42	9	1
1:A:278:GLN:NE2	1:A:302:GLU:OE1	0.53	2.42	10	1
1:A:267:ALA:O	1:A:270:ILE:N	0.52	2.41	11	22
1:A:252:TRP:O	1:A:293:ILE:N	0.52	2.42	26	6
1:A:282:LEU:N	1:A:282:LEU:HD23	0.52	2.19	13	5
1:A:248:GLU:N	1:A:248:GLU:CD	0.52	2.68	24	1
1:A:308:GLU:N	1:A:308:GLU:OE1	0.52	2.43	24	1
1:A:279:LEU:N	1:A:279:LEU:CD2	0.52	2.72	28	2
1:A:254:VAL:CG2	1:A:288:ALA:O	0.52	2.57	17	5
1:A:311:LYS:CD	1:A:311:LYS:C	0.52	2.81	22	2
1:A:297:GLU:CD	1:A:297:GLU:N	0.52	2.67	22	1
1:A:249:LYS:NZ	1:A:251:SER:O	0.52	2.42	29	1
1:A:309:ILE:C	1:A:311:LYS:N	0.52	2.66	8	30
1:A:249:LYS:O	1:A:252:TRP:NE1	0.52	2.43	1	10
1:A:268:SER:N	1:A:274:ILE:HD11	0.52	2.20	25	4
1:A:246:LEU:CD1	1:A:303:LEU:HD21	0.52	2.35	16	1
1:A:279:LEU:HD11	1:A:302:GLU:OE2	0.52	2.05	23	3
1:A:252:TRP:CZ3	1:A:256:ASP:OD1	0.52	2.62	25	1
1:A:271:TYR:O	1:A:274:ILE:CG2	0.52	2.58	3	9
1:A:270:ILE:O	1:A:270:ILE:HG22	0.52	2.05	28	17
1:A:270:ILE:HG22	1:A:270:ILE:O	0.52	2.03	17	4
1:A:250:ASP:OD2	1:A:250:ASP:N	0.52	2.42	30	1
1:A:262:GLY:O	1:A:265:ASN:OD1	0.51	2.28	13	9
1:A:245:VAL:O	1:A:263:LYS:NZ	0.51	2.42	16	3
1:A:282:LEU:HD21	1:A:296:THR:HG23	0.51	1.83	22	3
1:A:278:GLN:CD	1:A:278:GLN:N	0.51	2.69	15	1
1:A:275:LYS:NZ	1:A:302:GLU:OE2	0.51	2.43	22	2
1:A:302:GLU:OE1	1:A:306:ASN:ND2	0.51	2.44	23	1
1:A:303:LEU:C	1:A:303:LEU:CD1	0.50	2.84	5	30
1:A:252:TRP:CZ3	1:A:260:LEU:HD22	0.50	2.41	23	7
1:A:257:ILE:HB	1:A:283:LEU:HD21	0.50	1.82	18	6
1:A:255:ASN:ND2	1:A:259:LYS:NZ	0.50	2.59	21	1
1:A:282:LEU:HD12	1:A:293:ILE:CG2	0.50	2.37	25	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:309:ILE:C	1:A:311:LYS:H	0.50	2.13	7	26
1:A:246:LEU:HD23	1:A:260:LEU:HD11	0.50	1.81	18	1
1:A:301:LEU:C	1:A:301:LEU:CD1	0.49	2.85	29	1
1:A:275:LYS:CB	1:A:302:GLU:OE2	0.49	2.61	28	1
1:A:258:GLN:HG3	1:A:283:LEU:HD11	0.49	1.83	28	8
1:A:282:LEU:HD12	1:A:293:ILE:HG22	0.49	1.83	25	3
1:A:265:ASN:OD1	1:A:266:TRP:N	0.49	2.45	25	7
1:A:302:GLU:N	1:A:302:GLU:CD	0.48	2.70	2	2
1:A:274:ILE:N	1:A:309:ILE:CD1	0.48	2.75	3	2
1:A:245:VAL:HG22	1:A:246:LEU:N	0.48	2.24	6	5
1:A:291:GLU:OE1	1:A:292:VAL:N	0.48	2.47	16	1
1:A:252:TRP:CZ3	1:A:260:LEU:HD13	0.48	2.44	5	1
1:A:311:LYS:N	1:A:311:LYS:CD	0.48	2.76	16	2
1:A:264:LEU:O	1:A:268:SER:N	0.48	2.47	23	1
1:A:306:ASN:C	1:A:308:GLU:N	0.48	2.70	7	14
1:A:298:GLU:O	1:A:302:GLU:OE1	0.48	2.32	15	2
1:A:245:VAL:H	1:A:263:LYS:NZ	0.48	2.06	26	1
1:A:260:LEU:O	1:A:261:VAL:C	0.47	2.57	26	30
1:A:306:ASN:O	1:A:309:ILE:N	0.47	2.47	2	6
1:A:264:LEU:O	1:A:267:ALA:HB3	0.47	2.09	18	4
1:A:258:GLN:HG3	1:A:283:LEU:HD21	0.47	1.86	2	4
1:A:308:GLU:OE1	1:A:308:GLU:CA	0.47	2.63	24	1
1:A:296:THR:O	1:A:297:GLU:C	0.47	2.58	26	24
1:A:276:VAL:O	1:A:276:VAL:CG2	0.47	2.63	3	6
1:A:258:GLN:HG2	1:A:283:LEU:HD21	0.46	1.87	10	14
1:A:261:VAL:O	1:A:265:ASN:CG	0.46	2.58	27	9
1:A:253:THR:O	1:A:257:ILE:N	0.46	2.48	15	1
1:A:279:LEU:C	1:A:281:LYS:N	0.46	2.73	29	1
1:A:246:LEU:HD11	1:A:264:LEU:HD21	0.46	1.87	14	1
1:A:245:VAL:CG2	1:A:246:LEU:N	0.46	2.78	21	3
1:A:246:LEU:HD22	1:A:310:LEU:HD11	0.46	1.87	5	1
1:A:255:ASN:CG	1:A:289:LEU:HD23	0.46	2.35	11	1
1:A:301:LEU:C	1:A:301:LEU:CD2	0.46	2.87	18	1
1:A:250:ASP:N	1:A:250:ASP:OD1	0.46	2.47	1	1
1:A:248:GLU:CG	1:A:248:GLU:O	0.46	2.63	7	3
1:A:295:LEU:O	1:A:296:THR:C	0.46	2.59	20	3
1:A:296:THR:N	1:A:299:ALA:HB3	0.46	2.26	15	1
1:A:278:GLN:N	1:A:278:GLN:CD	0.45	2.74	7	3
1:A:268:SER:C	1:A:270:ILE:H	0.45	2.19	4	5
1:A:246:LEU:O	1:A:247:PRO:O	0.45	2.34	4	8
1:A:282:LEU:CD2	1:A:296:THR:HG23	0.45	2.41	26	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:306:ASN:O	1:A:308:GLU:N	0.45	2.49	7	2
1:A:255:ASN:HD21	1:A:259:LYS:NZ	0.45	2.08	21	1
1:A:298:GLU:HA	1:A:301:LEU:HD12	0.45	1.89	22	1
1:A:252:TRP:CE3	1:A:256:ASP:CG	0.45	2.94	2	2
1:A:281:LYS:C	1:A:283:LEU:N	0.45	2.73	12	2
1:A:253:THR:O	1:A:254:VAL:C	0.45	2.60	14	4
1:A:251:SER:O	1:A:251:SER:OG	0.44	2.35	26	13
1:A:268:SER:C	1:A:270:ILE:N	0.44	2.76	4	5
1:A:268:SER:OG	1:A:274:ILE:HG21	0.44	2.12	28	1
1:A:254:VAL:HG12	1:A:289:LEU:HD23	0.44	1.89	30	1
1:A:302:GLU:O	1:A:306:ASN:OD1	0.44	2.36	29	15
1:A:264:LEU:O	1:A:267:ALA:N	0.44	2.51	18	1
1:A:299:ALA:C	1:A:302:GLU:OE1	0.44	2.60	15	1
1:A:302:GLU:O	1:A:303:LEU:C	0.44	2.61	26	21
1:A:246:LEU:HD13	1:A:260:LEU:HD11	0.44	1.88	28	3
1:A:246:LEU:C	1:A:246:LEU:HD23	0.44	2.38	24	1
1:A:264:LEU:O	1:A:268:SER:OG	0.44	2.36	17	3
1:A:252:TRP:NE1	1:A:295:LEU:HD11	0.44	2.28	10	1
1:A:275:LYS:C	1:A:302:GLU:OE2	0.43	2.61	10	1
1:A:295:LEU:O	1:A:296:THR:O	0.43	2.36	17	1
1:A:288:ALA:C	1:A:290:THR:N	0.43	2.74	2	3
1:A:308:GLU:O	1:A:311:LYS:CG	0.43	2.66	21	1
1:A:246:LEU:C	1:A:246:LEU:CD2	0.43	2.92	24	1
1:A:275:LYS:C	1:A:302:GLU:OE1	0.43	2.61	20	1
1:A:256:ASP:OD1	1:A:256:ASP:O	0.43	2.37	17	1
1:A:277:ARG:O	1:A:280:SER:OG	0.43	2.37	16	2
1:A:250:ASP:OD1	1:A:250:ASP:N	0.43	2.45	17	1
1:A:298:GLU:O	1:A:302:GLU:OE2	0.43	2.36	19	1
1:A:291:GLU:OE2	1:A:292:VAL:O	0.43	2.36	12	1
1:A:299:ALA:O	1:A:302:GLU:OE1	0.43	2.36	15	1
1:A:244:ILE:HG22	1:A:310:LEU:HD13	0.43	1.91	19	1
1:A:306:ASN:O	1:A:307:ARG:C	0.43	2.62	4	7
1:A:276:VAL:O	1:A:280:SER:OG	0.43	2.37	20	1
1:A:245:VAL:H	1:A:263:LYS:HZ2	0.43	1.57	26	1
1:A:302:GLU:O	1:A:306:ASN:CG	0.43	2.62	2	8
1:A:248:GLU:O	1:A:248:GLU:CG	0.43	2.67	11	2
1:A:291:GLU:OE1	1:A:292:VAL:O	0.43	2.37	16	2
1:A:288:ALA:O	1:A:290:THR:N	0.42	2.52	2	1
1:A:307:ARG:CG	1:A:307:ARG:HH21	0.42	2.27	11	1
1:A:265:ASN:O	1:A:268:SER:CB	0.42	2.68	19	2
1:A:308:GLU:O	1:A:308:GLU:CD	0.42	2.62	7	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:255:ASN:O	1:A:255:ASN:ND2	0.42	2.52	9	1
1:A:275:LYS:NZ	1:A:302:GLU:OE1	0.42	2.53	10	1
1:A:309:ILE:O	1:A:312:GLU:N	0.42	2.52	28	2
1:A:257:ILE:O	1:A:258:GLN:C	0.42	2.62	20	8
1:A:282:LEU:HD21	1:A:296:THR:CG2	0.42	2.44	12	1
1:A:276:VAL:O	1:A:277:ARG:C	0.42	2.62	16	1
1:A:274:ILE:HG23	1:A:306:ASN:ND2	0.42	2.30	14	1
1:A:299:ALA:O	1:A:302:GLU:CD	0.42	2.62	15	1
1:A:260:LEU:C	1:A:262:GLY:N	0.42	2.78	12	3
1:A:299:ALA:O	1:A:302:GLU:OE2	0.42	2.38	15	1
1:A:255:ASN:HD21	1:A:259:LYS:HZ1	0.42	1.58	21	1
1:A:246:LEU:HD21	1:A:310:LEU:HD11	0.42	1.92	26	1
1:A:282:LEU:HD21	1:A:295:LEU:HA	0.41	1.90	6	3
1:A:246:LEU:C	1:A:246:LEU:CD1	0.41	2.92	8	1
1:A:247:PRO:C	1:A:248:GLU:OE1	0.41	2.63	8	1
1:A:247:PRO:O	1:A:248:GLU:O	0.41	2.37	21	1
1:A:250:ASP:O	1:A:250:ASP:CG	0.41	2.62	2	1
1:A:307:ARG:CG	1:A:307:ARG:NH2	0.41	2.82	11	1
1:A:303:LEU:O	1:A:304:ALA:C	0.41	2.63	2	1
1:A:278:GLN:N	1:A:278:GLN:OE1	0.41	2.53	7	1
1:A:296:THR:OG1	1:A:298:GLU:OE2	0.41	2.37	8	1
1:A:246:LEU:C	1:A:246:LEU:HD13	0.41	2.41	8	1
1:A:297:GLU:O	1:A:301:LEU:CB	0.41	2.68	29	1
1:A:259:LYS:O	1:A:260:LEU:C	0.41	2.63	9	1
1:A:263:LYS:O	1:A:267:ALA:CB	0.41	2.69	9	3
1:A:274:ILE:HG22	1:A:275:LYS:N	0.41	2.31	26	1
1:A:282:LEU:HD11	1:A:296:THR:HG23	0.41	1.93	7	2
1:A:307:ARG:CD	1:A:307:ARG:C	0.41	2.94	5	1
1:A:257:ILE:O	1:A:261:VAL:N	0.40	2.52	12	1
1:A:278:GLN:OE1	1:A:278:GLN:CA	0.40	2.70	12	1
1:A:310:LEU:HD23	1:A:310:LEU:N	0.40	2.30	3	1
1:A:253:THR:OG1	1:A:289:LEU:O	0.40	2.39	7	1
1:A:249:LYS:CD	1:A:249:LYS:H	0.40	2.29	9	1
1:A:246:LEU:HD21	1:A:303:LEU:CD2	0.40	2.46	14	1
1:A:309:ILE:O	1:A:310:LEU:C	0.40	2.65	3	1
1:A:261:VAL:HG13	1:A:276:VAL:HG21	0.40	1.91	9	1
1:A:293:ILE:O	1:A:293:ILE:HG22	0.40	2.15	10	1
1:A:264:LEU:HD13	1:A:279:LEU:HD13	0.40	1.93	11	1
1:A:297:GLU:CD	1:A:297:GLU:H	0.40	2.24	27	1
1:A:288:ALA:HB3	1:A:291:GLU:HB2	0.40	1.93	30	1

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	65/90 (72%)	53±2 (81±3%)	10±2 (16±3%)	2±1 (3±2%)	5	36
All	All	1950/2700 (72%)	1577 (81%)	311 (16%)	62 (3%)	5	36

All 9 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	288	ALA	17
1	A	247	PRO	15
1	A	310	LEU	11
1	A	276	VAL	7
1	A	248	GLU	4
1	A	296	THR	3
1	A	251	SER	2
1	A	289	LEU	2
1	A	307	ARG	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	59/82 (72%)	47±2 (79±4%)	12±2 (21±4%)	3	31
All	All	1770/2460 (72%)	1400 (79%)	370 (21%)	3	31

All 41 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	300	GLU	27

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Mol	Chain	Res	Type	Models (Total)
1	A	246	LEU	26
1	A	257	ILE	26
1	A	253	THR	25
1	A	254	VAL	24
1	A	249	LYS	22
1	A	283	LEU	22
1	A	275	LYS	17
1	A	281	LYS	16
1	A	297	GLU	16
1	A	274	ILE	15
1	A	296	THR	13
1	A	282	LEU	11
1	A	268	SER	10
1	A	244	ILE	8
1	A	311	LYS	8
1	A	278	GLN	7
1	A	263	LYS	7
1	A	280	SER	6
1	A	289	LEU	6
1	A	291	GLU	5
1	A	250	ASP	5
1	A	248	GLU	5
1	A	305	GLU	4
1	A	301	LEU	4
1	A	308	GLU	4
1	A	245	VAL	4
1	A	270	ILE	4
1	A	307	ARG	3
1	A	259	LYS	3
1	A	276	VAL	3
1	A	298	GLU	3
1	A	302	GLU	2
1	A	255	ASN	2
1	A	290	THR	1
1	A	303	LEU	1
1	A	279	LEU	1
1	A	310	LEU	1
1	A	293	ILE	1
1	A	266	TRP	1
1	A	292	VAL	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 82% for the well-defined parts and 72% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: 160902_2_chemical_shift.txt

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	939
Number of shifts mapped to atoms	939
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
$^{13}\text{C}_\alpha$	82	-0.28 ± 0.22	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	78	0.06 ± 0.08	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	76	0.14 ± 0.24	None needed (< 0.5 ppm)

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 82%, i.e. 774 atoms were assigned a chemical shift out of a possible 940. 0 out of 16 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	252/321 (79%)	125/129 (97%)	65/130 (50%)	62/62 (100%)
Sidechain	506/586 (86%)	339/382 (89%)	161/186 (87%)	6/18 (33%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	16/33 (48%)	14/16 (88%)	0/15 (0%)	2/2 (100%)
Overall	774/940 (82%)	478/527 (91%)	226/331 (68%)	70/82 (85%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 72%, i.e. 938 atoms were assigned a chemical shift out of a possible 1298. 0 out of 20 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	314/444 (71%)	156/179 (87%)	82/180 (46%)	76/85 (89%)
Sidechain	599/751 (80%)	398/489 (81%)	194/238 (82%)	7/24 (29%)
Aromatic	25/103 (24%)	22/54 (41%)	0/39 (0%)	3/10 (30%)
Overall	938/1298 (72%)	576/722 (80%)	276/457 (60%)	86/119 (72%)

7.1.4 Statistically unusual chemical shifts ⓘ

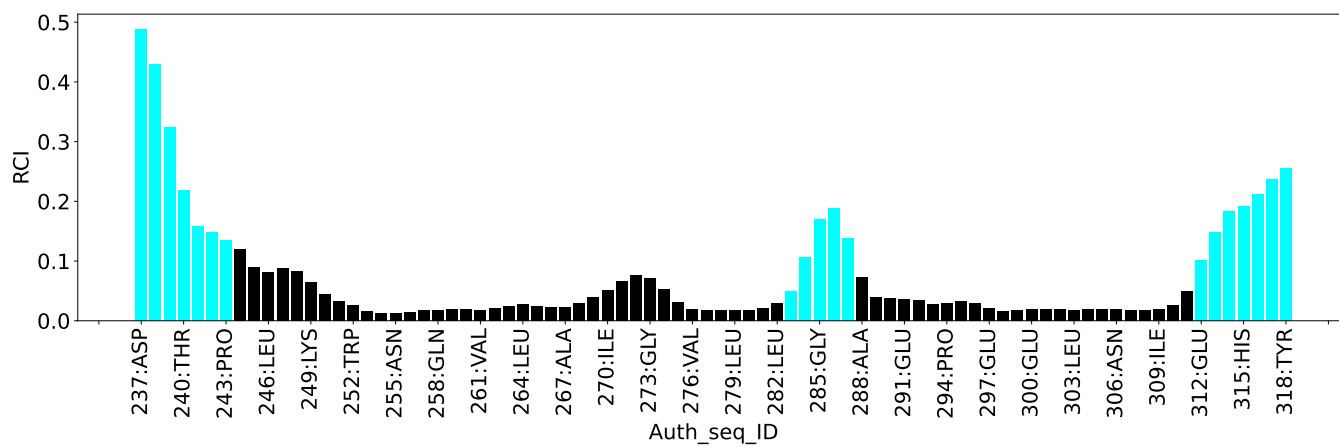
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	249	LYS	HB3	0.07	0.46 – 3.04	-6.5
1	A	278	GLN	H	11.48	5.39 – 11.05	5.8

7.1.5 Random Coil Index (RCI) plots ⓘ

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	2712
Intra-residue ($ i-j =0$)	1091
Sequential ($ i-j =1$)	617
Medium range ($ i-j >1$ and $ i-j <5$)	456
Long range ($ i-j \geq 5$)	456
Inter-chain	0
Hydrogen bond restraints	92
Disulfide bond restraints	0
Total dihedral-angle restraints	116
Number of unmapped restraints	0
Number of restraints per residue	31.4
Number of long range restraints per residue ¹	5.1

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)	41.0	0.2
0.2-0.5 (Medium)	15.4	0.47
>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.

Bins (°)	Average number of violations per model	Max (°)
1.0-10.0 (Small)	5.3	4.32
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis ⓘ

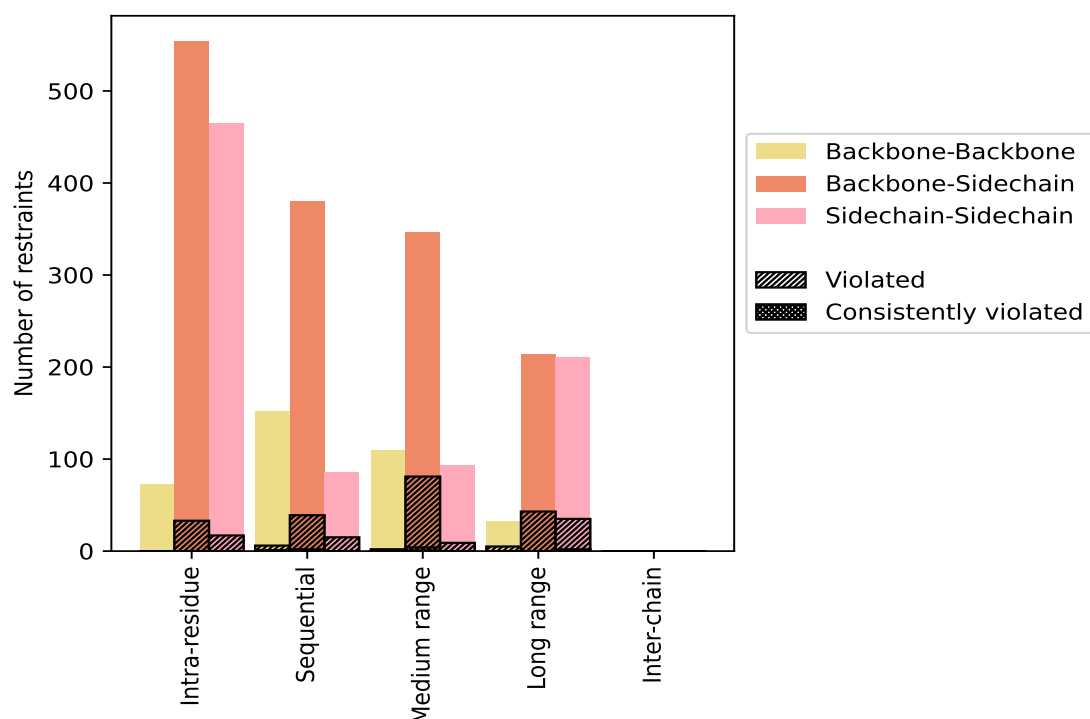
9.1 Summary of distance violations ⓘ

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 ($i-j =0$)	1091	40.2	50	4.6	1.8	0	0.0	0.0
Backbone-Backbone	72	2.7	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	554	20.4	33	6.0	1.2	0	0.0	0.0
Sidechain-Sidechain	465	17.1	17	3.7	0.6	0	0.0	0.0
Sequential ($i-j =1$)	617	22.8	60	9.7	2.2	3	0.5	0.1
Backbone-Backbone	152	5.6	6	3.9	0.2	1	0.7	0.0
Backbone-Sidechain	380	14.0	39	10.3	1.4	2	0.5	0.1
Sidechain-Sidechain	85	3.1	15	17.6	0.6	0	0.0	0.0
Medium range ($i-j >1$ & $i-j <5$)	456	16.8	56	12.3	2.1	2	0.4	0.1
Backbone-Backbone	109	4.0	2	1.8	0.1	0	0.0	0.0
Backbone-Sidechain	254	9.4	45	17.7	1.7	2	0.8	0.1
Sidechain-Sidechain	93	3.4	9	9.7	0.3	0	0.0	0.0
Long range ($i-j \geq 5$)	456	16.8	83	18.2	3.1	2	0.4	0.1
Backbone-Backbone	32	1.2	5	15.6	0.2	0	0.0	0.0
Backbone-Sidechain	214	7.9	43	20.1	1.6	0	0.0	0.0
Sidechain-Sidechain	210	7.7	35	16.7	1.3	2	1.0	0.1
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	92	3.4	36	39.1	1.3	2	2.2	0.1
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	2712	100.0	285	10.5	10.5	9	0.3	0.3
Backbone-Backbone	365	13.5	13	3.6	0.5	1	0.3	0.0
Backbone-Sidechain	1494	55.1	196	13.1	7.2	6	0.4	0.2
Sidechain-Sidechain	853	31.5	76	8.9	2.8	2	0.2	0.1

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	7	8	17	21	0	53	0.17	0.37	0.06	0.15
2	5	13	18	19	0	55	0.17	0.34	0.06	0.14
3	5	13	21	19	0	58	0.16	0.35	0.06	0.15
4	8	11	18	15	0	52	0.18	0.4	0.06	0.16
5	5	10	12	19	0	46	0.17	0.36	0.07	0.15
6	6	14	18	18	0	56	0.17	0.45	0.08	0.15
7	7	17	18	19	0	61	0.17	0.41	0.07	0.14
8	7	14	22	17	0	60	0.17	0.41	0.07	0.15
9	9	12	26	12	0	59	0.17	0.37	0.07	0.15
10	8	17	23	22	0	70	0.17	0.37	0.07	0.14

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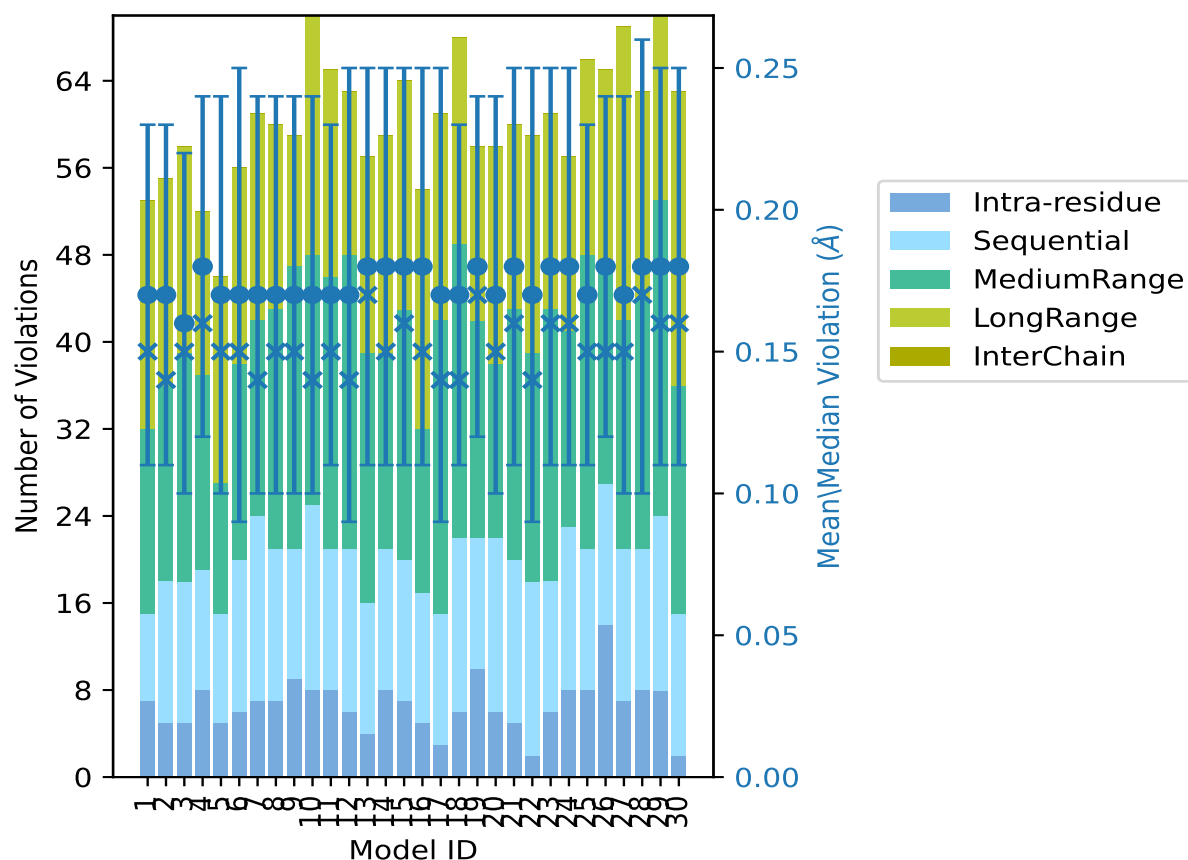
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	8	13	25	19	0	65	0.17	0.36	0.06	0.15
12	6	15	27	15	0	63	0.17	0.45	0.08	0.14
13	4	12	23	18	0	57	0.18	0.39	0.07	0.17
14	8	13	18	20	0	59	0.18	0.44	0.07	0.15
15	7	13	23	21	0	64	0.18	0.37	0.07	0.16
16	5	12	15	22	0	54	0.18	0.37	0.07	0.15
17	3	12	27	19	0	61	0.17	0.41	0.08	0.14
18	6	16	27	19	0	68	0.17	0.34	0.06	0.14
19	10	12	20	16	0	58	0.18	0.42	0.06	0.17
20	6	16	16	20	0	58	0.17	0.39	0.07	0.15
21	5	15	23	17	0	60	0.18	0.37	0.07	0.16
22	2	16	21	20	0	59	0.17	0.43	0.08	0.14
23	6	12	25	18	0	61	0.18	0.34	0.07	0.16
24	8	15	18	16	0	57	0.18	0.44	0.07	0.16
25	8	13	27	18	0	66	0.17	0.35	0.06	0.15
26	14	13	20	18	0	65	0.18	0.37	0.06	0.15
27	7	14	21	27	0	69	0.17	0.35	0.07	0.15
28	8	13	23	19	0	63	0.18	0.46	0.08	0.17
29	8	16	29	17	0	70	0.18	0.47	0.07	0.16
30	2	13	21	27	0	63	0.18	0.45	0.07	0.16

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 [i](#)



The mean(dot),median(x) and the standard deviation are shown in blue with respect to the y axis on the right

9.3 Distance violation statistics for the ensemble [i](#)

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, 2371(IR:1041, SQ:557, MR:400, LR:373, 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	%
14	20	21	22	0	77	1	3.3
12	7	2	10	0	31	2	6.7
6	7	4	5	0	22	3	10.0
3	2	4	7	0	16	4	13.3
1	2	2	6	0	11	5	16.7
4	2	3	4	0	13	6	20.0

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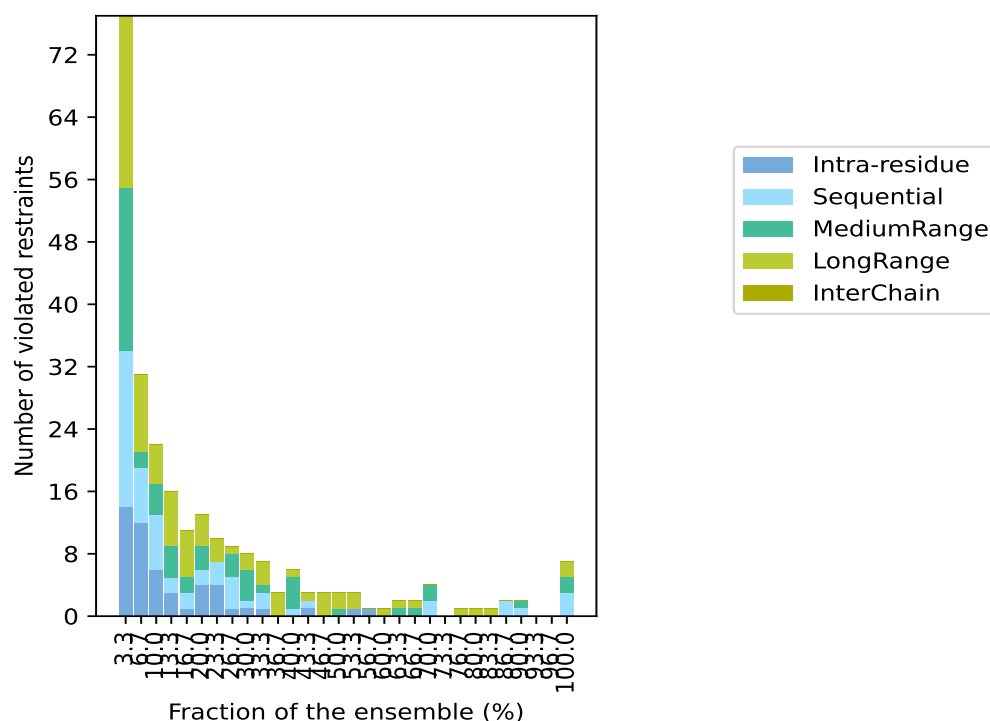
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Number of violated restraints						Fraction of the ensemble	
IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total	Count ⁶	%
4	3	0	3	0	10	7	23.3
1	4	3	1	0	9	8	26.7
1	1	4	2	0	8	9	30.0
1	2	1	3	0	7	10	33.3
0	0	0	3	0	3	11	36.7
0	1	4	1	0	6	12	40.0
1	1	0	1	0	3	13	43.3
0	0	0	3	0	3	14	46.7
0	0	1	2	0	3	15	50.0
1	0	0	2	0	3	16	53.3
1	0	0	0	0	1	17	56.7
0	0	0	1	0	1	18	60.0
0	0	1	1	0	2	19	63.3
0	0	1	1	0	2	20	66.7
0	2	2	0	0	4	21	70.0
0	0	0	0	0	0	22	73.3
0	0	0	1	0	1	23	76.7
0	0	0	1	0	1	24	80.0
0	0	0	1	0	1	25	83.3
0	2	0	0	0	2	26	86.7
0	1	1	0	0	2	27	90.0
0	0	0	0	0	0	28	93.3
0	0	0	0	0	0	29	96.7
0	3	2	2	0	7	30	100.0

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

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

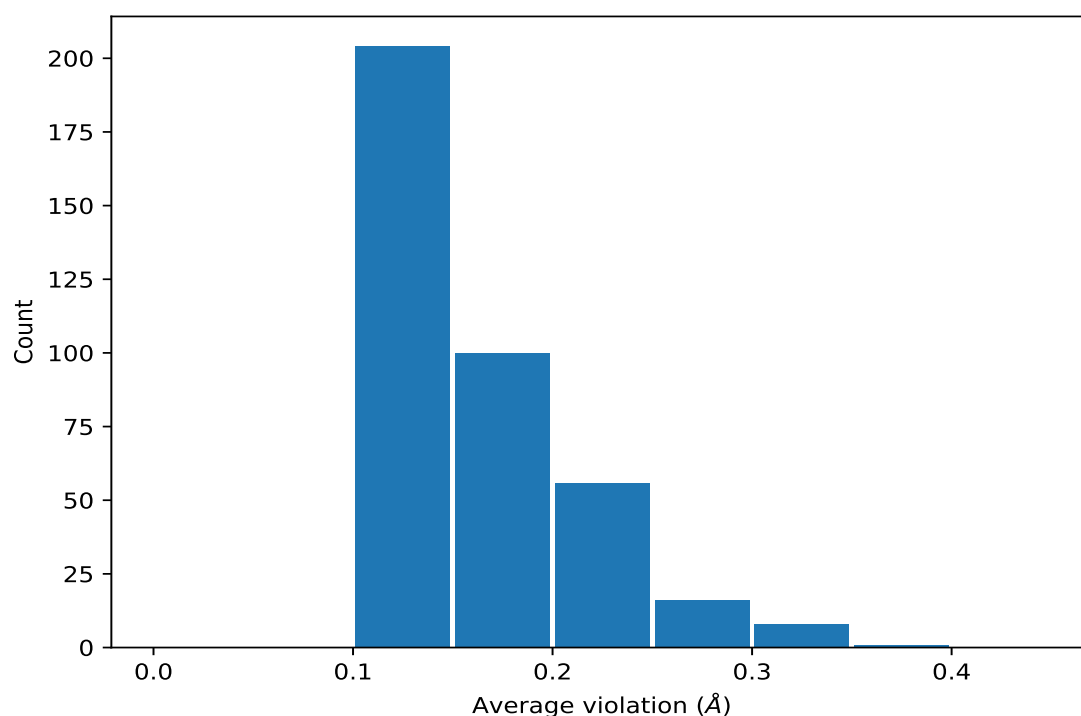
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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

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

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



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

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

Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	30	0.34	0.04	0.34
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	30	0.3	0.07	0.3
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	30	0.29	0.04	0.3
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	30	0.28	0.05	0.28
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	30	0.28	0.05	0.28
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	30	0.28	0.05	0.28
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	30	0.25	0.04	0.26
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	30	0.23	0.05	0.24
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	30	0.21	0.04	0.2
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	30	0.21	0.04	0.2
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	30	0.21	0.04	0.2
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	30	0.19	0.03	0.19
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	30	0.19	0.03	0.19
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	27	0.23	0.08	0.24
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	27	0.23	0.08	0.24
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	27	0.23	0.08	0.24

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	27	0.16	0.05	0.15
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	27	0.16	0.05	0.15
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	27	0.16	0.05	0.15
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	26	0.16	0.03	0.16
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	26	0.14	0.02	0.14
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	26	0.14	0.02	0.14
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	26	0.14	0.02	0.14
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	25	0.17	0.03	0.16
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	25	0.17	0.03	0.16
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	25	0.17	0.03	0.16
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	24	0.18	0.08	0.15
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	24	0.18	0.08	0.15
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	24	0.18	0.08	0.15
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	23	0.18	0.07	0.16
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	23	0.18	0.07	0.16
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	23	0.18	0.07	0.16
(3,2303)	1:238:A:LYS:H	1:239:A:TRP:HA	21	0.19	0.07	0.17
(3,1426)	1:293:A:ILE:HD11	1:292:A:VAL:H	21	0.18	0.06	0.16
(3,1426)	1:293:A:ILE:HD12	1:292:A:VAL:H	21	0.18	0.06	0.16
(3,1426)	1:293:A:ILE:HD13	1:292:A:VAL:H	21	0.18	0.06	0.16
(3,2357)	1:262:A:GLY:H	1:260:A:LEU:HB2	21	0.18	0.05	0.18
(3,1215)	1:276:A:VAL:HG11	1:279:A:LEU:HB2	21	0.15	0.02	0.15
(3,1215)	1:276:A:VAL:HG12	1:279:A:LEU:HB2	21	0.15	0.02	0.15
(3,1215)	1:276:A:VAL:HG13	1:279:A:LEU:HB2	21	0.15	0.02	0.15
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG21	20	0.16	0.03	0.17
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG22	20	0.16	0.03	0.17
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG23	20	0.16	0.03	0.17
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD11	20	0.15	0.05	0.14
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD12	20	0.15	0.05	0.14
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD13	20	0.15	0.05	0.14
(1,15)	1:302:A:GLU:H	1:298:A:GLU:O	20	0.13	0.02	0.12
(2,15)	1:302:A:GLU:H	1:298:A:GLU:O	20	0.13	0.02	0.12
(3,28)	1:310:A:LEU:HD21	1:271:A:TYR:HB2	19	0.18	0.04	0.18
(3,28)	1:310:A:LEU:HD22	1:271:A:TYR:HB2	19	0.18	0.04	0.18
(3,28)	1:310:A:LEU:HD23	1:271:A:TYR:HB2	19	0.18	0.04	0.18
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG21	19	0.16	0.03	0.16
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG22	19	0.16	0.03	0.16
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG23	19	0.16	0.03	0.16
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG21	18	0.18	0.04	0.18
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG22	18	0.18	0.04	0.18
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG23	18	0.18	0.04	0.18
(3,740)	1:238:A:LYS:HB2	1:238:A:LYS:HD3	17	0.18	0.02	0.17

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG11	16	0.25	0.08	0.26
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG12	16	0.25	0.08	0.26
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG13	16	0.25	0.08	0.26
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG21	16	0.23	0.08	0.2
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG22	16	0.23	0.08	0.2
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG23	16	0.23	0.08	0.2
(3,2540)	1:283:A:LEU:HD21	1:283:A:LEU:H	16	0.17	0.04	0.16
(3,2540)	1:283:A:LEU:HD22	1:283:A:LEU:H	16	0.17	0.04	0.16
(3,2540)	1:283:A:LEU:HD23	1:283:A:LEU:H	16	0.17	0.04	0.16
(1,21)	1:308:A:GLU:H	1:304:A:ALA:O	16	0.13	0.03	0.13
(2,21)	1:308:A:GLU:H	1:304:A:ALA:O	16	0.13	0.03	0.13
(3,2514)	1:273:A:GLY:H	1:271:A:TYR:HB3	15	0.18	0.03	0.18
(3,1462)	1:293:A:ILE:HD11	1:283:A:LEU:HB3	15	0.18	0.05	0.17
(3,1462)	1:293:A:ILE:HD12	1:283:A:LEU:HB3	15	0.18	0.05	0.17
(3,1462)	1:293:A:ILE:HD13	1:283:A:LEU:HB3	15	0.18	0.05	0.17
(3,871)	1:283:A:LEU:HD21	1:254:A:VAL:HA	15	0.17	0.03	0.16
(3,871)	1:283:A:LEU:HD22	1:254:A:VAL:HA	15	0.17	0.03	0.16
(3,871)	1:283:A:LEU:HD23	1:254:A:VAL:HA	15	0.17	0.03	0.16
(1,34)	1:268:A:SER:N	1:264:A:LEU:O	15	0.13	0.03	0.13
(2,34)	1:268:A:SER:N	1:264:A:LEU:O	15	0.13	0.03	0.13
(3,1139)	1:283:A:LEU:HD11	1:257:A:ILE:H	14	0.23	0.06	0.24
(3,1139)	1:283:A:LEU:HD12	1:257:A:ILE:H	14	0.23	0.06	0.24
(3,1139)	1:283:A:LEU:HD13	1:257:A:ILE:H	14	0.23	0.06	0.24
(3,2336)	1:295:A:LEU:H	1:300:A:GLU:HB2	14	0.16	0.04	0.15
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD21	14	0.12	0.02	0.12
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD22	14	0.12	0.02	0.12
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD23	14	0.12	0.02	0.12
(3,888)	1:287:A:LYS:HB2	1:287:A:LYS:HE2	13	0.26	0.06	0.29
(3,71)	1:290:A:THR:H	1:255:A:ASN:HB3	13	0.21	0.08	0.24
(3,2141)	1:299:A:ALA:H	1:300:A:GLU:HB2	13	0.13	0.02	0.13
(3,47)	1:306:A:ASN:H	1:310:A:LEU:HG	12	0.14	0.02	0.15
(3,2474)	1:256:A:ASP:H	1:258:A:GLN:HB3	12	0.14	0.02	0.13
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD11	12	0.13	0.02	0.13
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD12	12	0.13	0.02	0.13
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD13	12	0.13	0.02	0.13
(3,2448)	1:256:A:ASP:H	1:257:A:ILE:HG12	12	0.13	0.02	0.13
(3,1185)	1:262:A:GLY:HA3	1:265:A:ASN:HD22	12	0.13	0.02	0.13
(3,2401)	1:253:A:THR:H	1:292:A:VAL:H	12	0.13	0.03	0.12
(1,35)	1:269:A:GLN:N	1:265:A:ASN:O	12	0.12	0.02	0.12
(2,35)	1:269:A:GLN:N	1:265:A:ASN:O	12	0.12	0.02	0.12
(3,875)	1:283:A:LEU:HD11	1:258:A:GLN:HB3	11	0.16	0.03	0.15
(3,875)	1:283:A:LEU:HD12	1:258:A:GLN:HB3	11	0.16	0.03	0.15

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(3,875)	1:283:A:LEU:HD13	1:258:A:GLN:HB3	11	0.16	0.03	0.15
(3,2388)	1:255:A:ASN:H	1:289:A:LEU:HB2	11	0.13	0.02	0.12
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE1	11	0.12	0.02	0.12
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE2	11	0.12	0.02	0.12
(3,866)	1:283:A:LEU:HD21	1:261:A:VAL:HB	10	0.21	0.09	0.23
(3,866)	1:283:A:LEU:HD22	1:261:A:VAL:HB	10	0.21	0.09	0.23
(3,866)	1:283:A:LEU:HD23	1:261:A:VAL:HB	10	0.21	0.09	0.23
(3,1658)	1:240:A:THR:HB	1:239:A:TRP:HA	10	0.2	0.08	0.24
(3,1885)	1:281:A:LYS:H	1:281:A:LYS:HG2	10	0.18	0.05	0.18
(3,81)	1:262:A:GLY:H	1:260:A:LEU:HG	10	0.17	0.04	0.18
(3,29)	1:310:A:LEU:H	1:271:A:TYR:HE1	10	0.14	0.02	0.15
(3,29)	1:310:A:LEU:H	1:271:A:TYR:HE2	10	0.14	0.02	0.15
(3,2241)	1:258:A:GLN:HG2	1:257:A:ILE:H	10	0.14	0.02	0.15
(3,1496)	1:295:A:LEU:HD21	1:250:A:ASP:HA	10	0.12	0.02	0.12
(3,1496)	1:295:A:LEU:HD22	1:250:A:ASP:HA	10	0.12	0.02	0.12
(3,1496)	1:295:A:LEU:HD23	1:250:A:ASP:HA	10	0.12	0.02	0.12
(1,13)	1:282:A:LEU:H	1:278:A:GLN:O	10	0.12	0.02	0.12
(2,13)	1:282:A:LEU:H	1:278:A:GLN:O	10	0.12	0.02	0.12
(3,1186)	1:265:A:ASN:HB3	1:262:A:GLY:HA3	9	0.36	0.02	0.37
(3,825)	1:254:A:VAL:HG11	1:293:A:ILE:H	9	0.25	0.05	0.25
(3,825)	1:254:A:VAL:HG12	1:293:A:ILE:H	9	0.25	0.05	0.25
(3,825)	1:254:A:VAL:HG13	1:293:A:ILE:H	9	0.25	0.05	0.25
(3,72)	1:290:A:THR:H	1:253:A:THR:HA	9	0.19	0.06	0.22
(3,2295)	1:262:A:GLY:H	1:265:A:ASN:HB2	9	0.18	0.03	0.18
(3,2268)	1:274:A:ILE:HG13	1:271:A:TYR:H	9	0.17	0.03	0.16
(3,1211)	1:264:A:LEU:HG	1:265:A:ASN:H	9	0.15	0.03	0.14
(3,814)	1:275:A:LYS:HG2	1:275:A:LYS:HE3	9	0.14	0.06	0.12
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD11	9	0.13	0.02	0.12
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD12	9	0.13	0.02	0.12
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD13	9	0.13	0.02	0.12
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD11	8	0.34	0.06	0.32
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD12	8	0.34	0.06	0.32
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD13	8	0.34	0.06	0.32
(3,810)	1:275:A:LYS:HE3	1:275:A:LYS:HB3	8	0.2	0.07	0.2
(3,1953)	1:265:A:ASN:H	1:263:A:LYS:HB3	8	0.17	0.05	0.17
(3,2285)	1:271:A:TYR:H	1:270:A:ILE:HG13	8	0.14	0.03	0.14
(3,2434)	1:253:A:THR:HG21	1:254:A:VAL:H	8	0.14	0.03	0.12
(3,2434)	1:253:A:THR:HG22	1:254:A:VAL:H	8	0.14	0.03	0.12
(3,2434)	1:253:A:THR:HG23	1:254:A:VAL:H	8	0.14	0.03	0.12
(3,2058)	1:254:A:VAL:H	1:289:A:LEU:HB3	8	0.13	0.02	0.13
(3,1764)	1:270:A:ILE:HD11	1:271:A:TYR:HD1	8	0.13	0.01	0.13
(3,1764)	1:270:A:ILE:HD11	1:271:A:TYR:HD2	8	0.13	0.01	0.13

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(3,1764)	1:270:A:ILE:HD12	1:271:A:TYR:HD1	8	0.13	0.01	0.13
(3,1764)	1:270:A:ILE:HD12	1:271:A:TYR:HD2	8	0.13	0.01	0.13
(3,1764)	1:270:A:ILE:HD13	1:271:A:TYR:HD1	8	0.13	0.01	0.13
(3,1764)	1:270:A:ILE:HD13	1:271:A:TYR:HD2	8	0.13	0.01	0.13
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG21	8	0.12	0.02	0.11
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG22	8	0.12	0.02	0.11
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG23	8	0.12	0.02	0.11
(3,2206)	1:274:A:ILE:H	1:272:A:PRO:HD3	8	0.11	0.01	0.11
(3,2155)	1:287:A:LYS:H	1:287:A:LYS:HE2	7	0.2	0.04	0.21
(3,1148)	1:259:A:LYS:H	1:259:A:LYS:HD2	7	0.17	0.02	0.17
(3,2498)	1:287:A:LYS:H	1:287:A:LYS:HD2	7	0.16	0.03	0.18
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD11	7	0.16	0.02	0.16
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD12	7	0.16	0.02	0.16
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD13	7	0.16	0.02	0.16
(3,1052)	1:240:A:THR:HB	1:241:A:VAL:HB	7	0.14	0.05	0.12
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD11	7	0.14	0.01	0.14
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD12	7	0.14	0.01	0.14
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD13	7	0.14	0.01	0.14
(3,1441)	1:293:A:ILE:HG12	1:254:A:VAL:HB	7	0.13	0.01	0.13
(3,2550)	1:280:A:SER:H	1:302:A:GLU:HG2	7	0.12	0.01	0.12
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG21	7	0.12	0.01	0.11
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG22	7	0.12	0.01	0.11
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG23	7	0.12	0.01	0.11
(3,1907)	1:271:A:TYR:H	1:272:A:PRO:HB3	7	0.11	0.01	0.11
(3,872)	1:254:A:VAL:HA	1:283:A:LEU:HD11	6	0.25	0.05	0.26
(3,872)	1:254:A:VAL:HA	1:283:A:LEU:HD12	6	0.25	0.05	0.26
(3,872)	1:254:A:VAL:HA	1:283:A:LEU:HD13	6	0.25	0.05	0.26
(3,705)	1:287:A:LYS:HG2	1:287:A:LYS:HE2	6	0.18	0.03	0.18
(3,899)	1:288:A:ALA:HA	1:289:A:LEU:HG	6	0.18	0.06	0.16
(3,2367)	1:275:A:LYS:HG2	1:275:A:LYS:H	6	0.16	0.03	0.16
(3,867)	1:283:A:LEU:HD21	1:258:A:GLN:HB3	6	0.15	0.04	0.15
(3,867)	1:283:A:LEU:HD22	1:258:A:GLN:HB3	6	0.15	0.04	0.15
(3,867)	1:283:A:LEU:HD23	1:258:A:GLN:HB3	6	0.15	0.04	0.15
(3,857)	1:283:A:LEU:HD21	1:280:A:SER:HA	6	0.15	0.02	0.15
(3,857)	1:283:A:LEU:HD22	1:280:A:SER:HA	6	0.15	0.02	0.15
(3,857)	1:283:A:LEU:HD23	1:280:A:SER:HA	6	0.15	0.02	0.15
(3,2174)	1:304:A:ALA:H	1:302:A:GLU:HB2	6	0.15	0.05	0.12
(3,2414)	1:268:A:SER:H	1:274:A:ILE:HB	6	0.15	0.04	0.15
(3,2436)	1:291:A:GLU:H	1:291:A:GLU:HG2	6	0.13	0.02	0.13
(3,986)	1:304:A:ALA:H	1:302:A:GLU:HG2	6	0.12	0.02	0.12
(3,85)	1:244:A:ILE:HD11	1:270:A:ILE:HA	6	0.12	0.01	0.12
(3,85)	1:244:A:ILE:HD12	1:270:A:ILE:HA	6	0.12	0.01	0.12

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(3,85)	1:244:A:ILE:HD13	1:270:A:ILE:HA	6	0.12	0.01	0.12
(3,2273)	1:254:A:VAL:H	1:255:A:ASN:HA	6	0.12	0.01	0.12
(3,2457)	1:303:A:LEU:H	1:303:A:LEU:HG	6	0.11	0.01	0.11
(3,716)	1:287:A:LYS:HD3	1:287:A:LYS:H	5	0.21	0.04	0.21
(3,1518)	1:295:A:LEU:HD11	1:282:A:LEU:HD11	5	0.2	0.07	0.21
(3,1518)	1:295:A:LEU:HD11	1:282:A:LEU:HD12	5	0.2	0.07	0.21
(3,1518)	1:295:A:LEU:HD11	1:282:A:LEU:HD13	5	0.2	0.07	0.21
(3,1518)	1:295:A:LEU:HD12	1:282:A:LEU:HD11	5	0.2	0.07	0.21
(3,1518)	1:295:A:LEU:HD12	1:282:A:LEU:HD12	5	0.2	0.07	0.21
(3,1518)	1:295:A:LEU:HD12	1:282:A:LEU:HD13	5	0.2	0.07	0.21
(3,1518)	1:295:A:LEU:HD13	1:282:A:LEU:HD11	5	0.2	0.07	0.21
(3,1518)	1:295:A:LEU:HD13	1:282:A:LEU:HD12	5	0.2	0.07	0.21
(3,1518)	1:295:A:LEU:HD13	1:282:A:LEU:HD13	5	0.2	0.07	0.21
(3,80)	1:270:A:ILE:HD11	1:314:A:VAL:HG11	5	0.2	0.07	0.23
(3,80)	1:270:A:ILE:HD11	1:314:A:VAL:HG12	5	0.2	0.07	0.23
(3,80)	1:270:A:ILE:HD11	1:314:A:VAL:HG13	5	0.2	0.07	0.23
(3,80)	1:270:A:ILE:HD12	1:314:A:VAL:HG11	5	0.2	0.07	0.23
(3,80)	1:270:A:ILE:HD12	1:314:A:VAL:HG12	5	0.2	0.07	0.23
(3,80)	1:270:A:ILE:HD12	1:314:A:VAL:HG13	5	0.2	0.07	0.23
(3,80)	1:270:A:ILE:HD13	1:314:A:VAL:HG11	5	0.2	0.07	0.23
(3,80)	1:270:A:ILE:HD13	1:314:A:VAL:HG12	5	0.2	0.07	0.23
(3,80)	1:270:A:ILE:HD13	1:314:A:VAL:HG13	5	0.2	0.07	0.23
(3,1318)	1:274:A:ILE:HG21	1:275:A:LYS:HA	5	0.18	0.01	0.18
(3,1318)	1:274:A:ILE:HG22	1:275:A:LYS:HA	5	0.18	0.01	0.18
(3,1318)	1:274:A:ILE:HG23	1:275:A:LYS:HA	5	0.18	0.01	0.18
(3,1391)	1:287:A:LYS:HB3	1:254:A:VAL:HG21	5	0.16	0.07	0.14
(3,1391)	1:287:A:LYS:HB3	1:254:A:VAL:HG22	5	0.16	0.07	0.14
(3,1391)	1:287:A:LYS:HB3	1:254:A:VAL:HG23	5	0.16	0.07	0.14
(3,823)	1:291:A:GLU:HB3	1:254:A:VAL:HG11	5	0.16	0.07	0.13
(3,823)	1:291:A:GLU:HB3	1:254:A:VAL:HG12	5	0.16	0.07	0.13
(3,823)	1:291:A:GLU:HB3	1:254:A:VAL:HG13	5	0.16	0.07	0.13
(3,1482)	1:257:A:ILE:HD11	1:254:A:VAL:HB	5	0.16	0.03	0.16
(3,1482)	1:257:A:ILE:HD12	1:254:A:VAL:HB	5	0.16	0.03	0.16
(3,1482)	1:257:A:ILE:HD13	1:254:A:VAL:HB	5	0.16	0.03	0.16
(3,2163)	1:256:A:ASP:H	1:289:A:LEU:HD21	5	0.15	0.03	0.13
(3,2163)	1:256:A:ASP:H	1:289:A:LEU:HD22	5	0.15	0.03	0.13
(3,2163)	1:256:A:ASP:H	1:289:A:LEU:HD23	5	0.15	0.03	0.13
(3,2613)	1:255:A:ASN:HD22	1:289:A:LEU:HG	5	0.13	0.03	0.12
(1,11)	1:268:A:SER:H	1:264:A:LEU:O	5	0.12	0.02	0.13
(2,11)	1:268:A:SER:H	1:264:A:LEU:O	5	0.12	0.02	0.13
(3,74)	1:283:A:LEU:H	1:280:A:SER:HB2	5	0.12	0.02	0.11
(1,5)	1:262:A:GLY:H	1:258:A:GLN:O	5	0.12	0.02	0.12

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(2,5)	1:262:A:GLY:H	1:258:A:GLN:O	5	0.12	0.02	0.12
(3,2277)	1:269:A:GLN:H	1:270:A:ILE:HG21	5	0.11	0.0	0.11
(3,2277)	1:269:A:GLN:H	1:270:A:ILE:HG22	5	0.11	0.0	0.11
(3,2277)	1:269:A:GLN:H	1:270:A:ILE:HG23	5	0.11	0.0	0.11
(3,1616)	1:318:A:TYR:HB3	1:317:A:VAL:HB	4	0.33	0.11	0.36
(3,894)	1:254:A:VAL:HG11	1:287:A:LYS:HD2	4	0.24	0.03	0.24
(3,894)	1:254:A:VAL:HG12	1:287:A:LYS:HD2	4	0.24	0.03	0.24
(3,894)	1:254:A:VAL:HG13	1:287:A:LYS:HD2	4	0.24	0.03	0.24
(3,774)	1:263:A:LYS:HE2	1:263:A:LYS:H	4	0.2	0.05	0.21
(3,3)	1:314:A:VAL:HG11	1:315:A:HIS:HA	4	0.18	0.04	0.17
(3,3)	1:314:A:VAL:HG12	1:315:A:HIS:HA	4	0.18	0.04	0.17
(3,3)	1:314:A:VAL:HG13	1:315:A:HIS:HA	4	0.18	0.04	0.17
(3,1134)	1:254:A:VAL:HA	1:257:A:ILE:HG21	4	0.16	0.04	0.16
(3,1134)	1:254:A:VAL:HA	1:257:A:ILE:HG22	4	0.16	0.04	0.16
(3,1134)	1:254:A:VAL:HA	1:257:A:ILE:HG23	4	0.16	0.04	0.16
(3,1347)	1:280:A:SER:HA	1:276:A:VAL:HG21	4	0.16	0.06	0.14
(3,1347)	1:280:A:SER:HA	1:276:A:VAL:HG22	4	0.16	0.06	0.14
(3,1347)	1:280:A:SER:HA	1:276:A:VAL:HG23	4	0.16	0.06	0.14
(3,63)	1:293:A:ILE:H	1:252:A:TRP:HD1	4	0.15	0.02	0.15
(3,1470)	1:293:A:ILE:HG21	1:257:A:ILE:HB	4	0.15	0.04	0.14
(3,1470)	1:293:A:ILE:HG22	1:257:A:ILE:HB	4	0.15	0.04	0.14
(3,1470)	1:293:A:ILE:HG23	1:257:A:ILE:HB	4	0.15	0.04	0.14
(3,659)	1:281:A:LYS:HE3	1:281:A:LYS:HB2	4	0.14	0.04	0.14
(3,19)	1:314:A:VAL:HG21	1:312:A:GLU:HB2	4	0.14	0.04	0.12
(3,19)	1:314:A:VAL:HG22	1:312:A:GLU:HB2	4	0.14	0.04	0.12
(3,19)	1:314:A:VAL:HG23	1:312:A:GLU:HB2	4	0.14	0.04	0.12
(3,1966)	1:266:A:TRP:H	1:276:A:VAL:HG11	4	0.14	0.03	0.14
(3,1966)	1:266:A:TRP:H	1:276:A:VAL:HG12	4	0.14	0.03	0.14
(3,1966)	1:266:A:TRP:H	1:276:A:VAL:HG13	4	0.14	0.03	0.14
(3,1829)	1:276:A:VAL:HG21	1:283:A:LEU:H	4	0.13	0.03	0.12
(3,1829)	1:276:A:VAL:HG22	1:283:A:LEU:H	4	0.13	0.03	0.12
(3,1829)	1:276:A:VAL:HG23	1:283:A:LEU:H	4	0.13	0.03	0.12
(3,1373)	1:279:A:LEU:HD21	1:306:A:ASN:HB3	4	0.12	0.01	0.12
(3,1373)	1:279:A:LEU:HD22	1:306:A:ASN:HB3	4	0.12	0.01	0.12
(3,1373)	1:279:A:LEU:HD23	1:306:A:ASN:HB3	4	0.12	0.01	0.12
(1,22)	1:309:A:ILE:H	1:305:A:GLU:O	4	0.12	0.01	0.12
(2,22)	1:309:A:ILE:H	1:305:A:GLU:O	4	0.12	0.01	0.12
(3,78)	1:279:A:LEU:HD11	1:306:A:ASN:HD22	4	0.12	0.01	0.12
(3,78)	1:279:A:LEU:HD12	1:306:A:ASN:HD22	4	0.12	0.01	0.12
(3,78)	1:279:A:LEU:HD13	1:306:A:ASN:HD22	4	0.12	0.01	0.12
(3,1755)	1:264:A:LEU:HG	1:268:A:SER:H	4	0.11	0.01	0.11
(3,1916)	1:301:A:LEU:HD11	1:301:A:LEU:H	4	0.11	0.0	0.11

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(3,1916)	1:301:A:LEU:HD12	1:301:A:LEU:H	4	0.11	0.0	0.11
(3,1916)	1:301:A:LEU:HD13	1:301:A:LEU:H	4	0.11	0.0	0.11
(3,1538)	1:298:A:GLU:HA	1:301:A:LEU:HD21	3	0.31	0.11	0.23
(3,1538)	1:298:A:GLU:HA	1:301:A:LEU:HD22	3	0.31	0.11	0.23
(3,1538)	1:298:A:GLU:HA	1:301:A:LEU:HD23	3	0.31	0.11	0.23
(3,1915)	1:308:A:GLU:HG3	1:308:A:GLU:H	3	0.21	0.06	0.25
(3,1389)	1:286:A:THR:HG21	1:291:A:GLU:HG3	3	0.18	0.06	0.2
(3,1389)	1:286:A:THR:HG22	1:291:A:GLU:HG3	3	0.18	0.06	0.2
(3,1389)	1:286:A:THR:HG23	1:291:A:GLU:HG3	3	0.18	0.06	0.2
(3,1638)	1:319:A:LEU:HD21	1:318:A:TYR:HB3	3	0.17	0.04	0.19
(3,1638)	1:319:A:LEU:HD22	1:318:A:TYR:HB3	3	0.17	0.04	0.19
(3,1638)	1:319:A:LEU:HD23	1:318:A:TYR:HB3	3	0.17	0.04	0.19
(1,27)	1:261:A:VAL:N	1:257:A:ILE:O	3	0.16	0.01	0.16
(2,27)	1:261:A:VAL:N	1:257:A:ILE:O	3	0.16	0.01	0.16
(3,2)	1:314:A:VAL:HG21	1:313:A:PRO:HA	3	0.15	0.02	0.15
(3,2)	1:314:A:VAL:HG22	1:313:A:PRO:HA	3	0.15	0.02	0.15
(3,2)	1:314:A:VAL:HG23	1:313:A:PRO:HA	3	0.15	0.02	0.15
(3,1621)	1:317:A:VAL:HB	1:318:A:TYR:HE1	3	0.15	0.02	0.16
(3,1621)	1:317:A:VAL:HB	1:318:A:TYR:HE2	3	0.15	0.02	0.16
(3,2054)	1:263:A:LYS:H	1:263:A:LYS:HG3	3	0.15	0.01	0.14
(3,1660)	1:240:A:THR:HG21	1:315:A:HIS:HA	3	0.15	0.04	0.13
(3,1660)	1:240:A:THR:HG22	1:315:A:HIS:HA	3	0.15	0.04	0.13
(3,1660)	1:240:A:THR:HG23	1:315:A:HIS:HA	3	0.15	0.04	0.13
(3,623)	1:301:A:LEU:HB2	1:305:A:GLU:H	3	0.14	0.02	0.14
(3,1468)	1:293:A:ILE:HG21	1:286:A:THR:HB	3	0.14	0.03	0.12
(3,1468)	1:293:A:ILE:HG22	1:286:A:THR:HB	3	0.14	0.03	0.12
(3,1468)	1:293:A:ILE:HG23	1:286:A:THR:HB	3	0.14	0.03	0.12
(3,678)	1:281:A:LYS:HB3	1:281:A:LYS:HE2	3	0.13	0.01	0.13
(3,2061)	1:273:A:GLY:H	1:274:A:ILE:HG13	3	0.13	0.01	0.14
(3,2284)	1:281:A:LYS:HD3	1:281:A:LYS:H	3	0.13	0.01	0.14
(3,1351)	1:277:A:ARG:HG2	1:276:A:VAL:H	3	0.12	0.01	0.13
(3,2213)	1:266:A:TRP:H	1:276:A:VAL:HG21	3	0.12	0.01	0.11
(3,2213)	1:266:A:TRP:H	1:276:A:VAL:HG22	3	0.12	0.01	0.11
(3,2213)	1:266:A:TRP:H	1:276:A:VAL:HG23	3	0.12	0.01	0.11
(3,2435)	1:239:A:TRP:HA	1:239:A:TRP:HE1	3	0.12	0.01	0.11
(3,231)	1:276:A:VAL:H	1:275:A:LYS:HE3	3	0.12	0.0	0.12
(3,1506)	1:296:A:THR:HG21	1:301:A:LEU:H	3	0.12	0.0	0.12
(3,1506)	1:296:A:THR:HG22	1:301:A:LEU:H	3	0.12	0.0	0.12
(3,1506)	1:296:A:THR:HG23	1:301:A:LEU:H	3	0.12	0.0	0.12
(3,2051)	1:289:A:LEU:H	1:289:A:LEU:HG	3	0.11	0.01	0.12
(3,2366)	1:300:A:GLU:H	1:301:A:LEU:HA	3	0.11	0.01	0.12
(3,1136)	1:260:A:LEU:HB2	1:257:A:ILE:HG21	3	0.11	0.0	0.11

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(3,1136)	1:260:A:LEU:HB2	1:257:A:ILE:HG22	3	0.11	0.0	0.11
(3,1136)	1:260:A:LEU:HB2	1:257:A:ILE:HG23	3	0.11	0.0	0.11
(3,2150)	1:310:A:LEU:H	1:308:A:GLU:HG3	3	0.11	0.0	0.11
(3,2417)	1:308:A:GLU:H	1:307:A:ARG:HG3	2	0.24	0.03	0.24
(3,543)	1:287:A:LYS:H	1:287:A:LYS:HG2	2	0.24	0.08	0.24
(3,1149)	1:259:A:LYS:HD2	1:259:A:LYS:HA	2	0.23	0.11	0.23
(3,15)	1:240:A:THR:HG21	1:239:A:TRP:HB3	2	0.22	0.06	0.22
(3,15)	1:240:A:THR:HG22	1:239:A:TRP:HB3	2	0.22	0.06	0.22
(3,15)	1:240:A:THR:HG23	1:239:A:TRP:HB3	2	0.22	0.06	0.22
(3,1392)	1:288:A:ALA:HB1	1:254:A:VAL:HB	2	0.22	0.06	0.22
(3,1392)	1:288:A:ALA:HB2	1:254:A:VAL:HB	2	0.22	0.06	0.22
(3,1392)	1:288:A:ALA:HB3	1:254:A:VAL:HB	2	0.22	0.06	0.22
(3,2201)	1:311:A:LYS:H	1:311:A:LYS:HD2	2	0.22	0.01	0.22
(3,6)	1:314:A:VAL:H	1:315:A:HIS:HB2	2	0.2	0.06	0.2
(3,2340)	1:258:A:GLN:HE22	1:258:A:GLN:HB3	2	0.2	0.01	0.2
(3,1160)	1:259:A:LYS:HE3	1:259:A:LYS:HG2	2	0.19	0.09	0.19
(3,36)	1:308:A:GLU:H	1:306:A:ASN:HB3	2	0.18	0.08	0.18
(3,1346)	1:276:A:VAL:HG21	1:264:A:LEU:HB3	2	0.16	0.06	0.16
(3,1346)	1:276:A:VAL:HG22	1:264:A:LEU:HB3	2	0.16	0.06	0.16
(3,1346)	1:276:A:VAL:HG23	1:264:A:LEU:HB3	2	0.16	0.06	0.16
(3,1146)	1:259:A:LYS:HG3	1:259:A:LYS:HE2	2	0.16	0.02	0.16
(3,2022)	1:291:A:GLU:HG3	1:291:A:GLU:H	2	0.16	0.02	0.16
(3,2491)	1:255:A:ASN:HD22	1:289:A:LEU:HD11	2	0.16	0.02	0.16
(3,2491)	1:255:A:ASN:HD22	1:289:A:LEU:HD12	2	0.16	0.02	0.16
(3,2491)	1:255:A:ASN:HD22	1:289:A:LEU:HD13	2	0.16	0.02	0.16
(3,17)	1:241:A:VAL:HG21	1:271:A:TYR:HE1	2	0.15	0.03	0.15
(3,17)	1:241:A:VAL:HG21	1:271:A:TYR:HE2	2	0.15	0.03	0.15
(3,17)	1:241:A:VAL:HG22	1:271:A:TYR:HE1	2	0.15	0.03	0.15
(3,17)	1:241:A:VAL:HG22	1:271:A:TYR:HE2	2	0.15	0.03	0.15
(3,17)	1:241:A:VAL:HG23	1:271:A:TYR:HE1	2	0.15	0.03	0.15
(3,17)	1:241:A:VAL:HG23	1:271:A:TYR:HE2	2	0.15	0.03	0.15
(3,79)	1:270:A:ILE:HD11	1:314:A:VAL:HG21	2	0.14	0.03	0.14
(3,79)	1:270:A:ILE:HD11	1:314:A:VAL:HG22	2	0.14	0.03	0.14
(3,79)	1:270:A:ILE:HD11	1:314:A:VAL:HG23	2	0.14	0.03	0.14
(3,79)	1:270:A:ILE:HD12	1:314:A:VAL:HG21	2	0.14	0.03	0.14
(3,79)	1:270:A:ILE:HD12	1:314:A:VAL:HG22	2	0.14	0.03	0.14
(3,79)	1:270:A:ILE:HD12	1:314:A:VAL:HG23	2	0.14	0.03	0.14
(3,79)	1:270:A:ILE:HD13	1:314:A:VAL:HG21	2	0.14	0.03	0.14
(3,79)	1:270:A:ILE:HD13	1:314:A:VAL:HG22	2	0.14	0.03	0.14
(3,79)	1:270:A:ILE:HD13	1:314:A:VAL:HG23	2	0.14	0.03	0.14
(3,2482)	1:282:A:LEU:HD21	1:282:A:LEU:H	2	0.14	0.03	0.14
(3,2482)	1:282:A:LEU:HD22	1:282:A:LEU:H	2	0.14	0.03	0.14

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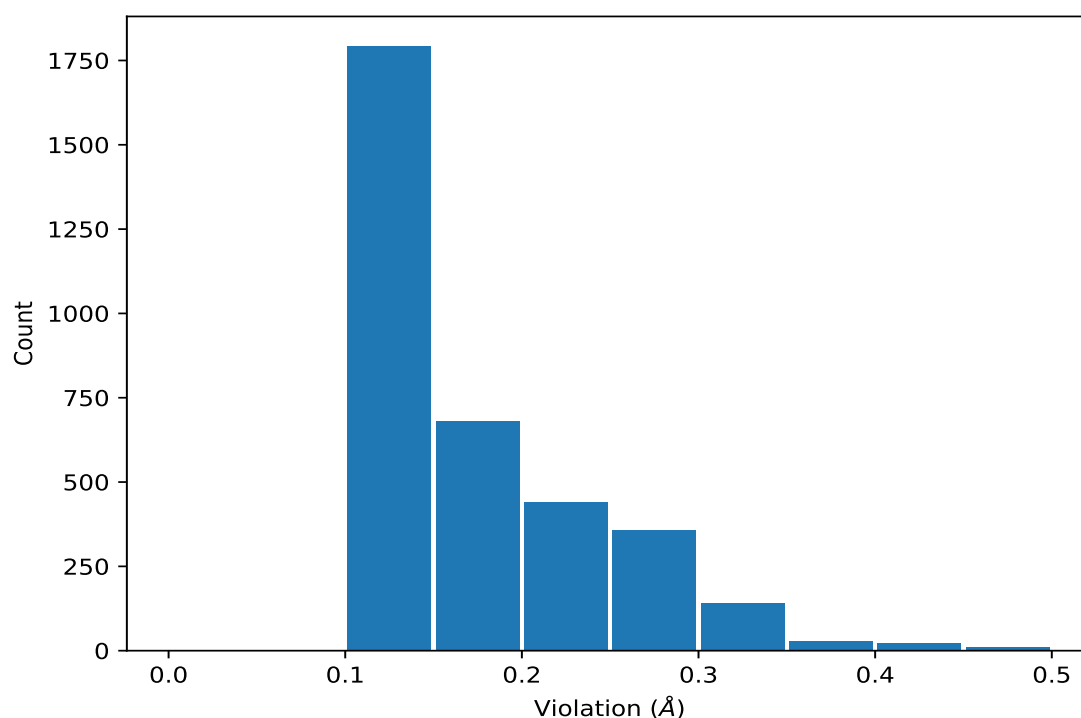
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(3,2482)	1:282:A:LEU:HD23	1:282:A:LEU:H	2	0.14	0.03	0.14
(3,2286)	1:255:A:ASN:H	1:289:A:LEU:HG	2	0.14	0.01	0.14
(3,7)	1:314:A:VAL:H	1:241:A:VAL:HG21	2	0.13	0.02	0.13
(3,7)	1:314:A:VAL:H	1:241:A:VAL:HG22	2	0.13	0.02	0.13
(3,7)	1:314:A:VAL:H	1:241:A:VAL:HG23	2	0.13	0.02	0.13
(3,1614)	1:318:A:TYR:HB3	1:317:A:VAL:HG21	2	0.13	0.01	0.13
(3,1614)	1:318:A:TYR:HB3	1:317:A:VAL:HG22	2	0.13	0.01	0.13
(3,1614)	1:318:A:TYR:HB3	1:317:A:VAL:HG23	2	0.13	0.01	0.13
(3,315)	1:282:A:LEU:HA	1:282:A:LEU:HD11	2	0.12	0.01	0.12
(3,315)	1:282:A:LEU:HA	1:282:A:LEU:HD12	2	0.12	0.01	0.12
(3,315)	1:282:A:LEU:HA	1:282:A:LEU:HD13	2	0.12	0.01	0.12
(3,1385)	1:286:A:THR:HG21	1:291:A:GLU:H	2	0.12	0.02	0.12
(3,1385)	1:286:A:THR:HG22	1:291:A:GLU:H	2	0.12	0.02	0.12
(3,1385)	1:286:A:THR:HG23	1:291:A:GLU:H	2	0.12	0.02	0.12
(3,2353)	1:268:A:SER:H	1:274:A:ILE:HG21	2	0.12	0.02	0.12
(3,2353)	1:268:A:SER:H	1:274:A:ILE:HG22	2	0.12	0.02	0.12
(3,2353)	1:268:A:SER:H	1:274:A:ILE:HG23	2	0.12	0.02	0.12
(3,706)	1:287:A:LYS:HE2	1:287:A:LYS:HG3	2	0.12	0.02	0.12
(1,42)	1:306:A:ASN:N	1:302:A:GLU:O	2	0.12	0.0	0.12
(2,42)	1:306:A:ASN:N	1:302:A:GLU:O	2	0.12	0.0	0.12
(3,2080)	1:299:A:ALA:H	1:300:A:GLU:HG3	2	0.12	0.0	0.12
(1,4)	1:261:A:VAL:H	1:257:A:ILE:O	2	0.11	0.01	0.11
(2,4)	1:261:A:VAL:H	1:257:A:ILE:O	2	0.11	0.01	0.11
(3,1096)	1:292:A:VAL:HG11	1:291:A:GLU:H	2	0.11	0.0	0.11
(3,1096)	1:292:A:VAL:HG12	1:291:A:GLU:H	2	0.11	0.0	0.11
(3,1096)	1:292:A:VAL:HG13	1:291:A:GLU:H	2	0.11	0.0	0.11
(3,1159)	1:259:A:LYS:HG2	1:259:A:LYS:HE2	2	0.11	0.01	0.11
(3,1759)	1:264:A:LEU:HG	1:306:A:ASN:HB2	2	0.11	0.0	0.11
(3,2526)	1:276:A:VAL:HG21	1:276:A:VAL:H	2	0.11	0.0	0.11
(3,2526)	1:276:A:VAL:HG22	1:276:A:VAL:H	2	0.11	0.0	0.11
(3,2526)	1:276:A:VAL:HG23	1:276:A:VAL:H	2	0.11	0.0	0.11
(3,1187)	1:265:A:ASN:HB2	1:262:A:GLY:HA3	2	0.11	0.0	0.11
(3,2430)	1:257:A:ILE:H	1:258:A:GLN:HB3	2	0.11	0.0	0.11

¹Number of violated models, ²Standard deviation

9.5 All violated distance restraints ⓘ

9.5.1 Histogram : Distribution of distance violations ⓘ

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)
(3,1538)	1:298:A:GLU:HA	1:301:A:LEU:HD21	29	0.47
(3,1538)	1:298:A:GLU:HA	1:301:A:LEU:HD22	29	0.47
(3,1538)	1:298:A:GLU:HA	1:301:A:LEU:HD23	29	0.47
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	28	0.46
(3,1882)	1:292:A:VAL:HG21	1:253:A:THR:H	30	0.45
(3,1882)	1:292:A:VAL:HG22	1:253:A:THR:H	30	0.45
(3,1882)	1:292:A:VAL:HG23	1:253:A:THR:H	30	0.45
(3,1616)	1:318:A:TYR:HB3	1:317:A:VAL:HB	12	0.45
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG11	6	0.45
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG12	6	0.45
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG13	6	0.45
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	14	0.44
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD11	24	0.44
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD12	24	0.44
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD13	24	0.44
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	22	0.43

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	19	0.42
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	17	0.41
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	17	0.41
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	17	0.41
(3,1616)	1:318:A:TYR:HB3	1:317:A:VAL:HB	7	0.41
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD11	8	0.41
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD12	8	0.41
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD13	8	0.41
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD11	28	0.41
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD12	28	0.41
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD13	28	0.41
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	4	0.4
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	28	0.4
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	28	0.4
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	28	0.4
(3,1186)	1:265:A:ASN:HB3	1:262:A:GLY:HA3	28	0.4
(3,2303)	1:238:A:LYS:H	1:239:A:TRP:HA	20	0.39
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	17	0.39
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	17	0.39
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	17	0.39
(3,1186)	1:265:A:ASN:HB3	1:262:A:GLY:HA3	13	0.39
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	8	0.38
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	12	0.38
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	29	0.38
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	1	0.37
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	6	0.37
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	16	0.37
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	26	0.37
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	4	0.37
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	7	0.37
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	10	0.37
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	15	0.37
(3,1186)	1:265:A:ASN:HB3	1:262:A:GLY:HA3	9	0.37
(3,1186)	1:265:A:ASN:HB3	1:262:A:GLY:HA3	16	0.37
(3,1186)	1:265:A:ASN:HB3	1:262:A:GLY:HA3	21	0.37
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	5	0.36
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	21	0.36
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	6	0.36
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	6	0.36
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	6	0.36
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	11	0.36
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	11	0.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	11	0.36
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	3	0.35
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	13	0.35
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	16	0.35
(3,1658)	1:240:A:THR:HB	1:239:A:TRP:HA	14	0.35
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG21	26	0.35
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG22	26	0.35
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG23	26	0.35
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	13	0.35
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	13	0.35
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	13	0.35
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	27	0.35
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	27	0.35
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	27	0.35
(3,1186)	1:265:A:ASN:HB3	1:262:A:GLY:HA3	10	0.35
(3,1186)	1:265:A:ASN:HB3	1:262:A:GLY:HA3	25	0.35
(3,1186)	1:265:A:ASN:HB3	1:262:A:GLY:HA3	26	0.35
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	3	0.34
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	5	0.34
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	11	0.34
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	12	0.34
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	17	0.34
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	10	0.34
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	27	0.34
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	17	0.34
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	2	0.34
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	6	0.34
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	17	0.34
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	23	0.34
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	18	0.34
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	18	0.34
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	18	0.34
(3,1149)	1:259:A:LYS:HD2	1:259:A:LYS:HA	6	0.34
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG11	8	0.34
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG12	8	0.34
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG13	8	0.34
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD11	17	0.34
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD12	17	0.34
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD13	17	0.34
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	6	0.33
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	16	0.33
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	18	0.33

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	22	0.33
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	30	0.33
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	2	0.33
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	15	0.33
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	14	0.33
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	29	0.33
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	29	0.33
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	29	0.33
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG21	17	0.33
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG22	17	0.33
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG23	17	0.33
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG21	19	0.33
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG22	19	0.33
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG23	19	0.33
(3,1186)	1:265:A:ASN:HB3	1:262:A:GLY:HA3	27	0.33
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG11	23	0.33
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG12	23	0.33
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG13	23	0.33
(3,888)	1:287:A:LYS:HB2	1:287:A:LYS:HE2	20	0.33
(3,866)	1:283:A:LEU:HD21	1:261:A:VAL:HB	11	0.33
(3,866)	1:283:A:LEU:HD22	1:261:A:VAL:HB	11	0.33
(3,866)	1:283:A:LEU:HD23	1:261:A:VAL:HB	11	0.33
(3,825)	1:254:A:VAL:HG11	1:293:A:ILE:H	30	0.33
(3,825)	1:254:A:VAL:HG12	1:293:A:ILE:H	30	0.33
(3,825)	1:254:A:VAL:HG13	1:293:A:ILE:H	30	0.33
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	20	0.32
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	26	0.32
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	27	0.32
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	29	0.32
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	9	0.32
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	11	0.32
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	25	0.32
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	7	0.32
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	8	0.32
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	24	0.32
(3,1426)	1:293:A:ILE:HD11	1:292:A:VAL:H	18	0.32
(3,1426)	1:293:A:ILE:HD12	1:292:A:VAL:H	18	0.32
(3,1426)	1:293:A:ILE:HD13	1:292:A:VAL:H	18	0.32
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG21	27	0.32
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG22	27	0.32
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG23	27	0.32
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	12	0.32

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	12	0.32
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	12	0.32
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	21	0.32
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	21	0.32
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	21	0.32
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	22	0.32
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	22	0.32
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	22	0.32
(3,1139)	1:283:A:LEU:HD11	1:257:A:ILE:H	15	0.32
(3,1139)	1:283:A:LEU:HD12	1:257:A:ILE:H	15	0.32
(3,1139)	1:283:A:LEU:HD13	1:257:A:ILE:H	15	0.32
(3,888)	1:287:A:LYS:HB2	1:287:A:LYS:HE2	6	0.32
(3,872)	1:254:A:VAL:HA	1:283:A:LEU:HD11	22	0.32
(3,872)	1:254:A:VAL:HA	1:283:A:LEU:HD12	22	0.32
(3,872)	1:254:A:VAL:HA	1:283:A:LEU:HD13	22	0.32
(3,866)	1:283:A:LEU:HD21	1:261:A:VAL:HB	23	0.32
(3,866)	1:283:A:LEU:HD22	1:261:A:VAL:HB	23	0.32
(3,866)	1:283:A:LEU:HD23	1:261:A:VAL:HB	23	0.32
(3,543)	1:287:A:LYS:H	1:287:A:LYS:HG2	24	0.32
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	9	0.31
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	7	0.31
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	17	0.31
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	24	0.31
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	28	0.31
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	4	0.31
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	4	0.31
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	4	0.31
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	20	0.31
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	20	0.31
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	20	0.31
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	26	0.31
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	26	0.31
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	26	0.31
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	24	0.31
(3,1518)	1:295:A:LEU:HD11	1:282:A:LEU:HD11	24	0.31
(3,1518)	1:295:A:LEU:HD11	1:282:A:LEU:HD12	24	0.31
(3,1518)	1:295:A:LEU:HD11	1:282:A:LEU:HD13	24	0.31
(3,1518)	1:295:A:LEU:HD12	1:282:A:LEU:HD11	24	0.31
(3,1518)	1:295:A:LEU:HD12	1:282:A:LEU:HD12	24	0.31
(3,1518)	1:295:A:LEU:HD12	1:282:A:LEU:HD13	24	0.31
(3,1518)	1:295:A:LEU:HD13	1:282:A:LEU:HD11	24	0.31
(3,1518)	1:295:A:LEU:HD13	1:282:A:LEU:HD12	24	0.31

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1518)	1:295:A:LEU:HD13	1:282:A:LEU:HD13	24	0.31
(3,1139)	1:283:A:LEU:HD11	1:257:A:ILE:H	23	0.31
(3,1139)	1:283:A:LEU:HD12	1:257:A:ILE:H	23	0.31
(3,1139)	1:283:A:LEU:HD13	1:257:A:ILE:H	23	0.31
(3,1139)	1:283:A:LEU:HD11	1:257:A:ILE:H	29	0.31
(3,1139)	1:283:A:LEU:HD12	1:257:A:ILE:H	29	0.31
(3,1139)	1:283:A:LEU:HD13	1:257:A:ILE:H	29	0.31
(3,888)	1:287:A:LYS:HB2	1:287:A:LYS:HE2	9	0.31
(3,825)	1:254:A:VAL:HG11	1:293:A:ILE:H	10	0.31
(3,825)	1:254:A:VAL:HG12	1:293:A:ILE:H	10	0.31
(3,825)	1:254:A:VAL:HG13	1:293:A:ILE:H	10	0.31
(3,814)	1:275:A:LYS:HG2	1:275:A:LYS:HE3	12	0.31
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	18	0.31
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	18	0.31
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	18	0.31
(3,71)	1:290:A:THR:H	1:255:A:ASN:HB3	1	0.31
(3,71)	1:290:A:THR:H	1:255:A:ASN:HB3	5	0.31
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	13	0.3
(3,2303)	1:238:A:LYS:H	1:239:A:TRP:HA	22	0.3
(3,2303)	1:238:A:LYS:H	1:239:A:TRP:HA	30	0.3
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	18	0.3
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	21	0.3
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	28	0.3
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	5	0.3
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	19	0.3
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	30	0.3
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	16	0.3
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	16	0.3
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	16	0.3
(3,1656)	1:240:A:THR:HG21	1:239:A:TRP:HE3	14	0.3
(3,1656)	1:240:A:THR:HG22	1:239:A:TRP:HE3	14	0.3
(3,1656)	1:240:A:THR:HG23	1:239:A:TRP:HE3	14	0.3
(3,1616)	1:318:A:TYR:HB3	1:317:A:VAL:HB	11	0.3
(3,1426)	1:293:A:ILE:HD11	1:292:A:VAL:H	8	0.3
(3,1426)	1:293:A:ILE:HD12	1:292:A:VAL:H	8	0.3
(3,1426)	1:293:A:ILE:HD13	1:292:A:VAL:H	8	0.3
(3,1396)	1:289:A:LEU:HD11	1:254:A:VAL:HB	30	0.3
(3,1396)	1:289:A:LEU:HD12	1:254:A:VAL:HB	30	0.3
(3,1396)	1:289:A:LEU:HD13	1:254:A:VAL:HB	30	0.3
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG21	4	0.3
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG22	4	0.3
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG23	4	0.3

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG11	29	0.3
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG12	29	0.3
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG13	29	0.3
(3,888)	1:287:A:LYS:HB2	1:287:A:LYS:HE2	2	0.3
(3,888)	1:287:A:LYS:HB2	1:287:A:LYS:HE2	29	0.3
(3,866)	1:283:A:LEU:HD21	1:261:A:VAL:HB	15	0.3
(3,866)	1:283:A:LEU:HD22	1:261:A:VAL:HB	15	0.3
(3,866)	1:283:A:LEU:HD23	1:261:A:VAL:HB	15	0.3
(3,823)	1:291:A:GLU:HB3	1:254:A:VAL:HG11	30	0.3
(3,823)	1:291:A:GLU:HB3	1:254:A:VAL:HG12	30	0.3
(3,823)	1:291:A:GLU:HB3	1:254:A:VAL:HG13	30	0.3
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	15	0.3
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	15	0.3
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	15	0.3
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	19	0.3
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	19	0.3
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	19	0.3
(3,80)	1:270:A:ILE:HD11	1:314:A:VAL:HG11	27	0.3
(3,80)	1:270:A:ILE:HD11	1:314:A:VAL:HG12	27	0.3
(3,80)	1:270:A:ILE:HD11	1:314:A:VAL:HG13	27	0.3
(3,80)	1:270:A:ILE:HD12	1:314:A:VAL:HG11	27	0.3
(3,80)	1:270:A:ILE:HD12	1:314:A:VAL:HG12	27	0.3
(3,80)	1:270:A:ILE:HD12	1:314:A:VAL:HG13	27	0.3
(3,80)	1:270:A:ILE:HD13	1:314:A:VAL:HG11	27	0.3
(3,80)	1:270:A:ILE:HD13	1:314:A:VAL:HG12	27	0.3
(3,80)	1:270:A:ILE:HD13	1:314:A:VAL:HG13	27	0.3
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	23	0.29
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	4	0.29
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	6	0.29
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	12	0.29
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	13	0.29
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	21	0.29
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	23	0.29
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	1	0.29
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	11	0.29
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	11	0.29
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	11	0.29
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	13	0.29
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	13	0.29
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	13	0.29
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	15	0.29
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	15	0.29

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	15	0.29
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	25	0.29
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	25	0.29
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	25	0.29
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	20	0.29
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	20	0.29
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	20	0.29
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	5	0.29
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	14	0.29
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	15	0.29
(3,1391)	1:287:A:LYS:HB3	1:254:A:VAL:HG21	18	0.29
(3,1391)	1:287:A:LYS:HB3	1:254:A:VAL:HG22	18	0.29
(3,1391)	1:287:A:LYS:HB3	1:254:A:VAL:HG23	18	0.29
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	8	0.29
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	8	0.29
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	8	0.29
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	20	0.29
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	20	0.29
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	20	0.29
(3,894)	1:254:A:VAL:HG11	1:287:A:LYS:HD2	16	0.29
(3,894)	1:254:A:VAL:HG12	1:287:A:LYS:HD2	16	0.29
(3,894)	1:254:A:VAL:HG13	1:287:A:LYS:HD2	16	0.29
(3,888)	1:287:A:LYS:HB2	1:287:A:LYS:HE2	11	0.29
(3,888)	1:287:A:LYS:HB2	1:287:A:LYS:HE2	23	0.29
(3,866)	1:283:A:LEU:HD21	1:261:A:VAL:HB	18	0.29
(3,866)	1:283:A:LEU:HD22	1:261:A:VAL:HB	18	0.29
(3,866)	1:283:A:LEU:HD23	1:261:A:VAL:HB	18	0.29
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD11	19	0.29
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD12	19	0.29
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD13	19	0.29
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD11	29	0.29
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD12	29	0.29
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD13	29	0.29
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	12	0.29
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	12	0.29
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	12	0.29
(3,15)	1:240:A:THR:HG21	1:239:A:TRP:HB3	5	0.29
(3,15)	1:240:A:THR:HG22	1:239:A:TRP:HB3	5	0.29
(3,15)	1:240:A:THR:HG23	1:239:A:TRP:HB3	5	0.29
(3,2357)	1:262:A:GLY:H	1:260:A:LEU:HB2	25	0.28
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	30	0.28
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	2	0.28

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	8	0.28
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	22	0.28
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	9	0.28
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	13	0.28
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	22	0.28
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	1	0.28
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	1	0.28
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	1	0.28
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	9	0.28
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	9	0.28
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	9	0.28
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	30	0.28
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	30	0.28
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	30	0.28
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	27	0.28
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	27	0.28
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	27	0.28
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	3	0.28
(3,1462)	1:293:A:ILE:HD11	1:283:A:LEU:HB3	21	0.28
(3,1462)	1:293:A:ILE:HD12	1:283:A:LEU:HB3	21	0.28
(3,1462)	1:293:A:ILE:HD13	1:283:A:LEU:HB3	21	0.28
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	18	0.28
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	18	0.28
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	18	0.28
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	29	0.28
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	29	0.28
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	29	0.28
(3,1160)	1:259:A:LYS:HE3	1:259:A:LYS:HG2	10	0.28
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG11	9	0.28
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG12	9	0.28
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG13	9	0.28
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG11	20	0.28
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG12	20	0.28
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG13	20	0.28
(3,888)	1:287:A:LYS:HB2	1:287:A:LYS:HE2	12	0.28
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD11	13	0.28
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD12	13	0.28
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD13	13	0.28
(3,72)	1:290:A:THR:H	1:253:A:THR:HA	6	0.28
(3,71)	1:290:A:THR:H	1:255:A:ASN:HB3	15	0.28
(3,71)	1:290:A:THR:H	1:255:A:ASN:HB3	30	0.28
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	1	0.27

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,2417)	1:308:A:GLU:H	1:307:A:ARG:HG3	14	0.27
(3,2357)	1:262:A:GLY:H	1:260:A:LEU:HB2	26	0.27
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	28	0.27
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	28	0.27
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	28	0.27
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	25	0.27
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	27	0.27
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	25	0.27
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	2	0.27
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	2	0.27
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	2	0.27
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	21	0.27
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	21	0.27
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	21	0.27
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	1	0.27
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	10	0.27
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	21	0.27
(3,1657)	1:240:A:THR:HB	1:242:A:GLN:H	1	0.27
(3,1426)	1:293:A:ILE:HD11	1:292:A:VAL:H	24	0.27
(3,1426)	1:293:A:ILE:HD12	1:292:A:VAL:H	24	0.27
(3,1426)	1:293:A:ILE:HD13	1:292:A:VAL:H	24	0.27
(3,1392)	1:288:A:ALA:HB1	1:254:A:VAL:HB	2	0.27
(3,1392)	1:288:A:ALA:HB2	1:254:A:VAL:HB	2	0.27
(3,1392)	1:288:A:ALA:HB3	1:254:A:VAL:HB	2	0.27
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	24	0.27
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	24	0.27
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	24	0.27
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	25	0.27
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	25	0.27
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	25	0.27
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	3	0.27
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	3	0.27
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	3	0.27
(3,899)	1:288:A:ALA:HA	1:289:A:LEU:HG	18	0.27
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG11	12	0.27
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG12	12	0.27
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG13	12	0.27
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG11	22	0.27
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG12	22	0.27
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG13	22	0.27
(3,888)	1:287:A:LYS:HB2	1:287:A:LYS:HE2	8	0.27
(3,872)	1:254:A:VAL:HA	1:283:A:LEU:HD11	12	0.27

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,872)	1:254:A:VAL:HA	1:283:A:LEU:HD12	12	0.27
(3,872)	1:254:A:VAL:HA	1:283:A:LEU:HD13	12	0.27
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD11	9	0.27
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD12	9	0.27
(3,858)	1:280:A:SER:HA	1:283:A:LEU:HD13	9	0.27
(3,825)	1:254:A:VAL:HG11	1:293:A:ILE:H	1	0.27
(3,825)	1:254:A:VAL:HG12	1:293:A:ILE:H	1	0.27
(3,825)	1:254:A:VAL:HG13	1:293:A:ILE:H	1	0.27
(3,810)	1:275:A:LYS:HE3	1:275:A:LYS:HB3	21	0.27
(3,716)	1:287:A:LYS:HD3	1:287:A:LYS:H	25	0.27
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	23	0.27
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	23	0.27
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	23	0.27
(3,71)	1:290:A:THR:H	1:255:A:ASN:HB3	10	0.27
(3,28)	1:310:A:LEU:HD21	1:271:A:TYR:HB2	2	0.27
(3,28)	1:310:A:LEU:HD22	1:271:A:TYR:HB2	2	0.27
(3,28)	1:310:A:LEU:HD23	1:271:A:TYR:HB2	2	0.27
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	7	0.26
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	8	0.26
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	10	0.26
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	14	0.26
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	23	0.26
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	24	0.26
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	25	0.26
(3,2540)	1:283:A:LEU:HD21	1:283:A:LEU:H	20	0.26
(3,2540)	1:283:A:LEU:HD22	1:283:A:LEU:H	20	0.26
(3,2540)	1:283:A:LEU:HD23	1:283:A:LEU:H	20	0.26
(3,2303)	1:238:A:LYS:H	1:239:A:TRP:HA	16	0.26
(3,2097)	1:299:A:ALA:H	1:300:A:GLU:HA	20	0.26
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	3	0.26
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	16	0.26
(3,1953)	1:265:A:ASN:H	1:263:A:LYS:HB3	21	0.26
(3,1885)	1:281:A:LYS:H	1:281:A:LYS:HG2	19	0.26
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	3	0.26
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	27	0.26
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	10	0.26
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	10	0.26
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	10	0.26
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	14	0.26
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	14	0.26
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	14	0.26
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	22	0.26

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	22	0.26
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	22	0.26
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	30	0.26
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	30	0.26
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	30	0.26
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	2	0.26
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	9	0.26
(3,1658)	1:240:A:THR:HB	1:239:A:TRP:HA	10	0.26
(3,1462)	1:293:A:ILE:HD11	1:283:A:LEU:HB3	3	0.26
(3,1462)	1:293:A:ILE:HD12	1:283:A:LEU:HB3	3	0.26
(3,1462)	1:293:A:ILE:HD13	1:283:A:LEU:HB3	3	0.26
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	16	0.26
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	16	0.26
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	16	0.26
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	28	0.26
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	28	0.26
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	28	0.26
(3,1139)	1:283:A:LEU:HD11	1:257:A:ILE:H	8	0.26
(3,1139)	1:283:A:LEU:HD12	1:257:A:ILE:H	8	0.26
(3,1139)	1:283:A:LEU:HD13	1:257:A:ILE:H	8	0.26
(3,1139)	1:283:A:LEU:HD11	1:257:A:ILE:H	28	0.26
(3,1139)	1:283:A:LEU:HD12	1:257:A:ILE:H	28	0.26
(3,1139)	1:283:A:LEU:HD13	1:257:A:ILE:H	28	0.26
(3,899)	1:288:A:ALA:HA	1:289:A:LEU:HG	24	0.26
(3,872)	1:254:A:VAL:HA	1:283:A:LEU:HD11	11	0.26
(3,872)	1:254:A:VAL:HA	1:283:A:LEU:HD12	11	0.26
(3,872)	1:254:A:VAL:HA	1:283:A:LEU:HD13	11	0.26
(3,872)	1:254:A:VAL:HA	1:283:A:LEU:HD11	23	0.26
(3,872)	1:254:A:VAL:HA	1:283:A:LEU:HD12	23	0.26
(3,872)	1:254:A:VAL:HA	1:283:A:LEU:HD13	23	0.26
(3,866)	1:283:A:LEU:HD21	1:261:A:VAL:HB	22	0.26
(3,866)	1:283:A:LEU:HD22	1:261:A:VAL:HB	22	0.26
(3,866)	1:283:A:LEU:HD23	1:261:A:VAL:HB	22	0.26
(3,810)	1:275:A:LYS:HE3	1:275:A:LYS:HB3	14	0.26
(3,810)	1:275:A:LYS:HE3	1:275:A:LYS:HB3	16	0.26
(3,810)	1:275:A:LYS:HE3	1:275:A:LYS:HB3	27	0.26
(3,774)	1:263:A:LYS:HE2	1:263:A:LYS:H	16	0.26
(3,71)	1:290:A:THR:H	1:255:A:ASN:HB3	14	0.26
(3,36)	1:308:A:GLU:H	1:306:A:ASN:HB3	14	0.26
(3,6)	1:314:A:VAL:H	1:315:A:HIS:HB2	29	0.26
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	2	0.25
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	4	0.25

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	15	0.25
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	19	0.25
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	21	0.25
(3,2571)	1:273:A:GLY:H	1:272:A:PRO:HD3	28	0.25
(3,2357)	1:262:A:GLY:H	1:260:A:LEU:HB2	28	0.25
(3,2174)	1:304:A:ALA:H	1:302:A:GLU:HB2	15	0.25
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	13	0.25
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	13	0.25
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	13	0.25
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	1	0.25
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	5	0.25
(3,1915)	1:308:A:GLU:HG3	1:308:A:GLU:H	3	0.25
(3,1915)	1:308:A:GLU:HG3	1:308:A:GLU:H	15	0.25
(3,1885)	1:281:A:LYS:H	1:281:A:LYS:HG2	29	0.25
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	12	0.25
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	5	0.25
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	5	0.25
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	5	0.25
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	8	0.25
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	8	0.25
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	8	0.25
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	6	0.25
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	6	0.25
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	6	0.25
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	23	0.25
(3,1658)	1:240:A:THR:HB	1:239:A:TRP:HA	22	0.25
(3,1658)	1:240:A:THR:HB	1:239:A:TRP:HA	24	0.25
(3,1426)	1:293:A:ILE:HD11	1:292:A:VAL:H	26	0.25
(3,1426)	1:293:A:ILE:HD12	1:292:A:VAL:H	26	0.25
(3,1426)	1:293:A:ILE:HD13	1:292:A:VAL:H	26	0.25
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG21	14	0.25
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG22	14	0.25
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG23	14	0.25
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG21	25	0.25
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG22	25	0.25
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG23	25	0.25
(3,1347)	1:280:A:SER:HA	1:276:A:VAL:HG21	29	0.25
(3,1347)	1:280:A:SER:HA	1:276:A:VAL:HG22	29	0.25
(3,1347)	1:280:A:SER:HA	1:276:A:VAL:HG23	29	0.25
(3,1139)	1:283:A:LEU:HD11	1:257:A:ILE:H	9	0.25
(3,1139)	1:283:A:LEU:HD12	1:257:A:ILE:H	9	0.25
(3,1139)	1:283:A:LEU:HD13	1:257:A:ILE:H	9	0.25

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1139)	1:283:A:LEU:HD11	1:257:A:ILE:H	13	0.25
(3,1139)	1:283:A:LEU:HD12	1:257:A:ILE:H	13	0.25
(3,1139)	1:283:A:LEU:HD13	1:257:A:ILE:H	13	0.25
(3,1052)	1:240:A:THR:HB	1:241:A:VAL:HB	1	0.25
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	9	0.25
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	9	0.25
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	9	0.25
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	12	0.25
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	12	0.25
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	12	0.25
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG11	2	0.25
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG12	2	0.25
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG13	2	0.25
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG11	21	0.25
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG12	21	0.25
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG13	21	0.25
(3,884)	1:286:A:THR:HA	1:287:A:LYS:HB3	30	0.25
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	10	0.25
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	10	0.25
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	10	0.25
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	15	0.25
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	15	0.25
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	15	0.25
(3,825)	1:254:A:VAL:HG11	1:293:A:ILE:H	5	0.25
(3,825)	1:254:A:VAL:HG12	1:293:A:ILE:H	5	0.25
(3,825)	1:254:A:VAL:HG13	1:293:A:ILE:H	5	0.25
(3,825)	1:254:A:VAL:HG11	1:293:A:ILE:H	14	0.25
(3,825)	1:254:A:VAL:HG12	1:293:A:ILE:H	14	0.25
(3,825)	1:254:A:VAL:HG13	1:293:A:ILE:H	14	0.25
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	22	0.25
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	22	0.25
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	22	0.25
(3,3)	1:314:A:VAL:HG11	1:315:A:HIS:HA	7	0.25
(3,3)	1:314:A:VAL:HG12	1:315:A:HIS:HA	7	0.25
(3,3)	1:314:A:VAL:HG13	1:315:A:HIS:HA	7	0.25
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	11	0.25
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	23	0.25
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	11	0.25
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	23	0.25
(3,2357)	1:262:A:GLY:H	1:260:A:LEU:HB2	9	0.24
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	10	0.24
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	10	0.24

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	10	0.24
(3,2155)	1:287:A:LYS:H	1:287:A:LYS:HE2	4	0.24
(3,2155)	1:287:A:LYS:H	1:287:A:LYS:HE2	26	0.24
(3,2155)	1:287:A:LYS:H	1:287:A:LYS:HE2	27	0.24
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG21	8	0.24
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG22	8	0.24
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG23	8	0.24
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG21	21	0.24
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG22	21	0.24
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG23	21	0.24
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	14	0.24
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	19	0.24
(3,1885)	1:281:A:LYS:H	1:281:A:LYS:HG2	9	0.24
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	29	0.24
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	7	0.24
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	7	0.24
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	7	0.24
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	22	0.24
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	22	0.24
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	22	0.24
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	23	0.24
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	23	0.24
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	23	0.24
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	5	0.24
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	5	0.24
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	5	0.24
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	16	0.24
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	16	0.24
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	16	0.24
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	26	0.24
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	26	0.24
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	26	0.24
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	29	0.24
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	29	0.24
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	29	0.24
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	11	0.24
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	16	0.24
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	20	0.24
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	22	0.24
(3,1658)	1:240:A:THR:HB	1:239:A:TRP:HA	3	0.24
(3,1658)	1:240:A:THR:HB	1:239:A:TRP:HA	21	0.24
(3,1426)	1:293:A:ILE:HD11	1:292:A:VAL:H	9	0.24

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1426)	1:293:A:ILE:HD12	1:292:A:VAL:H	9	0.24
(3,1426)	1:293:A:ILE:HD13	1:292:A:VAL:H	9	0.24
(3,1426)	1:293:A:ILE:HD11	1:292:A:VAL:H	15	0.24
(3,1426)	1:293:A:ILE:HD12	1:292:A:VAL:H	15	0.24
(3,1426)	1:293:A:ILE:HD13	1:292:A:VAL:H	15	0.24
(3,1389)	1:286:A:THR:HG21	1:291:A:GLU:HG3	20	0.24
(3,1389)	1:286:A:THR:HG22	1:291:A:GLU:HG3	20	0.24
(3,1389)	1:286:A:THR:HG23	1:291:A:GLU:HG3	20	0.24
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	7	0.24
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	7	0.24
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	7	0.24
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	19	0.24
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	19	0.24
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	19	0.24
(3,894)	1:254:A:VAL:HG11	1:287:A:LYS:HD2	3	0.24
(3,894)	1:254:A:VAL:HG12	1:287:A:LYS:HD2	3	0.24
(3,894)	1:254:A:VAL:HG13	1:287:A:LYS:HD2	3	0.24
(3,871)	1:283:A:LEU:HD21	1:254:A:VAL:HA	25	0.24
(3,871)	1:283:A:LEU:HD22	1:254:A:VAL:HA	25	0.24
(3,871)	1:283:A:LEU:HD23	1:254:A:VAL:HA	25	0.24
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD11	28	0.24
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD12	28	0.24
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD13	28	0.24
(3,774)	1:263:A:LYS:HE2	1:263:A:LYS:H	28	0.24
(3,748)	1:241:A:VAL:HA	1:240:A:THR:HA	4	0.24
(3,716)	1:287:A:LYS:HD3	1:287:A:LYS:H	19	0.24
(3,81)	1:262:A:GLY:H	1:260:A:LEU:HG	21	0.24
(3,80)	1:270:A:ILE:HD11	1:314:A:VAL:HG11	19	0.24
(3,80)	1:270:A:ILE:HD11	1:314:A:VAL:HG12	19	0.24
(3,80)	1:270:A:ILE:HD11	1:314:A:VAL:HG13	19	0.24
(3,80)	1:270:A:ILE:HD12	1:314:A:VAL:HG11	19	0.24
(3,80)	1:270:A:ILE:HD12	1:314:A:VAL:HG12	19	0.24
(3,80)	1:270:A:ILE:HD12	1:314:A:VAL:HG13	19	0.24
(3,80)	1:270:A:ILE:HD13	1:314:A:VAL:HG11	19	0.24
(3,80)	1:270:A:ILE:HD13	1:314:A:VAL:HG12	19	0.24
(3,80)	1:270:A:ILE:HD13	1:314:A:VAL:HG13	19	0.24
(3,72)	1:290:A:THR:H	1:253:A:THR:HA	22	0.24
(3,72)	1:290:A:THR:H	1:253:A:THR:HA	23	0.24
(3,71)	1:290:A:THR:H	1:255:A:ASN:HB3	17	0.24
(3,28)	1:310:A:LEU:HD21	1:271:A:TYR:HB2	19	0.24
(3,28)	1:310:A:LEU:HD22	1:271:A:TYR:HB2	19	0.24
(3,28)	1:310:A:LEU:HD23	1:271:A:TYR:HB2	19	0.24

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,28)	1:310:A:LEU:HD21	1:271:A:TYR:HB2	24	0.24
(3,28)	1:310:A:LEU:HD22	1:271:A:TYR:HB2	24	0.24
(3,28)	1:310:A:LEU:HD23	1:271:A:TYR:HB2	24	0.24
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	4	0.24
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	18	0.24
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	4	0.24
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	18	0.24
(3,2540)	1:283:A:LEU:HD21	1:283:A:LEU:H	5	0.23
(3,2540)	1:283:A:LEU:HD22	1:283:A:LEU:H	5	0.23
(3,2540)	1:283:A:LEU:HD23	1:283:A:LEU:H	5	0.23
(3,2540)	1:283:A:LEU:HD21	1:283:A:LEU:H	21	0.23
(3,2540)	1:283:A:LEU:HD22	1:283:A:LEU:H	21	0.23
(3,2540)	1:283:A:LEU:HD23	1:283:A:LEU:H	21	0.23
(3,2514)	1:273:A:GLY:H	1:271:A:TYR:HB3	15	0.23
(3,2357)	1:262:A:GLY:H	1:260:A:LEU:HB2	13	0.23
(3,2357)	1:262:A:GLY:H	1:260:A:LEU:HB2	16	0.23
(3,2303)	1:238:A:LYS:H	1:239:A:TRP:HA	15	0.23
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	27	0.23
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	27	0.23
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	27	0.23
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG21	27	0.23
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG22	27	0.23
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG23	27	0.23
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	10	0.23
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	26	0.23
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	13	0.23
(3,1538)	1:298:A:GLU:HA	1:301:A:LEU:HD21	20	0.23
(3,1538)	1:298:A:GLU:HA	1:301:A:LEU:HD22	20	0.23
(3,1538)	1:298:A:GLU:HA	1:301:A:LEU:HD23	20	0.23
(3,1538)	1:298:A:GLU:HA	1:301:A:LEU:HD21	22	0.23
(3,1538)	1:298:A:GLU:HA	1:301:A:LEU:HD22	22	0.23
(3,1538)	1:298:A:GLU:HA	1:301:A:LEU:HD23	22	0.23
(3,1462)	1:293:A:ILE:HD11	1:283:A:LEU:HB3	28	0.23
(3,1462)	1:293:A:ILE:HD12	1:283:A:LEU:HB3	28	0.23
(3,1462)	1:293:A:ILE:HD13	1:283:A:LEU:HB3	28	0.23
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG21	24	0.23
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG22	24	0.23
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG23	24	0.23
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	18	0.23
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	18	0.23
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	18	0.23
(3,894)	1:254:A:VAL:HG11	1:287:A:LYS:HD2	25	0.23

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,894)	1:254:A:VAL:HG12	1:287:A:LYS:HD2	25	0.23
(3,894)	1:254:A:VAL:HG13	1:287:A:LYS:HD2	25	0.23
(3,872)	1:254:A:VAL:HA	1:283:A:LEU:HD11	18	0.23
(3,872)	1:254:A:VAL:HA	1:283:A:LEU:HD12	18	0.23
(3,872)	1:254:A:VAL:HA	1:283:A:LEU:HD13	18	0.23
(3,871)	1:283:A:LEU:HD21	1:254:A:VAL:HA	26	0.23
(3,871)	1:283:A:LEU:HD22	1:254:A:VAL:HA	26	0.23
(3,871)	1:283:A:LEU:HD23	1:254:A:VAL:HA	26	0.23
(3,825)	1:254:A:VAL:HG11	1:293:A:ILE:H	15	0.23
(3,825)	1:254:A:VAL:HG12	1:293:A:ILE:H	15	0.23
(3,825)	1:254:A:VAL:HG13	1:293:A:ILE:H	15	0.23
(3,825)	1:254:A:VAL:HG11	1:293:A:ILE:H	24	0.23
(3,825)	1:254:A:VAL:HG12	1:293:A:ILE:H	24	0.23
(3,825)	1:254:A:VAL:HG13	1:293:A:ILE:H	24	0.23
(3,705)	1:287:A:LYS:HG2	1:287:A:LYS:HE2	25	0.23
(3,80)	1:270:A:ILE:HD11	1:314:A:VAL:HG11	22	0.23
(3,80)	1:270:A:ILE:HD11	1:314:A:VAL:HG12	22	0.23
(3,80)	1:270:A:ILE:HD11	1:314:A:VAL:HG13	22	0.23
(3,80)	1:270:A:ILE:HD12	1:314:A:VAL:HG11	22	0.23
(3,80)	1:270:A:ILE:HD12	1:314:A:VAL:HG12	22	0.23
(3,80)	1:270:A:ILE:HD12	1:314:A:VAL:HG13	22	0.23
(3,80)	1:270:A:ILE:HD13	1:314:A:VAL:HG11	22	0.23
(3,80)	1:270:A:ILE:HD13	1:314:A:VAL:HG12	22	0.23
(3,80)	1:270:A:ILE:HD13	1:314:A:VAL:HG13	22	0.23
(3,72)	1:290:A:THR:H	1:253:A:THR:HA	10	0.23
(2,34)	1:268:A:SER:N	1:264:A:LEU:O	23	0.23
(1,34)	1:268:A:SER:N	1:264:A:LEU:O	23	0.23
(3,2417)	1:308:A:GLU:H	1:307:A:ARG:HG3	12	0.22
(3,2336)	1:295:A:LEU:H	1:300:A:GLU:HB2	17	0.22
(3,2336)	1:295:A:LEU:H	1:300:A:GLU:HB2	20	0.22
(3,2336)	1:295:A:LEU:H	1:300:A:GLU:HB2	24	0.22
(3,2303)	1:238:A:LYS:H	1:239:A:TRP:HA	4	0.22
(3,2295)	1:262:A:GLY:H	1:265:A:ASN:HB2	28	0.22
(3,2268)	1:274:A:ILE:HG13	1:271:A:TYR:H	3	0.22
(3,2268)	1:274:A:ILE:HG13	1:271:A:TYR:H	17	0.22
(3,2201)	1:311:A:LYS:H	1:311:A:LYS:HD2	12	0.22
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	4	0.22
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	4	0.22
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	4	0.22
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	14	0.22
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	14	0.22
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	14	0.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG21	2	0.22
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG22	2	0.22
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG23	2	0.22
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG21	25	0.22
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG22	25	0.22
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG23	25	0.22
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	11	0.22
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	15	0.22
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	19	0.22
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	19	0.22
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	19	0.22
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	24	0.22
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	24	0.22
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	24	0.22
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	25	0.22
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	25	0.22
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	25	0.22
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	26	0.22
(3,1518)	1:295:A:LEU:HD11	1:282:A:LEU:HD11	7	0.22
(3,1518)	1:295:A:LEU:HD11	1:282:A:LEU:HD12	7	0.22
(3,1518)	1:295:A:LEU:HD11	1:282:A:LEU:HD13	7	0.22
(3,1518)	1:295:A:LEU:HD12	1:282:A:LEU:HD11	7	0.22
(3,1518)	1:295:A:LEU:HD12	1:282:A:LEU:HD12	7	0.22
(3,1518)	1:295:A:LEU:HD12	1:282:A:LEU:HD13	7	0.22
(3,1518)	1:295:A:LEU:HD13	1:282:A:LEU:HD11	7	0.22
(3,1518)	1:295:A:LEU:HD13	1:282:A:LEU:HD12	7	0.22
(3,1518)	1:295:A:LEU:HD13	1:282:A:LEU:HD13	7	0.22
(3,1462)	1:293:A:ILE:HD11	1:283:A:LEU:HB3	7	0.22
(3,1462)	1:293:A:ILE:HD12	1:283:A:LEU:HB3	7	0.22
(3,1462)	1:293:A:ILE:HD13	1:283:A:LEU:HB3	7	0.22
(3,1346)	1:276:A:VAL:HG21	1:264:A:LEU:HB3	13	0.22
(3,1346)	1:276:A:VAL:HG22	1:264:A:LEU:HB3	13	0.22
(3,1346)	1:276:A:VAL:HG23	1:264:A:LEU:HB3	13	0.22
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	11	0.22
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	11	0.22
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	11	0.22
(3,1139)	1:283:A:LEU:HD11	1:257:A:ILE:H	19	0.22
(3,1139)	1:283:A:LEU:HD12	1:257:A:ILE:H	19	0.22
(3,1139)	1:283:A:LEU:HD13	1:257:A:ILE:H	19	0.22
(3,894)	1:254:A:VAL:HG11	1:287:A:LYS:HD2	21	0.22
(3,894)	1:254:A:VAL:HG12	1:287:A:LYS:HD2	21	0.22
(3,894)	1:254:A:VAL:HG13	1:287:A:LYS:HD2	21	0.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD11	4	0.22
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD12	4	0.22
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD13	4	0.22
(3,740)	1:238:A:LYS:HB2	1:238:A:LYS:HD3	4	0.22
(3,72)	1:290:A:THR:H	1:253:A:THR:HA	12	0.22
(3,28)	1:310:A:LEU:HD21	1:271:A:TYR:HB2	13	0.22
(3,28)	1:310:A:LEU:HD22	1:271:A:TYR:HB2	13	0.22
(3,28)	1:310:A:LEU:HD23	1:271:A:TYR:HB2	13	0.22
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	15	0.22
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	26	0.22
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	28	0.22
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	15	0.22
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	26	0.22
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	28	0.22
(3,2540)	1:283:A:LEU:HD21	1:283:A:LEU:H	3	0.21
(3,2540)	1:283:A:LEU:HD22	1:283:A:LEU:H	3	0.21
(3,2540)	1:283:A:LEU:HD23	1:283:A:LEU:H	3	0.21
(3,2540)	1:283:A:LEU:HD21	1:283:A:LEU:H	7	0.21
(3,2540)	1:283:A:LEU:HD22	1:283:A:LEU:H	7	0.21
(3,2540)	1:283:A:LEU:HD23	1:283:A:LEU:H	7	0.21
(3,2514)	1:273:A:GLY:H	1:271:A:TYR:HB3	21	0.21
(3,2514)	1:273:A:GLY:H	1:271:A:TYR:HB3	23	0.21
(3,2414)	1:268:A:SER:H	1:274:A:ILE:HB	27	0.21
(3,2303)	1:238:A:LYS:H	1:239:A:TRP:HA	9	0.21
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG21	8	0.21
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG22	8	0.21
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG23	8	0.21
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG21	21	0.21
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG22	21	0.21
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG23	21	0.21
(3,2201)	1:311:A:LYS:H	1:311:A:LYS:HD2	7	0.21
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	15	0.21
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	15	0.21
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	15	0.21
(3,2155)	1:287:A:LYS:H	1:287:A:LYS:HE2	18	0.21
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG21	17	0.21
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG22	17	0.21
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG23	17	0.21
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	9	0.21
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	26	0.21
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	29	0.21
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	22	0.21

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	3	0.21
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	3	0.21
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	3	0.21
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	27	0.21
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	27	0.21
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	27	0.21
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	9	0.21
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	9	0.21
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	9	0.21
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	10	0.21
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	10	0.21
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	10	0.21
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	13	0.21
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	13	0.21
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	13	0.21
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	23	0.21
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	23	0.21
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	23	0.21
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	6	0.21
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	19	0.21
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	29	0.21
(3,1665)	1:242:A:GLN:HG3	1:241:A:VAL:H	20	0.21
(3,1518)	1:295:A:LEU:HD11	1:282:A:LEU:HD11	6	0.21
(3,1518)	1:295:A:LEU:HD11	1:282:A:LEU:HD12	6	0.21
(3,1518)	1:295:A:LEU:HD11	1:282:A:LEU:HD13	6	0.21
(3,1518)	1:295:A:LEU:HD12	1:282:A:LEU:HD11	6	0.21
(3,1518)	1:295:A:LEU:HD12	1:282:A:LEU:HD12	6	0.21
(3,1518)	1:295:A:LEU:HD12	1:282:A:LEU:HD13	6	0.21
(3,1518)	1:295:A:LEU:HD13	1:282:A:LEU:HD11	6	0.21
(3,1518)	1:295:A:LEU:HD13	1:282:A:LEU:HD12	6	0.21
(3,1518)	1:295:A:LEU:HD13	1:282:A:LEU:HD13	6	0.21
(3,1482)	1:257:A:ILE:HD11	1:254:A:VAL:HB	15	0.21
(3,1482)	1:257:A:ILE:HD12	1:254:A:VAL:HB	15	0.21
(3,1482)	1:257:A:ILE:HD13	1:254:A:VAL:HB	15	0.21
(3,1470)	1:293:A:ILE:HG21	1:257:A:ILE:HB	30	0.21
(3,1470)	1:293:A:ILE:HG22	1:257:A:ILE:HB	30	0.21
(3,1470)	1:293:A:ILE:HG23	1:257:A:ILE:HB	30	0.21
(3,1462)	1:293:A:ILE:HD11	1:283:A:LEU:HB3	2	0.21
(3,1462)	1:293:A:ILE:HD12	1:283:A:LEU:HB3	2	0.21
(3,1462)	1:293:A:ILE:HD13	1:283:A:LEU:HB3	2	0.21
(3,1426)	1:293:A:ILE:HD11	1:292:A:VAL:H	10	0.21
(3,1426)	1:293:A:ILE:HD12	1:292:A:VAL:H	10	0.21

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1426)	1:293:A:ILE:HD13	1:292:A:VAL:H	10	0.21
(3,1215)	1:276:A:VAL:HG11	1:279:A:LEU:HB2	12	0.21
(3,1215)	1:276:A:VAL:HG12	1:279:A:LEU:HB2	12	0.21
(3,1215)	1:276:A:VAL:HG13	1:279:A:LEU:HB2	12	0.21
(3,1211)	1:264:A:LEU:HG	1:265:A:ASN:H	26	0.21
(3,1148)	1:259:A:LYS:H	1:259:A:LYS:HD2	23	0.21
(3,1139)	1:283:A:LEU:HD11	1:257:A:ILE:H	17	0.21
(3,1139)	1:283:A:LEU:HD12	1:257:A:ILE:H	17	0.21
(3,1139)	1:283:A:LEU:HD13	1:257:A:ILE:H	17	0.21
(3,1134)	1:254:A:VAL:HA	1:257:A:ILE:HG21	29	0.21
(3,1134)	1:254:A:VAL:HA	1:257:A:ILE:HG22	29	0.21
(3,1134)	1:254:A:VAL:HA	1:257:A:ILE:HG23	29	0.21
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	17	0.21
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	17	0.21
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	17	0.21
(3,871)	1:283:A:LEU:HD21	1:254:A:VAL:HA	16	0.21
(3,871)	1:283:A:LEU:HD22	1:254:A:VAL:HA	16	0.21
(3,871)	1:283:A:LEU:HD23	1:254:A:VAL:HA	16	0.21
(3,867)	1:283:A:LEU:HD21	1:258:A:GLN:HB3	24	0.21
(3,867)	1:283:A:LEU:HD22	1:258:A:GLN:HB3	24	0.21
(3,867)	1:283:A:LEU:HD23	1:258:A:GLN:HB3	24	0.21
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	30	0.21
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	30	0.21
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	30	0.21
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD11	14	0.21
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD12	14	0.21
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD13	14	0.21
(3,779)	1:263:A:LYS:HD3	1:263:A:LYS:H	26	0.21
(3,740)	1:238:A:LYS:HB2	1:238:A:LYS:HD3	20	0.21
(3,716)	1:287:A:LYS:HD3	1:287:A:LYS:H	26	0.21
(3,705)	1:287:A:LYS:HG2	1:287:A:LYS:HE2	30	0.21
(3,659)	1:281:A:LYS:HE3	1:281:A:LYS:HB2	26	0.21
(3,81)	1:262:A:GLY:H	1:260:A:LEU:HG	28	0.21
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	21	0.21
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	25	0.21
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	21	0.21
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	25	0.21
(3,2514)	1:273:A:GLY:H	1:271:A:TYR:HB3	7	0.2
(3,2434)	1:253:A:THR:HG21	1:254:A:VAL:H	30	0.2
(3,2434)	1:253:A:THR:HG22	1:254:A:VAL:H	30	0.2
(3,2434)	1:253:A:THR:HG23	1:254:A:VAL:H	30	0.2
(3,2401)	1:253:A:THR:H	1:292:A:VAL:H	15	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,2357)	1:262:A:GLY:H	1:260:A:LEU:HB2	10	0.2
(3,2357)	1:262:A:GLY:H	1:260:A:LEU:HB2	21	0.2
(3,2357)	1:262:A:GLY:H	1:260:A:LEU:HB2	27	0.2
(3,2340)	1:258:A:GLN:HE22	1:258:A:GLN:HB3	2	0.2
(3,2336)	1:295:A:LEU:H	1:300:A:GLU:HB2	30	0.2
(3,2295)	1:262:A:GLY:H	1:265:A:ASN:HB2	26	0.2
(3,2285)	1:271:A:TYR:H	1:270:A:ILE:HG13	10	0.2
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG21	4	0.2
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG22	4	0.2
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG23	4	0.2
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG21	28	0.2
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG22	28	0.2
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG23	28	0.2
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG21	13	0.2
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG22	13	0.2
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG23	13	0.2
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	23	0.2
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	15	0.2
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	15	0.2
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	15	0.2
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	18	0.2
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	18	0.2
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	18	0.2
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	19	0.2
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	19	0.2
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	19	0.2
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	22	0.2
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	22	0.2
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	22	0.2
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	4	0.2
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	28	0.2
(3,1660)	1:240:A:THR:HG21	1:315:A:HIS:HA	23	0.2
(3,1660)	1:240:A:THR:HG22	1:315:A:HIS:HA	23	0.2
(3,1660)	1:240:A:THR:HG23	1:315:A:HIS:HA	23	0.2
(3,1638)	1:319:A:LEU:HD21	1:318:A:TYR:HB3	14	0.2
(3,1638)	1:319:A:LEU:HD22	1:318:A:TYR:HB3	14	0.2
(3,1638)	1:319:A:LEU:HD23	1:318:A:TYR:HB3	14	0.2
(3,1462)	1:293:A:ILE:HD11	1:283:A:LEU:HB3	16	0.2
(3,1462)	1:293:A:ILE:HD12	1:283:A:LEU:HB3	16	0.2
(3,1462)	1:293:A:ILE:HD13	1:283:A:LEU:HB3	16	0.2
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG21	10	0.2
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG22	10	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG23	10	0.2
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG21	24	0.2
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG22	24	0.2
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG23	24	0.2
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG21	28	0.2
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG22	28	0.2
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG23	28	0.2
(3,1389)	1:286:A:THR:HG21	1:291:A:GLU:HG3	23	0.2
(3,1389)	1:286:A:THR:HG22	1:291:A:GLU:HG3	23	0.2
(3,1389)	1:286:A:THR:HG23	1:291:A:GLU:HG3	23	0.2
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG21	8	0.2
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG22	8	0.2
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG23	8	0.2
(3,1139)	1:283:A:LEU:HD11	1:257:A:ILE:H	24	0.2
(3,1139)	1:283:A:LEU:HD12	1:257:A:ILE:H	24	0.2
(3,1139)	1:283:A:LEU:HD13	1:257:A:ILE:H	24	0.2
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	26	0.2
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	26	0.2
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	26	0.2
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG11	25	0.2
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG12	25	0.2
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG13	25	0.2
(3,888)	1:287:A:LYS:HB2	1:287:A:LYS:HE2	22	0.2
(3,875)	1:283:A:LEU:HD11	1:258:A:GLN:HB3	7	0.2
(3,875)	1:283:A:LEU:HD12	1:258:A:GLN:HB3	7	0.2
(3,875)	1:283:A:LEU:HD13	1:258:A:GLN:HB3	7	0.2
(3,867)	1:283:A:LEU:HD21	1:258:A:GLN:HB3	8	0.2
(3,867)	1:283:A:LEU:HD22	1:258:A:GLN:HB3	8	0.2
(3,867)	1:283:A:LEU:HD23	1:258:A:GLN:HB3	8	0.2
(3,866)	1:283:A:LEU:HD21	1:261:A:VAL:HB	12	0.2
(3,866)	1:283:A:LEU:HD22	1:261:A:VAL:HB	12	0.2
(3,866)	1:283:A:LEU:HD23	1:261:A:VAL:HB	12	0.2
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD11	7	0.2
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD12	7	0.2
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD13	7	0.2
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD11	13	0.2
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD12	13	0.2
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD13	13	0.2
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD11	30	0.2
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD12	30	0.2
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD13	30	0.2
(3,740)	1:238:A:LYS:HB2	1:238:A:LYS:HD3	14	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,581)	1:302:A:GLU:HG3	1:302:A:GLU:HA	15	0.2
(3,28)	1:310:A:LEU:HD21	1:271:A:TYR:HB2	1	0.2
(3,28)	1:310:A:LEU:HD22	1:271:A:TYR:HB2	1	0.2
(3,28)	1:310:A:LEU:HD23	1:271:A:TYR:HB2	1	0.2
(3,19)	1:314:A:VAL:HG21	1:312:A:GLU:HB2	19	0.2
(3,19)	1:314:A:VAL:HG22	1:312:A:GLU:HB2	19	0.2
(3,19)	1:314:A:VAL:HG23	1:312:A:GLU:HB2	19	0.2
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	2	0.2
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	7	0.2
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	10	0.2
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	12	0.2
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	29	0.2
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	2	0.2
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	7	0.2
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	10	0.2
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	12	0.2
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	29	0.2
(3,2540)	1:283:A:LEU:HD21	1:283:A:LEU:H	6	0.19
(3,2540)	1:283:A:LEU:HD22	1:283:A:LEU:H	6	0.19
(3,2540)	1:283:A:LEU:HD23	1:283:A:LEU:H	6	0.19
(3,2528)	1:253:A:THR:H	1:292:A:VAL:HG11	30	0.19
(3,2528)	1:253:A:THR:H	1:292:A:VAL:HG12	30	0.19
(3,2528)	1:253:A:THR:H	1:292:A:VAL:HG13	30	0.19
(3,2514)	1:273:A:GLY:H	1:271:A:TYR:HB3	2	0.19
(3,2514)	1:273:A:GLY:H	1:271:A:TYR:HB3	10	0.19
(3,2498)	1:287:A:LYS:H	1:287:A:LYS:HD2	4	0.19
(3,2498)	1:287:A:LYS:H	1:287:A:LYS:HD2	19	0.19
(3,2498)	1:287:A:LYS:H	1:287:A:LYS:HD2	27	0.19
(3,2474)	1:256:A:ASP:H	1:258:A:GLN:HB3	18	0.19
(3,2367)	1:275:A:LYS:HG2	1:275:A:LYS:H	25	0.19
(3,2357)	1:262:A:GLY:H	1:260:A:LEU:HB2	4	0.19
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD11	28	0.19
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD12	28	0.19
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD13	28	0.19
(3,2340)	1:258:A:GLN:HE22	1:258:A:GLN:HB3	10	0.19
(3,2303)	1:238:A:LYS:H	1:239:A:TRP:HA	7	0.19
(3,2303)	1:238:A:LYS:H	1:239:A:TRP:HA	23	0.19
(3,2303)	1:238:A:LYS:H	1:239:A:TRP:HA	26	0.19
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG21	24	0.19
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG22	24	0.19
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG23	24	0.19
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG21	29	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG22	29	0.19
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG23	29	0.19
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	2	0.19
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	2	0.19
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	2	0.19
(3,2155)	1:287:A:LYS:H	1:287:A:LYS:HE2	19	0.19
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG21	30	0.19
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG22	30	0.19
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG23	30	0.19
(3,1953)	1:265:A:ASN:H	1:263:A:LYS:HB3	13	0.19
(3,1953)	1:265:A:ASN:H	1:263:A:LYS:HB3	16	0.19
(3,1953)	1:265:A:ASN:H	1:263:A:LYS:HB3	27	0.19
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	17	0.19
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	25	0.19
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	30	0.19
(3,1885)	1:281:A:LYS:H	1:281:A:LYS:HG2	28	0.19
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	20	0.19
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG21	12	0.19
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG22	12	0.19
(3,1823)	1:272:A:PRO:HG3	1:309:A:ILE:HG23	12	0.19
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	11	0.19
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	11	0.19
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	11	0.19
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	17	0.19
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	17	0.19
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	17	0.19
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	7	0.19
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	8	0.19
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	30	0.19
(3,1638)	1:319:A:LEU:HD21	1:318:A:TYR:HB3	8	0.19
(3,1638)	1:319:A:LEU:HD22	1:318:A:TYR:HB3	8	0.19
(3,1638)	1:319:A:LEU:HD23	1:318:A:TYR:HB3	8	0.19
(3,1426)	1:293:A:ILE:HD11	1:292:A:VAL:H	13	0.19
(3,1426)	1:293:A:ILE:HD12	1:292:A:VAL:H	13	0.19
(3,1426)	1:293:A:ILE:HD13	1:292:A:VAL:H	13	0.19
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG21	5	0.19
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG22	5	0.19
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG23	5	0.19
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG21	13	0.19
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG22	13	0.19
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG23	13	0.19
(3,1318)	1:274:A:ILE:HG21	1:275:A:LYS:HA	18	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1318)	1:274:A:ILE:HG22	1:275:A:LYS:HA	18	0.19
(3,1318)	1:274:A:ILE:HG23	1:275:A:LYS:HA	18	0.19
(3,1318)	1:274:A:ILE:HG21	1:275:A:LYS:HA	25	0.19
(3,1318)	1:274:A:ILE:HG22	1:275:A:LYS:HA	25	0.19
(3,1318)	1:274:A:ILE:HG23	1:275:A:LYS:HA	25	0.19
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG21	2	0.19
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG22	2	0.19
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG23	2	0.19
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG21	4	0.19
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG22	4	0.19
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG23	4	0.19
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG21	29	0.19
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG22	29	0.19
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG23	29	0.19
(3,1211)	1:264:A:LEU:HG	1:265:A:ASN:H	11	0.19
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	1	0.19
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	1	0.19
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	1	0.19
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	2	0.19
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	2	0.19
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	2	0.19
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	30	0.19
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	30	0.19
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	30	0.19
(3,1139)	1:283:A:LEU:HD11	1:257:A:ILE:H	12	0.19
(3,1139)	1:283:A:LEU:HD12	1:257:A:ILE:H	12	0.19
(3,1139)	1:283:A:LEU:HD13	1:257:A:ILE:H	12	0.19
(3,1139)	1:283:A:LEU:HD11	1:257:A:ILE:H	18	0.19
(3,1139)	1:283:A:LEU:HD12	1:257:A:ILE:H	18	0.19
(3,1139)	1:283:A:LEU:HD13	1:257:A:ILE:H	18	0.19
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	29	0.19
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	29	0.19
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	29	0.19
(3,1012)	1:309:A:ILE:HA	1:308:A:GLU:HG3	28	0.19
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG11	16	0.19
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG12	16	0.19
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG13	16	0.19
(3,875)	1:283:A:LEU:HD11	1:258:A:GLN:HB3	27	0.19
(3,875)	1:283:A:LEU:HD12	1:258:A:GLN:HB3	27	0.19
(3,875)	1:283:A:LEU:HD13	1:258:A:GLN:HB3	27	0.19
(3,871)	1:283:A:LEU:HD21	1:254:A:VAL:HA	3	0.19
(3,871)	1:283:A:LEU:HD22	1:254:A:VAL:HA	3	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,871)	1:283:A:LEU:HD23	1:254:A:VAL:HA	3	0.19
(3,871)	1:283:A:LEU:HD21	1:254:A:VAL:HA	10	0.19
(3,871)	1:283:A:LEU:HD22	1:254:A:VAL:HA	10	0.19
(3,871)	1:283:A:LEU:HD23	1:254:A:VAL:HA	10	0.19
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	19	0.19
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	19	0.19
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	19	0.19
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	29	0.19
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	29	0.19
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	29	0.19
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD11	16	0.19
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD12	16	0.19
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD13	16	0.19
(3,825)	1:254:A:VAL:HG11	1:293:A:ILE:H	8	0.19
(3,825)	1:254:A:VAL:HG12	1:293:A:ILE:H	8	0.19
(3,825)	1:254:A:VAL:HG13	1:293:A:ILE:H	8	0.19
(3,825)	1:254:A:VAL:HG11	1:293:A:ILE:H	26	0.19
(3,825)	1:254:A:VAL:HG12	1:293:A:ILE:H	26	0.19
(3,825)	1:254:A:VAL:HG13	1:293:A:ILE:H	26	0.19
(3,705)	1:287:A:LYS:HG2	1:287:A:LYS:HE2	19	0.19
(3,81)	1:262:A:GLY:H	1:260:A:LEU:HG	10	0.19
(3,81)	1:262:A:GLY:H	1:260:A:LEU:HG	13	0.19
(3,81)	1:262:A:GLY:H	1:260:A:LEU:HG	27	0.19
(3,28)	1:310:A:LEU:HD21	1:271:A:TYR:HB2	21	0.19
(3,28)	1:310:A:LEU:HD22	1:271:A:TYR:HB2	21	0.19
(3,28)	1:310:A:LEU:HD23	1:271:A:TYR:HB2	21	0.19
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	8	0.19
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	9	0.19
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	17	0.19
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	30	0.19
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	8	0.19
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	9	0.19
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	17	0.19
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	30	0.19
(3,2613)	1:255:A:ASN:HD22	1:289:A:LEU:HG	16	0.18
(3,2514)	1:273:A:GLY:H	1:271:A:TYR:HB3	1	0.18
(3,2514)	1:273:A:GLY:H	1:271:A:TYR:HB3	19	0.18
(3,2514)	1:273:A:GLY:H	1:271:A:TYR:HB3	24	0.18
(3,2498)	1:287:A:LYS:H	1:287:A:LYS:HD2	26	0.18
(3,2491)	1:255:A:ASN:HD22	1:289:A:LEU:HD11	20	0.18
(3,2491)	1:255:A:ASN:HD22	1:289:A:LEU:HD12	20	0.18
(3,2491)	1:255:A:ASN:HD22	1:289:A:LEU:HD13	20	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,2482)	1:282:A:LEU:HD21	1:282:A:LEU:H	20	0.18
(3,2482)	1:282:A:LEU:HD22	1:282:A:LEU:H	20	0.18
(3,2482)	1:282:A:LEU:HD23	1:282:A:LEU:H	20	0.18
(3,2448)	1:256:A:ASP:H	1:257:A:ILE:HG12	24	0.18
(3,2434)	1:253:A:THR:HG21	1:254:A:VAL:H	6	0.18
(3,2434)	1:253:A:THR:HG22	1:254:A:VAL:H	6	0.18
(3,2434)	1:253:A:THR:HG23	1:254:A:VAL:H	6	0.18
(3,2367)	1:275:A:LYS:HG2	1:275:A:LYS:H	11	0.18
(3,2367)	1:275:A:LYS:HG2	1:275:A:LYS:H	29	0.18
(3,2357)	1:262:A:GLY:H	1:260:A:LEU:HB2	8	0.18
(3,2295)	1:262:A:GLY:H	1:265:A:ASN:HB2	13	0.18
(3,2295)	1:262:A:GLY:H	1:265:A:ASN:HB2	16	0.18
(3,2295)	1:262:A:GLY:H	1:265:A:ASN:HB2	21	0.18
(3,2295)	1:262:A:GLY:H	1:265:A:ASN:HB2	25	0.18
(3,2295)	1:262:A:GLY:H	1:265:A:ASN:HB2	27	0.18
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG21	2	0.18
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG22	2	0.18
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG23	2	0.18
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD11	12	0.18
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD12	12	0.18
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD13	12	0.18
(3,2163)	1:256:A:ASP:H	1:289:A:LEU:HD21	11	0.18
(3,2163)	1:256:A:ASP:H	1:289:A:LEU:HD22	11	0.18
(3,2163)	1:256:A:ASP:H	1:289:A:LEU:HD23	11	0.18
(3,2163)	1:256:A:ASP:H	1:289:A:LEU:HD21	29	0.18
(3,2163)	1:256:A:ASP:H	1:289:A:LEU:HD22	29	0.18
(3,2163)	1:256:A:ASP:H	1:289:A:LEU:HD23	29	0.18
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	5	0.18
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	5	0.18
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	5	0.18
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG21	4	0.18
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG22	4	0.18
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG23	4	0.18
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG21	28	0.18
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG22	28	0.18
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG23	28	0.18
(3,2022)	1:291:A:GLU:HG3	1:291:A:GLU:H	21	0.18
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	18	0.18
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	20	0.18
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	24	0.18
(3,2012)	1:291:A:GLU:H	1:289:A:LEU:HG	30	0.18
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	16	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	19	0.18
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	20	0.18
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	21	0.18
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	27	0.18
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	28	0.18
(3,1885)	1:281:A:LYS:H	1:281:A:LYS:HG2	17	0.18
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	3	0.18
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	3	0.18
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	3	0.18
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	14	0.18
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	14	0.18
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	14	0.18
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	21	0.18
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	21	0.18
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	21	0.18
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	28	0.18
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	28	0.18
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	28	0.18
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	28	0.18
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	28	0.18
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	28	0.18
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	12	0.18
(3,1468)	1:293:A:ILE:HG21	1:286:A:THR:HB	17	0.18
(3,1468)	1:293:A:ILE:HG22	1:286:A:THR:HB	17	0.18
(3,1468)	1:293:A:ILE:HG23	1:286:A:THR:HB	17	0.18
(3,1462)	1:293:A:ILE:HD11	1:283:A:LEU:HB3	13	0.18
(3,1462)	1:293:A:ILE:HD12	1:283:A:LEU:HB3	13	0.18
(3,1462)	1:293:A:ILE:HD13	1:283:A:LEU:HB3	13	0.18
(3,1318)	1:274:A:ILE:HG21	1:275:A:LYS:HA	29	0.18
(3,1318)	1:274:A:ILE:HG22	1:275:A:LYS:HA	29	0.18
(3,1318)	1:274:A:ILE:HG23	1:275:A:LYS:HA	29	0.18
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG21	5	0.18
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG22	5	0.18
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG23	5	0.18
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	15	0.18
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	15	0.18
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	15	0.18
(3,1148)	1:259:A:LYS:H	1:259:A:LYS:HD2	8	0.18
(3,1146)	1:259:A:LYS:HG3	1:259:A:LYS:HE2	6	0.18
(3,888)	1:287:A:LYS:HB2	1:287:A:LYS:HE2	24	0.18
(3,875)	1:283:A:LEU:HD11	1:258:A:GLN:HB3	25	0.18
(3,875)	1:283:A:LEU:HD12	1:258:A:GLN:HB3	25	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,875)	1:283:A:LEU:HD13	1:258:A:GLN:HB3	25	0.18
(3,875)	1:283:A:LEU:HD11	1:258:A:GLN:HB3	30	0.18
(3,875)	1:283:A:LEU:HD12	1:258:A:GLN:HB3	30	0.18
(3,875)	1:283:A:LEU:HD13	1:258:A:GLN:HB3	30	0.18
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	11	0.18
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	11	0.18
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	11	0.18
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	14	0.18
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	14	0.18
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	14	0.18
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	20	0.18
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	20	0.18
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	20	0.18
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	28	0.18
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	28	0.18
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	28	0.18
(3,774)	1:263:A:LYS:HE2	1:263:A:LYS:H	26	0.18
(3,740)	1:238:A:LYS:HB2	1:238:A:LYS:HD3	21	0.18
(3,740)	1:238:A:LYS:HB2	1:238:A:LYS:HD3	24	0.18
(3,679)	1:281:A:LYS:HB3	1:281:A:LYS:HE3	5	0.18
(3,79)	1:270:A:ILE:HD11	1:314:A:VAL:HG21	15	0.18
(3,79)	1:270:A:ILE:HD11	1:314:A:VAL:HG22	15	0.18
(3,79)	1:270:A:ILE:HD11	1:314:A:VAL:HG23	15	0.18
(3,79)	1:270:A:ILE:HD12	1:314:A:VAL:HG21	15	0.18
(3,79)	1:270:A:ILE:HD12	1:314:A:VAL:HG22	15	0.18
(3,79)	1:270:A:ILE:HD12	1:314:A:VAL:HG23	15	0.18
(3,79)	1:270:A:ILE:HD13	1:314:A:VAL:HG21	15	0.18
(3,79)	1:270:A:ILE:HD13	1:314:A:VAL:HG22	15	0.18
(3,79)	1:270:A:ILE:HD13	1:314:A:VAL:HG23	15	0.18
(3,71)	1:290:A:THR:H	1:255:A:ASN:HB3	3	0.18
(3,63)	1:293:A:ILE:H	1:252:A:TRP:HD1	10	0.18
(3,28)	1:310:A:LEU:HD21	1:271:A:TYR:HB2	7	0.18
(3,28)	1:310:A:LEU:HD22	1:271:A:TYR:HB2	7	0.18
(3,28)	1:310:A:LEU:HD23	1:271:A:TYR:HB2	7	0.18
(3,28)	1:310:A:LEU:HD21	1:271:A:TYR:HB2	8	0.18
(3,28)	1:310:A:LEU:HD22	1:271:A:TYR:HB2	8	0.18
(3,28)	1:310:A:LEU:HD23	1:271:A:TYR:HB2	8	0.18
(3,28)	1:310:A:LEU:HD21	1:271:A:TYR:HB2	10	0.18
(3,28)	1:310:A:LEU:HD22	1:271:A:TYR:HB2	10	0.18
(3,28)	1:310:A:LEU:HD23	1:271:A:TYR:HB2	10	0.18
(3,28)	1:310:A:LEU:HD21	1:271:A:TYR:HB2	14	0.18
(3,28)	1:310:A:LEU:HD22	1:271:A:TYR:HB2	14	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,28)	1:310:A:LEU:HD23	1:271:A:TYR:HB2	14	0.18
(3,28)	1:310:A:LEU:HD21	1:271:A:TYR:HB2	23	0.18
(3,28)	1:310:A:LEU:HD22	1:271:A:TYR:HB2	23	0.18
(3,28)	1:310:A:LEU:HD23	1:271:A:TYR:HB2	23	0.18
(3,3)	1:314:A:VAL:HG11	1:315:A:HIS:HA	30	0.18
(3,3)	1:314:A:VAL:HG12	1:315:A:HIS:HA	30	0.18
(3,3)	1:314:A:VAL:HG13	1:315:A:HIS:HA	30	0.18
(2,27)	1:261:A:VAL:N	1:257:A:ILE:O	12	0.18
(2,21)	1:308:A:GLU:H	1:304:A:ALA:O	26	0.18
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	13	0.18
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	19	0.18
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	20	0.18
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	24	0.18
(1,27)	1:261:A:VAL:N	1:257:A:ILE:O	12	0.18
(1,21)	1:308:A:GLU:H	1:304:A:ALA:O	26	0.18
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	13	0.18
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	19	0.18
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	20	0.18
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	24	0.18
(3,2607)	1:307:A:ARG:HG2	1:308:A:GLU:H	27	0.17
(3,2540)	1:283:A:LEU:HD21	1:283:A:LEU:H	25	0.17
(3,2540)	1:283:A:LEU:HD22	1:283:A:LEU:H	25	0.17
(3,2540)	1:283:A:LEU:HD23	1:283:A:LEU:H	25	0.17
(3,2540)	1:283:A:LEU:HD21	1:283:A:LEU:H	26	0.17
(3,2540)	1:283:A:LEU:HD22	1:283:A:LEU:H	26	0.17
(3,2540)	1:283:A:LEU:HD23	1:283:A:LEU:H	26	0.17
(3,2514)	1:273:A:GLY:H	1:271:A:TYR:HB3	4	0.17
(3,2514)	1:273:A:GLY:H	1:271:A:TYR:HB3	25	0.17
(3,2514)	1:273:A:GLY:H	1:271:A:TYR:HB3	28	0.17
(3,2474)	1:256:A:ASP:H	1:258:A:GLN:HB3	8	0.17
(3,2414)	1:268:A:SER:H	1:274:A:ILE:HB	6	0.17
(3,2414)	1:268:A:SER:H	1:274:A:ILE:HB	11	0.17
(3,2388)	1:255:A:ASN:H	1:289:A:LEU:HB2	3	0.17
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD11	19	0.17
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD12	19	0.17
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD13	19	0.17
(3,2336)	1:295:A:LEU:H	1:300:A:GLU:HB2	21	0.17
(3,2303)	1:238:A:LYS:H	1:239:A:TRP:HA	17	0.17
(3,2303)	1:238:A:LYS:H	1:239:A:TRP:HA	18	0.17
(3,2268)	1:274:A:ILE:HG13	1:271:A:TYR:H	6	0.17
(3,2268)	1:274:A:ILE:HG13	1:271:A:TYR:H	30	0.17
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG21	1	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG22	1	0.17
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG23	1	0.17
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG21	14	0.17
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG22	14	0.17
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG23	14	0.17
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG21	26	0.17
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG22	26	0.17
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG23	26	0.17
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG21	27	0.17
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG22	27	0.17
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG23	27	0.17
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	1	0.17
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	1	0.17
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	1	0.17
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG21	7	0.17
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG22	7	0.17
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG23	7	0.17
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG21	24	0.17
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG22	24	0.17
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG23	24	0.17
(3,1966)	1:266:A:TRP:H	1:276:A:VAL:HG11	9	0.17
(3,1966)	1:266:A:TRP:H	1:276:A:VAL:HG12	9	0.17
(3,1966)	1:266:A:TRP:H	1:276:A:VAL:HG13	9	0.17
(3,1939)	1:296:A:THR:HG21	1:298:A:GLU:H	29	0.17
(3,1939)	1:296:A:THR:HG22	1:298:A:GLU:H	29	0.17
(3,1939)	1:296:A:THR:HG23	1:298:A:GLU:H	29	0.17
(3,1885)	1:281:A:LYS:H	1:281:A:LYS:HG2	11	0.17
(3,1885)	1:281:A:LYS:H	1:281:A:LYS:HG2	13	0.17
(3,1829)	1:276:A:VAL:HG21	1:283:A:LEU:H	7	0.17
(3,1829)	1:276:A:VAL:HG22	1:283:A:LEU:H	7	0.17
(3,1829)	1:276:A:VAL:HG23	1:283:A:LEU:H	7	0.17
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	1	0.17
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	1	0.17
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	1	0.17
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	2	0.17
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	2	0.17
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	2	0.17
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	8	0.17
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	8	0.17
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	8	0.17
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	19	0.17
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	19	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	19	0.17
(3,1621)	1:317:A:VAL:HB	1:318:A:TYR:HE1	7	0.17
(3,1621)	1:317:A:VAL:HB	1:318:A:TYR:HE2	7	0.17
(3,1518)	1:295:A:LEU:HD11	1:282:A:LEU:HD11	16	0.17
(3,1518)	1:295:A:LEU:HD11	1:282:A:LEU:HD12	16	0.17
(3,1518)	1:295:A:LEU:HD11	1:282:A:LEU:HD13	16	0.17
(3,1518)	1:295:A:LEU:HD12	1:282:A:LEU:HD11	16	0.17
(3,1518)	1:295:A:LEU:HD12	1:282:A:LEU:HD12	16	0.17
(3,1518)	1:295:A:LEU:HD12	1:282:A:LEU:HD13	16	0.17
(3,1518)	1:295:A:LEU:HD13	1:282:A:LEU:HD11	16	0.17
(3,1518)	1:295:A:LEU:HD13	1:282:A:LEU:HD12	16	0.17
(3,1518)	1:295:A:LEU:HD13	1:282:A:LEU:HD13	16	0.17
(3,1462)	1:293:A:ILE:HD11	1:283:A:LEU:HB3	29	0.17
(3,1462)	1:293:A:ILE:HD12	1:283:A:LEU:HB3	29	0.17
(3,1462)	1:293:A:ILE:HD13	1:283:A:LEU:HB3	29	0.17
(3,1426)	1:293:A:ILE:HD11	1:292:A:VAL:H	28	0.17
(3,1426)	1:293:A:ILE:HD12	1:292:A:VAL:H	28	0.17
(3,1426)	1:293:A:ILE:HD13	1:292:A:VAL:H	28	0.17
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG21	1	0.17
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG22	1	0.17
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG23	1	0.17
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG21	14	0.17
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG22	14	0.17
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG23	14	0.17
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG21	18	0.17
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG22	18	0.17
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG23	18	0.17
(3,1215)	1:276:A:VAL:HG11	1:279:A:LEU:HB2	3	0.17
(3,1215)	1:276:A:VAL:HG12	1:279:A:LEU:HB2	3	0.17
(3,1215)	1:276:A:VAL:HG13	1:279:A:LEU:HB2	3	0.17
(3,1215)	1:276:A:VAL:HG11	1:279:A:LEU:HB2	6	0.17
(3,1215)	1:276:A:VAL:HG12	1:279:A:LEU:HB2	6	0.17
(3,1215)	1:276:A:VAL:HG13	1:279:A:LEU:HB2	6	0.17
(3,1215)	1:276:A:VAL:HG11	1:279:A:LEU:HB2	11	0.17
(3,1215)	1:276:A:VAL:HG12	1:279:A:LEU:HB2	11	0.17
(3,1215)	1:276:A:VAL:HG13	1:279:A:LEU:HB2	11	0.17
(3,1215)	1:276:A:VAL:HG11	1:279:A:LEU:HB2	22	0.17
(3,1215)	1:276:A:VAL:HG12	1:279:A:LEU:HB2	22	0.17
(3,1215)	1:276:A:VAL:HG13	1:279:A:LEU:HB2	22	0.17
(3,1211)	1:264:A:LEU:HG	1:265:A:ASN:H	19	0.17
(3,1148)	1:259:A:LYS:H	1:259:A:LYS:HD2	4	0.17
(3,1148)	1:259:A:LYS:H	1:259:A:LYS:HD2	11	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1148)	1:259:A:LYS:H	1:259:A:LYS:HD2	14	0.17
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG21	22	0.17
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG22	22	0.17
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG23	22	0.17
(3,1134)	1:254:A:VAL:HA	1:257:A:ILE:HG21	8	0.17
(3,1134)	1:254:A:VAL:HA	1:257:A:ILE:HG22	8	0.17
(3,1134)	1:254:A:VAL:HA	1:257:A:ILE:HG23	8	0.17
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	13	0.17
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	13	0.17
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	13	0.17
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	15	0.17
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	15	0.17
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	15	0.17
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	21	0.17
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	21	0.17
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	21	0.17
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	25	0.17
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	25	0.17
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	25	0.17
(3,899)	1:288:A:ALA:HA	1:289:A:LEU:HG	9	0.17
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG11	11	0.17
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG12	11	0.17
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG13	11	0.17
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG11	27	0.17
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG12	27	0.17
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG13	27	0.17
(3,875)	1:283:A:LEU:HD11	1:258:A:GLN:HB3	20	0.17
(3,875)	1:283:A:LEU:HD12	1:258:A:GLN:HB3	20	0.17
(3,875)	1:283:A:LEU:HD13	1:258:A:GLN:HB3	20	0.17
(3,871)	1:283:A:LEU:HD21	1:254:A:VAL:HA	20	0.17
(3,871)	1:283:A:LEU:HD22	1:254:A:VAL:HA	20	0.17
(3,871)	1:283:A:LEU:HD23	1:254:A:VAL:HA	20	0.17
(3,867)	1:283:A:LEU:HD21	1:258:A:GLN:HB3	13	0.17
(3,867)	1:283:A:LEU:HD22	1:258:A:GLN:HB3	13	0.17
(3,867)	1:283:A:LEU:HD23	1:258:A:GLN:HB3	13	0.17
(3,857)	1:283:A:LEU:HD21	1:280:A:SER:HA	12	0.17
(3,857)	1:283:A:LEU:HD22	1:280:A:SER:HA	12	0.17
(3,857)	1:283:A:LEU:HD23	1:280:A:SER:HA	12	0.17
(3,857)	1:283:A:LEU:HD21	1:280:A:SER:HA	23	0.17
(3,857)	1:283:A:LEU:HD22	1:280:A:SER:HA	23	0.17
(3,857)	1:283:A:LEU:HD23	1:280:A:SER:HA	23	0.17
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	9	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	9	0.17
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	9	0.17
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	26	0.17
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	26	0.17
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	26	0.17
(3,740)	1:238:A:LYS:HB2	1:238:A:LYS:HD3	1	0.17
(3,740)	1:238:A:LYS:HB2	1:238:A:LYS:HD3	3	0.17
(3,740)	1:238:A:LYS:HB2	1:238:A:LYS:HD3	7	0.17
(3,740)	1:238:A:LYS:HB2	1:238:A:LYS:HD3	10	0.17
(3,740)	1:238:A:LYS:HB2	1:238:A:LYS:HD3	11	0.17
(3,740)	1:238:A:LYS:HB2	1:238:A:LYS:HD3	19	0.17
(3,740)	1:238:A:LYS:HB2	1:238:A:LYS:HD3	28	0.17
(3,740)	1:238:A:LYS:HB2	1:238:A:LYS:HD3	29	0.17
(3,716)	1:287:A:LYS:HD3	1:287:A:LYS:H	4	0.17
(3,705)	1:287:A:LYS:HG2	1:287:A:LYS:HE2	26	0.17
(3,623)	1:301:A:LEU:HB2	1:305:A:GLU:H	29	0.17
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	5	0.17
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	5	0.17
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	5	0.17
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	10	0.17
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	10	0.17
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	10	0.17
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	20	0.17
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	20	0.17
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	20	0.17
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	29	0.17
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	29	0.17
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	29	0.17
(3,47)	1:306:A:ASN:H	1:310:A:LEU:HG	5	0.17
(3,47)	1:306:A:ASN:H	1:310:A:LEU:HG	13	0.17
(3,29)	1:310:A:LEU:H	1:271:A:TYR:HE1	11	0.17
(3,29)	1:310:A:LEU:H	1:271:A:TYR:HE2	11	0.17
(3,29)	1:310:A:LEU:H	1:271:A:TYR:HE1	12	0.17
(3,29)	1:310:A:LEU:H	1:271:A:TYR:HE2	12	0.17
(3,28)	1:310:A:LEU:HD21	1:271:A:TYR:HB2	15	0.17
(3,28)	1:310:A:LEU:HD22	1:271:A:TYR:HB2	15	0.17
(3,28)	1:310:A:LEU:HD23	1:271:A:TYR:HB2	15	0.17
(3,28)	1:310:A:LEU:HD21	1:271:A:TYR:HB2	17	0.17
(3,28)	1:310:A:LEU:HD22	1:271:A:TYR:HB2	17	0.17
(3,28)	1:310:A:LEU:HD23	1:271:A:TYR:HB2	17	0.17
(3,17)	1:241:A:VAL:HG21	1:271:A:TYR:HE1	15	0.17
(3,17)	1:241:A:VAL:HG21	1:271:A:TYR:HE2	15	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,17)	1:241:A:VAL:HG22	1:271:A:TYR:HE1	15	0.17
(3,17)	1:241:A:VAL:HG22	1:271:A:TYR:HE2	15	0.17
(3,17)	1:241:A:VAL:HG23	1:271:A:TYR:HE1	15	0.17
(3,17)	1:241:A:VAL:HG23	1:271:A:TYR:HE2	15	0.17
(3,2)	1:314:A:VAL:HG21	1:313:A:PRO:HA	20	0.17
(3,2)	1:314:A:VAL:HG22	1:313:A:PRO:HA	20	0.17
(3,2)	1:314:A:VAL:HG23	1:313:A:PRO:HA	20	0.17
(2,21)	1:308:A:GLU:H	1:304:A:ALA:O	18	0.17
(2,21)	1:308:A:GLU:H	1:304:A:ALA:O	19	0.17
(2,15)	1:302:A:GLU:H	1:298:A:GLU:O	15	0.17
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	1	0.17
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	3	0.17
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	6	0.17
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	14	0.17
(1,21)	1:308:A:GLU:H	1:304:A:ALA:O	18	0.17
(1,21)	1:308:A:GLU:H	1:304:A:ALA:O	19	0.17
(1,15)	1:302:A:GLU:H	1:298:A:GLU:O	15	0.17
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	1	0.17
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	3	0.17
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	6	0.17
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	14	0.17
(3,2498)	1:287:A:LYS:H	1:287:A:LYS:HD2	25	0.16
(3,2436)	1:291:A:GLU:H	1:291:A:GLU:HG2	9	0.16
(3,2388)	1:255:A:ASN:H	1:289:A:LEU:HB2	21	0.16
(3,2357)	1:262:A:GLY:H	1:260:A:LEU:HB2	24	0.16
(3,2357)	1:262:A:GLY:H	1:260:A:LEU:HB2	29	0.16
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD11	13	0.16
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD12	13	0.16
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD13	13	0.16
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD11	29	0.16
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD12	29	0.16
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD13	29	0.16
(3,2336)	1:295:A:LEU:H	1:300:A:GLU:HB2	4	0.16
(3,2303)	1:238:A:LYS:H	1:239:A:TRP:HA	24	0.16
(3,2285)	1:271:A:TYR:H	1:270:A:ILE:HG13	28	0.16
(3,2268)	1:274:A:ILE:HG13	1:271:A:TYR:H	12	0.16
(3,2268)	1:274:A:ILE:HG13	1:271:A:TYR:H	27	0.16
(3,2241)	1:258:A:GLN:HG2	1:257:A:ILE:H	21	0.16
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD11	15	0.16
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD12	15	0.16
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD13	15	0.16
(3,2174)	1:304:A:ALA:H	1:302:A:GLU:HB2	1	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	25	0.16
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	25	0.16
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	25	0.16
(3,2141)	1:299:A:ALA:H	1:300:A:GLU:HB2	15	0.16
(3,2141)	1:299:A:ALA:H	1:300:A:GLU:HB2	25	0.16
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD11	25	0.16
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD12	25	0.16
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD13	25	0.16
(3,2058)	1:254:A:VAL:H	1:289:A:LEU:HB3	10	0.16
(3,2058)	1:254:A:VAL:H	1:289:A:LEU:HB3	14	0.16
(3,2054)	1:263:A:LYS:H	1:263:A:LYS:HG3	23	0.16
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	6	0.16
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	13	0.16
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	4	0.16
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	4	0.16
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	4	0.16
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	7	0.16
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	7	0.16
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	7	0.16
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	24	0.16
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	24	0.16
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	24	0.16
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	23	0.16
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	23	0.16
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	23	0.16
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	17	0.16
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	18	0.16
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	27	0.16
(3,1621)	1:317:A:VAL:HB	1:318:A:TYR:HE1	12	0.16
(3,1621)	1:317:A:VAL:HB	1:318:A:TYR:HE2	12	0.16
(3,1616)	1:318:A:TYR:HB3	1:317:A:VAL:HB	6	0.16
(3,1496)	1:295:A:LEU:HD21	1:250:A:ASP:HA	30	0.16
(3,1496)	1:295:A:LEU:HD22	1:250:A:ASP:HA	30	0.16
(3,1496)	1:295:A:LEU:HD23	1:250:A:ASP:HA	30	0.16
(3,1483)	1:282:A:LEU:HD21	1:295:A:LEU:H	30	0.16
(3,1483)	1:282:A:LEU:HD22	1:295:A:LEU:H	30	0.16
(3,1483)	1:282:A:LEU:HD23	1:295:A:LEU:H	30	0.16
(3,1482)	1:257:A:ILE:HD11	1:254:A:VAL:HB	5	0.16
(3,1482)	1:257:A:ILE:HD12	1:254:A:VAL:HB	5	0.16
(3,1482)	1:257:A:ILE:HD13	1:254:A:VAL:HB	5	0.16
(3,1482)	1:257:A:ILE:HD11	1:254:A:VAL:HB	14	0.16
(3,1482)	1:257:A:ILE:HD12	1:254:A:VAL:HB	14	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1482)	1:257:A:ILE:HD13	1:254:A:VAL:HB	14	0.16
(3,1470)	1:293:A:ILE:HG21	1:257:A:ILE:HB	26	0.16
(3,1470)	1:293:A:ILE:HG22	1:257:A:ILE:HB	26	0.16
(3,1470)	1:293:A:ILE:HG23	1:257:A:ILE:HB	26	0.16
(3,1454)	1:293:A:ILE:HD11	1:286:A:THR:HA	17	0.16
(3,1454)	1:293:A:ILE:HD12	1:286:A:THR:HA	17	0.16
(3,1454)	1:293:A:ILE:HD13	1:286:A:THR:HA	17	0.16
(3,1426)	1:293:A:ILE:HD11	1:292:A:VAL:H	3	0.16
(3,1426)	1:293:A:ILE:HD12	1:292:A:VAL:H	3	0.16
(3,1426)	1:293:A:ILE:HD13	1:292:A:VAL:H	3	0.16
(3,1426)	1:293:A:ILE:HD11	1:292:A:VAL:H	17	0.16
(3,1426)	1:293:A:ILE:HD12	1:292:A:VAL:H	17	0.16
(3,1426)	1:293:A:ILE:HD13	1:292:A:VAL:H	17	0.16
(3,1392)	1:288:A:ALA:HB1	1:254:A:VAL:HB	6	0.16
(3,1392)	1:288:A:ALA:HB2	1:254:A:VAL:HB	6	0.16
(3,1392)	1:288:A:ALA:HB3	1:254:A:VAL:HB	6	0.16
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG21	1	0.16
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG22	1	0.16
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG23	1	0.16
(3,1318)	1:274:A:ILE:HG21	1:275:A:LYS:HA	11	0.16
(3,1318)	1:274:A:ILE:HG22	1:275:A:LYS:HA	11	0.16
(3,1318)	1:274:A:ILE:HG23	1:275:A:LYS:HA	11	0.16
(3,1318)	1:274:A:ILE:HG21	1:275:A:LYS:HA	20	0.16
(3,1318)	1:274:A:ILE:HG22	1:275:A:LYS:HA	20	0.16
(3,1318)	1:274:A:ILE:HG23	1:275:A:LYS:HA	20	0.16
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG21	6	0.16
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG22	6	0.16
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG23	6	0.16
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG21	11	0.16
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG22	11	0.16
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG23	11	0.16
(3,1215)	1:276:A:VAL:HG11	1:279:A:LEU:HB2	8	0.16
(3,1215)	1:276:A:VAL:HG12	1:279:A:LEU:HB2	8	0.16
(3,1215)	1:276:A:VAL:HG13	1:279:A:LEU:HB2	8	0.16
(3,1215)	1:276:A:VAL:HG11	1:279:A:LEU:HB2	17	0.16
(3,1215)	1:276:A:VAL:HG12	1:279:A:LEU:HB2	17	0.16
(3,1215)	1:276:A:VAL:HG13	1:279:A:LEU:HB2	17	0.16
(3,1215)	1:276:A:VAL:HG11	1:279:A:LEU:HB2	19	0.16
(3,1215)	1:276:A:VAL:HG12	1:279:A:LEU:HB2	19	0.16
(3,1215)	1:276:A:VAL:HG13	1:279:A:LEU:HB2	19	0.16
(3,1215)	1:276:A:VAL:HG11	1:279:A:LEU:HB2	30	0.16
(3,1215)	1:276:A:VAL:HG12	1:279:A:LEU:HB2	30	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1215)	1:276:A:VAL:HG13	1:279:A:LEU:HB2	30	0.16
(3,1185)	1:262:A:GLY:HA3	1:265:A:ASN:HD22	4	0.16
(3,1185)	1:262:A:GLY:HA3	1:265:A:ASN:HD22	29	0.16
(3,1148)	1:259:A:LYS:H	1:259:A:LYS:HD2	1	0.16
(3,1148)	1:259:A:LYS:H	1:259:A:LYS:HD2	19	0.16
(3,1052)	1:240:A:THR:HB	1:241:A:VAL:HB	22	0.16
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	1	0.16
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	1	0.16
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	1	0.16
(3,871)	1:283:A:LEU:HD21	1:254:A:VAL:HA	1	0.16
(3,871)	1:283:A:LEU:HD22	1:254:A:VAL:HA	1	0.16
(3,871)	1:283:A:LEU:HD23	1:254:A:VAL:HA	1	0.16
(3,871)	1:283:A:LEU:HD21	1:254:A:VAL:HA	6	0.16
(3,871)	1:283:A:LEU:HD22	1:254:A:VAL:HA	6	0.16
(3,871)	1:283:A:LEU:HD23	1:254:A:VAL:HA	6	0.16
(3,871)	1:283:A:LEU:HD21	1:254:A:VAL:HA	21	0.16
(3,871)	1:283:A:LEU:HD22	1:254:A:VAL:HA	21	0.16
(3,871)	1:283:A:LEU:HD23	1:254:A:VAL:HA	21	0.16
(3,871)	1:283:A:LEU:HD21	1:254:A:VAL:HA	27	0.16
(3,871)	1:283:A:LEU:HD22	1:254:A:VAL:HA	27	0.16
(3,871)	1:283:A:LEU:HD23	1:254:A:VAL:HA	27	0.16
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	4	0.16
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	4	0.16
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	4	0.16
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	13	0.16
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	13	0.16
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	13	0.16
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	18	0.16
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	18	0.16
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	18	0.16
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	24	0.16
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	24	0.16
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	24	0.16
(3,814)	1:275:A:LYS:HG2	1:275:A:LYS:HE3	23	0.16
(3,740)	1:238:A:LYS:HB2	1:238:A:LYS:HD3	2	0.16
(3,740)	1:238:A:LYS:HB2	1:238:A:LYS:HD3	15	0.16
(3,740)	1:238:A:LYS:HB2	1:238:A:LYS:HD3	18	0.16
(3,740)	1:238:A:LYS:HB2	1:238:A:LYS:HD3	25	0.16
(3,716)	1:287:A:LYS:HD3	1:287:A:LYS:H	27	0.16
(3,81)	1:262:A:GLY:H	1:260:A:LEU:HG	9	0.16
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD21	27	0.16
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD22	27	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD23	27	0.16
(3,74)	1:283:A:LEU:H	1:280:A:SER:HB2	27	0.16
(3,47)	1:306:A:ASN:H	1:310:A:LEU:HG	29	0.16
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE1	18	0.16
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE2	18	0.16
(3,15)	1:240:A:THR:HG21	1:239:A:TRP:HB3	23	0.16
(3,15)	1:240:A:THR:HG22	1:239:A:TRP:HB3	23	0.16
(3,15)	1:240:A:THR:HG23	1:239:A:TRP:HB3	23	0.16
(3,3)	1:314:A:VAL:HG11	1:315:A:HIS:HA	29	0.16
(3,3)	1:314:A:VAL:HG12	1:315:A:HIS:HA	29	0.16
(3,3)	1:314:A:VAL:HG13	1:315:A:HIS:HA	29	0.16
(2,35)	1:269:A:GLN:N	1:265:A:ASN:O	4	0.16
(2,27)	1:261:A:VAL:N	1:257:A:ILE:O	11	0.16
(2,21)	1:308:A:GLU:H	1:304:A:ALA:O	23	0.16
(2,15)	1:302:A:GLU:H	1:298:A:GLU:O	22	0.16
(2,13)	1:282:A:LEU:H	1:278:A:GLN:O	11	0.16
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	5	0.16
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	22	0.16
(1,35)	1:269:A:GLN:N	1:265:A:ASN:O	4	0.16
(1,27)	1:261:A:VAL:N	1:257:A:ILE:O	11	0.16
(1,21)	1:308:A:GLU:H	1:304:A:ALA:O	23	0.16
(1,15)	1:302:A:GLU:H	1:298:A:GLU:O	22	0.16
(1,13)	1:282:A:LEU:H	1:278:A:GLN:O	11	0.16
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	5	0.16
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	22	0.16
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD11	8	0.15
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD12	8	0.15
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD13	8	0.15
(3,2550)	1:280:A:SER:H	1:302:A:GLU:HG2	3	0.15
(3,2540)	1:283:A:LEU:HD21	1:283:A:LEU:H	14	0.15
(3,2540)	1:283:A:LEU:HD22	1:283:A:LEU:H	14	0.15
(3,2540)	1:283:A:LEU:HD23	1:283:A:LEU:H	14	0.15
(3,2540)	1:283:A:LEU:HD21	1:283:A:LEU:H	16	0.15
(3,2540)	1:283:A:LEU:HD22	1:283:A:LEU:H	16	0.15
(3,2540)	1:283:A:LEU:HD23	1:283:A:LEU:H	16	0.15
(3,2514)	1:273:A:GLY:H	1:271:A:TYR:HB3	8	0.15
(3,2514)	1:273:A:GLY:H	1:271:A:TYR:HB3	14	0.15
(3,2474)	1:256:A:ASP:H	1:258:A:GLN:HB3	13	0.15
(3,2474)	1:256:A:ASP:H	1:258:A:GLN:HB3	25	0.15
(3,2448)	1:256:A:ASP:H	1:257:A:ILE:HG12	21	0.15
(3,2401)	1:253:A:THR:H	1:292:A:VAL:H	5	0.15
(3,2388)	1:255:A:ASN:H	1:289:A:LEU:HB2	2	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,2357)	1:262:A:GLY:H	1:260:A:LEU:HB2	2	0.15
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD11	8	0.15
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD12	8	0.15
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD13	8	0.15
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD11	9	0.15
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD12	9	0.15
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD13	9	0.15
(3,2336)	1:295:A:LEU:H	1:300:A:GLU:HB2	2	0.15
(3,2336)	1:295:A:LEU:H	1:300:A:GLU:HB2	26	0.15
(3,2295)	1:262:A:GLY:H	1:265:A:ASN:HB2	10	0.15
(3,2286)	1:255:A:ASN:H	1:289:A:LEU:HG	1	0.15
(3,2285)	1:271:A:TYR:H	1:270:A:ILE:HG13	7	0.15
(3,2285)	1:271:A:TYR:H	1:270:A:ILE:HG13	15	0.15
(3,2268)	1:274:A:ILE:HG13	1:271:A:TYR:H	5	0.15
(3,2241)	1:258:A:GLN:HG2	1:257:A:ILE:H	2	0.15
(3,2241)	1:258:A:GLN:HG2	1:257:A:ILE:H	3	0.15
(3,2241)	1:258:A:GLN:HG2	1:257:A:ILE:H	10	0.15
(3,2241)	1:258:A:GLN:HG2	1:257:A:ILE:H	14	0.15
(3,2241)	1:258:A:GLN:HG2	1:257:A:ILE:H	27	0.15
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG21	13	0.15
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG22	13	0.15
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG23	13	0.15
(3,2206)	1:274:A:ILE:H	1:272:A:PRO:HD3	18	0.15
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD11	1	0.15
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD12	1	0.15
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD13	1	0.15
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	3	0.15
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	3	0.15
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	3	0.15
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG21	9	0.15
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG22	9	0.15
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG23	9	0.15
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG21	10	0.15
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG22	10	0.15
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG23	10	0.15
(3,1966)	1:266:A:TRP:H	1:276:A:VAL:HG11	8	0.15
(3,1966)	1:266:A:TRP:H	1:276:A:VAL:HG12	8	0.15
(3,1966)	1:266:A:TRP:H	1:276:A:VAL:HG13	8	0.15
(3,1953)	1:265:A:ASN:H	1:263:A:LYS:HB3	26	0.15
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	3	0.15
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	12	0.15
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	26	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	11	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	4	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	4	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	4	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	6	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	6	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	6	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	9	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	9	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	9	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	11	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	11	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	11	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	17	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	17	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	17	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	25	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	25	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	25	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	26	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	26	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	26	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	29	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	29	0.15
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	29	0.15
(3,1659)	1:240:A:THR:HG21	1:271:A:TYR:HE1	20	0.15
(3,1659)	1:240:A:THR:HG21	1:271:A:TYR:HE2	20	0.15
(3,1659)	1:240:A:THR:HG22	1:271:A:TYR:HE1	20	0.15
(3,1659)	1:240:A:THR:HG22	1:271:A:TYR:HE2	20	0.15
(3,1659)	1:240:A:THR:HG23	1:271:A:TYR:HE1	20	0.15
(3,1659)	1:240:A:THR:HG23	1:271:A:TYR:HE2	20	0.15
(3,1462)	1:293:A:ILE:HD11	1:283:A:LEU:HB3	8	0.15
(3,1462)	1:293:A:ILE:HD12	1:283:A:LEU:HB3	8	0.15
(3,1462)	1:293:A:ILE:HD13	1:283:A:LEU:HB3	8	0.15
(3,1462)	1:293:A:ILE:HD11	1:283:A:LEU:HB3	9	0.15
(3,1462)	1:293:A:ILE:HD12	1:283:A:LEU:HB3	9	0.15
(3,1462)	1:293:A:ILE:HD13	1:283:A:LEU:HB3	9	0.15
(3,1441)	1:293:A:ILE:HG12	1:254:A:VAL:HB	3	0.15
(3,1426)	1:293:A:ILE:HD11	1:292:A:VAL:H	5	0.15
(3,1426)	1:293:A:ILE:HD12	1:292:A:VAL:H	5	0.15
(3,1426)	1:293:A:ILE:HD13	1:292:A:VAL:H	5	0.15
(3,1426)	1:293:A:ILE:HD11	1:292:A:VAL:H	14	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1426)	1:293:A:ILE:HD12	1:292:A:VAL:H	14	0.15
(3,1426)	1:293:A:ILE:HD13	1:292:A:VAL:H	14	0.15
(3,1426)	1:293:A:ILE:HD11	1:292:A:VAL:H	19	0.15
(3,1426)	1:293:A:ILE:HD12	1:292:A:VAL:H	19	0.15
(3,1426)	1:293:A:ILE:HD13	1:292:A:VAL:H	19	0.15
(3,1391)	1:287:A:LYS:HB3	1:254:A:VAL:HG21	17	0.15
(3,1391)	1:287:A:LYS:HB3	1:254:A:VAL:HG22	17	0.15
(3,1391)	1:287:A:LYS:HB3	1:254:A:VAL:HG23	17	0.15
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG21	18	0.15
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG22	18	0.15
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG23	18	0.15
(3,1385)	1:286:A:THR:HG21	1:291:A:GLU:H	16	0.15
(3,1385)	1:286:A:THR:HG22	1:291:A:GLU:H	16	0.15
(3,1385)	1:286:A:THR:HG23	1:291:A:GLU:H	16	0.15
(3,1373)	1:279:A:LEU:HD21	1:306:A:ASN:HB3	18	0.15
(3,1373)	1:279:A:LEU:HD22	1:306:A:ASN:HB3	18	0.15
(3,1373)	1:279:A:LEU:HD23	1:306:A:ASN:HB3	18	0.15
(3,1347)	1:280:A:SER:HA	1:276:A:VAL:HG21	9	0.15
(3,1347)	1:280:A:SER:HA	1:276:A:VAL:HG22	9	0.15
(3,1347)	1:280:A:SER:HA	1:276:A:VAL:HG23	9	0.15
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG21	3	0.15
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG22	3	0.15
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG23	3	0.15
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG21	20	0.15
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG22	20	0.15
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG23	20	0.15
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG21	30	0.15
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG22	30	0.15
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG23	30	0.15
(3,1215)	1:276:A:VAL:HG11	1:279:A:LEU:HB2	9	0.15
(3,1215)	1:276:A:VAL:HG12	1:279:A:LEU:HB2	9	0.15
(3,1215)	1:276:A:VAL:HG13	1:279:A:LEU:HB2	9	0.15
(3,1215)	1:276:A:VAL:HG11	1:279:A:LEU:HB2	27	0.15
(3,1215)	1:276:A:VAL:HG12	1:279:A:LEU:HB2	27	0.15
(3,1215)	1:276:A:VAL:HG13	1:279:A:LEU:HB2	27	0.15
(3,1215)	1:276:A:VAL:HG11	1:279:A:LEU:HB2	29	0.15
(3,1215)	1:276:A:VAL:HG12	1:279:A:LEU:HB2	29	0.15
(3,1215)	1:276:A:VAL:HG13	1:279:A:LEU:HB2	29	0.15
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	4	0.15
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	4	0.15
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	4	0.15
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	10	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	10	0.15
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	10	0.15
(3,1185)	1:262:A:GLY:HA3	1:265:A:ASN:HD22	24	0.15
(3,1146)	1:259:A:LYS:HG3	1:259:A:LYS:HE2	14	0.15
(3,1134)	1:254:A:VAL:HA	1:257:A:ILE:HG21	28	0.15
(3,1134)	1:254:A:VAL:HA	1:257:A:ILE:HG22	28	0.15
(3,1134)	1:254:A:VAL:HA	1:257:A:ILE:HG23	28	0.15
(3,1112)	1:257:A:ILE:HB	1:252:A:TRP:HA	24	0.15
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	4	0.15
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	4	0.15
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	4	0.15
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	5	0.15
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	5	0.15
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	5	0.15
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	7	0.15
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	7	0.15
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	7	0.15
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	8	0.15
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	8	0.15
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	8	0.15
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	11	0.15
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	11	0.15
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	11	0.15
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	23	0.15
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	23	0.15
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	23	0.15
(3,899)	1:288:A:ALA:HA	1:289:A:LEU:HG	26	0.15
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG11	7	0.15
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG12	7	0.15
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG13	7	0.15
(3,888)	1:287:A:LYS:HB2	1:287:A:LYS:HE2	7	0.15
(3,875)	1:283:A:LEU:HD11	1:258:A:GLN:HB3	4	0.15
(3,875)	1:283:A:LEU:HD12	1:258:A:GLN:HB3	4	0.15
(3,875)	1:283:A:LEU:HD13	1:258:A:GLN:HB3	4	0.15
(3,875)	1:283:A:LEU:HD11	1:258:A:GLN:HB3	6	0.15
(3,875)	1:283:A:LEU:HD12	1:258:A:GLN:HB3	6	0.15
(3,875)	1:283:A:LEU:HD13	1:258:A:GLN:HB3	6	0.15
(3,875)	1:283:A:LEU:HD11	1:258:A:GLN:HB3	16	0.15
(3,875)	1:283:A:LEU:HD12	1:258:A:GLN:HB3	16	0.15
(3,875)	1:283:A:LEU:HD13	1:258:A:GLN:HB3	16	0.15
(3,871)	1:283:A:LEU:HD21	1:254:A:VAL:HA	4	0.15
(3,871)	1:283:A:LEU:HD22	1:254:A:VAL:HA	4	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,871)	1:283:A:LEU:HD23	1:254:A:VAL:HA	4	0.15
(3,857)	1:283:A:LEU:HD21	1:280:A:SER:HA	11	0.15
(3,857)	1:283:A:LEU:HD22	1:280:A:SER:HA	11	0.15
(3,857)	1:283:A:LEU:HD23	1:280:A:SER:HA	11	0.15
(3,857)	1:283:A:LEU:HD21	1:280:A:SER:HA	22	0.15
(3,857)	1:283:A:LEU:HD22	1:280:A:SER:HA	22	0.15
(3,857)	1:283:A:LEU:HD23	1:280:A:SER:HA	22	0.15
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	7	0.15
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	7	0.15
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	7	0.15
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD11	3	0.15
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD12	3	0.15
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD13	3	0.15
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD11	17	0.15
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD12	17	0.15
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD13	17	0.15
(3,705)	1:287:A:LYS:HG2	1:287:A:LYS:HE2	4	0.15
(3,673)	1:281:A:LYS:HA	1:281:A:LYS:HD3	26	0.15
(3,659)	1:281:A:LYS:HE3	1:281:A:LYS:HB2	5	0.15
(3,543)	1:287:A:LYS:H	1:287:A:LYS:HG2	28	0.15
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	26	0.15
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	26	0.15
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	26	0.15
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	28	0.15
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	28	0.15
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	28	0.15
(3,81)	1:262:A:GLY:H	1:260:A:LEU:HG	16	0.15
(3,72)	1:290:A:THR:H	1:253:A:THR:HA	14	0.15
(3,63)	1:293:A:ILE:H	1:252:A:TRP:HD1	5	0.15
(3,47)	1:306:A:ASN:H	1:310:A:LEU:HG	16	0.15
(3,47)	1:306:A:ASN:H	1:310:A:LEU:HG	22	0.15
(3,47)	1:306:A:ASN:H	1:310:A:LEU:HG	23	0.15
(3,29)	1:310:A:LEU:H	1:271:A:TYR:HE1	20	0.15
(3,29)	1:310:A:LEU:H	1:271:A:TYR:HE2	20	0.15
(3,29)	1:310:A:LEU:H	1:271:A:TYR:HE1	26	0.15
(3,29)	1:310:A:LEU:H	1:271:A:TYR:HE2	26	0.15
(3,29)	1:310:A:LEU:H	1:271:A:TYR:HE1	30	0.15
(3,29)	1:310:A:LEU:H	1:271:A:TYR:HE2	30	0.15
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE1	28	0.15
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE2	28	0.15
(3,7)	1:314:A:VAL:H	1:241:A:VAL:HG21	27	0.15
(3,7)	1:314:A:VAL:H	1:241:A:VAL:HG22	27	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,7)	1:314:A:VAL:H	1:241:A:VAL:HG23	27	0.15
(3,6)	1:314:A:VAL:H	1:315:A:HIS:HB2	13	0.15
(3,2)	1:314:A:VAL:HG21	1:313:A:PRO:HA	16	0.15
(3,2)	1:314:A:VAL:HG22	1:313:A:PRO:HA	16	0.15
(3,2)	1:314:A:VAL:HG23	1:313:A:PRO:HA	16	0.15
(2,35)	1:269:A:GLN:N	1:265:A:ASN:O	23	0.15
(2,34)	1:268:A:SER:N	1:264:A:LEU:O	21	0.15
(2,34)	1:268:A:SER:N	1:264:A:LEU:O	26	0.15
(2,34)	1:268:A:SER:N	1:264:A:LEU:O	28	0.15
(2,27)	1:261:A:VAL:N	1:257:A:ILE:O	18	0.15
(2,21)	1:308:A:GLU:H	1:304:A:ALA:O	21	0.15
(2,15)	1:302:A:GLU:H	1:298:A:GLU:O	19	0.15
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	16	0.15
(2,12)	1:269:A:GLN:H	1:265:A:ASN:O	27	0.15
(2,5)	1:262:A:GLY:H	1:258:A:GLN:O	6	0.15
(1,35)	1:269:A:GLN:N	1:265:A:ASN:O	23	0.15
(1,34)	1:268:A:SER:N	1:264:A:LEU:O	21	0.15
(1,34)	1:268:A:SER:N	1:264:A:LEU:O	26	0.15
(1,34)	1:268:A:SER:N	1:264:A:LEU:O	28	0.15
(1,27)	1:261:A:VAL:N	1:257:A:ILE:O	18	0.15
(1,21)	1:308:A:GLU:H	1:304:A:ALA:O	21	0.15
(1,15)	1:302:A:GLU:H	1:298:A:GLU:O	19	0.15
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	16	0.15
(1,12)	1:269:A:GLN:H	1:265:A:ASN:O	27	0.15
(1,5)	1:262:A:GLY:H	1:258:A:GLN:O	6	0.15
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD11	2	0.14
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD12	2	0.14
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD13	2	0.14
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD11	21	0.14
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD12	21	0.14
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD13	21	0.14
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD11	27	0.14
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD12	27	0.14
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD13	27	0.14
(3,2579)	1:298:A:GLU:H	1:301:A:LEU:HD21	29	0.14
(3,2579)	1:298:A:GLU:H	1:301:A:LEU:HD22	29	0.14
(3,2579)	1:298:A:GLU:H	1:301:A:LEU:HD23	29	0.14
(3,2540)	1:283:A:LEU:HD21	1:283:A:LEU:H	4	0.14
(3,2540)	1:283:A:LEU:HD22	1:283:A:LEU:H	4	0.14
(3,2540)	1:283:A:LEU:HD23	1:283:A:LEU:H	4	0.14
(3,2540)	1:283:A:LEU:HD21	1:283:A:LEU:H	27	0.14
(3,2540)	1:283:A:LEU:HD22	1:283:A:LEU:H	27	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,2540)	1:283:A:LEU:HD23	1:283:A:LEU:H	27	0.14
(3,2498)	1:287:A:LYS:H	1:287:A:LYS:HD2	18	0.14
(3,2448)	1:256:A:ASP:H	1:257:A:ILE:HG12	11	0.14
(3,2448)	1:256:A:ASP:H	1:257:A:ILE:HG12	12	0.14
(3,2448)	1:256:A:ASP:H	1:257:A:ILE:HG12	22	0.14
(3,2435)	1:239:A:TRP:HA	1:239:A:TRP:HE1	4	0.14
(3,2434)	1:253:A:THR:HG21	1:254:A:VAL:H	22	0.14
(3,2434)	1:253:A:THR:HG22	1:254:A:VAL:H	22	0.14
(3,2434)	1:253:A:THR:HG23	1:254:A:VAL:H	22	0.14
(3,2410)	1:276:A:VAL:H	1:275:A:LYS:HD3	10	0.14
(3,2401)	1:253:A:THR:H	1:292:A:VAL:H	1	0.14
(3,2401)	1:253:A:THR:H	1:292:A:VAL:H	10	0.14
(3,2388)	1:255:A:ASN:H	1:289:A:LEU:HB2	16	0.14
(3,2367)	1:275:A:LYS:HG2	1:275:A:LYS:H	1	0.14
(3,2357)	1:262:A:GLY:H	1:260:A:LEU:HB2	14	0.14
(3,2353)	1:268:A:SER:H	1:274:A:ILE:HG21	20	0.14
(3,2353)	1:268:A:SER:H	1:274:A:ILE:HG22	20	0.14
(3,2353)	1:268:A:SER:H	1:274:A:ILE:HG23	20	0.14
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD11	17	0.14
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD12	17	0.14
(3,2351)	1:283:A:LEU:H	1:283:A:LEU:HD13	17	0.14
(3,2336)	1:295:A:LEU:H	1:300:A:GLU:HB2	23	0.14
(3,2303)	1:238:A:LYS:H	1:239:A:TRP:HA	3	0.14
(3,2303)	1:238:A:LYS:H	1:239:A:TRP:HA	8	0.14
(3,2303)	1:238:A:LYS:H	1:239:A:TRP:HA	12	0.14
(3,2303)	1:238:A:LYS:H	1:239:A:TRP:HA	29	0.14
(3,2284)	1:281:A:LYS:HD3	1:281:A:LYS:H	7	0.14
(3,2284)	1:281:A:LYS:HD3	1:281:A:LYS:H	24	0.14
(3,2273)	1:254:A:VAL:H	1:255:A:ASN:HA	6	0.14
(3,2268)	1:274:A:ILE:HG13	1:271:A:TYR:H	22	0.14
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG21	6	0.14
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG22	6	0.14
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG23	6	0.14
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG21	10	0.14
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG22	10	0.14
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG23	10	0.14
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG21	16	0.14
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG22	16	0.14
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG23	16	0.14
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG21	25	0.14
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG22	25	0.14
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG23	25	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,2213)	1:266:A:TRP:H	1:276:A:VAL:HG21	7	0.14
(3,2213)	1:266:A:TRP:H	1:276:A:VAL:HG22	7	0.14
(3,2213)	1:266:A:TRP:H	1:276:A:VAL:HG23	7	0.14
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD11	4	0.14
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD12	4	0.14
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD13	4	0.14
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD11	7	0.14
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD12	7	0.14
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD13	7	0.14
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	11	0.14
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	11	0.14
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	11	0.14
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	18	0.14
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	18	0.14
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	18	0.14
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	19	0.14
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	19	0.14
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	19	0.14
(3,2155)	1:287:A:LYS:H	1:287:A:LYS:HE2	1	0.14
(3,2155)	1:287:A:LYS:H	1:287:A:LYS:HE2	14	0.14
(3,2141)	1:299:A:ALA:H	1:300:A:GLU:HB2	3	0.14
(3,2141)	1:299:A:ALA:H	1:300:A:GLU:HB2	13	0.14
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD11	9	0.14
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD12	9	0.14
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD13	9	0.14
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD11	27	0.14
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD12	27	0.14
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD13	27	0.14
(3,2061)	1:273:A:GLY:H	1:274:A:ILE:HG13	16	0.14
(3,2061)	1:273:A:GLY:H	1:274:A:ILE:HG13	17	0.14
(3,2058)	1:254:A:VAL:H	1:289:A:LEU:HB3	17	0.14
(3,2054)	1:263:A:LYS:H	1:263:A:LYS:HG3	25	0.14
(3,2054)	1:263:A:LYS:H	1:263:A:LYS:HG3	26	0.14
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG21	15	0.14
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG22	15	0.14
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG23	15	0.14
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG21	18	0.14
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG22	18	0.14
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG23	18	0.14
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG21	19	0.14
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG22	19	0.14
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG23	19	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1953)	1:265:A:ASN:H	1:263:A:LYS:HB3	9	0.14
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	7	0.14
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	9	0.14
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	10	0.14
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	18	0.14
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	24	0.14
(3,1937)	1:275:A:LYS:H	1:275:A:LYS:HD3	12	0.14
(3,1764)	1:270:A:ILE:HD11	1:271:A:TYR:HD1	14	0.14
(3,1764)	1:270:A:ILE:HD11	1:271:A:TYR:HD2	14	0.14
(3,1764)	1:270:A:ILE:HD12	1:271:A:TYR:HD1	14	0.14
(3,1764)	1:270:A:ILE:HD12	1:271:A:TYR:HD2	14	0.14
(3,1764)	1:270:A:ILE:HD13	1:271:A:TYR:HD1	14	0.14
(3,1764)	1:270:A:ILE:HD13	1:271:A:TYR:HD2	14	0.14
(3,1764)	1:270:A:ILE:HD11	1:271:A:TYR:HD1	25	0.14
(3,1764)	1:270:A:ILE:HD11	1:271:A:TYR:HD2	25	0.14
(3,1764)	1:270:A:ILE:HD12	1:271:A:TYR:HD1	25	0.14
(3,1764)	1:270:A:ILE:HD12	1:271:A:TYR:HD2	25	0.14
(3,1764)	1:270:A:ILE:HD13	1:271:A:TYR:HD1	25	0.14
(3,1764)	1:270:A:ILE:HD13	1:271:A:TYR:HD2	25	0.14
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	8	0.14
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	8	0.14
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	8	0.14
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	12	0.14
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	12	0.14
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	12	0.14
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	24	0.14
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	24	0.14
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	24	0.14
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	30	0.14
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	30	0.14
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	30	0.14
(3,1658)	1:240:A:THR:HB	1:239:A:TRP:HA	5	0.14
(3,1614)	1:318:A:TYR:HB3	1:317:A:VAL:HG21	30	0.14
(3,1614)	1:318:A:TYR:HB3	1:317:A:VAL:HG22	30	0.14
(3,1614)	1:318:A:TYR:HB3	1:317:A:VAL:HG23	30	0.14
(3,1496)	1:295:A:LEU:HD21	1:250:A:ASP:HA	21	0.14
(3,1496)	1:295:A:LEU:HD22	1:250:A:ASP:HA	21	0.14
(3,1496)	1:295:A:LEU:HD23	1:250:A:ASP:HA	21	0.14
(3,1496)	1:295:A:LEU:HD21	1:250:A:ASP:HA	25	0.14
(3,1496)	1:295:A:LEU:HD22	1:250:A:ASP:HA	25	0.14
(3,1496)	1:295:A:LEU:HD23	1:250:A:ASP:HA	25	0.14
(3,1482)	1:257:A:ILE:HD11	1:254:A:VAL:HB	1	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1482)	1:257:A:ILE:HD12	1:254:A:VAL:HB	1	0.14
(3,1482)	1:257:A:ILE:HD13	1:254:A:VAL:HB	1	0.14
(3,1462)	1:293:A:ILE:HD11	1:283:A:LEU:HB3	20	0.14
(3,1462)	1:293:A:ILE:HD12	1:283:A:LEU:HB3	20	0.14
(3,1462)	1:293:A:ILE:HD13	1:283:A:LEU:HB3	20	0.14
(3,1462)	1:293:A:ILE:HD11	1:283:A:LEU:HB3	27	0.14
(3,1462)	1:293:A:ILE:HD12	1:283:A:LEU:HB3	27	0.14
(3,1462)	1:293:A:ILE:HD13	1:283:A:LEU:HB3	27	0.14
(3,1462)	1:293:A:ILE:HD11	1:283:A:LEU:HB3	30	0.14
(3,1462)	1:293:A:ILE:HD12	1:283:A:LEU:HB3	30	0.14
(3,1462)	1:293:A:ILE:HD13	1:283:A:LEU:HB3	30	0.14
(3,1426)	1:293:A:ILE:HD11	1:292:A:VAL:H	2	0.14
(3,1426)	1:293:A:ILE:HD12	1:292:A:VAL:H	2	0.14
(3,1426)	1:293:A:ILE:HD13	1:292:A:VAL:H	2	0.14
(3,1391)	1:287:A:LYS:HB3	1:254:A:VAL:HG21	13	0.14
(3,1391)	1:287:A:LYS:HB3	1:254:A:VAL:HG22	13	0.14
(3,1391)	1:287:A:LYS:HB3	1:254:A:VAL:HG23	13	0.14
(3,1215)	1:276:A:VAL:HG11	1:279:A:LEU:HB2	4	0.14
(3,1215)	1:276:A:VAL:HG12	1:279:A:LEU:HB2	4	0.14
(3,1215)	1:276:A:VAL:HG13	1:279:A:LEU:HB2	4	0.14
(3,1215)	1:276:A:VAL:HG11	1:279:A:LEU:HB2	5	0.14
(3,1215)	1:276:A:VAL:HG12	1:279:A:LEU:HB2	5	0.14
(3,1215)	1:276:A:VAL:HG13	1:279:A:LEU:HB2	5	0.14
(3,1215)	1:276:A:VAL:HG11	1:279:A:LEU:HB2	10	0.14
(3,1215)	1:276:A:VAL:HG12	1:279:A:LEU:HB2	10	0.14
(3,1215)	1:276:A:VAL:HG13	1:279:A:LEU:HB2	10	0.14
(3,1215)	1:276:A:VAL:HG11	1:279:A:LEU:HB2	14	0.14
(3,1215)	1:276:A:VAL:HG12	1:279:A:LEU:HB2	14	0.14
(3,1215)	1:276:A:VAL:HG13	1:279:A:LEU:HB2	14	0.14
(3,1215)	1:276:A:VAL:HG11	1:279:A:LEU:HB2	24	0.14
(3,1215)	1:276:A:VAL:HG12	1:279:A:LEU:HB2	24	0.14
(3,1215)	1:276:A:VAL:HG13	1:279:A:LEU:HB2	24	0.14
(3,1211)	1:264:A:LEU:HG	1:265:A:ASN:H	24	0.14
(3,1211)	1:264:A:LEU:HG	1:265:A:ASN:H	29	0.14
(3,1185)	1:262:A:GLY:HA3	1:265:A:ASN:HD22	1	0.14
(3,1185)	1:262:A:GLY:HA3	1:265:A:ASN:HD22	8	0.14
(3,1139)	1:283:A:LEU:HD11	1:257:A:ILE:H	22	0.14
(3,1139)	1:283:A:LEU:HD12	1:257:A:ILE:H	22	0.14
(3,1139)	1:283:A:LEU:HD13	1:257:A:ILE:H	22	0.14
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG21	1	0.14
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG22	1	0.14
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG23	1	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	10	0.14
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	10	0.14
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	10	0.14
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	24	0.14
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	24	0.14
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	24	0.14
(3,986)	1:304:A:ALA:H	1:302:A:GLU:HG2	7	0.14
(3,986)	1:304:A:ALA:H	1:302:A:GLU:HG2	16	0.14
(3,888)	1:287:A:LYS:HB2	1:287:A:LYS:HE2	28	0.14
(3,875)	1:283:A:LEU:HD11	1:258:A:GLN:HB3	5	0.14
(3,875)	1:283:A:LEU:HD12	1:258:A:GLN:HB3	5	0.14
(3,875)	1:283:A:LEU:HD13	1:258:A:GLN:HB3	5	0.14
(3,872)	1:254:A:VAL:HA	1:283:A:LEU:HD11	15	0.14
(3,872)	1:254:A:VAL:HA	1:283:A:LEU:HD12	15	0.14
(3,872)	1:254:A:VAL:HA	1:283:A:LEU:HD13	15	0.14
(3,871)	1:283:A:LEU:HD21	1:254:A:VAL:HA	5	0.14
(3,871)	1:283:A:LEU:HD22	1:254:A:VAL:HA	5	0.14
(3,871)	1:283:A:LEU:HD23	1:254:A:VAL:HA	5	0.14
(3,871)	1:283:A:LEU:HD21	1:254:A:VAL:HA	7	0.14
(3,871)	1:283:A:LEU:HD22	1:254:A:VAL:HA	7	0.14
(3,871)	1:283:A:LEU:HD23	1:254:A:VAL:HA	7	0.14
(3,857)	1:283:A:LEU:HD21	1:280:A:SER:HA	18	0.14
(3,857)	1:283:A:LEU:HD22	1:280:A:SER:HA	18	0.14
(3,857)	1:283:A:LEU:HD23	1:280:A:SER:HA	18	0.14
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	1	0.14
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	1	0.14
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	1	0.14
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	2	0.14
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	2	0.14
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	2	0.14
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	3	0.14
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	3	0.14
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	3	0.14
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	21	0.14
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	21	0.14
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	21	0.14
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	25	0.14
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	25	0.14
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	25	0.14
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD11	21	0.14
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD12	21	0.14
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD13	21	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD11	25	0.14
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD12	25	0.14
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD13	25	0.14
(3,774)	1:263:A:LYS:HE2	1:263:A:LYS:H	11	0.14
(3,678)	1:281:A:LYS:HB3	1:281:A:LYS:HE2	20	0.14
(3,624)	1:301:A:LEU:HG	1:302:A:GLU:H	22	0.14
(3,623)	1:301:A:LEU:HB2	1:305:A:GLU:H	23	0.14
(3,85)	1:244:A:ILE:HD11	1:270:A:ILE:HA	19	0.14
(3,85)	1:244:A:ILE:HD12	1:270:A:ILE:HA	19	0.14
(3,85)	1:244:A:ILE:HD13	1:270:A:ILE:HA	19	0.14
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	3	0.14
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	3	0.14
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	3	0.14
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	4	0.14
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	4	0.14
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	4	0.14
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	21	0.14
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	21	0.14
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	21	0.14
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	25	0.14
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	25	0.14
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	25	0.14
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	27	0.14
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	27	0.14
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	27	0.14
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD21	21	0.14
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD22	21	0.14
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD23	21	0.14
(3,72)	1:290:A:THR:H	1:253:A:THR:HA	27	0.14
(3,63)	1:293:A:ILE:H	1:252:A:TRP:HD1	14	0.14
(3,47)	1:306:A:ASN:H	1:310:A:LEU:HG	11	0.14
(3,47)	1:306:A:ASN:H	1:310:A:LEU:HG	17	0.14
(3,41)	1:304:A:ALA:H	1:306:A:ASN:HD22	10	0.14
(3,29)	1:310:A:LEU:H	1:271:A:TYR:HE1	3	0.14
(3,29)	1:310:A:LEU:H	1:271:A:TYR:HE2	3	0.14
(3,29)	1:310:A:LEU:H	1:271:A:TYR:HE1	5	0.14
(3,29)	1:310:A:LEU:H	1:271:A:TYR:HE2	5	0.14
(3,28)	1:310:A:LEU:HD21	1:271:A:TYR:HB2	4	0.14
(3,28)	1:310:A:LEU:HD22	1:271:A:TYR:HB2	4	0.14
(3,28)	1:310:A:LEU:HD23	1:271:A:TYR:HB2	4	0.14
(3,28)	1:310:A:LEU:HD21	1:271:A:TYR:HB2	29	0.14
(3,28)	1:310:A:LEU:HD22	1:271:A:TYR:HB2	29	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,28)	1:310:A:LEU:HD23	1:271:A:TYR:HB2	29	0.14
(3,11)	1:317:A:VAL:H	1:238:A:LYS:HD2	14	0.14
(2,35)	1:269:A:GLN:N	1:265:A:ASN:O	15	0.14
(2,35)	1:269:A:GLN:N	1:265:A:ASN:O	25	0.14
(2,34)	1:268:A:SER:N	1:264:A:LEU:O	15	0.14
(2,34)	1:268:A:SER:N	1:264:A:LEU:O	25	0.14
(2,22)	1:309:A:ILE:H	1:305:A:GLU:O	20	0.14
(2,21)	1:308:A:GLU:H	1:304:A:ALA:O	9	0.14
(2,21)	1:308:A:GLU:H	1:304:A:ALA:O	11	0.14
(2,21)	1:308:A:GLU:H	1:304:A:ALA:O	22	0.14
(2,15)	1:302:A:GLU:H	1:298:A:GLU:O	2	0.14
(2,15)	1:302:A:GLU:H	1:298:A:GLU:O	14	0.14
(2,15)	1:302:A:GLU:H	1:298:A:GLU:O	28	0.14
(2,11)	1:268:A:SER:H	1:264:A:LEU:O	3	0.14
(2,11)	1:268:A:SER:H	1:264:A:LEU:O	17	0.14
(1,35)	1:269:A:GLN:N	1:265:A:ASN:O	15	0.14
(1,35)	1:269:A:GLN:N	1:265:A:ASN:O	25	0.14
(1,34)	1:268:A:SER:N	1:264:A:LEU:O	15	0.14
(1,34)	1:268:A:SER:N	1:264:A:LEU:O	25	0.14
(1,22)	1:309:A:ILE:H	1:305:A:GLU:O	20	0.14
(1,21)	1:308:A:GLU:H	1:304:A:ALA:O	9	0.14
(1,21)	1:308:A:GLU:H	1:304:A:ALA:O	11	0.14
(1,21)	1:308:A:GLU:H	1:304:A:ALA:O	22	0.14
(1,15)	1:302:A:GLU:H	1:298:A:GLU:O	2	0.14
(1,15)	1:302:A:GLU:H	1:298:A:GLU:O	14	0.14
(1,15)	1:302:A:GLU:H	1:298:A:GLU:O	28	0.14
(1,11)	1:268:A:SER:H	1:264:A:LEU:O	3	0.14
(1,11)	1:268:A:SER:H	1:264:A:LEU:O	17	0.14
(3,2614)	1:278:A:GLN:HE22	1:298:A:GLU:HA	28	0.13
(3,2613)	1:255:A:ASN:HD22	1:289:A:LEU:HG	27	0.13
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD11	3	0.13
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD12	3	0.13
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD13	3	0.13
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD11	16	0.13
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD12	16	0.13
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD13	16	0.13
(3,2550)	1:280:A:SER:H	1:302:A:GLU:HG2	6	0.13
(3,2550)	1:280:A:SER:H	1:302:A:GLU:HG2	26	0.13
(3,2540)	1:283:A:LEU:HD21	1:283:A:LEU:H	1	0.13
(3,2540)	1:283:A:LEU:HD22	1:283:A:LEU:H	1	0.13
(3,2540)	1:283:A:LEU:HD23	1:283:A:LEU:H	1	0.13
(3,2540)	1:283:A:LEU:HD21	1:283:A:LEU:H	2	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,2540)	1:283:A:LEU:HD22	1:283:A:LEU:H	2	0.13
(3,2540)	1:283:A:LEU:HD23	1:283:A:LEU:H	2	0.13
(3,2540)	1:283:A:LEU:HD21	1:283:A:LEU:H	30	0.13
(3,2540)	1:283:A:LEU:HD22	1:283:A:LEU:H	30	0.13
(3,2540)	1:283:A:LEU:HD23	1:283:A:LEU:H	30	0.13
(3,2514)	1:273:A:GLY:H	1:271:A:TYR:HB3	13	0.13
(3,2507)	1:255:A:ASN:HD22	1:253:A:THR:HG21	25	0.13
(3,2507)	1:255:A:ASN:HD22	1:253:A:THR:HG22	25	0.13
(3,2507)	1:255:A:ASN:HD22	1:253:A:THR:HG23	25	0.13
(3,2491)	1:255:A:ASN:HD22	1:289:A:LEU:HD11	11	0.13
(3,2491)	1:255:A:ASN:HD22	1:289:A:LEU:HD12	11	0.13
(3,2491)	1:255:A:ASN:HD22	1:289:A:LEU:HD13	11	0.13
(3,2474)	1:256:A:ASP:H	1:258:A:GLN:HB3	12	0.13
(3,2474)	1:256:A:ASP:H	1:258:A:GLN:HB3	14	0.13
(3,2474)	1:256:A:ASP:H	1:258:A:GLN:HB3	19	0.13
(3,2474)	1:256:A:ASP:H	1:258:A:GLN:HB3	28	0.13
(3,2448)	1:256:A:ASP:H	1:257:A:ILE:HG12	7	0.13
(3,2448)	1:256:A:ASP:H	1:257:A:ILE:HG12	18	0.13
(3,2436)	1:291:A:GLU:H	1:291:A:GLU:HG2	15	0.13
(3,2436)	1:291:A:GLU:H	1:291:A:GLU:HG2	28	0.13
(3,2436)	1:291:A:GLU:H	1:291:A:GLU:HG2	29	0.13
(3,2434)	1:253:A:THR:HG21	1:254:A:VAL:H	12	0.13
(3,2434)	1:253:A:THR:HG22	1:254:A:VAL:H	12	0.13
(3,2434)	1:253:A:THR:HG23	1:254:A:VAL:H	12	0.13
(3,2388)	1:255:A:ASN:H	1:289:A:LEU:HB2	14	0.13
(3,2357)	1:262:A:GLY:H	1:260:A:LEU:HB2	7	0.13
(3,2357)	1:262:A:GLY:H	1:260:A:LEU:HB2	20	0.13
(3,2336)	1:295:A:LEU:H	1:300:A:GLU:HB2	19	0.13
(3,2336)	1:295:A:LEU:H	1:300:A:GLU:HB2	28	0.13
(3,2336)	1:295:A:LEU:H	1:300:A:GLU:HB2	29	0.13
(3,2303)	1:238:A:LYS:H	1:239:A:TRP:HA	1	0.13
(3,2286)	1:255:A:ASN:H	1:289:A:LEU:HG	5	0.13
(3,2285)	1:271:A:TYR:H	1:270:A:ILE:HG13	9	0.13
(3,2285)	1:271:A:TYR:H	1:270:A:ILE:HG13	13	0.13
(3,2273)	1:254:A:VAL:H	1:255:A:ASN:HA	2	0.13
(3,2241)	1:258:A:GLN:HG2	1:257:A:ILE:H	20	0.13
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG21	3	0.13
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG22	3	0.13
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG23	3	0.13
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG21	17	0.13
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG22	17	0.13
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG23	17	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD11	20	0.13
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD12	20	0.13
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD13	20	0.13
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD11	30	0.13
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD12	30	0.13
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD13	30	0.13
(3,2174)	1:304:A:ALA:H	1:302:A:GLU:HB2	11	0.13
(3,2163)	1:256:A:ASP:H	1:289:A:LEU:HD21	19	0.13
(3,2163)	1:256:A:ASP:H	1:289:A:LEU:HD22	19	0.13
(3,2163)	1:256:A:ASP:H	1:289:A:LEU:HD23	19	0.13
(3,2163)	1:256:A:ASP:H	1:289:A:LEU:HD21	20	0.13
(3,2163)	1:256:A:ASP:H	1:289:A:LEU:HD22	20	0.13
(3,2163)	1:256:A:ASP:H	1:289:A:LEU:HD23	20	0.13
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	7	0.13
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	7	0.13
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	7	0.13
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	26	0.13
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	26	0.13
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	26	0.13
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	30	0.13
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	30	0.13
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	30	0.13
(3,2141)	1:299:A:ALA:H	1:300:A:GLU:HB2	7	0.13
(3,2141)	1:299:A:ALA:H	1:300:A:GLU:HB2	9	0.13
(3,2141)	1:299:A:ALA:H	1:300:A:GLU:HB2	11	0.13
(3,2141)	1:299:A:ALA:H	1:300:A:GLU:HB2	18	0.13
(3,2121)	1:301:A:LEU:HG	1:301:A:LEU:H	29	0.13
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD11	29	0.13
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD12	29	0.13
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD13	29	0.13
(3,2058)	1:254:A:VAL:H	1:289:A:LEU:HB3	24	0.13
(3,2058)	1:254:A:VAL:H	1:289:A:LEU:HB3	27	0.13
(3,2037)	1:241:A:VAL:H	1:315:A:HIS:HA	20	0.13
(3,2022)	1:291:A:GLU:HG3	1:291:A:GLU:H	17	0.13
(3,1953)	1:265:A:ASN:H	1:263:A:LYS:HB3	28	0.13
(3,1907)	1:271:A:TYR:H	1:272:A:PRO:HB3	7	0.13
(3,1907)	1:271:A:TYR:H	1:272:A:PRO:HB3	28	0.13
(3,1885)	1:281:A:LYS:H	1:281:A:LYS:HG2	12	0.13
(3,1874)	1:271:A:TYR:H	1:272:A:PRO:HG3	18	0.13
(3,1829)	1:276:A:VAL:HG21	1:283:A:LEU:H	2	0.13
(3,1829)	1:276:A:VAL:HG22	1:283:A:LEU:H	2	0.13
(3,1829)	1:276:A:VAL:HG23	1:283:A:LEU:H	2	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1812)	1:270:A:ILE:HB	1:269:A:GLN:HB3	18	0.13
(3,1764)	1:270:A:ILE:HD11	1:271:A:TYR:HD1	2	0.13
(3,1764)	1:270:A:ILE:HD11	1:271:A:TYR:HD2	2	0.13
(3,1764)	1:270:A:ILE:HD12	1:271:A:TYR:HD1	2	0.13
(3,1764)	1:270:A:ILE:HD12	1:271:A:TYR:HD2	2	0.13
(3,1764)	1:270:A:ILE:HD13	1:271:A:TYR:HD1	2	0.13
(3,1764)	1:270:A:ILE:HD13	1:271:A:TYR:HD2	2	0.13
(3,1764)	1:270:A:ILE:HD11	1:271:A:TYR:HD1	6	0.13
(3,1764)	1:270:A:ILE:HD11	1:271:A:TYR:HD2	6	0.13
(3,1764)	1:270:A:ILE:HD12	1:271:A:TYR:HD1	6	0.13
(3,1764)	1:270:A:ILE:HD12	1:271:A:TYR:HD2	6	0.13
(3,1764)	1:270:A:ILE:HD13	1:271:A:TYR:HD1	6	0.13
(3,1764)	1:270:A:ILE:HD13	1:271:A:TYR:HD2	6	0.13
(3,1764)	1:270:A:ILE:HD11	1:271:A:TYR:HD1	8	0.13
(3,1764)	1:270:A:ILE:HD11	1:271:A:TYR:HD2	8	0.13
(3,1764)	1:270:A:ILE:HD12	1:271:A:TYR:HD1	8	0.13
(3,1764)	1:270:A:ILE:HD12	1:271:A:TYR:HD2	8	0.13
(3,1764)	1:270:A:ILE:HD13	1:271:A:TYR:HD1	8	0.13
(3,1764)	1:270:A:ILE:HD13	1:271:A:TYR:HD2	8	0.13
(3,1757)	1:264:A:LEU:HG	1:306:A:ASN:HD22	18	0.13
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	18	0.13
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	18	0.13
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	18	0.13
(3,1723)	1:254:A:VAL:HA	1:258:A:GLN:HB3	25	0.13
(3,1660)	1:240:A:THR:HG21	1:315:A:HIS:HA	27	0.13
(3,1660)	1:240:A:THR:HG22	1:315:A:HIS:HA	27	0.13
(3,1660)	1:240:A:THR:HG23	1:315:A:HIS:HA	27	0.13
(3,1639)	1:319:A:LEU:HD11	1:318:A:TYR:HB3	6	0.13
(3,1639)	1:319:A:LEU:HD12	1:318:A:TYR:HB3	6	0.13
(3,1639)	1:319:A:LEU:HD13	1:318:A:TYR:HB3	6	0.13
(3,1600)	1:239:A:TRP:HB2	1:317:A:VAL:HA	20	0.13
(3,1441)	1:293:A:ILE:HG12	1:254:A:VAL:HB	9	0.13
(3,1441)	1:293:A:ILE:HG12	1:254:A:VAL:HB	19	0.13
(3,1441)	1:293:A:ILE:HG12	1:254:A:VAL:HB	22	0.13
(3,1426)	1:293:A:ILE:HD11	1:292:A:VAL:H	1	0.13
(3,1426)	1:293:A:ILE:HD12	1:292:A:VAL:H	1	0.13
(3,1426)	1:293:A:ILE:HD13	1:292:A:VAL:H	1	0.13
(3,1426)	1:293:A:ILE:HD11	1:292:A:VAL:H	21	0.13
(3,1426)	1:293:A:ILE:HD12	1:292:A:VAL:H	21	0.13
(3,1426)	1:293:A:ILE:HD13	1:292:A:VAL:H	21	0.13
(3,1351)	1:277:A:ARG:HG2	1:276:A:VAL:H	8	0.13
(3,1351)	1:277:A:ARG:HG2	1:276:A:VAL:H	30	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1215)	1:276:A:VAL:HG11	1:279:A:LEU:HB2	21	0.13
(3,1215)	1:276:A:VAL:HG12	1:279:A:LEU:HB2	21	0.13
(3,1215)	1:276:A:VAL:HG13	1:279:A:LEU:HB2	21	0.13
(3,1211)	1:264:A:LEU:HG	1:265:A:ASN:H	20	0.13
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	3	0.13
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	3	0.13
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	3	0.13
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	9	0.13
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	9	0.13
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	9	0.13
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	26	0.13
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	26	0.13
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	26	0.13
(3,1185)	1:262:A:GLY:HA3	1:265:A:ASN:HD22	14	0.13
(3,1185)	1:262:A:GLY:HA3	1:265:A:ASN:HD22	19	0.13
(3,1139)	1:283:A:LEU:HD11	1:257:A:ILE:H	11	0.13
(3,1139)	1:283:A:LEU:HD12	1:257:A:ILE:H	11	0.13
(3,1139)	1:283:A:LEU:HD13	1:257:A:ILE:H	11	0.13
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG21	23	0.13
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG22	23	0.13
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG23	23	0.13
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG21	26	0.13
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG22	26	0.13
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG23	26	0.13
(3,1052)	1:240:A:THR:HB	1:241:A:VAL:HB	10	0.13
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	2	0.13
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	2	0.13
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	2	0.13
(3,998)	1:303:A:LEU:HD11	1:307:A:ARG:HA	27	0.13
(3,998)	1:303:A:LEU:HD12	1:307:A:ARG:HA	27	0.13
(3,998)	1:303:A:LEU:HD13	1:307:A:ARG:HA	27	0.13
(3,986)	1:304:A:ALA:H	1:302:A:GLU:HG2	6	0.13
(3,899)	1:288:A:ALA:HA	1:289:A:LEU:HG	11	0.13
(3,875)	1:283:A:LEU:HD11	1:258:A:GLN:HB3	3	0.13
(3,875)	1:283:A:LEU:HD12	1:258:A:GLN:HB3	3	0.13
(3,875)	1:283:A:LEU:HD13	1:258:A:GLN:HB3	3	0.13
(3,871)	1:283:A:LEU:HD21	1:254:A:VAL:HA	2	0.13
(3,871)	1:283:A:LEU:HD22	1:254:A:VAL:HA	2	0.13
(3,871)	1:283:A:LEU:HD23	1:254:A:VAL:HA	2	0.13
(3,871)	1:283:A:LEU:HD21	1:254:A:VAL:HA	14	0.13
(3,871)	1:283:A:LEU:HD22	1:254:A:VAL:HA	14	0.13
(3,871)	1:283:A:LEU:HD23	1:254:A:VAL:HA	14	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	5	0.13
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	5	0.13
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	5	0.13
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	8	0.13
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	8	0.13
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	8	0.13
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	27	0.13
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	27	0.13
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	27	0.13
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD11	8	0.13
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD12	8	0.13
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD13	8	0.13
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD11	10	0.13
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD12	10	0.13
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD13	10	0.13
(3,823)	1:291:A:GLU:HB3	1:254:A:VAL:HG11	1	0.13
(3,823)	1:291:A:GLU:HB3	1:254:A:VAL:HG12	1	0.13
(3,823)	1:291:A:GLU:HB3	1:254:A:VAL:HG13	1	0.13
(3,823)	1:291:A:GLU:HB3	1:254:A:VAL:HG11	14	0.13
(3,823)	1:291:A:GLU:HB3	1:254:A:VAL:HG12	14	0.13
(3,823)	1:291:A:GLU:HB3	1:254:A:VAL:HG13	14	0.13
(3,814)	1:275:A:LYS:HG2	1:275:A:LYS:HE3	22	0.13
(3,810)	1:275:A:LYS:HE3	1:275:A:LYS:HB3	2	0.13
(3,810)	1:275:A:LYS:HE3	1:275:A:LYS:HB3	15	0.13
(3,810)	1:275:A:LYS:HE3	1:275:A:LYS:HB3	26	0.13
(3,706)	1:287:A:LYS:HE2	1:287:A:LYS:HG3	13	0.13
(3,705)	1:287:A:LYS:HG2	1:287:A:LYS:HE2	27	0.13
(3,678)	1:281:A:LYS:HB3	1:281:A:LYS:HE2	15	0.13
(3,315)	1:282:A:LEU:HA	1:282:A:LEU:HD11	19	0.13
(3,315)	1:282:A:LEU:HA	1:282:A:LEU:HD12	19	0.13
(3,315)	1:282:A:LEU:HA	1:282:A:LEU:HD13	19	0.13
(3,235)	1:275:A:LYS:HG3	1:275:A:LYS:HE3	20	0.13
(3,85)	1:244:A:ILE:HD11	1:270:A:ILE:HA	18	0.13
(3,85)	1:244:A:ILE:HD12	1:270:A:ILE:HA	18	0.13
(3,85)	1:244:A:ILE:HD13	1:270:A:ILE:HA	18	0.13
(3,81)	1:262:A:GLY:H	1:260:A:LEU:HG	26	0.13
(3,78)	1:279:A:LEU:HD11	1:306:A:ASN:HD22	30	0.13
(3,78)	1:279:A:LEU:HD12	1:306:A:ASN:HD22	30	0.13
(3,78)	1:279:A:LEU:HD13	1:306:A:ASN:HD22	30	0.13
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD21	6	0.13
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD22	6	0.13
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD23	6	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD21	15	0.13
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD22	15	0.13
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD23	15	0.13
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD21	23	0.13
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD22	23	0.13
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD23	23	0.13
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD21	26	0.13
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD22	26	0.13
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD23	26	0.13
(3,73)	1:288:A:ALA:H	1:290:A:THR:H	17	0.13
(3,71)	1:290:A:THR:H	1:255:A:ASN:HB3	11	0.13
(3,71)	1:290:A:THR:H	1:255:A:ASN:HB3	16	0.13
(3,63)	1:293:A:ILE:H	1:252:A:TRP:HD1	1	0.13
(3,47)	1:306:A:ASN:H	1:310:A:LEU:HG	18	0.13
(3,29)	1:310:A:LEU:H	1:271:A:TYR:HE1	18	0.13
(3,29)	1:310:A:LEU:H	1:271:A:TYR:HE2	18	0.13
(3,28)	1:310:A:LEU:HD21	1:271:A:TYR:HB2	11	0.13
(3,28)	1:310:A:LEU:HD22	1:271:A:TYR:HB2	11	0.13
(3,28)	1:310:A:LEU:HD23	1:271:A:TYR:HB2	11	0.13
(3,28)	1:310:A:LEU:HD21	1:271:A:TYR:HB2	28	0.13
(3,28)	1:310:A:LEU:HD22	1:271:A:TYR:HB2	28	0.13
(3,28)	1:310:A:LEU:HD23	1:271:A:TYR:HB2	28	0.13
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE1	27	0.13
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE2	27	0.13
(3,14)	1:239:A:TRP:HB2	1:238:A:LYS:HB2	20	0.13
(3,3)	1:314:A:VAL:HG11	1:315:A:HIS:HA	26	0.13
(3,3)	1:314:A:VAL:HG12	1:315:A:HIS:HA	26	0.13
(3,3)	1:314:A:VAL:HG13	1:315:A:HIS:HA	26	0.13
(3,2)	1:314:A:VAL:HG21	1:313:A:PRO:HA	15	0.13
(3,2)	1:314:A:VAL:HG22	1:313:A:PRO:HA	15	0.13
(3,2)	1:314:A:VAL:HG23	1:313:A:PRO:HA	15	0.13
(2,34)	1:268:A:SER:N	1:264:A:LEU:O	8	0.13
(2,34)	1:268:A:SER:N	1:264:A:LEU:O	18	0.13
(2,34)	1:268:A:SER:N	1:264:A:LEU:O	19	0.13
(2,15)	1:302:A:GLU:H	1:298:A:GLU:O	3	0.13
(2,15)	1:302:A:GLU:H	1:298:A:GLU:O	7	0.13
(2,15)	1:302:A:GLU:H	1:298:A:GLU:O	17	0.13
(2,15)	1:302:A:GLU:H	1:298:A:GLU:O	24	0.13
(2,13)	1:282:A:LEU:H	1:278:A:GLN:O	9	0.13
(2,13)	1:282:A:LEU:H	1:278:A:GLN:O	19	0.13
(2,13)	1:282:A:LEU:H	1:278:A:GLN:O	29	0.13
(2,11)	1:268:A:SER:H	1:264:A:LEU:O	30	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,8)	1:265:A:ASN:H	1:261:A:VAL:O	23	0.13
(1,34)	1:268:A:SER:N	1:264:A:LEU:O	8	0.13
(1,34)	1:268:A:SER:N	1:264:A:LEU:O	18	0.13
(1,34)	1:268:A:SER:N	1:264:A:LEU:O	19	0.13
(1,15)	1:302:A:GLU:H	1:298:A:GLU:O	3	0.13
(1,15)	1:302:A:GLU:H	1:298:A:GLU:O	7	0.13
(1,15)	1:302:A:GLU:H	1:298:A:GLU:O	17	0.13
(1,15)	1:302:A:GLU:H	1:298:A:GLU:O	24	0.13
(1,13)	1:282:A:LEU:H	1:278:A:GLN:O	9	0.13
(1,13)	1:282:A:LEU:H	1:278:A:GLN:O	19	0.13
(1,13)	1:282:A:LEU:H	1:278:A:GLN:O	29	0.13
(1,11)	1:268:A:SER:H	1:264:A:LEU:O	30	0.13
(1,8)	1:265:A:ASN:H	1:261:A:VAL:O	23	0.13
(3,2613)	1:255:A:ASN:HD22	1:289:A:LEU:HG	3	0.12
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD11	25	0.12
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD12	25	0.12
(3,2585)	1:290:A:THR:H	1:289:A:LEU:HD13	25	0.12
(3,2550)	1:280:A:SER:H	1:302:A:GLU:HG2	24	0.12
(3,2547)	1:299:A:ALA:H	1:278:A:GLN:H	30	0.12
(3,2474)	1:256:A:ASP:H	1:258:A:GLN:HB3	6	0.12
(3,2474)	1:256:A:ASP:H	1:258:A:GLN:HB3	27	0.12
(3,2457)	1:303:A:LEU:H	1:303:A:LEU:HG	9	0.12
(3,2448)	1:256:A:ASP:H	1:257:A:ILE:HG12	4	0.12
(3,2448)	1:256:A:ASP:H	1:257:A:ILE:HG12	8	0.12
(3,2436)	1:291:A:GLU:H	1:291:A:GLU:HG2	11	0.12
(3,2434)	1:253:A:THR:HG21	1:254:A:VAL:H	15	0.12
(3,2434)	1:253:A:THR:HG22	1:254:A:VAL:H	15	0.12
(3,2434)	1:253:A:THR:HG23	1:254:A:VAL:H	15	0.12
(3,2414)	1:268:A:SER:H	1:274:A:ILE:HB	29	0.12
(3,2401)	1:253:A:THR:H	1:292:A:VAL:H	8	0.12
(3,2401)	1:253:A:THR:H	1:292:A:VAL:H	14	0.12
(3,2401)	1:253:A:THR:H	1:292:A:VAL:H	24	0.12
(3,2388)	1:255:A:ASN:H	1:289:A:LEU:HB2	4	0.12
(3,2388)	1:255:A:ASN:H	1:289:A:LEU:HB2	8	0.12
(3,2388)	1:255:A:ASN:H	1:289:A:LEU:HB2	25	0.12
(3,2367)	1:275:A:LYS:HG2	1:275:A:LYS:H	14	0.12
(3,2367)	1:275:A:LYS:HG2	1:275:A:LYS:H	24	0.12
(3,2366)	1:300:A:GLU:H	1:301:A:LEU:HA	5	0.12
(3,2366)	1:300:A:GLU:H	1:301:A:LEU:HA	27	0.12
(3,2295)	1:262:A:GLY:H	1:265:A:ASN:HB2	9	0.12
(3,2282)	1:239:A:TRP:HE1	1:240:A:THR:H	20	0.12
(3,2277)	1:269:A:GLN:H	1:270:A:ILE:HG21	4	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,2277)	1:269:A:GLN:H	1:270:A:ILE:HG22	4	0.12
(3,2277)	1:269:A:GLN:H	1:270:A:ILE:HG23	4	0.12
(3,2273)	1:254:A:VAL:H	1:255:A:ASN:HA	27	0.12
(3,2241)	1:258:A:GLN:HG2	1:257:A:ILE:H	7	0.12
(3,2241)	1:258:A:GLN:HG2	1:257:A:ILE:H	16	0.12
(3,2174)	1:304:A:ALA:H	1:302:A:GLU:HB2	9	0.12
(3,2174)	1:304:A:ALA:H	1:302:A:GLU:HB2	25	0.12
(3,2163)	1:256:A:ASP:H	1:289:A:LEU:HD21	26	0.12
(3,2163)	1:256:A:ASP:H	1:289:A:LEU:HD22	26	0.12
(3,2163)	1:256:A:ASP:H	1:289:A:LEU:HD23	26	0.12
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	12	0.12
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	12	0.12
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	12	0.12
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	20	0.12
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	20	0.12
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	20	0.12
(3,2141)	1:299:A:ALA:H	1:300:A:GLU:HB2	10	0.12
(3,2141)	1:299:A:ALA:H	1:300:A:GLU:HB2	12	0.12
(3,2141)	1:299:A:ALA:H	1:300:A:GLU:HB2	27	0.12
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD11	5	0.12
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD12	5	0.12
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD13	5	0.12
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD11	10	0.12
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD12	10	0.12
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD13	10	0.12
(3,2080)	1:299:A:ALA:H	1:300:A:GLU:HG3	28	0.12
(3,2051)	1:289:A:LEU:H	1:289:A:LEU:HG	9	0.12
(3,2051)	1:289:A:LEU:H	1:289:A:LEU:HG	26	0.12
(3,2024)	1:302:A:GLU:H	1:278:A:GLN:H	8	0.12
(3,2023)	1:280:A:SER:H	1:279:A:LEU:HG	26	0.12
(3,1987)	1:256:A:ASP:H	1:252:A:TRP:HZ3	4	0.12
(3,1966)	1:266:A:TRP:H	1:276:A:VAL:HG11	19	0.12
(3,1966)	1:266:A:TRP:H	1:276:A:VAL:HG12	19	0.12
(3,1966)	1:266:A:TRP:H	1:276:A:VAL:HG13	19	0.12
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	4	0.12
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	15	0.12
(3,1934)	1:275:A:LYS:H	1:274:A:ILE:HD11	14	0.12
(3,1934)	1:275:A:LYS:H	1:274:A:ILE:HD12	14	0.12
(3,1934)	1:275:A:LYS:H	1:274:A:ILE:HD13	14	0.12
(3,1915)	1:308:A:GLU:HG3	1:308:A:GLU:H	16	0.12
(3,1907)	1:271:A:TYR:H	1:272:A:PRO:HB3	15	0.12
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG21	12	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG22	12	0.12
(3,1821)	1:270:A:ILE:HB	1:309:A:ILE:HG23	12	0.12
(3,1810)	1:270:A:ILE:HA	1:241:A:VAL:HG11	15	0.12
(3,1810)	1:270:A:ILE:HA	1:241:A:VAL:HG12	15	0.12
(3,1810)	1:270:A:ILE:HA	1:241:A:VAL:HG13	15	0.12
(3,1764)	1:270:A:ILE:HD11	1:271:A:TYR:HD1	10	0.12
(3,1764)	1:270:A:ILE:HD11	1:271:A:TYR:HD2	10	0.12
(3,1764)	1:270:A:ILE:HD12	1:271:A:TYR:HD1	10	0.12
(3,1764)	1:270:A:ILE:HD12	1:271:A:TYR:HD2	10	0.12
(3,1764)	1:270:A:ILE:HD13	1:271:A:TYR:HD1	10	0.12
(3,1764)	1:270:A:ILE:HD13	1:271:A:TYR:HD2	10	0.12
(3,1755)	1:264:A:LEU:HG	1:268:A:SER:H	9	0.12
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	21	0.12
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	21	0.12
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	21	0.12
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	27	0.12
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	27	0.12
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	27	0.12
(3,1621)	1:317:A:VAL:HB	1:318:A:TYR:HE1	19	0.12
(3,1621)	1:317:A:VAL:HB	1:318:A:TYR:HE2	19	0.12
(3,1614)	1:318:A:TYR:HB3	1:317:A:VAL:HG21	18	0.12
(3,1614)	1:318:A:TYR:HB3	1:317:A:VAL:HG22	18	0.12
(3,1614)	1:318:A:TYR:HB3	1:317:A:VAL:HG23	18	0.12
(3,1537)	1:297:A:GLU:HB3	1:296:A:THR:HB	22	0.12
(3,1506)	1:296:A:THR:HG21	1:301:A:LEU:H	26	0.12
(3,1506)	1:296:A:THR:HG22	1:301:A:LEU:H	26	0.12
(3,1506)	1:296:A:THR:HG23	1:301:A:LEU:H	26	0.12
(3,1506)	1:296:A:THR:HG21	1:301:A:LEU:H	29	0.12
(3,1506)	1:296:A:THR:HG22	1:301:A:LEU:H	29	0.12
(3,1506)	1:296:A:THR:HG23	1:301:A:LEU:H	29	0.12
(3,1496)	1:295:A:LEU:HD21	1:250:A:ASP:HA	11	0.12
(3,1496)	1:295:A:LEU:HD22	1:250:A:ASP:HA	11	0.12
(3,1496)	1:295:A:LEU:HD23	1:250:A:ASP:HA	11	0.12
(3,1496)	1:295:A:LEU:HD21	1:250:A:ASP:HA	17	0.12
(3,1496)	1:295:A:LEU:HD22	1:250:A:ASP:HA	17	0.12
(3,1496)	1:295:A:LEU:HD23	1:250:A:ASP:HA	17	0.12
(3,1496)	1:295:A:LEU:HD21	1:250:A:ASP:HA	22	0.12
(3,1496)	1:295:A:LEU:HD22	1:250:A:ASP:HA	22	0.12
(3,1496)	1:295:A:LEU:HD23	1:250:A:ASP:HA	22	0.12
(3,1496)	1:295:A:LEU:HD21	1:250:A:ASP:HA	23	0.12
(3,1496)	1:295:A:LEU:HD22	1:250:A:ASP:HA	23	0.12
(3,1496)	1:295:A:LEU:HD23	1:250:A:ASP:HA	23	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1470)	1:293:A:ILE:HG21	1:257:A:ILE:HB	11	0.12
(3,1470)	1:293:A:ILE:HG22	1:257:A:ILE:HB	11	0.12
(3,1470)	1:293:A:ILE:HG23	1:257:A:ILE:HB	11	0.12
(3,1468)	1:293:A:ILE:HG21	1:286:A:THR:HB	22	0.12
(3,1468)	1:293:A:ILE:HG22	1:286:A:THR:HB	22	0.12
(3,1468)	1:293:A:ILE:HG23	1:286:A:THR:HB	22	0.12
(3,1462)	1:293:A:ILE:HD11	1:283:A:LEU:HB3	17	0.12
(3,1462)	1:293:A:ILE:HD12	1:283:A:LEU:HB3	17	0.12
(3,1462)	1:293:A:ILE:HD13	1:283:A:LEU:HB3	17	0.12
(3,1441)	1:293:A:ILE:HG12	1:254:A:VAL:HB	5	0.12
(3,1426)	1:293:A:ILE:HD11	1:292:A:VAL:H	29	0.12
(3,1426)	1:293:A:ILE:HD12	1:292:A:VAL:H	29	0.12
(3,1426)	1:293:A:ILE:HD13	1:292:A:VAL:H	29	0.12
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG21	7	0.12
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG22	7	0.12
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG23	7	0.12
(3,1375)	1:280:A:SER:H	1:276:A:VAL:HB	24	0.12
(3,1373)	1:279:A:LEU:HD21	1:306:A:ASN:HB3	1	0.12
(3,1373)	1:279:A:LEU:HD22	1:306:A:ASN:HB3	1	0.12
(3,1373)	1:279:A:LEU:HD23	1:306:A:ASN:HB3	1	0.12
(3,1373)	1:279:A:LEU:HD21	1:306:A:ASN:HB3	8	0.12
(3,1373)	1:279:A:LEU:HD22	1:306:A:ASN:HB3	8	0.12
(3,1373)	1:279:A:LEU:HD23	1:306:A:ASN:HB3	8	0.12
(3,1363)	1:279:A:LEU:HG	1:299:A:ALA:HB1	28	0.12
(3,1363)	1:279:A:LEU:HG	1:299:A:ALA:HB2	28	0.12
(3,1363)	1:279:A:LEU:HG	1:299:A:ALA:HB3	28	0.12
(3,1347)	1:280:A:SER:HA	1:276:A:VAL:HG21	17	0.12
(3,1347)	1:280:A:SER:HA	1:276:A:VAL:HG22	17	0.12
(3,1347)	1:280:A:SER:HA	1:276:A:VAL:HG23	17	0.12
(3,1331)	1:274:A:ILE:HD11	1:271:A:TYR:HA	20	0.12
(3,1331)	1:274:A:ILE:HD12	1:271:A:TYR:HA	20	0.12
(3,1331)	1:274:A:ILE:HD13	1:271:A:TYR:HA	20	0.12
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG21	7	0.12
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG22	7	0.12
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG23	7	0.12
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG21	12	0.12
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG22	12	0.12
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG23	12	0.12
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG21	23	0.12
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG22	23	0.12
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG23	23	0.12
(3,1215)	1:276:A:VAL:HG11	1:279:A:LEU:HB2	25	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1215)	1:276:A:VAL:HG12	1:279:A:LEU:HB2	25	0.12
(3,1215)	1:276:A:VAL:HG13	1:279:A:LEU:HB2	25	0.12
(3,1185)	1:262:A:GLY:HA3	1:265:A:ASN:HD22	18	0.12
(3,1159)	1:259:A:LYS:HG2	1:259:A:LYS:HE2	6	0.12
(3,1149)	1:259:A:LYS:HD2	1:259:A:LYS:HA	18	0.12
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG21	6	0.12
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG22	6	0.12
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG23	6	0.12
(3,1052)	1:240:A:THR:HB	1:241:A:VAL:HB	3	0.12
(3,1052)	1:240:A:THR:HB	1:241:A:VAL:HB	29	0.12
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	19	0.12
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	19	0.12
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	19	0.12
(3,997)	1:303:A:LEU:HD21	1:307:A:ARG:HA	2	0.12
(3,997)	1:303:A:LEU:HD22	1:307:A:ARG:HA	2	0.12
(3,997)	1:303:A:LEU:HD23	1:307:A:ARG:HA	2	0.12
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG11	13	0.12
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG12	13	0.12
(3,893)	1:287:A:LYS:HB3	1:254:A:VAL:HG13	13	0.12
(3,867)	1:283:A:LEU:HD21	1:258:A:GLN:HB3	17	0.12
(3,867)	1:283:A:LEU:HD22	1:258:A:GLN:HB3	17	0.12
(3,867)	1:283:A:LEU:HD23	1:258:A:GLN:HB3	17	0.12
(3,857)	1:283:A:LEU:HD21	1:280:A:SER:HA	15	0.12
(3,857)	1:283:A:LEU:HD22	1:280:A:SER:HA	15	0.12
(3,857)	1:283:A:LEU:HD23	1:280:A:SER:HA	15	0.12
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD11	16	0.12
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD12	16	0.12
(3,838)	1:255:A:ASN:HB3	1:289:A:LEU:HD13	16	0.12
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD11	1	0.12
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD12	1	0.12
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD13	1	0.12
(3,814)	1:275:A:LYS:HG2	1:275:A:LYS:HE3	5	0.12
(3,814)	1:275:A:LYS:HG2	1:275:A:LYS:HE3	14	0.12
(3,814)	1:275:A:LYS:HG2	1:275:A:LYS:HE3	16	0.12
(3,814)	1:275:A:LYS:HG2	1:275:A:LYS:HE3	27	0.12
(3,810)	1:275:A:LYS:HE3	1:275:A:LYS:HB3	8	0.12
(3,678)	1:281:A:LYS:HB3	1:281:A:LYS:HE2	9	0.12
(3,659)	1:281:A:LYS:HE3	1:281:A:LYS:HB2	9	0.12
(3,629)	1:302:A:GLU:H	1:301:A:LEU:HD21	20	0.12
(3,629)	1:302:A:GLU:H	1:301:A:LEU:HD22	20	0.12
(3,629)	1:302:A:GLU:H	1:301:A:LEU:HD23	20	0.12
(3,623)	1:301:A:LEU:HB2	1:305:A:GLU:H	11	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,315)	1:282:A:LEU:HA	1:282:A:LEU:HD11	13	0.12
(3,315)	1:282:A:LEU:HA	1:282:A:LEU:HD12	13	0.12
(3,315)	1:282:A:LEU:HA	1:282:A:LEU:HD13	13	0.12
(3,231)	1:276:A:VAL:H	1:275:A:LYS:HE3	22	0.12
(3,231)	1:276:A:VAL:H	1:275:A:LYS:HE3	23	0.12
(3,85)	1:244:A:ILE:HD11	1:270:A:ILE:HA	27	0.12
(3,85)	1:244:A:ILE:HD12	1:270:A:ILE:HA	27	0.12
(3,85)	1:244:A:ILE:HD13	1:270:A:ILE:HA	27	0.12
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	1	0.12
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	1	0.12
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	1	0.12
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	24	0.12
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	24	0.12
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	24	0.12
(3,81)	1:262:A:GLY:H	1:260:A:LEU:HG	25	0.12
(3,80)	1:270:A:ILE:HD11	1:314:A:VAL:HG11	18	0.12
(3,80)	1:270:A:ILE:HD11	1:314:A:VAL:HG12	18	0.12
(3,80)	1:270:A:ILE:HD11	1:314:A:VAL:HG13	18	0.12
(3,80)	1:270:A:ILE:HD12	1:314:A:VAL:HG11	18	0.12
(3,80)	1:270:A:ILE:HD12	1:314:A:VAL:HG12	18	0.12
(3,80)	1:270:A:ILE:HD12	1:314:A:VAL:HG13	18	0.12
(3,80)	1:270:A:ILE:HD13	1:314:A:VAL:HG11	18	0.12
(3,80)	1:270:A:ILE:HD13	1:314:A:VAL:HG12	18	0.12
(3,80)	1:270:A:ILE:HD13	1:314:A:VAL:HG13	18	0.12
(3,78)	1:279:A:LEU:HD11	1:306:A:ASN:HD22	27	0.12
(3,78)	1:279:A:LEU:HD12	1:306:A:ASN:HD22	27	0.12
(3,78)	1:279:A:LEU:HD13	1:306:A:ASN:HD22	27	0.12
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD21	3	0.12
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD22	3	0.12
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD23	3	0.12
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD21	13	0.12
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD22	13	0.12
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD23	13	0.12
(3,74)	1:283:A:LEU:H	1:280:A:SER:HB2	29	0.12
(3,71)	1:290:A:THR:H	1:255:A:ASN:HB3	2	0.12
(3,71)	1:290:A:THR:H	1:255:A:ASN:HB3	29	0.12
(3,47)	1:306:A:ASN:H	1:310:A:LEU:HG	26	0.12
(3,39)	1:308:A:GLU:HA	1:310:A:LEU:HD21	28	0.12
(3,39)	1:308:A:GLU:HA	1:310:A:LEU:HD22	28	0.12
(3,39)	1:308:A:GLU:HA	1:310:A:LEU:HD23	28	0.12
(3,28)	1:310:A:LEU:HD21	1:271:A:TYR:HB2	26	0.12
(3,28)	1:310:A:LEU:HD22	1:271:A:TYR:HB2	26	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,28)	1:310:A:LEU:HD23	1:271:A:TYR:HB2	26	0.12
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE1	4	0.12
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE2	4	0.12
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE1	6	0.12
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE2	6	0.12
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE1	14	0.12
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE2	14	0.12
(3,19)	1:314:A:VAL:HG21	1:312:A:GLU:HB2	4	0.12
(3,19)	1:314:A:VAL:HG22	1:312:A:GLU:HB2	4	0.12
(3,19)	1:314:A:VAL:HG23	1:312:A:GLU:HB2	4	0.12
(3,17)	1:241:A:VAL:HG21	1:271:A:TYR:HE1	28	0.12
(3,17)	1:241:A:VAL:HG21	1:271:A:TYR:HE2	28	0.12
(3,17)	1:241:A:VAL:HG22	1:271:A:TYR:HE1	28	0.12
(3,17)	1:241:A:VAL:HG22	1:271:A:TYR:HE2	28	0.12
(3,17)	1:241:A:VAL:HG23	1:271:A:TYR:HE1	28	0.12
(3,17)	1:241:A:VAL:HG23	1:271:A:TYR:HE2	28	0.12
(2,42)	1:306:A:ASN:N	1:302:A:GLU:O	17	0.12
(2,38)	1:302:A:GLU:N	1:298:A:GLU:O	15	0.12
(2,35)	1:269:A:GLN:N	1:265:A:ASN:O	10	0.12
(2,35)	1:269:A:GLN:N	1:265:A:ASN:O	17	0.12
(2,35)	1:269:A:GLN:N	1:265:A:ASN:O	18	0.12
(2,34)	1:268:A:SER:N	1:264:A:LEU:O	7	0.12
(2,34)	1:268:A:SER:N	1:264:A:LEU:O	13	0.12
(2,22)	1:309:A:ILE:H	1:305:A:GLU:O	12	0.12
(2,21)	1:308:A:GLU:H	1:304:A:ALA:O	24	0.12
(2,21)	1:308:A:GLU:H	1:304:A:ALA:O	29	0.12
(2,15)	1:302:A:GLU:H	1:298:A:GLU:O	12	0.12
(2,15)	1:302:A:GLU:H	1:298:A:GLU:O	13	0.12
(2,13)	1:282:A:LEU:H	1:278:A:GLN:O	18	0.12
(2,5)	1:262:A:GLY:H	1:258:A:GLN:O	8	0.12
(2,5)	1:262:A:GLY:H	1:258:A:GLN:O	12	0.12
(2,4)	1:261:A:VAL:H	1:257:A:ILE:O	11	0.12
(1,42)	1:306:A:ASN:N	1:302:A:GLU:O	17	0.12
(1,38)	1:302:A:GLU:N	1:298:A:GLU:O	15	0.12
(1,35)	1:269:A:GLN:N	1:265:A:ASN:O	10	0.12
(1,35)	1:269:A:GLN:N	1:265:A:ASN:O	17	0.12
(1,35)	1:269:A:GLN:N	1:265:A:ASN:O	18	0.12
(1,34)	1:268:A:SER:N	1:264:A:LEU:O	7	0.12
(1,34)	1:268:A:SER:N	1:264:A:LEU:O	13	0.12
(1,22)	1:309:A:ILE:H	1:305:A:GLU:O	12	0.12
(1,21)	1:308:A:GLU:H	1:304:A:ALA:O	24	0.12
(1,21)	1:308:A:GLU:H	1:304:A:ALA:O	29	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,15)	1:302:A:GLU:H	1:298:A:GLU:O	12	0.12
(1,15)	1:302:A:GLU:H	1:298:A:GLU:O	13	0.12
(1,13)	1:282:A:LEU:H	1:278:A:GLN:O	18	0.12
(1,5)	1:262:A:GLY:H	1:258:A:GLN:O	8	0.12
(1,5)	1:262:A:GLY:H	1:258:A:GLN:O	12	0.12
(1,4)	1:261:A:VAL:H	1:257:A:ILE:O	11	0.12
(3,2613)	1:255:A:ASN:HD22	1:289:A:LEU:HG	5	0.11
(3,2550)	1:280:A:SER:H	1:302:A:GLU:HG2	7	0.11
(3,2550)	1:280:A:SER:H	1:302:A:GLU:HG2	12	0.11
(3,2550)	1:280:A:SER:H	1:302:A:GLU:HG2	28	0.11
(3,2540)	1:283:A:LEU:HD21	1:283:A:LEU:H	10	0.11
(3,2540)	1:283:A:LEU:HD22	1:283:A:LEU:H	10	0.11
(3,2540)	1:283:A:LEU:HD23	1:283:A:LEU:H	10	0.11
(3,2526)	1:276:A:VAL:HG21	1:276:A:VAL:H	10	0.11
(3,2526)	1:276:A:VAL:HG22	1:276:A:VAL:H	10	0.11
(3,2526)	1:276:A:VAL:HG23	1:276:A:VAL:H	10	0.11
(3,2526)	1:276:A:VAL:HG21	1:276:A:VAL:H	23	0.11
(3,2526)	1:276:A:VAL:HG22	1:276:A:VAL:H	23	0.11
(3,2526)	1:276:A:VAL:HG23	1:276:A:VAL:H	23	0.11
(3,2482)	1:282:A:LEU:HD21	1:282:A:LEU:H	24	0.11
(3,2482)	1:282:A:LEU:HD22	1:282:A:LEU:H	24	0.11
(3,2482)	1:282:A:LEU:HD23	1:282:A:LEU:H	24	0.11
(3,2474)	1:256:A:ASP:H	1:258:A:GLN:HB3	15	0.11
(3,2457)	1:303:A:LEU:H	1:303:A:LEU:HG	18	0.11
(3,2457)	1:303:A:LEU:H	1:303:A:LEU:HG	25	0.11
(3,2448)	1:256:A:ASP:H	1:257:A:ILE:HG12	2	0.11
(3,2448)	1:256:A:ASP:H	1:257:A:ILE:HG12	20	0.11
(3,2435)	1:239:A:TRP:HA	1:239:A:TRP:HE1	1	0.11
(3,2435)	1:239:A:TRP:HA	1:239:A:TRP:HE1	15	0.11
(3,2434)	1:253:A:THR:HG21	1:254:A:VAL:H	19	0.11
(3,2434)	1:253:A:THR:HG22	1:254:A:VAL:H	19	0.11
(3,2434)	1:253:A:THR:HG23	1:254:A:VAL:H	19	0.11
(3,2434)	1:253:A:THR:HG21	1:254:A:VAL:H	23	0.11
(3,2434)	1:253:A:THR:HG22	1:254:A:VAL:H	23	0.11
(3,2434)	1:253:A:THR:HG23	1:254:A:VAL:H	23	0.11
(3,2430)	1:257:A:ILE:H	1:258:A:GLN:HB3	25	0.11
(3,2414)	1:268:A:SER:H	1:274:A:ILE:HB	16	0.11
(3,2414)	1:268:A:SER:H	1:274:A:ILE:HB	30	0.11
(3,2402)	1:302:A:GLU:H	1:300:A:GLU:HA	29	0.11
(3,2401)	1:253:A:THR:H	1:292:A:VAL:H	11	0.11
(3,2401)	1:253:A:THR:H	1:292:A:VAL:H	21	0.11
(3,2401)	1:253:A:THR:H	1:292:A:VAL:H	23	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,2401)	1:253:A:THR:H	1:292:A:VAL:H	29	0.11
(3,2357)	1:262:A:GLY:H	1:260:A:LEU:HB2	6	0.11
(3,2357)	1:262:A:GLY:H	1:260:A:LEU:HB2	18	0.11
(3,2357)	1:262:A:GLY:H	1:260:A:LEU:HB2	23	0.11
(3,2357)	1:262:A:GLY:H	1:260:A:LEU:HB2	30	0.11
(3,2353)	1:268:A:SER:H	1:274:A:ILE:HG21	25	0.11
(3,2353)	1:268:A:SER:H	1:274:A:ILE:HG22	25	0.11
(3,2353)	1:268:A:SER:H	1:274:A:ILE:HG23	25	0.11
(3,2336)	1:295:A:LEU:H	1:300:A:GLU:HB2	13	0.11
(3,2303)	1:238:A:LYS:H	1:239:A:TRP:HA	5	0.11
(3,2303)	1:238:A:LYS:H	1:239:A:TRP:HA	14	0.11
(3,2285)	1:271:A:TYR:H	1:270:A:ILE:HG13	2	0.11
(3,2284)	1:281:A:LYS:HD3	1:281:A:LYS:H	26	0.11
(3,2277)	1:269:A:GLN:H	1:270:A:ILE:HG21	10	0.11
(3,2277)	1:269:A:GLN:H	1:270:A:ILE:HG22	10	0.11
(3,2277)	1:269:A:GLN:H	1:270:A:ILE:HG23	10	0.11
(3,2277)	1:269:A:GLN:H	1:270:A:ILE:HG21	15	0.11
(3,2277)	1:269:A:GLN:H	1:270:A:ILE:HG22	15	0.11
(3,2277)	1:269:A:GLN:H	1:270:A:ILE:HG23	15	0.11
(3,2277)	1:269:A:GLN:H	1:270:A:ILE:HG21	23	0.11
(3,2277)	1:269:A:GLN:H	1:270:A:ILE:HG22	23	0.11
(3,2277)	1:269:A:GLN:H	1:270:A:ILE:HG23	23	0.11
(3,2277)	1:269:A:GLN:H	1:270:A:ILE:HG21	25	0.11
(3,2277)	1:269:A:GLN:H	1:270:A:ILE:HG22	25	0.11
(3,2277)	1:269:A:GLN:H	1:270:A:ILE:HG23	25	0.11
(3,2273)	1:254:A:VAL:H	1:255:A:ASN:HA	12	0.11
(3,2273)	1:254:A:VAL:H	1:255:A:ASN:HA	14	0.11
(3,2268)	1:274:A:ILE:HG13	1:271:A:TYR:H	16	0.11
(3,2241)	1:258:A:GLN:HG2	1:257:A:ILE:H	26	0.11
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG21	30	0.11
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG22	30	0.11
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG23	30	0.11
(3,2213)	1:266:A:TRP:H	1:276:A:VAL:HG21	17	0.11
(3,2213)	1:266:A:TRP:H	1:276:A:VAL:HG22	17	0.11
(3,2213)	1:266:A:TRP:H	1:276:A:VAL:HG23	17	0.11
(3,2213)	1:266:A:TRP:H	1:276:A:VAL:HG21	30	0.11
(3,2213)	1:266:A:TRP:H	1:276:A:VAL:HG22	30	0.11
(3,2213)	1:266:A:TRP:H	1:276:A:VAL:HG23	30	0.11
(3,2206)	1:274:A:ILE:H	1:272:A:PRO:HD3	11	0.11
(3,2206)	1:274:A:ILE:H	1:272:A:PRO:HD3	12	0.11
(3,2206)	1:274:A:ILE:H	1:272:A:PRO:HD3	17	0.11
(3,2206)	1:274:A:ILE:H	1:272:A:PRO:HD3	26	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,2206)	1:274:A:ILE:H	1:272:A:PRO:HD3	29	0.11
(3,2185)	1:291:A:GLU:H	1:289:A:LEU:HB3	17	0.11
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD11	14	0.11
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD12	14	0.11
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD13	14	0.11
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD11	24	0.11
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD12	24	0.11
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD13	24	0.11
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD11	25	0.11
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD12	25	0.11
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD13	25	0.11
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD11	27	0.11
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD12	27	0.11
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD13	27	0.11
(3,2174)	1:304:A:ALA:H	1:302:A:GLU:HB2	8	0.11
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	16	0.11
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	16	0.11
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	16	0.11
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG11	22	0.11
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG12	22	0.11
(3,2156)	1:291:A:GLU:H	1:254:A:VAL:HG13	22	0.11
(3,2150)	1:310:A:LEU:H	1:308:A:GLU:HG3	1	0.11
(3,2150)	1:310:A:LEU:H	1:308:A:GLU:HG3	11	0.11
(3,2150)	1:310:A:LEU:H	1:308:A:GLU:HG3	29	0.11
(3,2141)	1:299:A:ALA:H	1:300:A:GLU:HB2	29	0.11
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD11	7	0.11
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD12	7	0.11
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD13	7	0.11
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD11	11	0.11
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD12	11	0.11
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD13	11	0.11
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD11	15	0.11
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD12	15	0.11
(3,2085)	1:298:A:GLU:H	1:301:A:LEU:HD13	15	0.11
(3,2080)	1:299:A:ALA:H	1:300:A:GLU:HG3	17	0.11
(3,2061)	1:273:A:GLY:H	1:274:A:ILE:HG13	5	0.11
(3,2058)	1:254:A:VAL:H	1:289:A:LEU:HB3	18	0.11
(3,2052)	1:255:A:ASN:HD22	1:289:A:LEU:HB2	9	0.11
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG21	26	0.11
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG22	26	0.11
(3,2046)	1:255:A:ASN:HD22	1:290:A:THR:HG23	26	0.11
(3,2008)	1:292:A:VAL:H	1:253:A:THR:HG21	27	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,2008)	1:292:A:VAL:H	1:253:A:THR:HG22	27	0.11
(3,2008)	1:292:A:VAL:H	1:253:A:THR:HG23	27	0.11
(3,2002)	1:284:A:ARG:H	1:283:A:LEU:HD21	11	0.11
(3,2002)	1:284:A:ARG:H	1:283:A:LEU:HD22	11	0.11
(3,2002)	1:284:A:ARG:H	1:283:A:LEU:HD23	11	0.11
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	11	0.11
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	29	0.11
(3,1916)	1:301:A:LEU:HD11	1:301:A:LEU:H	8	0.11
(3,1916)	1:301:A:LEU:HD12	1:301:A:LEU:H	8	0.11
(3,1916)	1:301:A:LEU:HD13	1:301:A:LEU:H	8	0.11
(3,1916)	1:301:A:LEU:HD11	1:301:A:LEU:H	11	0.11
(3,1916)	1:301:A:LEU:HD12	1:301:A:LEU:H	11	0.11
(3,1916)	1:301:A:LEU:HD13	1:301:A:LEU:H	11	0.11
(3,1907)	1:271:A:TYR:H	1:272:A:PRO:HB3	10	0.11
(3,1907)	1:271:A:TYR:H	1:272:A:PRO:HB3	24	0.11
(3,1885)	1:281:A:LYS:H	1:281:A:LYS:HG2	8	0.11
(3,1829)	1:276:A:VAL:HG21	1:283:A:LEU:H	1	0.11
(3,1829)	1:276:A:VAL:HG22	1:283:A:LEU:H	1	0.11
(3,1829)	1:276:A:VAL:HG23	1:283:A:LEU:H	1	0.11
(3,1764)	1:270:A:ILE:HD11	1:271:A:TYR:HD1	17	0.11
(3,1764)	1:270:A:ILE:HD11	1:271:A:TYR:HD2	17	0.11
(3,1764)	1:270:A:ILE:HD12	1:271:A:TYR:HD1	17	0.11
(3,1764)	1:270:A:ILE:HD12	1:271:A:TYR:HD2	17	0.11
(3,1764)	1:270:A:ILE:HD13	1:271:A:TYR:HD1	17	0.11
(3,1764)	1:270:A:ILE:HD13	1:271:A:TYR:HD2	17	0.11
(3,1764)	1:270:A:ILE:HD11	1:271:A:TYR:HD1	24	0.11
(3,1764)	1:270:A:ILE:HD11	1:271:A:TYR:HD2	24	0.11
(3,1764)	1:270:A:ILE:HD12	1:271:A:TYR:HD1	24	0.11
(3,1764)	1:270:A:ILE:HD12	1:271:A:TYR:HD2	24	0.11
(3,1764)	1:270:A:ILE:HD13	1:271:A:TYR:HD1	24	0.11
(3,1764)	1:270:A:ILE:HD13	1:271:A:TYR:HD2	24	0.11
(3,1759)	1:264:A:LEU:HG	1:306:A:ASN:HB2	6	0.11
(3,1759)	1:264:A:LEU:HG	1:306:A:ASN:HB2	15	0.11
(3,1755)	1:264:A:LEU:HG	1:268:A:SER:H	10	0.11
(3,1755)	1:264:A:LEU:HG	1:268:A:SER:H	18	0.11
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	2	0.11
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	2	0.11
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	2	0.11
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	7	0.11
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	7	0.11
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	7	0.11
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	10	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	10	0.11
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	10	0.11
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	13	0.11
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	13	0.11
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	13	0.11
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	16	0.11
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	16	0.11
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	16	0.11
(3,1696)	1:245:A:VAL:HA	1:310:A:LEU:HD21	14	0.11
(3,1696)	1:245:A:VAL:HA	1:310:A:LEU:HD22	14	0.11
(3,1696)	1:245:A:VAL:HA	1:310:A:LEU:HD23	14	0.11
(3,1660)	1:240:A:THR:HG21	1:315:A:HIS:HA	1	0.11
(3,1660)	1:240:A:THR:HG22	1:315:A:HIS:HA	1	0.11
(3,1660)	1:240:A:THR:HG23	1:315:A:HIS:HA	1	0.11
(3,1658)	1:240:A:THR:HB	1:239:A:TRP:HA	2	0.11
(3,1658)	1:240:A:THR:HB	1:239:A:TRP:HA	25	0.11
(3,1640)	1:319:A:LEU:HD11	1:318:A:TYR:HA	4	0.11
(3,1640)	1:319:A:LEU:HD12	1:318:A:TYR:HA	4	0.11
(3,1640)	1:319:A:LEU:HD13	1:318:A:TYR:HA	4	0.11
(3,1638)	1:319:A:LEU:HD21	1:318:A:TYR:HB3	18	0.11
(3,1638)	1:319:A:LEU:HD22	1:318:A:TYR:HB3	18	0.11
(3,1638)	1:319:A:LEU:HD23	1:318:A:TYR:HB3	18	0.11
(3,1524)	1:282:A:LEU:HD21	1:279:A:LEU:HD21	20	0.11
(3,1524)	1:282:A:LEU:HD21	1:279:A:LEU:HD22	20	0.11
(3,1524)	1:282:A:LEU:HD21	1:279:A:LEU:HD23	20	0.11
(3,1524)	1:282:A:LEU:HD22	1:279:A:LEU:HD21	20	0.11
(3,1524)	1:282:A:LEU:HD22	1:279:A:LEU:HD22	20	0.11
(3,1524)	1:282:A:LEU:HD22	1:279:A:LEU:HD23	20	0.11
(3,1524)	1:282:A:LEU:HD23	1:279:A:LEU:HD21	20	0.11
(3,1524)	1:282:A:LEU:HD23	1:279:A:LEU:HD22	20	0.11
(3,1524)	1:282:A:LEU:HD23	1:279:A:LEU:HD23	20	0.11
(3,1518)	1:295:A:LEU:HD11	1:282:A:LEU:HD11	30	0.11
(3,1518)	1:295:A:LEU:HD11	1:282:A:LEU:HD12	30	0.11
(3,1518)	1:295:A:LEU:HD11	1:282:A:LEU:HD13	30	0.11
(3,1518)	1:295:A:LEU:HD12	1:282:A:LEU:HD11	30	0.11
(3,1518)	1:295:A:LEU:HD12	1:282:A:LEU:HD12	30	0.11
(3,1518)	1:295:A:LEU:HD12	1:282:A:LEU:HD13	30	0.11
(3,1518)	1:295:A:LEU:HD13	1:282:A:LEU:HD11	30	0.11
(3,1518)	1:295:A:LEU:HD13	1:282:A:LEU:HD12	30	0.11
(3,1518)	1:295:A:LEU:HD13	1:282:A:LEU:HD13	30	0.11
(3,1506)	1:296:A:THR:HG21	1:301:A:LEU:H	16	0.11
(3,1506)	1:296:A:THR:HG22	1:301:A:LEU:H	16	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1506)	1:296:A:THR:HG23	1:301:A:LEU:H	16	0.11
(3,1496)	1:295:A:LEU:HD21	1:250:A:ASP:HA	13	0.11
(3,1496)	1:295:A:LEU:HD22	1:250:A:ASP:HA	13	0.11
(3,1496)	1:295:A:LEU:HD23	1:250:A:ASP:HA	13	0.11
(3,1496)	1:295:A:LEU:HD21	1:250:A:ASP:HA	20	0.11
(3,1496)	1:295:A:LEU:HD22	1:250:A:ASP:HA	20	0.11
(3,1496)	1:295:A:LEU:HD23	1:250:A:ASP:HA	20	0.11
(3,1496)	1:295:A:LEU:HD21	1:250:A:ASP:HA	27	0.11
(3,1496)	1:295:A:LEU:HD22	1:250:A:ASP:HA	27	0.11
(3,1496)	1:295:A:LEU:HD23	1:250:A:ASP:HA	27	0.11
(3,1482)	1:257:A:ILE:HD11	1:254:A:VAL:HB	2	0.11
(3,1482)	1:257:A:ILE:HD12	1:254:A:VAL:HB	2	0.11
(3,1482)	1:257:A:ILE:HD13	1:254:A:VAL:HB	2	0.11
(3,1470)	1:293:A:ILE:HG21	1:257:A:ILE:HB	17	0.11
(3,1470)	1:293:A:ILE:HG22	1:257:A:ILE:HB	17	0.11
(3,1470)	1:293:A:ILE:HG23	1:257:A:ILE:HB	17	0.11
(3,1468)	1:293:A:ILE:HG21	1:286:A:THR:HB	9	0.11
(3,1468)	1:293:A:ILE:HG22	1:286:A:THR:HB	9	0.11
(3,1468)	1:293:A:ILE:HG23	1:286:A:THR:HB	9	0.11
(3,1462)	1:293:A:ILE:HD11	1:283:A:LEU:HB3	6	0.11
(3,1462)	1:293:A:ILE:HD12	1:283:A:LEU:HB3	6	0.11
(3,1462)	1:293:A:ILE:HD13	1:283:A:LEU:HB3	6	0.11
(3,1441)	1:293:A:ILE:HG12	1:254:A:VAL:HB	10	0.11
(3,1441)	1:293:A:ILE:HG12	1:254:A:VAL:HB	15	0.11
(3,1426)	1:293:A:ILE:HD11	1:292:A:VAL:H	7	0.11
(3,1426)	1:293:A:ILE:HD12	1:292:A:VAL:H	7	0.11
(3,1426)	1:293:A:ILE:HD13	1:292:A:VAL:H	7	0.11
(3,1426)	1:293:A:ILE:HD11	1:292:A:VAL:H	16	0.11
(3,1426)	1:293:A:ILE:HD12	1:292:A:VAL:H	16	0.11
(3,1426)	1:293:A:ILE:HD13	1:292:A:VAL:H	16	0.11
(3,1391)	1:287:A:LYS:HB3	1:254:A:VAL:HG21	23	0.11
(3,1391)	1:287:A:LYS:HB3	1:254:A:VAL:HG22	23	0.11
(3,1391)	1:287:A:LYS:HB3	1:254:A:VAL:HG23	23	0.11
(3,1373)	1:279:A:LEU:HD21	1:306:A:ASN:HB3	29	0.11
(3,1373)	1:279:A:LEU:HD22	1:306:A:ASN:HB3	29	0.11
(3,1373)	1:279:A:LEU:HD23	1:306:A:ASN:HB3	29	0.11
(3,1351)	1:277:A:ARG:HG2	1:276:A:VAL:H	13	0.11
(3,1346)	1:276:A:VAL:HG21	1:264:A:LEU:HB3	7	0.11
(3,1346)	1:276:A:VAL:HG22	1:264:A:LEU:HB3	7	0.11
(3,1346)	1:276:A:VAL:HG23	1:264:A:LEU:HB3	7	0.11
(3,1313)	1:274:A:ILE:HG12	1:306:A:ASN:HA	25	0.11
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG21	15	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG22	15	0.11
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG23	15	0.11
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG21	22	0.11
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG22	22	0.11
(3,1228)	1:265:A:ASN:HB3	1:261:A:VAL:HG23	22	0.11
(3,1215)	1:276:A:VAL:HG11	1:279:A:LEU:HB2	18	0.11
(3,1215)	1:276:A:VAL:HG12	1:279:A:LEU:HB2	18	0.11
(3,1215)	1:276:A:VAL:HG13	1:279:A:LEU:HB2	18	0.11
(3,1215)	1:276:A:VAL:HG11	1:279:A:LEU:HB2	23	0.11
(3,1215)	1:276:A:VAL:HG12	1:279:A:LEU:HB2	23	0.11
(3,1215)	1:276:A:VAL:HG13	1:279:A:LEU:HB2	23	0.11
(3,1211)	1:264:A:LEU:HG	1:265:A:ASN:H	7	0.11
(3,1211)	1:264:A:LEU:HG	1:265:A:ASN:H	8	0.11
(3,1211)	1:264:A:LEU:HG	1:265:A:ASN:H	21	0.11
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	17	0.11
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	17	0.11
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	17	0.11
(3,1187)	1:265:A:ASN:HB2	1:262:A:GLY:HA3	27	0.11
(3,1185)	1:262:A:GLY:HA3	1:265:A:ASN:HD22	2	0.11
(3,1185)	1:262:A:GLY:HA3	1:265:A:ASN:HD22	7	0.11
(3,1185)	1:262:A:GLY:HA3	1:265:A:ASN:HD22	20	0.11
(3,1156)	1:259:A:LYS:HE2	1:259:A:LYS:HB3	6	0.11
(3,1136)	1:260:A:LEU:HB2	1:257:A:ILE:HG21	12	0.11
(3,1136)	1:260:A:LEU:HB2	1:257:A:ILE:HG22	12	0.11
(3,1136)	1:260:A:LEU:HB2	1:257:A:ILE:HG23	12	0.11
(3,1136)	1:260:A:LEU:HB2	1:257:A:ILE:HG21	15	0.11
(3,1136)	1:260:A:LEU:HB2	1:257:A:ILE:HG22	15	0.11
(3,1136)	1:260:A:LEU:HB2	1:257:A:ILE:HG23	15	0.11
(3,1136)	1:260:A:LEU:HB2	1:257:A:ILE:HG21	22	0.11
(3,1136)	1:260:A:LEU:HB2	1:257:A:ILE:HG22	22	0.11
(3,1136)	1:260:A:LEU:HB2	1:257:A:ILE:HG23	22	0.11
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG21	9	0.11
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG22	9	0.11
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG23	9	0.11
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG21	19	0.11
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG22	19	0.11
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG23	19	0.11
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG21	28	0.11
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG22	28	0.11
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG23	28	0.11
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG21	29	0.11
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG22	29	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG23	29	0.11
(3,1134)	1:254:A:VAL:HA	1:257:A:ILE:HG21	25	0.11
(3,1134)	1:254:A:VAL:HA	1:257:A:ILE:HG22	25	0.11
(3,1134)	1:254:A:VAL:HA	1:257:A:ILE:HG23	25	0.11
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG21	10	0.11
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG22	10	0.11
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG23	10	0.11
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG21	21	0.11
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG22	21	0.11
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG23	21	0.11
(3,1096)	1:292:A:VAL:HG11	1:291:A:GLU:H	6	0.11
(3,1096)	1:292:A:VAL:HG12	1:291:A:GLU:H	6	0.11
(3,1096)	1:292:A:VAL:HG13	1:291:A:GLU:H	6	0.11
(3,1096)	1:292:A:VAL:HG11	1:291:A:GLU:H	12	0.11
(3,1096)	1:292:A:VAL:HG12	1:291:A:GLU:H	12	0.11
(3,1096)	1:292:A:VAL:HG13	1:291:A:GLU:H	12	0.11
(3,1052)	1:240:A:THR:HB	1:241:A:VAL:HB	13	0.11
(3,1052)	1:240:A:THR:HB	1:241:A:VAL:HB	24	0.11
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	14	0.11
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	14	0.11
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	14	0.11
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	20	0.11
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	20	0.11
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	20	0.11
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	22	0.11
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	22	0.11
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	22	0.11
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	30	0.11
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	30	0.11
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	30	0.11
(3,986)	1:304:A:ALA:H	1:302:A:GLU:HG2	12	0.11
(3,986)	1:304:A:ALA:H	1:302:A:GLU:HG2	26	0.11
(3,895)	1:287:A:LYS:HE2	1:287:A:LYS:HA	3	0.11
(3,875)	1:283:A:LEU:HD11	1:258:A:GLN:HB3	2	0.11
(3,875)	1:283:A:LEU:HD12	1:258:A:GLN:HB3	2	0.11
(3,875)	1:283:A:LEU:HD13	1:258:A:GLN:HB3	2	0.11
(3,867)	1:283:A:LEU:HD21	1:258:A:GLN:HB3	23	0.11
(3,867)	1:283:A:LEU:HD22	1:258:A:GLN:HB3	23	0.11
(3,867)	1:283:A:LEU:HD23	1:258:A:GLN:HB3	23	0.11
(3,866)	1:283:A:LEU:HD21	1:261:A:VAL:HB	25	0.11
(3,866)	1:283:A:LEU:HD22	1:261:A:VAL:HB	25	0.11
(3,866)	1:283:A:LEU:HD23	1:261:A:VAL:HB	25	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,866)	1:283:A:LEU:HD21	1:261:A:VAL:HB	27	0.11
(3,866)	1:283:A:LEU:HD22	1:261:A:VAL:HB	27	0.11
(3,866)	1:283:A:LEU:HD23	1:261:A:VAL:HB	27	0.11
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD11	22	0.11
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD12	22	0.11
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD13	22	0.11
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD11	27	0.11
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD12	27	0.11
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD13	27	0.11
(3,823)	1:291:A:GLU:HB3	1:254:A:VAL:HG11	5	0.11
(3,823)	1:291:A:GLU:HB3	1:254:A:VAL:HG12	5	0.11
(3,823)	1:291:A:GLU:HB3	1:254:A:VAL:HG13	5	0.11
(3,823)	1:291:A:GLU:HB3	1:254:A:VAL:HG11	10	0.11
(3,823)	1:291:A:GLU:HB3	1:254:A:VAL:HG12	10	0.11
(3,823)	1:291:A:GLU:HB3	1:254:A:VAL:HG13	10	0.11
(3,814)	1:275:A:LYS:HG2	1:275:A:LYS:HE3	10	0.11
(3,814)	1:275:A:LYS:HG2	1:275:A:LYS:HE3	21	0.11
(3,741)	1:238:A:LYS:HB3	1:238:A:LYS:HD3	18	0.11
(3,668)	1:281:A:LYS:HE2	1:281:A:LYS:HB2	9	0.11
(3,335)	1:311:A:LYS:HG2	1:311:A:LYS:H	12	0.11
(3,231)	1:276:A:VAL:H	1:275:A:LYS:HE3	5	0.11
(3,230)	1:275:A:LYS:HE3	1:275:A:LYS:H	23	0.11
(3,85)	1:244:A:ILE:HD11	1:270:A:ILE:HA	1	0.11
(3,85)	1:244:A:ILE:HD12	1:270:A:ILE:HA	1	0.11
(3,85)	1:244:A:ILE:HD13	1:270:A:ILE:HA	1	0.11
(3,85)	1:244:A:ILE:HD11	1:270:A:ILE:HA	15	0.11
(3,85)	1:244:A:ILE:HD12	1:270:A:ILE:HA	15	0.11
(3,85)	1:244:A:ILE:HD13	1:270:A:ILE:HA	15	0.11
(3,85)	1:244:A:ILE:HD11	1:270:A:ILE:HA	28	0.11
(3,85)	1:244:A:ILE:HD12	1:270:A:ILE:HA	28	0.11
(3,85)	1:244:A:ILE:HD13	1:270:A:ILE:HA	28	0.11
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	2	0.11
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	2	0.11
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	2	0.11
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	30	0.11
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	30	0.11
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	30	0.11
(3,80)	1:270:A:ILE:HD11	1:314:A:VAL:HG11	23	0.11
(3,80)	1:270:A:ILE:HD11	1:314:A:VAL:HG12	23	0.11
(3,80)	1:270:A:ILE:HD11	1:314:A:VAL:HG13	23	0.11
(3,80)	1:270:A:ILE:HD12	1:314:A:VAL:HG11	23	0.11
(3,80)	1:270:A:ILE:HD12	1:314:A:VAL:HG12	23	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,80)	1:270:A:ILE:HD12	1:314:A:VAL:HG13	23	0.11
(3,80)	1:270:A:ILE:HD13	1:314:A:VAL:HG11	23	0.11
(3,80)	1:270:A:ILE:HD13	1:314:A:VAL:HG12	23	0.11
(3,80)	1:270:A:ILE:HD13	1:314:A:VAL:HG13	23	0.11
(3,79)	1:270:A:ILE:HD11	1:314:A:VAL:HG21	4	0.11
(3,79)	1:270:A:ILE:HD11	1:314:A:VAL:HG22	4	0.11
(3,79)	1:270:A:ILE:HD11	1:314:A:VAL:HG23	4	0.11
(3,79)	1:270:A:ILE:HD12	1:314:A:VAL:HG21	4	0.11
(3,79)	1:270:A:ILE:HD12	1:314:A:VAL:HG22	4	0.11
(3,79)	1:270:A:ILE:HD12	1:314:A:VAL:HG23	4	0.11
(3,79)	1:270:A:ILE:HD13	1:314:A:VAL:HG21	4	0.11
(3,79)	1:270:A:ILE:HD13	1:314:A:VAL:HG22	4	0.11
(3,79)	1:270:A:ILE:HD13	1:314:A:VAL:HG23	4	0.11
(3,78)	1:279:A:LEU:HD11	1:306:A:ASN:HD22	12	0.11
(3,78)	1:279:A:LEU:HD12	1:306:A:ASN:HD22	12	0.11
(3,78)	1:279:A:LEU:HD13	1:306:A:ASN:HD22	12	0.11
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD21	7	0.11
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD22	7	0.11
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD23	7	0.11
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD21	11	0.11
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD22	11	0.11
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD23	11	0.11
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD21	12	0.11
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD22	12	0.11
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD23	12	0.11
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD21	18	0.11
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD22	18	0.11
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD23	18	0.11
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD21	22	0.11
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD22	22	0.11
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD23	22	0.11
(3,74)	1:283:A:LEU:H	1:280:A:SER:HB2	10	0.11
(3,74)	1:283:A:LEU:H	1:280:A:SER:HB2	14	0.11
(3,74)	1:283:A:LEU:H	1:280:A:SER:HB2	30	0.11
(3,72)	1:290:A:THR:H	1:253:A:THR:HA	3	0.11
(3,71)	1:290:A:THR:H	1:255:A:ASN:HB3	20	0.11
(3,47)	1:306:A:ASN:H	1:310:A:LEU:HG	1	0.11
(3,47)	1:306:A:ASN:H	1:310:A:LEU:HG	8	0.11
(3,36)	1:308:A:GLU:H	1:306:A:ASN:HB3	12	0.11
(3,32)	1:309:A:ILE:H	1:306:A:ASN:HB3	18	0.11
(3,29)	1:310:A:LEU:H	1:271:A:TYR:HE1	6	0.11
(3,29)	1:310:A:LEU:H	1:271:A:TYR:HE2	6	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,29)	1:310:A:LEU:H	1:271:A:TYR:HE1	9	0.11
(3,29)	1:310:A:LEU:H	1:271:A:TYR:HE2	9	0.11
(3,28)	1:310:A:LEU:HD21	1:271:A:TYR:HB2	16	0.11
(3,28)	1:310:A:LEU:HD22	1:271:A:TYR:HB2	16	0.11
(3,28)	1:310:A:LEU:HD23	1:271:A:TYR:HB2	16	0.11
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE1	8	0.11
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE2	8	0.11
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE1	22	0.11
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE2	22	0.11
(3,19)	1:314:A:VAL:HG21	1:312:A:GLU:HB2	18	0.11
(3,19)	1:314:A:VAL:HG22	1:312:A:GLU:HB2	18	0.11
(3,19)	1:314:A:VAL:HG23	1:312:A:GLU:HB2	18	0.11
(3,19)	1:314:A:VAL:HG21	1:312:A:GLU:HB2	22	0.11
(3,19)	1:314:A:VAL:HG22	1:312:A:GLU:HB2	22	0.11
(3,19)	1:314:A:VAL:HG23	1:312:A:GLU:HB2	22	0.11
(3,7)	1:314:A:VAL:H	1:241:A:VAL:HG21	30	0.11
(3,7)	1:314:A:VAL:H	1:241:A:VAL:HG22	30	0.11
(3,7)	1:314:A:VAL:H	1:241:A:VAL:HG23	30	0.11
(2,42)	1:306:A:ASN:N	1:302:A:GLU:O	23	0.11
(2,35)	1:269:A:GLN:N	1:265:A:ASN:O	21	0.11
(2,35)	1:269:A:GLN:N	1:265:A:ASN:O	28	0.11
(2,35)	1:269:A:GLN:N	1:265:A:ASN:O	30	0.11
(2,34)	1:268:A:SER:N	1:264:A:LEU:O	9	0.11
(2,22)	1:309:A:ILE:H	1:305:A:GLU:O	3	0.11
(2,21)	1:308:A:GLU:H	1:304:A:ALA:O	2	0.11
(2,21)	1:308:A:GLU:H	1:304:A:ALA:O	7	0.11
(2,21)	1:308:A:GLU:H	1:304:A:ALA:O	12	0.11
(2,15)	1:302:A:GLU:H	1:298:A:GLU:O	4	0.11
(2,15)	1:302:A:GLU:H	1:298:A:GLU:O	6	0.11
(2,15)	1:302:A:GLU:H	1:298:A:GLU:O	9	0.11
(2,15)	1:302:A:GLU:H	1:298:A:GLU:O	11	0.11
(2,15)	1:302:A:GLU:H	1:298:A:GLU:O	21	0.11
(2,15)	1:302:A:GLU:H	1:298:A:GLU:O	26	0.11
(2,13)	1:282:A:LEU:H	1:278:A:GLN:O	10	0.11
(2,13)	1:282:A:LEU:H	1:278:A:GLN:O	12	0.11
(2,13)	1:282:A:LEU:H	1:278:A:GLN:O	17	0.11
(2,13)	1:282:A:LEU:H	1:278:A:GLN:O	22	0.11
(2,11)	1:268:A:SER:H	1:264:A:LEU:O	25	0.11
(2,6)	1:263:A:LYS:H	1:259:A:LYS:O	13	0.11
(2,5)	1:262:A:GLY:H	1:258:A:GLN:O	27	0.11
(2,2)	1:259:A:LYS:H	1:255:A:ASN:O	30	0.11
(1,42)	1:306:A:ASN:N	1:302:A:GLU:O	23	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,35)	1:269:A:GLN:N	1:265:A:ASN:O	21	0.11
(1,35)	1:269:A:GLN:N	1:265:A:ASN:O	28	0.11
(1,35)	1:269:A:GLN:N	1:265:A:ASN:O	30	0.11
(1,34)	1:268:A:SER:N	1:264:A:LEU:O	9	0.11
(1,22)	1:309:A:ILE:H	1:305:A:GLU:O	3	0.11
(1,21)	1:308:A:GLU:H	1:304:A:ALA:O	2	0.11
(1,21)	1:308:A:GLU:H	1:304:A:ALA:O	7	0.11
(1,21)	1:308:A:GLU:H	1:304:A:ALA:O	12	0.11
(1,15)	1:302:A:GLU:H	1:298:A:GLU:O	4	0.11
(1,15)	1:302:A:GLU:H	1:298:A:GLU:O	6	0.11
(1,15)	1:302:A:GLU:H	1:298:A:GLU:O	9	0.11
(1,15)	1:302:A:GLU:H	1:298:A:GLU:O	11	0.11
(1,15)	1:302:A:GLU:H	1:298:A:GLU:O	21	0.11
(1,15)	1:302:A:GLU:H	1:298:A:GLU:O	26	0.11
(1,13)	1:282:A:LEU:H	1:278:A:GLN:O	10	0.11
(1,13)	1:282:A:LEU:H	1:278:A:GLN:O	12	0.11
(1,13)	1:282:A:LEU:H	1:278:A:GLN:O	17	0.11
(1,13)	1:282:A:LEU:H	1:278:A:GLN:O	22	0.11
(1,11)	1:268:A:SER:H	1:264:A:LEU:O	25	0.11
(1,6)	1:263:A:LYS:H	1:259:A:LYS:O	13	0.11
(1,5)	1:262:A:GLY:H	1:258:A:GLN:O	27	0.11
(1,2)	1:259:A:LYS:H	1:255:A:ASN:O	30	0.11
(3,2613)	1:255:A:ASN:HD22	1:289:A:LEU:HG	13	0.1
(3,2498)	1:287:A:LYS:H	1:287:A:LYS:HD2	1	0.1
(3,2474)	1:256:A:ASP:H	1:258:A:GLN:HB3	30	0.1
(3,2457)	1:303:A:LEU:H	1:303:A:LEU:HG	5	0.1
(3,2457)	1:303:A:LEU:H	1:303:A:LEU:HG	8	0.1
(3,2457)	1:303:A:LEU:H	1:303:A:LEU:HG	29	0.1
(3,2448)	1:256:A:ASP:H	1:257:A:ILE:HG12	6	0.1
(3,2436)	1:291:A:GLU:H	1:291:A:GLU:HG2	24	0.1
(3,2434)	1:253:A:THR:HG21	1:254:A:VAL:H	28	0.1
(3,2434)	1:253:A:THR:HG22	1:254:A:VAL:H	28	0.1
(3,2434)	1:253:A:THR:HG23	1:254:A:VAL:H	28	0.1
(3,2430)	1:257:A:ILE:H	1:258:A:GLN:HB3	27	0.1
(3,2401)	1:253:A:THR:H	1:292:A:VAL:H	16	0.1
(3,2388)	1:255:A:ASN:H	1:289:A:LEU:HB2	12	0.1
(3,2388)	1:255:A:ASN:H	1:289:A:LEU:HB2	22	0.1
(3,2388)	1:255:A:ASN:H	1:289:A:LEU:HB2	27	0.1
(3,2366)	1:300:A:GLU:H	1:301:A:LEU:HA	22	0.1
(3,2336)	1:295:A:LEU:H	1:300:A:GLU:HB2	22	0.1
(3,2303)	1:238:A:LYS:H	1:239:A:TRP:HA	21	0.1
(3,2285)	1:271:A:TYR:H	1:270:A:ILE:HG13	21	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,2273)	1:254:A:VAL:H	1:255:A:ASN:HA	29	0.1
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG21	20	0.1
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG22	20	0.1
(3,2230)	1:265:A:ASN:HD21	1:261:A:VAL:HG23	20	0.1
(3,2206)	1:274:A:ILE:H	1:272:A:PRO:HD3	3	0.1
(3,2206)	1:274:A:ILE:H	1:272:A:PRO:HD3	6	0.1
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD11	8	0.1
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD12	8	0.1
(3,2184)	1:306:A:ASN:H	1:303:A:LEU:HD13	8	0.1
(3,2141)	1:299:A:ALA:H	1:300:A:GLU:HB2	1	0.1
(3,2058)	1:254:A:VAL:H	1:289:A:LEU:HB3	1	0.1
(3,2058)	1:254:A:VAL:H	1:289:A:LEU:HB3	16	0.1
(3,2051)	1:289:A:LEU:H	1:289:A:LEU:HG	19	0.1
(3,1966)	1:266:A:TRP:H	1:276:A:VAL:HG11	29	0.1
(3,1966)	1:266:A:TRP:H	1:276:A:VAL:HG12	29	0.1
(3,1966)	1:266:A:TRP:H	1:276:A:VAL:HG13	29	0.1
(3,1953)	1:265:A:ASN:H	1:263:A:LYS:HB3	10	0.1
(3,1938)	1:251:A:SER:H	1:252:A:TRP:HA	8	0.1
(3,1916)	1:301:A:LEU:HD11	1:301:A:LEU:H	7	0.1
(3,1916)	1:301:A:LEU:HD12	1:301:A:LEU:H	7	0.1
(3,1916)	1:301:A:LEU:HD13	1:301:A:LEU:H	7	0.1
(3,1916)	1:301:A:LEU:HD11	1:301:A:LEU:H	26	0.1
(3,1916)	1:301:A:LEU:HD12	1:301:A:LEU:H	26	0.1
(3,1916)	1:301:A:LEU:HD13	1:301:A:LEU:H	26	0.1
(3,1907)	1:271:A:TYR:H	1:272:A:PRO:HB3	21	0.1
(3,1907)	1:271:A:TYR:H	1:272:A:PRO:HB3	23	0.1
(3,1896)	1:301:A:LEU:HD21	1:301:A:LEU:H	28	0.1
(3,1896)	1:301:A:LEU:HD22	1:301:A:LEU:H	28	0.1
(3,1896)	1:301:A:LEU:HD23	1:301:A:LEU:H	28	0.1
(3,1885)	1:281:A:LYS:H	1:281:A:LYS:HG2	3	0.1
(3,1851)	1:255:A:ASN:HD22	1:258:A:GLN:HB3	20	0.1
(3,1829)	1:276:A:VAL:HG21	1:283:A:LEU:H	10	0.1
(3,1829)	1:276:A:VAL:HG22	1:283:A:LEU:H	10	0.1
(3,1829)	1:276:A:VAL:HG23	1:283:A:LEU:H	10	0.1
(3,1755)	1:264:A:LEU:HG	1:268:A:SER:H	23	0.1
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	3	0.1
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	3	0.1
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	3	0.1
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG21	20	0.1
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG22	20	0.1
(3,1732)	1:258:A:GLN:HB2	1:257:A:ILE:HG23	20	0.1
(3,1658)	1:240:A:THR:HB	1:239:A:TRP:HA	17	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1526)	1:282:A:LEU:HD11	1:280:A:SER:H	8	0.1
(3,1526)	1:282:A:LEU:HD12	1:280:A:SER:H	8	0.1
(3,1526)	1:282:A:LEU:HD13	1:280:A:SER:H	8	0.1
(3,1426)	1:293:A:ILE:HD11	1:292:A:VAL:H	27	0.1
(3,1426)	1:293:A:ILE:HD12	1:292:A:VAL:H	27	0.1
(3,1426)	1:293:A:ILE:HD13	1:292:A:VAL:H	27	0.1
(3,1391)	1:287:A:LYS:HB3	1:254:A:VAL:HG21	7	0.1
(3,1391)	1:287:A:LYS:HB3	1:254:A:VAL:HG22	7	0.1
(3,1391)	1:287:A:LYS:HB3	1:254:A:VAL:HG23	7	0.1
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG21	15	0.1
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG22	15	0.1
(3,1390)	1:287:A:LYS:HB2	1:254:A:VAL:HG23	15	0.1
(3,1389)	1:286:A:THR:HG21	1:291:A:GLU:HG3	25	0.1
(3,1389)	1:286:A:THR:HG22	1:291:A:GLU:HG3	25	0.1
(3,1389)	1:286:A:THR:HG23	1:291:A:GLU:HG3	25	0.1
(3,1385)	1:286:A:THR:HG21	1:291:A:GLU:H	22	0.1
(3,1385)	1:286:A:THR:HG22	1:291:A:GLU:H	22	0.1
(3,1385)	1:286:A:THR:HG23	1:291:A:GLU:H	22	0.1
(3,1347)	1:280:A:SER:HA	1:276:A:VAL:HG21	19	0.1
(3,1347)	1:280:A:SER:HA	1:276:A:VAL:HG22	19	0.1
(3,1347)	1:280:A:SER:HA	1:276:A:VAL:HG23	19	0.1
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD21	6	0.1
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD22	6	0.1
(3,1204)	1:265:A:ASN:H	1:264:A:LEU:HD23	6	0.1
(3,1187)	1:265:A:ASN:HB2	1:262:A:GLY:HA3	25	0.1
(3,1185)	1:262:A:GLY:HA3	1:265:A:ASN:HD22	11	0.1
(3,1160)	1:259:A:LYS:HE3	1:259:A:LYS:HG2	24	0.1
(3,1159)	1:259:A:LYS:HG2	1:259:A:LYS:HE2	10	0.1
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG21	6	0.1
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG22	6	0.1
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG23	6	0.1
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG21	10	0.1
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG22	10	0.1
(3,1135)	1:258:A:GLN:HB3	1:257:A:ILE:HG23	10	0.1
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG21	3	0.1
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG22	3	0.1
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG23	3	0.1
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG21	22	0.1
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG22	22	0.1
(3,1132)	1:279:A:LEU:H	1:257:A:ILE:HG23	22	0.1
(3,1028)	1:309:A:ILE:HD11	1:307:A:ARG:H	27	0.1
(3,1028)	1:309:A:ILE:HD12	1:307:A:ARG:H	27	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,1028)	1:309:A:ILE:HD13	1:307:A:ARG:H	27	0.1
(3,986)	1:304:A:ALA:H	1:302:A:GLU:HG2	3	0.1
(3,899)	1:288:A:ALA:HA	1:289:A:LEU:HG	19	0.1
(3,867)	1:283:A:LEU:HD21	1:258:A:GLN:HB3	19	0.1
(3,867)	1:283:A:LEU:HD22	1:258:A:GLN:HB3	19	0.1
(3,867)	1:283:A:LEU:HD23	1:258:A:GLN:HB3	19	0.1
(3,866)	1:283:A:LEU:HD21	1:261:A:VAL:HB	10	0.1
(3,866)	1:283:A:LEU:HD22	1:261:A:VAL:HB	10	0.1
(3,866)	1:283:A:LEU:HD23	1:261:A:VAL:HB	10	0.1
(3,866)	1:283:A:LEU:HD21	1:261:A:VAL:HB	16	0.1
(3,866)	1:283:A:LEU:HD22	1:261:A:VAL:HB	16	0.1
(3,866)	1:283:A:LEU:HD23	1:261:A:VAL:HB	16	0.1
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD11	2	0.1
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD12	2	0.1
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD13	2	0.1
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD11	5	0.1
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD12	5	0.1
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD13	5	0.1
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD11	6	0.1
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD12	6	0.1
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD13	6	0.1
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD11	12	0.1
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD12	12	0.1
(3,834)	1:255:A:ASN:HA	1:289:A:LEU:HD13	12	0.1
(3,706)	1:287:A:LYS:HE2	1:287:A:LYS:HG3	10	0.1
(3,659)	1:281:A:LYS:HE3	1:281:A:LYS:HB2	7	0.1
(3,319)	1:283:A:LEU:HD11	1:284:A:ARG:H	18	0.1
(3,319)	1:283:A:LEU:HD12	1:284:A:ARG:H	18	0.1
(3,319)	1:283:A:LEU:HD13	1:284:A:ARG:H	18	0.1
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	6	0.1
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	6	0.1
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	6	0.1
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG11	14	0.1
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG12	14	0.1
(3,82)	1:279:A:LEU:H	1:261:A:VAL:HG13	14	0.1
(3,81)	1:262:A:GLY:H	1:260:A:LEU:HG	17	0.1
(3,78)	1:279:A:LEU:HD11	1:306:A:ASN:HD22	28	0.1
(3,78)	1:279:A:LEU:HD12	1:306:A:ASN:HD22	28	0.1
(3,78)	1:279:A:LEU:HD13	1:306:A:ASN:HD22	28	0.1
(3,76)	1:281:A:LYS:H	1:284:A:ARG:HD2	15	0.1
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD21	10	0.1
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD22	10	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,75)	1:282:A:LEU:H	1:295:A:LEU:HD23	10	0.1
(3,72)	1:290:A:THR:H	1:253:A:THR:HA	2	0.1
(3,67)	1:293:A:ILE:HG21	1:252:A:TRP:H	30	0.1
(3,67)	1:293:A:ILE:HG22	1:252:A:TRP:H	30	0.1
(3,67)	1:293:A:ILE:HG23	1:252:A:TRP:H	30	0.1
(3,38)	1:308:A:GLU:HA	1:311:A:LYS:HB2	18	0.1
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE1	2	0.1
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE2	2	0.1
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE1	5	0.1
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE2	5	0.1
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE1	29	0.1
(3,21)	1:313:A:PRO:HG2	1:271:A:TYR:HE2	29	0.1
(3,18)	1:242:A:GLN:H	1:240:A:THR:HG21	5	0.1
(3,18)	1:242:A:GLN:H	1:240:A:THR:HG22	5	0.1
(3,18)	1:242:A:GLN:H	1:240:A:THR:HG23	5	0.1
(3,13)	1:239:A:TRP:HB3	1:238:A:LYS:HB2	30	0.1
(3,4)	1:314:A:VAL:H	1:271:A:TYR:HD1	16	0.1
(3,4)	1:314:A:VAL:H	1:271:A:TYR:HD2	16	0.1
(2,35)	1:269:A:GLN:N	1:265:A:ASN:O	2	0.1
(2,35)	1:269:A:GLN:N	1:265:A:ASN:O	3	0.1
(2,34)	1:268:A:SER:N	1:264:A:LEU:O	3	0.1
(2,34)	1:268:A:SER:N	1:264:A:LEU:O	29	0.1
(2,34)	1:268:A:SER:N	1:264:A:LEU:O	30	0.1
(2,22)	1:309:A:ILE:H	1:305:A:GLU:O	9	0.1
(2,21)	1:308:A:GLU:H	1:304:A:ALA:O	10	0.1
(2,21)	1:308:A:GLU:H	1:304:A:ALA:O	17	0.1
(2,21)	1:308:A:GLU:H	1:304:A:ALA:O	28	0.1
(2,15)	1:302:A:GLU:H	1:298:A:GLU:O	23	0.1
(2,15)	1:302:A:GLU:H	1:298:A:GLU:O	25	0.1
(2,14)	1:301:A:LEU:H	1:297:A:GLU:O	22	0.1
(2,13)	1:282:A:LEU:H	1:278:A:GLN:O	13	0.1
(2,11)	1:268:A:SER:H	1:264:A:LEU:O	16	0.1
(2,5)	1:262:A:GLY:H	1:258:A:GLN:O	21	0.1
(2,4)	1:261:A:VAL:H	1:257:A:ILE:O	6	0.1
(2,1)	1:258:A:GLN:H	1:254:A:VAL:O	1	0.1
(1,35)	1:269:A:GLN:N	1:265:A:ASN:O	2	0.1
(1,35)	1:269:A:GLN:N	1:265:A:ASN:O	3	0.1
(1,34)	1:268:A:SER:N	1:264:A:LEU:O	3	0.1
(1,34)	1:268:A:SER:N	1:264:A:LEU:O	29	0.1
(1,34)	1:268:A:SER:N	1:264:A:LEU:O	30	0.1
(1,22)	1:309:A:ILE:H	1:305:A:GLU:O	9	0.1
(1,21)	1:308:A:GLU:H	1:304:A:ALA:O	10	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,21)	1:308:A:GLU:H	1:304:A:ALA:O	17	0.1
(1,21)	1:308:A:GLU:H	1:304:A:ALA:O	28	0.1
(1,15)	1:302:A:GLU:H	1:298:A:GLU:O	23	0.1
(1,15)	1:302:A:GLU:H	1:298:A:GLU:O	25	0.1
(1,14)	1:301:A:LEU:H	1:297:A:GLU:O	22	0.1
(1,13)	1:282:A:LEU:H	1:278:A:GLN:O	13	0.1
(1,11)	1:268:A:SER:H	1:264:A:LEU:O	16	0.1
(1,5)	1:262:A:GLY:H	1:258:A:GLN:O	21	0.1
(1,4)	1:261:A:VAL:H	1:257:A:ILE:O	6	0.1
(1,1)	1:258:A:GLN:H	1:254:A:VAL:O	1	0.1

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

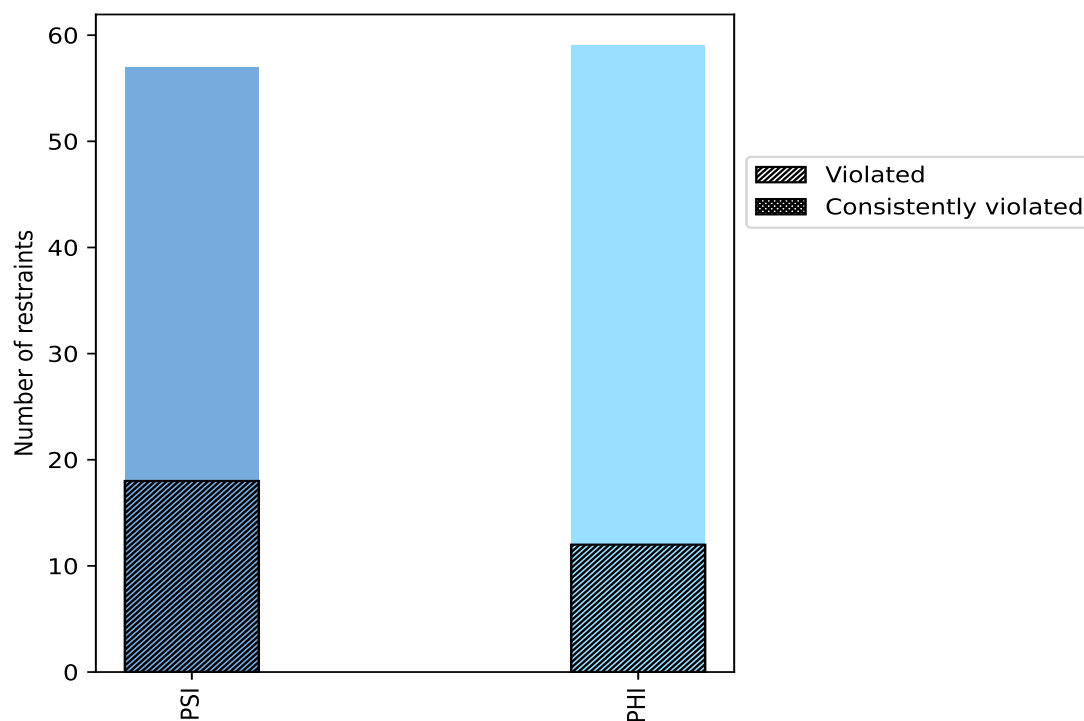
10.1 Summary of dihedral-angle violations [i](#)

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

Angle type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
PSI	57	49.1	18	31.6	15.5	0	0.0	0.0
PHI	59	50.9	12	20.3	10.3	0	0.0	0.0
Total	116	100.0	30	25.9	25.9	0	0.0	0.0

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

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



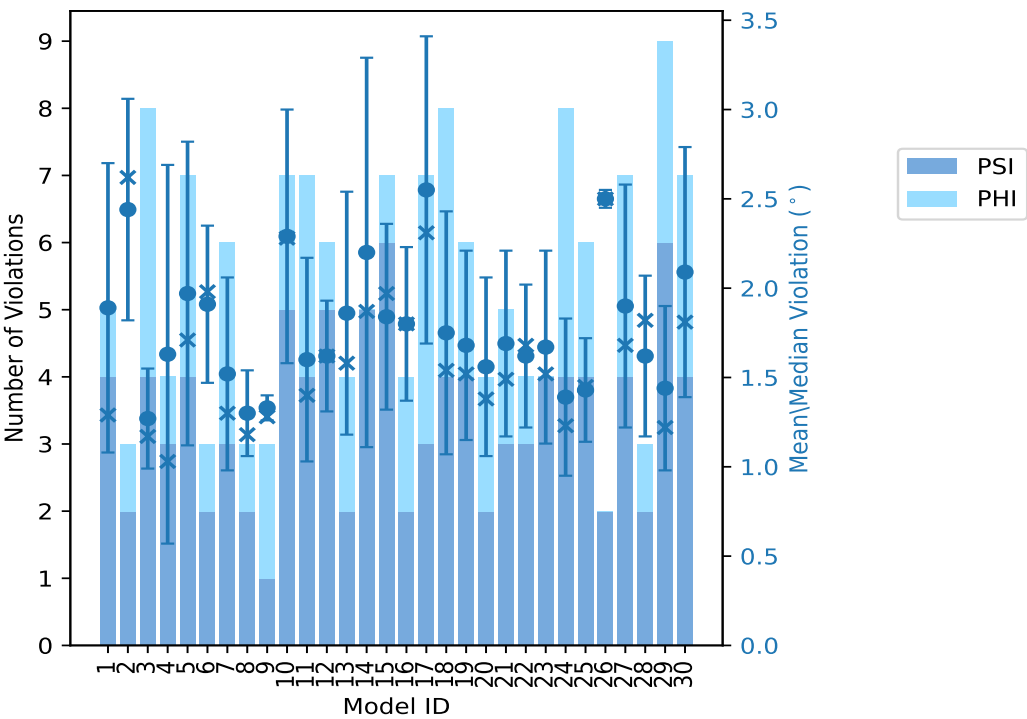
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

10.2 Dihedral-angle violation statistics for each model

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

Model ID	Number of violations			Mean (°)	Max (°)	SD (°)	Median (°)
	PSI	PHI	Total				
1	4	1	5	1.89	2.99	0.81	1.29
2	2	1	3	2.44	3.09	0.62	2.62
3	4	4	8	1.27	1.93	0.28	1.17
4	3	1	4	1.63	3.47	1.06	1.03
5	4	3	7	1.97	3.44	0.85	1.71
6	2	1	3	1.91	2.41	0.44	1.98
7	3	3	6	1.52	2.56	0.54	1.3
8	2	1	3	1.3	1.64	0.24	1.18
9	1	2	3	1.33	1.43	0.07	1.28
10	5	2	7	2.29	3.57	0.71	2.28
11	4	3	7	1.6	2.91	0.57	1.4
12	5	1	6	1.62	2.18	0.31	1.62
13	2	2	4	1.86	3.01	0.68	1.58
14	5	0	5	2.2	4.19	1.09	1.87
15	6	1	7	1.84	2.46	0.52	1.97
16	2	2	4	1.8	2.26	0.43	1.8
17	3	4	7	2.55	4.32	0.86	2.31
18	4	4	8	1.75	2.73	0.68	1.54
19	4	2	6	1.68	2.38	0.53	1.52
20	2	2	4	1.56	2.4	0.5	1.38
21	3	2	5	1.69	2.64	0.52	1.49
22	3	1	4	1.62	2.1	0.4	1.68
23	4	0	4	1.67	2.53	0.54	1.52
24	4	4	8	1.39	2.25	0.44	1.23
25	4	2	6	1.43	1.88	0.29	1.45
26	2	0	2	2.5	2.55	0.05	2.5
27	4	3	7	1.9	3.37	0.68	1.68
28	2	1	3	1.62	2.04	0.45	1.82
29	6	3	9	1.44	2.58	0.46	1.22
30	4	3	7	2.09	3.44	0.7	1.81

10.2.1 Bar graph : Dihedral 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

10.3 Dihedral-angle violation statistics for the ensemble ⓘ

Violation analysis may find that some restraints are violated in very few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of ensemble.

Number of violated restraints			Fraction of the ensemble	
PSI	PHI	Total	Count ¹	%
8	3	11	1	3.3
3	4	7	2	6.7
2	1	3	3	10.0
0	0	0	4	13.3
0	0	0	5	16.7
1	1	2	6	20.0
1	0	1	7	23.3
0	0	0	8	26.7
0	0	0	9	30.0
0	0	0	10	33.3
0	0	0	11	36.7

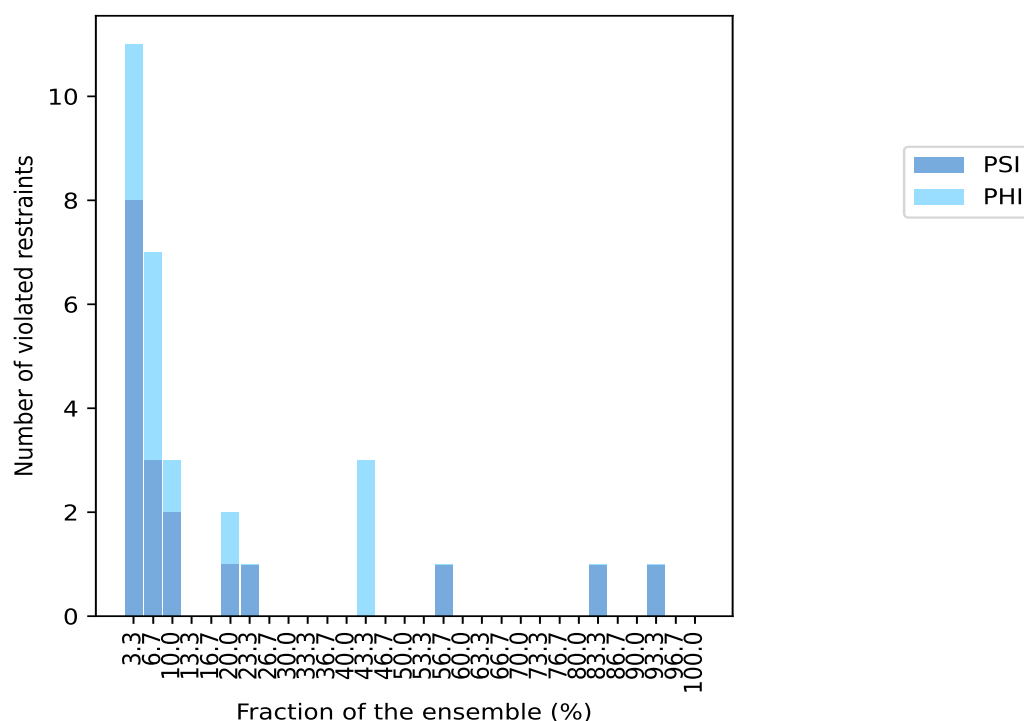
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Number of violated restraints			Fraction of the ensemble	
PSI	PHI	Total	Count ¹	%
0	0	0	12	40.0
0	3	3	13	43.3
0	0	0	14	46.7
0	0	0	15	50.0
0	0	0	16	53.3
1	0	1	17	56.7
0	0	0	18	60.0
0	0	0	19	63.3
0	0	0	20	66.7
0	0	0	21	70.0
0	0	0	22	73.3
0	0	0	23	76.7
0	0	0	24	80.0
1	0	1	25	83.3
0	0	0	26	86.7
0	0	0	27	90.0
1	0	1	28	93.3
0	0	0	29	96.7
0	0	0	30	100.0

¹ Number of models with violations

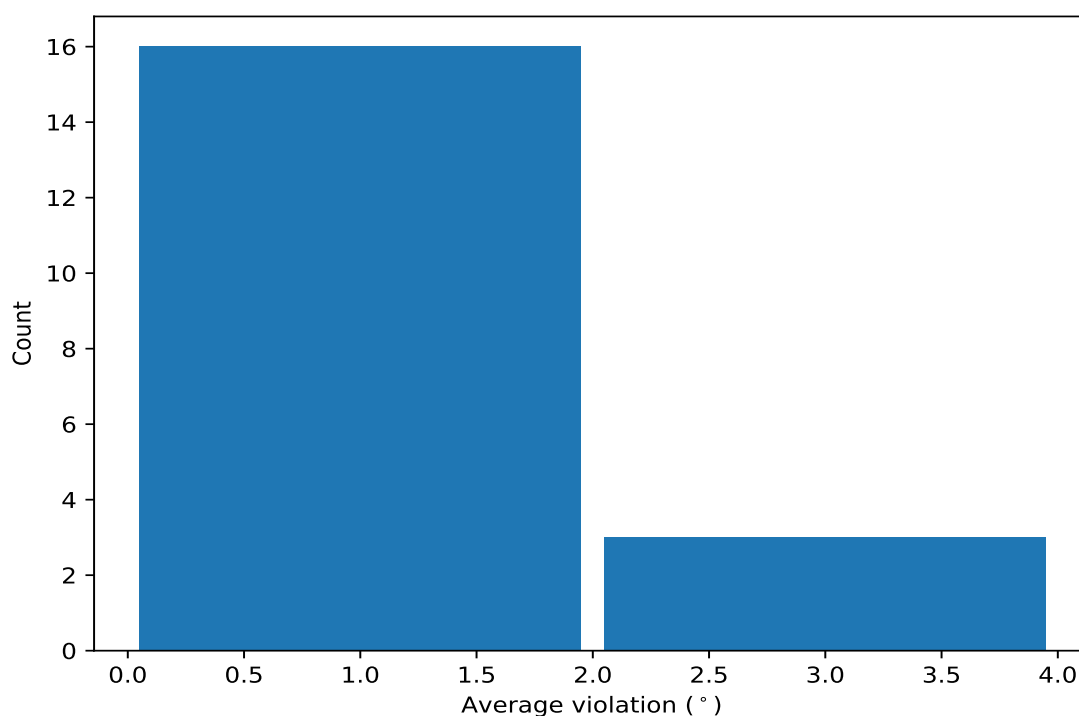
10.3.1 Bar graph : Dihedral-angle Violation statistics for the ensemble [i](#)



10.4 Most violated dihedral-angle restraints in the ensemble [i](#)

10.4.1 Histogram : Distribution of mean dihedral-angle 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



10.4.2 Table: Most violated dihedral-angle restraints [i](#)

The following table provides the mean and the standard deviation of the violation for each restraint sorted by number of violated models and the mean value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint.

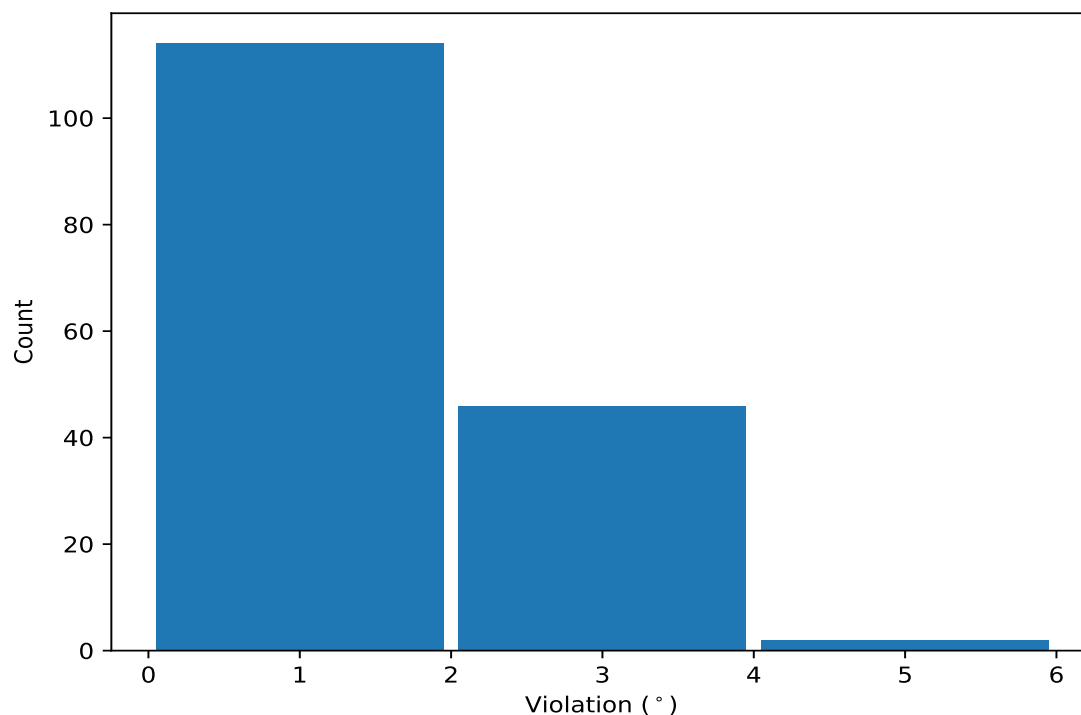
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	28	2.08	0.46	2.12
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	25	2.24	0.9	2.18
(1,70)	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	1:289:A:LEU:N	17	1.8	0.66	1.53
(1,48)	1:271:A:TYR:C	1:272:A:PRO:N	1:272:A:PRO:CA	1:272:A:PRO:C	13	1.79	0.46	1.76
(1,69)	1:287:A:LYS:C	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	13	1.67	0.59	1.47
(1,73)	1:289:A:LEU:C	1:290:A:THR:N	1:290:A:THR:CA	1:290:A:THR:C	13	1.64	0.54	1.43
(1,88)	1:298:A:GLU:N	1:298:A:GLU:CA	1:298:A:GLU:C	1:299:A:ALA:N	7	1.48	0.37	1.32
(1,72)	1:289:A:LEU:N	1:289:A:LEU:CA	1:289:A:LEU:C	1:290:A:THR:N	6	1.52	0.44	1.36
(1,35)	1:264:A:LEU:C	1:265:A:ASN:N	1:265:A:ASN:CA	1:265:A:ASN:C	6	1.23	0.13	1.27
(1,26)	1:260:A:LEU:N	1:260:A:LEU:CA	1:260:A:LEU:C	1:261:A:VAL:N	3	1.5	0.3	1.68
(1,62)	1:280:A:SER:N	1:280:A:SER:CA	1:280:A:SER:C	1:281:A:LYS:N	3	1.31	0.32	1.17
(1,9)	1:251:A:SER:C	1:252:A:TRP:N	1:252:A:TRP:CA	1:252:A:TRP:C	3	1.09	0.08	1.04
(1,71)	1:288:A:ALA:C	1:289:A:LEU:N	1:289:A:LEU:CA	1:289:A:LEU:C	2	2.78	1.54	2.78
(1,21)	1:257:A:ILE:C	1:258:A:GLN:N	1:258:A:GLN:CA	1:258:A:GLN:C	2	1.34	0.24	1.34
(1,22)	1:258:A:GLN:N	1:258:A:GLN:CA	1:258:A:GLN:C	1:259:A:LYS:N	2	1.25	0.07	1.25
(1,57)	1:277:A:ARG:C	1:278:A:GLN:N	1:278:A:GLN:CA	1:278:A:GLN:C	2	1.17	0.01	1.17
(1,36)	1:265:A:ASN:N	1:265:A:ASN:CA	1:265:A:ASN:C	1:266:A:TRP:N	2	1.16	0.05	1.16
(1,44)	1:269:A:GLN:N	1:269:A:GLN:CA	1:269:A:GLN:C	1:270:A:ILE:N	2	1.06	0.05	1.06
(1,39)	1:266:A:TRP:C	1:267:A:ALA:N	1:267:A:ALA:CA	1:267:A:ALA:C	2	1.03	0.02	1.03

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

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

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

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



10.5.2 Table: All violated dihedral-angle restraints [i](#)

The following table lists the absolute value of the violation for each restraint in the ensemble sorted by its value. The Key (restraint list ID, restraint ID) is the unique identifier for a given restraint.

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,71)	1:288:A:ALA:C	1:289:A:LEU:N	1:289:A:LEU:CA	1:289:A:LEU:C	17	4.32
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	14	4.19
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	10	3.57
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	4	3.47
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	5	3.44
(1,10)	1:252:A:TRP:N	1:252:A:TRP:CA	1:252:A:TRP:C	1:253:A:THR:N	30	3.44
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	27	3.37
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	2	3.09
(1,70)	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	1:289:A:LEU:N	5	3.02
(1,69)	1:287:A:LYS:C	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	13	3.01
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	1	2.99
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	11	2.91
(1,73)	1:289:A:LEU:C	1:290:A:THR:N	1:290:A:THR:CA	1:290:A:THR:C	17	2.88
(1,48)	1:271:A:TYR:C	1:272:A:PRO:N	1:272:A:PRO:CA	1:272:A:PRO:C	17	2.85

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,70)	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	1:289:A:LEU:N	1	2.76
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	18	2.73
(1,70)	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	1:289:A:LEU:N	30	2.73
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	21	2.64
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	2	2.62
(1,73)	1:289:A:LEU:C	1:290:A:THR:N	1:290:A:THR:CA	1:290:A:THR:C	10	2.59
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	29	2.58
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	7	2.56
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	26	2.55
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	23	2.53
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	18	2.53
(1,69)	1:287:A:LYS:C	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	18	2.49
(1,70)	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	1:289:A:LEU:N	15	2.46
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	26	2.44
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	15	2.44
(1,70)	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	1:289:A:LEU:N	14	2.44
(1,48)	1:271:A:TYR:C	1:272:A:PRO:N	1:272:A:PRO:CA	1:272:A:PRO:C	6	2.41
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	20	2.4
(1,70)	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	1:289:A:LEU:N	10	2.4
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	19	2.38
(1,69)	1:287:A:LYS:C	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	19	2.38
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	17	2.31
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	10	2.28
(1,72)	1:289:A:LEU:N	1:289:A:LEU:CA	1:289:A:LEU:C	1:290:A:THR:N	10	2.26
(1,48)	1:271:A:TYR:C	1:272:A:PRO:N	1:272:A:PRO:CA	1:272:A:PRO:C	16	2.26
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	24	2.25
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	17	2.21
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	16	2.19
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	12	2.18
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	27	2.13
(1,73)	1:289:A:LEU:C	1:290:A:THR:N	1:290:A:THR:CA	1:290:A:THR:C	15	2.11
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	22	2.1
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	30	2.08
(1,69)	1:287:A:LYS:C	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	28	2.04
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	6	1.98
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	24	1.98
(1,88)	1:298:A:GLU:N	1:298:A:GLU:CA	1:298:A:GLU:C	1:299:A:ALA:N	27	1.97
(1,72)	1:289:A:LEU:N	1:289:A:LEU:CA	1:289:A:LEU:C	1:290:A:THR:N	15	1.97
(1,48)	1:271:A:TYR:C	1:272:A:PRO:N	1:272:A:PRO:CA	1:272:A:PRO:C	5	1.94
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	3	1.93
(1,88)	1:298:A:GLU:N	1:298:A:GLU:CA	1:298:A:GLU:C	1:299:A:ALA:N	10	1.9
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	25	1.88
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	14	1.87
(1,60)	1:279:A:LEU:N	1:279:A:LEU:CA	1:279:A:LEU:C	1:280:A:SER:N	7	1.87
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	28	1.82
(1,48)	1:271:A:TYR:C	1:272:A:PRO:N	1:272:A:PRO:CA	1:272:A:PRO:C	22	1.82
(1,70)	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	1:289:A:LEU:N	21	1.81
(1,48)	1:271:A:TYR:C	1:272:A:PRO:N	1:272:A:PRO:CA	1:272:A:PRO:C	30	1.81
(1,88)	1:298:A:GLU:N	1:298:A:GLU:CA	1:298:A:GLU:C	1:299:A:ALA:N	29	1.8
(1,48)	1:271:A:TYR:C	1:272:A:PRO:N	1:272:A:PRO:CA	1:272:A:PRO:C	18	1.76
(1,62)	1:280:A:SER:N	1:280:A:SER:CA	1:280:A:SER:C	1:281:A:LYS:N	17	1.75

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,26)	1:260:A:LEU:N	1:260:A:LEU:CA	1:260:A:LEU:C	1:261:A:VAL:N	11	1.75
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	12	1.74
(1,73)	1:289:A:LEU:C	1:290:A:THR:N	1:290:A:THR:CA	1:290:A:THR:C	30	1.73
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	5	1.71
(1,70)	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	1:289:A:LEU:N	23	1.71
(1,73)	1:289:A:LEU:C	1:290:A:THR:N	1:290:A:THR:CA	1:290:A:THR:C	27	1.68
(1,26)	1:260:A:LEU:N	1:260:A:LEU:CA	1:260:A:LEU:C	1:261:A:VAL:N	12	1.68
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	30	1.67
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	15	1.66
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	8	1.64
(1,34)	1:264:A:LEU:N	1:264:A:LEU:CA	1:264:A:LEU:C	1:265:A:ASN:N	25	1.64
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	19	1.6
(1,69)	1:287:A:LYS:C	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	2	1.6
(1,48)	1:271:A:TYR:C	1:272:A:PRO:N	1:272:A:PRO:CA	1:272:A:PRO:C	29	1.59
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	13	1.58
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	25	1.58
(1,21)	1:257:A:ILE:C	1:258:A:GLN:N	1:258:A:GLN:CA	1:258:A:GLN:C	13	1.58
(1,48)	1:271:A:TYR:C	1:272:A:PRO:N	1:272:A:PRO:CA	1:272:A:PRO:C	12	1.57
(1,69)	1:287:A:LYS:C	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	17	1.55
(1,70)	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	1:289:A:LEU:N	22	1.53
(1,48)	1:271:A:TYR:C	1:272:A:PRO:N	1:272:A:PRO:CA	1:272:A:PRO:C	27	1.53
(1,73)	1:289:A:LEU:C	1:290:A:THR:N	1:290:A:THR:CA	1:290:A:THR:C	21	1.49
(1,70)	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	1:289:A:LEU:N	27	1.47
(1,69)	1:287:A:LYS:C	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	3	1.47
(1,85)	1:296:A:THR:C	1:297:A:GLU:N	1:297:A:GLU:CA	1:297:A:GLU:C	19	1.45
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	11	1.45
(1,96)	1:302:A:GLU:N	1:302:A:GLU:CA	1:302:A:GLU:C	1:303:A:LEU:N	20	1.44
(1,73)	1:289:A:LEU:C	1:290:A:THR:N	1:290:A:THR:CA	1:290:A:THR:C	9	1.43
(1,72)	1:289:A:LEU:N	1:289:A:LEU:CA	1:289:A:LEU:C	1:290:A:THR:N	5	1.43
(1,73)	1:289:A:LEU:C	1:290:A:THR:N	1:290:A:THR:CA	1:290:A:THR:C	16	1.42
(1,35)	1:264:A:LEU:C	1:265:A:ASN:N	1:265:A:ASN:CA	1:265:A:ASN:C	11	1.4
(1,69)	1:287:A:LYS:C	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	24	1.37
(1,48)	1:271:A:TYR:C	1:272:A:PRO:N	1:272:A:PRO:CA	1:272:A:PRO:C	11	1.37
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	7	1.35
(1,70)	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	1:289:A:LEU:N	12	1.35
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	6	1.33
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	23	1.33
(1,88)	1:298:A:GLU:N	1:298:A:GLU:CA	1:298:A:GLU:C	1:299:A:ALA:N	25	1.32
(1,70)	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	1:289:A:LEU:N	16	1.32
(1,35)	1:264:A:LEU:C	1:265:A:ASN:N	1:265:A:ASN:CA	1:265:A:ASN:C	20	1.32
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	21	1.31
(1,35)	1:264:A:LEU:C	1:265:A:ASN:N	1:265:A:ASN:CA	1:265:A:ASN:C	18	1.31
(1,22)	1:258:A:GLN:N	1:258:A:GLN:CA	1:258:A:GLN:C	1:259:A:LYS:N	14	1.31
(1,73)	1:289:A:LEU:C	1:290:A:THR:N	1:290:A:THR:CA	1:290:A:THR:C	24	1.29
(1,72)	1:289:A:LEU:N	1:289:A:LEU:CA	1:289:A:LEU:C	1:290:A:THR:N	1	1.29
(1,69)	1:287:A:LYS:C	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	9	1.28
(1,92)	1:300:A:GLU:N	1:300:A:GLU:CA	1:300:A:GLU:C	1:301:A:LEU:N	29	1.27
(1,70)	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	1:289:A:LEU:N	9	1.27
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	13	1.26
(1,73)	1:289:A:LEU:C	1:290:A:THR:N	1:290:A:THR:CA	1:290:A:THR:C	1	1.24
(1,71)	1:288:A:ALA:C	1:289:A:LEU:N	1:289:A:LEU:CA	1:289:A:LEU:C	7	1.24

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,48)	1:271:A:TYR:C	1:272:A:PRO:N	1:272:A:PRO:CA	1:272:A:PRO:C	3	1.23
(1,36)	1:265:A:ASN:N	1:265:A:ASN:CA	1:265:A:ASN:C	1:266:A:TRP:N	15	1.22
(1,35)	1:264:A:LEU:C	1:265:A:ASN:N	1:265:A:ASN:CA	1:265:A:ASN:C	29	1.22
(1,88)	1:298:A:GLU:N	1:298:A:GLU:CA	1:298:A:GLU:C	1:299:A:ALA:N	12	1.21
(1,73)	1:289:A:LEU:C	1:290:A:THR:N	1:290:A:THR:CA	1:290:A:THR:C	3	1.21
(1,70)	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	1:289:A:LEU:N	29	1.2
(1,9)	1:251:A:SER:C	1:252:A:TRP:N	1:252:A:TRP:CA	1:252:A:TRP:C	29	1.2
(1,73)	1:289:A:LEU:C	1:290:A:THR:N	1:290:A:THR:CA	1:290:A:THR:C	11	1.19
(1,69)	1:287:A:LYS:C	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	21	1.19
(1,69)	1:287:A:LYS:C	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	30	1.19
(1,72)	1:289:A:LEU:N	1:289:A:LEU:CA	1:289:A:LEU:C	1:290:A:THR:N	14	1.18
(1,57)	1:277:A:ARG:C	1:278:A:GLN:N	1:278:A:GLN:CA	1:278:A:GLN:C	5	1.18
(1,22)	1:258:A:GLN:N	1:258:A:GLN:CA	1:258:A:GLN:C	1:259:A:LYS:N	8	1.18
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	1	1.17
(1,62)	1:280:A:SER:N	1:280:A:SER:CA	1:280:A:SER:C	1:281:A:LYS:N	19	1.17
(1,57)	1:277:A:ARG:C	1:278:A:GLN:N	1:278:A:GLN:CA	1:278:A:GLN:C	24	1.16
(1,48)	1:271:A:TYR:C	1:272:A:PRO:N	1:272:A:PRO:CA	1:272:A:PRO:C	25	1.15
(1,111)	1:309:A:ILE:C	1:310:A:LEU:N	1:310:A:LEU:CA	1:310:A:LEU:C	3	1.14
(1,88)	1:298:A:GLU:N	1:298:A:GLU:CA	1:298:A:GLU:C	1:299:A:ALA:N	11	1.12
(1,69)	1:287:A:LYS:C	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	27	1.12
(1,70)	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	1:289:A:LEU:N	3	1.11
(1,44)	1:269:A:GLN:N	1:269:A:GLN:CA	1:269:A:GLN:C	1:270:A:ILE:N	23	1.11
(1,36)	1:265:A:ASN:N	1:265:A:ASN:CA	1:265:A:ASN:C	1:266:A:TRP:N	29	1.11
(1,21)	1:257:A:ILE:C	1:258:A:GLN:N	1:258:A:GLN:CA	1:258:A:GLN:C	20	1.1
(1,35)	1:264:A:LEU:C	1:265:A:ASN:N	1:265:A:ASN:CA	1:265:A:ASN:C	8	1.08
(1,26)	1:260:A:LEU:N	1:260:A:LEU:CA	1:260:A:LEU:C	1:261:A:VAL:N	18	1.08
(1,100)	1:304:A:ALA:N	1:304:A:ALA:CA	1:304:A:ALA:C	1:305:A:GLU:N	19	1.07
(1,70)	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	1:289:A:LEU:N	18	1.06
(1,39)	1:266:A:TRP:C	1:267:A:ALA:N	1:267:A:ALA:CA	1:267:A:ALA:C	4	1.05
(1,73)	1:289:A:LEU:C	1:290:A:THR:N	1:290:A:THR:CA	1:290:A:THR:C	5	1.04
(1,69)	1:287:A:LYS:C	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	7	1.04
(1,35)	1:264:A:LEU:C	1:265:A:ASN:N	1:265:A:ASN:CA	1:265:A:ASN:C	24	1.04
(1,9)	1:251:A:SER:C	1:252:A:TRP:N	1:252:A:TRP:CA	1:252:A:TRP:C	7	1.04
(1,88)	1:298:A:GLU:N	1:298:A:GLU:CA	1:298:A:GLU:C	1:299:A:ALA:N	3	1.03
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	22	1.03
(1,45)	1:269:A:GLN:C	1:270:A:ILE:N	1:270:A:ILE:CA	1:270:A:ILE:C	18	1.03
(1,9)	1:251:A:SER:C	1:252:A:TRP:N	1:252:A:TRP:CA	1:252:A:TRP:C	25	1.03
(1,76)	1:291:A:GLU:N	1:291:A:GLU:CA	1:291:A:GLU:C	1:292:A:VAL:N	29	1.02
(1,38)	1:266:A:TRP:N	1:266:A:TRP:CA	1:266:A:TRP:C	1:267:A:ALA:N	15	1.02
(1,72)	1:289:A:LEU:N	1:289:A:LEU:CA	1:289:A:LEU:C	1:290:A:THR:N	3	1.01
(1,70)	1:288:A:ALA:N	1:288:A:ALA:CA	1:288:A:ALA:C	1:289:A:LEU:N	24	1.01
(1,62)	1:280:A:SER:N	1:280:A:SER:CA	1:280:A:SER:C	1:281:A:LYS:N	24	1.01
(1,44)	1:269:A:GLN:N	1:269:A:GLN:CA	1:269:A:GLN:C	1:270:A:ILE:N	4	1.01
(1,39)	1:266:A:TRP:C	1:267:A:ALA:N	1:267:A:ALA:CA	1:267:A:ALA:C	10	1.01
(1,104)	1:306:A:ASN:N	1:306:A:ASN:CA	1:306:A:ASN:C	1:307:A:ARG:N	4	1.0
(1,68)	1:283:A:LEU:N	1:283:A:LEU:CA	1:283:A:LEU:C	1:284:A:ARG:N	28	1.0