



Full wwPDB NMR Structure Validation Report ⓘ

Mar 5, 2026 – 06:31 PM UTC

PDB ID : 2MP5 / pdb_00002mp5
BMRB ID : 19963
Title : Structure of Bitistatin B
Authors : Carbajo, R.J.; Calvete, J.; Sanz, L.; Perez, A.
Deposited on : 2014-05-11

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

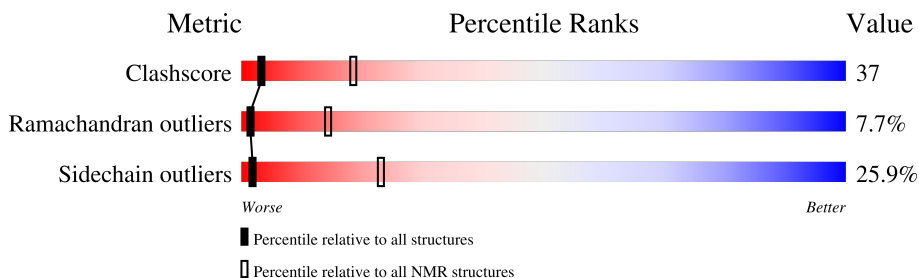
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 78%.

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	1	83	 31% 55% 11% .

2 Ensemble composition and analysis

This entry contains 43 models. Model 16 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	1:3-1:83 (81)	0.93	16

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

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

NmrClust was unable to cluster the ensemble.

Error message: NMCparsrange - Unexpected character.

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1165 atoms, of which 547 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Disintegrin bitistatin.

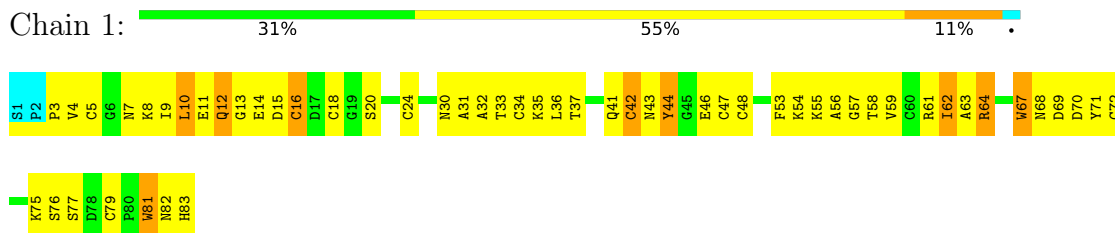
Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		S
1	1	83	1165	363	547	114	127	14	0

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: Disintegrin bitistatin

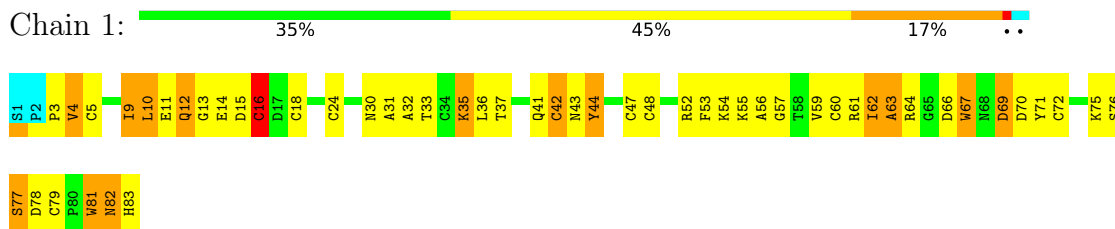


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

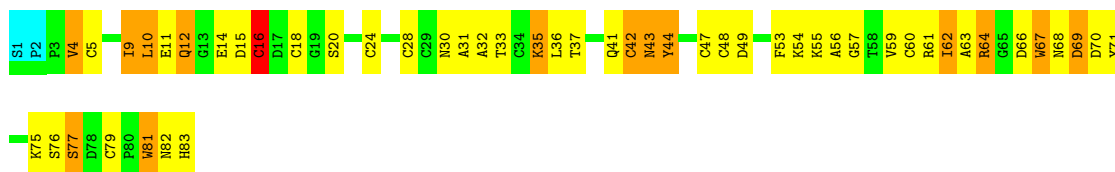
- Molecule 1: Disintegrin bitistatin



4.2.2 Score per residue for model 2

- Molecule 1: Disintegrin bitistatin

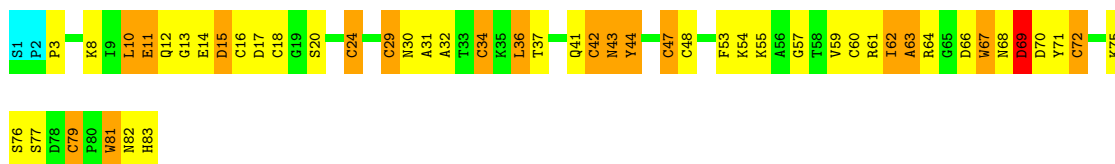




4.2.3 Score per residue for model 3

- Molecule 1: Disintegrin bitistatin

Chain 1: 37% 39% 20% ..



4.2.4 Score per residue for model 4

- Molecule 1: Disintegrin bitistatin

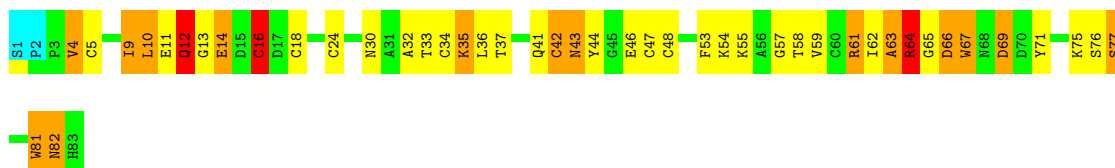
Chain 1: 37% 42% 17% ..



4.2.5 Score per residue for model 5

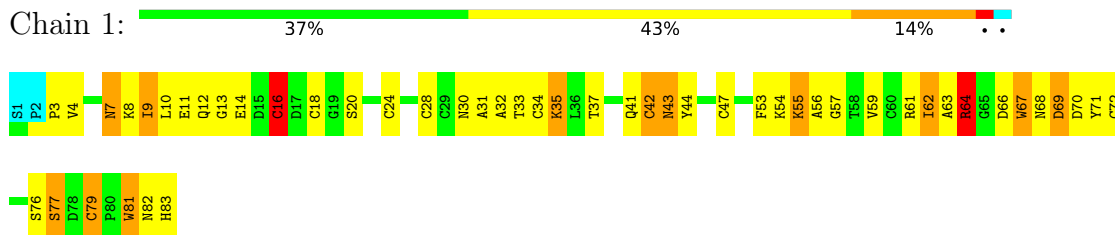
- Molecule 1: Disintegrin bitistatin

Chain 1: 43% 33% 18% ..



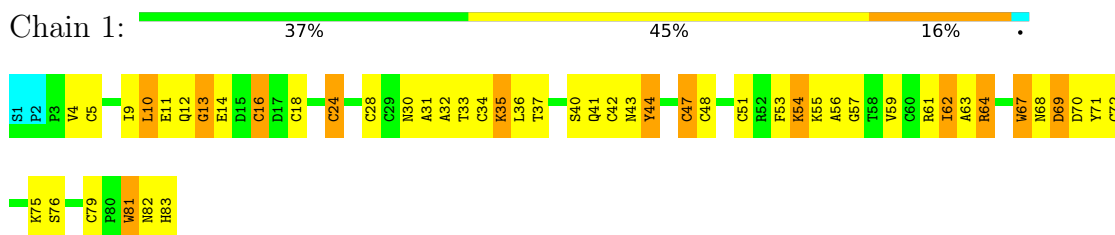
4.2.6 Score per residue for model 6

- Molecule 1: Disintegrin bitistatin



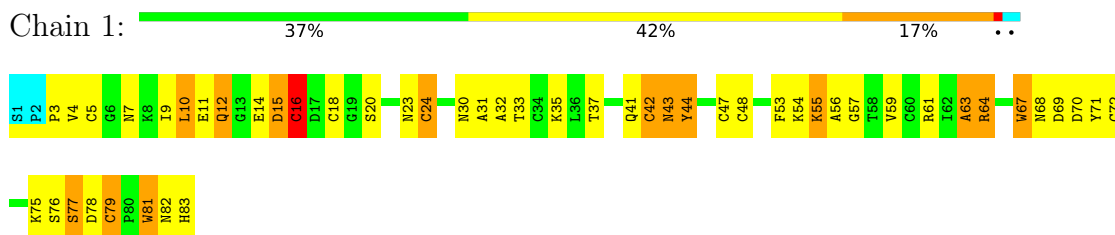
4.2.7 Score per residue for model 7

- Molecule 1: Disintegrin bitistatin



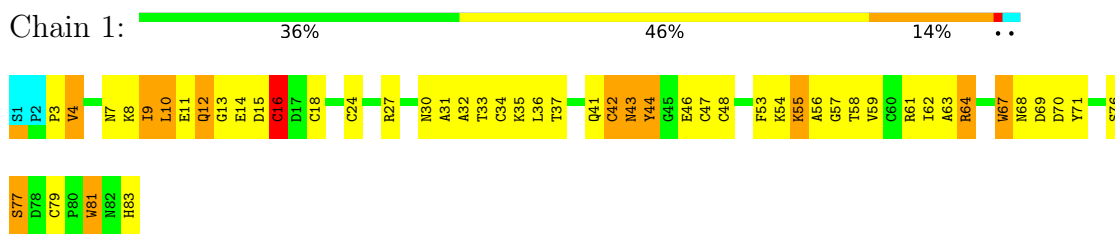
4.2.8 Score per residue for model 8

- Molecule 1: Disintegrin bitistatin



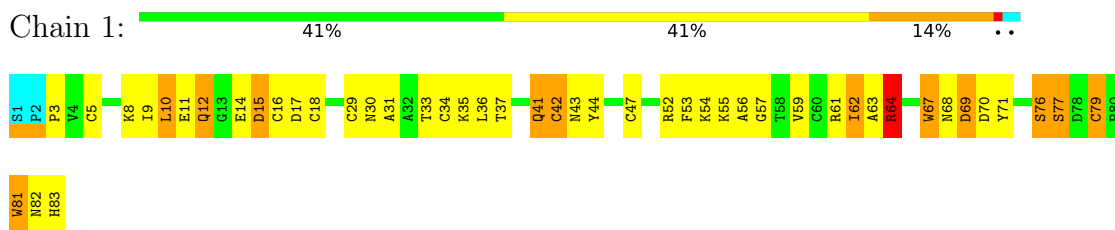
4.2.9 Score per residue for model 9

- Molecule 1: Disintegrin bitistatin



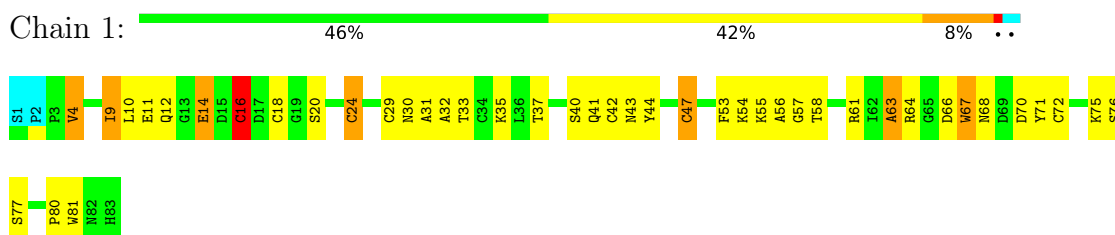
4.2.10 Score per residue for model 10

- Molecule 1: Disintegrin bitistatin



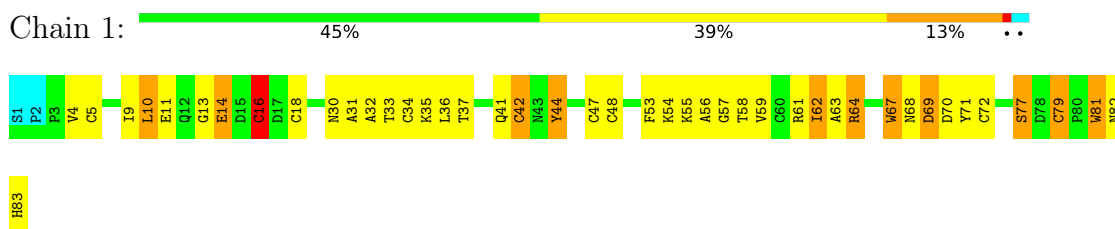
4.2.11 Score per residue for model 11

- Molecule 1: Disintegrin bitistatin



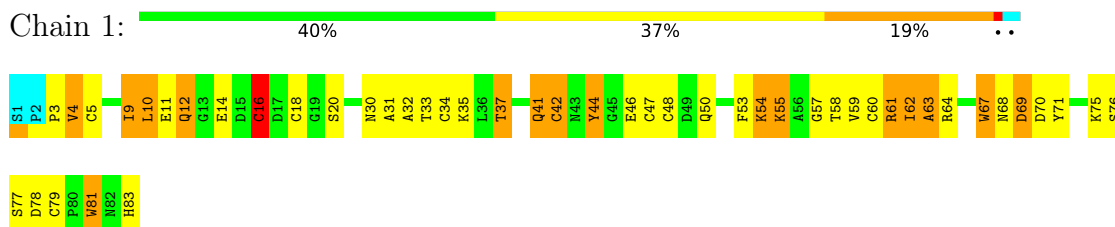
4.2.12 Score per residue for model 12

- Molecule 1: Disintegrin bitistatin



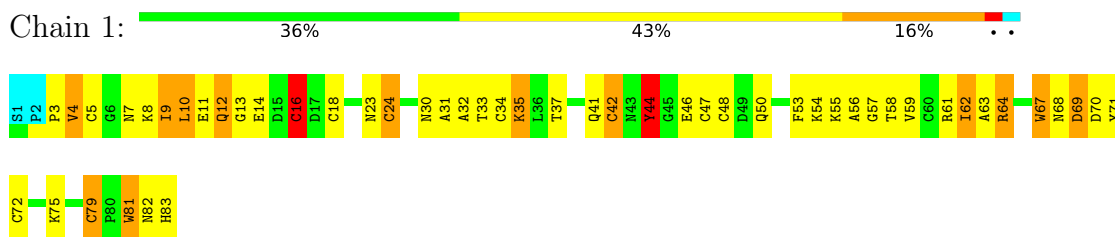
4.2.13 Score per residue for model 13

- Molecule 1: Disintegrin bitistatin



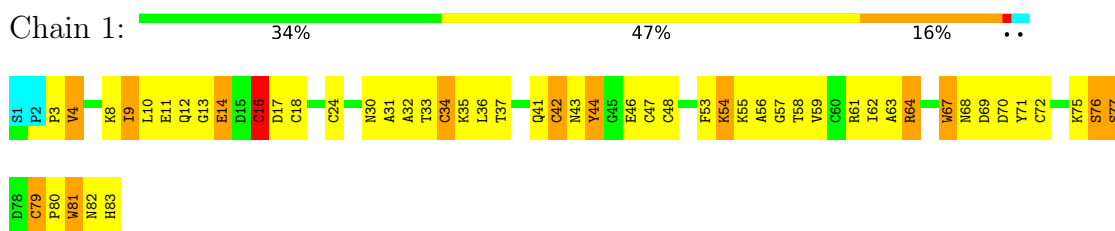
4.2.14 Score per residue for model 14

- Molecule 1: Disintegrin bitistatin



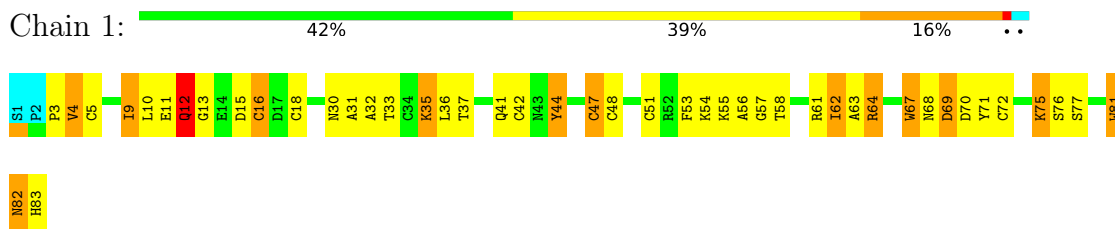
4.2.15 Score per residue for model 15

- Molecule 1: Disintegrin bitistatin



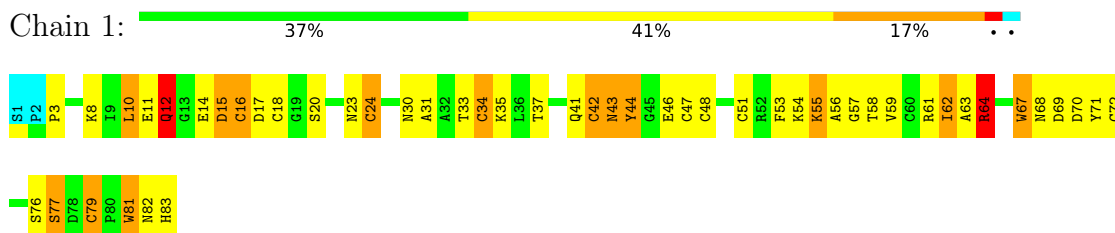
4.2.16 Score per residue for model 16 (medoid)

- Molecule 1: Disintegrin bitistatin



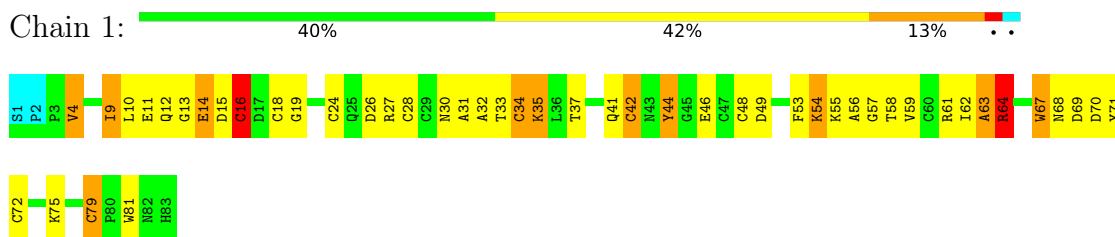
4.2.17 Score per residue for model 17

- Molecule 1: Disintegrin bitistatin



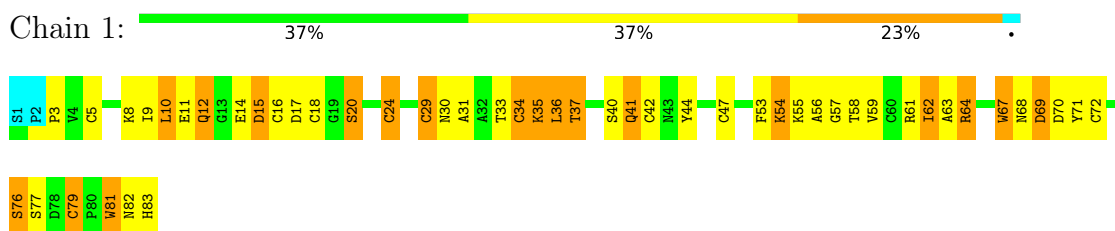
4.2.18 Score per residue for model 18

- Molecule 1: Disintegrin bitistatin



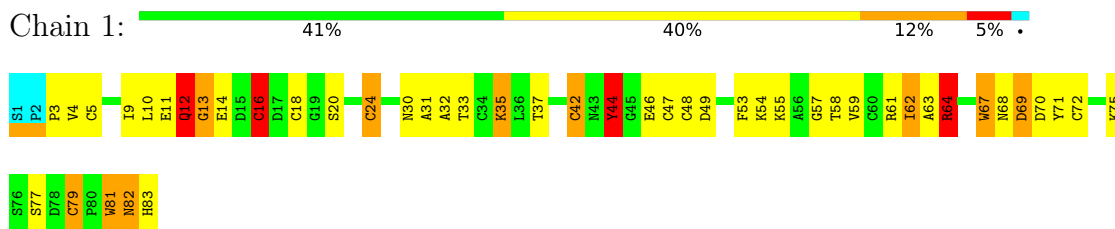
4.2.19 Score per residue for model 19

- Molecule 1: Disintegrin bitistatin



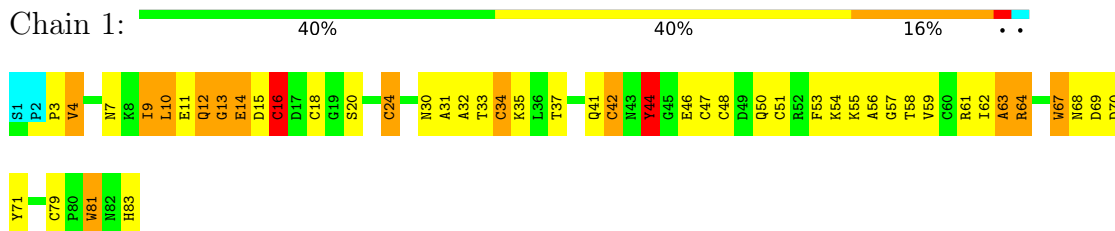
4.2.20 Score per residue for model 20

- Molecule 1: Disintegrin bitistatin



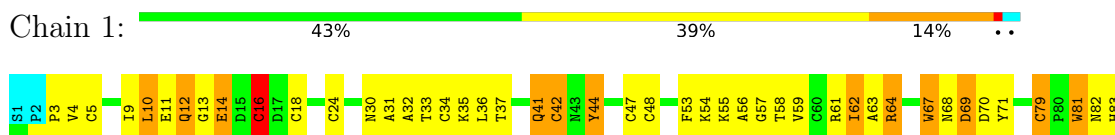
4.2.21 Score per residue for model 21

- Molecule 1: Disintegrin bitistatin



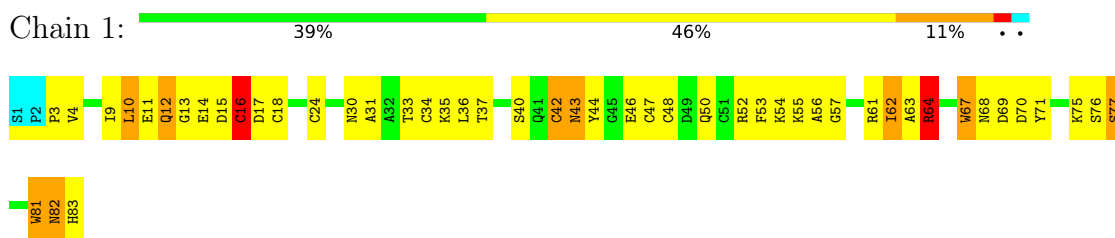
4.2.22 Score per residue for model 22

- Molecule 1: Disintegrin bitistatin



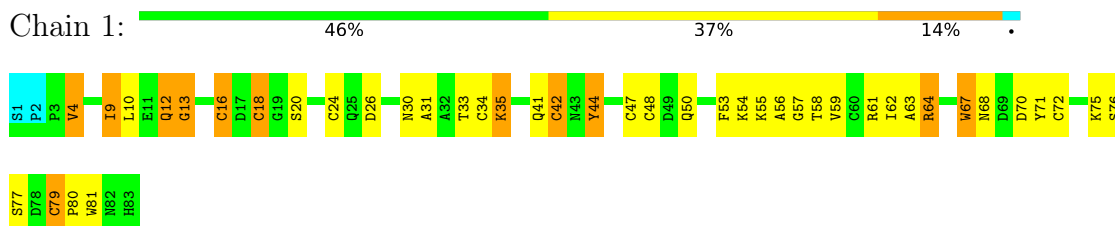
4.2.23 Score per residue for model 23

- Molecule 1: Disintegrin bitistatin



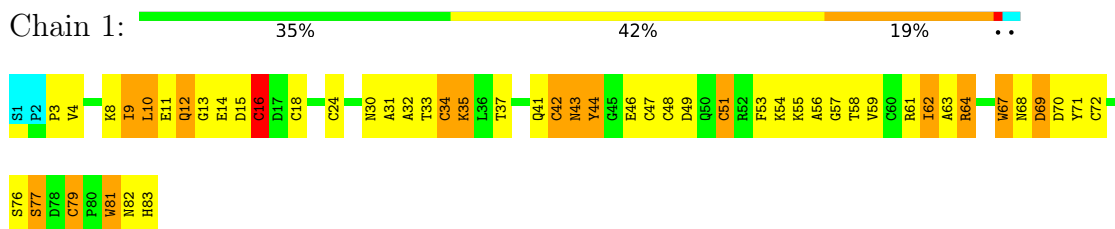
4.2.24 Score per residue for model 24

- Molecule 1: Disintegrin bitistatin



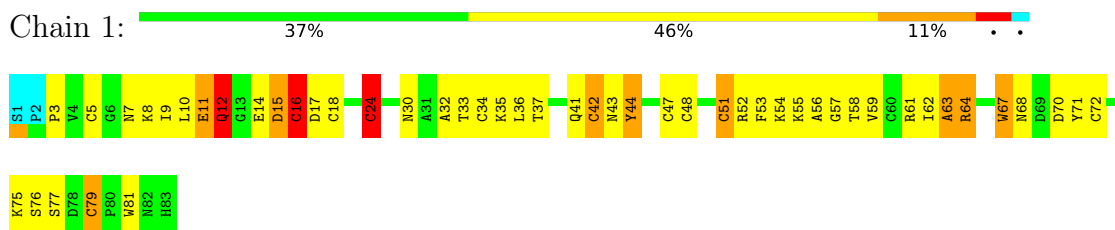
4.2.25 Score per residue for model 25

- Molecule 1: Disintegrin bitistatin



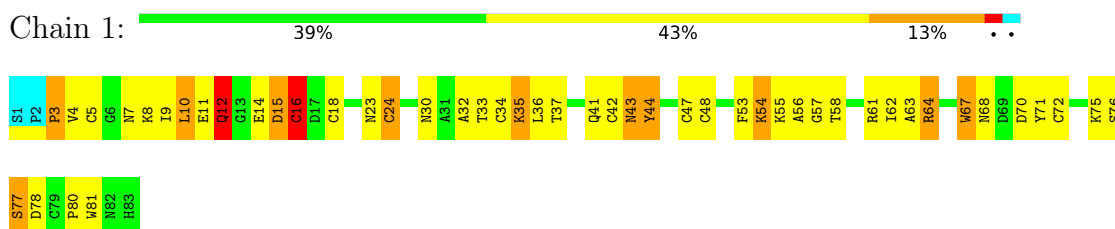
4.2.26 Score per residue for model 26

- Molecule 1: Disintegrin bitistatin



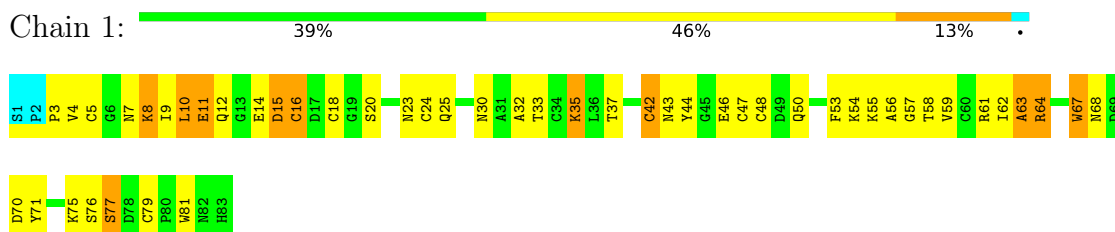
4.2.27 Score per residue for model 27

- Molecule 1: Disintegrin bitistatin



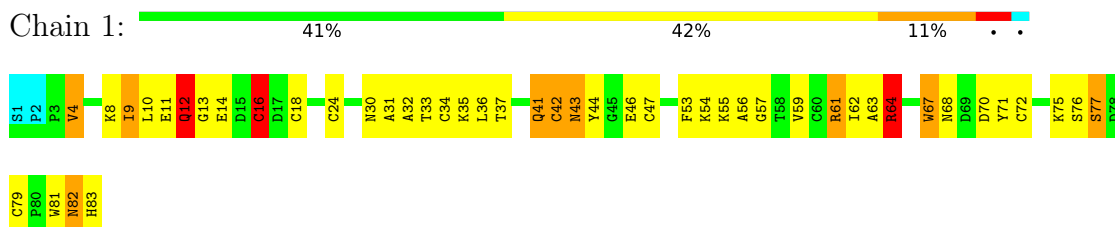
4.2.28 Score per residue for model 28

- Molecule 1: Disintegrin bitistatin



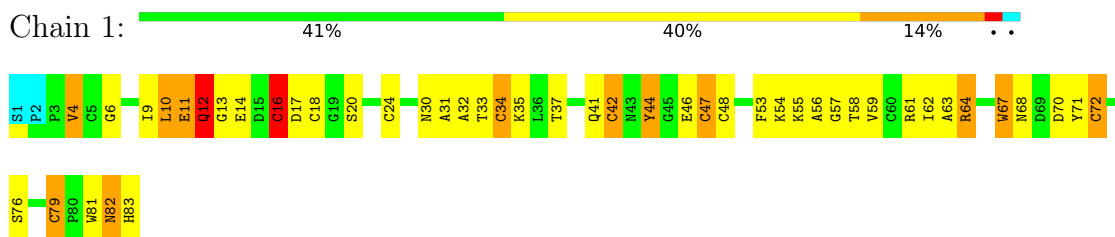
4.2.29 Score per residue for model 29

- Molecule 1: Disintegrin bitistatin



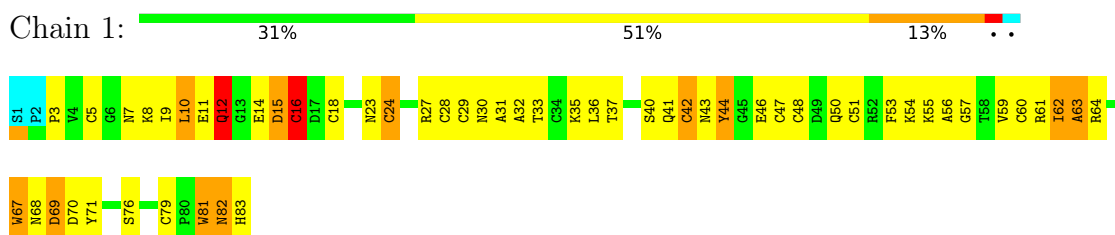
4.2.30 Score per residue for model 30

- Molecule 1: Disintegrin bitistatin



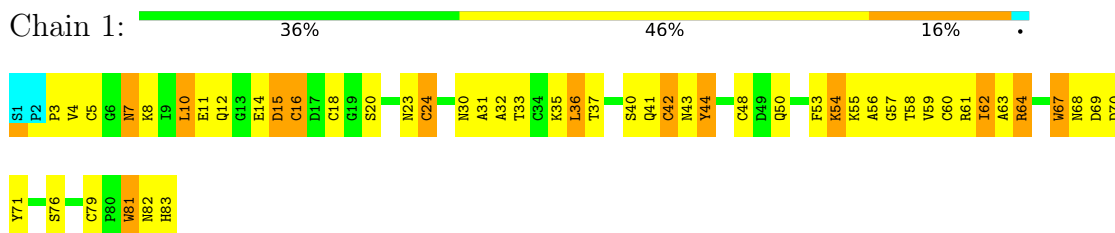
4.2.31 Score per residue for model 31

- Molecule 1: Disintegrin bitistatin



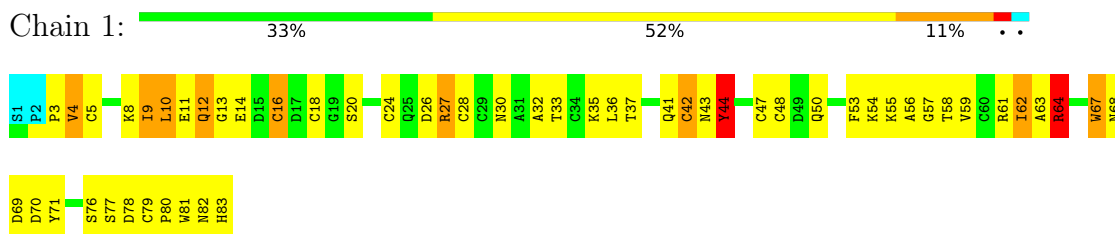
4.2.32 Score per residue for model 32

- Molecule 1: Disintegrin bitistatin



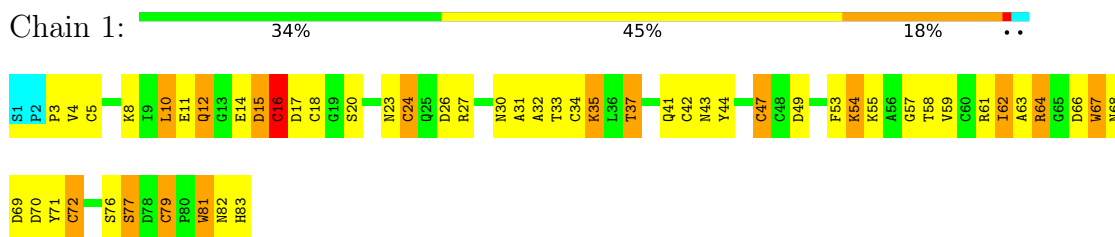
4.2.33 Score per residue for model 33

- Molecule 1: Disintegrin bitistatin



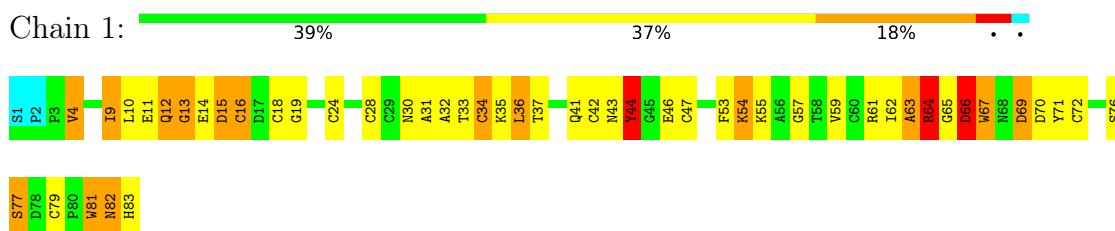
4.2.34 Score per residue for model 34

- Molecule 1: Disintegrin bitistatin



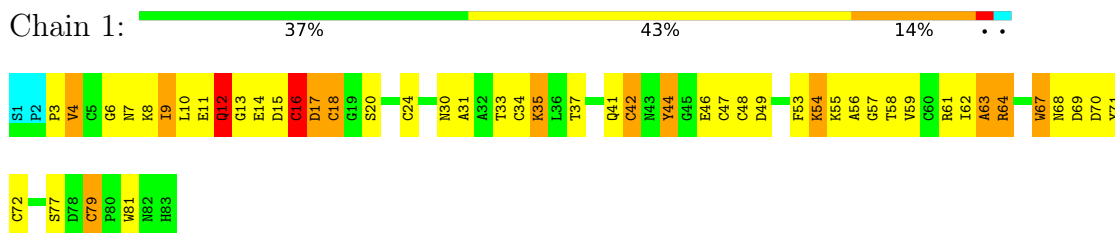
4.2.35 Score per residue for model 35

- Molecule 1: Disintegrin bitistatin



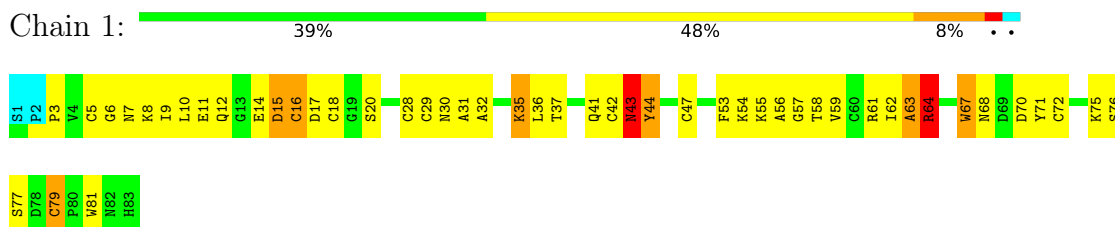
4.2.36 Score per residue for model 36

- Molecule 1: Disintegrin bitistatin



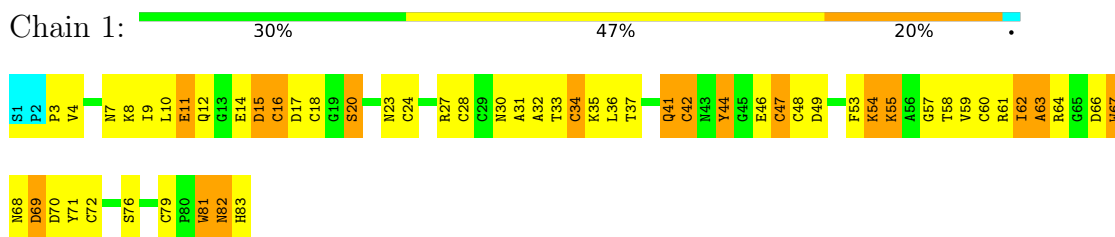
4.2.37 Score per residue for model 37

- Molecule 1: Disintegrin bitistatin



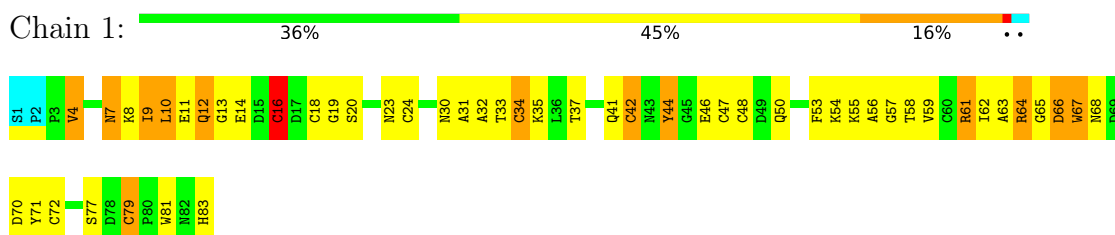
4.2.38 Score per residue for model 38

- Molecule 1: Disintegrin bitistatin



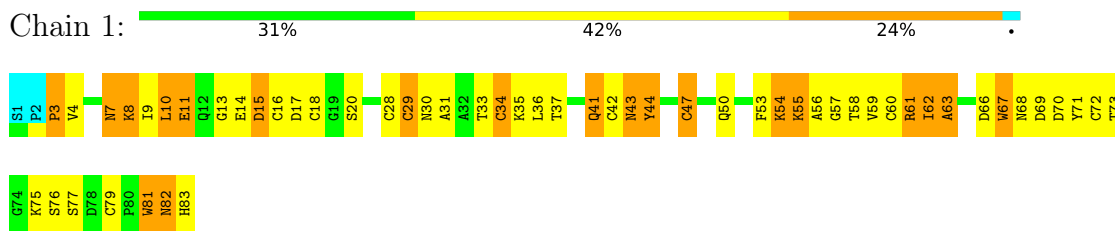
4.2.39 Score per residue for model 39

- Molecule 1: Disintegrin bitistatin



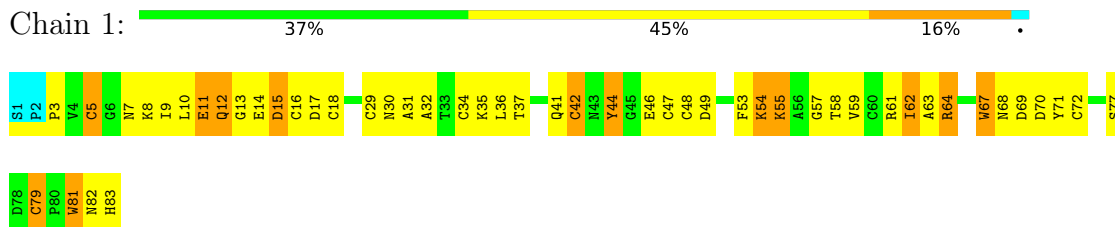
4.2.40 Score per residue for model 40

- Molecule 1: Disintegrin bitistatin



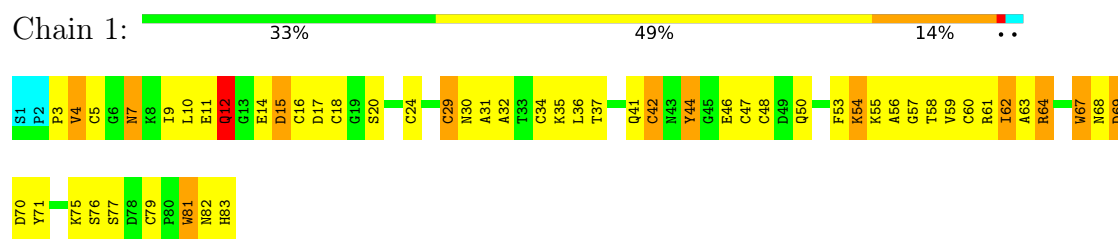
4.2.41 Score per residue for model 41

- Molecule 1: Disintegrin bitistatin



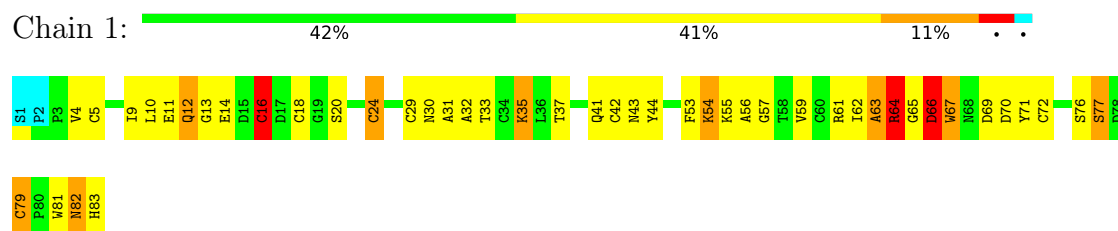
4.2.42 Score per residue for model 42

- Molecule 1: Disintegrin bitistatin



4.2.43 Score per residue for model 43

- Molecule 1: Disintegrin bitistatin



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 43 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
CNSSOLVE	structure solution	
CNSSOLVE	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	765
Number of shifts mapped to atoms	765
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	78%

6 Model quality i

6.1 Standard geometry i

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

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts i

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	1	605	533	532	42±5
All	All	26015	22919	22876	1813

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 37.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:1:18:CYS:CB	1:1:31:ALA:HB2	0.89	1.97	36	3
1:1:62:ILE:N	1:1:62:ILE:HD12	0.89	1.83	40	4
1:1:63:ALA:HB2	1:1:83:HIS:CE1	0.86	2.06	25	26
1:1:61:ARG:C	1:1:62:ILE:HD12	0.84	1.98	41	22
1:1:63:ALA:HB3	1:1:67:TRP:HE1	0.82	1.33	5	43
1:1:18:CYS:HB2	1:1:31:ALA:HB2	0.79	1.53	37	30
1:1:18:CYS:HB3	1:1:31:ALA:HB2	0.78	1.56	36	1
1:1:62:ILE:HD13	1:1:63:ALA:N	0.76	1.94	13	1
1:1:10:LEU:HD12	1:1:10:LEU:H	0.76	1.38	32	6
1:1:54:LYS:CD	1:1:58:THR:HG21	0.76	2.11	16	2
1:1:61:ARG:O	1:1:62:ILE:HD13	0.74	1.81	25	2
1:1:30:ASN:HB2	1:1:37:THR:HG22	0.74	1.60	33	29
1:1:4:VAL:HG23	1:1:9:ILE:HD12	0.72	1.59	2	4
1:1:61:ARG:C	1:1:62:ILE:HD13	0.71	2.10	25	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:1:54:LYS:HG2	1:1:58:THR:HG21	0.70	1.61	14	28
1:1:70:ASP:HA	1:1:81:TRP:HA	0.70	1.64	30	16
1:1:54:LYS:HD2	1:1:58:THR:HG21	0.68	1.65	30	2
1:1:10:LEU:HD21	1:1:44:TYR:CE2	0.68	2.24	37	1
1:1:44:TYR:C	1:1:44:TYR:CD1	0.66	2.71	35	22
1:1:62:ILE:HD12	1:1:62:ILE:N	0.66	2.06	6	19
1:1:9:ILE:HD12	1:1:11:GLU:CG	0.65	2.20	25	1
1:1:63:ALA:HB3	1:1:67:TRP:NE1	0.65	2.07	5	26
1:1:36:LEU:HD22	1:1:41:GLN:C	0.65	2.17	42	6
1:1:7:ASN:HB3	1:1:9:ILE:HD12	0.64	1.67	42	2
1:1:10:LEU:HD12	1:1:13:GLY:HA2	0.63	1.70	3	1
1:1:44:TYR:C	1:1:48:CYS:SG	0.63	2.81	39	16
1:1:9:ILE:HD12	1:1:11:GLU:HG2	0.63	1.71	25	1
1:1:10:LEU:HD23	1:1:15:ASP:HA	0.63	1.71	37	5
1:1:61:ARG:HG2	1:1:70:ASP:CB	0.62	2.24	35	1
1:1:62:ILE:HD13	1:1:62:ILE:C	0.62	2.19	13	1
1:1:7:ASN:O	1:1:9:ILE:HD12	0.62	1.95	31	4
1:1:30:ASN:HB3	1:1:33:THR:HG22	0.60	1.72	35	35
1:1:43:ASN:O	1:1:44:TYR:HB3	0.60	1.95	37	2
1:1:7:ASN:OD1	1:1:9:ILE:HD12	0.60	1.95	8	1
1:1:59:VAL:HG21	1:1:62:ILE:HD11	0.59	1.74	29	1
1:1:30:ASN:N	1:1:37:THR:HG23	0.59	2.12	19	4
1:1:10:LEU:HD22	1:1:44:TYR:CD2	0.58	2.33	7	2
1:1:15:ASP:OD2	1:1:36:LEU:HD11	0.58	1.98	42	1
1:1:62:ILE:HD12	1:1:69:ASP:OD1	0.58	1.98	5	1
1:1:61:ARG:C	1:1:62:ILE:CD1	0.58	2.77	41	20
1:1:16:CYS:SG	1:1:36:LEU:HD23	0.58	2.39	1	5
1:1:70:ASP:CB	1:1:81:TRP:HA	0.58	2.29	33	25
1:1:11:GLU:O	1:1:13:GLY:N	0.57	2.37	23	22
1:1:81:TRP:O	1:1:82:ASN:HB2	0.57	2.00	4	7
1:1:70:ASP:CA	1:1:81:TRP:HA	0.57	2.30	15	14
1:1:30:ASN:HD21	1:1:32:ALA:HB3	0.57	1.59	41	35
1:1:3:PRO:C	1:1:12:GLN:HB2	0.57	2.24	36	11
1:1:29:CYS:C	1:1:37:THR:HG23	0.57	2.24	40	5
1:1:54:LYS:CG	1:1:58:THR:HG21	0.56	2.29	13	18
1:1:4:VAL:HG11	1:1:7:ASN:CG	0.56	2.25	6	2
1:1:63:ALA:HB2	1:1:83:HIS:HE1	0.56	1.60	4	23
1:1:30:ASN:ND2	1:1:32:ALA:HB3	0.56	2.15	35	2
1:1:29:CYS:N	1:1:37:THR:HG23	0.56	2.15	42	2
1:1:62:ILE:HD13	1:1:69:ASP:HA	0.56	1.77	35	2
1:1:10:LEU:HD13	1:1:44:TYR:CD2	0.55	2.36	30	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:1:7:ASN:OD1	1:1:9:ILE:HD11	0.55	2.01	14	1
1:1:10:LEU:HD13	1:1:44:TYR:OH	0.55	1.99	10	1
1:1:10:LEU:O	1:1:11:GLU:C	0.55	2.50	34	16
1:1:62:ILE:N	1:1:62:ILE:CD1	0.55	2.58	38	12
1:1:36:LEU:HD22	1:1:40:SER:C	0.54	2.26	19	1
1:1:10:LEU:H	1:1:10:LEU:HD23	0.54	1.62	11	3
1:1:9:ILE:O	1:1:11:GLU:N	0.54	2.40	14	15
1:1:30:ASN:CB	1:1:37:THR:HG22	0.53	2.31	36	7
1:1:15:ASP:O	1:1:16:CYS:CB	0.53	2.57	28	11
1:1:81:TRP:O	1:1:83:HIS:CG	0.53	2.61	21	2
1:1:18:CYS:CB	1:1:24:CYS:HA	0.53	2.34	26	3
1:1:81:TRP:O	1:1:82:ASN:CB	0.53	2.57	5	18
1:1:14:GLU:O	1:1:15:ASP:CB	0.53	2.57	19	20
1:1:14:GLU:HB3	1:1:34:CYS:O	0.53	2.04	23	9
1:1:10:LEU:HD12	1:1:10:LEU:N	0.52	2.19	40	3
1:1:54:LYS:O	1:1:55:LYS:C	0.52	2.52	41	37
1:1:61:ARG:NE	1:1:81:TRP:CZ3	0.52	2.78	13	11
1:1:10:LEU:HD12	1:1:44:TYR:CD2	0.52	2.39	23	1
1:1:10:LEU:H	1:1:10:LEU:CD1	0.52	2.09	32	1
1:1:30:ASN:CG	1:1:33:THR:HG22	0.52	2.30	24	4
1:1:33:THR:HG23	1:1:35:LYS:N	0.52	2.19	24	26
1:1:61:ARG:O	1:1:70:ASP:HB3	0.52	2.04	33	22
1:1:36:LEU:HD22	1:1:40:SER:HB3	0.52	1.80	31	1
1:1:29:CYS:CA	1:1:37:THR:HG23	0.51	2.35	3	2
1:1:28:CYS:C	1:1:37:THR:HG23	0.51	2.29	35	1
1:1:42:CYS:C	1:1:44:TYR:H	0.51	2.12	10	8
1:1:10:LEU:HD22	1:1:44:TYR:CE2	0.51	2.40	32	1
1:1:81:TRP:CD1	1:1:81:TRP:N	0.51	2.78	21	3
1:1:61:ARG:NE	1:1:81:TRP:CE3	0.51	2.79	35	1
1:1:4:VAL:HG23	1:1:7:ASN:HB2	0.50	1.83	8	3
1:1:47:CYS:HB2	1:1:77:SER:HA	0.50	1.83	28	24
1:1:59:VAL:HA	1:1:70:ASP:O	0.50	2.06	30	15
1:1:42:CYS:HB3	1:1:48:CYS:HA	0.50	1.83	33	5
1:1:10:LEU:HD12	1:1:44:TYR:CE2	0.50	2.42	14	2
1:1:16:CYS:HB3	1:1:34:CYS:C	0.50	2.31	19	5
1:1:18:CYS:SG	1:1:31:ALA:HB2	0.49	2.47	31	1
1:1:3:PRO:HB2	1:1:12:GLN:CB	0.49	2.36	3	5
1:1:33:THR:HG23	1:1:35:LYS:H	0.49	1.68	5	14
1:1:63:ALA:CB	1:1:83:HIS:CE1	0.49	2.96	40	3
1:1:59:VAL:CG2	1:1:62:ILE:HD11	0.49	2.37	29	2
1:1:44:TYR:CD1	1:1:44:TYR:O	0.49	2.66	35	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:1:7:ASN:ND2	1:1:9:ILE:HD12	0.49	2.23	37	1
1:1:4:VAL:HB	1:1:7:ASN:HB2	0.48	1.85	39	2
1:1:55:LYS:O	1:1:56:ALA:C	0.48	2.56	11	33
1:1:10:LEU:N	1:1:17:ASP:CB	0.48	2.76	40	1
1:1:4:VAL:N	1:1:12:GLN:HB2	0.48	2.23	29	6
1:1:11:GLU:C	1:1:12:GLN:HG3	0.48	2.33	42	1
1:1:36:LEU:HD22	1:1:40:SER:O	0.48	2.08	19	2
1:1:44:TYR:CD1	1:1:44:TYR:C	0.48	2.92	5	18
1:1:10:LEU:O	1:1:14:GLU:N	0.48	2.44	3	2
1:1:7:ASN:HB3	1:1:9:ILE:HG13	0.48	1.84	9	2
1:1:5:CYS:CB	1:1:11:GLU:HG3	0.48	2.39	41	1
1:1:57:GLY:O	1:1:71:TYR:CD1	0.48	2.67	11	41
1:1:70:ASP:OD1	1:1:79:CYS:C	0.48	2.56	32	20
1:1:36:LEU:HD13	1:1:41:GLN:C	0.48	2.34	4	1
1:1:36:LEU:HD13	1:1:41:GLN:O	0.47	2.08	1	4
1:1:72:CYS:N	1:1:79:CYS:SG	0.47	2.87	8	20
1:1:81:TRP:CD1	1:1:81:TRP:H	0.47	2.28	21	12
1:1:64:ARG:C	1:1:67:TRP:CZ2	0.47	2.92	5	3
1:1:10:LEU:CD1	1:1:44:TYR:CD2	0.47	2.97	1	8
1:1:23:ASN:O	1:1:24:CYS:C	0.47	2.57	27	1
1:1:7:ASN:O	1:1:8:LYS:CB	0.47	2.63	40	4
1:1:36:LEU:HD23	1:1:43:ASN:HB3	0.47	1.85	40	1
1:1:18:CYS:H	1:1:31:ALA:HB2	0.47	1.70	20	7
1:1:4:VAL:CG2	1:1:9:ILE:CD1	0.47	2.93	13	10
1:1:63:ALA:O	1:1:64:ARG:HB2	0.47	2.09	25	2
1:1:61:ARG:NH2	1:1:70:ASP:OD2	0.47	2.48	21	3
1:1:61:ARG:C	1:1:70:ASP:HB3	0.47	2.35	40	5
1:1:53:PHE:CE1	1:1:77:SER:N	0.47	2.83	5	18
1:1:56:ALA:HB2	1:1:73:THR:O	0.47	2.10	40	1
1:1:11:GLU:HB3	1:1:14:GLU:CG	0.46	2.41	41	9
1:1:10:LEU:HD23	1:1:15:ASP:CA	0.46	2.39	38	2
1:1:36:LEU:HD23	1:1:43:ASN:CB	0.46	2.40	40	1
1:1:4:VAL:CG2	1:1:9:ILE:HD12	0.46	2.41	5	12
1:1:81:TRP:CB	1:1:83:HIS:CE1	0.46	2.99	31	11
1:1:59:VAL:O	1:1:59:VAL:HG13	0.46	2.10	39	25
1:1:10:LEU:N	1:1:17:ASP:HB3	0.46	2.25	19	7
1:1:36:LEU:HD21	1:1:42:CYS:O	0.46	2.10	40	1
1:1:41:GLN:O	1:1:53:PHE:CZ	0.46	2.69	4	36
1:1:81:TRP:HB2	1:1:83:HIS:CE1	0.46	2.46	35	3
1:1:16:CYS:O	1:1:34:CYS:HA	0.46	2.10	38	2
1:1:16:CYS:SG	1:1:30:ASN:C	0.46	2.99	19	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:1:18:CYS:HB3	1:1:24:CYS:HA	0.46	1.88	33	18
1:1:16:CYS:O	1:1:35:LYS:N	0.46	2.49	25	3
1:1:59:VAL:HB	1:1:71:TYR:CE1	0.46	2.46	17	24
1:1:61:ARG:C	1:1:62:ILE:HG12	0.46	2.36	5	1
1:1:53:PHE:CE2	1:1:76:SER:CA	0.46	2.99	35	4
1:1:42:CYS:SG	1:1:53:PHE:CE1	0.46	3.09	16	17
1:1:36:LEU:CD2	1:1:42:CYS:N	0.46	2.79	37	1
1:1:3:PRO:HB2	1:1:12:GLN:CG	0.46	2.41	42	1
1:1:47:CYS:O	1:1:54:LYS:N	0.45	2.49	11	30
1:1:64:ARG:O	1:1:67:TRP:CH2	0.45	2.68	5	3
1:1:41:GLN:O	1:1:53:PHE:CE2	0.45	2.70	34	9
1:1:42:CYS:CB	1:1:48:CYS:HA	0.45	2.41	15	11
1:1:54:LYS:HD3	1:1:58:THR:HG21	0.45	1.84	16	1
1:1:10:LEU:HD23	1:1:17:ASP:HB3	0.45	1.88	19	1
1:1:10:LEU:CD1	1:1:44:TYR:CE2	0.45	3.00	33	4
1:1:16:CYS:CB	1:1:35:LYS:N	0.45	2.80	37	4
1:1:61:ARG:NH2	1:1:81:TRP:CE2	0.45	2.85	3	1
1:1:14:GLU:CA	1:1:34:CYS:O	0.45	2.65	15	10
1:1:11:GLU:N	1:1:14:GLU:OE1	0.45	2.50	43	6
1:1:14:GLU:HB3	1:1:34:CYS:HB3	0.45	1.89	21	1
1:1:12:GLN:N	1:1:14:GLU:OE1	0.45	2.49	13	7
1:1:64:ARG:O	1:1:67:TRP:CZ2	0.45	2.69	35	36
1:1:30:ASN:ND2	1:1:33:THR:HG22	0.45	2.27	10	1
1:1:68:ASN:ND2	1:1:83:HIS:CD2	0.45	2.85	13	1
1:1:57:GLY:C	1:1:71:TYR:HD2	0.45	2.20	40	1
1:1:53:PHE:CE1	1:1:76:SER:C	0.45	2.95	10	22
1:1:16:CYS:HB2	1:1:35:LYS:C	0.45	2.37	28	5
1:1:54:LYS:O	1:1:72:CYS:SG	0.45	2.75	27	3
1:1:36:LEU:HD21	1:1:42:CYS:C	0.45	2.37	40	2
1:1:42:CYS:HB2	1:1:53:PHE:CD1	0.44	2.47	13	14
1:1:12:GLN:HB3	1:1:14:GLU:OE1	0.44	2.12	13	3
1:1:26:ASP:O	1:1:28:CYS:N	0.44	2.50	33	2
1:1:16:CYS:SG	1:1:30:ASN:N	0.44	2.90	37	3
1:1:42:CYS:HB2	1:1:48:CYS:HA	0.44	1.88	23	6
1:1:61:ARG:O	1:1:70:ASP:CB	0.44	2.65	2	10
1:1:16:CYS:HB2	1:1:35:LYS:CA	0.44	2.43	24	2
1:1:53:PHE:CE2	1:1:76:SER:HA	0.44	2.48	35	11
1:1:62:ILE:C	1:1:62:ILE:CD1	0.44	2.88	13	1
1:1:4:VAL:HB	1:1:7:ASN:HB3	0.44	1.89	14	1
1:1:3:PRO:HB3	1:1:12:GLN:CA	0.44	2.43	8	3
1:1:43:ASN:N	1:1:48:CYS:SG	0.44	2.90	23	9

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:1:61:ARG:CZ	1:1:81:TRP:CH2	0.44	3.00	12	2
1:1:6:GLY:N	1:1:17:ASP:OD1	0.44	2.48	36	1
1:1:61:ARG:H	1:1:70:ASP:HB3	0.44	1.73	16	5
1:1:42:CYS:SG	1:1:77:SER:CB	0.44	3.06	20	3
1:1:61:ARG:O	1:1:62:ILE:HG13	0.44	2.13	22	9
1:1:43:ASN:O	1:1:43:ASN:ND2	0.44	2.51	33	1
1:1:3:PRO:HB3	1:1:12:GLN:HA	0.44	1.89	41	2
1:1:41:GLN:O	1:1:53:PHE:CE1	0.44	2.71	43	10
1:1:53:PHE:CZ	1:1:77:SER:N	0.44	2.86	35	1
1:1:61:ARG:N	1:1:70:ASP:HB3	0.43	2.28	23	6
1:1:10:LEU:HD22	1:1:44:TYR:HD2	0.43	1.73	7	1
1:1:28:CYS:O	1:1:37:THR:HG23	0.43	2.12	18	2
1:1:9:ILE:O	1:1:17:ASP:OD2	0.43	2.36	38	1
1:1:30:ASN:O	1:1:34:CYS:N	0.43	2.51	9	2
1:1:57:GLY:O	1:1:71:TYR:CE1	0.43	2.72	42	17
1:1:36:LEU:HD21	1:1:43:ASN:CB	0.43	2.44	4	1
1:1:42:CYS:SG	1:1:53:PHE:CD1	0.43	3.11	20	2
1:1:14:GLU:OE2	1:1:17:ASP:HB3	0.43	2.14	15	1
1:1:53:PHE:CZ	1:1:76:SER:C	0.43	2.97	43	5
1:1:42:CYS:SG	1:1:43:ASN:N	0.43	2.92	43	7
1:1:61:ARG:NH2	1:1:79:CYS:O	0.43	2.52	4	4
1:1:3:PRO:HA	1:1:11:GLU:HB3	0.43	1.90	15	2
1:1:61:ARG:HB3	1:1:70:ASP:CB	0.43	2.44	30	2
1:1:12:GLN:N	1:1:14:GLU:CD	0.43	2.77	30	4
1:1:82:ASN:O	1:1:83:HIS:CD2	0.43	2.72	30	5
1:1:12:GLN:O	1:1:13:GLY:C	0.43	2.61	21	8
1:1:16:CYS:CB	1:1:35:LYS:C	0.43	2.92	26	21
1:1:81:TRP:HB2	1:1:83:HIS:ND1	0.43	2.29	3	10
1:1:20:SER:O	1:1:24:CYS:N	0.43	2.52	36	5
1:1:65:GLY:O	1:1:66:ASP:CB	0.43	2.67	43	3
1:1:15:ASP:O	1:1:16:CYS:SG	0.43	2.77	17	3
1:1:30:ASN:N	1:1:37:THR:CG2	0.43	2.82	4	1
1:1:70:ASP:OD2	1:1:79:CYS:O	0.43	2.37	30	2
1:1:36:LEU:CD2	1:1:42:CYS:O	0.43	2.67	35	1
1:1:10:LEU:HD13	1:1:13:GLY:H	0.43	1.74	40	1
1:1:9:ILE:HD12	1:1:11:GLU:HG3	0.42	1.90	25	1
1:1:70:ASP:HB2	1:1:81:TRP:HA	0.42	1.90	35	1
1:1:7:ASN:CB	1:1:9:ILE:HD12	0.42	2.43	41	1
1:1:3:PRO:CB	1:1:12:GLN:CG	0.42	2.97	27	3
1:1:12:GLN:O	1:1:14:GLU:N	0.42	2.52	21	1
1:1:61:ARG:CB	1:1:70:ASP:CB	0.42	2.97	40	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:1:70:ASP:HA	1:1:80:PRO:O	0.42	2.14	11	5
1:1:34:CYS:O	1:1:35:LYS:CG	0.42	2.68	23	6
1:1:61:ARG:CZ	1:1:70:ASP:OD2	0.42	2.67	33	4
1:1:30:ASN:OD1	1:1:33:THR:HG22	0.42	2.15	40	2
1:1:16:CYS:HB2	1:1:36:LEU:N	0.42	2.30	22	1
1:1:4:VAL:HG23	1:1:7:ASN:HB3	0.42	1.91	36	2
1:1:47:CYS:CB	1:1:76:SER:O	0.42	2.67	42	5
1:1:10:LEU:CD2	1:1:44:TYR:CE2	0.42	2.99	37	2
1:1:53:PHE:CE2	1:1:76:SER:N	0.42	2.88	33	1
1:1:30:ASN:HB2	1:1:37:THR:HG23	0.42	1.92	13	1
1:1:83:HIS:N	1:1:83:HIS:CD2	0.42	2.87	1	2
1:1:11:GLU:C	1:1:12:GLN:CG	0.42	2.92	3	1
1:1:9:ILE:O	1:1:14:GLU:OE2	0.42	2.38	5	1
1:1:61:ARG:CB	1:1:70:ASP:OD2	0.42	2.68	11	1
1:1:10:LEU:HA	1:1:17:ASP:HB3	0.42	1.92	17	3
1:1:14:GLU:CB	1:1:34:CYS:O	0.42	2.67	21	1
1:1:17:ASP:CG	1:1:18:CYS:N	0.42	2.78	23	1
1:1:62:ILE:HD12	1:1:62:ILE:H	0.42	1.67	40	1
1:1:41:GLN:O	1:1:53:PHE:CD2	0.42	2.73	29	4
1:1:42:CYS:O	1:1:51:CYS:HA	0.42	2.15	16	1
1:1:23:ASN:O	1:1:25:GLN:N	0.42	2.53	28	1
1:1:35:LYS:CG	1:1:36:LEU:N	0.42	2.81	29	2
1:1:11:GLU:O	1:1:11:GLU:CG	0.42	2.67	37	1
1:1:4:VAL:C	1:1:12:GLN:HB2	0.42	2.39	21	1
1:1:14:GLU:HG2	1:1:15:ASP:N	0.41	2.29	35	2
1:1:70:ASP:OD1	1:1:70:ASP:C	0.41	2.63	21	2
1:1:57:GLY:O	1:1:71:TYR:CE2	0.41	2.73	40	1
1:1:83:HIS:CD2	1:1:83:HIS:N	0.41	2.88	40	1
1:1:53:PHE:CE1	1:1:77:SER:CA	0.41	3.03	43	1
1:1:41:GLN:O	1:1:53:PHE:CD1	0.41	2.73	2	4
1:1:20:SER:O	1:1:23:ASN:N	0.41	2.53	38	6
1:1:44:TYR:O	1:1:44:TYR:CG	0.41	2.74	26	6
1:1:81:TRP:HB2	1:1:83:HIS:CD2	0.41	2.51	1	1
1:1:5:CYS:N	1:1:12:GLN:CB	0.41	2.84	22	1
1:1:23:ASN:O	1:1:24:CYS:O	0.41	2.39	31	1
1:1:42:CYS:C	1:1:44:TYR:N	0.41	2.78	10	4
1:1:14:GLU:HA	1:1:34:CYS:O	0.41	2.15	14	1
1:1:18:CYS:O	1:1:19:GLY:C	0.41	2.64	18	3
1:1:14:GLU:CG	1:1:34:CYS:HB3	0.41	2.45	27	2
1:1:9:ILE:O	1:1:9:ILE:CG2	0.41	2.69	29	1
1:1:81:TRP:O	1:1:83:HIS:CE1	0.41	2.74	39	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:1:61:ARG:CZ	1:1:81:TRP:CZ3	0.41	3.04	12	2
1:1:81:TRP:O	1:1:83:HIS:CD2	0.41	2.73	13	1
1:1:41:GLN:O	1:1:53:PHE:CG	0.41	2.74	29	4
1:1:67:TRP:CD1	1:1:83:HIS:CE1	0.41	3.09	40	2
1:1:69:ASP:HB3	1:1:71:TYR:CE2	0.41	2.51	13	1
1:1:42:CYS:SG	1:1:51:CYS:CA	0.41	3.09	26	2
1:1:7:ASN:O	1:1:8:LYS:HB2	0.41	2.16	28	2
1:1:44:TYR:C	1:1:44:TYR:HD1	0.41	2.21	35	1
1:1:14:GLU:HA	1:1:14:GLU:OE1	0.41	2.16	23	1
1:1:10:LEU:N	1:1:10:LEU:HD12	0.41	2.31	42	2
1:1:70:ASP:HB2	1:1:81:TRP:HB3	0.40	1.93	9	1
1:1:29:CYS:SG	1:1:43:ASN:ND2	0.40	2.94	31	1
1:1:16:CYS:HB2	1:1:35:LYS:N	0.40	2.30	37	1
1:1:59:VAL:HG13	1:1:59:VAL:O	0.40	2.16	12	1
1:1:53:PHE:CE2	1:1:75:LYS:O	0.40	2.75	16	1
1:1:6:GLY:N	1:1:17:ASP:OD2	0.40	2.53	30	1
1:1:53:PHE:CZ	1:1:76:SER:HA	0.40	2.52	30	2
1:1:9:ILE:C	1:1:17:ASP:CB	0.40	2.94	41	1
1:1:9:ILE:O	1:1:14:GLU:OE1	0.40	2.40	11	1
1:1:12:GLN:N	1:1:14:GLU:OE2	0.40	2.55	22	1
1:1:47:CYS:O	1:1:54:LYS:CG	0.40	2.70	1	1
1:1:3:PRO:O	1:1:12:GLN:CG	0.40	2.70	16	1
1:1:35:LYS:HE3	1:1:36:LEU:HD12	0.40	1.94	16	1
1:1:10:LEU:HD23	1:1:10:LEU:H	0.40	1.77	28	1
1:1:16:CYS:HB2	1:1:35:LYS:HA	0.40	1.92	36	2
1:1:61:ARG:CA	1:1:70:ASP:HB3	0.40	2.45	40	1
1:1:16:CYS:HB3	1:1:35:LYS:N	0.40	2.32	41	1
1:1:11:GLU:C	1:1:14:GLU:OE1	0.40	2.64	43	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	1	80/83 (96%)	60±3 (74±3%)	14±3 (18±4%)	6±2 (8±3%)	1 14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	3440/3569 (96%)	2561 (74%)	614 (18%)	265 (8%)	1 14

All 22 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	1	16	CYS	36
1	1	64	ARG	35
1	1	69	ASP	29
1	1	12	GLN	25
1	1	24	CYS	25
1	1	43	ASN	18
1	1	63	ALA	17
1	1	15	ASP	16
1	1	62	ILE	13
1	1	82	ASN	10
1	1	66	ASP	7
1	1	44	TYR	7
1	1	11	GLU	5
1	1	13	GLY	5
1	1	55	LYS	4
1	1	10	LEU	3
1	1	42	CYS	3
1	1	27	ARG	2
1	1	3	PRO	2
1	1	6	GLY	1
1	1	65	GLY	1
1	1	8	LYS	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	1	68/70 (97%)	50±2 (74±4%)	18±2 (26±4%)	2 23
All	All	2924/3010 (97%)	2167 (74%)	757 (26%)	2 23

All 54 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	1	67	TRP	43
1	1	68	ASN	38
1	1	10	LEU	35
1	1	16	CYS	32
1	1	42	CYS	30
1	1	44	TYR	30
1	1	81	TRP	30
1	1	4	VAL	27
1	1	9	ILE	27
1	1	79	CYS	27
1	1	12	GLN	25
1	1	62	ILE	24
1	1	5	CYS	23
1	1	75	LYS	23
1	1	35	LYS	22
1	1	69	ASP	22
1	1	46	GLU	22
1	1	77	SER	21
1	1	8	LYS	20
1	1	64	ARG	18
1	1	34	CYS	17
1	1	54	LYS	16
1	1	20	SER	15
1	1	50	GLN	12
1	1	37	THR	11
1	1	60	CYS	10
1	1	72	CYS	10
1	1	61	ARG	10
1	1	49	ASP	8
1	1	66	ASP	8
1	1	47	CYS	8
1	1	28	CYS	7
1	1	14	GLU	7
1	1	41	GLN	7
1	1	29	CYS	6
1	1	36	LEU	6
1	1	51	CYS	6
1	1	78	ASP	5
1	1	76	SER	5
1	1	7	ASN	5
1	1	27	ARG	5
1	1	15	ASP	4

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Mol	Chain	Res	Type	Models (Total)
1	1	52	ARG	4
1	1	55	LYS	4
1	1	82	ASN	4
1	1	18	CYS	4
1	1	43	ASN	3
1	1	40	SER	3
1	1	26	ASP	2
1	1	11	GLU	2
1	1	59	VAL	1
1	1	23	ASN	1
1	1	24	CYS	1
1	1	17	ASP	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 i

The completeness of assignment taking into account all chemical shift lists is 78% for the well-defined parts and 77% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping i

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	765
Number of shifts mapped to atoms	765
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

7.1.2 Chemical shift referencing i

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
¹³ C _α	67	0.21 \pm 0.23	None needed (< 0.5 ppm)
¹³ C _β	56	0.45 \pm 0.23	None needed (< 0.5 ppm)
¹³ C'	0	—	None (insufficient data)
¹⁵ N	77	-0.19 \pm 0.60	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments i

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 78%, i.e. 747 atoms were assigned a chemical shift out of a possible 961. 0 out of 4 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	307/405 (76%)	165/166 (99%)	65/162 (40%)	77/77 (100%)
Sidechain	412/496 (83%)	301/313 (96%)	104/156 (67%)	7/27 (26%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	28/60 (47%)	26/29 (90%)	0/27 (0%)	2/4 (50%)
Overall	747/961 (78%)	492/508 (97%)	169/345 (49%)	86/108 (80%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 77%, i.e. 756 atoms were assigned a chemical shift out of a possible 981. 0 out of 4 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	311/413 (75%)	167/169 (99%)	67/166 (40%)	77/78 (99%)
Sidechain	417/508 (82%)	305/321 (95%)	105/160 (66%)	7/27 (26%)
Aromatic	28/60 (47%)	26/29 (90%)	0/27 (0%)	2/4 (50%)
Overall	756/981 (77%)	498/519 (96%)	172/353 (49%)	86/109 (79%)

7.1.4 Statistically unusual chemical shifts [i](#)

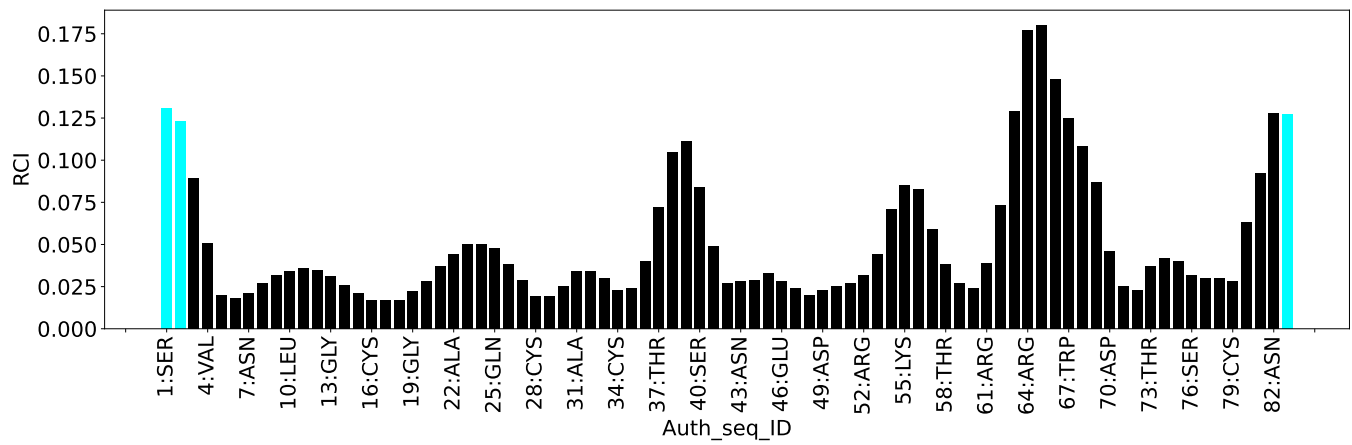
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	1	41	GLN	HB2	0.57	0.80 – 3.29	-5.9

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

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

Random coil index (RCI) for chain 1:



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	1615
Intra-residue ($ i-j =0$)	204
Sequential ($ i-j =1$)	488
Medium range ($ i-j >1$ and $ i-j <5$)	307
Long range ($ i-j \geq 5$)	586
Inter-chain	0
Hydrogen bond restraints	30
Disulfide bond restraints	0
Total dihedral-angle restraints	82
Number of unmapped restraints	0
Number of restraints per residue	20.4
Number of long range restraints per residue ¹	7.3

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)	9.4	0.2
0.2-0.5 (Medium)	12.4	0.5
>0.5 (Large)	28.8	3.36

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

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

Bins (°)	Average number of violations per model	Max (°)
1.0-10.0 (Small)	1.3	2.44
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis [i](#)

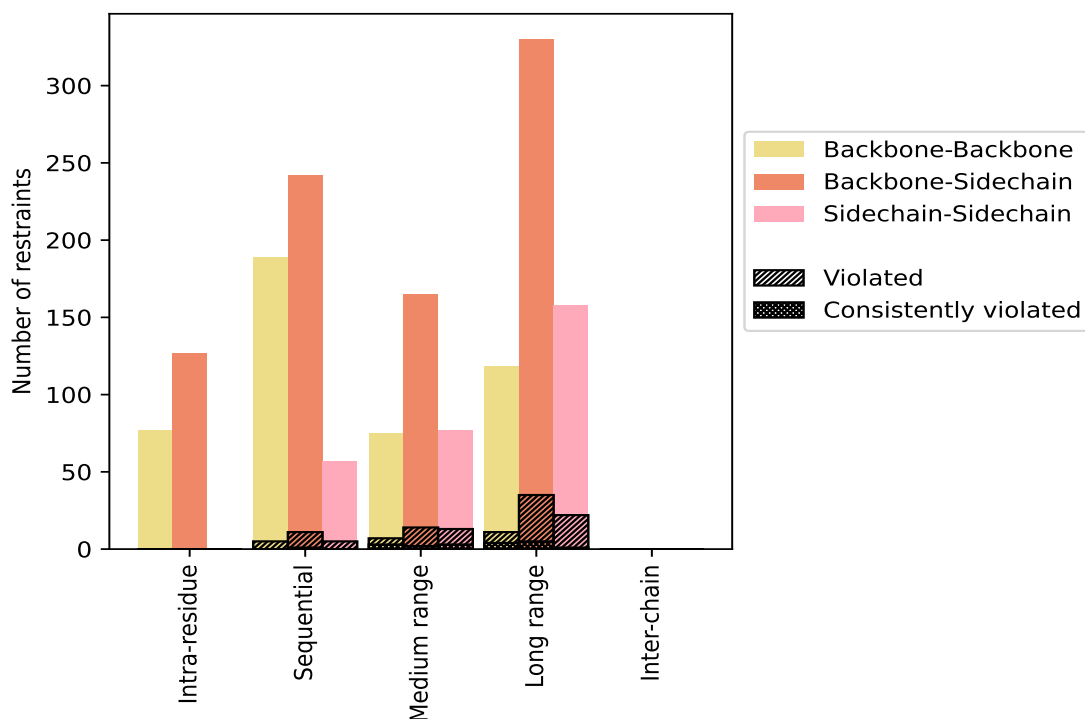
9.1 Summary of distance violations [i](#)

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 ($i-j =0$)	204	12.6	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	77	4.8	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	127	7.9	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sequential ($i-j =1$)	488	30.2	21	4.3	1.3	1	0.2	0.1
Backbone-Backbone	189	11.7	5	2.6	0.3	0	0.0	0.0
Backbone-Sidechain	242	15.0	11	4.5	0.7	1	0.4	0.1
Sidechain-Sidechain	57	3.5	5	8.8	0.3	0	0.0	0.0
Medium range ($i-j >1$ & $i-j <5$)	307	19.0	33	10.7	2.0	8	2.6	0.5
Backbone-Backbone	75	4.6	7	9.3	0.4	3	4.0	0.2
Backbone-Sidechain	155	9.6	13	8.4	0.8	2	1.3	0.1
Sidechain-Sidechain	77	4.8	13	16.9	0.8	3	3.9	0.2
Long range ($i-j \geq 5$)	586	36.3	67	11.4	4.1	10	1.7	0.6
Backbone-Backbone	118	7.3	11	9.3	0.7	4	3.4	0.2
Backbone-Sidechain	310	19.2	34	11.0	2.1	5	1.6	0.3
Sidechain-Sidechain	158	9.8	22	13.9	1.4	1	0.6	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	30	1.9	2	6.7	0.1	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	1615	100.0	123	7.6	7.6	19	1.2	1.2
Backbone-Backbone	459	28.4	23	5.0	1.4	7	1.5	0.4
Backbone-Sidechain	864	53.5	60	6.9	3.7	8	0.9	0.5
Sidechain-Sidechain	292	18.1	40	13.7	2.5	4	1.4	0.2

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

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



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

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

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

Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
1	0	2	13	27	0	42	0.67	1.32	0.35	0.74
2	0	6	15	32	0	53	0.63	2.33	0.43	0.64
3	0	6	17	33	0	56	0.6	2.36	0.41	0.54
4	0	3	16	31	0	50	0.63	2.54	0.44	0.64
5	0	4	16	35	0	55	0.65	3.23	0.49	0.61
6	0	4	15	31	0	50	0.62	2.71	0.46	0.48
7	0	4	16	30	0	50	0.65	2.47	0.43	0.68
8	0	6	16	31	0	53	0.61	2.5	0.43	0.5
9	0	3	15	38	0	56	0.69	3.32	0.48	0.71
10	0	4	16	31	0	51	0.65	2.46	0.44	0.71

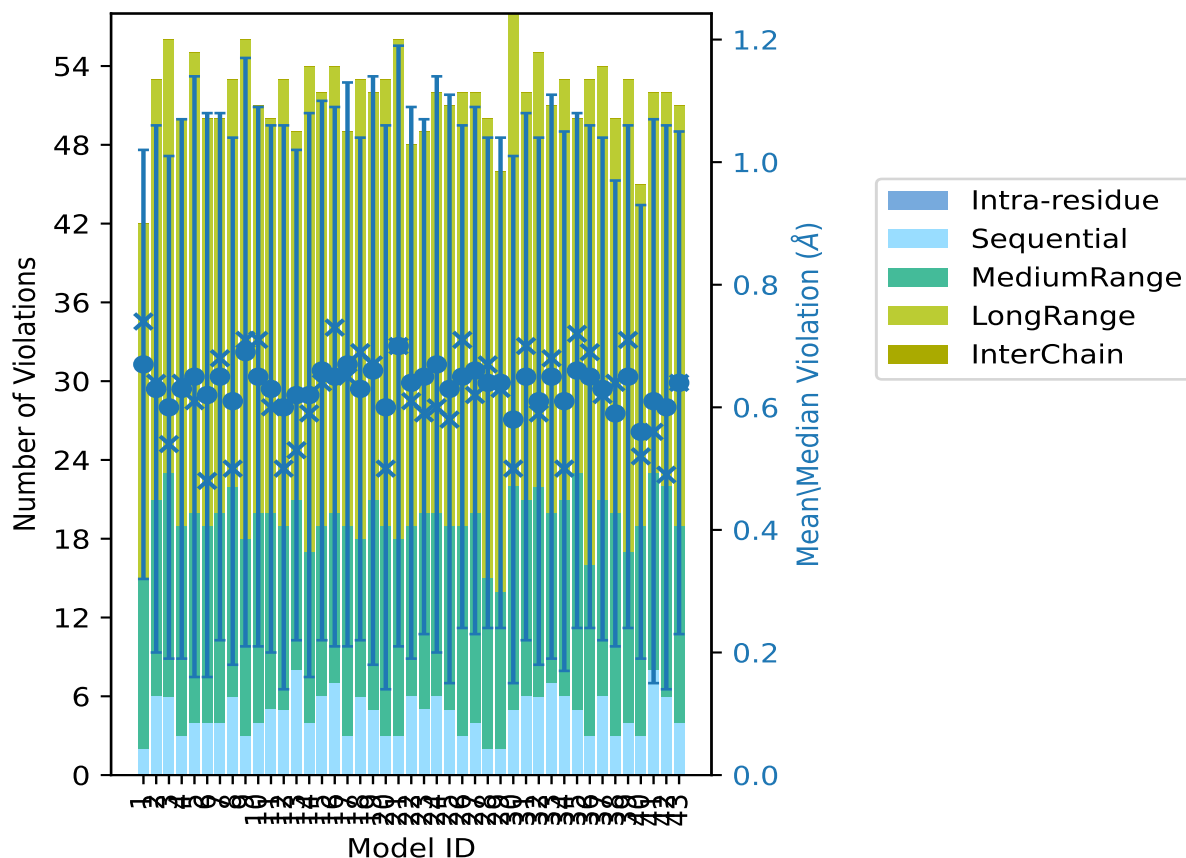
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	0	5	15	30	0	50	0.63	2.4	0.43	0.6
12	0	5	14	34	0	53	0.6	2.49	0.46	0.5
13	0	8	13	28	0	49	0.62	2.05	0.4	0.53
14	0	4	13	37	0	54	0.62	2.81	0.46	0.59
15	0	6	13	33	0	52	0.66	2.55	0.44	0.64
16	0	7	13	34	0	54	0.65	2.37	0.44	0.73
17	0	3	16	30	0	49	0.67	2.9	0.46	0.65
18	0	6	12	35	0	53	0.63	2.13	0.41	0.69
19	0	5	16	31	0	52	0.66	2.5	0.48	0.67
20	0	3	16	34	0	53	0.6	2.73	0.46	0.5
21	0	3	15	38	0	56	0.7	3.36	0.49	0.7
22	0	6	13	29	0	48	0.64	2.53	0.45	0.61
23	0	5	15	29	0	49	0.65	2.3	0.42	0.59
24	0	6	14	32	0	52	0.67	2.58	0.47	0.6
25	0	5	14	32	0	51	0.63	2.97	0.48	0.58
26	0	3	16	33	0	52	0.65	2.16	0.41	0.71
27	0	4	16	32	0	52	0.66	2.54	0.43	0.62
28	0	2	13	35	0	50	0.64	2.12	0.4	0.67
29	0	2	12	32	0	46	0.64	2.16	0.4	0.63
30	0	5	17	36	0	58	0.58	2.4	0.43	0.5
31	0	6	15	31	0	52	0.65	2.27	0.43	0.7
32	0	6	16	33	0	55	0.61	2.35	0.43	0.59
33	0	7	13	31	0	51	0.65	2.52	0.46	0.68
34	0	6	15	32	0	53	0.61	2.51	0.44	0.5
35	0	5	18	27	0	50	0.66	2.27	0.42	0.72
36	0	3	13	37	0	53	0.65	2.12	0.41	0.69
37	0	6	15	33	0	54	0.63	2.16	0.41	0.62
38	0	3	17	30	0	50	0.59	1.32	0.38	0.64
39	0	4	13	36	0	53	0.65	2.11	0.41	0.71
40	0	3	16	26	0	45	0.56	1.24	0.37	0.52
41	0	8	15	29	0	52	0.61	2.57	0.46	0.56
42	0	6	16	30	0	52	0.6	2.62	0.46	0.49
43	0	4	15	32	0	51	0.64	2.09	0.41	0.64

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, 1464(IR:204, SQ:467, MR:274, LR:519, IC:0) restraints are not violated in the ensemble.

Number of violated restraints						Fraction of the ensemble	
IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total	Count ⁶	%
0	4	5	6	0	15	1	2.3
0	6	4	4	0	14	2	4.7
0	2	1	8	0	11	3	7.0
0	1	1	2	0	4	4	9.3
0	1	0	1	0	2	5	11.6
0	0	1	0	0	1	6	14.0

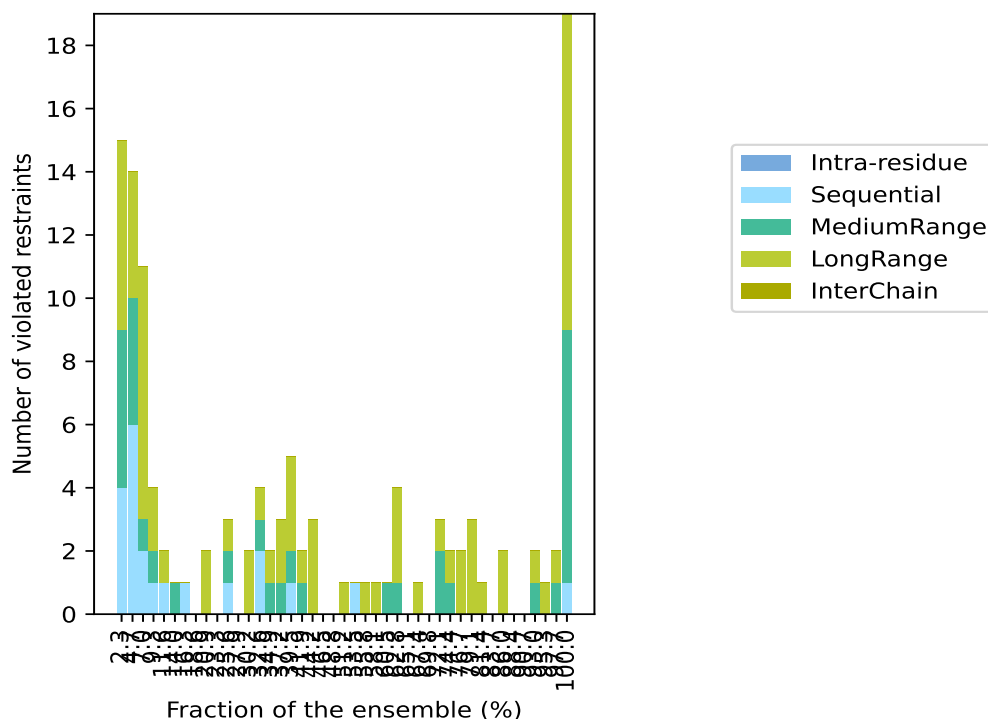
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Number of violated restraints						Fraction of the ensemble	
IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total	Count ⁶	%
0	1	0	0	0	1	7	16.3
0	0	0	0	0	0	8	18.6
0	0	0	2	0	2	9	20.9
0	0	0	0	0	0	10	23.3
0	1	1	1	0	3	11	25.6
0	0	0	0	0	0	12	27.9
0	0	0	2	0	2	13	30.2
0	2	1	1	0	4	14	32.6
0	0	1	1	0	2	15	34.9
0	0	1	2	0	3	16	37.2
0	1	1	3	0	5	17	39.5
0	0	1	1	0	2	18	41.9
0	0	0	3	0	3	19	44.2
0	0	0	0	0	0	20	46.5
0	0	0	0	0	0	21	48.8
0	0	0	1	0	1	22	51.2
0	1	0	0	0	1	23	53.5
0	0	0	1	0	1	24	55.8
0	0	0	1	0	1	25	58.1
0	0	1	0	0	1	26	60.5
0	0	1	3	0	4	27	62.8
0	0	0	0	0	0	28	65.1
0	0	0	1	0	1	29	67.4
0	0	0	0	0	0	30	69.8
0	0	2	1	0	3	31	72.1
0	0	1	1	0	2	32	74.4
0	0	0	2	0	2	33	76.7
0	0	0	3	0	3	34	79.1
0	0	0	1	0	1	35	81.4
0	0	0	0	0	0	36	83.7
0	0	0	2	0	2	37	86.0
0	0	0	0	0	0	38	88.4
0	0	0	0	0	0	39	90.7
0	0	1	1	0	2	40	93.0
0	0	0	1	0	1	41	95.3
0	0	1	1	0	2	42	97.7
0	1	8	10	0	19	43	100.0

¹Intra-residue restraints, ²Sequential restraints, ³Medium range restraints, ⁴Long range restraints, ⁵Inter-chain restraints, ⁶ Number of models with violations

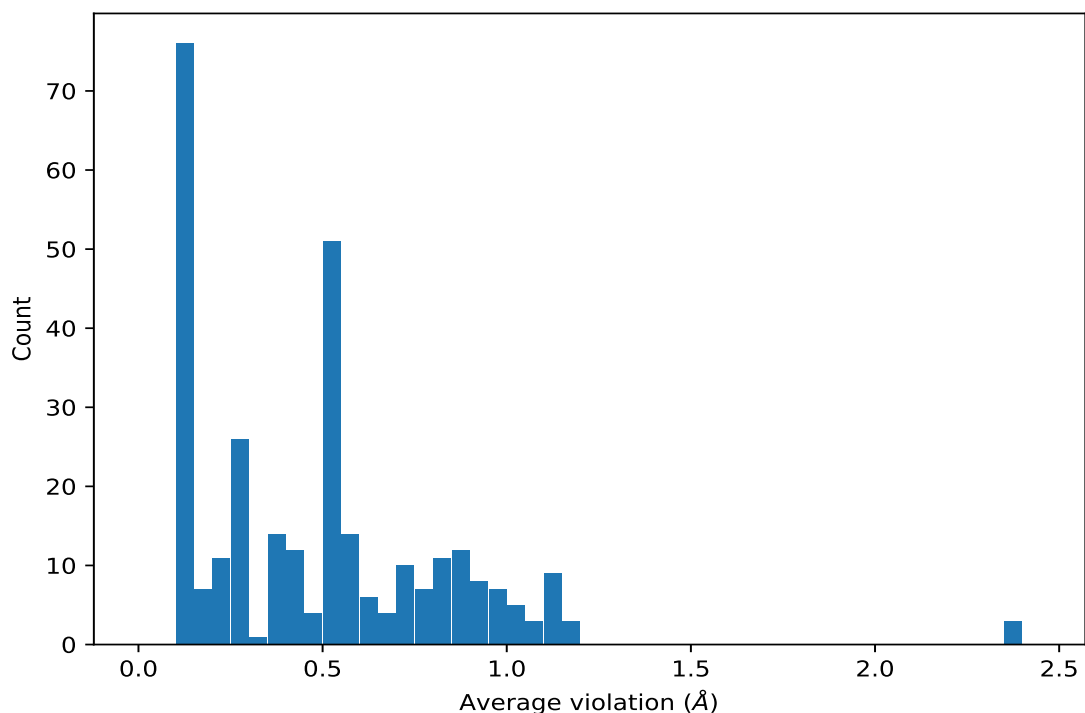
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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)
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB1	43	2.39	0.48	2.46
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB3	43	2.39	0.48	2.46
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB2	43	2.39	0.48	2.46
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	43	1.11	0.02	1.11
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	43	1.11	0.02	1.11
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	43	1.11	0.02	1.11
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	43	1.11	0.02	1.11
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	43	1.11	0.02	1.11
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	43	1.11	0.02	1.11
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	43	1.1	0.18	1.13
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	43	1.1	0.05	1.08
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	43	1.1	0.05	1.08
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	43	1.06	0.01	1.06
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	43	1.02	0.03	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	43	1.02	0.03	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	43	0.99	0.08	1.02

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	43	0.99	0.08	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	43	0.99	0.08	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	43	0.99	0.08	1.02
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	43	0.97	0.07	1.0
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	43	0.97	0.07	1.0
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	43	0.97	0.06	1.0
(2,583)	1:31:1:ALA:HB2	1:26:1:ASP:H	43	0.88	0.28	0.93
(2,583)	1:31:1:ALA:HB3	1:26:1:ASP:H	43	0.88	0.28	0.93
(2,583)	1:31:1:ALA:HB1	1:26:1:ASP:H	43	0.88	0.28	0.93
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	43	0.88	0.03	0.9
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	43	0.85	0.21	0.99
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	43	0.85	0.21	0.99
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	43	0.81	0.12	0.8
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	43	0.8	0.08	0.81
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	43	0.76	0.06	0.76
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	43	0.76	0.06	0.76
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	43	0.75	0.11	0.7
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	43	0.75	0.11	0.7
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	43	0.49	0.18	0.43
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	43	0.3	0.05	0.31
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	43	0.22	0.04	0.22
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	42	0.87	0.13	0.9
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	42	0.87	0.13	0.9
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	42	0.87	0.13	0.9
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	42	0.87	0.13	0.9
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	42	0.87	0.13	0.9
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	42	0.87	0.13	0.9
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	42	0.36	0.11	0.38
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	42	0.36	0.11	0.38
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	42	0.36	0.11	0.38
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	41	0.28	0.09	0.26
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	41	0.28	0.09	0.26
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	40	0.54	0.14	0.5
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	40	0.54	0.14	0.5
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	40	0.12	0.01	0.12
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	37	0.9	0.21	1.0
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	37	0.9	0.21	1.0
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	37	0.42	0.19	0.38
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	37	0.42	0.19	0.38
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	37	0.42	0.19	0.38
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	37	0.42	0.19	0.38
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	37	0.42	0.19	0.38

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	37	0.42	0.19	0.38
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	35	0.23	0.09	0.19
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	34	0.53	0.3	0.45
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	34	0.53	0.3	0.45
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	34	0.39	0.28	0.24
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	34	0.29	0.15	0.25
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	34	0.29	0.15	0.25
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	33	0.74	0.23	0.74

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	33	0.74	0.23	0.74
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	33	0.53	0.19	0.54
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	33	0.53	0.19	0.54
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	33	0.53	0.19	0.54
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	33	0.53	0.19	0.54
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	33	0.53	0.19	0.54
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	33	0.53	0.19	0.54
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	32	0.6	0.28	0.57
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	32	0.6	0.28	0.57
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	32	0.6	0.28	0.57
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	32	0.46	0.22	0.47
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD13	31	0.72	0.18	0.79
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD11	31	0.72	0.18	0.79
(2,578)	1:8:1:LYS:HA	1:4:1:VAL:HG23	31	0.72	0.18	0.79
(2,578)	1:8:1:LYS:HA	1:4:1:VAL:HG22	31	0.72	0.18	0.79
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD12	31	0.72	0.18	0.79
(2,578)	1:8:1:LYS:HA	1:4:1:VAL:HG21	31	0.72	0.18	0.79
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	31	0.24	0.11	0.22
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	31	0.24	0.11	0.22
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	31	0.12	0.02	0.12
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	31	0.12	0.02	0.12
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	29	0.31	0.17	0.28
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	27	1.05	0.01	1.04
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	27	1.05	0.01	1.04
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	27	1.0	0.05	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	27	1.0	0.05	1.01
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	27	0.88	0.31	0.82
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG2	27	0.88	0.31	0.82
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	27	0.29	0.1	0.31
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	27	0.29	0.1	0.31
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	27	0.29	0.1	0.31
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	27	0.29	0.1	0.31
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	27	0.29	0.1	0.31
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	27	0.29	0.1	0.31
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	26	0.93	0.16	0.98
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	26	0.93	0.16	0.98
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	26	0.93	0.16	0.98
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	26	0.93	0.16	0.98
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	26	0.93	0.16	0.98
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	26	0.93	0.16	0.98
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	25	0.15	0.07	0.13
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	25	0.15	0.07	0.13

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	25	0.15	0.07	0.13
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	25	0.15	0.07	0.13
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	24	0.64	0.41	1.01
(2,381)	1:61:1:ARG:HH21	1:62:1:ILE:H	23	0.71	0.28	0.8
(2,381)	1:61:1:ARG:HH11	1:62:1:ILE:H	23	0.71	0.28	0.8
(2,389)	1:61:1:ARG:HG2	1:70:1:ASP:HA	22	0.42	0.12	0.36
(2,389)	1:61:1:ARG:HG3	1:70:1:ASP:HA	22	0.42	0.12	0.36
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD2	19	0.8	0.23	0.87
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD3	19	0.8	0.23	0.87
(2,42)	1:9:1:ILE:H	1:17:1:ASP:H	19	0.63	0.3	0.7
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB2	19	0.28	0.07	0.26
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB3	19	0.28	0.07	0.26
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB2	19	0.28	0.07	0.26
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB3	19	0.28	0.07	0.26
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB2	19	0.28	0.07	0.26
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB3	19	0.28	0.07	0.26
(2,400)	1:61:1:ARG:HB2	1:81:1:TRP:HH2	18	0.85	0.19	0.84
(2,400)	1:61:1:ARG:HB3	1:81:1:TRP:HH2	18	0.85	0.19	0.84
(2,581)	1:25:1:GLN:HE21	1:26:1:ASP:HA	18	0.52	0.29	0.43
(2,581)	1:25:1:GLN:HE21	1:23:1:ASN:HA	18	0.52	0.29	0.43
(2,435)	1:62:1:ILE:HG21	1:67:1:TRP:HD1	17	0.66	0.11	0.66
(2,435)	1:62:1:ILE:HG22	1:67:1:TRP:HD1	17	0.66	0.11	0.66
(2,435)	1:62:1:ILE:HG23	1:67:1:TRP:HD1	17	0.66	0.11	0.66
(2,527)	1:72:1:CYS:HA	1:76:1:SER:H	17	0.19	0.06	0.17
(2,513)	1:70:1:ASP:HA	1:81:1:TRP:HD1	17	0.19	0.07	0.18
(1,591)	1:53:1:PHE:HE1	1:54:1:LYS:H	17	0.13	0.01	0.13
(1,591)	1:53:1:PHE:HE2	1:54:1:LYS:H	17	0.13	0.01	0.13
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE1	17	0.12	0.01	0.12
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE2	17	0.12	0.01	0.12
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE1	17	0.12	0.01	0.12
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE2	17	0.12	0.01	0.12
(2,402)	1:61:1:ARG:HG2	1:81:1:TRP:HH2	16	0.64	0.34	0.82
(2,402)	1:61:1:ARG:HG3	1:81:1:TRP:HH2	16	0.64	0.34	0.82
(2,575)	1:5:1:CYS:H	1:14:1:GLU:HB2	16	0.44	0.1	0.46
(2,575)	1:5:1:CYS:H	1:3:1:PRO:HB2	16	0.44	0.1	0.46
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG21	16	0.11	0.02	0.11
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG22	16	0.11	0.02	0.11
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG23	16	0.11	0.02	0.11
(2,434)	1:62:1:ILE:HG21	1:67:1:TRP:H	15	0.75	0.11	0.78
(2,434)	1:62:1:ILE:HG22	1:67:1:TRP:H	15	0.75	0.11	0.78
(2,434)	1:62:1:ILE:HG23	1:67:1:TRP:H	15	0.75	0.11	0.78
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB2	15	0.6	0.27	0.51

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB3	15	0.6	0.27	0.51
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB2	15	0.6	0.27	0.51
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB3	15	0.6	0.27	0.51
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB2	15	0.6	0.27	0.51
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB3	15	0.6	0.27	0.51
(2,430)	1:62:1:ILE:HG21	1:66:1:ASP:H	14	0.84	0.12	0.9
(2,430)	1:62:1:ILE:HG22	1:66:1:ASP:H	14	0.84	0.12	0.9
(2,430)	1:62:1:ILE:HG23	1:66:1:ASP:H	14	0.84	0.12	0.9
(1,777)	1:61:1:ARG:HH21	1:81:1:TRP:HZ2	14	0.3	0.11	0.29
(2,560)	1:80:1:PRO:HG2	1:81:1:TRP:HD1	14	0.3	0.08	0.29
(2,560)	1:80:1:PRO:HG3	1:81:1:TRP:HD1	14	0.3	0.08	0.29
(2,567)	1:81:1:TRP:HE3	1:82:1:ASN:H	14	0.12	0.02	0.12
(2,438)	1:62:1:ILE:HG21	1:81:1:TRP:HE3	13	0.29	0.12	0.26
(2,438)	1:62:1:ILE:HG22	1:81:1:TRP:HE3	13	0.29	0.12	0.26
(2,438)	1:62:1:ILE:HG23	1:81:1:TRP:HE3	13	0.29	0.12	0.26
(2,439)	1:62:1:ILE:HD11	1:81:1:TRP:HA	13	0.12	0.01	0.12
(2,439)	1:62:1:ILE:HD12	1:81:1:TRP:HA	13	0.12	0.01	0.12
(2,439)	1:62:1:ILE:HD13	1:81:1:TRP:HA	13	0.12	0.01	0.12
(2,577)	1:8:1:LYS:H	1:9:1:ILE:HG23	11	0.6	0.17	0.67
(2,577)	1:8:1:LYS:H	1:9:1:ILE:HG22	11	0.6	0.17	0.67
(2,577)	1:8:1:LYS:H	1:9:1:ILE:HG21	11	0.6	0.17	0.67
(2,577)	1:8:1:LYS:H	1:4:1:VAL:HG13	11	0.6	0.17	0.67
(2,577)	1:8:1:LYS:H	1:4:1:VAL:HG12	11	0.6	0.17	0.67
(2,441)	1:62:1:ILE:HD11	1:81:1:TRP:HE3	11	0.28	0.2	0.17
(2,441)	1:62:1:ILE:HD12	1:81:1:TRP:HE3	11	0.28	0.2	0.17
(2,441)	1:62:1:ILE:HD13	1:81:1:TRP:HE3	11	0.28	0.2	0.17
(2,483)	1:66:1:ASP:HB2	1:67:1:TRP:HE3	11	0.24	0.07	0.21
(2,483)	1:66:1:ASP:HB3	1:67:1:TRP:HE3	11	0.24	0.07	0.21
(2,411)	1:61:1:ARG:HH21	1:81:1:TRP:HH2	9	0.36	0.31	0.2
(2,191)	1:41:1:GLN:HA	1:53:1:PHE:HB2	9	0.21	0.11	0.19
(2,191)	1:41:1:GLN:HA	1:53:1:PHE:HB3	9	0.21	0.11	0.19
(2,595)	1:67:1:TRP:HE3	1:66:1:ASP:HA	7	0.12	0.01	0.11
(2,466)	1:64:1:ARG:HG2	1:67:1:TRP:HE1	6	0.21	0.1	0.18
(2,466)	1:64:1:ARG:HG3	1:67:1:TRP:HE1	6	0.21	0.1	0.18
(2,582)	1:30:1:ASN:HB3	1:35:1:LYS:HB3	5	1.19	0.65	1.05
(2,582)	1:30:1:ASN:HB3	1:35:1:LYS:HB2	5	1.19	0.65	1.05
(2,582)	1:30:1:ASN:HB3	1:36:1:LEU:HB3	5	1.19	0.65	1.05
(2,587)	1:56:1:ALA:HB2	1:75:1:LYS:HZ2	5	0.53	0.26	0.58
(2,587)	1:56:1:ALA:HB2	1:55:1:LYS:HZ1	5	0.53	0.26	0.58
(2,587)	1:56:1:ALA:HB1	1:75:1:LYS:HZ2	5	0.53	0.26	0.58
(2,422)	1:62:1:ILE:HG21	1:64:1:ARG:HD2	4	0.36	0.14	0.4
(2,422)	1:62:1:ILE:HG21	1:64:1:ARG:HD3	4	0.36	0.14	0.4

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(2,422)	1:62:1:ILE:HG22	1:64:1:ARG:HD2	4	0.36	0.14	0.4
(2,422)	1:62:1:ILE:HG22	1:64:1:ARG:HD3	4	0.36	0.14	0.4
(2,422)	1:62:1:ILE:HG23	1:64:1:ARG:HD2	4	0.36	0.14	0.4
(2,422)	1:62:1:ILE:HG23	1:64:1:ARG:HD3	4	0.36	0.14	0.4
(2,46)	1:10:1:LEU:HD11	1:11:1:GLU:HG2	4	0.15	0.01	0.15
(2,46)	1:10:1:LEU:HD11	1:11:1:GLU:HG3	4	0.15	0.01	0.15
(2,46)	1:10:1:LEU:HD12	1:11:1:GLU:HG2	4	0.15	0.01	0.15
(2,46)	1:10:1:LEU:HD12	1:11:1:GLU:HG3	4	0.15	0.01	0.15
(2,46)	1:10:1:LEU:HD13	1:11:1:GLU:HG2	4	0.15	0.01	0.15
(2,46)	1:10:1:LEU:HD13	1:11:1:GLU:HG3	4	0.15	0.01	0.15
(2,46)	1:10:1:LEU:HD21	1:11:1:GLU:HG2	4	0.15	0.01	0.15
(2,46)	1:10:1:LEU:HD21	1:11:1:GLU:HG3	4	0.15	0.01	0.15
(2,46)	1:10:1:LEU:HD22	1:11:1:GLU:HG2	4	0.15	0.01	0.15
(2,46)	1:10:1:LEU:HD22	1:11:1:GLU:HG3	4	0.15	0.01	0.15
(2,46)	1:10:1:LEU:HD23	1:11:1:GLU:HG2	4	0.15	0.01	0.15
(2,46)	1:10:1:LEU:HD23	1:11:1:GLU:HG3	4	0.15	0.01	0.15
(1,43)	1:5:1:CYS:HA	1:11:1:GLU:H	4	0.12	0.0	0.12
(2,71)	1:15:1:ASP:H	1:34:1:CYS:HA	4	0.11	0.01	0.11
(2,498)	1:68:1:ASN:HA	1:83:1:HIS:HD2	3	1.01	0.0	1.01
(2,412)	1:61:1:ARG:HH21	1:81:1:TRP:HZ3	3	0.69	0.23	0.85
(2,489)	1:67:1:TRP:HB2	1:83:1:HIS:HD2	3	0.54	0.11	0.55
(2,489)	1:67:1:TRP:HB3	1:83:1:HIS:HD2	3	0.54	0.11	0.55
(2,386)	1:61:1:ARG:HB2	1:69:1:ASP:HA	3	0.41	0.12	0.49
(2,386)	1:61:1:ARG:HB3	1:69:1:ASP:HA	3	0.41	0.12	0.49
(1,776)	1:61:1:ARG:HH21	1:81:1:TRP:HE3	3	0.37	0.08	0.33
(2,75)	1:16:1:CYS:HB2	1:29:1:CYS:H	3	0.37	0.28	0.22
(2,75)	1:16:1:CYS:HB3	1:29:1:CYS:H	3	0.37	0.28	0.22
(2,447)	1:63:1:ALA:HB1	1:67:1:TRP:HE3	3	0.16	0.02	0.15
(2,447)	1:63:1:ALA:HB2	1:67:1:TRP:HE3	3	0.16	0.02	0.15
(2,447)	1:63:1:ALA:HB3	1:67:1:TRP:HE3	3	0.16	0.02	0.15
(2,491)	1:67:1:TRP:HD1	1:83:1:HIS:HB2	3	0.13	0.03	0.12
(2,491)	1:67:1:TRP:HD1	1:83:1:HIS:HB3	3	0.13	0.03	0.12
(1,111)	1:10:1:LEU:HD11	1:11:1:GLU:HB2	3	0.13	0.01	0.13
(1,111)	1:10:1:LEU:HD11	1:11:1:GLU:HB3	3	0.13	0.01	0.13
(1,111)	1:10:1:LEU:HD12	1:11:1:GLU:HB2	3	0.13	0.01	0.13
(1,111)	1:10:1:LEU:HD12	1:11:1:GLU:HB3	3	0.13	0.01	0.13
(1,111)	1:10:1:LEU:HD13	1:11:1:GLU:HB2	3	0.13	0.01	0.13
(1,111)	1:10:1:LEU:HD13	1:11:1:GLU:HB3	3	0.13	0.01	0.13
(1,111)	1:10:1:LEU:HD21	1:11:1:GLU:HB2	3	0.13	0.01	0.13
(1,111)	1:10:1:LEU:HD21	1:11:1:GLU:HB3	3	0.13	0.01	0.13
(1,111)	1:10:1:LEU:HD22	1:11:1:GLU:HB2	3	0.13	0.01	0.13
(1,111)	1:10:1:LEU:HD22	1:11:1:GLU:HB3	3	0.13	0.01	0.13

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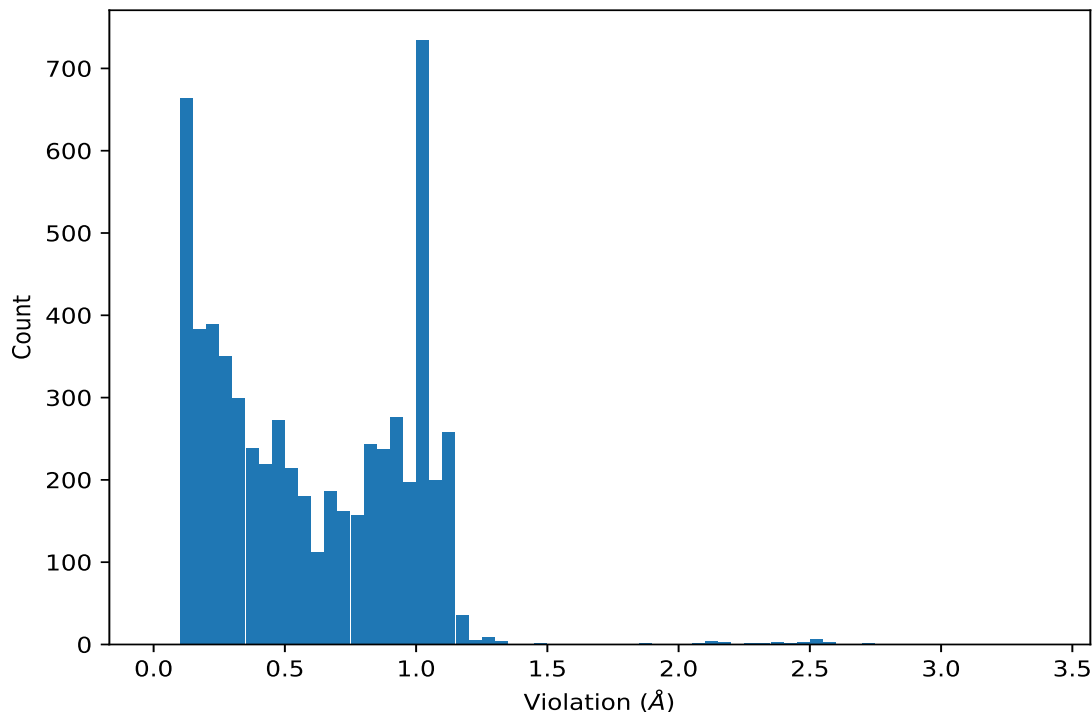
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,111)	1:10:1:LEU:HD23	1:11:1:GLU:HB2	3	0.13	0.01	0.13
(1,111)	1:10:1:LEU:HD23	1:11:1:GLU:HB3	3	0.13	0.01	0.13
(1,698)	1:58:1:THR:HG21	1:71:1:TYR:HE1	3	0.11	0.01	0.11
(1,698)	1:58:1:THR:HG21	1:71:1:TYR:HE2	3	0.11	0.01	0.11
(1,698)	1:58:1:THR:HG22	1:71:1:TYR:HE1	3	0.11	0.01	0.11
(1,698)	1:58:1:THR:HG22	1:71:1:TYR:HE2	3	0.11	0.01	0.11
(1,698)	1:58:1:THR:HG23	1:71:1:TYR:HE1	3	0.11	0.01	0.11
(1,698)	1:58:1:THR:HG23	1:71:1:TYR:HE2	3	0.11	0.01	0.11
(1,362)	1:33:1:THR:H	1:34:1:CYS:HA	3	0.1	0.0	0.1
(2,174)	1:40:1:SER:H	1:51:1:CYS:HB2	2	0.62	0.05	0.62
(2,174)	1:40:1:SER:H	1:51:1:CYS:HB3	2	0.62	0.05	0.62
(1,766)	1:61:1:ARG:HH11	1:79:1:CYS:HB2	2	0.45	0.28	0.45
(1,766)	1:61:1:ARG:HH21	1:79:1:CYS:HB2	2	0.45	0.28	0.45
(1,774)	1:61:1:ARG:HH21	1:81:1:TRP:HD1	2	0.22	0.02	0.22
(2,566)	1:81:1:TRP:HE1	1:82:1:ASN:H	2	0.18	0.04	0.18
(1,988)	1:25:1:GLN:H	1:26:1:ASP:HA	2	0.17	0.02	0.17
(2,221)	1:44:1:TYR:H	1:53:1:PHE:HD1	2	0.14	0.01	0.14
(2,221)	1:44:1:TYR:H	1:53:1:PHE:HD2	2	0.14	0.01	0.14
(2,507)	1:70:1:ASP:HB2	1:72:1:CYS:H	2	0.14	0.01	0.14
(2,507)	1:70:1:ASP:HB3	1:72:1:CYS:H	2	0.14	0.01	0.14
(1,288)	1:27:1:ARG:H	1:28:1:CYS:H	2	0.13	0.01	0.13
(2,25)	1:8:1:LYS:H	1:10:1:LEU:HD11	2	0.13	0.0	0.13
(2,25)	1:8:1:LYS:H	1:10:1:LEU:HD12	2	0.13	0.0	0.13
(2,25)	1:8:1:LYS:H	1:10:1:LEU:HD13	2	0.13	0.0	0.13
(2,25)	1:8:1:LYS:H	1:10:1:LEU:HD21	2	0.13	0.0	0.13
(2,25)	1:8:1:LYS:H	1:10:1:LEU:HD22	2	0.13	0.0	0.13
(2,25)	1:8:1:LYS:H	1:10:1:LEU:HD23	2	0.13	0.0	0.13
(1,279)	1:26:1:ASP:H	1:27:1:ARG:HB2	2	0.12	0.01	0.12
(1,279)	1:26:1:ASP:H	1:27:1:ARG:HB3	2	0.12	0.01	0.12
(1,160)	1:15:1:ASP:H	1:17:1:ASP:HB2	2	0.11	0.0	0.11
(1,160)	1:15:1:ASP:H	1:17:1:ASP:HB3	2	0.11	0.0	0.11
(1,260)	1:24:1:CYS:H	1:25:1:GLN:H	2	0.11	0.0	0.11
(1,464)	1:43:1:ASN:H	1:44:1:TYR:H	2	0.11	0.0	0.11
(1,867)	1:70:1:ASP:HA	1:71:1:TYR:HE1	2	0.1	0.0	0.1
(1,867)	1:70:1:ASP:HA	1:71:1:TYR:HE2	2	0.1	0.0	0.1
(3,3)	1:30:1:ASN:O	1:35:1:LYS:H	2	0.1	0.0	0.1

¹Number of violated models, ²Standard deviation

9.5 All violated distance restraints [i](#)

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

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



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

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

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB2	21	3.36
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB3	9	3.32
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB3	5	3.23
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB1	25	2.97
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB3	17	2.9
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB1	14	2.81
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB2	20	2.73
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB1	6	2.71
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB2	42	2.62
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB2	24	2.58

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB1	41	2.57
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB2	15	2.55
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB1	4	2.54
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB2	27	2.54
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB3	22	2.53
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB3	33	2.52
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB1	34	2.51
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB2	8	2.5
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB2	19	2.5
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB2	12	2.49
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB1	7	2.47
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB3	10	2.46
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB2	11	2.4
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB2	30	2.4
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB3	16	2.37
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB2	3	2.36
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB3	32	2.35
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB3	2	2.33
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB2	23	2.3
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB2	31	2.27
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB1	35	2.27
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB2	26	2.16
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB2	29	2.16
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB3	37	2.16
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB2	18	2.13
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB2	28	2.12
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB1	36	2.12
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB2	39	2.11
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB1	43	2.09
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB2	13	2.05
(2,582)	1:30:1:ASN:HB3	1:36:1:LEU:HB3	19	1.89
(2,582)	1:30:1:ASN:HB3	1:36:1:LEU:HB3	24	1.88
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	19	1.59
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	3	1.45
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	5	1.45
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	33	1.42
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	37	1.39
(2,583)	1:31:1:ALA:HB2	1:26:1:ASP:H	31	1.33
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	24	1.33
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	1	1.32
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB2	38	1.32
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	11	1.29

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,583)	1:31:1:ALA:HB1	1:26:1:ASP:H	25	1.27
(2,583)	1:31:1:ALA:HB2	1:26:1:ASP:H	2	1.26
(2,583)	1:31:1:ALA:HB2	1:26:1:ASP:H	21	1.26
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	32	1.26
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	10	1.26
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	27	1.26
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	31	1.26
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	38	1.25
(2,583)	1:31:1:ALA:HB3	1:26:1:ASP:H	39	1.24
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	40	1.24
(2,583)	1:31:1:ALA:HB1	1:26:1:ASP:H	16	1.2
(2,583)	1:31:1:ALA:HB1	1:26:1:ASP:H	43	1.2
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	15	1.2
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	2	1.19
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	43	1.19
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	39	1.18
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	39	1.18
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	26	1.18
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	30	1.18
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	39	1.18
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	36	1.17
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	18	1.17
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	18	1.17
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	27	1.17
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	27	1.17
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	28	1.17
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	28	1.17
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	36	1.17
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	36	1.17
(2,583)	1:31:1:ALA:HB3	1:26:1:ASP:H	4	1.16
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	11	1.16
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	11	1.16
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	15	1.16
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	15	1.16
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	24	1.16
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	24	1.16
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	26	1.16
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	26	1.16
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	33	1.16
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	33	1.16
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	37	1.16
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	37	1.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,583)	1:31:1:ALA:HB1	1:26:1:ASP:H	35	1.15
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	37	1.15
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	37	1.15
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	37	1.15
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	37	1.15
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	37	1.15
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	37	1.15
(2,583)	1:31:1:ALA:HB1	1:26:1:ASP:H	9	1.14
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG2	34	1.14
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	30	1.14
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	30	1.14
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	43	1.14
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	43	1.14
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	6	1.14
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	18	1.14
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	20	1.14
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	36	1.14
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	37	1.14
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB3	40	1.14
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	11	1.14
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	11	1.14
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	11	1.14
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	11	1.14
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	11	1.14
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	11	1.14
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	24	1.14
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	24	1.14
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	24	1.14
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	24	1.14
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	24	1.14
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	24	1.14
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	26	1.14
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	26	1.14
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	26	1.14
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	26	1.14
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	26	1.14
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	26	1.14
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	28	1.14
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	28	1.14
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	28	1.14
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	28	1.14
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	28	1.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	28	1.14
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	29	1.14
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	29	1.14
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	29	1.14
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	29	1.14
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	29	1.14
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	29	1.14
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	30	1.14
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	30	1.14
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	30	1.14
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	30	1.14
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	30	1.14
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	30	1.14
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	25	1.13
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	25	1.13
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	25	1.13
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	25	1.13
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	25	1.13
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	25	1.13
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	16	1.13
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	28	1.13
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	15	1.13
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	15	1.13
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	15	1.13
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	15	1.13
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	15	1.13
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	15	1.13
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	18	1.13
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	18	1.13
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	18	1.13
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	18	1.13
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	18	1.13
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	18	1.13
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	27	1.13
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	27	1.13
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	27	1.13
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	27	1.13
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	27	1.13
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	27	1.13
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	33	1.13
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	33	1.13
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	33	1.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	33	1.13
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	33	1.13
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	33	1.13
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	36	1.13
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	36	1.13
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	36	1.13
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	36	1.13
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	36	1.13
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	36	1.13
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	39	1.13
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	39	1.13
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	39	1.13
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	39	1.13
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	39	1.13
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	39	1.13
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	43	1.13
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	43	1.13
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	43	1.13
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	43	1.13
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	43	1.13
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	43	1.13
(2,583)	1:31:1:ALA:HB3	1:26:1:ASP:H	38	1.12
(2,581)	1:25:1:GLN:HE21	1:23:1:ASN:HA	35	1.12
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	29	1.12
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	29	1.12
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	32	1.12
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	9	1.12
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	9	1.12
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	9	1.12
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	9	1.12
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	9	1.12
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	9	1.12
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	21	1.12
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	21	1.12
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	21	1.12
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	21	1.12
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	21	1.12
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	21	1.12
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	40	1.12
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	40	1.12
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	40	1.12
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	40	1.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	40	1.12
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	40	1.12
(2,583)	1:31:1:ALA:HB3	1:26:1:ASP:H	22	1.11
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	27	1.11
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	4	1.11
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	4	1.11
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	14	1.11
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	17	1.11
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	25	1.11
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	42	1.11
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	1	1.11
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	1	1.11
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	1	1.11
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	1	1.11
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	1	1.11
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	1	1.11
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	2	1.11
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	2	1.11
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	2	1.11
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	2	1.11
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	2	1.11
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	2	1.11
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	5	1.11
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	5	1.11
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	5	1.11
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	5	1.11
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	5	1.11
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	5	1.11
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	8	1.11
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	8	1.11
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	8	1.11
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	8	1.11
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	8	1.11
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	8	1.11
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	13	1.11
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	13	1.11
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	13	1.11
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	13	1.11
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	13	1.11
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	13	1.11
(2,583)	1:31:1:ALA:HB1	1:26:1:ASP:H	18	1.1
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	20	1.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	20	1.1
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	3	1.1
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	3	1.1
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	3	1.1
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	3	1.1
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	3	1.1
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	3	1.1
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	12	1.1
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	12	1.1
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	12	1.1
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	12	1.1
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	12	1.1
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	12	1.1
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	14	1.1
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	14	1.1
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	14	1.1
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	14	1.1
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	14	1.1
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	14	1.1
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	20	1.1
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	20	1.1
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	20	1.1
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	20	1.1
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	20	1.1
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	20	1.1
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	22	1.1
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	22	1.1
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	22	1.1
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	22	1.1
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	22	1.1
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	22	1.1
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	23	1.1
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	23	1.1
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	23	1.1
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	23	1.1
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	23	1.1
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	23	1.1
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	31	1.1
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	31	1.1
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	31	1.1
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	31	1.1
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	31	1.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	31	1.1
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	32	1.1
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	32	1.1
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	32	1.1
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	32	1.1
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	32	1.1
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	32	1.1
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	38	1.1
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	38	1.1
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	38	1.1
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	38	1.1
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	38	1.1
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	38	1.1
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	42	1.1
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	42	1.1
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	42	1.1
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	42	1.1
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	42	1.1
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	42	1.1
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	41	1.1
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	41	1.1
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	41	1.1
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	41	1.1
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	41	1.1
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	41	1.1
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	41	1.1
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	41	1.1
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	41	1.1
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	41	1.1
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	41	1.1
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	41	1.1
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	41	1.1
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	41	1.1
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	41	1.1
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	41	1.1
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	41	1.1
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	41	1.1
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	41	1.1
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	41	1.1
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	41	1.1
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	41	1.1
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	41	1.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	41	1.1
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	41	1.1
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	41	1.1
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	41	1.1
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	41	1.1
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	41	1.1
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	41	1.1
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	41	1.1
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	41	1.1
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	41	1.1
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	41	1.1
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	41	1.1
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	41	1.1
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	9	1.09
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	9	1.09
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	31	1.09
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	31	1.09
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	43	1.09
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	43	1.09
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	4	1.09
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	4	1.09
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	4	1.09
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	4	1.09
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	4	1.09
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	4	1.09
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	6	1.09
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	6	1.09
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	6	1.09
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	6	1.09
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	6	1.09
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	6	1.09
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	7	1.09
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	7	1.09
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	7	1.09
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	7	1.09
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	7	1.09
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	7	1.09
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	10	1.09
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	10	1.09
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	10	1.09
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	10	1.09
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	10	1.09

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	10	1.09
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	16	1.09
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	16	1.09
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	16	1.09
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	16	1.09
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	16	1.09
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	16	1.09
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	17	1.09
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	17	1.09
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	17	1.09
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	17	1.09
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	17	1.09
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	17	1.09
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	19	1.09
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	19	1.09
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	19	1.09
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	19	1.09
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	19	1.09
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	19	1.09
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	25	1.09
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	25	1.09
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	25	1.09
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	25	1.09
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	25	1.09
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	25	1.09
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	34	1.09
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	34	1.09
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	34	1.09
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	34	1.09
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	34	1.09
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	34	1.09
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	35	1.09
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	35	1.09
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	35	1.09
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	35	1.09
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	35	1.09
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	35	1.09
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE1	41	1.09
(2,321)	1:56:1:ALA:HB1	1:71:1:TYR:HE2	41	1.09
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE1	41	1.09
(2,321)	1:56:1:ALA:HB2	1:71:1:TYR:HE2	41	1.09
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE1	41	1.09

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,321)	1:56:1:ALA:HB3	1:71:1:TYR:HE2	41	1.09
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	1	1.08
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	1	1.08
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	5	1.08
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	5	1.08
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	6	1.08
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	6	1.08
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	14	1.08
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	14	1.08
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	17	1.08
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	17	1.08
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	21	1.08
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	21	1.08
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	25	1.08
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	25	1.08
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	38	1.08
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	38	1.08
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	42	1.08
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	42	1.08
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	5	1.08
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	5	1.08
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	13	1.08
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	13	1.08
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	33	1.08
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	5	1.07
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	5	1.07
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	19	1.07
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	19	1.07
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	22	1.07
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	22	1.07
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	34	1.07
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	34	1.07
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	41	1.07
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	41	1.07
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	16	1.07
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	16	1.07
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	40	1.07
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	40	1.07
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	39	1.07
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	39	1.07
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	39	1.07
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	39	1.07

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	39	1.07
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	39	1.07
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	35	1.07
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	2	1.07
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	12	1.07
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	24	1.07
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	31	1.07
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	7	1.06
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	7	1.06
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	12	1.06
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	12	1.06
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	23	1.06
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	23	1.06
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	2	1.06
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	2	1.06
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	10	1.06
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	10	1.06
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	19	1.06
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	19	1.06
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	23	1.06
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	23	1.06
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	32	1.06
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	32	1.06
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	35	1.06
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	35	1.06
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	11	1.06
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	11	1.06
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	35	1.06
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	35	1.06
(2,400)	1:61:1:ARG:HB2	1:81:1:TRP:HH2	9	1.06
(2,400)	1:61:1:ARG:HB3	1:81:1:TRP:HH2	9	1.06
(2,400)	1:61:1:ARG:HB2	1:81:1:TRP:HH2	21	1.06
(2,400)	1:61:1:ARG:HB3	1:81:1:TRP:HH2	21	1.06
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	21	1.06
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	4	1.06
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	6	1.06
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	8	1.06
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	10	1.06
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	13	1.06
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	14	1.06
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	15	1.06
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	18	1.06

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	19	1.06
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	20	1.06
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	21	1.06
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	22	1.06
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	23	1.06
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	28	1.06
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	29	1.06
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	30	1.06
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	35	1.06
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	36	1.06
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	39	1.06
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	41	1.06
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	42	1.06
(2,582)	1:30:1:ASN:HB3	1:35:1:LYS:HB2	10	1.05
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	1	1.05
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	1	1.05
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	3	1.05
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	3	1.05
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	25	1.05
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	25	1.05
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	40	1.05
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	40	1.05
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	7	1.05
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	7	1.05
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	8	1.05
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	8	1.05
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	22	1.05
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	22	1.05
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	21	1.05
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	21	1.05
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	8	1.05
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	13	1.05
(2,381)	1:61:1:ARG:HH21	1:62:1:ILE:H	10	1.05
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	3	1.05
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	7	1.05
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	9	1.05
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	17	1.05
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	26	1.05
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	27	1.05
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	32	1.05
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	37	1.05
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	40	1.05

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	43	1.05
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	21	1.05
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	21	1.05
(2,583)	1:31:1:ALA:HB1	1:26:1:ASP:H	26	1.04
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	2	1.04
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	2	1.04
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	6	1.04
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	6	1.04
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	8	1.04
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	8	1.04
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	10	1.04
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	10	1.04
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	13	1.04
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	13	1.04
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	16	1.04
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	16	1.04
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	17	1.04
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	17	1.04
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	20	1.04
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	20	1.04
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	32	1.04
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	32	1.04
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	38	1.04
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	38	1.04
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	42	1.04
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	42	1.04
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	3	1.04
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	3	1.04
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	12	1.04
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	12	1.04
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	13	1.04
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	13	1.04
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	9	1.04
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	9	1.04
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	18	1.04
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	18	1.04
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	24	1.04
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	24	1.04
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	27	1.04
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	27	1.04
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	29	1.04
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	29	1.04

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	30	1.04
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	30	1.04
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	12	1.04
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	1	1.04
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	11	1.04
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	25	1.04
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	34	1.04
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	38	1.04
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	26	1.04
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	26	1.04
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	26	1.04
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	26	1.04
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	26	1.04
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	26	1.04
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	26	1.04
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	26	1.04
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	26	1.04
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	26	1.04
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	26	1.04
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	26	1.04
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	26	1.04
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	26	1.04
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	26	1.04
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	26	1.04
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	26	1.04
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	26	1.04
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	26	1.04
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	26	1.04
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	26	1.04
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	26	1.04
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	26	1.04
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	26	1.04
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	26	1.04
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	26	1.04
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	26	1.04
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	26	1.04
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	26	1.04
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	26	1.04
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	26	1.04
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	26	1.04
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	26	1.04
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	26	1.04

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	26	1.04
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	26	1.04
(2,583)	1:31:1:ALA:HB1	1:26:1:ASP:H	13	1.03
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	14	1.03
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	14	1.03
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	31	1.03
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	31	1.03
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	35	1.03
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	35	1.03
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	34	1.03
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	34	1.03
(2,504)	1:69:1:ASP:HB2	1:82:1:ASN:H	41	1.03
(2,504)	1:69:1:ASP:HB3	1:82:1:ASN:H	41	1.03
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	15	1.03
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	15	1.03
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	26	1.03
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	26	1.03
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	28	1.03
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	28	1.03
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	36	1.03
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	36	1.03
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	37	1.03
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	37	1.03
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	8	1.03
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	8	1.03
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	8	1.03
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	8	1.03
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	11	1.03
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	11	1.03
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	11	1.03
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	11	1.03
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	21	1.03
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	21	1.03
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	21	1.03
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	21	1.03
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	15	1.03
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	15	1.03
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	15	1.03
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	15	1.03
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	15	1.03
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	15	1.03
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	33	1.03

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	33	1.03
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	33	1.03
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	33	1.03
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	33	1.03
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	33	1.03
(2,400)	1:61:1:ARG:HB2	1:81:1:TRP:HH2	33	1.03
(2,400)	1:61:1:ARG:HB3	1:81:1:TRP:HH2	33	1.03
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	9	1.03
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	16	1.03
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	27	1.03
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	1	1.03
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	1	1.03
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	2	1.03
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	2	1.03
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	5	1.03
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	5	1.03
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	8	1.03
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	8	1.03
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	23	1.03
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	23	1.03
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	27	1.03
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	27	1.03
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	18	1.03
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	18	1.03
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	7	1.03
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	7	1.03
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	12	1.03
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	12	1.03
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	25	1.03
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	25	1.03
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	43	1.03
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	43	1.03
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	4	1.02
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	4	1.02
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	18	1.02
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	26	1.02
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	28	1.02
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	33	1.02
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	36	1.02
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	37	1.02
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	8	1.02
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	8	1.02

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	33	1.02
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	33	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	1	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	1	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	1	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	1	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	2	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	2	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	2	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	2	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	4	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	4	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	4	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	4	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	9	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	9	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	9	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	9	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	12	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	12	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	12	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	12	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	14	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	14	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	14	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	14	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	15	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	15	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	15	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	15	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	17	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	17	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	17	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	17	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	18	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	18	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	18	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	18	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	24	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	24	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	24	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	24	1.02

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	26	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	26	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	26	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	26	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	27	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	27	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	27	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	27	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	28	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	28	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	28	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	28	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	30	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	30	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	30	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	30	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	31	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	31	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	31	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	31	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	32	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	32	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	32	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	32	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	33	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	33	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	33	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	33	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	36	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	36	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	36	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	36	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	37	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	37	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	37	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	37	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	42	1.02
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	42	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	42	1.02
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	42	1.02
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	5	1.02
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	5	1.02

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	5	1.02
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	5	1.02
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	5	1.02
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	5	1.02
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	23	1.02
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	23	1.02
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	23	1.02
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	23	1.02
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	23	1.02
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	23	1.02
(2,400)	1:61:1:ARG:HB2	1:81:1:TRP:HH2	43	1.02
(2,400)	1:61:1:ARG:HB3	1:81:1:TRP:HH2	43	1.02
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	23	1.02
(2,337)	1:57:1:GLY:H	1:79:1:CYS:HA	5	1.02
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	11	1.02
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	23	1.02
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	3	1.02
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	3	1.02
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	6	1.02
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	6	1.02
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	9	1.02
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	9	1.02
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	10	1.02
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	10	1.02
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	11	1.02
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	11	1.02
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	17	1.02
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	17	1.02
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	25	1.02
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	25	1.02
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	26	1.02
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	26	1.02
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	28	1.02
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	28	1.02
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	40	1.02
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	40	1.02
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	35	1.02
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	35	1.02
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	24	1.02
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	36	1.02
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	1	1.02
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	1	1.02

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	14	1.02
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	14	1.02
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	15	1.02
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	15	1.02
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	17	1.02
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	17	1.02
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	27	1.02
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	27	1.02
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	28	1.02
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	28	1.02
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	32	1.02
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	32	1.02
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	33	1.02
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	33	1.02
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	1	1.02
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	1	1.02
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	22	1.02
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	22	1.02
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	23	1.02
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	23	1.02
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	35	1.02
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	35	1.02
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	14	1.02
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	14	1.02
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	14	1.02
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	14	1.02
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	14	1.02
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	14	1.02
(2,42)	1:9:1:ILE:H	1:17:1:ASP:H	26	1.02
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	38	1.02
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	38	1.02
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	38	1.02
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	38	1.02
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	38	1.02
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	38	1.02
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	38	1.02
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	38	1.02
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	38	1.02
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	38	1.02
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	38	1.02
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	38	1.02
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	38	1.02

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	38	1.02
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	38	1.02
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	38	1.02
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	38	1.02
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	38	1.02
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	38	1.02
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	38	1.02
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	38	1.02
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	38	1.02
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	38	1.02
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	38	1.02
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	38	1.02
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	38	1.02
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	38	1.02
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	38	1.02
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	38	1.02
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	38	1.02
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	38	1.02
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	38	1.02
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	38	1.02
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	38	1.02
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	38	1.02
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	38	1.02
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	24	1.01
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB2	4	1.01
(2,571)	1:81:1:TRP:HZ2	1:83:1:HIS:HB3	4	1.01
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	7	1.01
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	7	1.01
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	9	1.01
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	11	1.01
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	15	1.01
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	21	1.01
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	24	1.01
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	27	1.01
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	39	1.01
(2,498)	1:68:1:ASN:HA	1:83:1:HIS:HD2	29	1.01
(2,498)	1:68:1:ASN:HA	1:83:1:HIS:HD2	30	1.01
(2,498)	1:68:1:ASN:HA	1:83:1:HIS:HD2	43	1.01
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	31	1.01
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	31	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	1	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	1	1.01

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	3	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	3	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	4	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	4	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	6	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	6	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	7	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	7	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	10	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	10	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	12	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	12	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	14	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	14	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	16	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	16	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	17	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	17	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	19	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	19	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	20	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	20	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	22	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	22	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	23	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	23	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	31	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	31	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	32	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	32	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	34	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	34	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	41	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	41	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	42	1.01
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	42	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	3	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	3	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	3	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	3	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	6	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	6	1.01

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	6	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	6	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	7	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	7	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	7	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	7	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	10	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	10	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	10	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	10	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	16	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	16	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	16	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	16	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	19	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	19	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	19	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	19	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	20	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	20	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	20	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	20	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	22	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	22	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	22	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	22	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	23	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	23	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	23	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	23	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	25	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	25	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	25	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	25	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	29	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	29	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	29	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	29	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	34	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	34	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	34	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	34	1.01

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	38	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	38	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	38	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	38	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	40	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	40	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	40	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	40	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	41	1.01
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	41	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	41	1.01
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	41	1.01
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	6	1.01
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	6	1.01
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	6	1.01
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	6	1.01
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	6	1.01
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	6	1.01
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	20	1.01
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	20	1.01
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	20	1.01
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	20	1.01
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	20	1.01
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	20	1.01
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	22	1.01
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	22	1.01
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	22	1.01
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	22	1.01
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	22	1.01
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	22	1.01
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	41	1.01
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	41	1.01
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	41	1.01
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	41	1.01
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	41	1.01
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	41	1.01
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	3	1.01
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	3	1.01
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	3	1.01
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	8	1.01
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	8	1.01
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	8	1.01

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	22	1.01
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	22	1.01
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	22	1.01
(2,381)	1:61:1:ARG:HH21	1:62:1:ILE:H	12	1.01
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	8	1.01
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	9	1.01
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	15	1.01
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	16	1.01
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	17	1.01
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	19	1.01
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	25	1.01
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	38	1.01
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	42	1.01
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	40	1.01
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	7	1.01
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	7	1.01
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	29	1.01
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	29	1.01
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	32	1.01
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	32	1.01
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	37	1.01
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	37	1.01
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	42	1.01
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	42	1.01
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	2	1.01
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	2	1.01
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	12	1.01
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	12	1.01
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	13	1.01
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	13	1.01
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	14	1.01
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	14	1.01
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	22	1.01
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	22	1.01
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	24	1.01
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	24	1.01
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	30	1.01
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	30	1.01
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	36	1.01
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	36	1.01
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	39	1.01
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	39	1.01

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	5	1.01
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	5	1.01
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	12	1.01
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	12	1.01
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	18	1.01
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	18	1.01
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	26	1.01
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	26	1.01
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	31	1.01
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	31	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	2	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	2	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	5	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	5	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	13	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	13	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	14	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	14	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	15	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	15	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	18	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	18	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	20	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	20	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	24	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	24	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	29	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	29	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	30	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	30	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	33	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	33	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	36	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	36	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	39	1.01
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	39	1.01
(2,42)	1:9:1:ILE:H	1:17:1:ASP:H	38	1.01
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	31	1.01
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	31	1.01
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	31	1.01
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	31	1.01
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	31	1.01

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	31	1.01
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	31	1.01
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	31	1.01
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	31	1.01
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	31	1.01
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	31	1.01
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	31	1.01
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	31	1.01
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	31	1.01
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	31	1.01
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	31	1.01
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	31	1.01
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	31	1.01
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	31	1.01
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	31	1.01
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	31	1.01
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	31	1.01
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	31	1.01
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	31	1.01
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	31	1.01
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	31	1.01
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	31	1.01
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	31	1.01
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	31	1.01
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	31	1.01
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	31	1.01
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	31	1.01
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	31	1.01
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	31	1.01
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	31	1.01
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	31	1.01
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	1	1.0
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	1	1.0
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	4	1.0
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	4	1.0
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	8	1.0
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	8	1.0
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	34	1.0
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	34	1.0
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	36	1.0
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	36	1.0
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	41	1.0

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	41	1.0
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	2	1.0
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	2	1.0
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	25	1.0
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	25	1.0
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	17	1.0
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	17	1.0
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	17	1.0
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	17	1.0
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	17	1.0
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	17	1.0
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	33	1.0
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	33	1.0
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	33	1.0
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	33	1.0
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	33	1.0
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	33	1.0
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	34	1.0
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	34	1.0
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	34	1.0
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	34	1.0
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	34	1.0
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	34	1.0
(2,402)	1:61:1:ARG:HG2	1:81:1:TRP:HH2	9	1.0
(2,402)	1:61:1:ARG:HG3	1:81:1:TRP:HH2	9	1.0
(2,402)	1:61:1:ARG:HG2	1:81:1:TRP:HH2	15	1.0
(2,402)	1:61:1:ARG:HG3	1:81:1:TRP:HH2	15	1.0
(2,400)	1:61:1:ARG:HB2	1:81:1:TRP:HH2	11	1.0
(2,400)	1:61:1:ARG:HB3	1:81:1:TRP:HH2	11	1.0
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	34	1.0
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	34	1.0
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	34	1.0
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	41	1.0
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	41	1.0
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	41	1.0
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	1	1.0
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	2	1.0
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	10	1.0
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	13	1.0
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	26	1.0
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	29	1.0
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	30	1.0

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	31	1.0
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	36	1.0
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	39	1.0
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	4	1.0
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	4	1.0
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	19	1.0
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	19	1.0
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	34	1.0
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	34	1.0
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	35	1.0
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	35	1.0
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	43	1.0
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	43	1.0
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD2	5	1.0
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD3	5	1.0
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD2	12	1.0
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD3	12	1.0
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD2	16	1.0
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD3	16	1.0
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD2	20	1.0
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD3	20	1.0
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD2	31	1.0
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD3	31	1.0
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD2	35	1.0
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD3	35	1.0
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD2	42	1.0
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD3	42	1.0
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	1	1.0
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	1	1.0
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	7	1.0
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	7	1.0
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	9	1.0
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	9	1.0
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	16	1.0
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	16	1.0
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	20	1.0
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	20	1.0
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	23	1.0
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	23	1.0
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	32	1.0
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	32	1.0
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	33	1.0

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	33	1.0
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	41	1.0
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	41	1.0
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	42	1.0
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	42	1.0
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	16	1.0
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	6	1.0
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	6	1.0
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	7	1.0
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	7	1.0
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	8	1.0
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	8	1.0
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	23	1.0
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	23	1.0
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	29	1.0
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	29	1.0
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	38	1.0
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	38	1.0
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	4	1.0
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	4	1.0
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	16	1.0
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	16	1.0
(2,42)	1:9:1:ILE:H	1:17:1:ASP:H	10	1.0
(2,583)	1:31:1:ALA:HB1	1:26:1:ASP:H	24	0.99
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD13	39	0.99
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	35	0.99
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	35	0.99
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	43	0.99
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	43	0.99
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	25	0.99
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	25	0.99
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	7	0.99
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	7	0.99
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	7	0.99
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	7	0.99
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	7	0.99
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	7	0.99
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	19	0.99
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	19	0.99
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	19	0.99
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	19	0.99
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	19	0.99

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	19	0.99
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	31	0.99
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	31	0.99
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	31	0.99
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	31	0.99
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	31	0.99
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	31	0.99
(2,381)	1:61:1:ARG:HH21	1:62:1:ILE:H	16	0.99
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	6	0.99
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	12	0.99
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	21	0.99
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	27	0.99
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	27	0.99
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	37	0.99
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	2	0.99
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	2	0.99
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	16	0.99
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	16	0.99
(2,583)	1:31:1:ALA:HB1	1:26:1:ASP:H	32	0.98
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	32	0.98
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	32	0.98
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	35	0.98
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	35	0.98
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	5	0.98
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	5	0.98
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	7	0.98
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	7	0.98
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	7	0.98
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	7	0.98
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	7	0.98
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	7	0.98
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	14	0.98
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	14	0.98
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	14	0.98
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	14	0.98
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	14	0.98
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	14	0.98
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	4	0.98
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	4	0.98
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	4	0.98
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	4	0.98
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	4	0.98

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	4	0.98
(2,381)	1:61:1:ARG:HH21	1:62:1:ILE:H	23	0.98
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	24	0.98
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	43	0.98
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	15	0.98
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	15	0.98
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	11	0.98
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	11	0.98
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	11	0.98
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	11	0.98
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	11	0.98
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	11	0.98
(2,583)	1:31:1:ALA:HB2	1:26:1:ASP:H	33	0.97
(2,581)	1:25:1:GLN:HE21	1:23:1:ASN:HA	39	0.97
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	14	0.97
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	14	0.97
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	20	0.97
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	20	0.97
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	20	0.97
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	20	0.97
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	20	0.97
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	20	0.97
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	27	0.97
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	27	0.97
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	27	0.97
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	27	0.97
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	27	0.97
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	27	0.97
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	12	0.97
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	12	0.97
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	12	0.97
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	12	0.97
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	12	0.97
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	12	0.97
(2,402)	1:61:1:ARG:HG2	1:81:1:TRP:HH2	21	0.97
(2,402)	1:61:1:ARG:HG3	1:81:1:TRP:HH2	21	0.97
(2,400)	1:61:1:ARG:HB2	1:81:1:TRP:HH2	27	0.97
(2,400)	1:61:1:ARG:HB3	1:81:1:TRP:HH2	27	0.97
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	4	0.97
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	22	0.97
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	28	0.97
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	37	0.97

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	13	0.97
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	13	0.97
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	16	0.97
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	16	0.97
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	31	0.97
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	31	0.97
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	15	0.97
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	15	0.97
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	41	0.97
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	6	0.97
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	6	0.97
(2,583)	1:31:1:ALA:HB2	1:26:1:ASP:H	12	0.96
(2,583)	1:31:1:ALA:HB2	1:26:1:ASP:H	34	0.96
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	36	0.96
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	36	0.96
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	36	0.96
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	36	0.96
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	36	0.96
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	36	0.96
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	10	0.96
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	10	0.96
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	10	0.96
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	10	0.96
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	10	0.96
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	10	0.96
(2,381)	1:61:1:ARG:HH21	1:62:1:ILE:H	7	0.96
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	3	0.96
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	18	0.96
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	23	0.96
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	21	0.96
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	21	0.96
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	22	0.96
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	22	0.96
(2,582)	1:30:1:ASN:HB3	1:35:1:LYS:HB2	40	0.95
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	15	0.95
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	15	0.95
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	15	0.95
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	15	0.95
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	15	0.95
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	15	0.95
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	16	0.95
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	16	0.95

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	16	0.95
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	16	0.95
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	16	0.95
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	16	0.95
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	18	0.95
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	18	0.95
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	18	0.95
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	18	0.95
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	18	0.95
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	18	0.95
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	28	0.95
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	28	0.95
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	28	0.95
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	28	0.95
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	28	0.95
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	28	0.95
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	37	0.95
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	37	0.95
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	37	0.95
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	37	0.95
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	37	0.95
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	37	0.95
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	14	0.95
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	14	0.95
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	14	0.95
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	14	0.95
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	14	0.95
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	14	0.95
(2,411)	1:61:1:ARG:HH21	1:81:1:TRP:HH2	21	0.95
(2,400)	1:61:1:ARG:HB2	1:81:1:TRP:HH2	24	0.95
(2,400)	1:61:1:ARG:HB3	1:81:1:TRP:HH2	24	0.95
(2,400)	1:61:1:ARG:HB2	1:81:1:TRP:HH2	30	0.95
(2,400)	1:61:1:ARG:HB3	1:81:1:TRP:HH2	30	0.95
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	12	0.95
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	12	0.95
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	12	0.95
(2,381)	1:61:1:ARG:HH21	1:62:1:ILE:H	19	0.95
(2,381)	1:61:1:ARG:HH21	1:62:1:ILE:H	22	0.95
(2,381)	1:61:1:ARG:HH21	1:62:1:ILE:H	34	0.95
(2,381)	1:61:1:ARG:HH21	1:62:1:ILE:H	41	0.95
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	33	0.95
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	12	0.95

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	12	0.95
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	24	0.95
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	24	0.95
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	10	0.95
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	13	0.95
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	34	0.95
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	34	0.95
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	41	0.95
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	8	0.95
(2,42)	1:9:1:ILE:H	1:17:1:ASP:H	3	0.95
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	1	0.94
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	1	0.94
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	29	0.94
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	5	0.94
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	5	0.94
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	29	0.94
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	29	0.94
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	29	0.94
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	29	0.94
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	29	0.94
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	29	0.94
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	41	0.94
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	41	0.94
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	41	0.94
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	41	0.94
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	41	0.94
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	41	0.94
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	17	0.94
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	17	0.94
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	17	0.94
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	17	0.94
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	17	0.94
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	17	0.94
(2,411)	1:61:1:ARG:HH21	1:81:1:TRP:HH2	9	0.94
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	19	0.94
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	19	0.94
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	19	0.94
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	41	0.94
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	30	0.94
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	30	0.94
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	39	0.94
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	39	0.94

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	22	0.94
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	30	0.94
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	30	0.94
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	39	0.94
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	39	0.94
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	42	0.94
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	28	0.94
(2,583)	1:31:1:ALA:HB2	1:26:1:ASP:H	8	0.93
(2,583)	1:31:1:ALA:HB3	1:26:1:ASP:H	15	0.93
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD13	14	0.93
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	21	0.93
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	21	0.93
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	21	0.93
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	21	0.93
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	21	0.93
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	21	0.93
(2,430)	1:62:1:ILE:HG21	1:66:1:ASP:H	21	0.93
(2,430)	1:62:1:ILE:HG22	1:66:1:ASP:H	21	0.93
(2,430)	1:62:1:ILE:HG23	1:66:1:ASP:H	21	0.93
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	2	0.93
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	2	0.93
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	2	0.93
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	2	0.93
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	2	0.93
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	2	0.93
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	29	0.93
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	7	0.93
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	7	0.93
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	7	0.93
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	21	0.93
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	21	0.93
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	22	0.93
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	22	0.93
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	41	0.93
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	41	0.93
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	17	0.93
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	17	0.93
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	38	0.93
(2,587)	1:56:1:ALA:HB2	1:55:1:LYS:HZ1	27	0.92
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	3	0.92
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	30	0.92
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	38	0.92

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	38	0.92
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB2	40	0.92
(2,488)	1:67:1:TRP:HE1	1:70:1:ASP:HB3	40	0.92
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	43	0.92
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	43	0.92
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	4	0.92
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	4	0.92
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	4	0.92
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	4	0.92
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	4	0.92
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	4	0.92
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	19	0.92
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	19	0.92
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	19	0.92
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	19	0.92
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	19	0.92
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	19	0.92
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	26	0.92
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	26	0.92
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	26	0.92
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	26	0.92
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	26	0.92
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	26	0.92
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	34	0.92
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	34	0.92
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	34	0.92
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	34	0.92
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	34	0.92
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	34	0.92
(2,435)	1:62:1:ILE:HG21	1:67:1:TRP:HD1	43	0.92
(2,435)	1:62:1:ILE:HG22	1:67:1:TRP:HD1	43	0.92
(2,435)	1:62:1:ILE:HG23	1:67:1:TRP:HD1	43	0.92
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB2	27	0.92
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB3	27	0.92
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB2	27	0.92
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB3	27	0.92
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB2	27	0.92
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB3	27	0.92
(2,430)	1:62:1:ILE:HG21	1:66:1:ASP:H	11	0.92
(2,430)	1:62:1:ILE:HG22	1:66:1:ASP:H	11	0.92
(2,430)	1:62:1:ILE:HG23	1:66:1:ASP:H	11	0.92
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	16	0.92

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	16	0.92
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	16	0.92
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	16	0.92
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	16	0.92
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	16	0.92
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	32	0.92
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	32	0.92
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	32	0.92
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	32	0.92
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	32	0.92
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	32	0.92
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	5	0.92
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	36	0.92
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	36	0.92
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	3	0.92
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	3	0.92
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	13	0.92
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	13	0.92
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	37	0.92
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	9	0.92
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	9	0.92
(2,583)	1:31:1:ALA:HB2	1:26:1:ASP:H	30	0.91
(2,581)	1:25:1:GLN:HE21	1:23:1:ASN:HA	31	0.91
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	2	0.91
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	17	0.91
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	20	0.91
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	22	0.91
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	25	0.91
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	32	0.91
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	34	0.91
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	41	0.91
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	22	0.91
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	22	0.91
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	22	0.91
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	22	0.91
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	22	0.91
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	22	0.91
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	30	0.91
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	30	0.91
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	30	0.91
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	30	0.91
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	30	0.91

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	30	0.91
(2,434)	1:62:1:ILE:HG21	1:67:1:TRP:H	43	0.91
(2,434)	1:62:1:ILE:HG22	1:67:1:TRP:H	43	0.91
(2,434)	1:62:1:ILE:HG23	1:67:1:TRP:H	43	0.91
(2,430)	1:62:1:ILE:HG21	1:66:1:ASP:H	9	0.91
(2,430)	1:62:1:ILE:HG22	1:66:1:ASP:H	9	0.91
(2,430)	1:62:1:ILE:HG23	1:66:1:ASP:H	9	0.91
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	42	0.91
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	42	0.91
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	42	0.91
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	42	0.91
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	42	0.91
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	42	0.91
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	7	0.91
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	14	0.91
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	20	0.91
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	10	0.91
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	26	0.91
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	17	0.91
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	17	0.91
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	17	0.91
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	17	0.91
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	17	0.91
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	17	0.91
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	17	0.91
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	17	0.91
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	17	0.91
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	17	0.91
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	17	0.91
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	17	0.91
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	17	0.91
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	17	0.91
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	17	0.91
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	17	0.91
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	17	0.91
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	17	0.91
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	17	0.91
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	17	0.91
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	17	0.91
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	17	0.91
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	17	0.91
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	17	0.91

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	17	0.91
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	17	0.91
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	17	0.91
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	17	0.91
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	17	0.91
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	17	0.91
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	17	0.91
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	17	0.91
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	17	0.91
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	17	0.91
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	17	0.91
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	17	0.91
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	31	0.9
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD13	9	0.9
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	6	0.9
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	7	0.9
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	8	0.9
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	9	0.9
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	10	0.9
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	11	0.9
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	14	0.9
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	15	0.9
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	16	0.9
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	19	0.9
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	21	0.9
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	27	0.9
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	13	0.9
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	13	0.9
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	13	0.9
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	13	0.9
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	8	0.9
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	8	0.9
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	8	0.9
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	8	0.9
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	8	0.9
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	8	0.9
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	32	0.9
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	32	0.9
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	32	0.9
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	32	0.9
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	32	0.9
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	32	0.9

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	42	0.9
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	42	0.9
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	42	0.9
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	42	0.9
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	42	0.9
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	42	0.9
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB2	36	0.9
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB3	36	0.9
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB2	36	0.9
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB3	36	0.9
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB2	36	0.9
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB3	36	0.9
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB2	37	0.9
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB3	37	0.9
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB2	37	0.9
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB3	37	0.9
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB2	37	0.9
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB3	37	0.9
(2,430)	1:62:1:ILE:HG21	1:66:1:ASP:H	26	0.9
(2,430)	1:62:1:ILE:HG22	1:66:1:ASP:H	26	0.9
(2,430)	1:62:1:ILE:HG23	1:66:1:ASP:H	26	0.9
(2,430)	1:62:1:ILE:HG21	1:66:1:ASP:H	27	0.9
(2,430)	1:62:1:ILE:HG22	1:66:1:ASP:H	27	0.9
(2,430)	1:62:1:ILE:HG23	1:66:1:ASP:H	27	0.9
(2,430)	1:62:1:ILE:HG21	1:66:1:ASP:H	28	0.9
(2,430)	1:62:1:ILE:HG22	1:66:1:ASP:H	28	0.9
(2,430)	1:62:1:ILE:HG23	1:66:1:ASP:H	28	0.9
(2,430)	1:62:1:ILE:HG21	1:66:1:ASP:H	36	0.9
(2,430)	1:62:1:ILE:HG22	1:66:1:ASP:H	36	0.9
(2,430)	1:62:1:ILE:HG23	1:66:1:ASP:H	36	0.9
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	29	0.9
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	9	0.9
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	9	0.9
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	20	0.9
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	20	0.9
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD11	2	0.89
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	42	0.89
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	42	0.89
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	12	0.89
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	24	0.89
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	42	0.89
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	43	0.89

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	9	0.89
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	9	0.89
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	9	0.89
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	9	0.89
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	9	0.89
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	9	0.89
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	23	0.89
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	23	0.89
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	23	0.89
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	23	0.89
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	23	0.89
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	23	0.89
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	25	0.89
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	25	0.89
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	25	0.89
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	25	0.89
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	25	0.89
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	25	0.89
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB2	18	0.89
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB3	18	0.89
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB2	18	0.89
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB3	18	0.89
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB2	18	0.89
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB3	18	0.89
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB2	28	0.89
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB3	28	0.89
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB2	28	0.89
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB3	28	0.89
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB2	28	0.89
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB3	28	0.89
(2,430)	1:62:1:ILE:HG21	1:66:1:ASP:H	18	0.89
(2,430)	1:62:1:ILE:HG22	1:66:1:ASP:H	18	0.89
(2,430)	1:62:1:ILE:HG23	1:66:1:ASP:H	18	0.89
(2,430)	1:62:1:ILE:HG21	1:66:1:ASP:H	30	0.89
(2,430)	1:62:1:ILE:HG22	1:66:1:ASP:H	30	0.89
(2,430)	1:62:1:ILE:HG23	1:66:1:ASP:H	30	0.89
(2,402)	1:61:1:ARG:HG2	1:81:1:TRP:HH2	29	0.89
(2,402)	1:61:1:ARG:HG3	1:81:1:TRP:HH2	29	0.89
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	14	0.89
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	14	0.89
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD2	9	0.89
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD3	9	0.89

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	5	0.89
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	5	0.89
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	31	0.89
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	31	0.89
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	5	0.89
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	5	0.89
(2,42)	1:9:1:ILE:H	1:17:1:ASP:H	19	0.89
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	10	0.89
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	10	0.89
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	10	0.89
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	10	0.89
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	10	0.89
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	10	0.89
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	10	0.89
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	10	0.89
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	10	0.89
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	10	0.89
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	10	0.89
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	10	0.89
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	10	0.89
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	10	0.89
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	10	0.89
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	10	0.89
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	10	0.89
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	10	0.89
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	10	0.89
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	10	0.89
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	10	0.89
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	10	0.89
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	10	0.89
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	10	0.89
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	10	0.89
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	10	0.89
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	10	0.89
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	10	0.89
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	10	0.89
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	10	0.89
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	10	0.89
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	10	0.89
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	10	0.89
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	10	0.89
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	10	0.89

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	10	0.89
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	42	0.89
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	42	0.89
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	42	0.89
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	42	0.89
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	42	0.89
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	42	0.89
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	42	0.89
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	42	0.89
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	42	0.89
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	42	0.89
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	42	0.89
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	42	0.89
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	42	0.89
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	42	0.89
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	42	0.89
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	42	0.89
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	42	0.89
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	42	0.89
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	42	0.89
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	42	0.89
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	42	0.89
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	42	0.89
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	42	0.89
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	42	0.89
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	42	0.89
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	42	0.89
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	42	0.89
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	42	0.89
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	42	0.89
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	42	0.89
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	42	0.89
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	42	0.89
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	42	0.89
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	42	0.89
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	42	0.89
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	42	0.89
(2,583)	1:31:1:ALA:HB1	1:26:1:ASP:H	17	0.88
(2,581)	1:25:1:GLN:HE21	1:23:1:ASN:HA	38	0.88
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	20	0.88
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD12	33	0.88
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	23	0.88

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	26	0.88
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	35	0.88
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	2	0.88
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	2	0.88
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	2	0.88
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	2	0.88
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	2	0.88
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	2	0.88
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	12	0.88
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	12	0.88
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	12	0.88
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	12	0.88
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	12	0.88
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	12	0.88
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	24	0.88
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	24	0.88
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	24	0.88
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	24	0.88
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	24	0.88
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	24	0.88
(2,381)	1:61:1:ARG:HH21	1:62:1:ILE:H	2	0.88
(2,381)	1:61:1:ARG:HH21	1:62:1:ILE:H	32	0.88
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	34	0.88
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	21	0.88
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	21	0.88
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	6	0.88
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	40	0.88
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	17	0.88
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	27	0.88
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	37	0.88
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	33	0.87
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD13	1	0.87
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD13	5	0.87
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD11	6	0.87
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	10	0.87
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	10	0.87
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	33	0.87
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	33	0.87
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	4	0.87
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	31	0.87
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	33	0.87
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	40	0.87

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	6	0.87
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	6	0.87
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	6	0.87
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	6	0.87
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	6	0.87
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	6	0.87
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	10	0.87
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	10	0.87
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	10	0.87
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	10	0.87
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	10	0.87
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	10	0.87
(2,430)	1:62:1:ILE:HG21	1:66:1:ASP:H	37	0.87
(2,430)	1:62:1:ILE:HG22	1:66:1:ASP:H	37	0.87
(2,430)	1:62:1:ILE:HG23	1:66:1:ASP:H	37	0.87
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	15	0.87
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	18	0.87
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	18	0.87
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD2	3	0.87
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD3	3	0.87
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD2	39	0.87
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD3	39	0.87
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	1	0.87
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	12	0.87
(2,42)	1:9:1:ILE:H	1:17:1:ASP:H	40	0.87
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD12	13	0.86
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD11	18	0.86
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	1	0.86
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	38	0.86
(2,412)	1:61:1:ARG:HH21	1:81:1:TRP:HZ3	21	0.86
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	35	0.86
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	2	0.86
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	34	0.86
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	42	0.86
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	5	0.85
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	5	0.85
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	15	0.85
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	15	0.85
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	37	0.85
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	3	0.85
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	3	0.85
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	3	0.85

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	3	0.85
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	3	0.85
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	3	0.85
(2,434)	1:62:1:ILE:HG21	1:67:1:TRP:H	21	0.85
(2,434)	1:62:1:ILE:HG22	1:67:1:TRP:H	21	0.85
(2,434)	1:62:1:ILE:HG23	1:67:1:TRP:H	21	0.85
(2,430)	1:62:1:ILE:HG21	1:66:1:ASP:H	24	0.85
(2,430)	1:62:1:ILE:HG22	1:66:1:ASP:H	24	0.85
(2,430)	1:62:1:ILE:HG23	1:66:1:ASP:H	24	0.85
(2,412)	1:61:1:ARG:HH21	1:81:1:TRP:HZ3	9	0.85
(2,402)	1:61:1:ARG:HG2	1:81:1:TRP:HH2	18	0.85
(2,402)	1:61:1:ARG:HG3	1:81:1:TRP:HH2	18	0.85
(2,402)	1:61:1:ARG:HG2	1:81:1:TRP:HH2	36	0.85
(2,402)	1:61:1:ARG:HG3	1:81:1:TRP:HH2	36	0.85
(2,400)	1:61:1:ARG:HB2	1:81:1:TRP:HH2	29	0.85
(2,400)	1:61:1:ARG:HB3	1:81:1:TRP:HH2	29	0.85
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	4	0.85
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	19	0.85
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	21	0.85
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	40	0.85
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	41	0.85
(2,583)	1:31:1:ALA:HB2	1:26:1:ASP:H	10	0.84
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD11	24	0.84
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	11	0.84
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	11	0.84
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	18	0.84
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	28	0.84
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	36	0.84
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	17	0.84
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	17	0.84
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	35	0.84
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	35	0.84
(2,434)	1:62:1:ILE:HG21	1:67:1:TRP:H	11	0.84
(2,434)	1:62:1:ILE:HG22	1:67:1:TRP:H	11	0.84
(2,434)	1:62:1:ILE:HG23	1:67:1:TRP:H	11	0.84
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB2	21	0.84
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB3	21	0.84
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB2	21	0.84
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB3	21	0.84
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB2	21	0.84
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB3	21	0.84
(2,402)	1:61:1:ARG:HG2	1:81:1:TRP:HH2	39	0.84

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,402)	1:61:1:ARG:HG3	1:81:1:TRP:HH2	39	0.84
(2,400)	1:61:1:ARG:HB2	1:81:1:TRP:HH2	18	0.84
(2,400)	1:61:1:ARG:HB3	1:81:1:TRP:HH2	18	0.84
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	7	0.84
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	5	0.84
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	38	0.84
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	38	0.84
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD2	1	0.84
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD3	1	0.84
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	19	0.84
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	19	0.84
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	19	0.84
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	19	0.84
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	19	0.84
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	19	0.84
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	19	0.84
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	19	0.84
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	19	0.84
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	19	0.84
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	19	0.84
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	19	0.84
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	19	0.84
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	19	0.84
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	19	0.84
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	19	0.84
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	19	0.84
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	19	0.84
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	19	0.84
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	19	0.84
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	19	0.84
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	19	0.84
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	19	0.84
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	19	0.84
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	19	0.84
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	19	0.84
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	19	0.84
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	19	0.84
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	19	0.84
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	19	0.84
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	19	0.84
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	19	0.84
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	19	0.84

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	19	0.84
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	19	0.84
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	19	0.84
(2,583)	1:31:1:ALA:HB3	1:26:1:ASP:H	28	0.83
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG2	43	0.83
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD13	35	0.83
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	39	0.83
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	39	0.83
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	11	0.83
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	11	0.83
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	11	0.83
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	11	0.83
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	11	0.83
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	11	0.83
(2,402)	1:61:1:ARG:HG2	1:81:1:TRP:HH2	28	0.83
(2,402)	1:61:1:ARG:HG3	1:81:1:TRP:HH2	28	0.83
(2,400)	1:61:1:ARG:HB2	1:81:1:TRP:HH2	28	0.83
(2,400)	1:61:1:ARG:HB3	1:81:1:TRP:HH2	28	0.83
(2,400)	1:61:1:ARG:HB2	1:81:1:TRP:HH2	36	0.83
(2,400)	1:61:1:ARG:HB3	1:81:1:TRP:HH2	36	0.83
(2,400)	1:61:1:ARG:HB2	1:81:1:TRP:HH2	37	0.83
(2,400)	1:61:1:ARG:HB3	1:81:1:TRP:HH2	37	0.83
(2,400)	1:61:1:ARG:HB2	1:81:1:TRP:HH2	39	0.83
(2,400)	1:61:1:ARG:HB3	1:81:1:TRP:HH2	39	0.83
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	8	0.83
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	8	0.83
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	21	0.83
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	12	0.83
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	13	0.83
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	1	0.82
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	4	0.82
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	7	0.82
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD13	21	0.82
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	27	0.82
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	27	0.82
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	39	0.82
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	19	0.82
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	19	0.82
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB2	26	0.82
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB3	26	0.82
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB2	26	0.82
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB3	26	0.82

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB2	26	0.82
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB3	26	0.82
(2,402)	1:61:1:ARG:HG2	1:81:1:TRP:HH2	37	0.82
(2,402)	1:61:1:ARG:HG3	1:81:1:TRP:HH2	37	0.82
(2,400)	1:61:1:ARG:HB2	1:81:1:TRP:HH2	26	0.82
(2,400)	1:61:1:ARG:HB3	1:81:1:TRP:HH2	26	0.82
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	3	0.82
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	32	0.82
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	38	0.82
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	9	0.82
(2,42)	1:9:1:ILE:H	1:17:1:ASP:H	42	0.82
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	3	0.82
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	3	0.82
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	3	0.82
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	3	0.82
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	3	0.82
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	3	0.82
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	3	0.82
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	3	0.82
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	3	0.82
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	3	0.82
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	3	0.82
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	3	0.82
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	3	0.82
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	3	0.82
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	3	0.82
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	3	0.82
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	3	0.82
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	3	0.82
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	3	0.82
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	3	0.82
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	3	0.82
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	3	0.82
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	3	0.82
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	3	0.82
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	3	0.82
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	3	0.82
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	3	0.82
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	3	0.82
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	3	0.82
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	3	0.82
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	3	0.82

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	3	0.82
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	3	0.82
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	3	0.82
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	3	0.82
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	3	0.82
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD12	15	0.81
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	23	0.81
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	23	0.81
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	14	0.81
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	14	0.81
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	16	0.81
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	16	0.81
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	20	0.81
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	20	0.81
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	34	0.81
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	34	0.81
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	41	0.81
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	41	0.81
(2,434)	1:62:1:ILE:HG21	1:67:1:TRP:H	26	0.81
(2,434)	1:62:1:ILE:HG22	1:67:1:TRP:H	26	0.81
(2,434)	1:62:1:ILE:HG23	1:67:1:TRP:H	26	0.81
(2,402)	1:61:1:ARG:HG2	1:81:1:TRP:HH2	26	0.81
(2,402)	1:61:1:ARG:HG3	1:81:1:TRP:HH2	26	0.81
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	19	0.81
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	28	0.81
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	28	0.81
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	19	0.81
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	33	0.81
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	4	0.81
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	4	0.81
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	35	0.81
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	35	0.81
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	35	0.81
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	35	0.81
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	35	0.81
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	35	0.81
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	35	0.81
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	35	0.81
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	15	0.81
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	20	0.81
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	31	0.81
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	32	0.81

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,42)	1:9:1:ILE:H	1:17:1:ASP:H	17	0.81
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	34	0.8
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	34	0.8
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	13	0.8
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	15	0.8
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	15	0.8
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	22	0.8
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	22	0.8
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	23	0.8
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	23	0.8
(2,435)	1:62:1:ILE:HG21	1:67:1:TRP:HD1	21	0.8
(2,435)	1:62:1:ILE:HG22	1:67:1:TRP:HD1	21	0.8
(2,435)	1:62:1:ILE:HG23	1:67:1:TRP:HD1	21	0.8
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	4	0.8
(2,381)	1:61:1:ARG:HH21	1:62:1:ILE:H	13	0.8
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	8	0.8
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	14	0.8
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	43	0.8
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	24	0.8
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	37	0.8
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	37	0.8
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	37	0.8
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	37	0.8
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	37	0.8
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	37	0.8
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	37	0.8
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	37	0.8
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	37	0.8
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	37	0.8
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	37	0.8
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	37	0.8
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	37	0.8
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	37	0.8
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	37	0.8
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	37	0.8
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	37	0.8
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	37	0.8
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	37	0.8
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	37	0.8
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	37	0.8
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	37	0.8
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	37	0.8

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	37	0.8
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	37	0.8
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	37	0.8
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	37	0.8
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	37	0.8
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	37	0.8
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	37	0.8
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	37	0.8
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	37	0.8
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	37	0.8
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	37	0.8
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	37	0.8
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	37	0.8
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	2	0.79
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD13	11	0.79
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD11	16	0.79
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	2	0.79
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	2	0.79
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	6	0.79
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	6	0.79
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	7	0.79
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	7	0.79
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	25	0.79
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	25	0.79
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	35	0.79
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	35	0.79
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	42	0.79
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	42	0.79
(2,434)	1:62:1:ILE:HG21	1:67:1:TRP:H	28	0.79
(2,434)	1:62:1:ILE:HG22	1:67:1:TRP:H	28	0.79
(2,434)	1:62:1:ILE:HG23	1:67:1:TRP:H	28	0.79
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	23	0.79
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	23	0.79
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	23	0.79
(2,328)	1:56:1:ALA:H	1:76:1:SER:H	40	0.79
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	19	0.79
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	38	0.79
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	38	0.79
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	38	0.79
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	9	0.79
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	17	0.79
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	34	0.79

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	3	0.79
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	4	0.79
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	7	0.79
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	39	0.79
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB2	11	0.79
(2,63)	1:11:1:GLU:H	1:34:1:CYS:HB3	11	0.79
(2,583)	1:31:1:ALA:HB2	1:26:1:ASP:H	20	0.78
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	6	0.78
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	29	0.78
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	29	0.78
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	4	0.78
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	4	0.78
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	12	0.78
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	12	0.78
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	31	0.78
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	31	0.78
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	31	0.78
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	31	0.78
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	31	0.78
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	31	0.78
(2,434)	1:62:1:ILE:HG21	1:67:1:TRP:H	9	0.78
(2,434)	1:62:1:ILE:HG22	1:67:1:TRP:H	9	0.78
(2,434)	1:62:1:ILE:HG23	1:67:1:TRP:H	9	0.78
(2,434)	1:62:1:ILE:HG21	1:67:1:TRP:H	18	0.78
(2,434)	1:62:1:ILE:HG22	1:67:1:TRP:H	18	0.78
(2,434)	1:62:1:ILE:HG23	1:67:1:TRP:H	18	0.78
(2,434)	1:62:1:ILE:HG21	1:67:1:TRP:H	36	0.78
(2,434)	1:62:1:ILE:HG22	1:67:1:TRP:H	36	0.78
(2,434)	1:62:1:ILE:HG23	1:67:1:TRP:H	36	0.78
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	38	0.78
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	39	0.78
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	42	0.78
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	1	0.78
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	18	0.78
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	32	0.78
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	32	0.78
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	32	0.78
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	32	0.78
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	32	0.78
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	32	0.78
(2,583)	1:31:1:ALA:HB1	1:26:1:ASP:H	27	0.77
(2,581)	1:25:1:GLN:HE21	1:26:1:ASP:HA	16	0.77

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG2	11	0.77
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	18	0.77
(2,577)	1:8:1:LYS:H	1:9:1:ILE:HG22	31	0.77
(2,492)	1:68:1:ASN:HA	1:70:1:ASP:H	5	0.77
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	10	0.77
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	10	0.77
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	33	0.77
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	33	0.77
(2,434)	1:62:1:ILE:HG21	1:67:1:TRP:H	27	0.77
(2,434)	1:62:1:ILE:HG22	1:67:1:TRP:H	27	0.77
(2,434)	1:62:1:ILE:HG23	1:67:1:TRP:H	27	0.77
(2,434)	1:62:1:ILE:HG21	1:67:1:TRP:H	37	0.77
(2,434)	1:62:1:ILE:HG22	1:67:1:TRP:H	37	0.77
(2,434)	1:62:1:ILE:HG23	1:67:1:TRP:H	37	0.77
(2,381)	1:61:1:ARG:HH21	1:62:1:ILE:H	8	0.77
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD2	14	0.77
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD3	14	0.77
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	28	0.77
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	10	0.77
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	2	0.77
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	30	0.77
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	35	0.77
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	16	0.77
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	16	0.77
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	16	0.77
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	16	0.77
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	16	0.77
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	16	0.77
(2,42)	1:9:1:ILE:H	1:17:1:ASP:H	37	0.77
(2,577)	1:8:1:LYS:H	1:9:1:ILE:HG23	41	0.76
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	3	0.76
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	3	0.76
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	8	0.76
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	8	0.76
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	15	0.76
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	15	0.76
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	24	0.76
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	24	0.76
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	27	0.76
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	27	0.76
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	32	0.76
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	32	0.76

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	43	0.76
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	43	0.76
(2,434)	1:62:1:ILE:HG21	1:67:1:TRP:H	30	0.76
(2,434)	1:62:1:ILE:HG22	1:67:1:TRP:H	30	0.76
(2,434)	1:62:1:ILE:HG23	1:67:1:TRP:H	30	0.76
(2,430)	1:62:1:ILE:HG21	1:66:1:ASP:H	39	0.76
(2,430)	1:62:1:ILE:HG22	1:66:1:ASP:H	39	0.76
(2,430)	1:62:1:ILE:HG23	1:66:1:ASP:H	39	0.76
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	13	0.76
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	13	0.76
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	13	0.76
(2,381)	1:61:1:ARG:HH11	1:62:1:ILE:H	35	0.76
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	25	0.76
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	25	0.76
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	25	0.76
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	26	0.76
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	26	0.76
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	43	0.76
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	43	0.76
(2,75)	1:16:1:CYS:HB2	1:29:1:CYS:H	37	0.76
(2,75)	1:16:1:CYS:HB3	1:29:1:CYS:H	37	0.76
(2,583)	1:31:1:ALA:HB1	1:26:1:ASP:H	6	0.75
(2,583)	1:31:1:ALA:HB2	1:26:1:ASP:H	23	0.75
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	39	0.75
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD11	34	0.75
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	26	0.75
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	26	0.75
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	31	0.75
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	31	0.75
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	29	0.75
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	29	0.75
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	29	0.75
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	29	0.75
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	29	0.75
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	29	0.75
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	32	0.75
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	32	0.75
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	32	0.75
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	4	0.75
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	4	0.75
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	26	0.75
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	16	0.75

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	33	0.75
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	36	0.75
(2,583)	1:31:1:ALA:HB2	1:26:1:ASP:H	1	0.74
(2,583)	1:31:1:ALA:HB2	1:26:1:ASP:H	11	0.74
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	16	0.74
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD13	10	0.74
(2,578)	1:8:1:LYS:HA	1:4:1:VAL:HG23	36	0.74
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	28	0.74
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	28	0.74
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	3	0.74
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	3	0.74
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	7	0.74
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	7	0.74
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	11	0.74
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	11	0.74
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	29	0.74
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	29	0.74
(2,384)	1:61:1:ARG:HH21	1:63:1:ALA:HB1	1	0.74
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	2	0.74
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	2	0.74
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	2	0.74
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	16	0.74
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD2	43	0.74
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD3	43	0.74
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	25	0.74
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	25	0.74
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	6	0.74
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	14	0.74
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	14	0.73
(2,577)	1:8:1:LYS:H	1:9:1:ILE:HG23	10	0.73
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	37	0.73
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	37	0.73
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	13	0.73
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	13	0.73
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	2	0.73
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	2	0.73
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	30	0.73
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	30	0.73
(2,441)	1:62:1:ILE:HD11	1:81:1:TRP:HE3	5	0.73
(2,441)	1:62:1:ILE:HD12	1:81:1:TRP:HE3	5	0.73
(2,441)	1:62:1:ILE:HD13	1:81:1:TRP:HE3	5	0.73
(2,435)	1:62:1:ILE:HG21	1:67:1:TRP:HD1	11	0.73

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,435)	1:62:1:ILE:HG22	1:67:1:TRP:HD1	11	0.73
(2,435)	1:62:1:ILE:HG23	1:67:1:TRP:HD1	11	0.73
(2,434)	1:62:1:ILE:HG21	1:67:1:TRP:H	24	0.73
(2,434)	1:62:1:ILE:HG22	1:67:1:TRP:H	24	0.73
(2,434)	1:62:1:ILE:HG23	1:67:1:TRP:H	24	0.73
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	1	0.73
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	20	0.73
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	20	0.73
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	11	0.73
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	29	0.73
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	43	0.73
(1,766)	1:61:1:ARG:HH21	1:79:1:CYS:HB2	23	0.73
(2,583)	1:31:1:ALA:HB1	1:26:1:ASP:H	5	0.72
(2,583)	1:31:1:ALA:HB3	1:26:1:ASP:H	7	0.72
(2,583)	1:31:1:ALA:HB1	1:26:1:ASP:H	14	0.72
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	35	0.72
(2,577)	1:8:1:LYS:H	1:9:1:ILE:HG23	19	0.72
(2,577)	1:8:1:LYS:H	1:4:1:VAL:HG13	26	0.72
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	24	0.72
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	24	0.72
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	42	0.72
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	42	0.72
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	1	0.72
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	1	0.72
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	3	0.72
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	3	0.72
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	9	0.72
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	9	0.72
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	36	0.72
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	36	0.72
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	22	0.72
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	9	0.72
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	16	0.72
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	27	0.72
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	32	0.72
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	35	0.72
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	15	0.72
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	15	0.72
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	15	0.72
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	15	0.72
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	15	0.72
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	15	0.72

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	36	0.72
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	36	0.72
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	36	0.72
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	36	0.72
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	36	0.72
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	36	0.72
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	31	0.72
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	10	0.71
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	10	0.71
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	8	0.71
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	8	0.71
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	18	0.71
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	18	0.71
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	28	0.71
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	28	0.71
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	39	0.71
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	39	0.71
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	35	0.71
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	35	0.71
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	35	0.71
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	35	0.71
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	39	0.71
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	39	0.71
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	39	0.71
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	39	0.71
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	39	0.71
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	39	0.71
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	6	0.71
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	31	0.71
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	6	0.7
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	6	0.7
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	9	0.7
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	9	0.7
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	17	0.7
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	17	0.7
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	21	0.7
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	21	0.7
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	25	0.7
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	25	0.7
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	31	0.7
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	31	0.7
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	33	0.7

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	33	0.7
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	39	0.7
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	39	0.7
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	21	0.7
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	21	0.7
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	37	0.7
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	37	0.7
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	43	0.7
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	43	0.7
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	43	0.7
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	43	0.7
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	38	0.7
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	38	0.7
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	38	0.7
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	38	0.7
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	38	0.7
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	38	0.7
(2,435)	1:62:1:ILE:HG21	1:67:1:TRP:HD1	9	0.7
(2,435)	1:62:1:ILE:HG22	1:67:1:TRP:HD1	9	0.7
(2,435)	1:62:1:ILE:HG23	1:67:1:TRP:HD1	9	0.7
(2,435)	1:62:1:ILE:HG21	1:67:1:TRP:HD1	26	0.7
(2,435)	1:62:1:ILE:HG22	1:67:1:TRP:HD1	26	0.7
(2,435)	1:62:1:ILE:HG23	1:67:1:TRP:HD1	26	0.7
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	14	0.7
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	17	0.7
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	20	0.7
(2,292)	1:53:1:PHE:HD1	1:56:1:ALA:H	33	0.7
(2,292)	1:53:1:PHE:HD2	1:56:1:ALA:H	33	0.7
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD2	2	0.7
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD3	2	0.7
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	20	0.7
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	18	0.7
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	18	0.7
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	18	0.7
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	18	0.7
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	18	0.7
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	18	0.7
(2,42)	1:9:1:ILE:H	1:17:1:ASP:H	41	0.7
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	13	0.69
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	13	0.69
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	18	0.69
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	18	0.69

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	22	0.69
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	22	0.69
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	36	0.69
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	36	0.69
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	13	0.69
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	13	0.69
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD21	5	0.69
(2,479)	1:65:1:GLY:HA2	1:68:1:ASN:HD22	5	0.69
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD21	5	0.69
(2,479)	1:65:1:GLY:HA3	1:68:1:ASN:HD22	5	0.69
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	29	0.69
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	29	0.69
(2,435)	1:62:1:ILE:HG21	1:67:1:TRP:HD1	18	0.69
(2,435)	1:62:1:ILE:HG22	1:67:1:TRP:HD1	18	0.69
(2,435)	1:62:1:ILE:HG23	1:67:1:TRP:HD1	18	0.69
(2,435)	1:62:1:ILE:HG21	1:67:1:TRP:HD1	28	0.69
(2,435)	1:62:1:ILE:HG22	1:67:1:TRP:HD1	28	0.69
(2,435)	1:62:1:ILE:HG23	1:67:1:TRP:HD1	28	0.69
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	10	0.69
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	19	0.69
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	19	0.69
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	4	0.69
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	7	0.69
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	25	0.69
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	30	0.69
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	23	0.69
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	12	0.68
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	12	0.68
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	26	0.68
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	26	0.68
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	40	0.68
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	40	0.68
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	35	0.68
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	35	0.68
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	35	0.68
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	35	0.68
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	35	0.68
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	35	0.68
(2,435)	1:62:1:ILE:HG21	1:67:1:TRP:HD1	36	0.68
(2,435)	1:62:1:ILE:HG22	1:67:1:TRP:HD1	36	0.68
(2,435)	1:62:1:ILE:HG23	1:67:1:TRP:HD1	36	0.68
(2,430)	1:62:1:ILE:HG21	1:66:1:ASP:H	3	0.68

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,430)	1:62:1:ILE:HG22	1:66:1:ASP:H	3	0.68
(2,430)	1:62:1:ILE:HG23	1:66:1:ASP:H	3	0.68
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	42	0.68
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	36	0.68
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	36	0.68
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	33	0.68
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	33	0.68
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	33	0.68
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	33	0.68
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	33	0.68
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	33	0.68
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	32	0.68
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	5	0.68
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	5	0.68
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	5	0.68
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	5	0.68
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	5	0.68
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	5	0.68
(2,577)	1:8:1:LYS:H	1:9:1:ILE:HG21	3	0.67
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	19	0.67
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	19	0.67
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	19	0.67
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	19	0.67
(2,489)	1:67:1:TRP:HB2	1:83:1:HIS:HD2	30	0.67
(2,489)	1:67:1:TRP:HB3	1:83:1:HIS:HD2	30	0.67
(2,174)	1:40:1:SER:H	1:51:1:CYS:HB2	33	0.67
(2,174)	1:40:1:SER:H	1:51:1:CYS:HB3	33	0.67
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	19	0.67
(2,587)	1:56:1:ALA:HB1	1:75:1:LYS:HZ2	7	0.66
(2,577)	1:8:1:LYS:H	1:4:1:VAL:HG12	17	0.66
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	14	0.66
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	14	0.66
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	20	0.66
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	20	0.66
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	30	0.66
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	30	0.66
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	40	0.66
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	40	0.66
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	40	0.66
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	40	0.66
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	40	0.66
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	40	0.66

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,435)	1:62:1:ILE:HG21	1:67:1:TRP:HD1	37	0.66
(2,435)	1:62:1:ILE:HG22	1:67:1:TRP:HD1	37	0.66
(2,435)	1:62:1:ILE:HG23	1:67:1:TRP:HD1	37	0.66
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	1	0.66
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	25	0.66
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	10	0.66
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	10	0.66
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	10	0.66
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	7	0.66
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	3	0.66
(2,578)	1:8:1:LYS:HA	1:4:1:VAL:HG23	4	0.65
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB2	38	0.65
(2,487)	1:67:1:TRP:HD1	1:70:1:ASP:HB3	38	0.65
(2,435)	1:62:1:ILE:HG21	1:67:1:TRP:HD1	13	0.65
(2,435)	1:62:1:ILE:HG22	1:67:1:TRP:HD1	13	0.65
(2,435)	1:62:1:ILE:HG23	1:67:1:TRP:HD1	13	0.65
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	38	0.65
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	34	0.65
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	16	0.65
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	16	0.65
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	16	0.65
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	17	0.65
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD2	32	0.65
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD3	32	0.65
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	31	0.65
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	26	0.65
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	28	0.65
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	28	0.65
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	28	0.65
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	28	0.65
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	28	0.65
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	28	0.65
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	28	0.65
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	28	0.65
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	28	0.65
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	28	0.65
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	28	0.65
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	28	0.65
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	28	0.65
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	28	0.65
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	28	0.65
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	28	0.65

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	28	0.65
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	28	0.65
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	28	0.65
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	28	0.65
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	28	0.65
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	28	0.65
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	28	0.65
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	28	0.65
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	28	0.65
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	28	0.65
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	28	0.65
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	28	0.65
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	28	0.65
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	28	0.65
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	28	0.65
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	28	0.65
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	28	0.65
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	28	0.65
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	28	0.65
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	28	0.65
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	28	0.65
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	32	0.65
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	32	0.65
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	32	0.65
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	32	0.65
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	32	0.65
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	32	0.65
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	32	0.65
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	32	0.65
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	32	0.65
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	32	0.65
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	32	0.65
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	32	0.65
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	32	0.65
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	32	0.65
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	32	0.65
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	32	0.65
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	32	0.65
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	32	0.65
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	32	0.65
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	32	0.65
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	32	0.65

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	32	0.65
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	32	0.65
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	32	0.65
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	32	0.65
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	32	0.65
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	32	0.65
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	32	0.65
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	32	0.65
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	32	0.65
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	32	0.65
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	32	0.65
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	32	0.65
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	32	0.65
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	32	0.65
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	32	0.65
(2,583)	1:31:1:ALA:HB2	1:26:1:ASP:H	29	0.64
(2,583)	1:31:1:ALA:HB2	1:26:1:ASP:H	40	0.64
(2,575)	1:5:1:CYS:H	1:3:1:PRO:HB2	38	0.64
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	5	0.64
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	5	0.64
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	30	0.64
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	30	0.64
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	38	0.64
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	38	0.64
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	41	0.64
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	41	0.64
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	21	0.64
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	21	0.64
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	24	0.64
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	24	0.64
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	40	0.64
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	38	0.64
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	43	0.64
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	43	0.64
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	15	0.64
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	17	0.64
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	11	0.64
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	2	0.64
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	2	0.64
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	2	0.64
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	2	0.64
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	2	0.64

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	2	0.64
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	33	0.64
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	33	0.64
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	33	0.64
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	33	0.64
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	33	0.64
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	33	0.64
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	43	0.64
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	43	0.64
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	43	0.64
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	43	0.64
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	43	0.64
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	43	0.64
(2,578)	1:8:1:LYS:HA	1:4:1:VAL:HG21	30	0.63
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	40	0.63
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	40	0.63
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	15	0.63
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	15	0.63
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	27	0.63
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	27	0.63
(2,435)	1:62:1:ILE:HG21	1:67:1:TRP:HD1	8	0.63
(2,435)	1:62:1:ILE:HG22	1:67:1:TRP:HD1	8	0.63
(2,435)	1:62:1:ILE:HG23	1:67:1:TRP:HD1	8	0.63
(2,435)	1:62:1:ILE:HG21	1:67:1:TRP:HD1	30	0.63
(2,435)	1:62:1:ILE:HG22	1:67:1:TRP:HD1	30	0.63
(2,435)	1:62:1:ILE:HG23	1:67:1:TRP:HD1	30	0.63
(2,392)	1:61:1:ARG:HH21	1:70:1:ASP:H	41	0.63
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	4	0.63
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	4	0.63
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	4	0.63
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	4	0.63
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	4	0.63
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	4	0.63
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	6	0.63
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	6	0.63
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	6	0.63
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	6	0.63
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	6	0.63
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	6	0.63
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	22	0.63
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	22	0.63
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	22	0.63

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	22	0.63
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	22	0.63
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	22	0.63
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	22	0.63
(2,578)	1:8:1:LYS:HA	1:4:1:VAL:HG23	20	0.62
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	9	0.62
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	9	0.62
(2,435)	1:62:1:ILE:HG21	1:67:1:TRP:HD1	27	0.62
(2,435)	1:62:1:ILE:HG22	1:67:1:TRP:HD1	27	0.62
(2,435)	1:62:1:ILE:HG23	1:67:1:TRP:HD1	27	0.62
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	29	0.62
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	29	0.62
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	29	0.62
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	29	0.62
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	29	0.62
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	29	0.62
(2,402)	1:61:1:ARG:HG2	1:81:1:TRP:HH2	5	0.61
(2,402)	1:61:1:ARG:HG3	1:81:1:TRP:HH2	5	0.61
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	7	0.61
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	7	0.61
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	7	0.61
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	7	0.61
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	7	0.61
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	7	0.61
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	12	0.61
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	12	0.61
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	12	0.61
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	12	0.61
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	12	0.61
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	12	0.61
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	21	0.61
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	21	0.61
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	21	0.61
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	21	0.61
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	21	0.61
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	21	0.61
(2,581)	1:25:1:GLN:HE21	1:26:1:ASP:HA	17	0.6
(2,389)	1:61:1:ARG:HG2	1:70:1:ASP:HA	26	0.6
(2,389)	1:61:1:ARG:HG3	1:70:1:ASP:HA	26	0.6
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	25	0.6
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	25	0.6
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	25	0.6

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	3	0.6
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	22	0.59
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD13	23	0.59
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD11	25	0.59
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD13	29	0.59
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD11	43	0.59
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB2	16	0.59
(2,540)	1:73:1:THR:H	1:80:1:PRO:HB3	16	0.59
(2,435)	1:62:1:ILE:HG21	1:67:1:TRP:HD1	39	0.59
(2,435)	1:62:1:ILE:HG22	1:67:1:TRP:HD1	39	0.59
(2,435)	1:62:1:ILE:HG23	1:67:1:TRP:HD1	39	0.59
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	32	0.59
(2,587)	1:56:1:ALA:HB2	1:55:1:LYS:HZ1	8	0.58
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG2	41	0.58
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD11	22	0.58
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	16	0.58
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	16	0.58
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	33	0.58
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	33	0.58
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	36	0.58
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	36	0.58
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	37	0.58
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	37	0.58
(2,434)	1:62:1:ILE:HG21	1:67:1:TRP:H	39	0.58
(2,434)	1:62:1:ILE:HG22	1:67:1:TRP:H	39	0.58
(2,434)	1:62:1:ILE:HG23	1:67:1:TRP:H	39	0.58
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	2	0.58
(2,389)	1:61:1:ARG:HG2	1:70:1:ASP:HA	37	0.58
(2,389)	1:61:1:ARG:HG3	1:70:1:ASP:HA	37	0.58
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD2	10	0.58
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD3	10	0.58
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD2	23	0.58
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD3	23	0.58
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	34	0.58
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	34	0.58
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	34	0.58
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	34	0.58
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	34	0.58
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	34	0.58
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	36	0.58
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	25	0.58
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	25	0.58

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	25	0.58
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	25	0.58
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	25	0.58
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	25	0.58
(2,42)	1:9:1:ILE:H	1:17:1:ASP:H	31	0.58
(2,575)	1:5:1:CYS:H	1:3:1:PRO:HB2	42	0.57
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	38	0.57
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	38	0.57
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	40	0.57
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	40	0.57
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	18	0.57
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	18	0.57
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	28	0.57
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	28	0.57
(2,389)	1:61:1:ARG:HG2	1:70:1:ASP:HA	28	0.57
(2,389)	1:61:1:ARG:HG3	1:70:1:ASP:HA	28	0.57
(2,389)	1:61:1:ARG:HG2	1:70:1:ASP:HA	39	0.57
(2,389)	1:61:1:ARG:HG3	1:70:1:ASP:HA	39	0.57
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	9	0.57
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	9	0.57
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	9	0.57
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	17	0.57
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	17	0.57
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	17	0.57
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	34	0.57
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	34	0.57
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	30	0.57
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	30	0.57
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	30	0.57
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	30	0.57
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	30	0.57
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	30	0.57
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	39	0.57
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	39	0.57
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	39	0.57
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	39	0.57
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	39	0.57
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	39	0.57
(2,42)	1:9:1:ILE:H	1:17:1:ASP:H	28	0.57
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	27	0.57
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	27	0.57
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	27	0.57

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	27	0.57
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	27	0.57
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	27	0.57
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	27	0.57
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	27	0.57
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	27	0.57
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	27	0.57
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	27	0.57
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	27	0.57
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	27	0.57
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	27	0.57
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	27	0.57
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	27	0.57
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	27	0.57
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	27	0.57
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	27	0.57
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	27	0.57
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	27	0.57
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	27	0.57
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	27	0.57
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	27	0.57
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	27	0.57
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	27	0.57
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	27	0.57
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	27	0.57
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	27	0.57
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	27	0.57
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	27	0.57
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	27	0.57
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	27	0.57
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	27	0.57
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	27	0.57
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	27	0.57
(2,581)	1:25:1:GLN:HE21	1:26:1:ASP:HA	2	0.56
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	23	0.56
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	23	0.56
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	21	0.56
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	21	0.56
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	26	0.56
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	26	0.56
(2,441)	1:62:1:ILE:HD11	1:81:1:TRP:HE3	25	0.56
(2,441)	1:62:1:ILE:HD12	1:81:1:TRP:HE3	25	0.56

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,441)	1:62:1:ILE:HD13	1:81:1:TRP:HE3	25	0.56
(2,435)	1:62:1:ILE:HG21	1:67:1:TRP:HD1	24	0.56
(2,435)	1:62:1:ILE:HG22	1:67:1:TRP:HD1	24	0.56
(2,435)	1:62:1:ILE:HG23	1:67:1:TRP:HD1	24	0.56
(2,434)	1:62:1:ILE:HG21	1:67:1:TRP:H	3	0.56
(2,434)	1:62:1:ILE:HG22	1:67:1:TRP:H	3	0.56
(2,434)	1:62:1:ILE:HG23	1:67:1:TRP:H	3	0.56
(2,389)	1:61:1:ARG:HG2	1:70:1:ASP:HA	36	0.56
(2,389)	1:61:1:ARG:HG3	1:70:1:ASP:HA	36	0.56
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	43	0.56
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	43	0.56
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	16	0.56
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	16	0.56
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	11	0.56
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	11	0.56
(2,174)	1:40:1:SER:H	1:51:1:CYS:HB2	8	0.56
(2,174)	1:40:1:SER:H	1:51:1:CYS:HB3	8	0.56
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	29	0.56
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	29	0.56
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	29	0.56
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	29	0.56
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	29	0.56
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	29	0.56
(2,581)	1:25:1:GLN:HE21	1:23:1:ASN:HA	19	0.55
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD13	7	0.55
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	30	0.55
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	30	0.55
(2,489)	1:67:1:TRP:HB2	1:83:1:HIS:HD2	43	0.55
(2,489)	1:67:1:TRP:HB3	1:83:1:HIS:HD2	43	0.55
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	11	0.55
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	11	0.55
(2,438)	1:62:1:ILE:HG21	1:81:1:TRP:HE3	21	0.55
(2,438)	1:62:1:ILE:HG22	1:81:1:TRP:HE3	21	0.55
(2,438)	1:62:1:ILE:HG23	1:81:1:TRP:HE3	21	0.55
(2,435)	1:62:1:ILE:HG21	1:67:1:TRP:HD1	3	0.55
(2,435)	1:62:1:ILE:HG22	1:67:1:TRP:HD1	3	0.55
(2,435)	1:62:1:ILE:HG23	1:67:1:TRP:HD1	3	0.55
(2,389)	1:61:1:ARG:HG2	1:70:1:ASP:HA	18	0.55
(2,389)	1:61:1:ARG:HG3	1:70:1:ASP:HA	18	0.55
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	21	0.55
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	21	0.55
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	21	0.55

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	24	0.55
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	24	0.55
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	24	0.55
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	24	0.55
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	24	0.55
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	24	0.55
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	41	0.55
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	41	0.55
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	41	0.55
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	41	0.55
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	41	0.55
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	41	0.55
(1,777)	1:61:1:ARG:HH21	1:81:1:TRP:HZ2	9	0.55
(1,777)	1:61:1:ARG:HH21	1:81:1:TRP:HZ2	21	0.55
(2,575)	1:5:1:CYS:H	1:3:1:PRO:HB2	10	0.54
(2,575)	1:5:1:CYS:H	1:3:1:PRO:HB2	41	0.54
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	5	0.54
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	5	0.54
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	5	0.54
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	5	0.54
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	5	0.54
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	5	0.54
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	1	0.54
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	1	0.54
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	1	0.54
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	1	0.54
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	1	0.54
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	1	0.54
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	16	0.54
(2,381)	1:61:1:ARG:HH11	1:62:1:ILE:H	20	0.54
(2,72)	1:15:1:ASP:H	1:35:1:LYS:H	25	0.54
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	1	0.54
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	1	0.54
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	1	0.54
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	1	0.54
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	1	0.54
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	1	0.54
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	21	0.54
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	21	0.54
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	21	0.54
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	21	0.54
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	21	0.54

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	21	0.54
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	21	0.54
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	21	0.54
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	21	0.54
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	21	0.54
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	21	0.54
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	21	0.54
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	21	0.54
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	21	0.54
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	21	0.54
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	21	0.54
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	21	0.54
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	21	0.54
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	21	0.54
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	21	0.54
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	21	0.54
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	21	0.54
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	21	0.54
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	21	0.54
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	21	0.54
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	21	0.54
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	21	0.54
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	21	0.54
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	21	0.54
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	21	0.54
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	21	0.54
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	21	0.54
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	21	0.54
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	21	0.54
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	21	0.54
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	21	0.54
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	3	0.53
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	3	0.53
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	38	0.53
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	38	0.53
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	38	0.53
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	38	0.53
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	38	0.53
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	38	0.53
(2,389)	1:61:1:ARG:HG2	1:70:1:ASP:HA	21	0.53
(2,389)	1:61:1:ARG:HG3	1:70:1:ASP:HA	21	0.53
(2,381)	1:61:1:ARG:HH11	1:62:1:ILE:H	17	0.53

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD2	15	0.53
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD3	15	0.53
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	13	0.53
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	13	0.53
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	13	0.53
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	13	0.53
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	13	0.53
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	13	0.53
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	15	0.53
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	15	0.53
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	15	0.53
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	15	0.53
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	15	0.53
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	15	0.53
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	15	0.53
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	15	0.53
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	15	0.53
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	15	0.53
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	15	0.53
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	15	0.53
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	15	0.53
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	15	0.53
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	15	0.53
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	15	0.53
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	15	0.53
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	15	0.53
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	15	0.53
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	15	0.53
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	15	0.53
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	15	0.53
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	15	0.53
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	15	0.53
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	15	0.53
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	15	0.53
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	15	0.53
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	15	0.53
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	15	0.53
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	15	0.53
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	15	0.53
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	15	0.53
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	15	0.53
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	15	0.53

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	15	0.53
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	15	0.53
(2,583)	1:31:1:ALA:HB3	1:26:1:ASP:H	42	0.52
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	17	0.52
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	17	0.52
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	43	0.52
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	43	0.52
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	43	0.52
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	43	0.52
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	43	0.52
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	43	0.52
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB2	40	0.52
(2,425)	1:62:1:ILE:HD11	1:64:1:ARG:HB3	40	0.52
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB2	40	0.52
(2,425)	1:62:1:ILE:HD12	1:64:1:ARG:HB3	40	0.52
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB2	40	0.52
(2,425)	1:62:1:ILE:HD13	1:64:1:ARG:HB3	40	0.52
(2,400)	1:61:1:ARG:HB2	1:81:1:TRP:HH2	15	0.52
(2,400)	1:61:1:ARG:HB3	1:81:1:TRP:HH2	15	0.52
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	14	0.52
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	14	0.52
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	14	0.52
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	29	0.52
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	29	0.52
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	38	0.52
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	38	0.52
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	10	0.52
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	10	0.52
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	10	0.52
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	10	0.52
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	10	0.52
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	10	0.52
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	11	0.52
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	11	0.52
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	11	0.52
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	11	0.52
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	11	0.52
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	11	0.52
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	43	0.52
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	43	0.52
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	43	0.52
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	43	0.52

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	43	0.52
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	43	0.52
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	15	0.52
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	15	0.52
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	15	0.52
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	15	0.52
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	15	0.52
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	15	0.52
(2,42)	1:9:1:ILE:H	1:17:1:ASP:H	32	0.52
(2,575)	1:5:1:CYS:H	1:3:1:PRO:HB2	37	0.51
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	12	0.51
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	12	0.51
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	41	0.51
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	41	0.51
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB2	11	0.51
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB3	11	0.51
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB2	11	0.51
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB3	11	0.51
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB2	11	0.51
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB3	11	0.51
(2,422)	1:62:1:ILE:HG21	1:64:1:ARG:HD2	13	0.51
(2,422)	1:62:1:ILE:HG21	1:64:1:ARG:HD3	13	0.51
(2,422)	1:62:1:ILE:HG22	1:64:1:ARG:HD2	13	0.51
(2,422)	1:62:1:ILE:HG22	1:64:1:ARG:HD3	13	0.51
(2,422)	1:62:1:ILE:HG23	1:64:1:ARG:HD2	13	0.51
(2,422)	1:62:1:ILE:HG23	1:64:1:ARG:HD3	13	0.51
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	36	0.51
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	36	0.51
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	36	0.51
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	24	0.51
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	24	0.51
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	8	0.51
(2,583)	1:31:1:ALA:HB1	1:26:1:ASP:H	37	0.5
(2,578)	1:8:1:LYS:HA	1:4:1:VAL:HG22	12	0.5
(2,575)	1:5:1:CYS:H	1:3:1:PRO:HB2	26	0.5
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	8	0.5
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	8	0.5
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	17	0.5
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	17	0.5
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	34	0.5
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	34	0.5
(2,430)	1:62:1:ILE:HG21	1:66:1:ASP:H	8	0.5

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,430)	1:62:1:ILE:HG22	1:66:1:ASP:H	8	0.5
(2,430)	1:62:1:ILE:HG23	1:66:1:ASP:H	8	0.5
(2,389)	1:61:1:ARG:HG2	1:70:1:ASP:HA	9	0.5
(2,389)	1:61:1:ARG:HG3	1:70:1:ASP:HA	9	0.5
(2,386)	1:61:1:ARG:HB2	1:69:1:ASP:HA	5	0.5
(2,386)	1:61:1:ARG:HB3	1:69:1:ASP:HA	5	0.5
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	20	0.5
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	20	0.5
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	20	0.5
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	39	0.5
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	39	0.5
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	39	0.5
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	23	0.5
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	29	0.5
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	29	0.5
(2,103)	1:21:1:PRO:HA	1:25:1:GLN:H	18	0.5
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	21	0.5
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	22	0.5
(2,575)	1:5:1:CYS:H	1:3:1:PRO:HB2	31	0.49
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	20	0.49
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	20	0.49
(2,441)	1:62:1:ILE:HD11	1:81:1:TRP:HE3	4	0.49
(2,441)	1:62:1:ILE:HD12	1:81:1:TRP:HE3	4	0.49
(2,441)	1:62:1:ILE:HD13	1:81:1:TRP:HE3	4	0.49
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	7	0.49
(2,389)	1:61:1:ARG:HG2	1:70:1:ASP:HA	29	0.49
(2,389)	1:61:1:ARG:HG3	1:70:1:ASP:HA	29	0.49
(2,386)	1:61:1:ARG:HB2	1:69:1:ASP:HA	35	0.49
(2,386)	1:61:1:ARG:HB3	1:69:1:ASP:HA	35	0.49
(2,381)	1:61:1:ARG:HH11	1:62:1:ILE:H	14	0.49
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	21	0.49
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	21	0.49
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	21	0.49
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	35	0.49
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	37	0.49
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	37	0.49
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	6	0.49
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	6	0.49
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	6	0.49
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	6	0.49
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	6	0.49
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	6	0.49

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	6	0.49
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	6	0.49
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	6	0.49
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	6	0.49
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	6	0.49
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	6	0.49
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	6	0.49
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	6	0.49
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	6	0.49
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	6	0.49
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	6	0.49
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	6	0.49
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	6	0.49
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	6	0.49
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	6	0.49
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	6	0.49
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	6	0.49
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	6	0.49
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	6	0.49
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	6	0.49
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	6	0.49
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	6	0.49
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	6	0.49
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	6	0.49
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	6	0.49
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	6	0.49
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	6	0.49
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	6	0.49
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	6	0.49
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	6	0.49
(1,776)	1:61:1:ARG:HH21	1:81:1:TRP:HE3	5	0.49
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	4	0.48
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	4	0.48
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	7	0.48
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	7	0.48
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	13	0.48
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	13	0.48
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	19	0.48
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	19	0.48
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	23	0.48
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	23	0.48
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	25	0.48

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	25	0.48
(2,438)	1:62:1:ILE:HG21	1:81:1:TRP:HE3	9	0.48
(2,438)	1:62:1:ILE:HG22	1:81:1:TRP:HE3	9	0.48
(2,438)	1:62:1:ILE:HG23	1:81:1:TRP:HE3	9	0.48
(2,434)	1:62:1:ILE:HG21	1:67:1:TRP:H	8	0.48
(2,434)	1:62:1:ILE:HG22	1:67:1:TRP:H	8	0.48
(2,434)	1:62:1:ILE:HG23	1:67:1:TRP:H	8	0.48
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB2	43	0.48
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB3	43	0.48
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB2	43	0.48
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB3	43	0.48
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB2	43	0.48
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB3	43	0.48
(2,381)	1:61:1:ARG:HH21	1:62:1:ILE:H	3	0.48
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	24	0.48
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	24	0.48
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	24	0.48
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	31	0.48
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	31	0.48
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	31	0.48
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	31	0.48
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	31	0.48
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	31	0.48
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	6	0.47
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	6	0.47
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	14	0.47
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	14	0.47
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	32	0.47
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	32	0.47
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB2	1	0.47
(2,445)	1:63:1:ALA:HB1	1:66:1:ASP:HB3	1	0.47
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB2	1	0.47
(2,445)	1:63:1:ALA:HB2	1:66:1:ASP:HB3	1	0.47
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB2	1	0.47
(2,445)	1:63:1:ALA:HB3	1:66:1:ASP:HB3	1	0.47
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	6	0.47
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	6	0.47
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	6	0.47
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	13	0.47
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	13	0.47
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	13	0.47
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	40	0.47

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,191)	1:41:1:GLN:HA	1:53:1:PHE:HB2	33	0.47
(2,191)	1:41:1:GLN:HA	1:53:1:PHE:HB3	33	0.47
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	39	0.47
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	39	0.47
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	39	0.47
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	39	0.47
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	39	0.47
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	39	0.47
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	29	0.47
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	40	0.47
(2,575)	1:5:1:CYS:H	1:3:1:PRO:HB2	17	0.46
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	6	0.46
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	6	0.46
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	22	0.46
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	22	0.46
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	42	0.46
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	42	0.46
(2,400)	1:61:1:ARG:HB2	1:81:1:TRP:HH2	5	0.46
(2,400)	1:61:1:ARG:HB3	1:81:1:TRP:HH2	5	0.46
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	15	0.46
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	15	0.46
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	27	0.46
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	27	0.46
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	10	0.46
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	10	0.46
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	10	0.46
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	12	0.46
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	12	0.46
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	12	0.46
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	31	0.46
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	31	0.46
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	31	0.46
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	42	0.46
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	42	0.46
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	42	0.46
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	30	0.46
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	30	0.46
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	14	0.46
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	14	0.46
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	14	0.46
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	14	0.46
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	14	0.46

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	14	0.46
(2,575)	1:5:1:CYS:H	1:14:1:GLU:HB2	32	0.45
(2,560)	1:80:1:PRO:HG2	1:81:1:TRP:HD1	13	0.45
(2,560)	1:80:1:PRO:HG3	1:81:1:TRP:HD1	13	0.45
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	12	0.45
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	12	0.45
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	9	0.45
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	9	0.45
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	9	0.45
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	9	0.45
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	9	0.45
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	9	0.45
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	12	0.45
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	18	0.45
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	18	0.45
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	24	0.45
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	24	0.45
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	28	0.45
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	28	0.45
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	6	0.45
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	6	0.45
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	6	0.45
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	18	0.45
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	18	0.45
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	18	0.45
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	30	0.45
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	30	0.45
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	30	0.45
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	15	0.45
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	15	0.45
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	32	0.45
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	37	0.45
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	11	0.45
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	4	0.45
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	4	0.45
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	4	0.45
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	4	0.45
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	4	0.45
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	4	0.45
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	18	0.45
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	18	0.45
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	18	0.45

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	18	0.45
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	18	0.45
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	18	0.45
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	20	0.45
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	20	0.45
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	20	0.45
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	20	0.45
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	20	0.45
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	20	0.45
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	8	0.45
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	8	0.45
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	8	0.45
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	8	0.45
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	8	0.45
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	8	0.45
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	8	0.45
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	8	0.45
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	8	0.45
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	8	0.45
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	8	0.45
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	8	0.45
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	8	0.45
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	8	0.45
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	8	0.45
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	8	0.45
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	8	0.45
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	8	0.45
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	8	0.45
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	8	0.45
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	8	0.45
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	8	0.45
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	8	0.45
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	8	0.45
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	8	0.45
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	8	0.45
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	8	0.45
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	8	0.45
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	8	0.45
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	8	0.45
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	8	0.45
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	8	0.45
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	8	0.45

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	8	0.45
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	8	0.45
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	8	0.45
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	9	0.45
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	9	0.45
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	9	0.45
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	9	0.45
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	9	0.45
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	9	0.45
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	9	0.45
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	9	0.45
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	9	0.45
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	9	0.45
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	9	0.45
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	9	0.45
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	9	0.45
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	9	0.45
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	9	0.45
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	9	0.45
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	9	0.45
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	9	0.45
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	9	0.45
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	9	0.45
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	9	0.45
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	9	0.45
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	9	0.45
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	9	0.45
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	9	0.45
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	9	0.45
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	9	0.45
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	9	0.45
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	9	0.45
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	9	0.45
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	9	0.45
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	9	0.45
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	9	0.45
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	9	0.45
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	9	0.45
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	9	0.45
(2,577)	1:8:1:LYS:H	1:9:1:ILE:HG22	2	0.44
(2,577)	1:8:1:LYS:H	1:9:1:ILE:HG23	32	0.44
(2,575)	1:5:1:CYS:H	1:14:1:GLU:HB2	27	0.44

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	2	0.44
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	2	0.44
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	5	0.44
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	5	0.44
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	5	0.44
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	5	0.44
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	5	0.44
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	5	0.44
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	19	0.44
(2,381)	1:61:1:ARG:HH11	1:62:1:ILE:H	6	0.44
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	30	0.44
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	30	0.44
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	37	0.44
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	37	0.44
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	22	0.44
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	22	0.44
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	22	0.44
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	41	0.44
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	41	0.44
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	41	0.44
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	3	0.44
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	27	0.44
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	33	0.44
(2,581)	1:25:1:GLN:HE21	1:26:1:ASP:HA	24	0.43
(2,581)	1:25:1:GLN:HE21	1:23:1:ASN:HA	27	0.43
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	10	0.43
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	10	0.43
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	16	0.43
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	16	0.43
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	21	0.43
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	21	0.43
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	21	0.43
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	21	0.43
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	21	0.43
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	21	0.43
(2,422)	1:62:1:ILE:HG21	1:64:1:ARG:HD2	26	0.43
(2,422)	1:62:1:ILE:HG21	1:64:1:ARG:HD3	26	0.43
(2,422)	1:62:1:ILE:HG22	1:64:1:ARG:HD2	26	0.43
(2,422)	1:62:1:ILE:HG22	1:64:1:ARG:HD3	26	0.43
(2,422)	1:62:1:ILE:HG23	1:64:1:ARG:HD2	26	0.43
(2,422)	1:62:1:ILE:HG23	1:64:1:ARG:HD3	26	0.43
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	11	0.43

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	11	0.43
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	33	0.43
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	33	0.43
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	36	0.43
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	36	0.43
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	37	0.43
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	34	0.43
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	34	0.43
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	9	0.43
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	23	0.43
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	34	0.43
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	39	0.43
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	39	0.43
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	39	0.43
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	39	0.43
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	39	0.43
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	39	0.43
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	39	0.43
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	39	0.43
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	39	0.43
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	39	0.43
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	39	0.43
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	39	0.43
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	39	0.43
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	39	0.43
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	39	0.43
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	39	0.43
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	39	0.43
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	39	0.43
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	39	0.43
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	39	0.43
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	39	0.43
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	39	0.43
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	39	0.43
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	39	0.43
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	39	0.43
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	39	0.43
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	39	0.43
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	39	0.43
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	39	0.43
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	39	0.43
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	39	0.43

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	39	0.43
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	39	0.43
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	39	0.43
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	39	0.43
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	39	0.43
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	22	0.42
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	22	0.42
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	33	0.42
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	33	0.42
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	33	0.42
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	7	0.42
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	7	0.42
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	1	0.42
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	13	0.42
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	13	0.42
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	13	0.42
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	13	0.42
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	13	0.42
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	13	0.42
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	6	0.42
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	16	0.42
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	34	0.42
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	34	0.42
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	34	0.42
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	34	0.42
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	34	0.42
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	34	0.42
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	34	0.42
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	34	0.42
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	34	0.42
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	34	0.42
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	34	0.42
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	34	0.42
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	34	0.42
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	34	0.42
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	34	0.42
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	34	0.42
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	34	0.42
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	34	0.42
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	34	0.42
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	34	0.42
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	34	0.42

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	34	0.42
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	34	0.42
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	34	0.42
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	34	0.42
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	34	0.42
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	34	0.42
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	34	0.42
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	34	0.42
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	34	0.42
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	34	0.42
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	34	0.42
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	34	0.42
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	34	0.42
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	34	0.42
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	34	0.42
(2,583)	1:31:1:ALA:HB3	1:26:1:ASP:H	36	0.41
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	20	0.41
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	20	0.41
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	30	0.41
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	30	0.41
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	30	0.41
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	30	0.41
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	30	0.41
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	30	0.41
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	39	0.41
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	39	0.41
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	8	0.41
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	8	0.41
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	8	0.41
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	14	0.41
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	14	0.41
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	14	0.41
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	29	0.41
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	29	0.41
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	29	0.41
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	40	0.41
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	40	0.41
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	30	0.41
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	9	0.41
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	9	0.41
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	9	0.41
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	9	0.41

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	9	0.41
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	9	0.41
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	17	0.41
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	17	0.41
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	17	0.41
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	17	0.41
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	17	0.41
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	17	0.41
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	23	0.41
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	23	0.41
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	23	0.41
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	23	0.41
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	23	0.41
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	23	0.41
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	28	0.41
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	28	0.41
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	28	0.41
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	28	0.41
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	28	0.41
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	28	0.41
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	11	0.41
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	27	0.41
(2,581)	1:25:1:GLN:HE21	1:26:1:ASP:HA	32	0.4
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	9	0.4
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	9	0.4
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	9	0.4
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	9	0.4
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	24	0.4
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	24	0.4
(2,489)	1:67:1:TRP:HB2	1:83:1:HIS:HD2	29	0.4
(2,489)	1:67:1:TRP:HB3	1:83:1:HIS:HD2	29	0.4
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB2	25	0.4
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB3	25	0.4
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB2	25	0.4
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB3	25	0.4
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB2	25	0.4
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB3	25	0.4
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	11	0.4
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	11	0.4
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	11	0.4
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	26	0.4
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	26	0.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	26	0.4
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	19	0.4
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	19	0.4
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	5	0.4
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	14	0.4
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	24	0.4
(2,581)	1:25:1:GLN:HE21	1:23:1:ASN:HA	7	0.39
(2,483)	1:66:1:ASP:HB2	1:67:1:TRP:HE3	15	0.39
(2,483)	1:66:1:ASP:HB3	1:67:1:TRP:HE3	15	0.39
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	22	0.39
(2,400)	1:61:1:ARG:HB2	1:81:1:TRP:HH2	4	0.39
(2,400)	1:61:1:ARG:HB3	1:81:1:TRP:HH2	4	0.39
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	24	0.39
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	24	0.39
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	24	0.39
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	28	0.39
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	28	0.39
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	28	0.39
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	27	0.39
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	3	0.39
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	3	0.39
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	4	0.39
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	25	0.39
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	30	0.39
(2,583)	1:31:1:ALA:HB3	1:26:1:ASP:H	19	0.38
(2,577)	1:8:1:LYS:H	1:9:1:ILE:HG21	40	0.38
(2,560)	1:80:1:PRO:HG2	1:81:1:TRP:HD1	3	0.38
(2,560)	1:80:1:PRO:HG3	1:81:1:TRP:HD1	3	0.38
(2,483)	1:66:1:ASP:HB2	1:67:1:TRP:HE3	24	0.38
(2,483)	1:66:1:ASP:HB3	1:67:1:TRP:HE3	24	0.38
(2,435)	1:62:1:ILE:HG21	1:67:1:TRP:HD1	35	0.38
(2,435)	1:62:1:ILE:HG22	1:67:1:TRP:HD1	35	0.38
(2,435)	1:62:1:ILE:HG23	1:67:1:TRP:HD1	35	0.38
(2,422)	1:62:1:ILE:HG21	1:64:1:ARG:HD2	27	0.38
(2,422)	1:62:1:ILE:HG21	1:64:1:ARG:HD3	27	0.38
(2,422)	1:62:1:ILE:HG22	1:64:1:ARG:HD2	27	0.38
(2,422)	1:62:1:ILE:HG22	1:64:1:ARG:HD3	27	0.38
(2,422)	1:62:1:ILE:HG23	1:64:1:ARG:HD2	27	0.38
(2,422)	1:62:1:ILE:HG23	1:64:1:ARG:HD3	27	0.38
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	34	0.38
(2,389)	1:61:1:ARG:HG2	1:70:1:ASP:HA	25	0.38
(2,389)	1:61:1:ARG:HG3	1:70:1:ASP:HA	25	0.38

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	5	0.38
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	5	0.38
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	5	0.38
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	15	0.38
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	15	0.38
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	15	0.38
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	26	0.38
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	26	0.38
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	20	0.38
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	20	0.38
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	20	0.38
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	3	0.38
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	3	0.38
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	3	0.38
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	3	0.38
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	3	0.38
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	3	0.38
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	43	0.38
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	15	0.37
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	17	0.37
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	25	0.37
(2,575)	1:5:1:CYS:H	1:14:1:GLU:HB2	34	0.37
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	11	0.37
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	21	0.37
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	21	0.37
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	21	0.37
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	21	0.37
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	31	0.37
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	31	0.37
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	31	0.37
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	31	0.37
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	31	0.37
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	31	0.37
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB2	4	0.37
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB3	4	0.37
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB2	4	0.37
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB3	4	0.37
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB2	4	0.37
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB3	4	0.37
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB2	17	0.37
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB3	17	0.37
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB2	17	0.37

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB3	17	0.37
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB2	17	0.37
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB3	17	0.37
(2,412)	1:61:1:ARG:HH21	1:81:1:TRP:HZ3	5	0.37
(2,389)	1:61:1:ARG:HG2	1:70:1:ASP:HA	31	0.37
(2,389)	1:61:1:ARG:HG3	1:70:1:ASP:HA	31	0.37
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	23	0.37
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	23	0.37
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	14	0.37
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	14	0.37
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	14	0.37
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	14	0.37
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	14	0.37
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	14	0.37
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	14	0.37
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	14	0.37
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	14	0.37
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	14	0.37
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	14	0.37
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	14	0.37
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	14	0.37
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	14	0.37
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	14	0.37
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	14	0.37
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	14	0.37
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	14	0.37
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	14	0.37
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	14	0.37
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	14	0.37
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	14	0.37
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	14	0.37
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	14	0.37
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	14	0.37
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	14	0.37
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	14	0.37
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	14	0.37
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	14	0.37
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	14	0.37
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	14	0.37
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	14	0.37
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	14	0.37
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	14	0.37

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	14	0.37
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	14	0.37
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	33	0.36
(2,560)	1:80:1:PRO:HG2	1:81:1:TRP:HD1	8	0.36
(2,560)	1:80:1:PRO:HG3	1:81:1:TRP:HD1	8	0.36
(2,466)	1:64:1:ARG:HG2	1:67:1:TRP:HE1	5	0.36
(2,466)	1:64:1:ARG:HG3	1:67:1:TRP:HE1	5	0.36
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	13	0.36
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	13	0.36
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	13	0.36
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	13	0.36
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	13	0.36
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	13	0.36
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	26	0.36
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	26	0.36
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	26	0.36
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	26	0.36
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	26	0.36
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	26	0.36
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB2	42	0.36
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB3	42	0.36
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB2	42	0.36
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB3	42	0.36
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB2	42	0.36
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB3	42	0.36
(2,438)	1:62:1:ILE:HG21	1:81:1:TRP:HE3	17	0.36
(2,438)	1:62:1:ILE:HG22	1:81:1:TRP:HE3	17	0.36
(2,438)	1:62:1:ILE:HG23	1:81:1:TRP:HE3	17	0.36
(2,417)	1:62:1:ILE:HD11	1:63:1:ALA:HA	25	0.36
(2,417)	1:62:1:ILE:HD12	1:63:1:ALA:HA	25	0.36
(2,417)	1:62:1:ILE:HD13	1:63:1:ALA:HA	25	0.36
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	23	0.36
(2,389)	1:61:1:ARG:HG2	1:70:1:ASP:HA	38	0.36
(2,389)	1:61:1:ARG:HG3	1:70:1:ASP:HA	38	0.36
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	5	0.36
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	5	0.36
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	23	0.36
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	23	0.36
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	12	0.36
(2,42)	1:9:1:ILE:H	1:17:1:ASP:H	27	0.36
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	22	0.35
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	34	0.35

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	41	0.35
(2,587)	1:56:1:ALA:HB2	1:75:1:LYS:HZ2	2	0.35
(2,527)	1:72:1:CYS:HA	1:76:1:SER:H	7	0.35
(2,513)	1:70:1:ASP:HA	1:81:1:TRP:HD1	13	0.35
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	35	0.35
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	35	0.35
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	35	0.35
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	35	0.35
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	35	0.35
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	35	0.35
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	41	0.35
(2,389)	1:61:1:ARG:HG2	1:70:1:ASP:HA	2	0.35
(2,389)	1:61:1:ARG:HG3	1:70:1:ASP:HA	2	0.35
(2,389)	1:61:1:ARG:HG2	1:70:1:ASP:HA	6	0.35
(2,389)	1:61:1:ARG:HG3	1:70:1:ASP:HA	6	0.35
(2,389)	1:61:1:ARG:HG2	1:70:1:ASP:HA	14	0.35
(2,389)	1:61:1:ARG:HG3	1:70:1:ASP:HA	14	0.35
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	27	0.35
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	27	0.35
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	27	0.35
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	42	0.35
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	42	0.35
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	42	0.35
(2,381)	1:61:1:ARG:HH11	1:62:1:ILE:H	42	0.35
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	9	0.35
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	9	0.35
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	4	0.35
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	4	0.35
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	6	0.35
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	6	0.35
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	23	0.35
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	23	0.35
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	23	0.35
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	23	0.35
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	23	0.35
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	23	0.35
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	1	0.35
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	2	0.35
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	13	0.35
(2,42)	1:9:1:ILE:H	1:17:1:ASP:H	8	0.35
(2,42)	1:9:1:ILE:H	1:17:1:ASP:H	34	0.35
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	2	0.35

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	2	0.35
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	2	0.35
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	2	0.35
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	2	0.35
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	2	0.35
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	2	0.35
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	2	0.35
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	2	0.35
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	2	0.35
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	2	0.35
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	2	0.35
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	2	0.35
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	2	0.35
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	2	0.35
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	2	0.35
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	2	0.35
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	2	0.35
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	2	0.35
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	2	0.35
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	2	0.35
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	2	0.35
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	2	0.35
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	2	0.35
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	2	0.35
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	2	0.35
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	2	0.35
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	2	0.35
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	2	0.35
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	2	0.35
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	2	0.35
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	2	0.35
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	2	0.35
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	2	0.35
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	2	0.35
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	2	0.35
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	7	0.34
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	14	0.34
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	16	0.34
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	19	0.34
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	20	0.34
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	29	0.34
(2,581)	1:25:1:GLN:HE21	1:26:1:ASP:HA	13	0.34

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,575)	1:5:1:CYS:H	1:14:1:GLU:HB2	8	0.34
(2,560)	1:80:1:PRO:HG2	1:81:1:TRP:HD1	34	0.34
(2,560)	1:80:1:PRO:HG3	1:81:1:TRP:HD1	34	0.34
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	27	0.34
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	31	0.34
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	31	0.34
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	27	0.34
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	27	0.34
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	27	0.34
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	27	0.34
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	27	0.34
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	27	0.34
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	37	0.34
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	37	0.34
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	37	0.34
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	37	0.34
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	37	0.34
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	37	0.34
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB2	14	0.34
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB3	14	0.34
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB2	14	0.34
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB3	14	0.34
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB2	14	0.34
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB3	14	0.34
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB2	20	0.34
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB3	20	0.34
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB2	20	0.34
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB3	20	0.34
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB2	20	0.34
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB3	20	0.34
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	3	0.34
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	8	0.34
(2,389)	1:61:1:ARG:HG2	1:70:1:ASP:HA	20	0.34
(2,389)	1:61:1:ARG:HG3	1:70:1:ASP:HA	20	0.34
(2,389)	1:61:1:ARG:HG2	1:70:1:ASP:HA	32	0.34
(2,389)	1:61:1:ARG:HG3	1:70:1:ASP:HA	32	0.34
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	2	0.34
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	2	0.34
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	2	0.34
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	3	0.34
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	3	0.34
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	3	0.34

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	23	0.34
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	23	0.34
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	23	0.34
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	37	0.34
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	37	0.34
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	37	0.34
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	27	0.34
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	27	0.34
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	42	0.34
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	42	0.34
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	16	0.34
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	16	0.34
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	16	0.34
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	16	0.34
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	16	0.34
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	16	0.34
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	20	0.34
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	43	0.34
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	4	0.33
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	6	0.33
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	10	0.33
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	23	0.33
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	42	0.33
(2,575)	1:5:1:CYS:H	1:14:1:GLU:HB2	3	0.33
(2,560)	1:80:1:PRO:HG2	1:81:1:TRP:HD1	41	0.33
(2,560)	1:80:1:PRO:HG3	1:81:1:TRP:HD1	41	0.33
(2,466)	1:64:1:ARG:HG2	1:67:1:TRP:HE1	35	0.33
(2,466)	1:64:1:ARG:HG3	1:67:1:TRP:HE1	35	0.33
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	8	0.33
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	8	0.33
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	8	0.33
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	8	0.33
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	8	0.33
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	8	0.33
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB2	30	0.33
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB3	30	0.33
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB2	30	0.33
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB3	30	0.33
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB2	30	0.33
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB3	30	0.33
(2,389)	1:61:1:ARG:HG2	1:70:1:ASP:HA	42	0.33
(2,389)	1:61:1:ARG:HG3	1:70:1:ASP:HA	42	0.33

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	16	0.33
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	16	0.33
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	16	0.33
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	38	0.33
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	38	0.33
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	38	0.33
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	43	0.33
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	43	0.33
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	43	0.33
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	32	0.33
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	32	0.33
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	40	0.33
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	40	0.33
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	19	0.33
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	19	0.33
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	19	0.33
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	19	0.33
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	19	0.33
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	19	0.33
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	7	0.33
(1,777)	1:61:1:ARG:HH21	1:81:1:TRP:HZ2	26	0.33
(1,776)	1:61:1:ARG:HH21	1:81:1:TRP:HE3	21	0.33
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	15	0.33
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	12	0.32
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	24	0.32
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	32	0.32
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	29	0.32
(2,575)	1:5:1:CYS:H	1:14:1:GLU:HB2	19	0.32
(2,560)	1:80:1:PRO:HG2	1:81:1:TRP:HD1	22	0.32
(2,560)	1:80:1:PRO:HG3	1:81:1:TRP:HD1	22	0.32
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	43	0.32
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB2	6	0.32
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB3	6	0.32
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB2	6	0.32
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB3	6	0.32
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB2	6	0.32
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB3	6	0.32
(2,438)	1:62:1:ILE:HG21	1:81:1:TRP:HE3	25	0.32
(2,438)	1:62:1:ILE:HG22	1:81:1:TRP:HE3	25	0.32
(2,438)	1:62:1:ILE:HG23	1:81:1:TRP:HE3	25	0.32
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB2	8	0.32
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB3	8	0.32

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB2	8	0.32
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB3	8	0.32
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB2	8	0.32
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB3	8	0.32
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB2	24	0.32
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB3	24	0.32
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB2	24	0.32
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB3	24	0.32
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB2	24	0.32
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB3	24	0.32
(2,389)	1:61:1:ARG:HG2	1:70:1:ASP:HA	17	0.32
(2,389)	1:61:1:ARG:HG3	1:70:1:ASP:HA	17	0.32
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	35	0.32
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	35	0.32
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	19	0.32
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	19	0.32
(1,777)	1:61:1:ARG:HH21	1:81:1:TRP:HZ2	37	0.32
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	2	0.31
(2,575)	1:5:1:CYS:H	1:14:1:GLU:HB2	40	0.31
(2,560)	1:80:1:PRO:HG2	1:81:1:TRP:HD1	7	0.31
(2,560)	1:80:1:PRO:HG3	1:81:1:TRP:HD1	7	0.31
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	31	0.31
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	11	0.31
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	11	0.31
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	11	0.31
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	11	0.31
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	11	0.31
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	11	0.31
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	24	0.31
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	24	0.31
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	24	0.31
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	24	0.31
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	24	0.31
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	24	0.31
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	39	0.31
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	39	0.31
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	39	0.31
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	39	0.31
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	39	0.31
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	39	0.31
(2,438)	1:62:1:ILE:HG21	1:81:1:TRP:HE3	14	0.31
(2,438)	1:62:1:ILE:HG22	1:81:1:TRP:HE3	14	0.31

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,438)	1:62:1:ILE:HG23	1:81:1:TRP:HE3	14	0.31
(2,389)	1:61:1:ARG:HG2	1:70:1:ASP:HA	15	0.31
(2,389)	1:61:1:ARG:HG3	1:70:1:ASP:HA	15	0.31
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	21	0.31
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	21	0.31
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	27	0.31
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	27	0.31
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	27	0.31
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	34	0.31
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	34	0.31
(2,191)	1:41:1:GLN:HA	1:53:1:PHE:HB2	20	0.31
(2,191)	1:41:1:GLN:HA	1:53:1:PHE:HB3	20	0.31
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	7	0.31
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	7	0.31
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	7	0.31
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	7	0.31
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	7	0.31
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	7	0.31
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	17	0.31
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	17	0.31
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	17	0.31
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	17	0.31
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	17	0.31
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	17	0.31
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	15	0.31
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	33	0.31
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	39	0.31
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	8	0.31
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	8	0.31
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	8	0.31
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	8	0.31
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	8	0.31
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	8	0.31
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	9	0.31
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	9	0.31
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	9	0.31
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	9	0.31
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	9	0.31
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	9	0.31
(1,777)	1:61:1:ARG:HH21	1:81:1:TRP:HZ2	28	0.31
(1,777)	1:61:1:ARG:HH21	1:81:1:TRP:HZ2	29	0.31
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	3	0.3

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	18	0.3
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	27	0.3
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	28	0.3
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	36	0.3
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	28	0.3
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	28	0.3
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	28	0.3
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	28	0.3
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	28	0.3
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	28	0.3
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB2	3	0.3
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB3	3	0.3
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB2	3	0.3
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB3	3	0.3
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB2	3	0.3
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB3	3	0.3
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	13	0.3
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	13	0.3
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	13	0.3
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	15	0.3
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	21	0.3
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	21	0.3
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	21	0.3
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	21	0.3
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	21	0.3
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	21	0.3
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	30	0.3
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	30	0.3
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	30	0.3
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	30	0.3
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	30	0.3
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	30	0.3
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	18	0.3
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	35	0.3
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	6	0.3
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	6	0.3
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	6	0.3
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	6	0.3
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	6	0.3
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	6	0.3
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	35	0.3
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	35	0.3

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	35	0.3
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	35	0.3
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	35	0.3
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	35	0.3
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	13	0.3
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	13	0.3
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	13	0.3
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	13	0.3
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	13	0.3
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	13	0.3
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	13	0.3
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	13	0.3
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	13	0.3
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	13	0.3
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	13	0.3
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	13	0.3
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	13	0.3
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	13	0.3
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	13	0.3
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	13	0.3
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	13	0.3
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	13	0.3
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	13	0.3
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	13	0.3
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	13	0.3
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	13	0.3
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	13	0.3
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	13	0.3
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	13	0.3
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	13	0.3
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	13	0.3
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	13	0.3
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	13	0.3
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	13	0.3
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	13	0.3
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	13	0.3
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	13	0.3
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	13	0.3
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	13	0.3
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	13	0.3
(1,776)	1:61:1:ARG:HH21	1:81:1:TRP:HE3	9	0.3
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	5	0.29

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	37	0.29
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	23	0.29
(2,527)	1:72:1:CYS:HA	1:76:1:SER:H	43	0.29
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	18	0.29
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	18	0.29
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	18	0.29
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	18	0.29
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	18	0.29
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	18	0.29
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	30	0.29
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	30	0.29
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	30	0.29
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	34	0.29
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	34	0.29
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	34	0.29
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	30	0.29
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	9	0.29
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	9	0.29
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	27	0.29
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	27	0.29
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	5	0.29
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	35	0.29
(2,179)	1:41:1:GLN:HB2	1:51:1:CYS:H	10	0.29
(2,179)	1:41:1:GLN:HB3	1:51:1:CYS:H	10	0.29
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	22	0.29
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	22	0.29
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	22	0.29
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	22	0.29
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	22	0.29
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	22	0.29
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	25	0.29
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	25	0.29
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	25	0.29
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	25	0.29
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	25	0.29
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	25	0.29
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	5	0.29
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	5	0.29
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	5	0.29
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	5	0.29
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	5	0.29
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	5	0.29

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	5	0.29
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	5	0.29
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	5	0.29
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	5	0.29
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	5	0.29
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	5	0.29
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	5	0.29
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	5	0.29
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	5	0.29
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	5	0.29
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	5	0.29
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	5	0.29
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	5	0.29
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	5	0.29
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	5	0.29
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	5	0.29
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	5	0.29
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	5	0.29
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	5	0.29
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	5	0.29
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	5	0.29
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	5	0.29
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	5	0.29
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	5	0.29
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	5	0.29
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	5	0.29
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	5	0.29
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	5	0.29
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	5	0.29
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	5	0.29
(1,777)	1:61:1:ARG:HH21	1:81:1:TRP:HZ2	18	0.29
(1,777)	1:61:1:ARG:HH21	1:81:1:TRP:HZ2	36	0.29
(1,777)	1:61:1:ARG:HH21	1:81:1:TRP:HZ2	39	0.29
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	11	0.28
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	26	0.28
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	35	0.28
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	43	0.28
(2,577)	1:8:1:LYS:H	1:4:1:VAL:HG13	38	0.28
(2,575)	1:5:1:CYS:H	1:14:1:GLU:HB2	28	0.28
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	7	0.28
(2,513)	1:70:1:ASP:HA	1:81:1:TRP:HD1	3	0.28
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	36	0.28

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	36	0.28
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	36	0.28
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	36	0.28
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	36	0.28
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	36	0.28
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB2	10	0.28
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB3	10	0.28
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB2	10	0.28
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB3	10	0.28
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB2	10	0.28
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB3	10	0.28
(2,438)	1:62:1:ILE:HG21	1:81:1:TRP:HE3	6	0.28
(2,438)	1:62:1:ILE:HG22	1:81:1:TRP:HE3	6	0.28
(2,438)	1:62:1:ILE:HG23	1:81:1:TRP:HE3	6	0.28
(2,381)	1:61:1:ARG:HH11	1:62:1:ILE:H	25	0.28
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	7	0.28
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	7	0.28
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	7	0.28
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	3	0.28
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	3	0.28
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	8	0.28
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	8	0.28
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	11	0.28
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	11	0.28
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	41	0.28
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	41	0.28
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	4	0.28
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	5	0.28
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	5	0.28
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	5	0.28
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	5	0.28
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	5	0.28
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	5	0.28
(2,77)	1:16:1:CYS:H	1:34:1:CYS:H	24	0.28
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	27	0.28
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	27	0.28
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	27	0.28
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	27	0.28
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	27	0.28
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	27	0.28
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	1	0.28
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	1	0.28

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	1	0.28
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	1	0.28
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	1	0.28
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	1	0.28
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	1	0.28
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	1	0.28
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	1	0.28
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	1	0.28
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	1	0.28
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	1	0.28
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	1	0.28
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	1	0.28
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	1	0.28
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	1	0.28
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	1	0.28
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	1	0.28
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	1	0.28
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	1	0.28
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	1	0.28
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	1	0.28
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	1	0.28
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	1	0.28
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	1	0.28
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	1	0.28
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	1	0.28
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	1	0.28
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	1	0.28
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	1	0.28
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	1	0.28
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	1	0.28
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	1	0.28
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	1	0.28
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	1	0.28
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	1	0.28
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	9	0.27
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	30	0.27
(2,560)	1:80:1:PRO:HG2	1:81:1:TRP:HD1	19	0.27
(2,560)	1:80:1:PRO:HG3	1:81:1:TRP:HD1	19	0.27
(2,527)	1:72:1:CYS:HA	1:76:1:SER:H	5	0.27
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	8	0.27
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	22	0.27
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB2	31	0.27

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB3	31	0.27
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB2	31	0.27
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB3	31	0.27
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB2	31	0.27
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB3	31	0.27
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB2	9	0.27
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB3	9	0.27
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB2	9	0.27
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB3	9	0.27
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB2	9	0.27
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB3	9	0.27
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	43	0.27
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	43	0.27
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	10	0.27
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	10	0.27
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	17	0.27
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	17	0.27
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	21	0.27
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	21	0.27
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	25	0.27
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	25	0.27
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	31	0.27
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	31	0.27
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	8	0.26
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	31	0.26
(2,585)	1:54:1:LYS:HZ3	1:60:1:CYS:HA	15	0.26
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD13	37	0.26
(2,560)	1:80:1:PRO:HG2	1:81:1:TRP:HD1	2	0.26
(2,560)	1:80:1:PRO:HG3	1:81:1:TRP:HD1	2	0.26
(2,560)	1:80:1:PRO:HG2	1:81:1:TRP:HD1	12	0.26
(2,560)	1:80:1:PRO:HG3	1:81:1:TRP:HD1	12	0.26
(2,560)	1:80:1:PRO:HG2	1:81:1:TRP:HD1	23	0.26
(2,560)	1:80:1:PRO:HG3	1:81:1:TRP:HD1	23	0.26
(2,560)	1:80:1:PRO:HG2	1:81:1:TRP:HD1	35	0.26
(2,560)	1:80:1:PRO:HG3	1:81:1:TRP:HD1	35	0.26
(2,483)	1:66:1:ASP:HB2	1:67:1:TRP:HE3	9	0.26
(2,483)	1:66:1:ASP:HB3	1:67:1:TRP:HE3	9	0.26
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	1	0.26
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	1	0.26
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	1	0.26
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	1	0.26
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	1	0.26

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	1	0.26
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	43	0.26
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	43	0.26
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	43	0.26
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	43	0.26
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	43	0.26
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	43	0.26
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB2	41	0.26
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB3	41	0.26
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB2	41	0.26
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB3	41	0.26
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB2	41	0.26
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB3	41	0.26
(2,438)	1:62:1:ILE:HG21	1:81:1:TRP:HE3	5	0.26
(2,438)	1:62:1:ILE:HG22	1:81:1:TRP:HE3	5	0.26
(2,438)	1:62:1:ILE:HG23	1:81:1:TRP:HE3	5	0.26
(2,438)	1:62:1:ILE:HG21	1:81:1:TRP:HE3	20	0.26
(2,438)	1:62:1:ILE:HG22	1:81:1:TRP:HE3	20	0.26
(2,438)	1:62:1:ILE:HG23	1:81:1:TRP:HE3	20	0.26
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	3	0.26
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	3	0.26
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	4	0.26
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	6	0.26
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	6	0.26
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	12	0.26
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	12	0.26
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	22	0.26
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	22	0.26
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	34	0.26
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	9	0.26
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	21	0.26
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	39	0.26
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	21	0.25
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	38	0.25
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	40	0.25
(2,583)	1:31:1:ALA:HB2	1:26:1:ASP:H	3	0.25
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	2	0.25
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	3	0.25
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	8	0.25
(2,527)	1:72:1:CYS:HA	1:76:1:SER:H	4	0.25
(2,513)	1:70:1:ASP:HA	1:81:1:TRP:HD1	2	0.25
(2,513)	1:70:1:ASP:HA	1:81:1:TRP:HD1	8	0.25

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,513)	1:70:1:ASP:HA	1:81:1:TRP:HD1	32	0.25
(2,441)	1:62:1:ILE:HD11	1:81:1:TRP:HE3	17	0.25
(2,441)	1:62:1:ILE:HD12	1:81:1:TRP:HE3	17	0.25
(2,441)	1:62:1:ILE:HD13	1:81:1:TRP:HE3	17	0.25
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB2	16	0.25
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB3	16	0.25
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB2	16	0.25
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB3	16	0.25
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB2	16	0.25
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB3	16	0.25
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB2	22	0.25
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB3	22	0.25
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB2	22	0.25
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB3	22	0.25
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB2	22	0.25
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB3	22	0.25
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB2	39	0.25
(2,432)	1:62:1:ILE:HG21	1:66:1:ASP:HB3	39	0.25
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB2	39	0.25
(2,432)	1:62:1:ILE:HG22	1:66:1:ASP:HB3	39	0.25
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB2	39	0.25
(2,432)	1:62:1:ILE:HG23	1:66:1:ASP:HB3	39	0.25
(2,389)	1:61:1:ARG:HG2	1:70:1:ASP:HA	40	0.25
(2,389)	1:61:1:ARG:HG3	1:70:1:ASP:HA	40	0.25
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	35	0.25
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	35	0.25
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	35	0.25
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	9	0.25
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	9	0.25
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	9	0.25
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	15	0.25
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	15	0.25
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	15	0.25
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	43	0.25
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	5	0.25
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	5	0.25
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	29	0.25
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	29	0.25
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	37	0.25
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	37	0.25
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	19	0.25
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	20	0.25

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	20	0.25
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	20	0.25
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	20	0.25
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	20	0.25
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	20	0.25
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	34	0.25
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	34	0.25
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	34	0.25
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	34	0.25
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	34	0.25
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	34	0.25
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	33	0.25
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	33	0.25
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	33	0.25
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	33	0.25
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	33	0.25
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	33	0.25
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	33	0.25
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	33	0.25
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	33	0.25
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	33	0.25
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	33	0.25
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	33	0.25
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	33	0.25
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	33	0.25
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	33	0.25
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	33	0.25
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	33	0.25
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	33	0.25
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	33	0.25
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	33	0.25
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	33	0.25
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	33	0.25
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	33	0.25
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	33	0.25
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	33	0.25
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	33	0.25
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	33	0.25
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	33	0.25
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	33	0.25
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	33	0.25
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	33	0.25

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	33	0.25
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	33	0.25
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	33	0.25
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	33	0.25
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	33	0.25
(1,774)	1:61:1:ARG:HH21	1:81:1:TRP:HD1	4	0.25
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	4	0.25
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	18	0.25
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	26	0.25
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	28	0.25
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	29	0.25
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	36	0.25
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	37	0.25
(2,581)	1:25:1:GLN:HE21	1:23:1:ASN:HA	3	0.24
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	20	0.24
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	30	0.24
(2,527)	1:72:1:CYS:HA	1:76:1:SER:H	11	0.24
(2,483)	1:66:1:ASP:HB2	1:67:1:TRP:HE3	30	0.24
(2,483)	1:66:1:ASP:HB3	1:67:1:TRP:HE3	30	0.24
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB2	19	0.24
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB3	19	0.24
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB2	19	0.24
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB3	19	0.24
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB2	19	0.24
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB3	19	0.24
(2,438)	1:62:1:ILE:HG21	1:81:1:TRP:HE3	4	0.24
(2,438)	1:62:1:ILE:HG22	1:81:1:TRP:HE3	4	0.24
(2,438)	1:62:1:ILE:HG23	1:81:1:TRP:HE3	4	0.24
(2,386)	1:61:1:ARG:HB2	1:69:1:ASP:HA	13	0.24
(2,386)	1:61:1:ARG:HB3	1:69:1:ASP:HA	13	0.24
(2,381)	1:61:1:ARG:HH11	1:62:1:ILE:H	15	0.24
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	2	0.24
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	2	0.24
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	18	0.24
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	20	0.24
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	26	0.24
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	13	0.24
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	13	0.24
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	33	0.24
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	33	0.24
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	1	0.24
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	1	0.24

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	2	0.24
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	2	0.24
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	14	0.24
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	14	0.24
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	28	0.24
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	28	0.24
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	36	0.24
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	36	0.24
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	39	0.24
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	39	0.24
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	42	0.24
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	42	0.24
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	42	0.24
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	42	0.24
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	42	0.24
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	42	0.24
(2,18)	1:6:1:GLY:H	1:17:1:ASP:HA	34	0.24
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	18	0.24
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	18	0.24
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	18	0.24
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	18	0.24
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	18	0.24
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	18	0.24
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	18	0.24
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	18	0.24
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	18	0.24
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	18	0.24
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	18	0.24
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	18	0.24
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	18	0.24
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	18	0.24
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	18	0.24
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	18	0.24
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	18	0.24
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	18	0.24
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	18	0.24
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	18	0.24
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	18	0.24
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	18	0.24
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	18	0.24
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	18	0.24
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	18	0.24

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	18	0.24
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	18	0.24
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	18	0.24
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	18	0.24
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	18	0.24
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	18	0.24
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	18	0.24
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	18	0.24
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	18	0.24
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	18	0.24
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	18	0.24
(1,777)	1:61:1:ARG:HH21	1:81:1:TRP:HZ2	33	0.24
(1,473)	1:44:1:TYR:HA	1:45:1:GLY:H	35	0.24
(2,583)	1:31:1:ALA:HB1	1:26:1:ASP:H	41	0.23
(2,566)	1:81:1:TRP:HE1	1:82:1:ASN:H	5	0.23
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	12	0.23
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	14	0.23
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	18	0.23
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	22	0.23
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	26	0.23
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	41	0.23
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB2	34	0.23
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB3	34	0.23
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB2	34	0.23
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB3	34	0.23
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB2	34	0.23
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB3	34	0.23
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	13	0.23
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	8	0.23
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	8	0.23
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	32	0.23
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	32	0.23
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	17	0.23
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	17	0.23
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	17	0.23
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	19	0.23
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	19	0.23
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	19	0.23
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	25	0.23
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	25	0.23
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	25	0.23
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	32	0.23

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	32	0.23
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	32	0.23
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	9	0.23
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	9	0.23
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	24	0.23
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	24	0.23
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	26	0.23
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	26	0.23
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	12	0.23
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	12	0.23
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	12	0.23
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	12	0.23
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	12	0.23
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	12	0.23
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	12	0.23
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	36	0.23
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	36	0.23
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	36	0.23
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	36	0.23
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	36	0.23
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	36	0.23
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	36	0.23
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	36	0.23
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	36	0.23
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	36	0.23
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	36	0.23
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	36	0.23
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	36	0.23
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	36	0.23
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	36	0.23
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	36	0.23
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	36	0.23
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	36	0.23
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	36	0.23
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	36	0.23
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	36	0.23
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	36	0.23
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	36	0.23
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	36	0.23
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	36	0.23
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	36	0.23
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	36	0.23

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	36	0.23
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	36	0.23
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	36	0.23
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	36	0.23
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	36	0.23
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	36	0.23
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	36	0.23
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	36	0.23
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	36	0.23
(1,777)	1:61:1:ARG:HH21	1:81:1:TRP:HZ2	27	0.23
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	1	0.22
(2,581)	1:25:1:GLN:HE21	1:26:1:ASP:HA	30	0.22
(2,581)	1:25:1:GLN:HE21	1:26:1:ASP:HA	37	0.22
(2,560)	1:80:1:PRO:HG2	1:81:1:TRP:HD1	32	0.22
(2,560)	1:80:1:PRO:HG3	1:81:1:TRP:HD1	32	0.22
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	25	0.22
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	28	0.22
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	33	0.22
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	35	0.22
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	36	0.22
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	38	0.22
(2,527)	1:72:1:CYS:HA	1:76:1:SER:H	34	0.22
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	3	0.22
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	3	0.22
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	3	0.22
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	3	0.22
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	3	0.22
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	3	0.22
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB2	12	0.22
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB3	12	0.22
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB2	12	0.22
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB3	12	0.22
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB2	12	0.22
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB3	12	0.22
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB2	23	0.22
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB3	23	0.22
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB2	23	0.22
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB3	23	0.22
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB2	23	0.22
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB3	23	0.22
(2,438)	1:62:1:ILE:HG21	1:81:1:TRP:HE3	10	0.22
(2,438)	1:62:1:ILE:HG22	1:81:1:TRP:HE3	10	0.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,438)	1:62:1:ILE:HG23	1:81:1:TRP:HE3	10	0.22
(2,403)	1:61:1:ARG:HG2	1:81:1:TRP:HZ3	5	0.22
(2,403)	1:61:1:ARG:HG3	1:81:1:TRP:HZ3	5	0.22
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	38	0.22
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	38	0.22
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	20	0.22
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	20	0.22
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	41	0.22
(2,191)	1:41:1:GLN:HA	1:53:1:PHE:HB2	14	0.22
(2,191)	1:41:1:GLN:HA	1:53:1:PHE:HB3	14	0.22
(2,75)	1:16:1:CYS:HB2	1:29:1:CYS:H	10	0.22
(2,75)	1:16:1:CYS:HB3	1:29:1:CYS:H	10	0.22
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	24	0.22
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	24	0.22
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	24	0.22
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	24	0.22
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	24	0.22
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	24	0.22
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	24	0.22
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	24	0.22
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	24	0.22
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	24	0.22
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	24	0.22
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	24	0.22
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	24	0.22
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	24	0.22
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	24	0.22
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	24	0.22
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	24	0.22
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	24	0.22
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	24	0.22
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	24	0.22
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	24	0.22
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	24	0.22
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	24	0.22
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	24	0.22
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	24	0.22
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	24	0.22
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	24	0.22
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	24	0.22
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	24	0.22
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	24	0.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	24	0.22
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	24	0.22
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	24	0.22
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	24	0.22
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	24	0.22
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	24	0.22
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	35	0.22
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	35	0.22
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	35	0.22
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	35	0.22
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	35	0.22
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	35	0.22
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	35	0.22
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	35	0.22
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	35	0.22
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	35	0.22
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	35	0.22
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	35	0.22
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	35	0.22
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	35	0.22
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	35	0.22
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	35	0.22
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	35	0.22
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	35	0.22
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	35	0.22
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	35	0.22
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	35	0.22
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	35	0.22
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	35	0.22
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	35	0.22
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	35	0.22
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	35	0.22
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	35	0.22
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	35	0.22
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	35	0.22
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	35	0.22
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	35	0.22
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	35	0.22
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	35	0.22
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	35	0.22
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	35	0.22
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	35	0.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	9	0.21
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	21	0.21
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	24	0.21
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	29	0.21
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	31	0.21
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	37	0.21
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	39	0.21
(2,483)	1:66:1:ASP:HB2	1:67:1:TRP:HE3	19	0.21
(2,483)	1:66:1:ASP:HB3	1:67:1:TRP:HE3	19	0.21
(2,483)	1:66:1:ASP:HB2	1:67:1:TRP:HE3	41	0.21
(2,483)	1:66:1:ASP:HB3	1:67:1:TRP:HE3	41	0.21
(2,466)	1:64:1:ARG:HG2	1:67:1:TRP:HE1	43	0.21
(2,466)	1:64:1:ARG:HG3	1:67:1:TRP:HE1	43	0.21
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	2	0.21
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	2	0.21
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	2	0.21
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	2	0.21
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	2	0.21
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	2	0.21
(2,441)	1:62:1:ILE:HD11	1:81:1:TRP:HE3	14	0.21
(2,441)	1:62:1:ILE:HD12	1:81:1:TRP:HE3	14	0.21
(2,441)	1:62:1:ILE:HD13	1:81:1:TRP:HE3	14	0.21
(2,438)	1:62:1:ILE:HG21	1:81:1:TRP:HE3	42	0.21
(2,438)	1:62:1:ILE:HG22	1:81:1:TRP:HE3	42	0.21
(2,438)	1:62:1:ILE:HG23	1:81:1:TRP:HE3	42	0.21
(2,411)	1:61:1:ARG:HH21	1:81:1:TRP:HH2	37	0.21
(2,389)	1:61:1:ARG:HG2	1:70:1:ASP:HA	1	0.21
(2,389)	1:61:1:ARG:HG3	1:70:1:ASP:HA	1	0.21
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	33	0.21
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	33	0.21
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	33	0.21
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	40	0.21
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	40	0.21
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	28	0.21
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	28	0.21
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	15	0.21
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	15	0.21
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	18	0.21
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	18	0.21
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	36	0.21
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	30	0.21
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	1	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	5	0.2
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	6	0.2
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	10	0.2
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	13	0.2
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	34	0.2
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	40	0.2
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	42	0.2
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	3	0.2
(2,513)	1:70:1:ASP:HA	1:81:1:TRP:HD1	1	0.2
(2,483)	1:66:1:ASP:HB2	1:67:1:TRP:HE3	4	0.2
(2,483)	1:66:1:ASP:HB3	1:67:1:TRP:HE3	4	0.2
(2,411)	1:61:1:ARG:HH21	1:81:1:TRP:HH2	26	0.2
(2,411)	1:61:1:ARG:HH21	1:81:1:TRP:HH2	28	0.2
(2,411)	1:61:1:ARG:HH21	1:81:1:TRP:HH2	29	0.2
(2,402)	1:61:1:ARG:HG2	1:81:1:TRP:HH2	10	0.2
(2,402)	1:61:1:ARG:HG3	1:81:1:TRP:HH2	10	0.2
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	25	0.2
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	25	0.2
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	28	0.2
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	26	0.2
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	26	0.2
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	22	0.2
(2,57)	1:10:1:LEU:HD11	1:18:1:CYS:H	36	0.2
(2,57)	1:10:1:LEU:HD12	1:18:1:CYS:H	36	0.2
(2,57)	1:10:1:LEU:HD13	1:18:1:CYS:H	36	0.2
(2,57)	1:10:1:LEU:HD21	1:18:1:CYS:H	36	0.2
(2,57)	1:10:1:LEU:HD22	1:18:1:CYS:H	36	0.2
(2,57)	1:10:1:LEU:HD23	1:18:1:CYS:H	36	0.2
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	4	0.2
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	4	0.2
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	4	0.2
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	4	0.2
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	4	0.2
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	4	0.2
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	4	0.2
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	4	0.2
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	4	0.2
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	4	0.2
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	4	0.2
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	4	0.2
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	4	0.2
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	4	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	4	0.2
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	4	0.2
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	4	0.2
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	4	0.2
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	4	0.2
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	4	0.2
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	4	0.2
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	4	0.2
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	4	0.2
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	4	0.2
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	4	0.2
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	4	0.2
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	4	0.2
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	4	0.2
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	4	0.2
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	4	0.2
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	4	0.2
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	4	0.2
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	4	0.2
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	4	0.2
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	4	0.2
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	4	0.2
(1,777)	1:61:1:ARG:HH21	1:81:1:TRP:HZ2	11	0.2
(1,774)	1:61:1:ARG:HH21	1:81:1:TRP:HD1	25	0.2
(2,579)	1:16:1:CYS:H	1:35:1:LYS:HG3	25	0.19
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	4	0.19
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	32	0.19
(2,527)	1:72:1:CYS:HA	1:76:1:SER:H	32	0.19
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	19	0.19
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	34	0.19
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	35	0.19
(2,513)	1:70:1:ASP:HA	1:81:1:TRP:HD1	22	0.19
(2,513)	1:70:1:ASP:HA	1:81:1:TRP:HD1	34	0.19
(2,483)	1:66:1:ASP:HB2	1:67:1:TRP:HE3	12	0.19
(2,483)	1:66:1:ASP:HB3	1:67:1:TRP:HE3	12	0.19
(2,483)	1:66:1:ASP:HB2	1:67:1:TRP:HE3	23	0.19
(2,483)	1:66:1:ASP:HB3	1:67:1:TRP:HE3	23	0.19
(2,483)	1:66:1:ASP:HB2	1:67:1:TRP:HE3	42	0.19
(2,483)	1:66:1:ASP:HB3	1:67:1:TRP:HE3	42	0.19
(2,447)	1:63:1:ALA:HB1	1:67:1:TRP:HE3	1	0.19
(2,447)	1:63:1:ALA:HB2	1:67:1:TRP:HE3	1	0.19
(2,447)	1:63:1:ALA:HB3	1:67:1:TRP:HE3	1	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB2	2	0.19
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB3	2	0.19
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB2	2	0.19
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB3	2	0.19
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB2	2	0.19
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB3	2	0.19
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB2	7	0.19
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB3	7	0.19
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB2	7	0.19
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB3	7	0.19
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB2	7	0.19
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB3	7	0.19
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	11	0.19
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	11	0.19
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	11	0.19
(2,381)	1:61:1:ARG:HH11	1:62:1:ILE:H	31	0.19
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	4	0.19
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	4	0.19
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	4	0.19
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	2	0.19
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	14	0.19
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	33	0.19
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	33	0.19
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	26	0.19
(2,191)	1:41:1:GLN:HA	1:53:1:PHE:HB2	22	0.19
(2,191)	1:41:1:GLN:HA	1:53:1:PHE:HB3	22	0.19
(2,191)	1:41:1:GLN:HA	1:53:1:PHE:HB2	42	0.19
(2,191)	1:41:1:GLN:HA	1:53:1:PHE:HB3	42	0.19
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	2	0.19
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	2	0.19
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	2	0.19
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	2	0.19
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	2	0.19
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	2	0.19
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	40	0.19
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	40	0.19
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	40	0.19
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	40	0.19
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	40	0.19
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	40	0.19
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	40	0.19
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	40	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	40	0.19
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	40	0.19
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	40	0.19
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	40	0.19
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	40	0.19
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	40	0.19
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	40	0.19
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	40	0.19
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	40	0.19
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	40	0.19
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	40	0.19
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	40	0.19
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	40	0.19
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	40	0.19
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	40	0.19
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	40	0.19
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	40	0.19
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	40	0.19
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	40	0.19
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	40	0.19
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	40	0.19
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	40	0.19
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	40	0.19
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	40	0.19
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	40	0.19
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	40	0.19
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	40	0.19
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	40	0.19
(1,988)	1:25:1:GLN:H	1:26:1:ASP:HA	31	0.19
(1,777)	1:61:1:ARG:HH21	1:81:1:TRP:HZ2	24	0.19
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	6	0.19
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	14	0.19
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	17	0.19
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	31	0.19
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	42	0.19
(2,578)	1:8:1:LYS:HA	1:9:1:ILE:HD13	8	0.18
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	17	0.18
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	19	0.18
(2,527)	1:72:1:CYS:HA	1:76:1:SER:H	23	0.18
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	8	0.18
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	8	0.18
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	8	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	8	0.18
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	25	0.18
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	25	0.18
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	25	0.18
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	25	0.18
(2,513)	1:70:1:ASP:HA	1:81:1:TRP:HD1	41	0.18
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	38	0.18
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	38	0.18
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	38	0.18
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	38	0.18
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	38	0.18
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	38	0.18
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB2	32	0.18
(2,440)	1:62:1:ILE:HD11	1:81:1:TRP:HB3	32	0.18
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB2	32	0.18
(2,440)	1:62:1:ILE:HD12	1:81:1:TRP:HB3	32	0.18
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB2	32	0.18
(2,440)	1:62:1:ILE:HD13	1:81:1:TRP:HB3	32	0.18
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	9	0.18
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	21	0.18
(2,411)	1:61:1:ARG:HH21	1:81:1:TRP:HH2	18	0.18
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	3	0.18
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	7	0.18
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	33	0.18
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	41	0.18
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	24	0.18
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG21	24	0.18
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG22	24	0.18
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG23	24	0.18
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	10	0.18
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	20	0.18
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	25	0.18
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	38	0.18
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	40	0.18
(1,766)	1:61:1:ARG:HH11	1:79:1:CYS:HB2	16	0.18
(2,582)	1:30:1:ASN:HB3	1:35:1:LYS:HB3	3	0.17
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	16	0.17
(2,527)	1:72:1:CYS:HA	1:76:1:SER:H	42	0.17
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	41	0.17
(2,513)	1:70:1:ASP:HA	1:81:1:TRP:HD1	7	0.17
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD21	27	0.17
(2,496)	1:68:1:ASN:H	1:82:1:ASN:HD22	27	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,491)	1:67:1:TRP:HD1	1:83:1:HIS:HB2	29	0.17
(2,491)	1:67:1:TRP:HD1	1:83:1:HIS:HB3	29	0.17
(2,441)	1:62:1:ILE:HD11	1:81:1:TRP:HE3	42	0.17
(2,441)	1:62:1:ILE:HD12	1:81:1:TRP:HE3	42	0.17
(2,441)	1:62:1:ILE:HD13	1:81:1:TRP:HE3	42	0.17
(2,411)	1:61:1:ARG:HH21	1:81:1:TRP:HH2	36	0.17
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	10	0.17
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	10	0.17
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	40	0.17
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	40	0.17
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	42	0.17
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	42	0.17
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	32	0.17
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	32	0.17
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	43	0.17
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	43	0.17
(2,220)	1:44:1:TYR:HE1	1:46:1:GLU:H	35	0.17
(2,220)	1:44:1:TYR:HE2	1:46:1:GLU:H	35	0.17
(2,191)	1:41:1:GLN:HA	1:53:1:PHE:HB2	30	0.17
(2,191)	1:41:1:GLN:HA	1:53:1:PHE:HB3	30	0.17
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	11	0.17
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	11	0.17
(2,42)	1:9:1:ILE:H	1:17:1:ASP:H	16	0.17
(1,777)	1:61:1:ARG:HH21	1:81:1:TRP:HZ2	30	0.17
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	35	0.17
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	9	0.17
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	9	0.17
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	13	0.16
(2,581)	1:25:1:GLN:HE21	1:26:1:ASP:HA	11	0.16
(2,527)	1:72:1:CYS:HA	1:76:1:SER:H	3	0.16
(2,527)	1:72:1:CYS:HA	1:76:1:SER:H	6	0.16
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	5	0.16
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	5	0.16
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	5	0.16
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	5	0.16
(2,513)	1:70:1:ASP:HA	1:81:1:TRP:HD1	25	0.16
(2,483)	1:66:1:ASP:HB2	1:67:1:TRP:HE3	31	0.16
(2,483)	1:66:1:ASP:HB3	1:67:1:TRP:HE3	31	0.16
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	32	0.16
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	32	0.16
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	32	0.16
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	32	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	32	0.16
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	32	0.16
(2,441)	1:62:1:ILE:HD11	1:81:1:TRP:HE3	6	0.16
(2,441)	1:62:1:ILE:HD12	1:81:1:TRP:HE3	6	0.16
(2,441)	1:62:1:ILE:HD13	1:81:1:TRP:HE3	6	0.16
(2,441)	1:62:1:ILE:HD11	1:81:1:TRP:HE3	15	0.16
(2,441)	1:62:1:ILE:HD12	1:81:1:TRP:HE3	15	0.16
(2,441)	1:62:1:ILE:HD13	1:81:1:TRP:HE3	15	0.16
(2,441)	1:62:1:ILE:HD11	1:81:1:TRP:HE3	20	0.16
(2,441)	1:62:1:ILE:HD12	1:81:1:TRP:HE3	20	0.16
(2,441)	1:62:1:ILE:HD13	1:81:1:TRP:HE3	20	0.16
(2,411)	1:61:1:ARG:HH21	1:81:1:TRP:HH2	39	0.16
(2,402)	1:61:1:ARG:HG2	1:81:1:TRP:HH2	31	0.16
(2,402)	1:61:1:ARG:HG3	1:81:1:TRP:HH2	31	0.16
(2,402)	1:61:1:ARG:HG2	1:81:1:TRP:HH2	38	0.16
(2,402)	1:61:1:ARG:HG3	1:81:1:TRP:HH2	38	0.16
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	31	0.16
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	31	0.16
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	31	0.16
(2,115)	1:25:1:GLN:H	1:31:1:ALA:HB1	32	0.16
(2,115)	1:25:1:GLN:H	1:31:1:ALA:HB2	32	0.16
(2,115)	1:25:1:GLN:H	1:31:1:ALA:HB3	32	0.16
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	1	0.16
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	1	0.16
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	1	0.16
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	1	0.16
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	1	0.16
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	1	0.16
(2,46)	1:10:1:LEU:HD11	1:11:1:GLU:HG2	38	0.16
(2,46)	1:10:1:LEU:HD11	1:11:1:GLU:HG3	38	0.16
(2,46)	1:10:1:LEU:HD12	1:11:1:GLU:HG2	38	0.16
(2,46)	1:10:1:LEU:HD12	1:11:1:GLU:HG3	38	0.16
(2,46)	1:10:1:LEU:HD13	1:11:1:GLU:HG2	38	0.16
(2,46)	1:10:1:LEU:HD13	1:11:1:GLU:HG3	38	0.16
(2,46)	1:10:1:LEU:HD21	1:11:1:GLU:HG2	38	0.16
(2,46)	1:10:1:LEU:HD21	1:11:1:GLU:HG3	38	0.16
(2,46)	1:10:1:LEU:HD22	1:11:1:GLU:HG2	38	0.16
(2,46)	1:10:1:LEU:HD22	1:11:1:GLU:HG3	38	0.16
(2,46)	1:10:1:LEU:HD23	1:11:1:GLU:HG2	38	0.16
(2,46)	1:10:1:LEU:HD23	1:11:1:GLU:HG3	38	0.16
(2,42)	1:9:1:ILE:H	1:17:1:ASP:H	39	0.16
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	5	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,587)	1:56:1:ALA:HB2	1:55:1:LYS:HZ1	3	0.15
(2,581)	1:25:1:GLN:HE21	1:23:1:ASN:HA	43	0.15
(2,567)	1:81:1:TRP:HE3	1:82:1:ASN:H	11	0.15
(2,567)	1:81:1:TRP:HE3	1:82:1:ASN:H	27	0.15
(2,548)	1:75:1:LYS:H	1:77:1:SER:H	15	0.15
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	13	0.15
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	13	0.15
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	13	0.15
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	13	0.15
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	16	0.15
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	16	0.15
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	16	0.15
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	16	0.15
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	7	0.15
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	12	0.15
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	12	0.15
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	12	0.15
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	12	0.15
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	12	0.15
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	12	0.15
(2,447)	1:63:1:ALA:HB1	1:67:1:TRP:HE3	40	0.15
(2,447)	1:63:1:ALA:HB2	1:67:1:TRP:HE3	40	0.15
(2,447)	1:63:1:ALA:HB3	1:67:1:TRP:HE3	40	0.15
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	22	0.15
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	22	0.15
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	12	0.15
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	22	0.15
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	23	0.15
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	34	0.15
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	2	0.15
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	2	0.15
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	8	0.15
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	8	0.15
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	20	0.15
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	20	0.15
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	37	0.15
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	37	0.15
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	2	0.15
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE1	3	0.15
(2,88)	1:17:1:ASP:H	1:44:1:TYR:HE2	3	0.15
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	32	0.15
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	32	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	32	0.15
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	32	0.15
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	32	0.15
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	32	0.15
(2,46)	1:10:1:LEU:HD11	1:11:1:GLU:HG2	26	0.15
(2,46)	1:10:1:LEU:HD11	1:11:1:GLU:HG3	26	0.15
(2,46)	1:10:1:LEU:HD12	1:11:1:GLU:HG2	26	0.15
(2,46)	1:10:1:LEU:HD12	1:11:1:GLU:HG3	26	0.15
(2,46)	1:10:1:LEU:HD13	1:11:1:GLU:HG2	26	0.15
(2,46)	1:10:1:LEU:HD13	1:11:1:GLU:HG3	26	0.15
(2,46)	1:10:1:LEU:HD21	1:11:1:GLU:HG2	26	0.15
(2,46)	1:10:1:LEU:HD21	1:11:1:GLU:HG3	26	0.15
(2,46)	1:10:1:LEU:HD22	1:11:1:GLU:HG2	26	0.15
(2,46)	1:10:1:LEU:HD22	1:11:1:GLU:HG3	26	0.15
(2,46)	1:10:1:LEU:HD23	1:11:1:GLU:HG2	26	0.15
(2,46)	1:10:1:LEU:HD23	1:11:1:GLU:HG3	26	0.15
(2,46)	1:10:1:LEU:HD11	1:11:1:GLU:HG2	37	0.15
(2,46)	1:10:1:LEU:HD11	1:11:1:GLU:HG3	37	0.15
(2,46)	1:10:1:LEU:HD12	1:11:1:GLU:HG2	37	0.15
(2,46)	1:10:1:LEU:HD12	1:11:1:GLU:HG3	37	0.15
(2,46)	1:10:1:LEU:HD13	1:11:1:GLU:HG2	37	0.15
(2,46)	1:10:1:LEU:HD13	1:11:1:GLU:HG3	37	0.15
(2,46)	1:10:1:LEU:HD21	1:11:1:GLU:HG2	37	0.15
(2,46)	1:10:1:LEU:HD21	1:11:1:GLU:HG3	37	0.15
(2,46)	1:10:1:LEU:HD22	1:11:1:GLU:HG2	37	0.15
(2,46)	1:10:1:LEU:HD22	1:11:1:GLU:HG3	37	0.15
(2,46)	1:10:1:LEU:HD23	1:11:1:GLU:HG2	37	0.15
(2,46)	1:10:1:LEU:HD23	1:11:1:GLU:HG3	37	0.15
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	11	0.15
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	11	0.15
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	11	0.15
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	11	0.15
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	11	0.15
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	11	0.15
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	11	0.15
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	11	0.15
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	11	0.15
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	11	0.15
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	11	0.15
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	11	0.15
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	11	0.15
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	11	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	11	0.15
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	11	0.15
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	11	0.15
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	11	0.15
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	11	0.15
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	11	0.15
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	11	0.15
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	11	0.15
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	11	0.15
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	11	0.15
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	11	0.15
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	11	0.15
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	11	0.15
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	11	0.15
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	11	0.15
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	11	0.15
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	11	0.15
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	11	0.15
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	11	0.15
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	11	0.15
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	11	0.15
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	11	0.15
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD11	16	0.15
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD12	16	0.15
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD13	16	0.15
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD21	16	0.15
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD22	16	0.15
(2,12)	1:4:1:VAL:HG11	1:10:1:LEU:HD23	16	0.15
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD11	16	0.15
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD12	16	0.15
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD13	16	0.15
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD21	16	0.15
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD22	16	0.15
(2,12)	1:4:1:VAL:HG12	1:10:1:LEU:HD23	16	0.15
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD11	16	0.15
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD12	16	0.15
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD13	16	0.15
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD21	16	0.15
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD22	16	0.15
(2,12)	1:4:1:VAL:HG13	1:10:1:LEU:HD23	16	0.15
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD11	16	0.15
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD12	16	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD13	16	0.15
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD21	16	0.15
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD22	16	0.15
(2,12)	1:4:1:VAL:HG21	1:10:1:LEU:HD23	16	0.15
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD11	16	0.15
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD12	16	0.15
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD13	16	0.15
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD21	16	0.15
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD22	16	0.15
(2,12)	1:4:1:VAL:HG22	1:10:1:LEU:HD23	16	0.15
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD11	16	0.15
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD12	16	0.15
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD13	16	0.15
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD21	16	0.15
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD22	16	0.15
(2,12)	1:4:1:VAL:HG23	1:10:1:LEU:HD23	16	0.15
(1,988)	1:25:1:GLN:H	1:26:1:ASP:HA	27	0.15
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	16	0.15
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	38	0.15
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	3	0.15
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	3	0.15
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	27	0.15
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	27	0.15
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	36	0.15
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	36	0.15
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	39	0.15
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	39	0.15
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	41	0.15
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	41	0.15
(2,595)	1:67:1:TRP:HE3	1:66:1:ASP:HA	5	0.14
(2,567)	1:81:1:TRP:HE3	1:82:1:ASN:H	24	0.14
(2,567)	1:81:1:TRP:HE3	1:82:1:ASN:H	33	0.14
(2,566)	1:81:1:TRP:HE1	1:82:1:ASN:H	13	0.14
(2,527)	1:72:1:CYS:HA	1:76:1:SER:H	2	0.14
(2,527)	1:72:1:CYS:HA	1:76:1:SER:H	8	0.14
(2,527)	1:72:1:CYS:HA	1:76:1:SER:H	10	0.14
(2,527)	1:72:1:CYS:HA	1:76:1:SER:H	35	0.14
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	3	0.14
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	3	0.14
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	3	0.14
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	3	0.14
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	23	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	23	0.14
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	23	0.14
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	23	0.14
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	26	0.14
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	26	0.14
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	26	0.14
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	26	0.14
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	38	0.14
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	38	0.14
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	38	0.14
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	38	0.14
(2,507)	1:70:1:ASP:HB2	1:72:1:CYS:H	21	0.14
(2,507)	1:70:1:ASP:HB3	1:72:1:CYS:H	21	0.14
(2,466)	1:64:1:ARG:HG2	1:67:1:TRP:HE1	29	0.14
(2,466)	1:64:1:ARG:HG3	1:67:1:TRP:HE1	29	0.14
(2,447)	1:63:1:ALA:HB1	1:67:1:TRP:HE3	38	0.14
(2,447)	1:63:1:ALA:HB2	1:67:1:TRP:HE3	38	0.14
(2,447)	1:63:1:ALA:HB3	1:67:1:TRP:HE3	38	0.14
(2,422)	1:62:1:ILE:HG21	1:64:1:ARG:HD2	1	0.14
(2,422)	1:62:1:ILE:HG21	1:64:1:ARG:HD3	1	0.14
(2,422)	1:62:1:ILE:HG22	1:64:1:ARG:HD2	1	0.14
(2,422)	1:62:1:ILE:HG22	1:64:1:ARG:HD3	1	0.14
(2,422)	1:62:1:ILE:HG23	1:64:1:ARG:HD2	1	0.14
(2,422)	1:62:1:ILE:HG23	1:64:1:ARG:HD3	1	0.14
(2,414)	1:61:1:ARG:HH21	1:82:1:ASN:H	5	0.14
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	30	0.14
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	12	0.14
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	12	0.14
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	20	0.14
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	20	0.14
(2,351)	1:59:1:VAL:H	1:61:1:ARG:H	35	0.14
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	5	0.14
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	5	0.14
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	5	0.14
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	11	0.14
(2,221)	1:44:1:TYR:H	1:53:1:PHE:HD1	33	0.14
(2,221)	1:44:1:TYR:H	1:53:1:PHE:HD2	33	0.14
(2,48)	1:10:1:LEU:HD11	1:12:1:GLN:H	21	0.14
(2,48)	1:10:1:LEU:HD12	1:12:1:GLN:H	21	0.14
(2,48)	1:10:1:LEU:HD13	1:12:1:GLN:H	21	0.14
(2,48)	1:10:1:LEU:HD21	1:12:1:GLN:H	21	0.14
(2,48)	1:10:1:LEU:HD22	1:12:1:GLN:H	21	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,48)	1:10:1:LEU:HD23	1:12:1:GLN:H	21	0.14
(2,46)	1:10:1:LEU:HD11	1:11:1:GLU:HG2	42	0.14
(2,46)	1:10:1:LEU:HD11	1:11:1:GLU:HG3	42	0.14
(2,46)	1:10:1:LEU:HD12	1:11:1:GLU:HG2	42	0.14
(2,46)	1:10:1:LEU:HD12	1:11:1:GLU:HG3	42	0.14
(2,46)	1:10:1:LEU:HD13	1:11:1:GLU:HG2	42	0.14
(2,46)	1:10:1:LEU:HD13	1:11:1:GLU:HG3	42	0.14
(2,46)	1:10:1:LEU:HD21	1:11:1:GLU:HG2	42	0.14
(2,46)	1:10:1:LEU:HD21	1:11:1:GLU:HG3	42	0.14
(2,46)	1:10:1:LEU:HD22	1:11:1:GLU:HG2	42	0.14
(2,46)	1:10:1:LEU:HD22	1:11:1:GLU:HG3	42	0.14
(2,46)	1:10:1:LEU:HD23	1:11:1:GLU:HG2	42	0.14
(2,46)	1:10:1:LEU:HD23	1:11:1:GLU:HG3	42	0.14
(1,591)	1:53:1:PHE:HE1	1:54:1:LYS:H	21	0.14
(1,591)	1:53:1:PHE:HE2	1:54:1:LYS:H	21	0.14
(1,591)	1:53:1:PHE:HE1	1:54:1:LYS:H	24	0.14
(1,591)	1:53:1:PHE:HE2	1:54:1:LYS:H	24	0.14
(1,591)	1:53:1:PHE:HE1	1:54:1:LYS:H	30	0.14
(1,591)	1:53:1:PHE:HE2	1:54:1:LYS:H	30	0.14
(1,591)	1:53:1:PHE:HE1	1:54:1:LYS:H	42	0.14
(1,591)	1:53:1:PHE:HE2	1:54:1:LYS:H	42	0.14
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE1	16	0.14
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE2	16	0.14
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE1	16	0.14
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE2	16	0.14
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	4	0.14
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	5	0.14
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	13	0.14
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	15	0.14
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	36	0.14
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	41	0.14
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	42	0.14
(1,288)	1:27:1:ARG:H	1:28:1:CYS:H	18	0.14
(1,111)	1:10:1:LEU:HD11	1:11:1:GLU:HB2	41	0.14
(1,111)	1:10:1:LEU:HD11	1:11:1:GLU:HB3	41	0.14
(1,111)	1:10:1:LEU:HD12	1:11:1:GLU:HB2	41	0.14
(1,111)	1:10:1:LEU:HD12	1:11:1:GLU:HB3	41	0.14
(1,111)	1:10:1:LEU:HD13	1:11:1:GLU:HB2	41	0.14
(1,111)	1:10:1:LEU:HD13	1:11:1:GLU:HB3	41	0.14
(1,111)	1:10:1:LEU:HD21	1:11:1:GLU:HB2	41	0.14
(1,111)	1:10:1:LEU:HD21	1:11:1:GLU:HB3	41	0.14
(1,111)	1:10:1:LEU:HD22	1:11:1:GLU:HB2	41	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,111)	1:10:1:LEU:HD22	1:11:1:GLU:HB3	41	0.14
(1,111)	1:10:1:LEU:HD23	1:11:1:GLU:HB2	41	0.14
(1,111)	1:10:1:LEU:HD23	1:11:1:GLU:HB3	41	0.14
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	6	0.14
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	6	0.14
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	8	0.14
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	8	0.14
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	21	0.14
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	21	0.14
(2,567)	1:81:1:TRP:HE3	1:82:1:ASN:H	15	0.13
(2,567)	1:81:1:TRP:HE3	1:82:1:ASN:H	30	0.13
(2,567)	1:81:1:TRP:HE3	1:82:1:ASN:H	43	0.13
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	28	0.13
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	28	0.13
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	28	0.13
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	28	0.13
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	41	0.13
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	41	0.13
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	41	0.13
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	41	0.13
(2,513)	1:70:1:ASP:HA	1:81:1:TRP:HD1	12	0.13
(2,513)	1:70:1:ASP:HA	1:81:1:TRP:HD1	19	0.13
(2,507)	1:70:1:ASP:HB2	1:72:1:CYS:H	9	0.13
(2,507)	1:70:1:ASP:HB3	1:72:1:CYS:H	9	0.13
(2,439)	1:62:1:ILE:HD11	1:81:1:TRP:HA	16	0.13
(2,439)	1:62:1:ILE:HD12	1:81:1:TRP:HA	16	0.13
(2,439)	1:62:1:ILE:HD13	1:81:1:TRP:HA	16	0.13
(2,439)	1:62:1:ILE:HD11	1:81:1:TRP:HA	23	0.13
(2,439)	1:62:1:ILE:HD12	1:81:1:TRP:HA	23	0.13
(2,439)	1:62:1:ILE:HD13	1:81:1:TRP:HA	23	0.13
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	24	0.13
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	27	0.13
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB1	4	0.13
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB2	4	0.13
(2,383)	1:61:1:ARG:HE	1:63:1:ALA:HB3	4	0.13
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	7	0.13
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	7	0.13
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	10	0.13
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	10	0.13
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	17	0.13
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	17	0.13
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	1	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	1	0.13
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	1	0.13
(2,329)	1:56:1:ALA:HB1	1:76:1:SER:H	35	0.13
(2,329)	1:56:1:ALA:HB2	1:76:1:SER:H	35	0.13
(2,329)	1:56:1:ALA:HB3	1:76:1:SER:H	35	0.13
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	32	0.13
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	6	0.13
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	6	0.13
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	25	0.13
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	25	0.13
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	14	0.13
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	42	0.13
(2,221)	1:44:1:TYR:H	1:53:1:PHE:HD1	20	0.13
(2,221)	1:44:1:TYR:H	1:53:1:PHE:HD2	20	0.13
(2,191)	1:41:1:GLN:HA	1:53:1:PHE:HB2	12	0.13
(2,191)	1:41:1:GLN:HA	1:53:1:PHE:HB3	12	0.13
(2,191)	1:41:1:GLN:HA	1:53:1:PHE:HB2	16	0.13
(2,191)	1:41:1:GLN:HA	1:53:1:PHE:HB3	16	0.13
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG21	36	0.13
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG22	36	0.13
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG23	36	0.13
(2,75)	1:16:1:CYS:HB2	1:29:1:CYS:H	19	0.13
(2,75)	1:16:1:CYS:HB3	1:29:1:CYS:H	19	0.13
(2,71)	1:15:1:ASP:H	1:34:1:CYS:HA	34	0.13
(2,42)	1:9:1:ILE:H	1:17:1:ASP:H	14	0.13
(2,25)	1:8:1:LYS:H	1:10:1:LEU:HD11	32	0.13
(2,25)	1:8:1:LYS:H	1:10:1:LEU:HD12	32	0.13
(2,25)	1:8:1:LYS:H	1:10:1:LEU:HD13	32	0.13
(2,25)	1:8:1:LYS:H	1:10:1:LEU:HD21	32	0.13
(2,25)	1:8:1:LYS:H	1:10:1:LEU:HD22	32	0.13
(2,25)	1:8:1:LYS:H	1:10:1:LEU:HD23	32	0.13
(2,25)	1:8:1:LYS:H	1:10:1:LEU:HD11	40	0.13
(2,25)	1:8:1:LYS:H	1:10:1:LEU:HD12	40	0.13
(2,25)	1:8:1:LYS:H	1:10:1:LEU:HD13	40	0.13
(2,25)	1:8:1:LYS:H	1:10:1:LEU:HD21	40	0.13
(2,25)	1:8:1:LYS:H	1:10:1:LEU:HD22	40	0.13
(2,25)	1:8:1:LYS:H	1:10:1:LEU:HD23	40	0.13
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	2	0.13
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	13	0.13
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	32	0.13
(1,591)	1:53:1:PHE:HE1	1:54:1:LYS:H	16	0.13
(1,591)	1:53:1:PHE:HE2	1:54:1:LYS:H	16	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,591)	1:53:1:PHE:HE1	1:54:1:LYS:H	22	0.13
(1,591)	1:53:1:PHE:HE2	1:54:1:LYS:H	22	0.13
(1,591)	1:53:1:PHE:HE1	1:54:1:LYS:H	31	0.13
(1,591)	1:53:1:PHE:HE2	1:54:1:LYS:H	31	0.13
(1,591)	1:53:1:PHE:HE1	1:54:1:LYS:H	33	0.13
(1,591)	1:53:1:PHE:HE2	1:54:1:LYS:H	33	0.13
(1,591)	1:53:1:PHE:HE1	1:54:1:LYS:H	36	0.13
(1,591)	1:53:1:PHE:HE2	1:54:1:LYS:H	36	0.13
(1,591)	1:53:1:PHE:HE1	1:54:1:LYS:H	39	0.13
(1,591)	1:53:1:PHE:HE2	1:54:1:LYS:H	39	0.13
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE1	13	0.13
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE2	13	0.13
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE1	13	0.13
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE2	13	0.13
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE1	38	0.13
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE2	38	0.13
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE1	38	0.13
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE2	38	0.13
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	1	0.13
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	6	0.13
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	19	0.13
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	28	0.13
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	30	0.13
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	31	0.13
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	39	0.13
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	43	0.13
(1,279)	1:26:1:ASP:H	1:27:1:ARG:HB2	33	0.13
(1,279)	1:26:1:ASP:H	1:27:1:ARG:HB3	33	0.13
(1,111)	1:10:1:LEU:HD11	1:11:1:GLU:HB2	42	0.13
(1,111)	1:10:1:LEU:HD11	1:11:1:GLU:HB3	42	0.13
(1,111)	1:10:1:LEU:HD12	1:11:1:GLU:HB2	42	0.13
(1,111)	1:10:1:LEU:HD12	1:11:1:GLU:HB3	42	0.13
(1,111)	1:10:1:LEU:HD13	1:11:1:GLU:HB2	42	0.13
(1,111)	1:10:1:LEU:HD13	1:11:1:GLU:HB3	42	0.13
(1,111)	1:10:1:LEU:HD21	1:11:1:GLU:HB2	42	0.13
(1,111)	1:10:1:LEU:HD21	1:11:1:GLU:HB3	42	0.13
(1,111)	1:10:1:LEU:HD22	1:11:1:GLU:HB2	42	0.13
(1,111)	1:10:1:LEU:HD22	1:11:1:GLU:HB3	42	0.13
(1,111)	1:10:1:LEU:HD23	1:11:1:GLU:HB2	42	0.13
(1,111)	1:10:1:LEU:HD23	1:11:1:GLU:HB3	42	0.13
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	14	0.13
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	14	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	15	0.13
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	15	0.13
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	34	0.13
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	34	0.13
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	42	0.13
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	42	0.13
(2,595)	1:67:1:TRP:HE3	1:66:1:ASP:HA	15	0.12
(2,594)	1:67:1:TRP:HZ2	1:66:1:ASP:HA	39	0.12
(2,591)	1:59:1:VAL:H	1:57:1:GLY:H	40	0.12
(2,527)	1:72:1:CYS:HA	1:76:1:SER:H	20	0.12
(2,527)	1:72:1:CYS:HA	1:76:1:SER:H	30	0.12
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	10	0.12
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	10	0.12
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	10	0.12
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	10	0.12
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	17	0.12
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	17	0.12
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	17	0.12
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	17	0.12
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	22	0.12
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	22	0.12
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	22	0.12
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	22	0.12
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	29	0.12
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	29	0.12
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	29	0.12
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	29	0.12
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	37	0.12
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	37	0.12
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	37	0.12
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	37	0.12
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	12	0.12
(2,513)	1:70:1:ASP:HA	1:81:1:TRP:HD1	38	0.12
(2,495)	1:68:1:ASN:HB2	1:71:1:TYR:HE1	30	0.12
(2,495)	1:68:1:ASN:HB2	1:71:1:TYR:HE2	30	0.12
(2,495)	1:68:1:ASN:HB3	1:71:1:TYR:HE1	30	0.12
(2,495)	1:68:1:ASN:HB3	1:71:1:TYR:HE2	30	0.12
(2,491)	1:67:1:TRP:HD1	1:83:1:HIS:HB2	25	0.12
(2,491)	1:67:1:TRP:HD1	1:83:1:HIS:HB3	25	0.12
(2,466)	1:64:1:ARG:HG2	1:67:1:TRP:HE1	30	0.12
(2,466)	1:64:1:ARG:HG3	1:67:1:TRP:HE1	30	0.12
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	33	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	33	0.12
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	33	0.12
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	33	0.12
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	33	0.12
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	33	0.12
(2,439)	1:62:1:ILE:HD11	1:81:1:TRP:HA	2	0.12
(2,439)	1:62:1:ILE:HD12	1:81:1:TRP:HA	2	0.12
(2,439)	1:62:1:ILE:HD13	1:81:1:TRP:HA	2	0.12
(2,439)	1:62:1:ILE:HD11	1:81:1:TRP:HA	6	0.12
(2,439)	1:62:1:ILE:HD12	1:81:1:TRP:HA	6	0.12
(2,439)	1:62:1:ILE:HD13	1:81:1:TRP:HA	6	0.12
(2,439)	1:62:1:ILE:HD11	1:81:1:TRP:HA	14	0.12
(2,439)	1:62:1:ILE:HD12	1:81:1:TRP:HA	14	0.12
(2,439)	1:62:1:ILE:HD13	1:81:1:TRP:HA	14	0.12
(2,439)	1:62:1:ILE:HD11	1:81:1:TRP:HA	17	0.12
(2,439)	1:62:1:ILE:HD12	1:81:1:TRP:HA	17	0.12
(2,439)	1:62:1:ILE:HD13	1:81:1:TRP:HA	17	0.12
(2,439)	1:62:1:ILE:HD11	1:81:1:TRP:HA	20	0.12
(2,439)	1:62:1:ILE:HD12	1:81:1:TRP:HA	20	0.12
(2,439)	1:62:1:ILE:HD13	1:81:1:TRP:HA	20	0.12
(2,439)	1:62:1:ILE:HD11	1:81:1:TRP:HA	31	0.12
(2,439)	1:62:1:ILE:HD12	1:81:1:TRP:HA	31	0.12
(2,439)	1:62:1:ILE:HD13	1:81:1:TRP:HA	31	0.12
(2,439)	1:62:1:ILE:HD11	1:81:1:TRP:HA	42	0.12
(2,439)	1:62:1:ILE:HD12	1:81:1:TRP:HA	42	0.12
(2,439)	1:62:1:ILE:HD13	1:81:1:TRP:HA	42	0.12
(2,438)	1:62:1:ILE:HG21	1:81:1:TRP:HE3	16	0.12
(2,438)	1:62:1:ILE:HG22	1:81:1:TRP:HE3	16	0.12
(2,438)	1:62:1:ILE:HG23	1:81:1:TRP:HE3	16	0.12
(2,402)	1:61:1:ARG:HG2	1:81:1:TRP:HH2	40	0.12
(2,402)	1:61:1:ARG:HG3	1:81:1:TRP:HH2	40	0.12
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	6	0.12
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	6	0.12
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	16	0.12
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	16	0.12
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	29	0.12
(2,299)	1:53:1:PHE:H	1:76:1:SER:H	36	0.12
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	17	0.12
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	17	0.12
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	28	0.12
(2,191)	1:41:1:GLN:HA	1:53:1:PHE:HB2	4	0.12
(2,191)	1:41:1:GLN:HA	1:53:1:PHE:HB3	4	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	26	0.12
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	26	0.12
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	26	0.12
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	26	0.12
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	26	0.12
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	26	0.12
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG21	26	0.12
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG22	26	0.12
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG23	26	0.12
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG21	38	0.12
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG22	38	0.12
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG23	38	0.12
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	12	0.12
(1,773)	1:61:1:ARG:HH21	1:81:1:TRP:HA	23	0.12
(1,698)	1:58:1:THR:HG21	1:71:1:TYR:HE1	30	0.12
(1,698)	1:58:1:THR:HG21	1:71:1:TYR:HE2	30	0.12
(1,698)	1:58:1:THR:HG22	1:71:1:TYR:HE1	30	0.12
(1,698)	1:58:1:THR:HG22	1:71:1:TYR:HE2	30	0.12
(1,698)	1:58:1:THR:HG23	1:71:1:TYR:HE1	30	0.12
(1,698)	1:58:1:THR:HG23	1:71:1:TYR:HE2	30	0.12
(1,591)	1:53:1:PHE:HE1	1:54:1:LYS:H	12	0.12
(1,591)	1:53:1:PHE:HE2	1:54:1:LYS:H	12	0.12
(1,591)	1:53:1:PHE:HE1	1:54:1:LYS:H	13	0.12
(1,591)	1:53:1:PHE:HE2	1:54:1:LYS:H	13	0.12
(1,591)	1:53:1:PHE:HE1	1:54:1:LYS:H	14	0.12
(1,591)	1:53:1:PHE:HE2	1:54:1:LYS:H	14	0.12
(1,591)	1:53:1:PHE:HE1	1:54:1:LYS:H	18	0.12
(1,591)	1:53:1:PHE:HE2	1:54:1:LYS:H	18	0.12
(1,591)	1:53:1:PHE:HE1	1:54:1:LYS:H	20	0.12
(1,591)	1:53:1:PHE:HE2	1:54:1:LYS:H	20	0.12
(1,591)	1:53:1:PHE:HE1	1:54:1:LYS:H	38	0.12
(1,591)	1:53:1:PHE:HE2	1:54:1:LYS:H	38	0.12
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE1	12	0.12
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE2	12	0.12
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE1	12	0.12
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE2	12	0.12
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE1	14	0.12
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE2	14	0.12
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE1	14	0.12
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE2	14	0.12
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE1	18	0.12
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE2	18	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE1	18	0.12
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE2	18	0.12
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE1	20	0.12
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE2	20	0.12
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE1	20	0.12
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE2	20	0.12
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE1	22	0.12
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE2	22	0.12
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE1	22	0.12
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE2	22	0.12
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE1	24	0.12
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE2	24	0.12
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE1	24	0.12
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE2	24	0.12
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE1	31	0.12
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE2	31	0.12
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE1	31	0.12
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE2	31	0.12
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE1	36	0.12
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE2	36	0.12
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE1	36	0.12
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE2	36	0.12
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE1	39	0.12
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE2	39	0.12
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE1	39	0.12
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE2	39	0.12
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE1	41	0.12
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE2	41	0.12
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE1	41	0.12
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE2	41	0.12
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE1	42	0.12
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE2	42	0.12
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE1	42	0.12
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE2	42	0.12
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	10	0.12
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	12	0.12
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	16	0.12
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	17	0.12
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	18	0.12
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	21	0.12
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	24	0.12
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	25	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	26	0.12
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	29	0.12
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	32	0.12
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	34	0.12
(1,288)	1:27:1:ARG:H	1:28:1:CYS:H	33	0.12
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	10	0.12
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	10	0.12
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	17	0.12
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	17	0.12
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	25	0.12
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	25	0.12
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	37	0.12
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	37	0.12
(1,43)	1:5:1:CYS:HA	1:11:1:GLU:H	20	0.12
(1,43)	1:5:1:CYS:HA	1:11:1:GLU:H	43	0.12
(3,19)	1:55:1:LYS:O	1:58:1:THR:H	40	0.11
(2,595)	1:67:1:TRP:HE3	1:66:1:ASP:HA	6	0.11
(2,595)	1:67:1:TRP:HE3	1:66:1:ASP:HA	11	0.11
(2,595)	1:67:1:TRP:HE3	1:66:1:ASP:HA	22	0.11
(2,595)	1:67:1:TRP:HE3	1:66:1:ASP:HA	25	0.11
(2,595)	1:67:1:TRP:HE3	1:66:1:ASP:HA	34	0.11
(2,567)	1:81:1:TRP:HE3	1:82:1:ASN:H	3	0.11
(2,567)	1:81:1:TRP:HE3	1:82:1:ASN:H	36	0.11
(2,567)	1:81:1:TRP:HE3	1:82:1:ASN:H	39	0.11
(2,560)	1:80:1:PRO:HG2	1:81:1:TRP:HD1	16	0.11
(2,560)	1:80:1:PRO:HG3	1:81:1:TRP:HD1	16	0.11
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	6	0.11
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	6	0.11
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	6	0.11
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	6	0.11
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	14	0.11
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	14	0.11
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	14	0.11
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	14	0.11
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	18	0.11
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	18	0.11
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	18	0.11
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	18	0.11
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	19	0.11
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	19	0.11
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	19	0.11
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	19	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	34	0.11
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	34	0.11
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	34	0.11
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	34	0.11
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	36	0.11
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	36	0.11
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	36	0.11
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	36	0.11
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD2	39	0.11
(2,522)	1:71:1:TYR:HD1	1:80:1:PRO:HD3	39	0.11
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD2	39	0.11
(2,522)	1:71:1:TYR:HD2	1:80:1:PRO:HD3	39	0.11
(2,513)	1:70:1:ASP:HA	1:81:1:TRP:HD1	31	0.11
(2,513)	1:70:1:ASP:HA	1:81:1:TRP:HD1	35	0.11
(2,491)	1:67:1:TRP:HD1	1:83:1:HIS:HB2	30	0.11
(2,491)	1:67:1:TRP:HD1	1:83:1:HIS:HB3	30	0.11
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	19	0.11
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	19	0.11
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	19	0.11
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	19	0.11
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	19	0.11
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	19	0.11
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB2	42	0.11
(2,453)	1:63:1:ALA:HB1	1:69:1:ASP:HB3	42	0.11
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB2	42	0.11
(2,453)	1:63:1:ALA:HB2	1:69:1:ASP:HB3	42	0.11
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB2	42	0.11
(2,453)	1:63:1:ALA:HB3	1:69:1:ASP:HB3	42	0.11
(2,441)	1:62:1:ILE:HD11	1:81:1:TRP:HE3	10	0.11
(2,441)	1:62:1:ILE:HD12	1:81:1:TRP:HE3	10	0.11
(2,441)	1:62:1:ILE:HD13	1:81:1:TRP:HE3	10	0.11
(2,439)	1:62:1:ILE:HD11	1:81:1:TRP:HA	10	0.11
(2,439)	1:62:1:ILE:HD12	1:81:1:TRP:HA	10	0.11
(2,439)	1:62:1:ILE:HD13	1:81:1:TRP:HA	10	0.11
(2,439)	1:62:1:ILE:HD11	1:81:1:TRP:HA	32	0.11
(2,439)	1:62:1:ILE:HD12	1:81:1:TRP:HA	32	0.11
(2,439)	1:62:1:ILE:HD13	1:81:1:TRP:HA	32	0.11
(2,438)	1:62:1:ILE:HG21	1:81:1:TRP:HE3	15	0.11
(2,438)	1:62:1:ILE:HG22	1:81:1:TRP:HE3	15	0.11
(2,438)	1:62:1:ILE:HG23	1:81:1:TRP:HE3	15	0.11
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	11	0.11
(2,402)	1:61:1:ARG:HG2	1:81:1:TRP:HH2	6	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,402)	1:61:1:ARG:HG3	1:81:1:TRP:HH2	6	0.11
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	14	0.11
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	14	0.11
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	34	0.11
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	34	0.11
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	41	0.11
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	41	0.11
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	11	0.11
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	11	0.11
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	39	0.11
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	39	0.11
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG2	41	0.11
(2,285)	1:52:1:ARG:H	1:54:1:LYS:HG3	41	0.11
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	18	0.11
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD2	18	0.11
(2,182)	1:41:1:GLN:HA	1:52:1:ARG:HD3	18	0.11
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG21	5	0.11
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG22	5	0.11
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG23	5	0.11
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG21	10	0.11
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG22	10	0.11
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG23	10	0.11
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG21	11	0.11
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG22	11	0.11
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG23	11	0.11
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG21	12	0.11
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG22	12	0.11
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG23	12	0.11
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG21	23	0.11
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG22	23	0.11
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG23	23	0.11
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG21	30	0.11
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG22	30	0.11
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG23	30	0.11
(2,71)	1:15:1:ASP:H	1:34:1:CYS:HA	8	0.11
(2,71)	1:15:1:ASP:H	1:34:1:CYS:HA	38	0.11
(1,698)	1:58:1:THR:HG21	1:71:1:TYR:HE1	43	0.11
(1,698)	1:58:1:THR:HG21	1:71:1:TYR:HE2	43	0.11
(1,698)	1:58:1:THR:HG22	1:71:1:TYR:HE1	43	0.11
(1,698)	1:58:1:THR:HG22	1:71:1:TYR:HE2	43	0.11
(1,698)	1:58:1:THR:HG23	1:71:1:TYR:HE1	43	0.11
(1,698)	1:58:1:THR:HG23	1:71:1:TYR:HE2	43	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,591)	1:53:1:PHE:HE1	1:54:1:LYS:H	41	0.11
(1,591)	1:53:1:PHE:HE2	1:54:1:LYS:H	41	0.11
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE1	21	0.11
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE2	21	0.11
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE1	21	0.11
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE2	21	0.11
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE1	30	0.11
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE2	30	0.11
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE1	30	0.11
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE2	30	0.11
(1,464)	1:43:1:ASN:H	1:44:1:TYR:H	4	0.11
(1,464)	1:43:1:ASN:H	1:44:1:TYR:H	43	0.11
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	2	0.11
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	3	0.11
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	7	0.11
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	8	0.11
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	9	0.11
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	11	0.11
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	14	0.11
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	22	0.11
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	27	0.11
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	37	0.11
(1,279)	1:26:1:ASP:H	1:27:1:ARG:HB2	18	0.11
(1,279)	1:26:1:ASP:H	1:27:1:ARG:HB3	18	0.11
(1,260)	1:24:1:CYS:H	1:25:1:GLN:H	33	0.11
(1,260)	1:24:1:CYS:H	1:25:1:GLN:H	40	0.11
(1,160)	1:15:1:ASP:H	1:17:1:ASP:HB2	19	0.11
(1,160)	1:15:1:ASP:H	1:17:1:ASP:HB3	19	0.11
(1,160)	1:15:1:ASP:H	1:17:1:ASP:HB2	37	0.11
(1,160)	1:15:1:ASP:H	1:17:1:ASP:HB3	37	0.11
(1,111)	1:10:1:LEU:HD11	1:11:1:GLU:HB2	37	0.11
(1,111)	1:10:1:LEU:HD11	1:11:1:GLU:HB3	37	0.11
(1,111)	1:10:1:LEU:HD12	1:11:1:GLU:HB2	37	0.11
(1,111)	1:10:1:LEU:HD12	1:11:1:GLU:HB3	37	0.11
(1,111)	1:10:1:LEU:HD13	1:11:1:GLU:HB2	37	0.11
(1,111)	1:10:1:LEU:HD13	1:11:1:GLU:HB3	37	0.11
(1,111)	1:10:1:LEU:HD21	1:11:1:GLU:HB2	37	0.11
(1,111)	1:10:1:LEU:HD21	1:11:1:GLU:HB3	37	0.11
(1,111)	1:10:1:LEU:HD22	1:11:1:GLU:HB2	37	0.11
(1,111)	1:10:1:LEU:HD22	1:11:1:GLU:HB3	37	0.11
(1,111)	1:10:1:LEU:HD23	1:11:1:GLU:HB2	37	0.11
(1,111)	1:10:1:LEU:HD23	1:11:1:GLU:HB3	37	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	7	0.11
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	7	0.11
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	12	0.11
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	12	0.11
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	19	0.11
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	19	0.11
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	20	0.11
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	20	0.11
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	23	0.11
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	23	0.11
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	30	0.11
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	30	0.11
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	40	0.11
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	40	0.11
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	43	0.11
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	43	0.11
(1,43)	1:5:1:CYS:HA	1:11:1:GLU:H	7	0.11
(1,43)	1:5:1:CYS:HA	1:11:1:GLU:H	12	0.11
(3,3)	1:30:1:ASN:O	1:35:1:LYS:H	8	0.1
(3,3)	1:30:1:ASN:O	1:35:1:LYS:H	38	0.1
(2,567)	1:81:1:TRP:HE3	1:82:1:ASN:H	18	0.1
(2,567)	1:81:1:TRP:HE3	1:82:1:ASN:H	26	0.1
(2,567)	1:81:1:TRP:HE3	1:82:1:ASN:H	28	0.1
(2,567)	1:81:1:TRP:HE3	1:82:1:ASN:H	37	0.1
(2,517)	1:70:1:ASP:HA	1:83:1:HIS:HD2	32	0.1
(2,513)	1:70:1:ASP:HA	1:81:1:TRP:HD1	40	0.1
(2,466)	1:64:1:ARG:HG2	1:67:1:TRP:HE1	24	0.1
(2,466)	1:64:1:ARG:HG3	1:67:1:TRP:HE1	24	0.1
(2,463)	1:64:1:ARG:HB2	1:67:1:TRP:HD1	38	0.1
(2,463)	1:64:1:ARG:HB3	1:67:1:TRP:HD1	38	0.1
(2,441)	1:62:1:ILE:HD11	1:81:1:TRP:HE3	33	0.1
(2,441)	1:62:1:ILE:HD12	1:81:1:TRP:HE3	33	0.1
(2,441)	1:62:1:ILE:HD13	1:81:1:TRP:HE3	33	0.1
(2,439)	1:62:1:ILE:HD11	1:81:1:TRP:HA	4	0.1
(2,439)	1:62:1:ILE:HD12	1:81:1:TRP:HA	4	0.1
(2,439)	1:62:1:ILE:HD13	1:81:1:TRP:HA	4	0.1
(2,439)	1:62:1:ILE:HD11	1:81:1:TRP:HA	12	0.1
(2,439)	1:62:1:ILE:HD12	1:81:1:TRP:HA	12	0.1
(2,439)	1:62:1:ILE:HD13	1:81:1:TRP:HA	12	0.1
(2,413)	1:61:1:ARG:HE	1:82:1:ASN:H	43	0.1
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB2	19	0.1
(2,359)	1:59:1:VAL:H	1:69:1:ASP:HB3	19	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,349)	1:58:1:THR:HB	1:73:1:THR:H	37	0.1
(2,244)	1:47:1:CYS:HB2	1:72:1:CYS:H	7	0.1
(2,244)	1:47:1:CYS:HB3	1:72:1:CYS:H	7	0.1
(2,232)	1:46:1:GLU:HA	1:79:1:CYS:H	27	0.1
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD11	28	0.1
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD12	28	0.1
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD13	28	0.1
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD21	28	0.1
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD22	28	0.1
(2,86)	1:17:1:ASP:H	1:36:1:LEU:HD23	28	0.1
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG21	7	0.1
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG22	7	0.1
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG23	7	0.1
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG21	9	0.1
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG22	9	0.1
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG23	9	0.1
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG21	14	0.1
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG22	14	0.1
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG23	14	0.1
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG21	15	0.1
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG22	15	0.1
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG23	15	0.1
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG21	21	0.1
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG22	21	0.1
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG23	21	0.1
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG21	28	0.1
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG22	28	0.1
(2,76)	1:16:1:CYS:HA	1:33:1:THR:HG23	28	0.1
(2,71)	1:15:1:ASP:H	1:34:1:CYS:HA	41	0.1
(1,867)	1:70:1:ASP:HA	1:71:1:TYR:HE1	8	0.1
(1,867)	1:70:1:ASP:HA	1:71:1:TYR:HE2	8	0.1
(1,867)	1:70:1:ASP:HA	1:71:1:TYR:HE1	13	0.1
(1,867)	1:70:1:ASP:HA	1:71:1:TYR:HE2	13	0.1
(1,703)	1:58:1:THR:HB	1:72:1:CYS:HA	40	0.1
(1,698)	1:58:1:THR:HG21	1:71:1:TYR:HE1	29	0.1
(1,698)	1:58:1:THR:HG21	1:71:1:TYR:HE2	29	0.1
(1,698)	1:58:1:THR:HG22	1:71:1:TYR:HE1	29	0.1
(1,698)	1:58:1:THR:HG22	1:71:1:TYR:HE2	29	0.1
(1,698)	1:58:1:THR:HG23	1:71:1:TYR:HE1	29	0.1
(1,698)	1:58:1:THR:HG23	1:71:1:TYR:HE2	29	0.1
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE1	33	0.1
(1,529)	1:48:1:CYS:HB2	1:53:1:PHE:HE2	33	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE1	33	0.1
(1,529)	1:48:1:CYS:HB3	1:53:1:PHE:HE2	33	0.1
(1,477)	1:44:1:TYR:HE1	1:45:1:GLY:H	16	0.1
(1,477)	1:44:1:TYR:HE2	1:45:1:GLY:H	16	0.1
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	20	0.1
(1,456)	1:42:1:CYS:HA	1:48:1:CYS:H	23	0.1
(1,362)	1:33:1:THR:H	1:34:1:CYS:HA	32	0.1
(1,362)	1:33:1:THR:H	1:34:1:CYS:HA	34	0.1
(1,362)	1:33:1:THR:H	1:34:1:CYS:HA	41	0.1
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	2	0.1
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	2	0.1
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	4	0.1
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	4	0.1
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	26	0.1
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	26	0.1
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	28	0.1
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	28	0.1
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	29	0.1
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	29	0.1
(1,63)	1:7:1:ASN:HB2	1:12:1:GLN:H	31	0.1
(1,63)	1:7:1:ASN:HB3	1:12:1:GLN:H	31	0.1

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

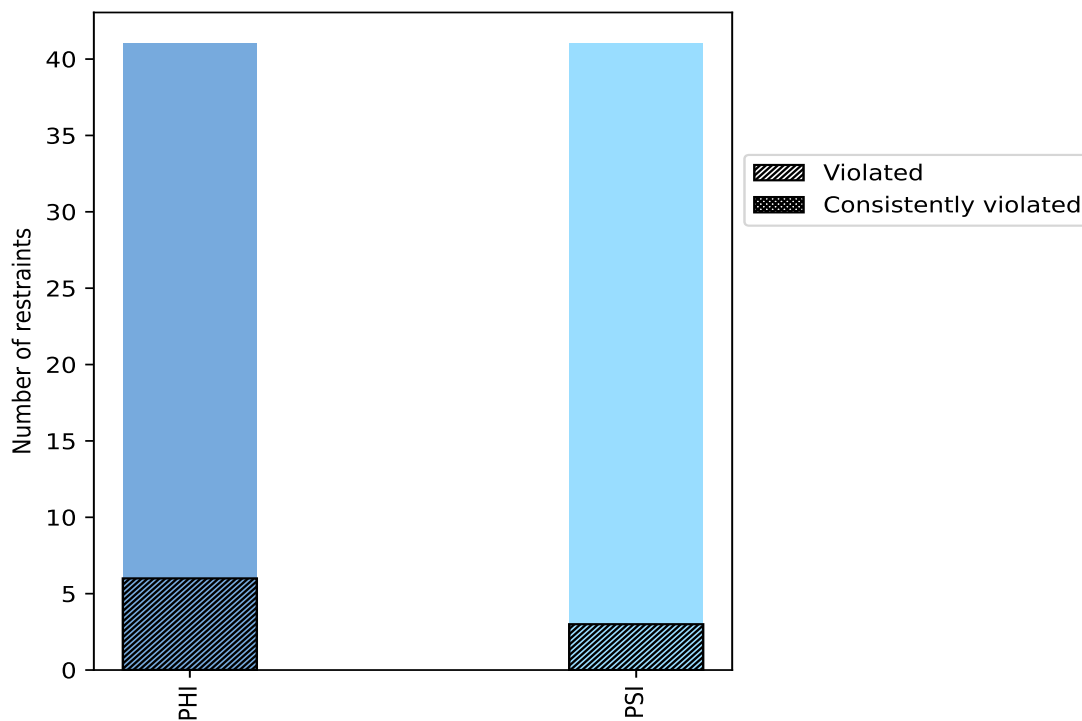
10.1 Summary of dihedral-angle violations [i](#)

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
PHI	41	50.0	6	14.6	7.3	0	0.0	0.0
PSI	41	50.0	3	7.3	3.7	0	0.0	0.0
Total	82	100.0	9	11.0	11.0	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 [i](#)

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.

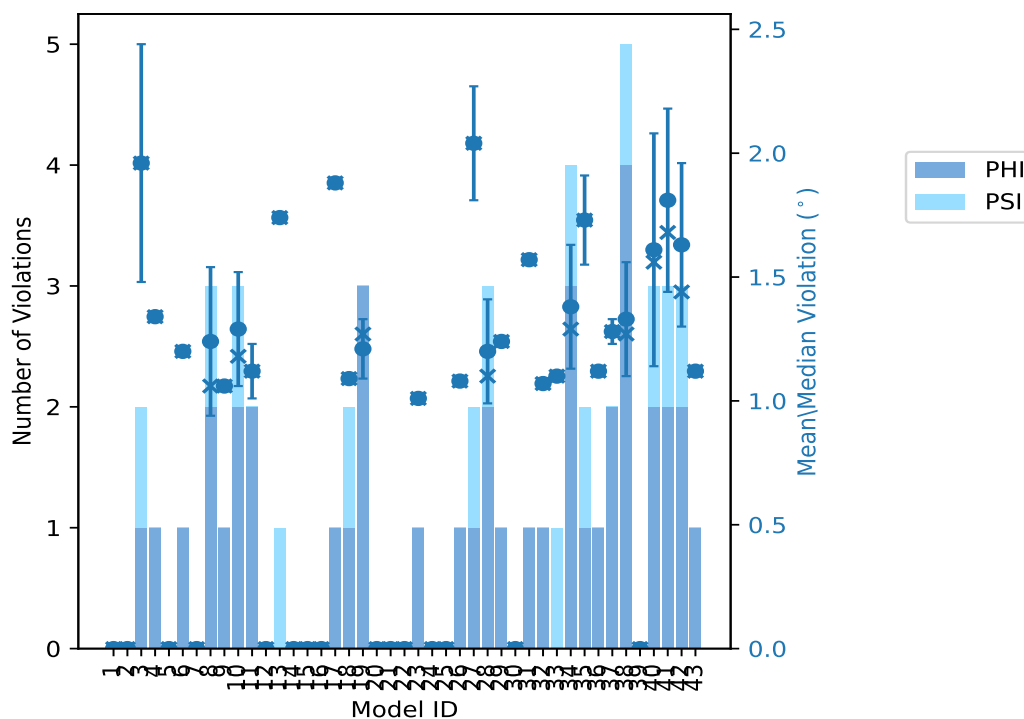
Model ID	Number of violations			Mean (°)	Max (°)	SD (°)	Median (°)
	PHI	PSI	Total				
1	0	0	0	0.0	0.0	0.0	0.0
2	0	0	0	0.0	0.0	0.0	0.0
3	1	1	2	1.96	2.44	0.48	1.96
4	1	0	1	1.34	1.34	0.0	1.34
5	0	0	0	0.0	0.0	0.0	0.0
6	1	0	1	1.2	1.2	0.0	1.2
7	0	0	0	0.0	0.0	0.0	0.0
8	2	1	3	1.24	1.66	0.3	1.06
9	1	0	1	1.06	1.06	0.0	1.06
10	2	1	3	1.29	1.62	0.23	1.18
11	2	0	2	1.12	1.23	0.11	1.12
12	0	0	0	0.0	0.0	0.0	0.0
13	0	1	1	1.74	1.74	0.0	1.74
14	0	0	0	0.0	0.0	0.0	0.0
15	0	0	0	0.0	0.0	0.0	0.0
16	0	0	0	0.0	0.0	0.0	0.0
17	1	0	1	1.88	1.88	0.0	1.88
18	1	1	2	1.09	1.09	0.0	1.09
19	3	0	3	1.21	1.31	0.12	1.27
20	0	0	0	0.0	0.0	0.0	0.0
21	0	0	0	0.0	0.0	0.0	0.0
22	0	0	0	0.0	0.0	0.0	0.0
23	1	0	1	1.01	1.01	0.0	1.01
24	0	0	0	0.0	0.0	0.0	0.0
25	0	0	0	0.0	0.0	0.0	0.0
26	1	0	1	1.08	1.08	0.0	1.08
27	1	1	2	2.04	2.27	0.23	2.04
28	2	1	3	1.2	1.5	0.21	1.1
29	1	0	1	1.24	1.24	0.0	1.24
30	0	0	0	0.0	0.0	0.0	0.0
31	1	0	1	1.57	1.57	0.0	1.57
32	1	0	1	1.07	1.07	0.0	1.07
33	0	1	1	1.1	1.1	0.0	1.1
34	3	1	4	1.38	1.77	0.25	1.29
35	1	1	2	1.73	1.91	0.18	1.73
36	1	0	1	1.12	1.12	0.0	1.12
37	2	0	2	1.28	1.33	0.05	1.28
38	4	1	5	1.33	1.77	0.23	1.27

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Model ID	Number of violations			Mean (°)	Max (°)	SD (°)	Median (°)
	PHI	PSI	Total				
39	0	0	0	0.0	0.0	0.0	0.0
40	2	1	3	1.61	2.21	0.47	1.56
41	2	1	3	1.81	2.31	0.37	1.68
42	2	1	3	1.63	2.09	0.33	1.44
43	1	0	1	1.12	1.12	0.0	1.12

10.2.1 Bar graph : Dihedral violation statistics for each model [i](#)



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

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

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

Number of violated restraints			Fraction of the ensemble	
PHI	PSI	Total	Count ¹	%
2	0	2	1	2.3

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Number of violated restraints			Fraction of the ensemble	
PHI	PSI	Total	Count ¹	%
0	2	2	2	4.7
0	0	0	3	7.0
0	0	0	4	9.3
1	0	1	5	11.6
1	0	1	6	14.0
0	0	0	7	16.3
0	0	0	8	18.6
0	0	0	9	20.9
0	1	1	10	23.3
0	0	0	11	25.6
1	0	1	12	27.9
0	0	0	13	30.2
0	0	0	14	32.6
0	0	0	15	34.9
1	0	1	16	37.2
0	0	0	17	39.5
0	0	0	18	41.9
0	0	0	19	44.2
0	0	0	20	46.5
0	0	0	21	48.8
0	0	0	22	51.2
0	0	0	23	53.5
0	0	0	24	55.8
0	0	0	25	58.1
0	0	0	26	60.5
0	0	0	27	62.8
0	0	0	28	65.1
0	0	0	29	67.4
0	0	0	30	69.8
0	0	0	31	72.1
0	0	0	32	74.4
0	0	0	33	76.7
0	0	0	34	79.1
0	0	0	35	81.4
0	0	0	36	83.7
0	0	0	37	86.0
0	0	0	38	88.4
0	0	0	39	90.7
0	0	0	40	93.0
0	0	0	41	95.3
0	0	0	42	97.7

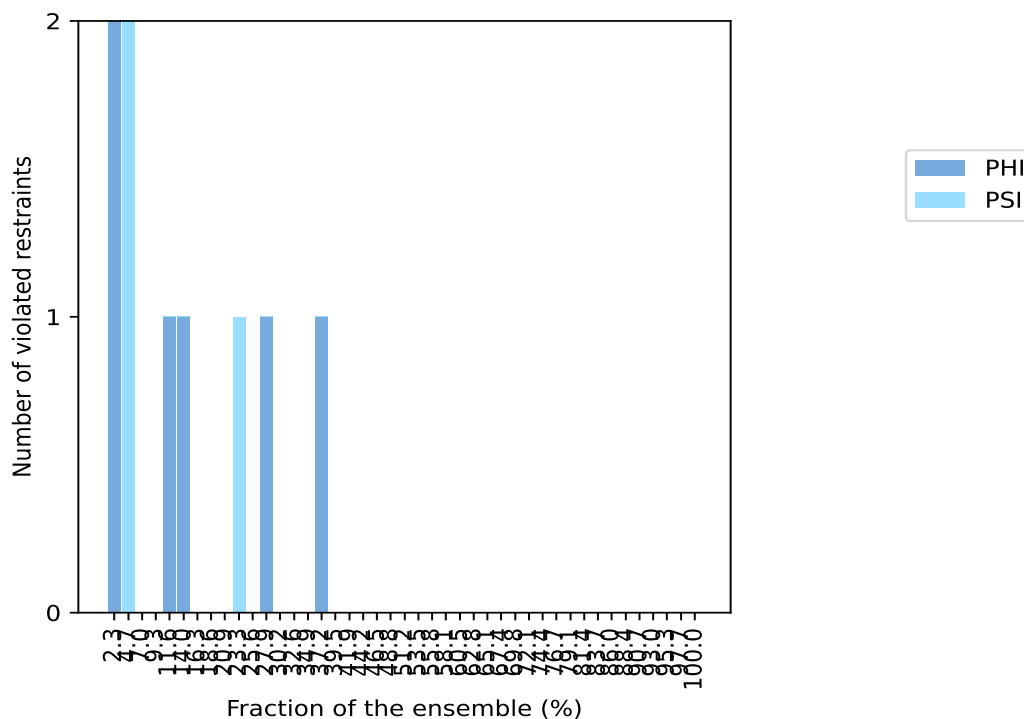
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Number of violated restraints			Fraction of the ensemble	
PHI	PSI	Total	Count ¹	%
0	0	0	43	100.0

¹ Number of models with violations

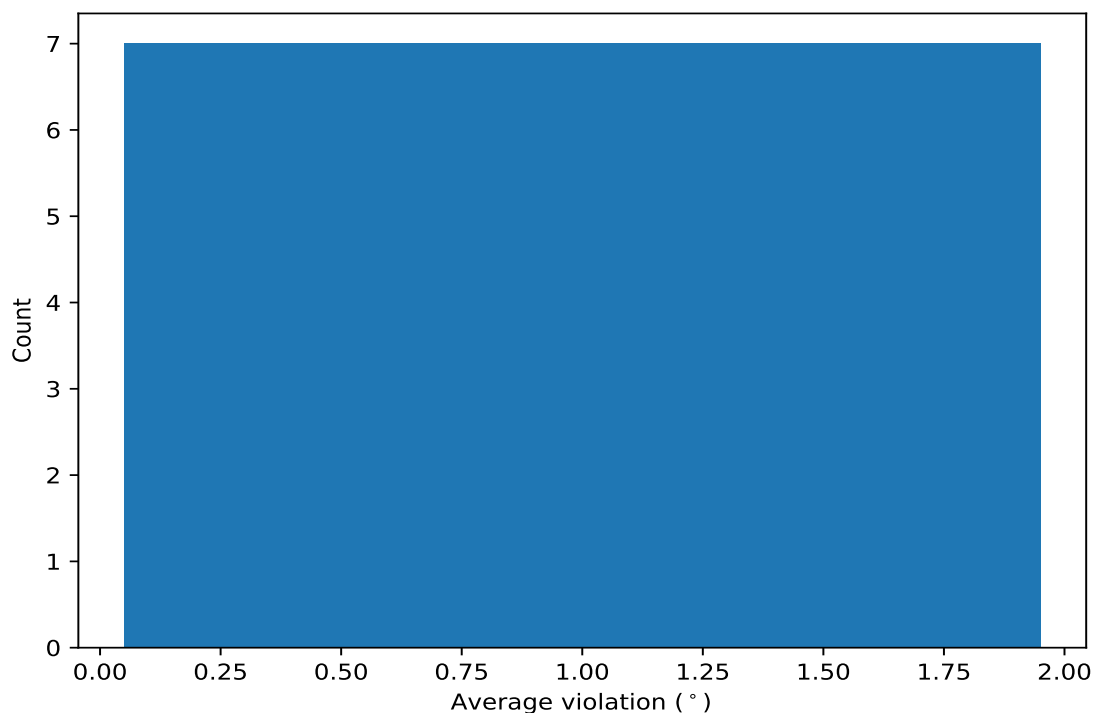
10.3.1 Bar graph : Dihedral-angle Violation statistics for the ensemble [i](#)



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.

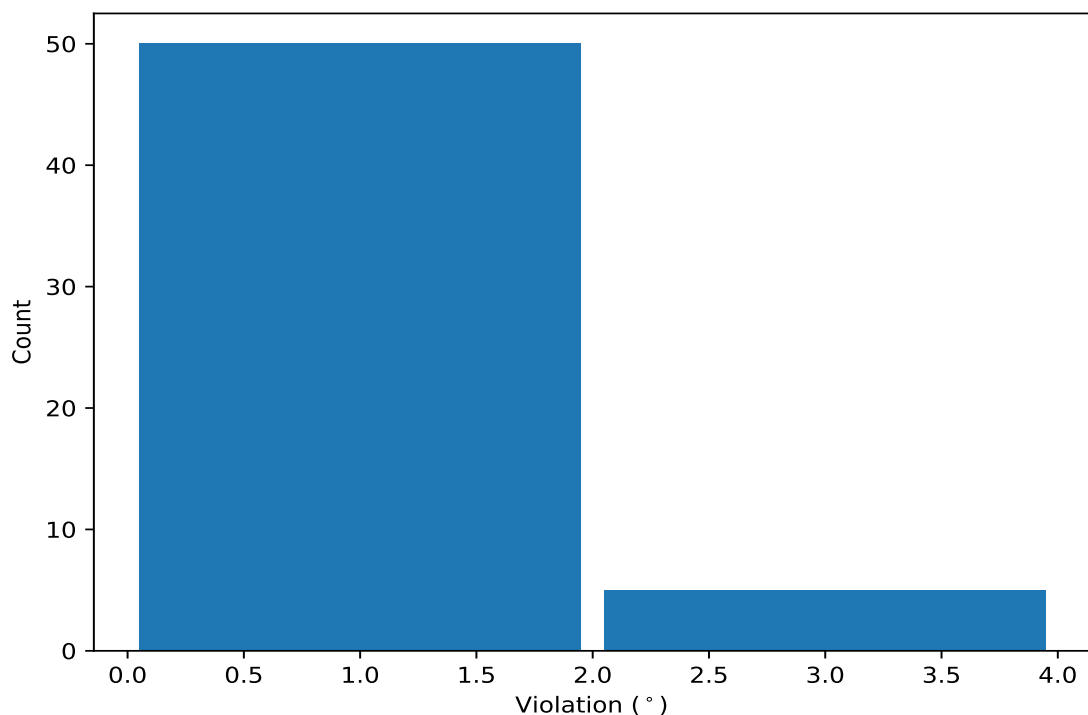
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,3)	1:4:1:VAL:C	1:5:1:CYS:N	1:5:1:CYS:CA	1:5:1:CYS:C	16	1.74	0.42	1.72
(1,44)	1:47:1:CYS:C	1:48:1:CYS:N	1:48:1:CYS:CA	1:48:1:CYS:C	12	1.2	0.1	1.21
(1,2)	1:4:1:VAL:N	1:4:1:VAL:CA	1:4:1:VAL:C	1:5:1:CYS:N	10	1.38	0.26	1.42
(1,10)	1:14:1:GLU:C	1:15:1:ASP:N	1:15:1:ASP:CA	1:15:1:ASP:C	6	1.22	0.15	1.21
(1,1)	1:3:1:PRO:C	1:4:1:VAL:N	1:4:1:VAL:CA	1:4:1:VAL:C	5	1.06	0.04	1.06
(1,61)	1:61:1:ARG:N	1:61:1:ARG:CA	1:61:1:ARG:C	1:62:1:ILE:N	2	1.64	0.09	1.64
(1,25)	1:26:1:ASP:N	1:26:1:ASP:CA	1:26:1:ASP:C	1:27:1:ARG:N	2	1.1	0.01	1.1

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 (°)
(1,3)	1:4:1:VAL:C	1:5:1:CYS:N	1:5:1:CYS:CA	1:5:1:CYS:C	3	2.44
(1,3)	1:4:1:VAL:C	1:5:1:CYS:N	1:5:1:CYS:CA	1:5:1:CYS:C	41	2.31
(1,3)	1:4:1:VAL:C	1:5:1:CYS:N	1:5:1:CYS:CA	1:5:1:CYS:C	27	2.27
(1,3)	1:4:1:VAL:C	1:5:1:CYS:N	1:5:1:CYS:CA	1:5:1:CYS:C	40	2.21
(1,3)	1:4:1:VAL:C	1:5:1:CYS:N	1:5:1:CYS:CA	1:5:1:CYS:C	42	2.09
(1,60)	1:60:1:CYS:C	1:61:1:ARG:N	1:61:1:ARG:CA	1:61:1:ARG:C	35	1.91
(1,3)	1:4:1:VAL:C	1:5:1:CYS:N	1:5:1:CYS:CA	1:5:1:CYS:C	17	1.88
(1,2)	1:4:1:VAL:N	1:4:1:VAL:CA	1:4:1:VAL:C	1:5:1:CYS:N	27	1.81
(1,3)	1:4:1:VAL:C	1:5:1:CYS:N	1:5:1:CYS:CA	1:5:1:CYS:C	34	1.77
(1,3)	1:4:1:VAL:C	1:5:1:CYS:N	1:5:1:CYS:CA	1:5:1:CYS:C	38	1.77
(1,61)	1:61:1:ARG:N	1:61:1:ARG:CA	1:61:1:ARG:C	1:62:1:ILE:N	13	1.74
(1,2)	1:4:1:VAL:N	1:4:1:VAL:CA	1:4:1:VAL:C	1:5:1:CYS:N	41	1.68
(1,3)	1:4:1:VAL:C	1:5:1:CYS:N	1:5:1:CYS:CA	1:5:1:CYS:C	8	1.66
(1,3)	1:4:1:VAL:C	1:5:1:CYS:N	1:5:1:CYS:CA	1:5:1:CYS:C	10	1.62
(1,3)	1:4:1:VAL:C	1:5:1:CYS:N	1:5:1:CYS:CA	1:5:1:CYS:C	31	1.57
(1,2)	1:4:1:VAL:N	1:4:1:VAL:CA	1:4:1:VAL:C	1:5:1:CYS:N	40	1.56
(1,61)	1:61:1:ARG:N	1:61:1:ARG:CA	1:61:1:ARG:C	1:62:1:ILE:N	35	1.55
(1,3)	1:4:1:VAL:C	1:5:1:CYS:N	1:5:1:CYS:CA	1:5:1:CYS:C	28	1.5
(1,2)	1:4:1:VAL:N	1:4:1:VAL:CA	1:4:1:VAL:C	1:5:1:CYS:N	3	1.48
(1,10)	1:14:1:GLU:C	1:15:1:ASP:N	1:15:1:ASP:CA	1:15:1:ASP:C	41	1.44
(1,2)	1:4:1:VAL:N	1:4:1:VAL:CA	1:4:1:VAL:C	1:5:1:CYS:N	42	1.44

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,2)	1:4:1:VAL:N	1:4:1:VAL:CA	1:4:1:VAL:C	1:5:1:CYS:N	34	1.4
(1,10)	1:14:1:GLU:C	1:15:1:ASP:N	1:15:1:ASP:CA	1:15:1:ASP:C	42	1.36
(1,44)	1:47:1:CYS:C	1:48:1:CYS:N	1:48:1:CYS:CA	1:48:1:CYS:C	4	1.34
(1,3)	1:4:1:VAL:C	1:5:1:CYS:N	1:5:1:CYS:CA	1:5:1:CYS:C	37	1.33
(1,44)	1:47:1:CYS:C	1:48:1:CYS:N	1:48:1:CYS:CA	1:48:1:CYS:C	19	1.31
(1,44)	1:47:1:CYS:C	1:48:1:CYS:N	1:48:1:CYS:CA	1:48:1:CYS:C	38	1.31
(1,10)	1:14:1:GLU:C	1:15:1:ASP:N	1:15:1:ASP:CA	1:15:1:ASP:C	38	1.27
(1,3)	1:4:1:VAL:C	1:5:1:CYS:N	1:5:1:CYS:CA	1:5:1:CYS:C	19	1.27
(1,44)	1:47:1:CYS:C	1:48:1:CYS:N	1:48:1:CYS:CA	1:48:1:CYS:C	29	1.24
(1,2)	1:4:1:VAL:N	1:4:1:VAL:CA	1:4:1:VAL:C	1:5:1:CYS:N	38	1.24
(1,44)	1:47:1:CYS:C	1:48:1:CYS:N	1:48:1:CYS:CA	1:48:1:CYS:C	11	1.23
(1,44)	1:47:1:CYS:C	1:48:1:CYS:N	1:48:1:CYS:CA	1:48:1:CYS:C	37	1.23
(1,44)	1:47:1:CYS:C	1:48:1:CYS:N	1:48:1:CYS:CA	1:48:1:CYS:C	6	1.2
(1,44)	1:47:1:CYS:C	1:48:1:CYS:N	1:48:1:CYS:CA	1:48:1:CYS:C	10	1.18
(1,44)	1:47:1:CYS:C	1:48:1:CYS:N	1:48:1:CYS:CA	1:48:1:CYS:C	34	1.18
(1,10)	1:14:1:GLU:C	1:15:1:ASP:N	1:15:1:ASP:CA	1:15:1:ASP:C	34	1.16
(1,44)	1:47:1:CYS:C	1:48:1:CYS:N	1:48:1:CYS:CA	1:48:1:CYS:C	43	1.12
(1,1)	1:3:1:PRO:C	1:4:1:VAL:N	1:4:1:VAL:CA	1:4:1:VAL:C	36	1.12
(1,25)	1:26:1:ASP:N	1:26:1:ASP:CA	1:26:1:ASP:C	1:27:1:ARG:N	33	1.1
(1,2)	1:4:1:VAL:N	1:4:1:VAL:CA	1:4:1:VAL:C	1:5:1:CYS:N	28	1.1
(1,26)	1:27:1:ARG:C	1:28:1:CYS:N	1:28:1:CYS:CA	1:28:1:CYS:C	18	1.09
(1,25)	1:26:1:ASP:N	1:26:1:ASP:CA	1:26:1:ASP:C	1:27:1:ARG:N	18	1.09
(1,3)	1:4:1:VAL:C	1:5:1:CYS:N	1:5:1:CYS:CA	1:5:1:CYS:C	26	1.08
(1,2)	1:4:1:VAL:N	1:4:1:VAL:CA	1:4:1:VAL:C	1:5:1:CYS:N	10	1.08
(1,1)	1:3:1:PRO:C	1:4:1:VAL:N	1:4:1:VAL:CA	1:4:1:VAL:C	38	1.08
(1,3)	1:4:1:VAL:C	1:5:1:CYS:N	1:5:1:CYS:CA	1:5:1:CYS:C	32	1.07
(1,44)	1:47:1:CYS:C	1:48:1:CYS:N	1:48:1:CYS:CA	1:48:1:CYS:C	40	1.06
(1,10)	1:14:1:GLU:C	1:15:1:ASP:N	1:15:1:ASP:CA	1:15:1:ASP:C	8	1.06
(1,1)	1:3:1:PRO:C	1:4:1:VAL:N	1:4:1:VAL:CA	1:4:1:VAL:C	9	1.06
(1,10)	1:14:1:GLU:C	1:15:1:ASP:N	1:15:1:ASP:CA	1:15:1:ASP:C	19	1.04
(1,44)	1:47:1:CYS:C	1:48:1:CYS:N	1:48:1:CYS:CA	1:48:1:CYS:C	28	1.01
(1,1)	1:3:1:PRO:C	1:4:1:VAL:N	1:4:1:VAL:CA	1:4:1:VAL:C	11	1.01
(1,1)	1:3:1:PRO:C	1:4:1:VAL:N	1:4:1:VAL:CA	1:4:1:VAL:C	23	1.01
(1,2)	1:4:1:VAL:N	1:4:1:VAL:CA	1:4:1:VAL:C	1:5:1:CYS:N	8	1.0