



Full wwPDB NMR Structure Validation Report ⓘ

Mar 5, 2026 – 04:30 AM UTC

PDB ID : 6QEB / pdb_00006qeb
BMRB ID : 34347
Title : Assessment of a large enzyme-drug complex by proton-detected solid-state NMR without deuteration
Authors : Vasa, S.K.
Deposited on : 2019-01-07

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
Mogul : 2022.3.0, CSD as543be (2022)
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

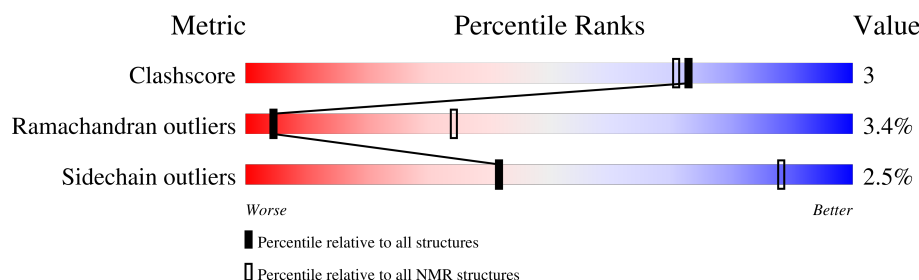
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLID-STATE NMR

The overall completeness of chemical shifts assignment is 71%.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	260	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA and RNA chains that are outliers for geometric criteria:

Mol	Chain	Compound	Res	Total models with violations	
				Chirality	Geometry
3	A	AZM	302	-	20

2 Ensemble composition and analysis

This entry contains 20 models. Model 1 is the overall representative, medoid model (most similar to other models).

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

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:29-A:196, A:203-A:231, A:239-A:260 (219)	2.50	1

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

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

The models can be grouped into 2 clusters and 9 single-model clusters were found.

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

3 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4122 atoms, of which 2035 are hydrogens and 0 are deuteriums.

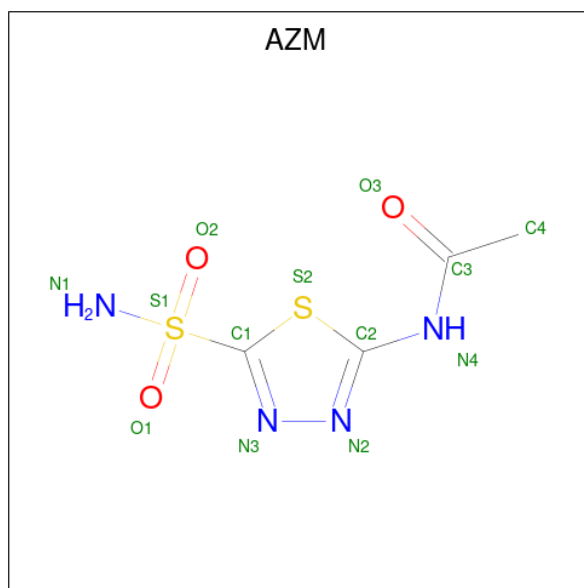
- Molecule 1 is a protein called Carbonic anhydrase 2.

Mol	Chain	Residues	Atoms						Trace
1	A	260	Total	C	H	N	O	S	0
			4108	1329	2035	357	384	3	

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	
2	A	1	Total	Zn
			1	1

- Molecule 3 is 5-ACETAMIDO-1,3,4-THIADIAZOLE-2-SULFONAMIDE (CCD ID: AZM) (formula: C₄H₆N₄O₃S₂).



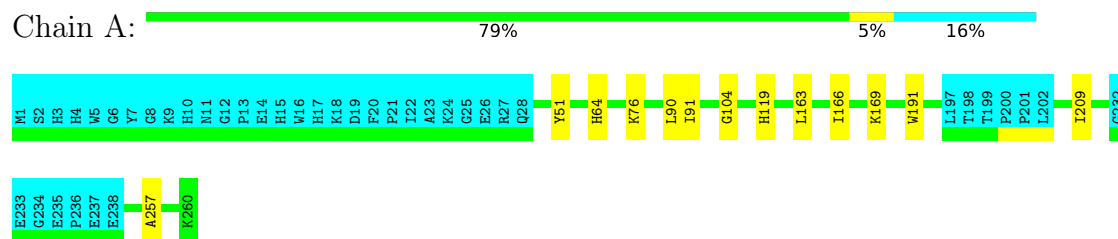
Mol	Chain	Residues	Atoms				
3	A	1	Total	C	N	O	S
			13	4	4	3	2

4 Residue-property plots [i](#)

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: Carbonic anhydrase 2

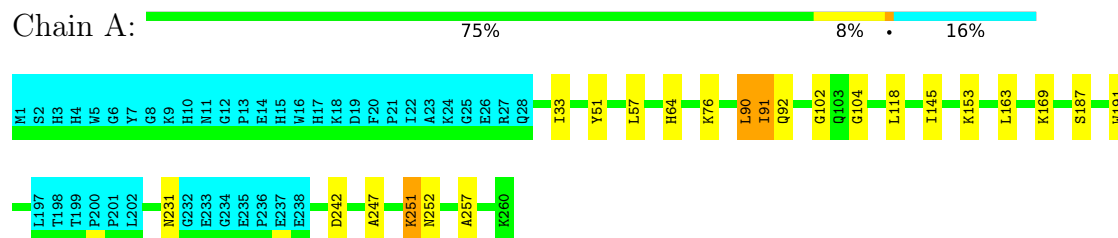


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1 (medoid)

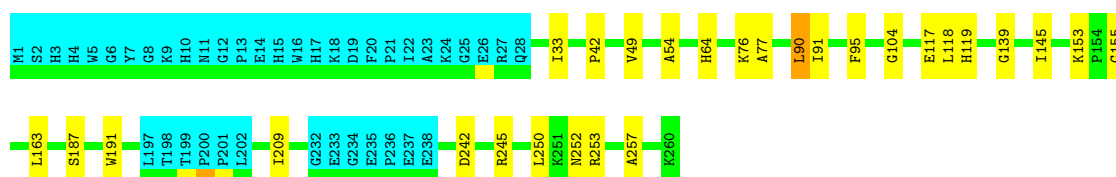
- Molecule 1: Carbonic anhydrase 2



4.2.2 Score per residue for model 2

- Molecule 1: Carbonic anhydrase 2

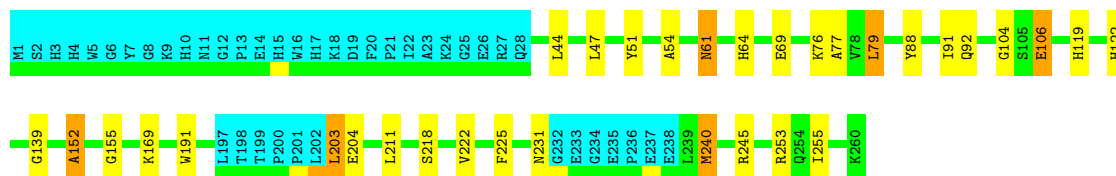




4.2.3 Score per residue for model 3

- Molecule 1: Carbonic anhydrase 2

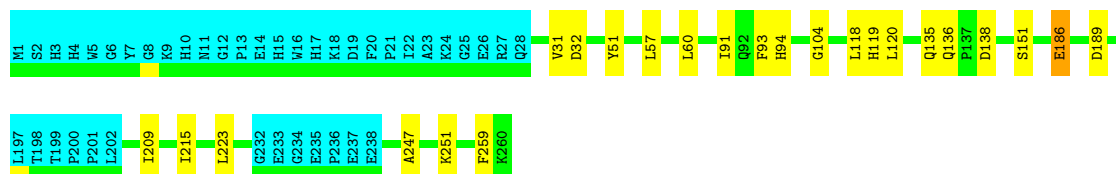
Chain A: 72% 10% 16%



4.2.4 Score per residue for model 4

- Molecule 1: Carbonic anhydrase 2

Chain A: 75% 9% 16%



4.2.5 Score per residue for model 5

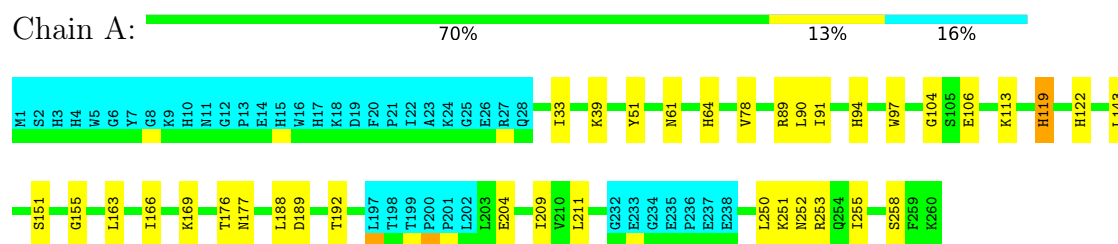
- Molecule 1: Carbonic anhydrase 2

Chain A: 70% 14% 16%



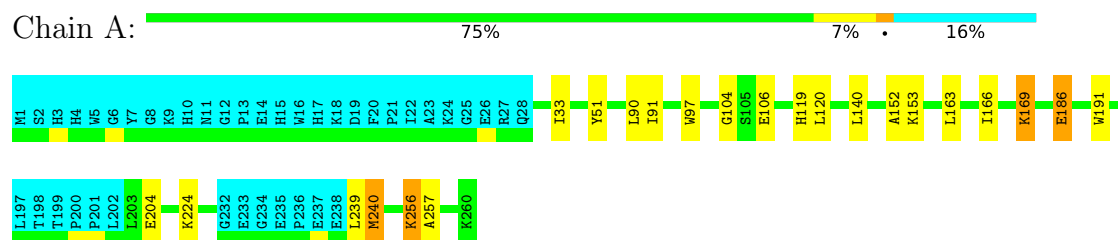
4.2.6 Score per residue for model 6

- Molecule 1: Carbonic anhydrase 2



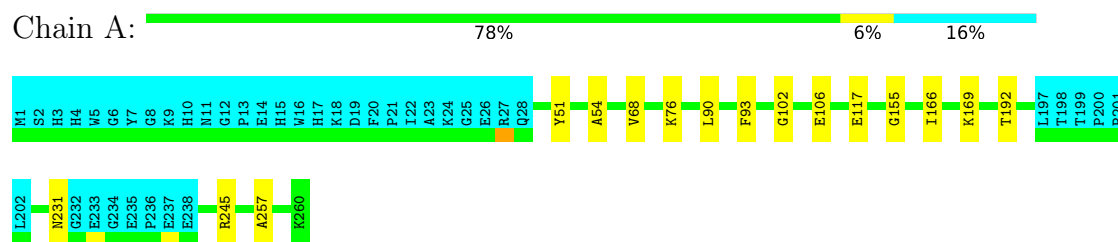
4.2.7 Score per residue for model 7

- Molecule 1: Carbonic anhydrase 2



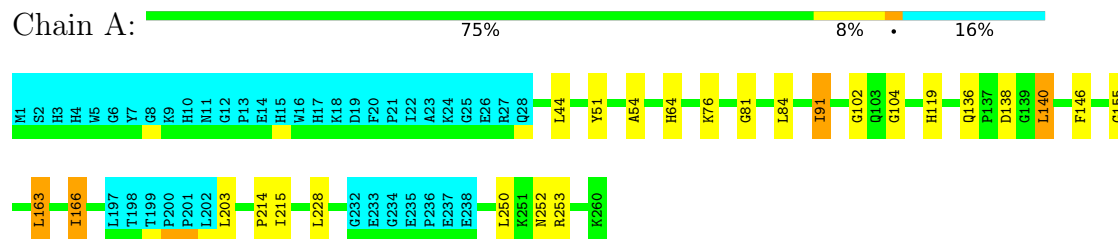
4.2.8 Score per residue for model 8

- Molecule 1: Carbonic anhydrase 2



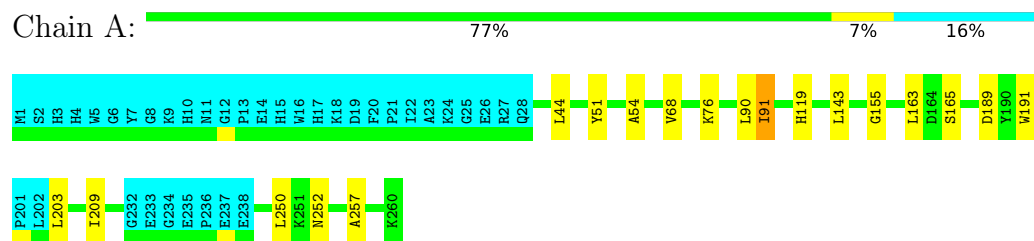
4.2.9 Score per residue for model 9

- Molecule 1: Carbonic anhydrase 2



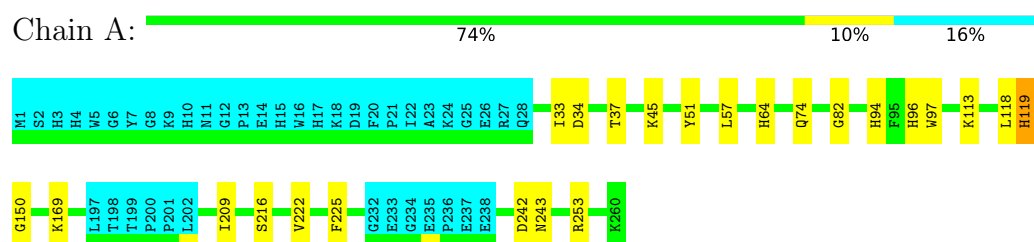
4.2.10 Score per residue for model 10

- Molecule 1: Carbonic anhydrase 2



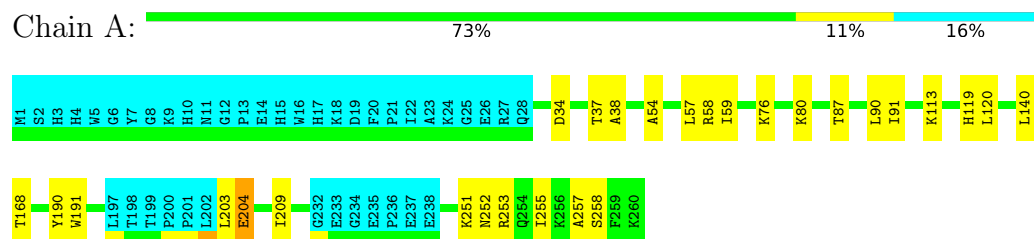
4.2.11 Score per residue for model 11

- Molecule 1: Carbonic anhydrase 2



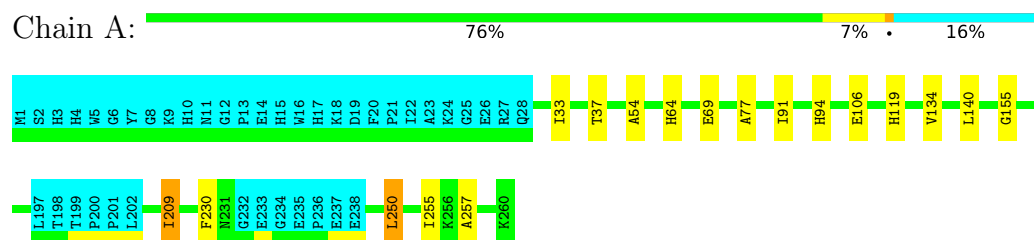
4.2.12 Score per residue for model 12

- Molecule 1: Carbonic anhydrase 2



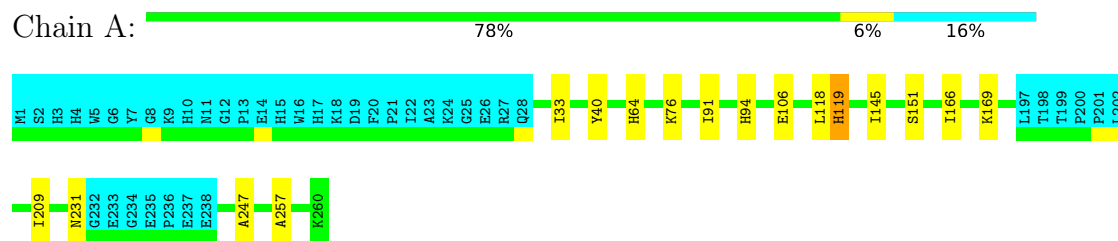
4.2.13 Score per residue for model 13

- Molecule 1: Carbonic anhydrase 2



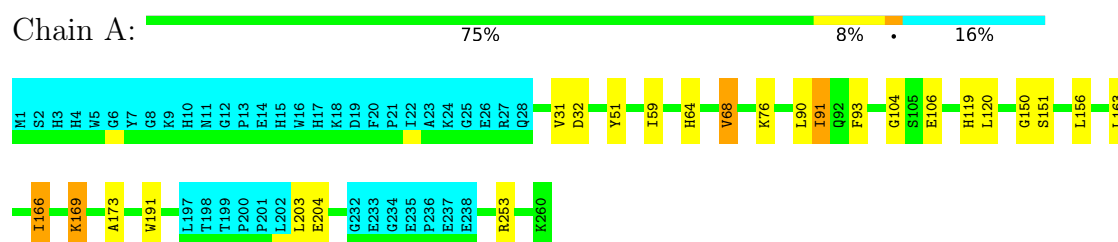
4.2.14 Score per residue for model 14

- Molecule 1: Carbonic anhydrase 2



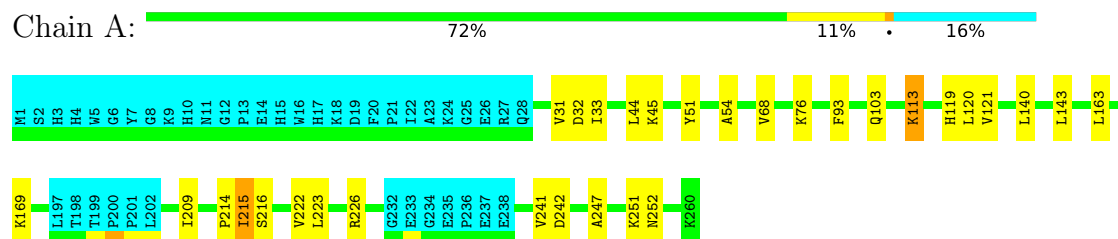
4.2.15 Score per residue for model 15

- Molecule 1: Carbonic anhydrase 2



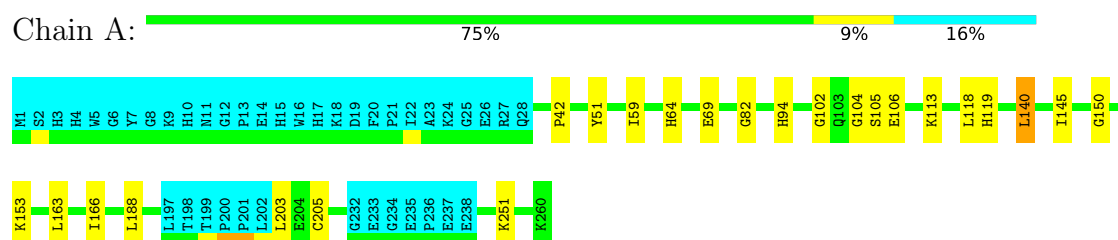
4.2.16 Score per residue for model 16

- Molecule 1: Carbonic anhydrase 2



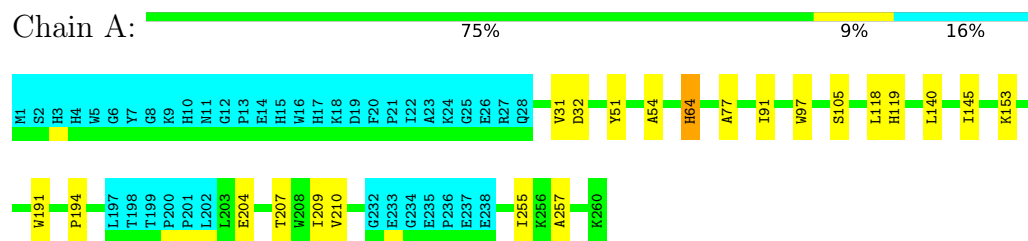
4.2.17 Score per residue for model 17

- Molecule 1: Carbonic anhydrase 2



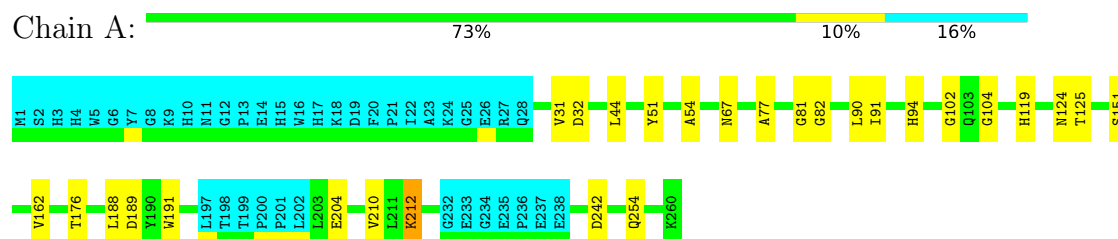
4.2.18 Score per residue for model 18

- Molecule 1: Carbonic anhydrase 2



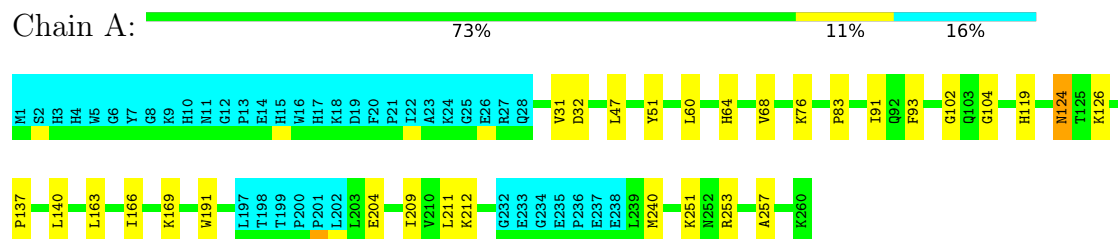
4.2.19 Score per residue for model 19

- Molecule 1: Carbonic anhydrase 2



4.2.20 Score per residue for model 20

- Molecule 1: Carbonic anhydrase 2



5 Refinement protocol and experimental data overview

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

Of the 20 calculated structures, 20 were deposited, based on the following criterion: *lowest energy*.

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

Software name	Classification	Version
ARIA	refinement	
ARIA	structure calculation	

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

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	2450
Number of shifts mapped to atoms	2450
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	71%

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

6 Model quality

6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: AZM, ZN

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

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	1739	1730	1726	10±3
3	A	13	0	6	1±0
All	All	35060	34600	34625	227

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 3.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
3:A:302:AZM:C1	3:A:302:AZM:S2	1.48	2.01	12	17
1:A:90:LEU:H	1:A:90:LEU:HD23	0.62	1.54	12	1
1:A:118:LEU:HD21	1:A:145:ILE:HB	0.60	1.72	14	1
1:A:215:ILE:HD13	1:A:215:ILE:H	0.58	1.58	16	1
1:A:191:TRP:HA	1:A:257:ALA:HB1	0.54	1.77	10	9
1:A:176:THR:HG23	1:A:177:ASN:HD22	0.54	1.63	6	1
1:A:59:ILE:HB	1:A:166:ILE:HD12	0.53	1.79	17	1
1:A:250:LEU:H	1:A:250:LEU:HD23	0.53	1.63	2	1
1:A:166:ILE:HG23	1:A:173:ALA:HB2	0.53	1.80	15	1
1:A:54:ALA:HB2	1:A:77:ALA:HB2	0.52	1.80	18	5
1:A:93:PHE:HB3	1:A:120:LEU:HD13	0.52	1.81	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:90:LEU:HD13	1:A:90:LEU:N	0.52	2.20	1	1
1:A:212:LYS:H	1:A:212:LYS:HD2	0.52	1.65	19	1
1:A:143:LEU:HD13	1:A:209:ILE:HB	0.50	1.82	16	1
1:A:141:ALA:HB1	1:A:209:ILE:HD13	0.50	1.82	5	1
1:A:124:ASN:HD22	1:A:124:ASN:N	0.50	2.04	20	1
1:A:91:ILE:HG22	1:A:92:GLN:HG3	0.49	1.83	3	2
1:A:68:VAL:HG21	1:A:93:PHE:CE1	0.49	2.43	15	1
1:A:118:LEU:HB2	1:A:145:ILE:HB	0.48	1.84	2	4
1:A:209:ILE:N	1:A:209:ILE:HD12	0.48	2.24	5	7
1:A:134:VAL:HA	1:A:140:LEU:HD22	0.48	1.84	13	1
1:A:140:LEU:H	1:A:140:LEU:HD23	0.48	1.68	16	2
1:A:140:LEU:HD22	1:A:140:LEU:N	0.48	2.23	17	2
1:A:169:LYS:N	1:A:169:LYS:HD2	0.48	2.23	3	1
1:A:91:ILE:HD12	1:A:91:ILE:N	0.48	2.23	12	8
1:A:79:LEU:HD22	1:A:79:LEU:N	0.47	2.24	3	1
1:A:31:VAL:HG22	1:A:32:ASP:H	0.47	1.69	18	4
1:A:47:LEU:HD23	1:A:47:LEU:H	0.47	1.69	3	1
1:A:94:HIS:NE2	1:A:119:HIS:HB2	0.47	2.25	19	7
1:A:31:VAL:HG12	1:A:32:ASP:N	0.47	2.25	19	3
1:A:54:ALA:HA	1:A:76:LYS:HB3	0.46	1.87	10	5
1:A:136:GLN:HE21	1:A:138:ASP:HB2	0.46	1.69	9	1
1:A:90:LEU:HD23	1:A:122:HIS:HA	0.46	1.88	6	1
1:A:192:THR:H	1:A:257:ALA:HA	0.46	1.70	8	1
1:A:91:ILE:N	1:A:91:ILE:HD13	0.46	2.26	9	3
1:A:203:LEU:O	1:A:203:LEU:HD12	0.46	2.10	5	1
1:A:54:ALA:HA	1:A:76:LYS:HG3	0.45	1.87	2	1
1:A:90:LEU:N	1:A:90:LEU:HD22	0.45	2.26	2	1
1:A:78:VAL:HA	1:A:89:ARG:HG3	0.45	1.88	6	1
1:A:169:LYS:N	1:A:169:LYS:HE3	0.45	2.26	7	1
1:A:81:GLY:HA3	1:A:84:LEU:HD21	0.45	1.87	9	1
1:A:34:ASP:HB2	1:A:37:THR:HG22	0.45	1.87	11	2
1:A:103:GLN:HA	1:A:113:LYS:HD2	0.45	1.89	16	1
1:A:211:LEU:HG	1:A:212:LYS:H	0.45	1.72	20	1
1:A:61:ASN:ND2	1:A:166:ILE:HG21	0.44	2.26	5	1
1:A:106:GLU:HA	1:A:245:ARG:HB3	0.44	1.90	3	1
1:A:90:LEU:HD12	1:A:90:LEU:N	0.44	2.28	10	4
1:A:44:LEU:HD22	1:A:44:LEU:N	0.44	2.28	9	2
1:A:33:ILE:HD12	1:A:33:ILE:N	0.44	2.28	6	7
1:A:240:MET:SD	1:A:240:MET:N	0.44	2.91	3	1
1:A:37:THR:HG23	1:A:255:ILE:HG22	0.44	1.89	13	1
1:A:152:ALA:HB2	1:A:218:SER:HB3	0.44	1.89	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:169:LYS:HD2	1:A:169:LYS:N	0.43	2.27	8	4
1:A:106:GLU:HA	1:A:245:ARG:HB2	0.43	1.89	5	1
1:A:120:LEU:HD23	1:A:121:VAL:N	0.43	2.28	16	1
1:A:105:SER:H	1:A:113:LYS:HE2	0.43	1.73	17	1
1:A:69:GLU:HA	1:A:92:GLN:HG2	0.43	1.89	3	2
1:A:255:ILE:N	1:A:255:ILE:HD12	0.43	2.29	3	1
1:A:68:VAL:HG12	1:A:93:PHE:CD2	0.43	2.49	8	1
1:A:194:PRO:HA	1:A:207:THR:HG23	0.43	1.90	5	2
1:A:44:LEU:HD23	1:A:45:LYS:N	0.43	2.29	16	1
1:A:61:ASN:HD22	1:A:61:ASN:N	0.43	2.12	3	1
1:A:203:LEU:HD13	1:A:204:GLU:H	0.43	1.73	3	1
1:A:60:LEU:N	1:A:60:LEU:HD22	0.43	2.29	4	1
1:A:192:THR:HG22	1:A:258:SER:N	0.43	2.29	6	1
1:A:88:TYR:HB3	1:A:122:HIS:HB3	0.43	1.90	3	1
1:A:191:TRP:HB2	1:A:211:LEU:HD22	0.43	1.90	3	1
1:A:122:HIS:NE2	1:A:143:LEU:HG	0.43	2.27	5	1
1:A:44:LEU:HD12	1:A:44:LEU:N	0.43	2.29	3	1
1:A:222:VAL:HB	1:A:225:PHE:HB2	0.43	1.90	11	1
1:A:153:LYS:HB3	1:A:156:LEU:HB2	0.43	1.91	18	1
1:A:250:LEU:HD22	1:A:250:LEU:N	0.42	2.28	6	3
1:A:256:LYS:H	1:A:256:LYS:HD2	0.42	1.73	7	1
1:A:91:ILE:HG12	1:A:92:GLN:N	0.42	2.28	1	1
1:A:146:PHE:H	1:A:214:PRO:HG2	0.42	1.74	9	1
1:A:190:TYR:HB2	1:A:258:SER:HB3	0.42	1.91	12	1
1:A:44:LEU:HD11	1:A:81:GLY:HA3	0.42	1.91	19	1
1:A:124:ASN:HD22	1:A:125:THR:N	0.42	2.11	19	1
1:A:118:LEU:HD21	1:A:145:ILE:HD12	0.42	1.90	11	1
1:A:80:LYS:HD2	1:A:87:THR:HB	0.42	1.90	12	1
1:A:209:ILE:HD13	1:A:209:ILE:N	0.42	2.30	13	1
1:A:59:ILE:HD12	1:A:59:ILE:N	0.42	2.30	15	1
1:A:68:VAL:HG23	1:A:93:PHE:O	0.42	2.15	15	2
1:A:203:LEU:HD22	1:A:203:LEU:N	0.42	2.29	17	1
1:A:143:LEU:HA	1:A:209:ILE:HB	0.42	1.92	10	1
1:A:245:ARG:HA	1:A:245:ARG:HE	0.42	1.75	8	1
1:A:163:LEU:HD12	1:A:228:LEU:HD11	0.42	1.92	9	1
1:A:203:LEU:HD23	1:A:203:LEU:N	0.42	2.30	10	1
1:A:58:ARG:HG3	1:A:59:ILE:N	0.42	2.30	12	1
1:A:68:VAL:HG22	1:A:93:PHE:O	0.42	2.15	16	1
1:A:188:LEU:HG	1:A:189:ASP:H	0.42	1.73	19	1
1:A:137:PRO:HB3	1:A:204:GLU:HG3	0.42	1.90	20	1
1:A:90:LEU:HD22	1:A:90:LEU:H	0.41	1.75	1	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:108:THR:HG23	1:A:113:LYS:N	0.41	2.31	5	1
1:A:96:HIS:ND1	1:A:243:ASN:HB3	0.41	2.31	11	1
1:A:57:LEU:N	1:A:57:LEU:HD12	0.41	2.30	12	1
1:A:140:LEU:HD23	1:A:140:LEU:N	0.41	2.30	12	1
1:A:33:ILE:HG23	1:A:255:ILE:HG12	0.41	1.92	5	1
1:A:91:ILE:N	1:A:91:ILE:HD12	0.41	2.30	3	1
1:A:136:GLN:HG2	1:A:138:ASP:H	0.41	1.75	4	1
1:A:43:SER:C	1:A:44:LEU:HD22	0.41	2.41	5	1
1:A:192:THR:HG22	1:A:257:ALA:HA	0.41	1.93	5	1
1:A:239:LEU:O	1:A:240:MET:C	0.41	2.63	7	1
1:A:40:TYR:HA	1:A:257:ALA:HA	0.41	1.91	14	1
1:A:169:LYS:HE2	1:A:169:LYS:N	0.41	2.30	15	1
1:A:191:TRP:HB3	1:A:210:VAL:HB	0.41	1.92	18	1
1:A:95:PHE:N	1:A:95:PHE:CD1	0.41	2.88	2	1
1:A:166:ILE:HD13	1:A:166:ILE:N	0.41	2.30	9	1
1:A:31:VAL:O	1:A:33:ILE:HD12	0.41	2.16	16	1
1:A:255:ILE:HD12	1:A:255:ILE:N	0.41	2.30	18	1
1:A:93:PHE:HB3	1:A:120:LEU:HA	0.41	1.93	4	1
1:A:97:TRP:HB2	1:A:240:MET:HE2	0.41	1.93	7	1
1:A:222:VAL:HB	1:A:225:PHE:HB3	0.41	1.92	3	1
1:A:156:LEU:N	1:A:156:LEU:HD23	0.41	2.31	15	1
1:A:64:HIS:HA	1:A:169:LYS:HG2	0.41	1.93	18	1
1:A:186:GLU:H	1:A:186:GLU:CD	0.41	2.24	4	2
1:A:33:ILE:HB	1:A:109:VAL:HG12	0.41	1.91	5	1
1:A:211:LEU:N	1:A:211:LEU:HD22	0.41	2.31	6	1
1:A:54:ALA:HA	1:A:76:LYS:HG2	0.41	1.93	3	1
1:A:189:ASP:HB3	1:A:259:PHE:HB2	0.41	1.92	4	1
1:A:33:ILE:HG23	1:A:255:ILE:HG21	0.41	1.93	6	1
1:A:188:LEU:HD23	1:A:189:ASP:N	0.41	2.31	6	1
1:A:38:ALA:HA	1:A:255:ILE:HG22	0.41	1.91	12	1
1:A:166:ILE:HG22	1:A:171:LYS:CB	0.41	2.46	13	1
1:A:140:LEU:N	1:A:140:LEU:HD23	0.41	2.31	9	1
1:A:204:GLU:H	1:A:204:GLU:CD	0.41	2.24	12	1
1:A:215:ILE:H	1:A:215:ILE:HD12	0.40	1.76	4	1
1:A:224:LYS:N	1:A:224:LYS:HD2	0.40	2.31	7	1
1:A:143:LEU:HD23	1:A:209:ILE:HB	0.40	1.92	11	1
1:A:245:ARG:HA	1:A:245:ARG:NE	0.40	2.31	2	1
3:A:302:AZM:O3	3:A:302:AZM:N2	0.40	2.52	4	3
1:A:90:LEU:HD23	1:A:120:LEU:HD21	0.40	1.92	7	1
1:A:97:TRP:H	1:A:243:ASN:HB2	0.40	1.76	11	1
1:A:120:LEU:HD23	1:A:143:LEU:HB3	0.40	1.93	12	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:162:VAL:HG11	1:A:176:THR:HG21	0.40	1.92	19	1
1:A:61:ASN:HD22	1:A:169:LYS:HA	0.40	1.76	6	1
1:A:143:LEU:HD22	1:A:143:LEU:N	0.40	2.32	6	1
1:A:191:TRP:HB2	1:A:210:VAL:HB	0.40	1.93	19	1
1:A:163:LEU:C	1:A:165:SER:N	0.40	2.79	10	1
1:A:250:LEU:HD23	1:A:250:LEU:H	0.40	1.75	13	1
1:A:223:LEU:HD12	1:A:226:ARG:HD2	0.40	1.93	16	1

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	218/260 (84%)	190±4 (87±2%)	21±3 (9±2%)	7±3 (3±1%)	4	34
All	All	4360/5200 (84%)	3799 (87%)	413 (9%)	148 (3%)	4	34

All 39 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	51	TYR	16
1	A	64	HIS	13
1	A	104	GLY	11
1	A	251	LYS	8
1	A	253	ARG	8
1	A	106	GLU	8
1	A	252	ASN	7
1	A	155	GLY	7
1	A	102	GLY	6
1	A	242	ASP	6
1	A	151	SER	5
1	A	76	LYS	4
1	A	231	ASN	4
1	A	247	ALA	4
1	A	166	ILE	4

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Mol	Chain	Res	Type	Models (Total)
1	A	139	GLY	3
1	A	152	ALA	3
1	A	82	GLY	3
1	A	150	GLY	3
1	A	187	SER	2
1	A	42	PRO	2
1	A	97	TRP	2
1	A	216	SER	2
1	A	69	GLU	2
1	A	49	VAL	1
1	A	147	LEU	1
1	A	91	ILE	1
1	A	240	MET	1
1	A	215	ILE	1
1	A	189	ASP	1
1	A	74	GLN	1
1	A	214	PRO	1
1	A	222	VAL	1
1	A	241	VAL	1
1	A	188	LEU	1
1	A	205	CYS	1
1	A	105	SER	1
1	A	47	LEU	1
1	A	83	PRO	1

6.3.2 Protein sidechains ⓘ

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	191/225 (85%)	186±2 (97±1%)	5±2 (3±1%)	42 88
All	All	3820/4500 (85%)	3723 (97%)	97 (3%)	42 88

All 37 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	119	HIS	14

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Mol	Chain	Res	Type	Models (Total)
1	A	163	LEU	11
1	A	91	ILE	6
1	A	204	GLU	5
1	A	166	ILE	5
1	A	153	LYS	4
1	A	203	LEU	4
1	A	113	LYS	4
1	A	169	LYS	4
1	A	57	LEU	3
1	A	90	LEU	3
1	A	209	ILE	3
1	A	140	LEU	3
1	A	117	GLU	2
1	A	240	MET	2
1	A	186	GLU	2
1	A	68	VAL	2
1	A	251	LYS	1
1	A	61	ASN	1
1	A	79	LEU	1
1	A	118	LEU	1
1	A	135	GLN	1
1	A	223	LEU	1
1	A	158	LYS	1
1	A	255	ILE	1
1	A	39	LYS	1
1	A	256	LYS	1
1	A	45	LYS	1
1	A	250	LEU	1
1	A	191	TRP	1
1	A	215	ILE	1
1	A	67	ASN	1
1	A	212	LYS	1
1	A	254	GLN	1
1	A	60	LEU	1
1	A	124	ASN	1
1	A	126	LYS	1

6.3.3 RNA ⓘ

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](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
3	AZM	A	302	2	13,13,13	11.78±0.01	7±0 (50±3%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
3	AZM	A	302	2	19,19,19	11.85±0.01	10±0 (52±0%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	AZM	A	302	2	-	2±0, 10,10,10	0±0,1,1,1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
3	A	302	AZM	C1-S2	27.25	2.01	1.73	15	20
3	A	302	AZM	C1-N3	24.12	1.47	1.29	10	20
3	A	302	AZM	N3-N2	15.87	1.05	1.39	12	20
3	A	302	AZM	C2-S2	13.73	1.50	1.73	5	20
3	A	302	AZM	C2-N2	5.95	1.22	1.31	6	20
3	A	302	AZM	S1-N1	3.49	1.66	1.58	4	20
3	A	302	AZM	C2-N4	2.10	1.41	1.38	1	11

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
3	A	302	AZM	C1-N3-N2	34.04	90.39	111.48	10	20
3	A	302	AZM	C1-S2-C2	32.57	70.01	85.47	16	20
3	A	302	AZM	S2-C1-N3	15.59	107.89	116.10	15	20
3	A	302	AZM	S2-C2-N4	9.58	110.89	123.72	18	20
3	A	302	AZM	C2-N2-N3	9.57	124.20	112.02	4	20
3	A	302	AZM	S2-C1-S1	4.16	127.14	121.62	12	20
3	A	302	AZM	O2-S1-O1	3.40	125.13	120.27	3	20
3	A	302	AZM	C4-C3-N4	2.89	119.94	115.27	12	20
3	A	302	AZM	S1-C1-N3	2.63	124.99	121.95	9	20
3	A	302	AZM	O2-S1-N1	2.18	105.34	108.39	1	20

There are no chirality outliers.

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

Mol	Chain	Res	Type	Atoms	Models (Total)
3	A	302	AZM	N2-C2-N4-C3	20
3	A	302	AZM	S2-C2-N4-C3	20

There are no ring outliers.

6.7 Other polymers ⓘ

There are no such molecules in this entry.

6.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

7 Chemical shift validation [i](#)

The completeness of assignment taking into account all chemical shift lists is 71% for the well-defined parts and 69% for the entire structure.

7.1 Chemical shift list 1

File name: `working_cs.cif`

Chemical shift list name: *starch_output*

7.1.1 Bookkeeping [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	2450
Number of shifts mapped to atoms	2450
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	11

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
$^{13}\text{C}_\alpha$	254	0.78 ± 0.13	Should be applied
$^{13}\text{C}_\beta$	213	0.72 ± 0.19	Should be applied
$^{13}\text{C}'$	221	0.61 ± 0.11	Should be applied
^{15}N	237	1.17 ± 0.17	Should be applied

7.1.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 71%, i.e. 2139 atoms were assigned a chemical shift out of a possible 2994. 0 out of 41 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	1029/1087 (95%)	413/442 (93%)	409/438 (93%)	207/207 (100%)
Sidechain	1110/1621 (68%)	706/1052 (67%)	404/511 (79%)	0/58 (0%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	0/286 (0%)	0/141 (0%)	0/129 (0%)	0/16 (0%)
Overall	2139/2994 (71%)	1119/1635 (68%)	813/1078 (75%)	207/281 (74%)

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 69%, i.e. 2444 atoms were assigned a chemical shift out of a possible 3538. 0 out of 43 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	1189/1288 (92%)	477/525 (91%)	475/520 (91%)	237/243 (98%)
Sidechain	1255/1881 (67%)	796/1218 (65%)	459/597 (77%)	0/66 (0%)
Aromatic	0/369 (0%)	0/182 (0%)	0/159 (0%)	0/28 (0%)
Overall	2444/3538 (69%)	1273/1925 (66%)	934/1276 (73%)	237/337 (70%)

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

7.1.4 Statistically unusual chemical shifts ⓘ

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

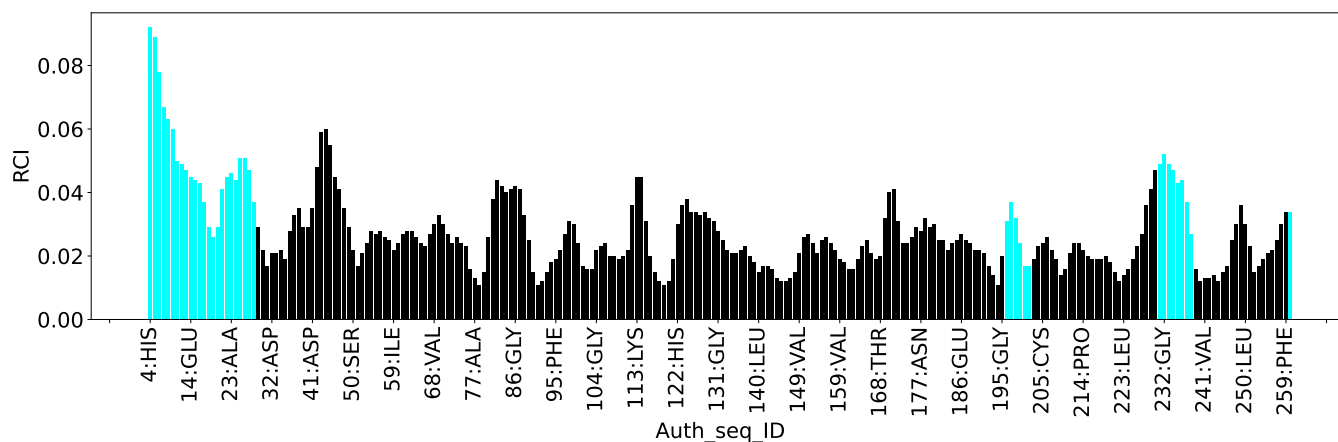
List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	27	ARG	CZ	60.10	141.81 – 177.93	-27.6
1	A	153	LYS	CD	58.40	23.50 – 34.42	27.0
1	A	198	THR	HG1	5.90	0.08 – 2.19	22.6
1	A	194	PRO	CA	45.76	55.85 – 70.84	-11.7
1	A	108	THR	CG2	29.34	16.06 – 27.03	7.1
1	A	147	LEU	CB	29.66	33.11 – 51.34	-6.9
1	A	254	GLN	CB	40.82	20.34 – 37.98	6.6
1	A	242	ASP	CB	30.78	32.98 – 48.76	-6.4
1	A	197	LEU	CG	33.20	21.37 – 32.19	5.9
1	A	118	LEU	HB2	3.37	-0.07 – 3.30	5.2
1	A	118	LEU	HB3	3.37	-0.26 – 3.31	5.2

7.1.5 Random Coil Index (RCI) plots ⓘ

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from

the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:



8 NMR restraints analysis

8.1 Conformationally restricting restraints

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

Description	Value
Total distance restraints	1823
Intra-residue ($ i-j =0$)	530
Sequential ($ i-j =1$)	712
Medium range ($ i-j >1$ and $ i-j <5$)	240
Long range ($ i-j \geq 5$)	341
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	352
Number of unmapped restraints	0
Number of restraints per residue	8.3
Number of long range restraints per residue ¹	1.3

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)	71.4	0.2
0.2-0.5 (Medium)	115.0	0.5
>0.5 (Large)	89.8	62.69

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)	0.8	2.02
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis ⓘ

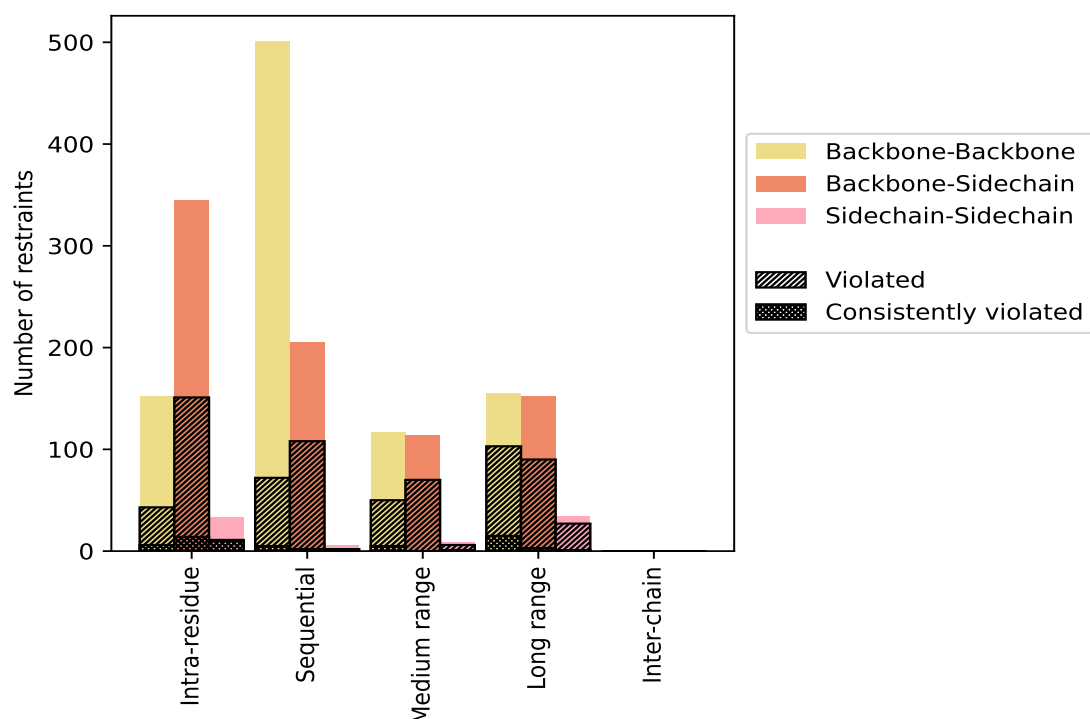
9.1 Summary of distance violations ⓘ

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

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue ($i-j =0$)	530	29.1	205	38.7	11.2	30	5.7	1.6
Backbone-Backbone	152	8.3	43	28.3	2.4	6	3.9	0.3
Backbone-Sidechain	345	18.9	151	43.8	8.3	14	4.1	0.8
Sidechain-Sidechain	33	1.8	11	33.3	0.6	10	30.3	0.5
Sequential ($i-j =1$)	712	39.1	182	25.6	10.0	7	1.0	0.4
Backbone-Backbone	501	27.5	72	14.4	3.9	5	1.0	0.3
Backbone-Sidechain	205	11.2	108	52.7	5.9	2	1.0	0.1
Sidechain-Sidechain	6	0.3	2	33.3	0.1	0	0.0	0.0
Medium range ($i-j >1$ & $i-j <5$)	240	13.2	126	52.5	6.9	6	2.5	0.3
Backbone-Backbone	117	6.4	50	42.7	2.7	5	4.3	0.3
Backbone-Sidechain	114	6.3	70	61.4	3.8	0	0.0	0.0
Sidechain-Sidechain	9	0.5	6	66.7	0.3	1	11.1	0.1
Long range ($i-j \geq 5$)	341	18.7	220	64.5	12.1	19	5.6	1.0
Backbone-Backbone	155	8.5	103	66.5	5.7	15	9.7	0.8
Backbone-Sidechain	152	8.3	90	59.2	4.9	3	2.0	0.2
Sidechain-Sidechain	34	1.9	27	79.4	1.5	1	2.9	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	0	0.0	0	0.0	0.0	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	1823	100.0	733	40.2	40.2	62	3.4	3.4
Backbone-Backbone	925	50.7	268	29.0	14.7	31	3.4	1.7
Backbone-Sidechain	816	44.8	419	51.3	23.0	19	2.3	1.0
Sidechain-Sidechain	82	4.5	46	56.1	2.5	12	14.6	0.7

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

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



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

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

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

Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
1	126	43	36	73	0	278	1.0	62.69	4.5	0.35
2	127	47	32	70	0	276	1.01	55.14	4.2	0.31
3	114	41	33	76	0	264	0.99	51.42	4.03	0.35
4	115	50	32	76	0	273	1.11	56.2	4.24	0.37
5	124	48	29	85	0	286	0.91	51.93	3.95	0.32
6	132	54	30	56	0	272	0.88	34.88	3.02	0.3
7	114	60	27	65	0	266	1.04	53.6	4.21	0.33
8	140	38	29	76	0	283	1.0	47.82	3.78	0.34
9	111	33	35	73	0	252	1.03	50.87	4.13	0.33
10	123	51	37	97	0	308	1.04	53.22	3.99	0.34

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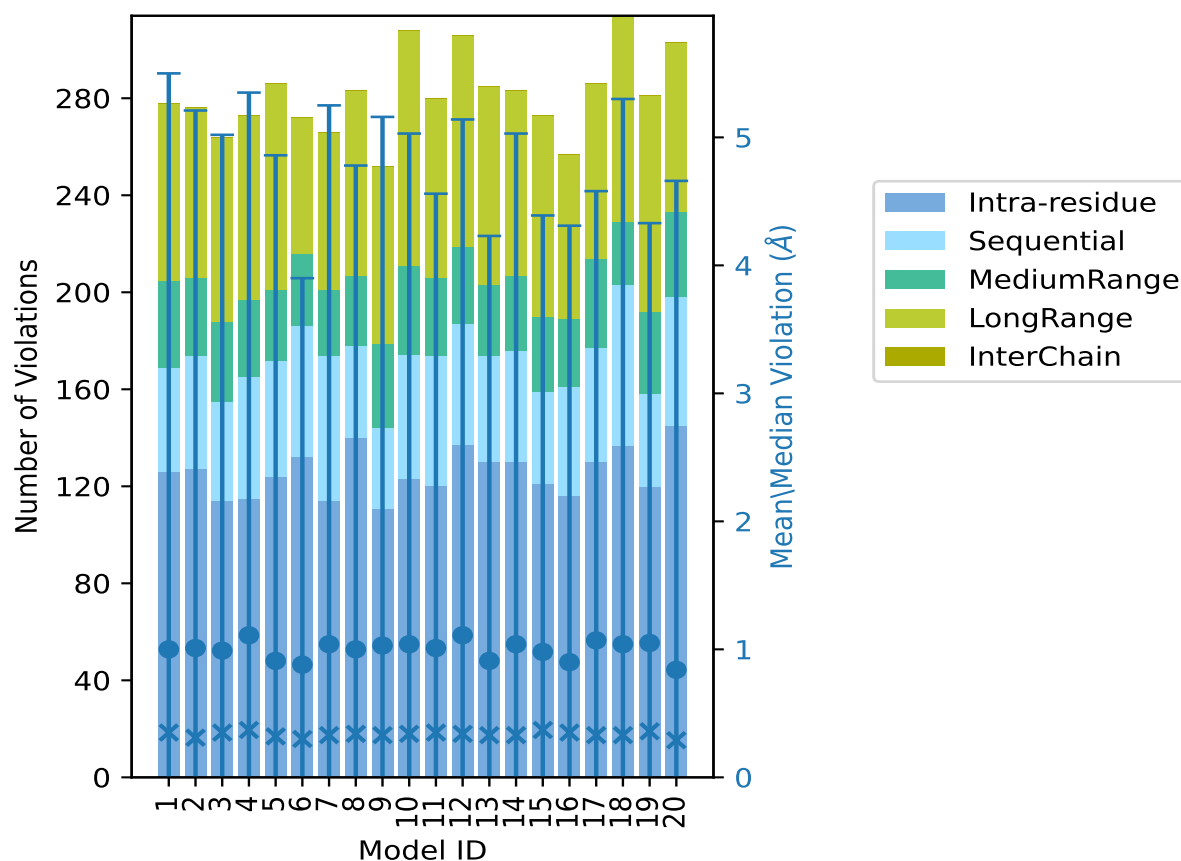
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	120	54	32	74	0	280	1.01	39.7	3.55	0.35
12	137	50	32	87	0	306	1.11	52.33	4.03	0.34
13	130	44	29	82	0	285	0.91	38.39	3.32	0.33
14	130	46	31	76	0	283	1.04	52.81	3.99	0.33
15	121	38	31	83	0	273	0.98	39.66	3.41	0.37
16	116	45	28	68	0	257	0.9	35.56	3.41	0.35
17	130	47	37	72	0	286	1.07	39.04	3.51	0.33
18	137	66	26	85	0	314	1.04	60.92	4.26	0.33
19	120	38	34	89	0	281	1.05	35.93	3.28	0.36
20	145	53	35	70	0	303	0.84	54.01	3.82	0.29

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

⁵Inter-chain restraints, ⁶Standard deviation

9.2.1 Bar graph : Distance Violation statistics for each model ⓘ



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

9.3 Distance violation statistics for the ensemble

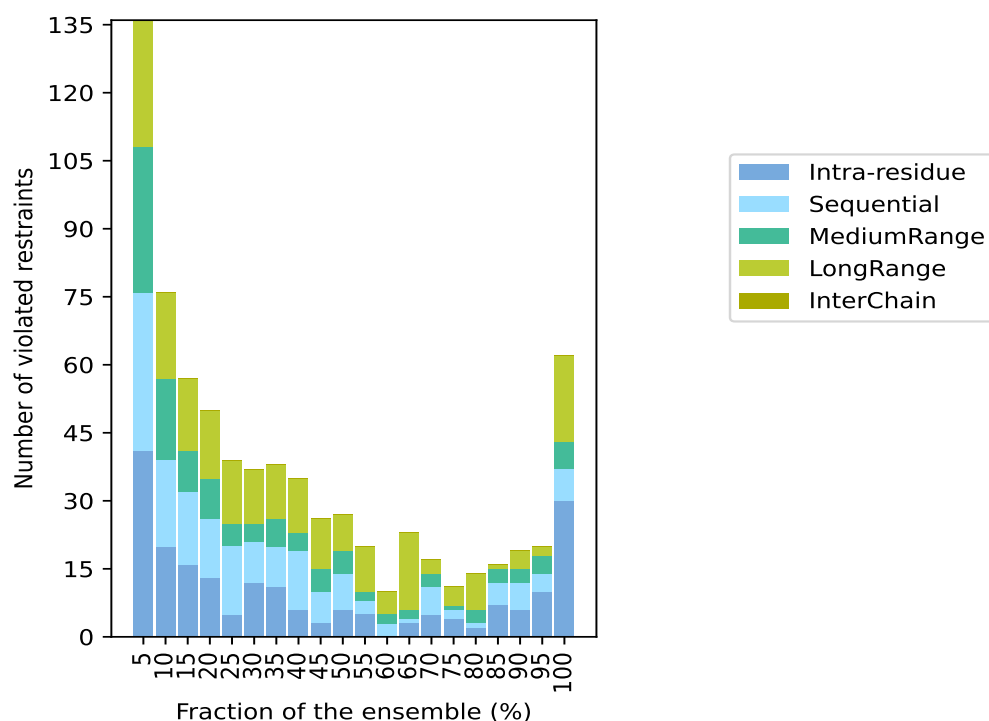
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 1090(IR:325, SQ:530, MR:114, LR:121, IC:0) restraints are 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	%
41	35	32	28	0	136	1	5.0
20	19	18	19	0	76	2	10.0
16	16	9	16	0	57	3	15.0
13	13	9	15	0	50	4	20.0
5	15	5	14	0	39	5	25.0
12	9	4	12	0	37	6	30.0
11	9	6	12	0	38	7	35.0
6	13	4	12	0	35	8	40.0
3	7	5	11	0	26	9	45.0
6	8	5	8	0	27	10	50.0
5	3	2	10	0	20	11	55.0
0	3	2	5	0	10	12	60.0
3	1	2	17	0	23	13	65.0
5	6	3	3	0	17	14	70.0
4	2	1	4	0	11	15	75.0
2	1	3	8	0	14	16	80.0
7	5	3	1	0	16	17	85.0
6	6	3	4	0	19	18	90.0
10	4	4	2	0	20	19	95.0
30	7	6	19	0	62	20	100.0

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

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

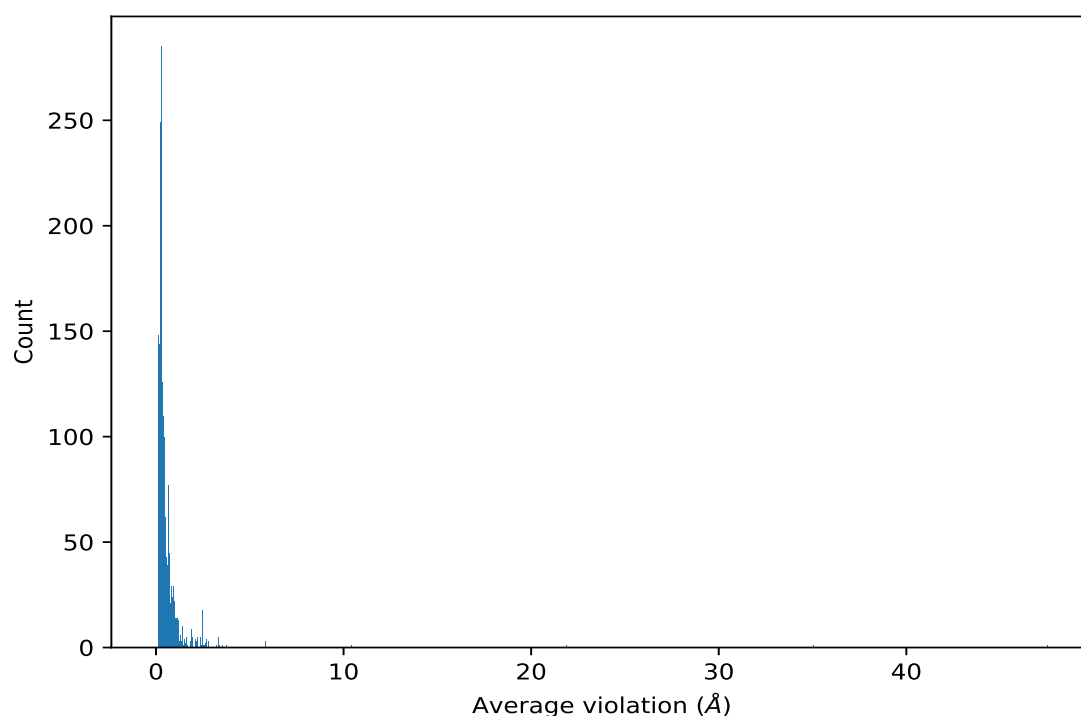
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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

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

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



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

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

Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(3,304)	1:7:A:TYR:H	1:168:A:THR:H	20	47.51	10.03	51.68
(3,303)	1:86:A:GLY:H	1:168:A:THR:H	20	35.0	1.63	35.12
(3,321)	1:127:A:TYR:H	1:184:A:LEU:H	20	21.87	1.54	21.89
(3,301)	1:63:A:GLY:H	1:227:A:LYS:H	20	10.4	0.77	10.42
(3,76)	1:227:A:LYS:H	1:240:A:MET:H	20	3.76	2.2	2.64
(3,98)	1:12:A:GLY:H	1:7:A:TYR:H	20	3.35	1.38	3.37
(3,261)	1:240:A:MET:H	1:228:A:LEU:H	20	2.8	2.26	1.78
(3,264)	1:240:A:MET:H	1:228:A:LEU:H	20	2.5	2.26	1.48
(4,61)	1:229:A:ASN:H	1:163:A:LEU:HD22	20	2.46	0.68	2.6
(4,61)	1:59:A:ILE:H	1:163:A:LEU:HD21	20	2.46	0.68	2.6
(4,61)	1:158:A:LYS:H	1:163:A:LEU:HD23	20	2.46	0.68	2.6
(4,61)	1:229:A:ASN:H	1:163:A:LEU:HD21	20	2.46	0.68	2.6
(4,61)	1:229:A:ASN:H	1:163:A:LEU:HD23	20	2.46	0.68	2.6
(4,61)	1:158:A:LYS:H	1:163:A:LEU:HD21	20	2.46	0.68	2.6
(4,61)	1:158:A:LYS:H	1:163:A:LEU:HD22	20	2.46	0.68	2.6
(4,72)	1:229:A:ASN:H	1:163:A:LEU:HD22	20	2.46	0.68	2.6

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,72)	1:59:A:ILE:H	1:163:A:LEU:HD21	20	2.46	0.68	2.6
(4,72)	1:158:A:LYS:H	1:163:A:LEU:HD23	20	2.46	0.68	2.6
(4,72)	1:229:A:ASN:H	1:163:A:LEU:HD21	20	2.46	0.68	2.6
(4,72)	1:229:A:ASN:H	1:163:A:LEU:HD23	20	2.46	0.68	2.6
(4,72)	1:158:A:LYS:H	1:163:A:LEU:HD21	20	2.46	0.68	2.6
(4,72)	1:158:A:LYS:H	1:163:A:LEU:HD22	20	2.46	0.68	2.6
(3,37)	1:206:A:VAL:H	1:140:A:LEU:H	20	1.69	0.6	1.64
(3,271)	1:140:A:LEU:H	1:206:A:VAL:H	20	1.39	0.6	1.34
(3,17)	1:169:A:LYS:H	1:63:A:GLY:H	20	1.05	0.51	0.93
(3,286)	1:70:A:PHE:H	1:92:A:GLN:H	20	1.04	0.53	0.97
(4,363)	1:251:A:LYS:HD2	1:251:A:LYS:HE3	20	0.8	0.03	0.81
(4,363)	1:158:A:LYS:HD2	1:158:A:LYS:HE3	20	0.8	0.03	0.81
(4,363)	1:169:A:LYS:HD2	1:169:A:LYS:HE2	20	0.8	0.03	0.81
(4,363)	1:76:A:LYS:HD2	1:76:A:LYS:HE3	20	0.8	0.03	0.81
(4,363)	1:39:A:LYS:HD3	1:39:A:LYS:HE2	20	0.8	0.03	0.81
(4,363)	1:76:A:LYS:HD2	1:76:A:LYS:HE2	20	0.8	0.03	0.81
(4,363)	1:169:A:LYS:HD2	1:169:A:LYS:HE3	20	0.8	0.03	0.81
(4,363)	1:80:A:LYS:HD3	1:80:A:LYS:HE2	20	0.8	0.03	0.81
(4,363)	1:167:A:LYS:HD2	1:167:A:LYS:HE3	20	0.8	0.03	0.81
(4,363)	1:169:A:LYS:HD3	1:169:A:LYS:HE2	20	0.8	0.03	0.81
(4,363)	1:158:A:LYS:HD3	1:158:A:LYS:HE2	20	0.8	0.03	0.81
(4,363)	1:251:A:LYS:HD2	1:251:A:LYS:HE2	20	0.8	0.03	0.81
(4,363)	1:167:A:LYS:HD3	1:167:A:LYS:HE2	20	0.8	0.03	0.81
(4,773)	1:135:A:GLN:H	1:135:A:GLN:HA	20	0.76	0.14	0.8
(4,773)	1:24:A:LYS:H	1:24:A:LYS:HA	20	0.76	0.14	0.8
(4,773)	1:92:A:GLN:H	1:91:A:ILE:HA	20	0.76	0.14	0.8
(4,773)	1:224:A:LYS:H	1:224:A:LYS:HA	20	0.76	0.14	0.8
(4,773)	1:222:A:VAL:H	1:222:A:VAL:HA	20	0.76	0.14	0.8
(4,293)	1:32:A:ASP:HB2	1:32:A:ASP:HA	20	0.71	0.11	0.74
(4,293)	1:66:A:PHE:HB3	1:66:A:PHE:HA	20	0.71	0.11	0.74
(4,293)	1:85:A:ASP:HB3	1:85:A:ASP:HA	20	0.71	0.11	0.74
(4,293)	1:179:A:ASP:HB3	1:179:A:ASP:HA	20	0.71	0.11	0.74
(4,293)	1:229:A:ASN:HB2	1:168:A:THR:HA	20	0.71	0.11	0.74
(4,293)	1:66:A:PHE:HB2	1:66:A:PHE:HA	20	0.71	0.11	0.74
(4,293)	1:259:A:PHE:HB2	1:259:A:PHE:HA	20	0.71	0.11	0.74
(4,293)	1:41:A:ASP:HB2	1:41:A:ASP:HA	20	0.71	0.11	0.74
(4,293)	1:174:A:ASP:HB3	1:174:A:ASP:HA	20	0.71	0.11	0.74
(4,293)	1:231:A:ASN:HB2	1:231:A:ASN:HA	20	0.71	0.11	0.74
(4,423)	1:39:A:LYS:HE2	1:39:A:LYS:HB2	20	0.71	0.17	0.6
(4,423)	1:39:A:LYS:HE2	1:39:A:LYS:HB3	20	0.71	0.17	0.6
(4,423)	1:39:A:LYS:HE3	1:39:A:LYS:HB2	20	0.71	0.17	0.6
(4,423)	1:158:A:LYS:HG2	1:158:A:LYS:HE2	20	0.71	0.17	0.6

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,423)	1:39:A:LYS:HD3	1:39:A:LYS:HE2	20	0.71	0.17	0.6
(4,423)	1:76:A:LYS:HD2	1:76:A:LYS:HE2	20	0.71	0.17	0.6
(4,423)	1:169:A:LYS:HD2	1:169:A:LYS:HE3	20	0.71	0.17	0.6
(4,423)	1:39:A:LYS:HE3	1:39:A:LYS:HB3	20	0.71	0.17	0.6
(4,423)	1:169:A:LYS:HD3	1:169:A:LYS:HE2	20	0.71	0.17	0.6
(4,423)	1:167:A:LYS:HE2	1:167:A:LYS:HB3	20	0.71	0.17	0.6
(4,423)	1:158:A:LYS:HD3	1:158:A:LYS:HE2	20	0.71	0.17	0.6
(4,423)	1:251:A:LYS:HD2	1:251:A:LYS:HE3	20	0.71	0.17	0.6
(4,423)	1:167:A:LYS:HE3	1:167:A:LYS:HB3	20	0.71	0.17	0.6
(4,389)	1:190:A:TYR:HB3	1:190:A:TYR:HA	20	0.56	0.03	0.57
(4,389)	1:127:A:TYR:HA	1:127:A:TYR:HB3	20	0.56	0.03	0.57
(4,389)	1:93:A:PHE:HB2	1:93:A:PHE:HA	20	0.56	0.03	0.57
(4,389)	1:117:A:GLU:HB2	1:117:A:GLU:HA	20	0.56	0.03	0.57
(4,389)	1:117:A:GLU:HB3	1:117:A:GLU:HA	20	0.56	0.03	0.57
(4,389)	1:174:A:ASP:HB3	1:174:A:ASP:HA	20	0.56	0.03	0.57
(4,389)	1:164:A:ASP:HB2	1:164:A:ASP:HA	20	0.56	0.03	0.57
(4,445)	1:76:A:LYS:HB3	1:76:A:LYS:HG2	20	0.54	0.04	0.56
(4,445)	1:241:A:VAL:HB	1:241:A:VAL:HG21	20	0.54	0.04	0.56
(4,445)	1:76:A:LYS:HB2	1:76:A:LYS:HD2	20	0.54	0.04	0.56
(4,445)	1:260:A:LYS:HB2	1:260:A:LYS:HG3	20	0.54	0.04	0.56
(4,445)	1:76:A:LYS:HB2	1:76:A:LYS:HG3	20	0.54	0.04	0.56
(4,445)	1:76:A:LYS:HB3	1:76:A:LYS:HG3	20	0.54	0.04	0.56
(4,445)	1:109:A:VAL:HB	1:109:A:VAL:HG21	20	0.54	0.04	0.56
(4,445)	1:76:A:LYS:HB3	1:76:A:LYS:HD3	20	0.54	0.04	0.56
(4,879)	1:247:A:ALA:H	1:247:A:ALA:HA	20	0.52	0.06	0.52
(4,879)	1:228:A:LEU:H	1:228:A:LEU:HA	20	0.52	0.06	0.52
(4,879)	1:100:A:LEU:H	1:99:A:SER:HB2	20	0.52	0.06	0.52
(4,879)	1:100:A:LEU:H	1:99:A:SER:HB3	20	0.52	0.06	0.52
(4,408)	1:134:A:VAL:HA	1:134:A:VAL:HB	20	0.5	0.13	0.55
(4,408)	1:48:A:SER:HB3	1:80:A:LYS:HD2	20	0.5	0.13	0.55
(4,408)	1:80:A:LYS:HB2	1:87:A:THR:HA	20	0.5	0.13	0.55
(4,408)	1:206:A:VAL:HB	1:206:A:VAL:HA	20	0.5	0.13	0.55
(4,408)	1:219:A:SER:HA	1:222:A:VAL:HB	20	0.5	0.13	0.55
(4,371)	1:22:A:ILE:HB	1:20:A:PHE:HB2	20	0.5	0.27	0.44
(4,371)	1:146:A:PHE:HB3	1:114:A:TYR:HB3	20	0.5	0.27	0.44
(4,371)	1:22:A:ILE:HB	1:20:A:PHE:HB3	20	0.5	0.27	0.44
(4,371)	1:146:A:PHE:HB3	1:114:A:TYR:HB2	20	0.5	0.27	0.44
(4,371)	1:146:A:PHE:HB2	1:114:A:TYR:HB3	20	0.5	0.27	0.44
(4,118)	1:165:A:SER:H	1:163:A:LEU:HA	20	0.5	0.09	0.5
(4,118)	1:164:A:ASP:H	1:163:A:LEU:HA	20	0.5	0.09	0.5
(4,414)	1:163:A:LEU:HB2	1:163:A:LEU:HA	20	0.49	0.03	0.48
(4,414)	1:260:A:LYS:HA	1:260:A:LYS:HB3	20	0.49	0.03	0.48

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,414)	1:250:A:LEU:HB3	1:250:A:LEU:HA	20	0.49	0.03	0.48
(4,414)	1:226:A:ARG:HA	1:226:A:ARG:HB2	20	0.49	0.03	0.48
(4,418)	1:163:A:LEU:HB2	1:163:A:LEU:HA	20	0.49	0.04	0.48
(4,458)	1:169:A:LYS:HB3	1:169:A:LYS:HG2	20	0.48	0.05	0.49
(4,458)	1:224:A:LYS:HB2	1:224:A:LYS:HD3	20	0.48	0.05	0.49
(4,458)	1:89:A:ARG:HB2	1:89:A:ARG:HG3	20	0.48	0.05	0.49
(4,458)	1:126:A:LYS:HB2	1:126:A:LYS:HG3	20	0.48	0.05	0.49
(4,458)	1:212:A:LYS:HB2	1:212:A:LYS:HG3	20	0.48	0.05	0.49
(4,733)	1:24:A:LYS:H	1:24:A:LYS:HA	20	0.47	0.01	0.47
(4,733)	1:92:A:GLN:H	1:92:A:GLN:HA	20	0.47	0.01	0.47
(4,733)	1:222:A:VAL:H	1:222:A:VAL:HA	20	0.47	0.01	0.47
(4,733)	1:127:A:TYR:H	1:127:A:TYR:HA	20	0.47	0.01	0.47
(4,733)	1:19:A:ASP:H	1:19:A:ASP:HA	20	0.47	0.01	0.47
(4,852)	1:160:A:VAL:H	1:160:A:VAL:HA	20	0.45	0.04	0.44
(4,380)	1:74:A:GLN:HA	1:74:A:GLN:HB3	20	0.45	0.02	0.46
(4,380)	1:122:A:HIS:HB3	1:122:A:HIS:HA	20	0.45	0.02	0.46
(4,380)	1:100:A:LEU:HB3	1:100:A:LEU:HA	20	0.45	0.02	0.46
(4,380)	1:259:A:PHE:HB2	1:259:A:PHE:HA	20	0.45	0.02	0.46
(4,380)	1:122:A:HIS:HB2	1:122:A:HIS:HA	20	0.45	0.02	0.46
(4,380)	1:245:A:ARG:HA	1:245:A:ARG:HB3	20	0.45	0.02	0.46
(4,457)	1:78:A:VAL:HB	1:78:A:VAL:HG21	20	0.44	0.07	0.46
(4,457)	1:78:A:VAL:HB	1:78:A:VAL:HG22	20	0.44	0.07	0.46
(4,457)	1:80:A:LYS:HB3	1:80:A:LYS:HG2	20	0.44	0.07	0.46
(4,457)	1:202:A:LEU:HB2	1:202:A:LEU:HD23	20	0.44	0.07	0.46
(4,457)	1:78:A:VAL:HB	1:78:A:VAL:HG23	20	0.44	0.07	0.46
(4,457)	1:78:A:VAL:HB	1:87:A:THR:HG22	20	0.44	0.07	0.46
(4,457)	1:80:A:LYS:HB2	1:80:A:LYS:HG3	20	0.44	0.07	0.46
(4,457)	1:202:A:LEU:HB3	1:202:A:LEU:HD22	20	0.44	0.07	0.46
(4,457)	1:202:A:LEU:HB3	1:202:A:LEU:HD23	20	0.44	0.07	0.46
(4,451)	1:203:A:LEU:HB3	1:203:A:LEU:HD21	20	0.42	0.04	0.44
(4,451)	1:250:A:LEU:HB3	1:250:A:LEU:HD23	20	0.42	0.04	0.44
(4,451)	1:239:A:LEU:HB3	1:239:A:LEU:HD23	20	0.42	0.04	0.44
(4,451)	1:223:A:LEU:HB2	1:223:A:LEU:HG	20	0.42	0.04	0.44
(4,451)	1:203:A:LEU:HB3	1:203:A:LEU:HD23	20	0.42	0.04	0.44
(4,451)	1:250:A:LEU:HB2	1:250:A:LEU:HD21	20	0.42	0.04	0.44
(4,451)	1:203:A:LEU:HB3	1:203:A:LEU:HD22	20	0.42	0.04	0.44
(4,451)	1:183:A:LEU:HB3	1:183:A:LEU:HD22	20	0.42	0.04	0.44
(4,451)	1:183:A:LEU:HB3	1:183:A:LEU:HD23	20	0.42	0.04	0.44
(4,451)	1:250:A:LEU:HB3	1:250:A:LEU:HD22	20	0.42	0.04	0.44
(4,451)	1:183:A:LEU:HB2	1:183:A:LEU:HD21	20	0.42	0.04	0.44
(4,451)	1:183:A:LEU:HB3	1:183:A:LEU:HD21	20	0.42	0.04	0.44
(4,451)	1:223:A:LEU:HB3	1:223:A:LEU:HD22	20	0.42	0.04	0.44

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,451)	1:239:A:LEU:HB3	1:239:A:LEU:HD22	20	0.42	0.04	0.44
(4,723)	1:24:A:LYS:H	1:24:A:LYS:HA	20	0.41	0.01	0.4
(4,723)	1:227:A:LYS:H	1:227:A:LYS:HA	20	0.41	0.01	0.4
(4,723)	1:222:A:VAL:H	1:222:A:VAL:HA	20	0.41	0.01	0.4
(4,723)	1:19:A:ASP:H	1:19:A:ASP:HA	20	0.41	0.01	0.4
(4,857)	1:241:A:VAL:H	1:241:A:VAL:HA	20	0.4	0.02	0.4
(4,857)	1:135:A:GLN:H	1:135:A:GLN:HA	20	0.4	0.02	0.4
(4,857)	1:224:A:LYS:H	1:224:A:LYS:HA	20	0.4	0.02	0.4
(4,365)	1:122:A:HIS:HB3	1:122:A:HIS:HA	20	0.4	0.02	0.4
(4,365)	1:85:A:ASP:HB3	1:85:A:ASP:HA	20	0.4	0.02	0.4
(4,365)	1:259:A:PHE:HB2	1:259:A:PHE:HA	20	0.4	0.02	0.4
(4,365)	1:122:A:HIS:HB2	1:122:A:HIS:HA	20	0.4	0.02	0.4
(4,365)	1:53:A:GLN:HB3	1:53:A:GLN:HA	20	0.4	0.02	0.4
(4,365)	1:85:A:ASP:HB2	1:85:A:ASP:HA	20	0.4	0.02	0.4
(4,365)	1:32:A:ASP:HB2	1:32:A:ASP:HA	20	0.4	0.02	0.4
(4,232)	1:34:A:ASP:H	1:34:A:ASP:HB2	20	0.4	0.08	0.42
(4,232)	1:259:A:PHE:H	1:259:A:PHE:HB3	20	0.4	0.08	0.42
(4,232)	1:66:A:PHE:H	1:66:A:PHE:HB2	20	0.4	0.08	0.42
(4,232)	1:179:A:ASP:HB3	1:182:A:GLY:H	20	0.4	0.08	0.42
(4,232)	1:169:A:LYS:H	1:229:A:ASN:HB2	20	0.4	0.08	0.42
(4,421)	1:181:A:ARG:HA	1:181:A:ARG:HB3	20	0.39	0.03	0.4
(4,421)	1:167:A:LYS:HA	1:167:A:LYS:HB2	20	0.39	0.03	0.4
(4,421)	1:147:A:LEU:HA	1:147:A:LEU:HB3	20	0.39	0.03	0.4
(4,421)	1:167:A:LYS:HA	1:167:A:LYS:HG3	20	0.39	0.03	0.4
(4,421)	1:167:A:LYS:HA	1:167:A:LYS:HB3	20	0.39	0.03	0.4
(4,421)	1:158:A:LYS:HA	1:158:A:LYS:HG3	20	0.39	0.03	0.4
(4,446)	1:22:A:ILE:HD12	1:22:A:ILE:HA	20	0.39	0.14	0.4
(4,446)	1:22:A:ILE:HD11	1:22:A:ILE:HA	20	0.39	0.14	0.4
(4,446)	1:221:A:GLN:HA	1:160:A:VAL:HG21	20	0.39	0.14	0.4
(4,446)	1:22:A:ILE:HG22	1:22:A:ILE:HA	20	0.39	0.14	0.4
(4,446)	1:37:A:THR:HA	1:37:A:THR:HG23	20	0.39	0.14	0.4
(4,446)	1:68:A:VAL:HA	1:68:A:VAL:HG22	20	0.39	0.14	0.4
(4,446)	1:22:A:ILE:HG23	1:22:A:ILE:HA	20	0.39	0.14	0.4
(4,446)	1:22:A:ILE:HG21	1:22:A:ILE:HA	20	0.39	0.14	0.4
(4,446)	1:22:A:ILE:HD13	1:22:A:ILE:HA	20	0.39	0.14	0.4
(4,446)	1:37:A:THR:HA	1:37:A:THR:HG22	20	0.39	0.14	0.4
(4,437)	1:35:A:THR:HG23	1:35:A:THR:HB	20	0.38	0.02	0.39
(4,437)	1:35:A:THR:HG22	1:35:A:THR:HB	20	0.38	0.02	0.39
(4,437)	1:199:A:THR:HB	1:199:A:THR:HG21	20	0.38	0.02	0.39
(4,437)	1:199:A:THR:HB	1:199:A:THR:HG23	20	0.38	0.02	0.39
(4,437)	1:199:A:THR:HB	1:199:A:THR:HG22	20	0.38	0.02	0.39
(4,437)	1:35:A:THR:HG21	1:35:A:THR:HB	20	0.38	0.02	0.39

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,219)	1:105:A:SER:H	1:105:A:SER:HB3	20	0.35	0.14	0.3
(4,219)	1:44:A:LEU:H	1:43:A:SER:HB3	20	0.35	0.14	0.3
(4,219)	1:134:A:VAL:H	1:134:A:VAL:HA	20	0.35	0.14	0.3
(4,219)	1:105:A:SER:H	1:105:A:SER:HB2	20	0.35	0.14	0.3
(4,238)	1:92:A:GLN:H	1:92:A:GLN:HA	20	0.34	0.01	0.34
(4,238)	1:222:A:VAL:H	1:222:A:VAL:HA	20	0.34	0.01	0.34
(4,238)	1:66:A:PHE:H	1:66:A:PHE:HA	20	0.34	0.01	0.34
(4,699)	1:176:A:THR:H	1:176:A:THR:HA	20	0.34	0.02	0.35
(4,705)	1:64:A:HIS:H	1:64:A:HIS:HA	20	0.34	0.04	0.33
(4,705)	1:29:A:SER:H	1:29:A:SER:HA	20	0.34	0.04	0.33
(4,677)	1:173:A:ALA:H	1:173:A:ALA:HA	20	0.33	0.03	0.32
(4,677)	1:39:A:LYS:H	1:39:A:LYS:HA	20	0.33	0.03	0.32
(4,396)	1:67:A:ASN:HB3	1:67:A:ASN:HA	20	0.29	0.03	0.29
(4,396)	1:153:A:LYS:HA	1:153:A:LYS:HB2	20	0.29	0.03	0.29
(4,396)	1:148:A:LYS:HB3	1:148:A:LYS:HA	20	0.29	0.03	0.29
(4,396)	1:138:A:ASP:HB3	1:138:A:ASP:HA	20	0.29	0.03	0.29
(4,396)	1:67:A:ASN:HB2	1:67:A:ASN:HA	20	0.29	0.03	0.29
(4,396)	1:153:A:LYS:HA	1:153:A:LYS:HB3	20	0.29	0.03	0.29
(4,557)	1:222:A:VAL:H	1:223:A:LEU:H	20	0.27	0.05	0.27
(4,557)	1:222:A:VAL:H	1:221:A:GLN:H	20	0.27	0.05	0.27
(4,557)	1:162:A:VAL:H	1:161:A:ASP:H	20	0.27	0.05	0.27
(4,557)	1:160:A:VAL:H	1:161:A:ASP:H	20	0.27	0.05	0.27
(4,453)	1:209:A:ILE:HG12	1:209:A:ILE:HG13	20	0.27	0.0	0.27
(4,874)	1:84:A:LEU:H	1:84:A:LEU:HA	20	0.25	0.03	0.26
(4,874)	1:247:A:ALA:H	1:247:A:ALA:HA	20	0.25	0.03	0.26
(4,435)	1:159:A:VAL:HA	1:159:A:VAL:HG23	20	0.25	0.05	0.25
(4,435)	1:35:A:THR:HG21	1:35:A:THR:HA	20	0.25	0.05	0.25
(4,435)	1:35:A:THR:HG22	1:35:A:THR:HA	20	0.25	0.05	0.25
(4,435)	1:160:A:VAL:HA	1:160:A:VAL:HG21	20	0.25	0.05	0.25
(4,435)	1:160:A:VAL:HA	1:160:A:VAL:HG23	20	0.25	0.05	0.25
(4,435)	1:159:A:VAL:HA	1:159:A:VAL:HG21	20	0.25	0.05	0.25
(4,435)	1:35:A:THR:HG23	1:35:A:THR:HA	20	0.25	0.05	0.25
(4,1109)	1:133:A:ALA:H	1:133:A:ALA:HB1	20	0.25	0.05	0.25
(4,1109)	1:133:A:ALA:H	1:133:A:ALA:HB3	20	0.25	0.05	0.25
(4,1109)	1:204:A:GLU:H	1:204:A:GLU:HB2	20	0.25	0.05	0.25
(4,1109)	1:209:A:ILE:H	1:209:A:ILE:HB	20	0.25	0.05	0.25
(4,1109)	1:133:A:ALA:H	1:133:A:ALA:HB2	20	0.25	0.05	0.25
(4,1109)	1:204:A:GLU:H	1:203:A:LEU:HB2	20	0.25	0.05	0.25
(4,1109)	1:204:A:GLU:H	1:203:A:LEU:HB3	20	0.25	0.05	0.25
(4,245)	1:228:A:LEU:H	1:228:A:LEU:HA	20	0.24	0.05	0.25
(4,1025)	1:164:A:ASP:H	1:164:A:ASP:HB2	20	0.24	0.05	0.26
(4,1025)	1:28:A:GLN:H	1:28:A:GLN:HB2	20	0.24	0.05	0.26

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,1025)	1:164:A:ASP:H	1:164:A:ASP:HB3	20	0.24	0.05	0.26
(4,324)	1:67:A:ASN:HB3	1:67:A:ASN:HA	20	0.23	0.03	0.24
(4,324)	1:230:A:PHE:HB2	1:230:A:PHE:HA	20	0.23	0.03	0.24
(4,324)	1:60:A:LEU:HB2	1:60:A:LEU:HA	20	0.23	0.03	0.24
(4,324)	1:230:A:PHE:HB3	1:230:A:PHE:HA	20	0.23	0.03	0.24
(4,324)	1:178:A:PHE:HB2	1:178:A:PHE:HA	20	0.23	0.03	0.24
(4,324)	1:60:A:LEU:HB3	1:60:A:LEU:HA	20	0.23	0.03	0.24
(4,762)	1:93:A:PHE:H	1:93:A:PHE:HA	20	0.21	0.02	0.2
(4,369)	1:94:A:HIS:HB3	1:94:A:HIS:HA	20	0.21	0.02	0.21
(4,369)	1:231:A:ASN:HB2	1:231:A:ASN:HA	20	0.21	0.02	0.21
(4,369)	1:20:A:PHE:HB3	1:20:A:PHE:HA	20	0.21	0.02	0.21
(4,369)	1:94:A:HIS:HB2	1:94:A:HIS:HA	20	0.21	0.02	0.21
(4,431)	1:192:A:THR:HG23	1:192:A:THR:HB	20	0.2	0.03	0.21
(4,431)	1:192:A:THR:HG22	1:192:A:THR:HB	20	0.2	0.03	0.21
(4,431)	1:55:A:THR:HB	1:55:A:THR:HG22	20	0.2	0.03	0.21
(4,431)	1:192:A:THR:HG21	1:192:A:THR:HB	20	0.2	0.03	0.21
(4,431)	1:55:A:THR:HB	1:55:A:THR:HG23	20	0.2	0.03	0.21
(4,431)	1:55:A:THR:HB	1:55:A:THR:HG21	20	0.2	0.03	0.21
(4,431)	1:108:A:THR:HG23	1:108:A:THR:HB	20	0.2	0.03	0.21
(4,431)	1:108:A:THR:HG21	1:108:A:THR:HB	20	0.2	0.03	0.21
(4,702)	1:121:A:VAL:H	1:121:A:VAL:HA	20	0.18	0.01	0.19
(4,736)	1:43:A:SER:H	1:43:A:SER:HA	20	0.17	0.03	0.18
(4,736)	1:218:A:SER:H	1:218:A:SER:HA	20	0.17	0.03	0.18
(4,736)	1:127:A:TYR:H	1:127:A:TYR:HA	20	0.17	0.03	0.18
(1,69)	1:87:A:THR:HB	1:87:A:THR:HG23	20	0.16	0.02	0.17
(1,69)	1:87:A:THR:HB	1:87:A:THR:HG21	20	0.16	0.02	0.17
(1,69)	1:87:A:THR:HB	1:87:A:THR:HG22	20	0.16	0.02	0.17
(4,867)	1:157:A:GLN:H	1:157:A:GLN:HA	20	0.15	0.02	0.14
(4,867)	1:189:A:ASP:H	1:189:A:ASP:HA	20	0.15	0.02	0.14
(4,683)	1:138:A:ASP:H	1:138:A:ASP:HA	20	0.14	0.02	0.14
(4,683)	1:92:A:GLN:H	1:92:A:GLN:HA	20	0.14	0.02	0.14
(4,62)	1:211:A:LEU:H	1:210:A:VAL:HA	20	0.13	0.01	0.13
(4,62)	1:257:A:ALA:H	1:256:A:LYS:HA	20	0.13	0.01	0.13
(4,62)	1:238:A:GLU:H	1:237:A:GLU:HA	20	0.13	0.01	0.13
(4,62)	1:254:A:GLN:HA	1:255:A:ILE:H	20	0.13	0.01	0.13
(4,62)	1:85:A:ASP:H	1:84:A:LEU:HA	20	0.13	0.01	0.13
(4,62)	1:55:A:THR:H	1:54:A:ALA:HA	20	0.13	0.01	0.13
(4,62)	1:240:A:MET:H	1:239:A:LEU:HA	20	0.13	0.01	0.13
(4,62)	1:123:A:TRP:H	1:122:A:HIS:HA	20	0.13	0.01	0.13
(4,62)	1:101:A:ASP:H	1:100:A:LEU:HA	20	0.13	0.01	0.13
(3,181)	1:153:A:LYS:H	1:157:A:GLN:H	19	2.43	0.55	2.31
(3,282)	1:202:A:LEU:H	1:199:A:THR:H	19	0.98	0.77	0.66

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(3,306)	1:156:A:LEU:H	1:159:A:VAL:H	19	0.7	0.23	0.68
(3,305)	1:166:A:ILE:H	1:168:A:THR:H	19	0.57	0.13	0.58
(4,411)	1:212:A:LYS:HA	1:212:A:LYS:HB2	19	0.53	0.1	0.57
(4,411)	1:250:A:LEU:HB2	1:250:A:LEU:HA	19	0.53	0.1	0.57
(4,411)	1:23:A:ALA:HB3	1:17:A:HIS:HA	19	0.53	0.1	0.57
(4,411)	1:23:A:ALA:HB2	1:17:A:HIS:HA	19	0.53	0.1	0.57
(4,411)	1:26:A:GLU:HA	1:26:A:GLU:HB3	19	0.53	0.1	0.57
(4,411)	1:26:A:GLU:HA	1:26:A:GLU:HB2	19	0.53	0.1	0.57
(4,411)	1:23:A:ALA:HB1	1:17:A:HIS:HA	19	0.53	0.1	0.57
(4,411)	1:250:A:LEU:HB3	1:250:A:LEU:HA	19	0.53	0.1	0.57
(4,411)	1:226:A:ARG:HA	1:226:A:ARG:HB2	19	0.53	0.1	0.57
(4,411)	1:226:A:ARG:HA	1:226:A:ARG:HB3	19	0.53	0.1	0.57
(4,411)	1:233:A:GLU:HA	1:233:A:GLU:HB2	19	0.53	0.1	0.57
(4,412)	1:233:A:GLU:HA	1:233:A:GLU:HB2	19	0.53	0.1	0.57
(4,412)	1:250:A:LEU:HB2	1:250:A:LEU:HA	19	0.53	0.1	0.57
(4,412)	1:23:A:ALA:HB3	1:17:A:HIS:HA	19	0.53	0.1	0.57
(4,412)	1:23:A:ALA:HB2	1:17:A:HIS:HA	19	0.53	0.1	0.57
(4,412)	1:26:A:GLU:HA	1:26:A:GLU:HB3	19	0.53	0.1	0.57
(4,412)	1:26:A:GLU:HA	1:26:A:GLU:HB2	19	0.53	0.1	0.57
(4,412)	1:23:A:ALA:HB1	1:17:A:HIS:HA	19	0.53	0.1	0.57
(4,412)	1:250:A:LEU:HB3	1:250:A:LEU:HA	19	0.53	0.1	0.57
(4,412)	1:226:A:ARG:HA	1:226:A:ARG:HB2	19	0.53	0.1	0.57
(4,412)	1:226:A:ARG:HA	1:226:A:ARG:HB3	19	0.53	0.1	0.57
(4,132)	1:93:A:PHE:H	1:93:A:PHE:HB3	19	0.48	0.08	0.51
(4,370)	1:251:A:LYS:HG2	1:251:A:LYS:HE2	19	0.43	0.08	0.46
(4,370)	1:45:A:LYS:HG2	1:45:A:LYS:HE2	19	0.43	0.08	0.46
(4,370)	1:251:A:LYS:HG3	1:251:A:LYS:HE2	19	0.43	0.08	0.46
(4,370)	1:132:A:LYS:HG3	1:132:A:LYS:HE3	19	0.43	0.08	0.46
(4,370)	1:132:A:LYS:HG2	1:129:A:ASP:HB2	19	0.43	0.08	0.46
(4,370)	1:45:A:LYS:HG3	1:45:A:LYS:HE3	19	0.43	0.08	0.46
(4,370)	1:111:A:LYS:HG3	1:111:A:LYS:HE2	19	0.43	0.08	0.46
(4,370)	1:158:A:LYS:HG2	1:158:A:LYS:HE3	19	0.43	0.08	0.46
(4,370)	1:158:A:LYS:HG2	1:158:A:LYS:HE2	19	0.43	0.08	0.46
(4,370)	1:132:A:LYS:HG2	1:132:A:LYS:HE2	19	0.43	0.08	0.46
(4,370)	1:45:A:LYS:HG3	1:45:A:LYS:HE2	19	0.43	0.08	0.46
(4,370)	1:158:A:LYS:HG3	1:158:A:LYS:HE2	19	0.43	0.08	0.46
(4,1227)	1:23:A:ALA:H	1:23:A:ALA:HB3	19	0.37	0.12	0.38
(4,1227)	1:23:A:ALA:H	1:23:A:ALA:HB2	19	0.37	0.12	0.38
(4,1227)	1:90:A:LEU:H	1:90:A:LEU:HB2	19	0.37	0.12	0.38
(4,1227)	1:23:A:ALA:H	1:23:A:ALA:HB1	19	0.37	0.12	0.38
(4,1227)	1:91:A:ILE:H	1:91:A:ILE:HG13	19	0.37	0.12	0.38
(4,1227)	1:91:A:ILE:H	1:91:A:ILE:HG12	19	0.37	0.12	0.38

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,1227)	1:257:A:ALA:H	1:257:A:ALA:HB3	19	0.37	0.12	0.38
(4,1227)	1:65:A:ALA:H	1:65:A:ALA:HB3	19	0.37	0.12	0.38
(4,1227)	1:23:A:ALA:H	1:22:A:ILE:HG22	19	0.37	0.12	0.38
(4,1227)	1:90:A:LEU:H	1:90:A:LEU:HB3	19	0.37	0.12	0.38
(4,112)	1:73:A:SER:H	1:73:A:SER:HA	19	0.33	0.03	0.32
(4,112)	1:147:A:LEU:H	1:147:A:LEU:HA	19	0.33	0.03	0.32
(4,112)	1:181:A:ARG:H	1:181:A:ARG:HA	19	0.33	0.03	0.32
(4,789)	1:9:A:LYS:H	1:8:A:GLY:HA2	19	0.31	0.14	0.31
(4,789)	1:106:A:GLU:H	1:105:A:SER:HA	19	0.31	0.14	0.31
(4,789)	1:147:A:LEU:H	1:147:A:LEU:HA	19	0.31	0.14	0.31
(4,789)	1:152:A:ALA:H	1:152:A:ALA:HA	19	0.31	0.14	0.31
(4,789)	1:36:A:HIS:H	1:35:A:THR:HB	19	0.31	0.14	0.31
(4,789)	1:178:A:PHE:H	1:177:A:ASN:HA	19	0.31	0.14	0.31
(4,789)	1:7:A:TYR:H	1:7:A:TYR:HA	19	0.31	0.14	0.31
(4,1075)	1:28:A:GLN:H	1:28:A:GLN:HB3	19	0.3	0.05	0.33
(4,1075)	1:164:A:ASP:H	1:164:A:ASP:HB2	19	0.3	0.05	0.33
(4,1075)	1:28:A:GLN:H	1:28:A:GLN:HB2	19	0.3	0.05	0.33
(4,1075)	1:164:A:ASP:H	1:164:A:ASP:HB3	19	0.3	0.05	0.33
(4,1075)	1:164:A:ASP:H	1:163:A:LEU:HG	19	0.3	0.05	0.33
(4,433)	1:173:A:ALA:HA	1:173:A:ALA:HB3	19	0.3	0.01	0.3
(4,433)	1:173:A:ALA:HA	1:173:A:ALA:HB1	19	0.3	0.01	0.3
(4,433)	1:173:A:ALA:HA	1:173:A:ALA:HB2	19	0.3	0.01	0.3
(4,1051)	1:170:A:GLY:H	1:61:A:ASN:HB3	19	0.3	0.12	0.31
(4,1051)	1:57:A:LEU:H	1:57:A:LEU:HB2	19	0.3	0.12	0.31
(4,1051)	1:26:A:GLU:H	1:26:A:GLU:HG2	19	0.3	0.12	0.31
(4,1051)	1:57:A:LEU:H	1:57:A:LEU:HB3	19	0.3	0.12	0.31
(4,1051)	1:26:A:GLU:H	1:26:A:GLU:HB3	19	0.3	0.12	0.31
(4,1051)	1:26:A:GLU:H	1:26:A:GLU:HB2	19	0.3	0.12	0.31
(4,1051)	1:26:A:GLU:H	1:26:A:GLU:HG3	19	0.3	0.12	0.31
(4,224)	1:159:A:VAL:H	1:159:A:VAL:HA	19	0.3	0.13	0.33
(4,224)	1:44:A:LEU:H	1:43:A:SER:HB3	19	0.3	0.13	0.33
(4,224)	1:160:A:VAL:H	1:160:A:VAL:HA	19	0.3	0.13	0.33
(4,224)	1:259:A:PHE:H	1:258:A:SER:HB3	19	0.3	0.13	0.33
(4,1102)	1:26:A:GLU:H	1:26:A:GLU:HB3	19	0.29	0.14	0.27
(4,1102)	1:140:A:LEU:H	1:140:A:LEU:HG	19	0.29	0.14	0.27
(4,1102)	1:140:A:LEU:H	1:140:A:LEU:HB3	19	0.29	0.14	0.27
(4,1102)	1:26:A:GLU:H	1:26:A:GLU:HB2	19	0.29	0.14	0.27
(4,1102)	1:170:A:GLY:H	1:169:A:LYS:HB3	19	0.29	0.14	0.27
(4,1102)	1:219:A:SER:H	1:149:A:VAL:HB	19	0.29	0.14	0.27
(4,1102)	1:57:A:LEU:H	1:57:A:LEU:HG	19	0.29	0.14	0.27
(4,1114)	1:171:A:LYS:H	1:171:A:LYS:HB2	19	0.27	0.07	0.27
(4,1114)	1:84:A:LEU:H	1:84:A:LEU:HB3	19	0.27	0.07	0.27

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,1114)	1:22:A:ILE:H	1:22:A:ILE:HB	19	0.27	0.07	0.27
(4,1114)	1:223:A:LEU:H	1:223:A:LEU:HB2	19	0.27	0.07	0.27
(4,1114)	1:84:A:LEU:H	1:84:A:LEU:HB2	19	0.27	0.07	0.27
(4,572)	1:227:A:LYS:H	1:228:A:LEU:H	19	0.23	0.05	0.23
(4,572)	1:159:A:VAL:H	1:160:A:VAL:H	19	0.23	0.05	0.23
(4,572)	1:222:A:VAL:H	1:221:A:GLN:H	19	0.23	0.05	0.23
(4,572)	1:135:A:GLN:H	1:136:A:GLN:H	19	0.23	0.05	0.23
(4,205)	1:54:A:ALA:H	1:54:A:ALA:HB1	19	0.23	0.05	0.24
(4,205)	1:54:A:ALA:H	1:54:A:ALA:HB3	19	0.23	0.05	0.24
(4,205)	1:66:A:PHE:H	1:65:A:ALA:HB1	19	0.23	0.05	0.24
(4,205)	1:66:A:PHE:H	1:65:A:ALA:HB3	19	0.23	0.05	0.24
(4,205)	1:54:A:ALA:H	1:54:A:ALA:HB2	19	0.23	0.05	0.24
(4,205)	1:66:A:PHE:H	1:65:A:ALA:HB2	19	0.23	0.05	0.24
(4,205)	1:115:A:ALA:H	1:115:A:ALA:HB3	19	0.23	0.05	0.24
(4,207)	1:159:A:VAL:H	1:159:A:VAL:HA	19	0.18	0.03	0.18
(4,180)	1:98:A:GLY:H	1:240:A:MET:HA	18	1.91	0.72	2.04
(4,180)	1:228:A:LEU:H	1:240:A:MET:HA	18	1.91	0.72	2.04
(4,180)	1:66:A:PHE:H	1:240:A:MET:HA	18	1.91	0.72	2.04
(4,180)	1:169:A:LYS:H	1:240:A:MET:HA	18	1.91	0.72	2.04
(3,237)	1:189:A:ASP:H	1:212:A:LYS:H	18	1.53	0.86	1.31
(3,110)	1:12:A:GLY:H	1:8:A:GLY:H	18	1.28	0.69	1.27
(3,314)	1:229:A:ASN:H	1:168:A:THR:H	18	1.27	0.89	1.1
(3,115)	1:12:A:GLY:H	1:8:A:GLY:H	18	1.18	0.69	1.16
(3,114)	1:241:A:VAL:H	1:243:A:ASN:H	18	0.73	0.46	0.66
(4,165)	1:260:A:LYS:H	1:260:A:LYS:HA	18	0.37	0.04	0.36
(4,165)	1:166:A:ILE:H	1:163:A:LEU:HA	18	0.37	0.04	0.36
(4,182)	1:166:A:ILE:H	1:163:A:LEU:HA	18	0.36	0.13	0.39
(4,182)	1:165:A:SER:H	1:163:A:LEU:HA	18	0.36	0.13	0.39
(4,379)	1:260:A:LYS:HG2	1:260:A:LYS:HE2	18	0.35	0.08	0.34
(4,379)	1:260:A:LYS:HG3	1:260:A:LYS:HE3	18	0.35	0.08	0.34
(4,379)	1:260:A:LYS:HG3	1:260:A:LYS:HE2	18	0.35	0.08	0.34
(4,379)	1:260:A:LYS:HG2	1:260:A:LYS:HE3	18	0.35	0.08	0.34
(4,379)	1:169:A:LYS:HG3	1:61:A:ASN:HB2	18	0.35	0.08	0.34
(4,379)	1:140:A:LEU:HD21	1:130:A:PHE:HB2	18	0.35	0.08	0.34
(4,202)	1:34:A:ASP:H	1:34:A:ASP:HB2	18	0.32	0.07	0.32
(4,202)	1:37:A:THR:H	1:34:A:ASP:HB2	18	0.32	0.07	0.32
(4,202)	1:162:A:VAL:H	1:161:A:ASP:HB3	18	0.32	0.07	0.32
(4,202)	1:162:A:VAL:H	1:161:A:ASP:HB2	18	0.32	0.07	0.32
(4,202)	1:37:A:THR:H	1:34:A:ASP:HB3	18	0.32	0.07	0.32
(4,167)	1:32:A:ASP:H	1:32:A:ASP:HB3	18	0.3	0.05	0.31
(4,167)	1:179:A:ASP:H	1:179:A:ASP:HB2	18	0.3	0.05	0.31
(4,167)	1:32:A:ASP:H	1:32:A:ASP:HB2	18	0.3	0.05	0.31

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,1055)	1:18:A:LYS:H	1:18:A:LYS:HB2	18	0.28	0.05	0.28
(4,1055)	1:100:A:LEU:H	1:100:A:LEU:HB2	18	0.28	0.05	0.28
(4,1055)	1:100:A:LEU:H	1:100:A:LEU:HB3	18	0.28	0.05	0.28
(4,1055)	1:253:A:ARG:H	1:253:A:ARG:HB3	18	0.28	0.05	0.28
(4,1055)	1:253:A:ARG:H	1:253:A:ARG:HB2	18	0.28	0.05	0.28
(4,449)	1:159:A:VAL:HA	1:159:A:VAL:HG23	18	0.26	0.05	0.28
(4,449)	1:160:A:VAL:HA	1:160:A:VAL:HG21	18	0.26	0.05	0.28
(4,449)	1:160:A:VAL:HA	1:160:A:VAL:HG22	18	0.26	0.05	0.28
(4,449)	1:160:A:VAL:HA	1:160:A:VAL:HG23	18	0.26	0.05	0.28
(4,449)	1:159:A:VAL:HA	1:159:A:VAL:HG21	18	0.26	0.05	0.28
(4,449)	1:159:A:VAL:HA	1:159:A:VAL:HG22	18	0.26	0.05	0.28
(4,758)	1:252:A:ASN:H	1:252:A:ASN:HA	18	0.25	0.05	0.24
(4,758)	1:259:A:PHE:H	1:259:A:PHE:HA	18	0.25	0.05	0.24
(4,758)	1:252:A:ASN:H	1:251:A:LYS:HA	18	0.25	0.05	0.24
(4,817)	1:103:A:GLN:H	1:103:A:GLN:HA	18	0.22	0.06	0.24
(4,817)	1:205:A:CYS:H	1:205:A:CYS:HA	18	0.22	0.06	0.24
(4,817)	1:205:A:CYS:H	1:204:A:GLU:HA	18	0.22	0.06	0.24
(4,993)	1:205:A:CYS:H	1:205:A:CYS:HB2	18	0.22	0.05	0.22
(4,993)	1:127:A:TYR:H	1:127:A:TYR:HB2	18	0.22	0.05	0.22
(4,993)	1:162:A:VAL:H	1:161:A:ASP:HB2	18	0.22	0.05	0.22
(4,993)	1:159:A:VAL:H	1:159:A:VAL:HB	18	0.22	0.05	0.22
(4,993)	1:127:A:TYR:H	1:127:A:TYR:HB3	18	0.22	0.05	0.22
(4,835)	1:229:A:ASN:H	1:228:A:LEU:HA	18	0.21	0.05	0.22
(4,835)	1:106:A:GLU:H	1:105:A:SER:HA	18	0.21	0.05	0.22
(4,835)	1:147:A:LEU:H	1:147:A:LEU:HA	18	0.21	0.05	0.22
(4,835)	1:152:A:ALA:H	1:152:A:ALA:HA	18	0.21	0.05	0.22
(4,835)	1:9:A:LYS:H	1:8:A:GLY:HA2	18	0.21	0.05	0.22
(4,835)	1:152:A:ALA:H	1:151:A:SER:HB2	18	0.21	0.05	0.22
(4,835)	1:152:A:ALA:H	1:218:A:SER:HB2	18	0.21	0.05	0.22
(4,450)	1:147:A:LEU:HA	1:147:A:LEU:HD22	18	0.17	0.08	0.15
(4,450)	1:147:A:LEU:HA	1:147:A:LEU:HD21	18	0.17	0.08	0.15
(4,450)	1:147:A:LEU:HA	1:147:A:LEU:HD23	18	0.17	0.08	0.15
(4,157)	1:207:A:THR:H	1:207:A:THR:HB	18	0.16	0.09	0.14
(4,157)	1:36:A:HIS:H	1:35:A:THR:HB	18	0.16	0.09	0.14
(1,123)	1:63:A:GLY:H	1:169:A:LYS:HG3	17	1.33	0.98	1.71
(1,123)	1:63:A:GLY:H	1:169:A:LYS:HG2	17	1.33	0.98	1.71
(3,234)	1:8:A:GLY:H	1:12:A:GLY:H	17	1.14	0.67	1.09
(4,386)	1:232:A:GLY:HA2	1:229:A:ASN:HB2	17	0.69	0.32	0.79
(4,386)	1:26:A:GLU:HG3	1:25:A:GLY:HA3	17	0.69	0.32	0.79
(4,386)	1:26:A:GLU:HG2	1:25:A:GLY:HA3	17	0.69	0.32	0.79
(4,386)	1:26:A:GLU:HG3	1:25:A:GLY:HA2	17	0.69	0.32	0.79
(4,386)	1:235:A:GLU:HG2	1:234:A:GLY:HA3	17	0.69	0.32	0.79

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,386)	1:25:A:GLY:HA2	1:28:A:GLN:HB2	17	0.69	0.32	0.79
(4,386)	1:235:A:GLU:HG3	1:234:A:GLY:HA3	17	0.69	0.32	0.79
(4,386)	1:26:A:GLU:HG2	1:25:A:GLY:HA2	17	0.69	0.32	0.79
(4,386)	1:235:A:GLU:HG3	1:232:A:GLY:HA3	17	0.69	0.32	0.79
(4,1021)	1:112:A:LYS:H	1:110:A:ASP:HB3	17	0.66	0.21	0.61
(4,1021)	1:112:A:LYS:H	1:110:A:ASP:HB2	17	0.66	0.21	0.61
(4,1021)	1:133:A:ALA:H	1:127:A:TYR:HB3	17	0.66	0.21	0.61
(4,1021)	1:260:A:LYS:H	1:259:A:PHE:HB3	17	0.66	0.21	0.61
(4,1021)	1:193:A:TYR:H	1:208:A:TRP:HB2	17	0.66	0.21	0.61
(4,1021)	1:193:A:TYR:H	1:208:A:TRP:HB3	17	0.66	0.21	0.61
(4,1021)	1:112:A:LYS:H	1:111:A:LYS:HB2	17	0.66	0.21	0.61
(4,1022)	1:112:A:LYS:H	1:110:A:ASP:HB3	17	0.62	0.25	0.62
(4,1022)	1:112:A:LYS:H	1:110:A:ASP:HB2	17	0.62	0.25	0.62
(4,1022)	1:133:A:ALA:H	1:127:A:TYR:HB3	17	0.62	0.25	0.62
(4,1022)	1:260:A:LYS:H	1:259:A:PHE:HB3	17	0.62	0.25	0.62
(4,1022)	1:193:A:TYR:H	1:208:A:TRP:HB2	17	0.62	0.25	0.62
(4,1022)	1:76:A:LYS:H	1:74:A:GLN:HB2	17	0.62	0.25	0.62
(4,1022)	1:193:A:TYR:H	1:208:A:TRP:HB3	17	0.62	0.25	0.62
(4,1022)	1:112:A:LYS:H	1:111:A:LYS:HB2	17	0.62	0.25	0.62
(4,828)	1:135:A:GLN:H	1:135:A:GLN:HA	17	0.42	0.04	0.42
(4,828)	1:205:A:CYS:H	1:205:A:CYS:HA	17	0.42	0.04	0.42
(4,828)	1:160:A:VAL:H	1:160:A:VAL:HA	17	0.42	0.04	0.42
(4,828)	1:227:A:LYS:H	1:227:A:LYS:HA	17	0.42	0.04	0.42
(4,828)	1:24:A:LYS:H	1:24:A:LYS:HA	17	0.42	0.04	0.42
(4,828)	1:205:A:CYS:H	1:204:A:GLU:HA	17	0.42	0.04	0.42
(4,836)	1:129:A:ASP:H	1:128:A:GLY:HA3	17	0.36	0.17	0.31
(4,836)	1:166:A:ILE:H	1:165:A:SER:HB3	17	0.36	0.17	0.31
(4,836)	1:28:A:GLN:H	1:28:A:GLN:HA	17	0.36	0.17	0.31
(4,836)	1:166:A:ILE:H	1:163:A:LEU:HA	17	0.36	0.17	0.31
(4,836)	1:166:A:ILE:H	1:165:A:SER:HB2	17	0.36	0.17	0.31
(4,805)	1:129:A:ASP:H	1:128:A:GLY:HA3	17	0.34	0.17	0.29
(4,805)	1:166:A:ILE:H	1:165:A:SER:HB3	17	0.34	0.17	0.29
(4,805)	1:28:A:GLN:H	1:28:A:GLN:HA	17	0.34	0.17	0.29
(4,805)	1:166:A:ILE:H	1:165:A:SER:HB2	17	0.34	0.17	0.29
(4,1228)	1:152:A:ALA:H	1:152:A:ALA:HB2	17	0.34	0.21	0.28
(4,1228)	1:152:A:ALA:H	1:152:A:ALA:HB1	17	0.34	0.21	0.28
(4,1228)	1:147:A:LEU:H	1:147:A:LEU:HG	17	0.34	0.21	0.28
(4,1228)	1:152:A:ALA:H	1:152:A:ALA:HB3	17	0.34	0.21	0.28
(4,1228)	1:84:A:LEU:H	1:84:A:LEU:HG	17	0.34	0.21	0.28
(4,189)	1:34:A:ASP:H	1:34:A:ASP:HB2	17	0.33	0.07	0.33
(4,189)	1:37:A:THR:H	1:34:A:ASP:HB2	17	0.33	0.07	0.33
(4,189)	1:162:A:VAL:H	1:161:A:ASP:HB3	17	0.33	0.07	0.33

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,189)	1:162:A:VAL:H	1:161:A:ASP:HB2	17	0.33	0.07	0.33
(4,189)	1:37:A:THR:H	1:34:A:ASP:HB3	17	0.33	0.07	0.33
(4,189)	1:74:A:GLN:H	1:76:A:LYS:HE3	17	0.33	0.07	0.33
(4,1128)	1:251:A:LYS:H	1:250:A:LEU:HB3	17	0.31	0.17	0.24
(4,1128)	1:251:A:LYS:H	1:250:A:LEU:HB2	17	0.31	0.17	0.24
(4,1128)	1:251:A:LYS:H	1:251:A:LYS:HG2	17	0.31	0.17	0.24
(4,1139)	1:256:A:LYS:H	1:256:A:LYS:HG3	17	0.26	0.08	0.28
(4,1139)	1:239:A:LEU:H	1:239:A:LEU:HB2	17	0.26	0.08	0.28
(4,1139)	1:211:A:LEU:H	1:211:A:LEU:HB2	17	0.26	0.08	0.28
(4,1139)	1:141:A:ALA:H	1:140:A:LEU:HB2	17	0.26	0.08	0.28
(4,1139)	1:209:A:ILE:H	1:209:A:ILE:HG12	17	0.26	0.08	0.28
(4,1139)	1:256:A:LYS:H	1:256:A:LYS:HB2	17	0.26	0.08	0.28
(4,1139)	1:256:A:LYS:H	1:256:A:LYS:HG2	17	0.26	0.08	0.28
(4,742)	1:71:A:ASP:H	1:70:A:PHE:HA	17	0.22	0.09	0.23
(4,742)	1:197:A:LEU:H	1:197:A:LEU:HA	17	0.22	0.09	0.23
(4,742)	1:197:A:LEU:H	1:196:A:SER:HA	17	0.22	0.09	0.23
(4,119)	1:231:A:ASN:H	1:229:A:ASN:HB3	17	0.2	0.04	0.21
(4,119)	1:232:A:GLY:H	1:231:A:ASN:HB3	17	0.2	0.04	0.21
(4,119)	1:179:A:ASP:H	1:179:A:ASP:HB2	17	0.2	0.04	0.21
(4,119)	1:36:A:HIS:H	1:34:A:ASP:HB3	17	0.2	0.04	0.21
(4,119)	1:161:A:ASP:H	1:161:A:ASP:HB3	17	0.2	0.04	0.21
(4,119)	1:70:A:PHE:H	1:70:A:PHE:HB2	17	0.2	0.04	0.21
(4,119)	1:229:A:ASN:H	1:229:A:ASN:HB2	17	0.2	0.04	0.21
(4,119)	1:174:A:ASP:H	1:174:A:ASP:HB2	17	0.2	0.04	0.21
(4,119)	1:32:A:ASP:H	1:32:A:ASP:HB3	17	0.2	0.04	0.21
(4,208)	1:45:A:LYS:H	1:44:A:LEU:HA	17	0.2	0.07	0.17
(4,191)	1:159:A:VAL:H	1:159:A:VAL:HG22	17	0.17	0.02	0.17
(4,191)	1:160:A:VAL:H	1:160:A:VAL:HG23	17	0.17	0.02	0.17
(4,191)	1:160:A:VAL:H	1:160:A:VAL:HG21	17	0.17	0.02	0.17
(4,191)	1:159:A:VAL:H	1:159:A:VAL:HG23	17	0.17	0.02	0.17
(4,191)	1:160:A:VAL:H	1:160:A:VAL:HG22	17	0.17	0.02	0.17
(4,191)	1:126:A:LYS:H	1:126:A:LYS:HG3	17	0.17	0.02	0.17
(4,191)	1:159:A:VAL:H	1:159:A:VAL:HG21	17	0.17	0.02	0.17
(3,302)	1:229:A:ASN:H	1:168:A:THR:H	16	1.2	0.85	0.98
(3,252)	1:196:A:SER:H	1:206:A:VAL:H	16	1.06	0.71	1.06
(3,290)	1:196:A:SER:H	1:206:A:VAL:H	16	1.06	0.71	1.06
(3,158)	1:57:A:LEU:H	1:70:A:PHE:H	16	0.87	0.98	0.59
(4,1006)	1:79:A:LEU:H	1:88:A:TYR:HB2	16	0.66	0.34	0.62
(4,1006)	1:141:A:ALA:H	1:122:A:HIS:HB2	16	0.66	0.34	0.62
(4,1006)	1:141:A:ALA:H	1:122:A:HIS:HB3	16	0.66	0.34	0.62
(4,1006)	1:141:A:ALA:H	1:123:A:TRP:HB3	16	0.66	0.34	0.62
(4,666)	1:226:A:ARG:H	1:222:A:VAL:H	16	0.58	0.27	0.46

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,1316)	1:165:A:SER:H	1:166:A:ILE:HD13	16	0.48	0.35	0.42
(4,1316)	1:165:A:SER:H	1:166:A:ILE:HD11	16	0.48	0.35	0.42
(4,1316)	1:165:A:SER:H	1:166:A:ILE:HD12	16	0.48	0.35	0.42
(4,1316)	1:205:A:CYS:H	1:206:A:VAL:HG21	16	0.48	0.35	0.42
(4,1316)	1:205:A:CYS:H	1:206:A:VAL:HG23	16	0.48	0.35	0.42
(4,1316)	1:205:A:CYS:H	1:206:A:VAL:HG22	16	0.48	0.35	0.42
(1,106)	1:226:A:ARG:H	1:225:A:PHE:HB2	16	0.44	0.22	0.36
(1,106)	1:226:A:ARG:H	1:225:A:PHE:HB3	16	0.44	0.22	0.36
(4,204)	1:253:A:ARG:H	1:253:A:ARG:HG2	16	0.39	0.38	0.28
(4,204)	1:100:A:LEU:H	1:100:A:LEU:HG	16	0.39	0.38	0.28
(4,204)	1:183:A:LEU:H	1:183:A:LEU:HG	16	0.39	0.38	0.28
(4,204)	1:253:A:ARG:H	1:253:A:ARG:HG3	16	0.39	0.38	0.28
(4,204)	1:34:A:ASP:H	1:255:A:ILE:HG13	16	0.39	0.38	0.28
(4,406)	1:133:A:ALA:HB1	1:130:A:PHE:HA	16	0.35	0.16	0.42
(4,406)	1:133:A:ALA:HB3	1:130:A:PHE:HA	16	0.35	0.16	0.42
(4,406)	1:149:A:VAL:HA	1:149:A:VAL:HB	16	0.35	0.16	0.42
(4,406)	1:133:A:ALA:HB2	1:130:A:PHE:HA	16	0.35	0.16	0.42
(1,105)	1:6:A:GLY:H	1:6:A:GLY:HA3	16	0.3	0.06	0.32
(4,903)	1:49:A:VAL:H	1:49:A:VAL:HA	16	0.3	0.09	0.35
(4,903)	1:49:A:VAL:H	1:48:A:SER:HB2	16	0.3	0.09	0.35
(4,903)	1:49:A:VAL:H	1:48:A:SER:HB3	16	0.3	0.09	0.35
(4,862)	1:78:A:VAL:H	1:50:A:SER:HB2	16	0.26	0.09	0.27
(4,862)	1:78:A:VAL:H	1:50:A:SER:HB3	16	0.26	0.09	0.27
(4,862)	1:43:A:SER:H	1:43:A:SER:HB3	16	0.26	0.09	0.27
(4,862)	1:218:A:SER:H	1:218:A:SER:HB2	16	0.26	0.09	0.27
(4,862)	1:218:A:SER:H	1:218:A:SER:HB3	16	0.26	0.09	0.27
(4,177)	1:41:A:ASP:H	1:41:A:ASP:HA	16	0.13	0.02	0.14
(4,177)	1:179:A:ASP:H	1:179:A:ASP:HA	16	0.13	0.02	0.14
(4,519)	1:50:A:SER:H	1:49:A:VAL:H	15	0.96	0.42	0.88
(4,519)	1:152:A:ALA:H	1:151:A:SER:H	15	0.96	0.42	0.88
(4,519)	1:230:A:PHE:H	1:239:A:LEU:H	15	0.96	0.42	0.88
(3,173)	1:57:A:LEU:H	1:175:A:PHE:H	15	0.7	0.72	0.45
(4,540)	1:89:A:ARG:H	1:123:A:TRP:H	15	0.65	0.3	0.71
(4,540)	1:97:A:TRP:H	1:98:A:GLY:H	15	0.65	0.3	0.71
(4,540)	1:243:A:ASN:H	1:97:A:TRP:H	15	0.65	0.3	0.71
(4,540)	1:71:A:ASP:H	1:55:A:THR:H	15	0.65	0.3	0.71
(4,540)	1:147:A:LEU:H	1:148:A:LYS:H	15	0.65	0.3	0.71
(4,1321)	1:205:A:CYS:H	1:206:A:VAL:HG23	15	0.6	0.35	0.6
(4,1321)	1:205:A:CYS:H	1:203:A:LEU:HD22	15	0.6	0.35	0.6
(4,1321)	1:205:A:CYS:H	1:206:A:VAL:HG21	15	0.6	0.35	0.6
(4,1321)	1:205:A:CYS:H	1:206:A:VAL:HG22	15	0.6	0.35	0.6
(4,801)	1:166:A:ILE:H	1:165:A:SER:HB3	15	0.35	0.17	0.29

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,801)	1:156:A:LEU:H	1:156:A:LEU:HA	15	0.35	0.17	0.29
(4,801)	1:28:A:GLN:H	1:28:A:GLN:HA	15	0.35	0.17	0.29
(4,801)	1:129:A:ASP:H	1:128:A:GLY:HA3	15	0.35	0.17	0.29
(4,801)	1:166:A:ILE:H	1:165:A:SER:HB2	15	0.35	0.17	0.29
(4,1223)	1:152:A:ALA:H	1:152:A:ALA:HB2	15	0.28	0.11	0.26
(4,1223)	1:152:A:ALA:H	1:152:A:ALA:HB1	15	0.28	0.11	0.26
(4,1223)	1:147:A:LEU:H	1:147:A:LEU:HG	15	0.28	0.11	0.26
(4,1223)	1:152:A:ALA:H	1:152:A:ALA:HB3	15	0.28	0.11	0.26
(4,1223)	1:124:A:ASN:H	1:133:A:ALA:HB2	15	0.28	0.11	0.26
(4,1223)	1:124:A:ASN:H	1:133:A:ALA:HB3	15	0.28	0.11	0.26
(4,1261)	1:152:A:ALA:H	1:152:A:ALA:HB2	15	0.27	0.19	0.21
(4,1261)	1:152:A:ALA:H	1:152:A:ALA:HB1	15	0.27	0.19	0.21
(4,1261)	1:152:A:ALA:H	1:152:A:ALA:HB3	15	0.27	0.19	0.21
(4,1261)	1:216:A:SER:H	1:147:A:LEU:HD22	15	0.27	0.19	0.21
(4,1172)	1:256:A:LYS:H	1:256:A:LYS:HG3	15	0.26	0.08	0.24
(4,1172)	1:239:A:LEU:H	1:239:A:LEU:HB2	15	0.26	0.08	0.24
(4,1172)	1:141:A:ALA:H	1:140:A:LEU:HB2	15	0.26	0.08	0.24
(4,1172)	1:256:A:LYS:H	1:256:A:LYS:HG2	15	0.26	0.08	0.24
(4,1172)	1:209:A:ILE:H	1:209:A:ILE:HG12	15	0.26	0.08	0.24
(4,1172)	1:239:A:LEU:H	1:239:A:LEU:HB3	15	0.26	0.08	0.24
(4,1172)	1:256:A:LYS:H	1:256:A:LYS:HB2	15	0.26	0.08	0.24
(4,1162)	1:133:A:ALA:H	1:133:A:ALA:HB3	15	0.22	0.04	0.22
(4,1162)	1:204:A:GLU:H	1:204:A:GLU:HB2	15	0.22	0.04	0.22
(4,1162)	1:209:A:ILE:H	1:209:A:ILE:HB	15	0.22	0.04	0.22
(4,1162)	1:47:A:LEU:H	1:47:A:LEU:HB3	15	0.22	0.04	0.22
(4,1162)	1:133:A:ALA:H	1:133:A:ALA:HB2	15	0.22	0.04	0.22
(4,1162)	1:133:A:ALA:H	1:133:A:ALA:HB1	15	0.22	0.04	0.22
(4,1162)	1:209:A:ILE:H	1:209:A:ILE:HG12	15	0.22	0.04	0.22
(4,870)	1:258:A:SER:H	1:258:A:SER:HB3	15	0.19	0.11	0.16
(4,870)	1:78:A:VAL:H	1:50:A:SER:HB2	15	0.19	0.11	0.16
(4,870)	1:258:A:SER:H	1:258:A:SER:HA	15	0.19	0.11	0.16
(4,870)	1:78:A:VAL:H	1:50:A:SER:HB3	15	0.19	0.11	0.16
(4,173)	1:157:A:GLN:H	1:157:A:GLN:HA	15	0.12	0.02	0.11
(4,173)	1:167:A:LYS:H	1:167:A:LYS:HA	15	0.12	0.02	0.11
(4,156)	1:223:A:LEU:H	1:224:A:LYS:HG2	14	0.95	0.17	0.98
(4,156)	1:157:A:GLN:H	1:158:A:LYS:HG3	14	0.95	0.17	0.98
(4,156)	1:157:A:GLN:H	1:158:A:LYS:HG2	14	0.95	0.17	0.98
(4,156)	1:164:A:ASP:H	1:163:A:LEU:HG	14	0.95	0.17	0.98
(4,150)	1:223:A:LEU:H	1:224:A:LYS:HG2	14	0.95	0.19	0.98
(4,150)	1:164:A:ASP:H	1:163:A:LEU:HG	14	0.95	0.19	0.98
(4,469)	1:140:A:LEU:HB3	1:134:A:VAL:HG23	14	0.7	0.31	0.64
(4,469)	1:140:A:LEU:HB2	1:91:A:ILE:HD12	14	0.7	0.31	0.64

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,469)	1:140:A:LEU:HB3	1:134:A:VAL:HG22	14	0.7	0.31	0.64
(4,469)	1:140:A:LEU:HB3	1:134:A:VAL:HG21	14	0.7	0.31	0.64
(4,469)	1:140:A:LEU:HB2	1:91:A:ILE:HD13	14	0.7	0.31	0.64
(4,469)	1:140:A:LEU:HB3	1:91:A:ILE:HD12	14	0.7	0.31	0.64
(4,469)	1:140:A:LEU:HB3	1:91:A:ILE:HD13	14	0.7	0.31	0.64
(4,454)	1:87:A:THR:HA	1:87:A:THR:HG22	14	0.48	0.13	0.5
(4,454)	1:49:A:VAL:HG22	1:49:A:VAL:HA	14	0.48	0.13	0.5
(4,454)	1:50:A:SER:HB3	1:78:A:VAL:HG23	14	0.48	0.13	0.5
(4,454)	1:37:A:THR:HA	1:37:A:THR:HG22	14	0.48	0.13	0.5
(4,454)	1:37:A:THR:HA	1:37:A:THR:HG23	14	0.48	0.13	0.5
(4,454)	1:50:A:SER:HB2	1:78:A:VAL:HG21	14	0.48	0.13	0.5
(4,454)	1:87:A:THR:HA	1:87:A:THR:HG21	14	0.48	0.13	0.5
(4,454)	1:49:A:VAL:HG21	1:49:A:VAL:HA	14	0.48	0.13	0.5
(4,454)	1:49:A:VAL:HG23	1:49:A:VAL:HA	14	0.48	0.13	0.5
(4,374)	1:127:A:TYR:HB3	1:133:A:ALA:HA	14	0.44	0.2	0.46
(4,374)	1:124:A:ASN:HB2	1:133:A:ALA:HA	14	0.44	0.2	0.46
(4,374)	1:124:A:ASN:HB3	1:133:A:ALA:HA	14	0.44	0.2	0.46
(1,132)	1:135:A:GLN:H	1:134:A:VAL:HG22	14	0.42	0.38	0.34
(1,132)	1:135:A:GLN:H	1:134:A:VAL:HG21	14	0.42	0.38	0.34
(1,132)	1:135:A:GLN:H	1:134:A:VAL:HG23	14	0.42	0.38	0.34
(4,1243)	1:163:A:LEU:H	1:162:A:VAL:HG23	14	0.38	0.15	0.46
(4,1243)	1:247:A:ALA:H	1:247:A:ALA:HB3	14	0.38	0.15	0.46
(4,1243)	1:247:A:ALA:H	1:247:A:ALA:HB2	14	0.38	0.15	0.46
(4,1243)	1:163:A:LEU:H	1:162:A:VAL:HG22	14	0.38	0.15	0.46
(4,1243)	1:163:A:LEU:H	1:162:A:VAL:HG21	14	0.38	0.15	0.46
(4,1243)	1:247:A:ALA:H	1:247:A:ALA:HB1	14	0.38	0.15	0.46
(4,998)	1:175:A:PHE:H	1:175:A:PHE:HB3	14	0.33	0.1	0.34
(4,998)	1:175:A:PHE:H	1:174:A:ASP:HB3	14	0.33	0.1	0.34
(4,998)	1:175:A:PHE:H	1:174:A:ASP:HB2	14	0.33	0.1	0.34
(4,998)	1:112:A:LYS:H	1:110:A:ASP:HB3	14	0.33	0.1	0.34
(4,998)	1:175:A:PHE:H	1:175:A:PHE:HB2	14	0.33	0.1	0.34
(4,962)	1:129:A:ASP:H	1:129:A:ASP:HB2	14	0.31	0.12	0.26
(4,962)	1:166:A:ILE:H	1:163:A:LEU:HA	14	0.31	0.12	0.26
(4,962)	1:129:A:ASP:H	1:127:A:TYR:HB2	14	0.31	0.12	0.26
(4,962)	1:129:A:ASP:H	1:127:A:TYR:HB3	14	0.31	0.12	0.26
(4,962)	1:129:A:ASP:H	1:129:A:ASP:HB3	14	0.31	0.12	0.26
(4,460)	1:224:A:LYS:HA	1:224:A:LYS:HD2	14	0.29	0.13	0.28
(4,460)	1:169:A:LYS:HA	1:169:A:LYS:HG3	14	0.29	0.13	0.28
(4,460)	1:99:A:SER:HA	1:241:A:VAL:HG23	14	0.29	0.13	0.28
(4,460)	1:223:A:LEU:HA	1:226:A:ARG:HG2	14	0.29	0.13	0.28
(4,460)	1:223:A:LEU:HA	1:223:A:LEU:HD23	14	0.29	0.13	0.28
(4,460)	1:169:A:LYS:HA	1:169:A:LYS:HG2	14	0.29	0.13	0.28

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,460)	1:224:A:LYS:HA	1:227:A:LYS:HG2	14	0.29	0.13	0.28
(4,460)	1:224:A:LYS:HA	1:224:A:LYS:HD3	14	0.29	0.13	0.28
(4,1083)	1:248:A:GLN:H	1:248:A:GLN:HG2	14	0.24	0.08	0.22
(4,1083)	1:237:A:GLU:H	1:237:A:GLU:HG2	14	0.24	0.08	0.22
(4,1083)	1:237:A:GLU:H	1:237:A:GLU:HG3	14	0.24	0.08	0.22
(4,1083)	1:69:A:GLU:H	1:69:A:GLU:HB2	14	0.24	0.08	0.22
(4,1083)	1:248:A:GLN:H	1:248:A:GLN:HG3	14	0.24	0.08	0.22
(4,1083)	1:233:A:GLU:H	1:233:A:GLU:HG2	14	0.24	0.08	0.22
(4,1083)	1:237:A:GLU:H	1:237:A:GLU:HB2	14	0.24	0.08	0.22
(4,330)	1:247:A:ALA:HB2	1:247:A:ALA:HA	14	0.22	0.03	0.22
(4,330)	1:152:A:ALA:HB2	1:152:A:ALA:HA	14	0.22	0.03	0.22
(4,330)	1:192:A:THR:HG21	1:192:A:THR:HB	14	0.22	0.03	0.22
(4,330)	1:23:A:ALA:HB2	1:17:A:HIS:HA	14	0.22	0.03	0.22
(4,330)	1:152:A:ALA:HB3	1:152:A:ALA:HA	14	0.22	0.03	0.22
(4,330)	1:192:A:THR:HG23	1:192:A:THR:HB	14	0.22	0.03	0.22
(4,330)	1:152:A:ALA:HB1	1:152:A:ALA:HA	14	0.22	0.03	0.22
(4,330)	1:247:A:ALA:HB3	1:247:A:ALA:HA	14	0.22	0.03	0.22
(4,330)	1:54:A:ALA:HB3	1:54:A:ALA:HA	14	0.22	0.03	0.22
(4,438)	1:133:A:ALA:HB3	1:130:A:PHE:HA	14	0.21	0.09	0.19
(4,438)	1:255:A:ILE:HA	1:255:A:ILE:HG13	14	0.21	0.09	0.19
(4,438)	1:255:A:ILE:HG21	1:255:A:ILE:HA	14	0.21	0.09	0.19
(4,438)	1:255:A:ILE:HD11	1:255:A:ILE:HA	14	0.21	0.09	0.19
(4,438)	1:255:A:ILE:HD13	1:255:A:ILE:HA	14	0.21	0.09	0.19
(4,438)	1:133:A:ALA:HB2	1:130:A:PHE:HA	14	0.21	0.09	0.19
(4,438)	1:133:A:ALA:HB1	1:130:A:PHE:HA	14	0.21	0.09	0.19
(4,438)	1:22:A:ILE:HD13	1:22:A:ILE:HA	14	0.21	0.09	0.19
(4,438)	1:22:A:ILE:HD12	1:22:A:ILE:HA	14	0.21	0.09	0.19
(4,438)	1:22:A:ILE:HG22	1:22:A:ILE:HA	14	0.21	0.09	0.19
(4,404)	1:49:A:VAL:HA	1:49:A:VAL:HB	14	0.2	0.05	0.21
(4,404)	1:160:A:VAL:HA	1:160:A:VAL:HB	14	0.2	0.05	0.21
(4,404)	1:134:A:VAL:HA	1:134:A:VAL:HB	14	0.2	0.05	0.21
(4,404)	1:189:A:ASP:HB3	1:258:A:SER:HB3	14	0.2	0.05	0.21
(4,404)	1:163:A:LEU:HB3	1:160:A:VAL:HA	14	0.2	0.05	0.21
(4,404)	1:159:A:VAL:HA	1:159:A:VAL:HB	14	0.2	0.05	0.21
(4,845)	1:151:A:SER:H	1:151:A:SER:HA	14	0.2	0.14	0.12
(4,845)	1:151:A:SER:H	1:150:A:GLY:HA2	14	0.2	0.14	0.12
(4,845)	1:151:A:SER:H	1:151:A:SER:HB2	14	0.2	0.14	0.12
(4,845)	1:151:A:SER:H	1:150:A:GLY:HA3	14	0.2	0.14	0.12
(4,283)	1:95:A:PHE:HB2	1:95:A:PHE:HA	14	0.15	0.01	0.15
(4,981)	1:164:A:ASP:H	1:164:A:ASP:HB2	14	0.14	0.01	0.14
(4,981)	1:164:A:ASP:H	1:164:A:ASP:HB3	14	0.14	0.01	0.14
(3,60)	1:29:A:SER:H	1:196:A:SER:H	13	2.23	1.96	1.36

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(3,251)	1:242:A:ASP:H	1:100:A:LEU:H	13	2.21	1.13	2.2
(3,320)	1:97:A:TRP:H	1:244:A:TRP:H	13	1.28	1.15	0.74
(4,273)	1:113:A:LYS:HD3	1:244:A:TRP:HA	13	1.17	1.1	0.79
(4,273)	1:113:A:LYS:HD2	1:244:A:TRP:HA	13	1.17	1.1	0.79
(4,273)	1:226:A:ARG:HG2	1:97:A:TRP:HA	13	1.17	1.1	0.79
(4,273)	1:113:A:LYS:HD3	1:97:A:TRP:HA	13	1.17	1.1	0.79
(3,255)	1:147:A:LEU:H	1:115:A:ALA:H	13	1.05	0.74	0.97
(3,120)	1:248:A:GLN:H	1:32:A:ASP:H	13	1.05	1.05	0.63
(3,210)	1:197:A:LEU:H	1:205:A:CYS:H	13	1.02	0.93	0.67
(4,466)	1:243:A:ASN:HB2	1:241:A:VAL:HG21	13	0.93	0.36	1.08
(4,466)	1:106:A:GLU:HG3	1:113:A:LYS:HD3	13	0.93	0.36	1.08
(4,466)	1:243:A:ASN:HB2	1:241:A:VAL:HG22	13	0.93	0.36	1.08
(4,466)	1:33:A:ILE:HD12	1:106:A:GLU:HG2	13	0.93	0.36	1.08
(4,466)	1:33:A:ILE:HD13	1:106:A:GLU:HG2	13	0.93	0.36	1.08
(4,466)	1:243:A:ASN:HB2	1:241:A:VAL:HG23	13	0.93	0.36	1.08
(3,166)	1:205:A:CYS:H	1:197:A:LEU:H	13	0.92	0.93	0.57
(1,78)	1:117:A:GLU:H	1:96:A:HIS:H	13	0.66	0.67	0.37
(3,9)	1:256:A:LYS:H	1:192:A:THR:H	13	0.63	0.35	0.45
(3,79)	1:192:A:THR:H	1:256:A:LYS:H	13	0.63	0.35	0.45
(4,1129)	1:195:A:GLY:H	1:207:A:THR:HG23	13	0.62	0.46	0.47
(4,1129)	1:195:A:GLY:H	1:207:A:THR:HG22	13	0.62	0.46	0.47
(4,1129)	1:195:A:GLY:H	1:207:A:THR:HG21	13	0.62	0.46	0.47
(4,1129)	1:111:A:LYS:H	1:33:A:ILE:HB	13	0.62	0.46	0.47
(4,1129)	1:111:A:LYS:H	1:108:A:THR:HG22	13	0.62	0.46	0.47
(4,1129)	1:195:A:GLY:H	1:204:A:GLU:HG3	13	0.62	0.46	0.47
(4,1129)	1:111:A:LYS:H	1:108:A:THR:HG21	13	0.62	0.46	0.47
(4,463)	1:174:A:ASP:HA	1:176:A:THR:HG22	13	0.6	0.31	0.56
(4,463)	1:174:A:ASP:HA	1:176:A:THR:HG21	13	0.6	0.31	0.56
(4,463)	1:174:A:ASP:HA	1:176:A:THR:HG23	13	0.6	0.31	0.56
(4,463)	1:174:A:ASP:HA	1:57:A:LEU:HD21	13	0.6	0.31	0.56
(4,215)	1:242:A:ASP:H	1:241:A:VAL:HA	13	0.4	0.14	0.43
(4,1214)	1:89:A:ARG:H	1:89:A:ARG:HB3	13	0.39	0.09	0.41
(4,1214)	1:89:A:ARG:H	1:89:A:ARG:HB2	13	0.39	0.09	0.41
(4,1214)	1:233:A:GLU:H	1:233:A:GLU:HB3	13	0.39	0.09	0.41
(4,1214)	1:80:A:LYS:H	1:80:A:LYS:HG2	13	0.39	0.09	0.41
(4,1214)	1:89:A:ARG:H	1:89:A:ARG:HG3	13	0.39	0.09	0.41
(4,1214)	1:89:A:ARG:H	1:89:A:ARG:HG2	13	0.39	0.09	0.41
(4,1214)	1:248:A:GLN:H	1:247:A:ALA:HB3	13	0.39	0.09	0.41
(4,1214)	1:248:A:GLN:H	1:247:A:ALA:HB1	13	0.39	0.09	0.41
(4,1214)	1:50:A:SER:H	1:78:A:VAL:HG23	13	0.39	0.09	0.41
(4,948)	1:166:A:ILE:H	1:163:A:LEU:HA	13	0.36	0.14	0.34
(4,948)	1:129:A:ASP:H	1:127:A:TYR:HB2	13	0.36	0.14	0.34

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,948)	1:64:A:HIS:H	1:62:A:ASN:HB2	13	0.36	0.14	0.34
(4,948)	1:64:A:HIS:H	1:63:A:GLY:HA3	13	0.36	0.14	0.34
(4,87)	1:234:A:GLY:H	1:233:A:GLU:HB2	13	0.29	0.06	0.29
(4,87)	1:256:A:LYS:H	1:256:A:LYS:HD2	13	0.29	0.06	0.29
(4,87)	1:55:A:THR:H	1:76:A:LYS:HD3	13	0.29	0.06	0.29
(4,87)	1:233:A:GLU:H	1:233:A:GLU:HB2	13	0.29	0.06	0.29
(4,87)	1:181:A:ARG:H	1:181:A:ARG:HB2	13	0.29	0.06	0.29
(4,87)	1:233:A:GLU:H	1:233:A:GLU:HB3	13	0.29	0.06	0.29
(4,87)	1:91:A:ILE:H	1:91:A:ILE:HG13	13	0.29	0.06	0.29
(4,405)	1:49:A:VAL:HA	1:49:A:VAL:HB	13	0.28	0.21	0.2
(4,405)	1:160:A:VAL:HA	1:160:A:VAL:HB	13	0.28	0.21	0.2
(4,405)	1:159:A:VAL:HA	1:159:A:VAL:HB	13	0.28	0.21	0.2
(4,405)	1:189:A:ASP:HB3	1:258:A:SER:HB3	13	0.28	0.21	0.2
(4,933)	1:129:A:ASP:H	1:129:A:ASP:HA	13	0.26	0.04	0.28
(4,933)	1:166:A:ILE:H	1:163:A:LEU:HA	13	0.26	0.04	0.28
(4,933)	1:129:A:ASP:H	1:127:A:TYR:HB2	13	0.26	0.04	0.28
(4,722)	1:57:A:LEU:H	1:56:A:SER:HA	13	0.21	0.12	0.18
(4,722)	1:64:A:HIS:H	1:64:A:HIS:HA	13	0.21	0.12	0.18
(4,327)	1:106:A:GLU:HG3	1:106:A:GLU:HA	13	0.15	0.03	0.15
(4,327)	1:148:A:LYS:HB3	1:148:A:LYS:HA	13	0.15	0.03	0.15
(4,327)	1:117:A:GLU:HB2	1:117:A:GLU:HA	13	0.15	0.03	0.15
(4,327)	1:117:A:GLU:HB3	1:117:A:GLU:HA	13	0.15	0.03	0.15
(4,327)	1:221:A:GLN:HG2	1:221:A:GLN:HA	13	0.15	0.03	0.15
(4,200)	1:108:A:THR:H	1:107:A:HIS:HA	13	0.15	0.03	0.16
(3,59)	1:197:A:LEU:H	1:204:A:GLU:H	12	1.23	1.35	0.62
(3,150)	1:206:A:VAL:H	1:197:A:LEU:H	12	1.07	0.76	0.92
(1,64)	1:60:A:LEU:HB2	1:172:A:SER:HB2	12	0.97	0.82	0.48
(1,64)	1:60:A:LEU:HB3	1:172:A:SER:HB3	12	0.97	0.82	0.48
(1,64)	1:60:A:LEU:HB2	1:172:A:SER:HB3	12	0.97	0.82	0.48
(4,1253)	1:198:A:THR:H	1:199:A:THR:HG21	12	0.96	0.33	0.97
(4,1253)	1:198:A:THR:H	1:199:A:THR:HG23	12	0.96	0.33	0.97
(4,1253)	1:99:A:SER:H	1:241:A:VAL:HG21	12	0.96	0.33	0.97
(4,1253)	1:198:A:THR:H	1:199:A:THR:HG22	12	0.96	0.33	0.97
(4,266)	1:244:A:TRP:H	1:241:A:VAL:HG21	12	0.95	0.45	1.0
(4,266)	1:166:A:ILE:HD13	1:168:A:THR:H	12	0.95	0.45	1.0
(4,266)	1:166:A:ILE:HD11	1:168:A:THR:H	12	0.95	0.45	1.0
(4,266)	1:244:A:TRP:H	1:241:A:VAL:HG22	12	0.95	0.45	1.0
(4,266)	1:244:A:TRP:H	1:241:A:VAL:HG23	12	0.95	0.45	1.0
(4,266)	1:166:A:ILE:HD12	1:168:A:THR:H	12	0.95	0.45	1.0
(1,100)	1:245:A:ARG:H	1:244:A:TRP:HB2	12	0.8	0.56	0.6
(1,100)	1:245:A:ARG:H	1:244:A:TRP:HB3	12	0.8	0.56	0.6
(3,141)	1:87:A:THR:H	1:125:A:THR:H	12	0.74	0.41	0.75

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,1289)	1:203:A:LEU:H	1:22:A:ILE:HG23	12	0.39	0.24	0.32
(4,1289)	1:203:A:LEU:H	1:22:A:ILE:HD13	12	0.39	0.24	0.32
(4,1289)	1:203:A:LEU:H	1:22:A:ILE:HD12	12	0.39	0.24	0.32
(4,1289)	1:203:A:LEU:H	1:203:A:LEU:HD22	12	0.39	0.24	0.32
(4,1289)	1:203:A:LEU:H	1:203:A:LEU:HD23	12	0.39	0.24	0.32
(4,1225)	1:64:A:HIS:H	1:169:A:LYS:HG2	12	0.35	0.22	0.31
(4,1225)	1:166:A:ILE:H	1:166:A:ILE:HG22	12	0.35	0.22	0.31
(4,1225)	1:166:A:ILE:H	1:166:A:ILE:HG21	12	0.35	0.22	0.31
(4,1225)	1:164:A:ASP:H	1:163:A:LEU:HG	12	0.35	0.22	0.31
(4,1225)	1:129:A:ASP:H	1:132:A:LYS:HG3	12	0.35	0.22	0.31
(4,1293)	1:213:A:GLU:H	1:212:A:LYS:HG3	12	0.27	0.13	0.21
(4,1293)	1:153:A:LYS:H	1:152:A:ALA:HB1	12	0.27	0.13	0.21
(4,1293)	1:91:A:ILE:H	1:91:A:ILE:HD13	12	0.27	0.13	0.21
(4,1293)	1:91:A:ILE:H	1:91:A:ILE:HD11	12	0.27	0.13	0.21
(4,1293)	1:153:A:LYS:H	1:152:A:ALA:HB2	12	0.27	0.13	0.21
(4,1293)	1:91:A:ILE:H	1:91:A:ILE:HD12	12	0.27	0.13	0.21
(4,1293)	1:23:A:ALA:H	1:22:A:ILE:HG22	12	0.27	0.13	0.21
(3,155)	1:169:A:LYS:H	1:231:A:ASN:H	11	1.85	1.7	1.18
(3,284)	1:48:A:SER:H	1:82:A:GLY:H	11	1.43	0.76	1.26
(3,231)	1:191:A:TRP:H	1:212:A:LYS:H	11	1.32	1.08	0.95
(3,160)	1:205:A:CYS:H	1:197:A:LEU:H	11	0.96	0.94	0.54
(3,163)	1:205:A:CYS:H	1:197:A:LEU:H	11	0.96	0.94	0.54
(3,222)	1:197:A:LEU:H	1:205:A:CYS:H	11	0.96	0.94	0.54
(4,467)	1:86:A:GLY:HA3	1:84:A:LEU:HD21	11	0.89	0.59	1.03
(4,467)	1:95:A:PHE:HB3	1:118:A:LEU:HD23	11	0.89	0.59	1.03
(4,467)	1:80:A:LYS:HE2	1:47:A:LEU:HD23	11	0.89	0.59	1.03
(4,467)	1:82:A:GLY:HA3	1:44:A:LEU:HD23	11	0.89	0.59	1.03
(4,467)	1:82:A:GLY:HA3	1:47:A:LEU:HD23	11	0.89	0.59	1.03
(4,467)	1:78:A:VAL:HG21	1:80:A:LYS:HE3	11	0.89	0.59	1.03
(4,467)	1:78:A:VAL:HG22	1:80:A:LYS:HE3	11	0.89	0.59	1.03
(4,467)	1:80:A:LYS:HE2	1:84:A:LEU:HD22	11	0.89	0.59	1.03
(4,467)	1:82:A:GLY:HA3	1:44:A:LEU:HD22	11	0.89	0.59	1.03
(2,20)	1:229:A:ASN:H	1:168:A:THR:H	11	0.89	0.75	0.57
(4,399)	1:50:A:SER:HA	1:52:A:ASP:HB3	11	0.88	0.2	0.8
(4,399)	1:50:A:SER:HA	1:53:A:GLN:HG2	11	0.88	0.2	0.8
(4,399)	1:50:A:SER:HA	1:78:A:VAL:HB	11	0.88	0.2	0.8
(3,92)	1:55:A:THR:H	1:77:A:ALA:H	11	0.66	0.35	0.67
(4,419)	1:205:A:CYS:HB3	1:140:A:LEU:HG	11	0.48	0.3	0.4
(4,419)	1:94:A:HIS:HB2	1:65:A:ALA:HB1	11	0.48	0.3	0.4
(4,419)	1:203:A:LEU:HB3	1:205:A:CYS:HB2	11	0.48	0.3	0.4
(4,419)	1:94:A:HIS:HB2	1:65:A:ALA:HB3	11	0.48	0.3	0.4
(4,419)	1:203:A:LEU:HB2	1:205:A:CYS:HB3	11	0.48	0.3	0.4

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,419)	1:205:A:CYS:HB2	1:140:A:LEU:HG	11	0.48	0.3	0.4
(4,419)	1:203:A:LEU:HB3	1:205:A:CYS:HB3	11	0.48	0.3	0.4
(4,419)	1:205:A:CYS:HB2	1:140:A:LEU:HB2	11	0.48	0.3	0.4
(4,419)	1:205:A:CYS:HB2	1:134:A:VAL:HB	11	0.48	0.3	0.4
(4,1086)	1:86:A:GLY:H	1:84:A:LEU:HB2	11	0.34	0.22	0.2
(4,1086)	1:25:A:GLY:H	1:24:A:LYS:HB2	11	0.34	0.22	0.2
(4,1086)	1:25:A:GLY:H	1:24:A:LYS:HB3	11	0.34	0.22	0.2
(4,1086)	1:98:A:GLY:H	1:116:A:ALA:HB3	11	0.34	0.22	0.2
(4,1138)	1:238:A:GLU:H	1:238:A:GLU:HB2	11	0.3	0.15	0.3
(4,1138)	1:238:A:GLU:H	1:238:A:GLU:HB3	11	0.3	0.15	0.3
(4,1138)	1:40:A:TYR:H	1:39:A:LYS:HB3	11	0.3	0.15	0.3
(4,1138)	1:40:A:TYR:H	1:39:A:LYS:HG3	11	0.3	0.15	0.3
(4,1027)	1:103:A:GLN:H	1:103:A:GLN:HG2	11	0.3	0.2	0.23
(4,1027)	1:103:A:GLN:H	1:100:A:LEU:HB3	11	0.3	0.2	0.23
(4,1027)	1:165:A:SER:H	1:164:A:ASP:HB3	11	0.3	0.2	0.23
(4,1027)	1:103:A:GLN:H	1:100:A:LEU:HB2	11	0.3	0.2	0.23
(4,1027)	1:103:A:GLN:H	1:103:A:GLN:HG3	11	0.3	0.2	0.23
(4,975)	1:133:A:ALA:H	1:133:A:ALA:HA	11	0.29	0.08	0.32
(4,975)	1:126:A:LYS:H	1:124:A:ASN:HB3	11	0.29	0.08	0.32
(4,975)	1:126:A:LYS:H	1:124:A:ASN:HB2	11	0.29	0.08	0.32
(4,1126)	1:228:A:LEU:H	1:228:A:LEU:HB2	11	0.2	0.05	0.19
(4,1126)	1:228:A:LEU:H	1:228:A:LEU:HG	11	0.2	0.05	0.19
(4,1126)	1:18:A:LYS:H	1:18:A:LYS:HG2	11	0.2	0.05	0.19
(4,80)	1:93:A:PHE:H	1:92:A:GLN:HB2	11	0.2	0.07	0.18
(4,80)	1:240:A:MET:H	1:240:A:MET:HB3	11	0.2	0.07	0.18
(4,80)	1:119:A:HIS:H	1:119:A:HIS:HB2	11	0.2	0.07	0.18
(4,80)	1:213:A:GLU:H	1:212:A:LYS:HB2	11	0.2	0.07	0.18
(4,898)	1:49:A:VAL:H	1:49:A:VAL:HA	11	0.19	0.04	0.2
(4,898)	1:256:A:LYS:H	1:193:A:TYR:HB2	11	0.19	0.04	0.2
(4,662)	1:51:A:TYR:H	1:51:A:TYR:HA	11	0.18	0.03	0.19
(4,662)	1:241:A:VAL:H	1:240:A:MET:H	11	0.18	0.03	0.19
(4,410)	1:35:A:THR:HG22	1:35:A:THR:HA	11	0.15	0.03	0.15
(4,410)	1:35:A:THR:HG21	1:35:A:THR:HA	11	0.15	0.03	0.15
(4,410)	1:35:A:THR:HG23	1:35:A:THR:HA	11	0.15	0.03	0.15
(1,126)	1:78:A:VAL:H	1:78:A:VAL:HG22	10	2.14	0.05	2.13
(1,126)	1:78:A:VAL:H	1:78:A:VAL:HG23	10	2.14	0.05	2.13
(1,126)	1:78:A:VAL:H	1:78:A:VAL:HG21	10	2.14	0.05	2.13
(3,226)	1:231:A:ASN:H	1:169:A:LYS:H	10	1.49	1.73	0.71
(1,42)	1:116:A:ALA:HB1	1:97:A:TRP:HA	10	1.21	1.73	0.38
(1,42)	1:116:A:ALA:HB3	1:97:A:TRP:HA	10	1.21	1.73	0.38
(1,42)	1:116:A:ALA:HB2	1:97:A:TRP:HA	10	1.21	1.73	0.38
(3,103)	1:82:A:GLY:H	1:48:A:SER:H	10	1.14	0.73	0.88

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,1266)	1:66:A:PHE:H	1:169:A:LYS:HG3	10	1.02	0.7	0.72
(4,1266)	1:66:A:PHE:H	1:68:A:VAL:HG21	10	1.02	0.7	0.72
(4,1266)	1:66:A:PHE:H	1:68:A:VAL:HG22	10	1.02	0.7	0.72
(4,1266)	1:66:A:PHE:H	1:169:A:LYS:HG2	10	1.02	0.7	0.72
(4,190)	1:127:A:TYR:H	1:123:A:TRP:HB3	10	1.0	0.5	0.9
(4,190)	1:92:A:GLN:H	1:123:A:TRP:HB3	10	1.0	0.5	0.9
(4,190)	1:133:A:ALA:H	1:123:A:TRP:HB3	10	1.0	0.5	0.9
(4,190)	1:130:A:PHE:H	1:123:A:TRP:HB3	10	1.0	0.5	0.9
(4,190)	1:134:A:VAL:H	1:123:A:TRP:HB3	10	1.0	0.5	0.9
(3,58)	1:70:A:PHE:H	1:57:A:LEU:H	10	0.82	1.09	0.27
(3,323)	1:181:A:ARG:H	1:184:A:LEU:H	10	0.81	0.5	0.7
(4,1176)	1:234:A:GLY:H	1:233:A:GLU:HB3	10	0.69	0.56	0.48
(4,1176)	1:234:A:GLY:H	1:233:A:GLU:HB2	10	0.69	0.56	0.48
(4,1176)	1:93:A:PHE:H	1:68:A:VAL:HB	10	0.69	0.56	0.48
(4,1205)	1:231:A:ASN:H	1:169:A:LYS:HD3	10	0.68	0.41	0.52
(4,1205)	1:198:A:THR:H	1:199:A:THR:HG23	10	0.68	0.41	0.52
(4,1205)	1:198:A:THR:H	1:199:A:THR:HG22	10	0.68	0.41	0.52
(4,1205)	1:198:A:THR:H	1:199:A:THR:HG21	10	0.68	0.41	0.52
(4,42)	1:38:A:ALA:HA	1:255:A:ILE:H	10	0.51	0.3	0.54
(4,1003)	1:76:A:LYS:H	1:76:A:LYS:HE2	10	0.49	0.16	0.52
(4,1003)	1:133:A:ALA:H	1:127:A:TYR:HB3	10	0.49	0.16	0.52
(4,1003)	1:126:A:LYS:H	1:124:A:ASN:HB3	10	0.49	0.16	0.52
(4,1003)	1:76:A:LYS:H	1:74:A:GLN:HB2	10	0.49	0.16	0.52
(1,38)	1:77:A:ALA:HA	1:51:A:TYR:HA	10	0.37	0.52	0.2
(4,1125)	1:248:A:GLN:H	1:248:A:GLN:HB3	10	0.29	0.08	0.3
(4,1125)	1:233:A:GLU:H	1:233:A:GLU:HB3	10	0.29	0.08	0.3
(4,1125)	1:80:A:LYS:H	1:80:A:LYS:HG2	10	0.29	0.08	0.3
(4,1125)	1:22:A:ILE:H	1:22:A:ILE:HB	10	0.29	0.08	0.3
(4,1125)	1:248:A:GLN:H	1:248:A:GLN:HB2	10	0.29	0.08	0.3
(4,1125)	1:233:A:GLU:H	1:233:A:GLU:HG3	10	0.29	0.08	0.3
(4,1125)	1:223:A:LEU:H	1:223:A:LEU:HB2	10	0.29	0.08	0.3
(4,1125)	1:149:A:VAL:H	1:148:A:LYS:HB2	10	0.29	0.08	0.3
(4,1125)	1:171:A:LYS:H	1:171:A:LYS:HB2	10	0.29	0.08	0.3
(4,12)	1:34:A:ASP:HB3	1:35:A:THR:H	10	0.29	0.04	0.31
(4,12)	1:178:A:PHE:HB2	1:56:A:SER:H	10	0.29	0.04	0.31
(4,12)	1:178:A:PHE:HB3	1:56:A:SER:H	10	0.29	0.04	0.31
(4,753)	1:172:A:SER:H	1:171:A:LYS:HA	10	0.25	0.02	0.26
(4,983)	1:119:A:HIS:H	1:119:A:HIS:HB2	10	0.23	0.1	0.21
(4,983)	1:65:A:ALA:H	1:62:A:ASN:HB2	10	0.23	0.1	0.21
(4,983)	1:68:A:VAL:H	1:67:A:ASN:HB3	10	0.23	0.1	0.21
(4,832)	1:247:A:ALA:H	1:247:A:ALA:HA	10	0.23	0.04	0.24
(4,832)	1:253:A:ARG:H	1:253:A:ARG:HA	10	0.23	0.04	0.24

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,1168)	1:229:A:ASN:H	1:228:A:LEU:HB3	10	0.22	0.07	0.22
(4,1168)	1:190:A:TYR:H	1:189:A:ASP:HB3	10	0.22	0.07	0.22
(4,1168)	1:152:A:ALA:H	1:152:A:ALA:HB3	10	0.22	0.07	0.22
(4,1168)	1:147:A:LEU:H	1:147:A:LEU:HG	10	0.22	0.07	0.22
(4,1168)	1:152:A:ALA:H	1:152:A:ALA:HB2	10	0.22	0.07	0.22
(4,1168)	1:124:A:ASN:H	1:133:A:ALA:HB3	10	0.22	0.07	0.22
(4,1168)	1:152:A:ALA:H	1:152:A:ALA:HB1	10	0.22	0.07	0.22
(4,1283)	1:152:A:ALA:H	1:152:A:ALA:HB3	10	0.2	0.05	0.22
(4,1283)	1:148:A:LYS:H	1:148:A:LYS:HG3	10	0.2	0.05	0.22
(4,1283)	1:152:A:ALA:H	1:152:A:ALA:HB2	10	0.2	0.05	0.22
(4,1283)	1:152:A:ALA:H	1:152:A:ALA:HB1	10	0.2	0.05	0.22
(4,1283)	1:148:A:LYS:H	1:148:A:LYS:HG2	10	0.2	0.05	0.22
(4,1195)	1:228:A:LEU:H	1:228:A:LEU:HB2	10	0.18	0.05	0.18
(4,1195)	1:228:A:LEU:H	1:228:A:LEU:HG	10	0.18	0.05	0.18
(4,1195)	1:18:A:LYS:H	1:18:A:LYS:HG2	10	0.18	0.05	0.18
(4,1007)	1:85:A:ASP:H	1:85:A:ASP:HB2	10	0.18	0.06	0.16
(4,1007)	1:119:A:HIS:H	1:119:A:HIS:HB2	10	0.18	0.06	0.16
(4,1007)	1:122:A:HIS:H	1:122:A:HIS:HB2	10	0.18	0.06	0.16
(4,999)	1:85:A:ASP:H	1:85:A:ASP:HB2	10	0.16	0.06	0.14
(4,999)	1:65:A:ALA:H	1:62:A:ASN:HB2	10	0.16	0.06	0.14
(4,999)	1:119:A:HIS:H	1:119:A:HIS:HB2	10	0.16	0.06	0.14
(4,999)	1:122:A:HIS:H	1:122:A:HIS:HB2	10	0.16	0.06	0.14
(4,767)	1:70:A:PHE:H	1:69:A:GLU:HA	10	0.16	0.04	0.15
(4,767)	1:190:A:TYR:H	1:189:A:ASP:HA	10	0.16	0.04	0.15
(4,767)	1:71:A:ASP:H	1:70:A:PHE:HA	10	0.16	0.04	0.15
(4,767)	1:197:A:LEU:H	1:197:A:LEU:HA	10	0.16	0.04	0.15
(4,767)	1:229:A:ASN:H	1:228:A:LEU:HA	10	0.16	0.04	0.15
(4,1041)	1:60:A:LEU:H	1:60:A:LEU:HB3	10	0.15	0.04	0.16
(4,1041)	1:153:A:LYS:H	1:153:A:LYS:HB2	10	0.15	0.04	0.16
(4,1041)	1:240:A:MET:H	1:240:A:MET:HB3	10	0.15	0.04	0.16
(4,1041)	1:153:A:LYS:H	1:153:A:LYS:HB3	10	0.15	0.04	0.16
(4,1041)	1:119:A:HIS:H	1:119:A:HIS:HB2	10	0.15	0.04	0.16
(4,1097)	1:157:A:GLN:H	1:157:A:GLN:HB2	10	0.13	0.02	0.13
(4,1097)	1:157:A:GLN:H	1:157:A:GLN:HB3	10	0.13	0.02	0.13
(4,1097)	1:237:A:GLU:H	1:237:A:GLU:HB2	10	0.13	0.02	0.13
(4,1097)	1:237:A:GLU:H	1:237:A:GLU:HB3	10	0.13	0.02	0.13
(4,148)	1:164:A:ASP:H	1:164:A:ASP:HB2	10	0.12	0.01	0.12
(4,148)	1:164:A:ASP:H	1:164:A:ASP:HB3	10	0.12	0.01	0.12
(3,7)	1:56:A:SER:H	1:177:A:ASN:H	9	2.57	1.62	2.82
(3,11)	1:177:A:ASN:H	1:56:A:SER:H	9	2.37	1.62	2.62
(1,128)	1:81:A:GLY:H	1:84:A:LEU:HD21	9	1.63	0.82	2.16
(1,128)	1:81:A:GLY:H	1:84:A:LEU:HD23	9	1.63	0.82	2.16

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,356)	1:153:A:LYS:HD3	1:158:A:LYS:HE2	9	1.12	0.5	1.06
(4,356)	1:153:A:LYS:HD2	1:158:A:LYS:HE2	9	1.12	0.5	1.06
(4,356)	1:153:A:LYS:HD3	1:158:A:LYS:HE3	9	1.12	0.5	1.06
(4,356)	1:153:A:LYS:HD2	1:224:A:LYS:HE3	9	1.12	0.5	1.06
(4,356)	1:153:A:LYS:HD3	1:224:A:LYS:HE2	9	1.12	0.5	1.06
(4,356)	1:153:A:LYS:HD3	1:159:A:VAL:HA	9	1.12	0.5	1.06
(4,356)	1:153:A:LYS:HD2	1:159:A:VAL:HA	9	1.12	0.5	1.06
(1,6)	1:169:A:LYS:HB3	1:63:A:GLY:H	9	0.95	1.15	0.54
(1,7)	1:59:A:ILE:H	1:166:A:ILE:HD11	9	0.86	0.36	0.94
(1,7)	1:59:A:ILE:H	1:166:A:ILE:HD12	9	0.86	0.36	0.94
(1,7)	1:59:A:ILE:H	1:166:A:ILE:HD13	9	0.86	0.36	0.94
(4,1091)	1:81:A:GLY:H	1:80:A:LYS:HB3	9	0.82	0.53	1.14
(4,1091)	1:81:A:GLY:H	1:84:A:LEU:HB3	9	0.82	0.53	1.14
(4,253)	1:135:A:GLN:H	1:127:A:TYR:HB3	9	0.62	0.44	0.75
(4,253)	1:135:A:GLN:H	1:127:A:TYR:HB2	9	0.62	0.44	0.75
(4,253)	1:61:A:ASN:HB2	1:168:A:THR:H	9	0.62	0.44	0.75
(4,654)	1:199:A:THR:H	1:202:A:LEU:H	9	0.61	0.61	0.31
(4,654)	1:199:A:THR:H	1:196:A:SER:H	9	0.61	0.61	0.31
(4,654)	1:162:A:VAL:H	1:174:A:ASP:H	9	0.61	0.61	0.31
(4,97)	1:161:A:ASP:H	1:163:A:LEU:HA	9	0.6	0.15	0.62
(4,97)	1:204:A:GLU:H	1:202:A:LEU:HA	9	0.6	0.15	0.62
(4,97)	1:23:A:ALA:H	1:202:A:LEU:HA	9	0.6	0.15	0.62
(4,1257)	1:78:A:VAL:H	1:77:A:ALA:HB3	9	0.49	0.22	0.45
(4,1257)	1:78:A:VAL:H	1:77:A:ALA:HB2	9	0.49	0.22	0.45
(4,1257)	1:251:A:LYS:H	1:251:A:LYS:HG2	9	0.49	0.22	0.45
(4,1257)	1:78:A:VAL:H	1:77:A:ALA:HB1	9	0.49	0.22	0.45
(4,1257)	1:251:A:LYS:H	1:251:A:LYS:HG3	9	0.49	0.22	0.45
(4,664)	1:54:A:ALA:H	1:51:A:TYR:HA	9	0.48	0.12	0.51
(4,439)	1:260:A:LYS:HA	1:260:A:LYS:HG3	9	0.47	0.09	0.48
(4,439)	1:260:A:LYS:HA	1:260:A:LYS:HG2	9	0.47	0.09	0.48
(4,439)	1:22:A:ILE:HG22	1:202:A:LEU:HA	9	0.47	0.09	0.48
(4,650)	1:199:A:THR:H	1:202:A:LEU:H	9	0.44	0.29	0.31
(4,650)	1:19:A:ASP:H	1:14:A:GLU:H	9	0.44	0.29	0.31
(4,650)	1:199:A:THR:H	1:196:A:SER:H	9	0.44	0.29	0.31
(4,650)	1:162:A:VAL:H	1:174:A:ASP:H	9	0.44	0.29	0.31
(4,1178)	1:177:A:ASN:H	1:55:A:THR:HG21	9	0.41	0.32	0.33
(4,1178)	1:177:A:ASN:H	1:176:A:THR:HG22	9	0.41	0.32	0.33
(4,1178)	1:177:A:ASN:H	1:176:A:THR:HG21	9	0.41	0.32	0.33
(4,1178)	1:177:A:ASN:H	1:176:A:THR:HG23	9	0.41	0.32	0.33
(4,1178)	1:177:A:ASN:H	1:55:A:THR:HG22	9	0.41	0.32	0.33
(4,1189)	1:34:A:ASP:H	1:255:A:ILE:HG22	9	0.41	0.13	0.44
(4,1189)	1:34:A:ASP:H	1:37:A:THR:HG22	9	0.41	0.13	0.44

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,1189)	1:34:A:ASP:H	1:255:A:ILE:HG21	9	0.41	0.13	0.44
(4,1189)	1:34:A:ASP:H	1:37:A:THR:HG23	9	0.41	0.13	0.44
(4,1189)	1:34:A:ASP:H	1:37:A:THR:HG21	9	0.41	0.13	0.44
(4,185)	1:92:A:GLN:H	1:91:A:ILE:HD12	9	0.41	0.24	0.36
(4,185)	1:142:A:VAL:H	1:209:A:ILE:HD12	9	0.41	0.24	0.36
(4,185)	1:142:A:VAL:H	1:209:A:ILE:HD11	9	0.41	0.24	0.36
(4,185)	1:22:A:ILE:H	1:22:A:ILE:HD12	9	0.41	0.24	0.36
(4,185)	1:255:A:ILE:HD11	1:34:A:ASP:H	9	0.41	0.24	0.36
(4,185)	1:22:A:ILE:H	1:22:A:ILE:HD13	9	0.41	0.24	0.36
(1,79)	1:68:A:VAL:H	1:93:A:PHE:H	9	0.31	0.18	0.24
(4,1121)	1:48:A:SER:H	1:47:A:LEU:HB3	9	0.29	0.09	0.32
(4,1121)	1:106:A:GLU:H	1:106:A:GLU:HB2	9	0.29	0.09	0.32
(4,1121)	1:147:A:LEU:H	1:146:A:PHE:HB3	9	0.29	0.09	0.32
(4,1121)	1:9:A:LYS:H	1:9:A:LYS:HB2	9	0.29	0.09	0.32
(4,1121)	1:48:A:SER:H	1:47:A:LEU:HB2	9	0.29	0.09	0.32
(4,1121)	1:106:A:GLU:H	1:106:A:GLU:HB3	9	0.29	0.09	0.32
(4,880)	1:224:A:LYS:H	1:224:A:LYS:HA	9	0.27	0.07	0.3
(4,880)	1:241:A:VAL:H	1:241:A:VAL:HA	9	0.27	0.07	0.3
(4,880)	1:166:A:ILE:H	1:165:A:SER:HB3	9	0.27	0.07	0.3
(4,880)	1:166:A:ILE:H	1:163:A:LEU:HA	9	0.27	0.07	0.3
(4,1135)	1:221:A:GLN:H	1:221:A:GLN:HB2	9	0.22	0.06	0.21
(4,1135)	1:221:A:GLN:H	1:221:A:GLN:HB3	9	0.22	0.06	0.21
(4,1135)	1:28:A:GLN:H	1:28:A:GLN:HB3	9	0.22	0.06	0.21
(4,923)	1:7:A:TYR:H	1:7:A:TYR:HB2	9	0.21	0.08	0.17
(4,923)	1:243:A:ASN:H	1:243:A:ASN:HB2	9	0.21	0.08	0.17
(4,923)	1:124:A:ASN:H	1:123:A:TRP:HB2	9	0.21	0.08	0.17
(4,923)	1:9:A:LYS:H	1:8:A:GLY:HA3	9	0.21	0.08	0.17
(4,923)	1:243:A:ASN:H	1:243:A:ASN:HB3	9	0.21	0.08	0.17
(4,114)	1:61:A:ASN:H	1:60:A:LEU:HG	9	0.2	0.05	0.17
(4,114)	1:254:A:GLN:H	1:253:A:ARG:HG3	9	0.2	0.05	0.17
(4,114)	1:256:A:LYS:H	1:255:A:ILE:HG13	9	0.2	0.05	0.17
(4,114)	1:89:A:ARG:H	1:89:A:ARG:HG2	9	0.2	0.05	0.17
(4,114)	1:27:A:ARG:H	1:27:A:ARG:HG3	9	0.2	0.05	0.17
(4,114)	1:250:A:LEU:H	1:250:A:LEU:HG	9	0.2	0.05	0.17
(4,1282)	1:152:A:ALA:H	1:152:A:ALA:HB3	9	0.2	0.04	0.22
(4,1282)	1:148:A:LYS:H	1:148:A:LYS:HG3	9	0.2	0.04	0.22
(4,1282)	1:152:A:ALA:H	1:152:A:ALA:HB2	9	0.2	0.04	0.22
(4,1282)	1:148:A:LYS:H	1:148:A:LYS:HG2	9	0.2	0.04	0.22
(4,670)	1:39:A:LYS:H	1:39:A:LYS:HA	9	0.16	0.05	0.14
(4,670)	1:52:A:ASP:H	1:51:A:TYR:HA	9	0.16	0.05	0.14
(4,1130)	1:260:A:LYS:H	1:260:A:LYS:HB2	9	0.12	0.02	0.11
(4,1130)	1:133:A:ALA:H	1:133:A:ALA:HB3	9	0.12	0.02	0.11

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,1130)	1:133:A:ALA:H	1:133:A:ALA:HB1	9	0.12	0.02	0.11
(1,56)	1:255:A:ILE:HD13	1:193:A:TYR:HB2	8	2.83	1.4	3.11
(1,56)	1:255:A:ILE:HD11	1:193:A:TYR:HB2	8	2.83	1.4	3.11
(1,56)	1:255:A:ILE:HD12	1:193:A:TYR:HB2	8	2.83	1.4	3.11
(4,1304)	1:177:A:ASN:H	1:57:A:LEU:HD23	8	2.67	1.5	2.46
(4,1304)	1:177:A:ASN:H	1:162:A:VAL:HG21	8	2.67	1.5	2.46
(4,1304)	1:177:A:ASN:H	1:57:A:LEU:HD22	8	2.67	1.5	2.46
(4,1304)	1:177:A:ASN:H	1:57:A:LEU:HD21	8	2.67	1.5	2.46
(1,75)	1:172:A:SER:HB2	1:60:A:LEU:HD11	8	2.21	0.72	2.41
(1,75)	1:172:A:SER:HB3	1:60:A:LEU:HD13	8	2.21	0.72	2.41
(1,75)	1:172:A:SER:HB3	1:60:A:LEU:HD11	8	2.21	0.72	2.41
(1,121)	1:93:A:PHE:H	1:68:A:VAL:HG21	8	2.15	1.24	2.42
(1,121)	1:93:A:PHE:H	1:68:A:VAL:HG23	8	2.15	1.24	2.42
(1,121)	1:93:A:PHE:H	1:68:A:VAL:HG22	8	2.15	1.24	2.42
(1,47)	1:240:A:MET:HA	1:230:A:PHE:HA	8	1.91	1.09	2.13
(3,245)	1:191:A:TRP:H	1:212:A:LYS:H	8	1.55	0.96	1.38
(3,249)	1:191:A:TRP:H	1:212:A:LYS:H	8	1.55	0.96	1.38
(3,325)	1:197:A:LEU:H	1:203:A:LEU:H	8	1.43	0.8	1.18
(4,468)	1:76:A:LYS:HG2	1:51:A:TYR:HA	8	1.21	0.87	1.1
(4,468)	1:76:A:LYS:HG3	1:51:A:TYR:HA	8	1.21	0.87	1.1
(4,468)	1:51:A:TYR:HA	1:78:A:VAL:HG23	8	1.21	0.87	1.1
(3,164)	1:203:A:LEU:H	1:197:A:LEU:H	8	1.13	0.8	0.88
(4,1325)	1:59:A:ILE:H	1:166:A:ILE:HD11	8	0.89	0.37	1.02
(4,1325)	1:59:A:ILE:H	1:166:A:ILE:HD12	8	0.89	0.37	1.02
(4,1325)	1:59:A:ILE:H	1:166:A:ILE:HD13	8	0.89	0.37	1.02
(4,382)	1:193:A:TYR:HB3	1:208:A:TRP:HB2	8	0.67	0.46	0.56
(4,382)	1:89:A:ARG:HD2	1:75:A:ASP:HB2	8	0.67	0.46	0.56
(4,382)	1:75:A:ASP:HB2	1:74:A:GLN:HB3	8	0.67	0.46	0.56
(4,382)	1:193:A:TYR:HB3	1:208:A:TRP:HB3	8	0.67	0.46	0.56
(1,28)	1:241:A:VAL:H	1:240:A:MET:HA	8	0.61	0.09	0.62
(4,260)	1:203:A:LEU:H	1:203:A:LEU:HB3	8	0.55	0.17	0.54
(4,260)	1:203:A:LEU:H	1:203:A:LEU:HB2	8	0.55	0.17	0.54
(4,1249)	1:169:A:LYS:H	1:169:A:LYS:HG3	8	0.54	0.38	0.46
(4,1249)	1:163:A:LEU:H	1:162:A:VAL:HG23	8	0.54	0.38	0.46
(4,1249)	1:171:A:LYS:H	1:171:A:LYS:HG3	8	0.54	0.38	0.46
(4,1249)	1:163:A:LEU:H	1:162:A:VAL:HG21	8	0.54	0.38	0.46
(4,487)	1:152:A:ALA:H	1:151:A:SER:H	8	0.48	0.27	0.53
(4,487)	1:48:A:SER:H	1:47:A:LEU:H	8	0.48	0.27	0.53
(4,487)	1:48:A:SER:H	1:80:A:LYS:H	8	0.48	0.27	0.53
(4,1274)	1:113:A:LYS:H	1:112:A:LYS:HG2	8	0.46	0.19	0.51
(4,1274)	1:126:A:LYS:H	1:125:A:THR:HG21	8	0.46	0.19	0.51
(4,1274)	1:126:A:LYS:H	1:125:A:THR:HG22	8	0.46	0.19	0.51

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,1274)	1:126:A:LYS:H	1:125:A:THR:HG23	8	0.46	0.19	0.51
(4,1274)	1:113:A:LYS:H	1:112:A:LYS:HG3	8	0.46	0.19	0.51
(4,989)	1:41:A:ASP:H	1:41:A:ASP:HB2	8	0.38	0.2	0.4
(4,989)	1:179:A:ASP:H	1:179:A:ASP:HB2	8	0.38	0.2	0.4
(4,989)	1:179:A:ASP:H	1:179:A:ASP:HB3	8	0.38	0.2	0.4
(4,989)	1:41:A:ASP:H	1:40:A:TYR:HB2	8	0.38	0.2	0.4
(4,397)	1:163:A:LEU:HB3	1:160:A:VAL:HA	8	0.36	0.15	0.38
(4,397)	1:159:A:VAL:HA	1:159:A:VAL:HB	8	0.36	0.15	0.38
(4,397)	1:159:A:VAL:HA	1:162:A:VAL:HB	8	0.36	0.15	0.38
(4,1147)	1:231:A:ASN:H	1:169:A:LYS:HD3	8	0.31	0.11	0.28
(4,1147)	1:231:A:ASN:H	1:169:A:LYS:HB2	8	0.31	0.11	0.28
(4,1147)	1:99:A:SER:H	1:100:A:LEU:HG	8	0.31	0.11	0.28
(1,114)	1:66:A:PHE:H	1:65:A:ALA:HB2	8	0.3	0.18	0.26
(1,114)	1:66:A:PHE:H	1:65:A:ALA:HB1	8	0.3	0.18	0.26
(1,114)	1:66:A:PHE:H	1:65:A:ALA:HB3	8	0.3	0.18	0.26
(4,1005)	1:175:A:PHE:H	1:175:A:PHE:HB3	8	0.3	0.08	0.29
(4,1005)	1:175:A:PHE:H	1:174:A:ASP:HB3	8	0.3	0.08	0.29
(4,1005)	1:175:A:PHE:H	1:175:A:PHE:HB2	8	0.3	0.08	0.29
(4,869)	1:129:A:ASP:H	1:129:A:ASP:HA	8	0.27	0.07	0.31
(4,869)	1:166:A:ILE:H	1:165:A:SER:HB3	8	0.27	0.07	0.31
(4,869)	1:166:A:ILE:H	1:163:A:LEU:HA	8	0.27	0.07	0.31
(4,13)	1:56:A:SER:H	1:76:A:LYS:HG2	8	0.26	0.16	0.2
(4,13)	1:113:A:LYS:HG2	1:245:A:ARG:H	8	0.26	0.16	0.2
(4,13)	1:56:A:SER:H	1:76:A:LYS:HG3	8	0.26	0.16	0.2
(4,13)	1:63:A:GLY:H	1:60:A:LEU:HD13	8	0.26	0.16	0.2
(4,13)	1:63:A:GLY:H	1:60:A:LEU:HD11	8	0.26	0.16	0.2
(4,48)	1:202:A:LEU:H	1:202:A:LEU:HB2	8	0.26	0.11	0.24
(4,48)	1:202:A:LEU:H	1:202:A:LEU:HB3	8	0.26	0.11	0.24
(4,48)	1:117:A:GLU:H	1:117:A:GLU:HB3	8	0.26	0.11	0.24
(4,48)	1:232:A:GLY:H	1:235:A:GLU:HG3	8	0.26	0.11	0.24
(4,48)	1:148:A:LYS:H	1:148:A:LYS:HB3	8	0.26	0.11	0.24
(4,48)	1:26:A:GLU:H	1:26:A:GLU:HG3	8	0.26	0.11	0.24
(4,980)	1:191:A:TRP:H	1:191:A:TRP:HB2	8	0.26	0.12	0.26
(4,980)	1:191:A:TRP:H	1:190:A:TYR:HB3	8	0.26	0.12	0.26
(4,980)	1:191:A:TRP:H	1:190:A:TYR:HB2	8	0.26	0.12	0.26
(4,980)	1:191:A:TRP:H	1:191:A:TRP:HB3	8	0.26	0.12	0.26
(4,1107)	1:48:A:SER:H	1:47:A:LEU:HB3	8	0.24	0.08	0.25
(4,1107)	1:229:A:ASN:H	1:228:A:LEU:HB2	8	0.24	0.08	0.25
(4,1107)	1:147:A:LEU:H	1:146:A:PHE:HB3	8	0.24	0.08	0.25
(4,1107)	1:147:A:LEU:H	1:147:A:LEU:HG	8	0.24	0.08	0.25
(4,1107)	1:229:A:ASN:H	1:228:A:LEU:HB3	8	0.24	0.08	0.25
(4,1107)	1:106:A:GLU:H	1:106:A:GLU:HB3	8	0.24	0.08	0.25

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(3,205)	1:124:A:ASN:H	1:127:A:TYR:H	8	0.24	0.07	0.22
(4,335)	1:22:A:ILE:HG21	1:22:A:ILE:HA	8	0.22	0.1	0.21
(4,335)	1:134:A:VAL:HG23	1:131:A:GLY:HA2	8	0.22	0.1	0.21
(4,335)	1:22:A:ILE:HG22	1:22:A:ILE:HA	8	0.22	0.1	0.21
(4,335)	1:49:A:VAL:HG21	1:49:A:VAL:HA	8	0.22	0.1	0.21
(4,335)	1:49:A:VAL:HG22	1:49:A:VAL:HA	8	0.22	0.1	0.21
(4,1060)	1:260:A:LYS:H	1:260:A:LYS:HB2	8	0.22	0.15	0.18
(4,1060)	1:260:A:LYS:H	1:260:A:LYS:HB3	8	0.22	0.15	0.18
(4,1060)	1:133:A:ALA:H	1:132:A:LYS:HB2	8	0.22	0.15	0.18
(1,103)	1:118:A:LEU:H	1:118:A:LEU:HB3	8	0.19	0.09	0.16
(1,103)	1:118:A:LEU:H	1:118:A:LEU:HB2	8	0.19	0.09	0.16
(4,611)	1:19:A:ASP:H	1:20:A:PHE:H	8	0.16	0.03	0.16
(4,611)	1:163:A:LEU:H	1:164:A:ASP:H	8	0.16	0.03	0.16
(4,1127)	1:197:A:LEU:H	1:197:A:LEU:HG	8	0.14	0.03	0.13
(4,1127)	1:167:A:LYS:H	1:167:A:LYS:HB2	8	0.14	0.03	0.13
(4,1127)	1:221:A:GLN:H	1:221:A:GLN:HB2	8	0.14	0.03	0.13
(4,1127)	1:197:A:LEU:H	1:197:A:LEU:HB2	8	0.14	0.03	0.13
(4,1127)	1:183:A:LEU:H	1:183:A:LEU:HB2	8	0.14	0.03	0.13
(4,1127)	1:20:A:PHE:H	1:19:A:ASP:HB3	8	0.14	0.03	0.13
(1,83)	1:37:A:THR:H	1:38:A:ALA:H	8	0.13	0.02	0.12
(4,711)	1:122:A:HIS:H	1:121:A:VAL:HA	8	0.13	0.02	0.12
(4,711)	1:51:A:TYR:H	1:50:A:SER:HA	8	0.13	0.02	0.12
(4,711)	1:188:A:LEU:H	1:187:A:SER:HA	8	0.13	0.02	0.12
(4,711)	1:90:A:LEU:H	1:89:A:ARG:HA	8	0.13	0.02	0.12
(3,10)	1:178:A:PHE:H	1:56:A:SER:H	7	2.6	1.04	2.93
(3,126)	1:56:A:SER:H	1:178:A:PHE:H	7	2.6	1.04	2.93
(4,1270)	1:93:A:PHE:H	1:68:A:VAL:HG23	7	2.35	1.04	2.33
(4,1270)	1:94:A:HIS:H	1:121:A:VAL:HG23	7	2.35	1.04	2.33
(4,1270)	1:93:A:PHE:H	1:68:A:VAL:HG21	7	2.35	1.04	2.33
(4,1270)	1:93:A:PHE:H	1:68:A:VAL:HG22	7	2.35	1.04	2.33
(1,76)	1:115:A:ALA:HB1	1:149:A:VAL:HG23	7	1.85	2.38	0.47
(1,76)	1:115:A:ALA:HB2	1:149:A:VAL:HG21	7	1.85	2.38	0.47
(1,76)	1:115:A:ALA:HB3	1:149:A:VAL:HG21	7	1.85	2.38	0.47
(1,76)	1:115:A:ALA:HB3	1:149:A:VAL:HG22	7	1.85	2.38	0.47
(1,76)	1:115:A:ALA:HB2	1:149:A:VAL:HG23	7	1.85	2.38	0.47
(4,66)	1:23:A:ALA:H	1:22:A:ILE:HD12	7	1.44	0.63	1.65
(4,66)	1:202:A:LEU:H	1:22:A:ILE:HD11	7	1.44	0.63	1.65
(4,66)	1:204:A:GLU:H	1:22:A:ILE:HD12	7	1.44	0.63	1.65
(4,66)	1:23:A:ALA:H	1:22:A:ILE:HD11	7	1.44	0.63	1.65
(4,66)	1:23:A:ALA:H	1:22:A:ILE:HD13	7	1.44	0.63	1.65
(4,328)	1:240:A:MET:HA	1:230:A:PHE:HA	7	1.31	0.42	1.47
(4,328)	1:240:A:MET:HA	1:239:A:LEU:HA	7	1.31	0.42	1.47

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,1258)	1:202:A:LEU:H	1:22:A:ILE:HG22	7	0.96	0.92	0.44
(4,1258)	1:202:A:LEU:H	1:22:A:ILE:HG23	7	0.96	0.92	0.44
(4,1258)	1:202:A:LEU:H	1:22:A:ILE:HD12	7	0.96	0.92	0.44
(4,1258)	1:202:A:LEU:H	1:202:A:LEU:HD21	7	0.96	0.92	0.44
(4,1258)	1:123:A:TRP:H	1:91:A:ILE:HG13	7	0.96	0.92	0.44
(4,1258)	1:123:A:TRP:H	1:91:A:ILE:HG12	7	0.96	0.92	0.44
(4,15)	1:255:A:ILE:HG12	1:35:A:THR:H	7	0.95	0.51	1.12
(4,15)	1:192:A:THR:H	1:255:A:ILE:HG13	7	0.95	0.51	1.12
(4,15)	1:192:A:THR:H	1:255:A:ILE:HG12	7	0.95	0.51	1.12
(4,478)	1:190:A:TYR:H	1:258:A:SER:H	7	0.9	0.32	1.08
(4,478)	1:32:A:ASP:H	1:250:A:LEU:H	7	0.9	0.32	1.08
(4,478)	1:243:A:ASN:H	1:97:A:TRP:H	7	0.9	0.32	1.08
(4,1218)	1:172:A:SER:H	1:171:A:LYS:HD2	7	0.66	0.39	0.76
(4,1218)	1:78:A:VAL:H	1:77:A:ALA:HB2	7	0.66	0.39	0.76
(4,1218)	1:172:A:SER:H	1:166:A:ILE:HG23	7	0.66	0.39	0.76
(4,1218)	1:172:A:SER:H	1:166:A:ILE:HG22	7	0.66	0.39	0.76
(4,1218)	1:78:A:VAL:H	1:77:A:ALA:HB3	7	0.66	0.39	0.76
(4,1218)	1:78:A:VAL:H	1:77:A:ALA:HB1	7	0.66	0.39	0.76
(4,416)	1:23:A:ALA:HB1	1:16:A:TRP:HB2	7	0.66	1.08	0.22
(4,416)	1:23:A:ALA:HB2	1:16:A:TRP:HB2	7	0.66	1.08	0.22
(4,416)	1:23:A:ALA:HB1	1:17:A:HIS:HB3	7	0.66	1.08	0.22
(4,416)	1:23:A:ALA:HB2	1:17:A:HIS:HB2	7	0.66	1.08	0.22
(4,416)	1:23:A:ALA:HB3	1:16:A:TRP:HB3	7	0.66	1.08	0.22
(4,416)	1:24:A:LYS:HG3	1:17:A:HIS:HB3	7	0.66	1.08	0.22
(3,23)	1:138:A:ASP:H	1:140:A:LEU:H	7	0.64	0.26	0.58
(4,470)	1:219:A:SER:H	1:150:A:GLY:H	7	0.58	0.43	0.61
(4,470)	1:170:A:GLY:H	1:63:A:GLY:H	7	0.58	0.43	0.61
(4,251)	1:259:A:PHE:H	1:40:A:TYR:HB2	7	0.41	0.21	0.31
(4,252)	1:259:A:PHE:H	1:40:A:TYR:HB2	7	0.38	0.14	0.31
(4,252)	1:40:A:TYR:HB3	1:259:A:PHE:H	7	0.38	0.14	0.31
(4,1242)	1:247:A:ALA:H	1:247:A:ALA:HB3	7	0.34	0.11	0.35
(4,1242)	1:247:A:ALA:H	1:247:A:ALA:HB1	7	0.34	0.11	0.35
(4,1242)	1:247:A:ALA:H	1:247:A:ALA:HB2	7	0.34	0.11	0.35
(4,963)	1:121:A:VAL:H	1:122:A:HIS:HB2	7	0.32	0.19	0.24
(4,100)	1:141:A:ALA:H	1:140:A:LEU:HB2	7	0.3	0.11	0.29
(4,1160)	1:224:A:LYS:H	1:224:A:LYS:HG2	7	0.3	0.09	0.27
(4,1160)	1:135:A:GLN:H	1:135:A:GLN:HB2	7	0.3	0.09	0.27
(4,1160)	1:224:A:LYS:H	1:224:A:LYS:HG3	7	0.3	0.09	0.27
(4,1160)	1:224:A:LYS:H	1:224:A:LYS:HB2	7	0.3	0.09	0.27
(4,1160)	1:92:A:GLN:H	1:91:A:ILE:HB	7	0.3	0.09	0.27
(4,1173)	1:22:A:ILE:H	1:22:A:ILE:HB	7	0.29	0.06	0.32
(4,1173)	1:223:A:LEU:H	1:223:A:LEU:HB2	7	0.29	0.06	0.32

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,1173)	1:233:A:GLU:H	1:233:A:GLU:HB3	7	0.29	0.06	0.32
(4,1173)	1:80:A:LYS:H	1:80:A:LYS:HG2	7	0.29	0.06	0.32
(4,1173)	1:89:A:ARG:H	1:89:A:ARG:HG2	7	0.29	0.06	0.32
(4,1173)	1:27:A:ARG:H	1:27:A:ARG:HG3	7	0.29	0.06	0.32
(1,73)	1:134:A:VAL:HG22	1:131:A:GLY:HA2	7	0.27	0.09	0.26
(1,73)	1:134:A:VAL:HG21	1:131:A:GLY:HA2	7	0.27	0.09	0.26
(1,73)	1:134:A:VAL:HG23	1:131:A:GLY:HA2	7	0.27	0.09	0.26
(4,968)	1:129:A:ASP:H	1:129:A:ASP:HB2	7	0.25	0.13	0.22
(4,968)	1:166:A:ILE:H	1:163:A:LEU:HA	7	0.25	0.13	0.22
(4,968)	1:129:A:ASP:H	1:127:A:TYR:HB2	7	0.25	0.13	0.22
(4,968)	1:129:A:ASP:H	1:129:A:ASP:HB3	7	0.25	0.13	0.22
(4,968)	1:241:A:VAL:H	1:240:A:MET:HA	7	0.25	0.13	0.22
(4,1264)	1:204:A:GLU:H	1:22:A:ILE:HD13	7	0.23	0.14	0.18
(4,1264)	1:204:A:GLU:H	1:22:A:ILE:HD11	7	0.23	0.14	0.18
(4,1264)	1:210:A:VAL:H	1:209:A:ILE:HG22	7	0.23	0.14	0.18
(4,1264)	1:90:A:LEU:H	1:89:A:ARG:HG2	7	0.23	0.14	0.18
(4,1264)	1:210:A:VAL:H	1:209:A:ILE:HG23	7	0.23	0.14	0.18
(4,922)	1:65:A:ALA:H	1:62:A:ASN:HB3	7	0.23	0.1	0.23
(4,922)	1:119:A:HIS:H	1:118:A:LEU:HB3	7	0.23	0.1	0.23
(4,922)	1:65:A:ALA:H	1:62:A:ASN:HB2	7	0.23	0.1	0.23
(4,922)	1:188:A:LEU:H	1:187:A:SER:HB2	7	0.23	0.1	0.23
(4,922)	1:122:A:HIS:H	1:122:A:HIS:HB2	7	0.23	0.1	0.23
(4,922)	1:188:A:LEU:H	1:187:A:SER:HB3	7	0.23	0.1	0.23
(4,1016)	1:43:A:SER:H	1:41:A:ASP:HB3	7	0.22	0.09	0.23
(4,1016)	1:218:A:SER:H	1:221:A:GLN:HG3	7	0.22	0.09	0.23
(4,1016)	1:218:A:SER:H	1:221:A:GLN:HB3	7	0.22	0.09	0.23
(4,704)	1:16:A:TRP:H	1:16:A:TRP:HA	7	0.21	0.04	0.22
(4,704)	1:189:A:ASP:H	1:188:A:LEU:HA	7	0.21	0.04	0.22
(4,964)	1:174:A:ASP:H	1:174:A:ASP:HB3	7	0.19	0.1	0.15
(4,964)	1:52:A:ASP:H	1:52:A:ASP:HB2	7	0.19	0.1	0.15
(4,964)	1:174:A:ASP:H	1:174:A:ASP:HB2	7	0.19	0.1	0.15
(4,1299)	1:213:A:GLU:H	1:212:A:LYS:HG3	7	0.19	0.07	0.18
(4,1299)	1:91:A:ILE:H	1:91:A:ILE:HD13	7	0.19	0.07	0.18
(4,1299)	1:79:A:LEU:H	1:78:A:VAL:HG23	7	0.19	0.07	0.18
(4,1299)	1:91:A:ILE:H	1:91:A:ILE:HD12	7	0.19	0.07	0.18
(4,1299)	1:23:A:ALA:H	1:22:A:ILE:HG22	7	0.19	0.07	0.18
(4,775)	1:106:A:GLU:H	1:105:A:SER:HA	7	0.19	0.08	0.15
(4,775)	1:147:A:LEU:H	1:147:A:LEU:HA	7	0.19	0.08	0.15
(4,775)	1:148:A:LYS:H	1:147:A:LEU:HA	7	0.19	0.08	0.15
(4,775)	1:7:A:TYR:H	1:7:A:TYR:HA	7	0.19	0.08	0.15
(4,628)	1:181:A:ARG:H	1:182:A:GLY:H	7	0.18	0.06	0.16
(4,628)	1:221:A:GLN:H	1:220:A:GLU:H	7	0.18	0.06	0.16

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,237)	1:167:A:LYS:H	1:166:A:ILE:HA	7	0.18	0.06	0.16
(4,237)	1:166:A:ILE:H	1:166:A:ILE:HA	7	0.18	0.06	0.16
(4,1191)	1:9:A:LYS:H	1:9:A:LYS:HB2	7	0.18	0.08	0.16
(4,1191)	1:148:A:LYS:H	1:148:A:LYS:HG3	7	0.18	0.08	0.16
(4,1191)	1:9:A:LYS:H	1:9:A:LYS:HB3	7	0.18	0.08	0.16
(4,1174)	1:148:A:LYS:H	1:148:A:LYS:HG3	7	0.17	0.06	0.18
(4,1174)	1:152:A:ALA:H	1:152:A:ALA:HB2	7	0.17	0.06	0.18
(4,1174)	1:152:A:ALA:H	1:152:A:ALA:HB1	7	0.17	0.06	0.18
(4,1174)	1:147:A:LEU:H	1:147:A:LEU:HG	7	0.17	0.06	0.18
(4,1174)	1:152:A:ALA:H	1:152:A:ALA:HB3	7	0.17	0.06	0.18
(4,1174)	1:9:A:LYS:H	1:9:A:LYS:HB2	7	0.17	0.06	0.18
(4,768)	1:16:A:TRP:H	1:16:A:TRP:HA	7	0.15	0.03	0.14
(4,768)	1:189:A:ASP:H	1:189:A:ASP:HA	7	0.15	0.03	0.14
(4,462)	1:159:A:VAL:HA	1:159:A:VAL:HG23	7	0.15	0.01	0.15
(4,462)	1:159:A:VAL:HA	1:159:A:VAL:HG22	7	0.15	0.01	0.15
(4,462)	1:159:A:VAL:HA	1:159:A:VAL:HG21	7	0.15	0.01	0.15
(4,823)	1:184:A:LEU:H	1:184:A:LEU:HA	7	0.15	0.04	0.12
(4,823)	1:184:A:LEU:H	1:181:A:ARG:HA	7	0.15	0.04	0.12
(4,242)	1:57:A:LEU:HB2	1:58:A:ARG:H	7	0.14	0.04	0.12
(4,242)	1:57:A:LEU:HB3	1:58:A:ARG:H	7	0.14	0.04	0.12
(4,242)	1:129:A:ASP:H	1:129:A:ASP:HB2	7	0.14	0.04	0.12
(4,1010)	1:52:A:ASP:H	1:52:A:ASP:HB2	7	0.13	0.02	0.13
(4,1010)	1:174:A:ASP:H	1:174:A:ASP:HB2	7	0.13	0.02	0.13
(4,1010)	1:174:A:ASP:H	1:174:A:ASP:HB3	7	0.13	0.02	0.13
(4,1010)	1:27:A:ARG:H	1:27:A:ARG:HB2	7	0.13	0.02	0.13
(4,1259)	1:93:A:PHE:H	1:68:A:VAL:HG23	6	2.46	0.42	2.46
(4,1259)	1:234:A:GLY:H	1:168:A:THR:HG21	6	2.46	0.42	2.46
(4,1259)	1:93:A:PHE:H	1:68:A:VAL:HG21	6	2.46	0.42	2.46
(4,1259)	1:93:A:PHE:H	1:68:A:VAL:HG22	6	2.46	0.42	2.46
(4,163)	1:231:A:ASN:H	1:240:A:MET:HA	6	1.03	0.33	0.96
(1,8)	1:95:A:PHE:H	1:95:A:PHE:HB2	6	0.84	0.03	0.84
(4,147)	1:243:A:ASN:H	1:240:A:MET:HA	6	0.83	0.43	0.76
(4,147)	1:231:A:ASN:H	1:240:A:MET:HA	6	0.83	0.43	0.76
(3,67)	1:169:A:LYS:H	1:229:A:ASN:H	6	0.79	0.91	0.41
(4,1198)	1:22:A:ILE:H	1:22:A:ILE:HD13	6	0.75	0.4	1.0
(4,1198)	1:22:A:ILE:H	1:22:A:ILE:HD11	6	0.75	0.4	1.0
(4,1198)	1:22:A:ILE:H	1:22:A:ILE:HD12	6	0.75	0.4	1.0
(4,1198)	1:157:A:GLN:H	1:153:A:LYS:HG2	6	0.75	0.4	1.0
(4,1198)	1:189:A:ASP:H	1:188:A:LEU:HB3	6	0.75	0.4	1.0
(4,6)	1:113:A:LYS:HG3	1:245:A:ARG:H	6	0.72	0.7	0.28
(4,6)	1:113:A:LYS:HG3	1:107:A:HIS:H	6	0.72	0.7	0.28
(4,393)	1:63:A:GLY:HA2	1:169:A:LYS:HB2	6	0.62	0.32	0.64

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,393)	1:232:A:GLY:HA2	1:169:A:LYS:HB2	6	0.62	0.32	0.64
(4,393)	1:232:A:GLY:HA3	1:169:A:LYS:HB2	6	0.62	0.32	0.64
(4,1279)	1:211:A:LEU:H	1:211:A:LEU:HG	6	0.56	0.45	0.47
(4,1279)	1:250:A:LEU:H	1:250:A:LEU:HD22	6	0.56	0.45	0.47
(4,1279)	1:145:A:ILE:H	1:118:A:LEU:HG	6	0.56	0.45	0.47
(4,1279)	1:49:A:VAL:H	1:49:A:VAL:HG21	6	0.56	0.45	0.47
(4,332)	1:22:A:ILE:HD12	1:204:A:GLU:HA	6	0.56	0.57	0.3
(4,332)	1:22:A:ILE:HD11	1:204:A:GLU:HA	6	0.56	0.57	0.3
(4,332)	1:22:A:ILE:HD13	1:22:A:ILE:HA	6	0.56	0.57	0.3
(4,332)	1:22:A:ILE:HD11	1:22:A:ILE:HA	6	0.56	0.57	0.3
(4,332)	1:22:A:ILE:HD12	1:22:A:ILE:HA	6	0.56	0.57	0.3
(4,626)	1:245:A:ARG:H	1:247:A:ALA:H	6	0.53	0.28	0.52
(4,626)	1:245:A:ARG:H	1:105:A:SER:H	6	0.53	0.28	0.52
(4,1123)	1:218:A:SER:H	1:221:A:GLN:HB2	6	0.49	0.49	0.3
(4,1123)	1:218:A:SER:H	1:221:A:GLN:HB3	6	0.49	0.49	0.3
(4,1123)	1:172:A:SER:H	1:171:A:LYS:HB3	6	0.49	0.49	0.3
(4,378)	1:22:A:ILE:HD13	1:20:A:PHE:HB3	6	0.44	0.46	0.15
(4,378)	1:22:A:ILE:HD11	1:20:A:PHE:HB3	6	0.44	0.46	0.15
(4,378)	1:22:A:ILE:HD11	1:28:A:GLN:HB2	6	0.44	0.46	0.15
(4,378)	1:22:A:ILE:HD12	1:28:A:GLN:HB2	6	0.44	0.46	0.15
(4,772)	1:158:A:LYS:H	1:158:A:LYS:HA	6	0.41	0.18	0.52
(4,772)	1:87:A:THR:H	1:86:A:GLY:HA2	6	0.41	0.18	0.52
(4,772)	1:164:A:ASP:H	1:164:A:ASP:HA	6	0.41	0.18	0.52
(1,25)	1:169:A:LYS:H	1:168:A:THR:HB	6	0.39	0.44	0.21
(3,71)	1:138:A:ASP:H	1:140:A:LEU:H	6	0.39	0.25	0.32
(4,1322)	1:203:A:LEU:H	1:22:A:ILE:HD12	6	0.39	0.19	0.35
(4,1322)	1:203:A:LEU:H	1:203:A:LEU:HD22	6	0.39	0.19	0.35
(4,1322)	1:203:A:LEU:H	1:22:A:ILE:HD13	6	0.39	0.19	0.35
(4,1322)	1:203:A:LEU:H	1:203:A:LEU:HD23	6	0.39	0.19	0.35
(4,231)	1:226:A:ARG:H	1:226:A:ARG:HB2	6	0.39	0.06	0.4
(4,231)	1:169:A:LYS:H	1:169:A:LYS:HD2	6	0.39	0.06	0.4
(4,231)	1:135:A:GLN:H	1:135:A:GLN:HB2	6	0.39	0.06	0.4
(4,1202)	1:198:A:THR:H	1:199:A:THR:HG23	6	0.31	0.11	0.28
(4,1202)	1:231:A:ASN:H	1:169:A:LYS:HD3	6	0.31	0.11	0.28
(4,1202)	1:99:A:SER:H	1:100:A:LEU:HG	6	0.31	0.11	0.28
(4,1202)	1:99:A:SER:H	1:241:A:VAL:HG21	6	0.31	0.11	0.28
(4,957)	1:191:A:TRP:H	1:191:A:TRP:HB3	6	0.28	0.14	0.28
(4,856)	1:167:A:LYS:H	1:167:A:LYS:HA	6	0.28	0.03	0.27
(4,856)	1:221:A:GLN:H	1:218:A:SER:HB3	6	0.28	0.03	0.27
(3,318)	1:171:A:LYS:H	1:168:A:THR:H	6	0.28	0.1	0.3
(4,1134)	1:197:A:LEU:H	1:197:A:LEU:HB3	6	0.26	0.11	0.21
(4,1134)	1:253:A:ARG:H	1:253:A:ARG:HB2	6	0.26	0.11	0.21

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,1134)	1:136:A:GLN:H	1:136:A:GLN:HB2	6	0.26	0.11	0.21
(4,1134)	1:197:A:LEU:H	1:197:A:LEU:HB2	6	0.26	0.11	0.21
(1,49)	1:224:A:LYS:HG2	1:224:A:LYS:HA	6	0.25	0.09	0.22
(4,1012)	1:18:A:LYS:H	1:17:A:HIS:HB2	6	0.25	0.11	0.24
(4,1012)	1:253:A:ARG:H	1:252:A:ASN:HB3	6	0.25	0.11	0.24
(4,1012)	1:18:A:LYS:H	1:17:A:HIS:HB3	6	0.25	0.11	0.24
(4,1012)	1:253:A:ARG:H	1:252:A:ASN:HB2	6	0.25	0.11	0.24
(4,901)	1:167:A:LYS:H	1:167:A:LYS:HA	6	0.24	0.02	0.24
(4,901)	1:221:A:GLN:H	1:218:A:SER:HB3	6	0.24	0.02	0.24
(4,624)	1:103:A:GLN:H	1:102:A:GLY:H	6	0.24	0.12	0.2
(4,624)	1:159:A:VAL:H	1:160:A:VAL:H	6	0.24	0.12	0.2
(4,1059)	1:147:A:LEU:H	1:146:A:PHE:HB3	6	0.23	0.03	0.24
(4,1059)	1:229:A:ASN:H	1:228:A:LEU:HB3	6	0.23	0.03	0.24
(4,1059)	1:124:A:ASN:H	1:124:A:ASN:HB3	6	0.23	0.03	0.24
(4,849)	1:198:A:THR:H	1:197:A:LEU:HA	6	0.22	0.02	0.22
(4,849)	1:198:A:THR:H	1:198:A:THR:HA	6	0.22	0.02	0.22
(4,849)	1:99:A:SER:H	1:99:A:SER:HA	6	0.22	0.02	0.22
(4,849)	1:116:A:ALA:H	1:116:A:ALA:HA	6	0.22	0.02	0.22
(4,258)	1:252:A:ASN:H	1:252:A:ASN:HB2	6	0.21	0.05	0.2
(4,258)	1:252:A:ASN:H	1:252:A:ASN:HB3	6	0.21	0.05	0.2
(4,258)	1:242:A:ASP:H	1:97:A:TRP:HB2	6	0.21	0.05	0.2
(4,258)	1:242:A:ASP:H	1:242:A:ASP:HB3	6	0.21	0.05	0.2
(4,1292)	1:91:A:ILE:H	1:91:A:ILE:HD13	6	0.19	0.07	0.2
(4,1292)	1:79:A:LEU:H	1:78:A:VAL:HG23	6	0.19	0.07	0.2
(4,1292)	1:91:A:ILE:H	1:91:A:ILE:HD12	6	0.19	0.07	0.2
(4,1292)	1:23:A:ALA:H	1:22:A:ILE:HG22	6	0.19	0.07	0.2
(4,987)	1:244:A:TRP:H	1:244:A:TRP:HB3	6	0.16	0.04	0.16
(4,987)	1:241:A:VAL:H	1:240:A:MET:HA	6	0.16	0.04	0.16
(4,1268)	1:204:A:GLU:H	1:22:A:ILE:HD11	6	0.16	0.04	0.17
(4,1268)	1:210:A:VAL:H	1:209:A:ILE:HG22	6	0.16	0.04	0.17
(4,1268)	1:204:A:GLU:H	1:22:A:ILE:HD12	6	0.16	0.04	0.17
(4,1268)	1:204:A:GLU:H	1:22:A:ILE:HD13	6	0.16	0.04	0.17
(4,1268)	1:210:A:VAL:H	1:209:A:ILE:HG23	6	0.16	0.04	0.17
(4,1186)	1:117:A:GLU:H	1:116:A:ALA:HB3	6	0.16	0.02	0.16
(4,1186)	1:9:A:LYS:H	1:9:A:LYS:HB3	6	0.16	0.02	0.16
(4,1186)	1:9:A:LYS:H	1:9:A:LYS:HB2	6	0.16	0.02	0.16
(4,1146)	1:135:A:GLN:H	1:135:A:GLN:HB2	6	0.15	0.03	0.15
(4,1146)	1:227:A:LYS:H	1:227:A:LYS:HB2	6	0.15	0.03	0.15
(4,1146)	1:162:A:VAL:H	1:162:A:VAL:HB	6	0.15	0.03	0.15
(4,1158)	1:84:A:LEU:H	1:84:A:LEU:HB3	6	0.14	0.03	0.13
(4,1158)	1:223:A:LEU:H	1:223:A:LEU:HB2	6	0.14	0.03	0.13
(4,1158)	1:147:A:LEU:H	1:147:A:LEU:HB2	6	0.14	0.03	0.13

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,1158)	1:84:A:LEU:H	1:84:A:LEU:HB2	6	0.14	0.03	0.13
(4,1158)	1:22:A:ILE:H	1:22:A:ILE:HB	6	0.14	0.03	0.13
(1,10)	1:55:A:THR:H	1:55:A:THR:HB	6	0.13	0.03	0.12
(1,36)	1:203:A:LEU:H	1:22:A:ILE:HD13	5	5.81	6.65	2.48
(1,36)	1:203:A:LEU:H	1:22:A:ILE:HD11	5	5.81	6.65	2.48
(1,36)	1:203:A:LEU:H	1:22:A:ILE:HD12	5	5.81	6.65	2.48
(1,77)	1:224:A:LYS:HB2	1:163:A:LEU:HD22	5	3.33	2.53	4.09
(1,77)	1:224:A:LYS:HB2	1:163:A:LEU:HD23	5	3.33	2.53	4.09
(1,77)	1:224:A:LYS:HB3	1:163:A:LEU:HD22	5	3.33	2.53	4.09
(1,77)	1:224:A:LYS:HB3	1:163:A:LEU:HD21	5	3.33	2.53	4.09
(4,1271)	1:231:A:ASN:H	1:169:A:LYS:HG2	5	1.81	1.62	1.33
(4,1271)	1:231:A:ASN:H	1:168:A:THR:HG22	5	1.81	1.62	1.33
(4,1339)	1:93:A:PHE:H	1:91:A:ILE:HD12	5	1.18	0.91	0.87
(4,1339)	1:116:A:ALA:H	1:149:A:VAL:HG21	5	1.18	0.91	0.87
(4,1339)	1:116:A:ALA:H	1:149:A:VAL:HG22	5	1.18	0.91	0.87
(4,1339)	1:116:A:ALA:H	1:149:A:VAL:HG23	5	1.18	0.91	0.87
(4,398)	1:123:A:TRP:HB3	1:140:A:LEU:HB3	5	1.13	1.11	0.81
(4,398)	1:130:A:PHE:HB3	1:123:A:TRP:HB2	5	1.13	1.11	0.81
(3,322)	1:108:A:THR:H	1:31:A:VAL:H	5	1.1	0.43	1.23
(4,275)	1:117:A:GLU:HB2	1:146:A:PHE:HA	5	1.06	0.66	0.93
(4,275)	1:243:A:ASN:HB2	1:244:A:TRP:HA	5	1.06	0.66	0.93
(4,275)	1:243:A:ASN:HB3	1:244:A:TRP:HA	5	1.06	0.66	0.93
(4,275)	1:117:A:GLU:HB3	1:146:A:PHE:HA	5	1.06	0.66	0.93
(4,88)	1:210:A:VAL:H	1:192:A:THR:HB	5	0.99	0.65	0.65
(4,88)	1:71:A:ASP:H	1:55:A:THR:HB	5	0.99	0.65	0.65
(4,1224)	1:123:A:TRP:H	1:89:A:ARG:HB2	5	0.73	0.45	0.86
(4,1224)	1:229:A:ASN:H	1:228:A:LEU:HD23	5	0.73	0.45	0.86
(4,1224)	1:123:A:TRP:H	1:91:A:ILE:HG12	5	0.73	0.45	0.86
(4,1224)	1:148:A:LYS:H	1:148:A:LYS:HG3	5	0.73	0.45	0.86
(4,1224)	1:229:A:ASN:H	1:168:A:THR:HG21	5	0.73	0.45	0.86
(4,32)	1:191:A:TRP:H	1:211:A:LEU:HG	5	0.71	0.62	0.29
(4,32)	1:211:A:LEU:HG	1:144:A:GLY:H	5	0.71	0.62	0.29
(4,32)	1:121:A:VAL:H	1:90:A:LEU:HG	5	0.71	0.62	0.29
(3,125)	1:245:A:ARG:H	1:106:A:GLU:H	5	0.63	0.48	0.44
(4,1153)	1:96:A:HIS:H	1:116:A:ALA:HB3	5	0.63	0.1	0.6
(4,1153)	1:78:A:VAL:H	1:77:A:ALA:HB3	5	0.63	0.1	0.6
(4,1153)	1:78:A:VAL:H	1:77:A:ALA:HB1	5	0.63	0.1	0.6
(4,1308)	1:189:A:ASP:H	1:188:A:LEU:HD23	5	0.61	0.44	0.42
(4,1308)	1:212:A:LYS:H	1:211:A:LEU:HD23	5	0.61	0.44	0.42
(4,1308)	1:212:A:LYS:H	1:211:A:LEU:HD22	5	0.61	0.44	0.42
(4,1308)	1:212:A:LYS:H	1:212:A:LYS:HG2	5	0.61	0.44	0.42
(4,1309)	1:163:A:LEU:H	1:163:A:LEU:HD23	5	0.55	0.37	0.33

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,1309)	1:163:A:LEU:H	1:162:A:VAL:HG23	5	0.55	0.37	0.33
(4,1309)	1:212:A:LYS:H	1:211:A:LEU:HD22	5	0.55	0.37	0.33
(4,1309)	1:169:A:LYS:H	1:169:A:LYS:HG3	5	0.55	0.37	0.33
(4,1309)	1:212:A:LYS:H	1:211:A:LEU:HD23	5	0.55	0.37	0.33
(4,668)	1:29:A:SER:H	1:198:A:THR:HG1	5	0.46	0.24	0.37
(4,668)	1:29:A:SER:H	1:31:A:VAL:H	5	0.46	0.24	0.37
(4,669)	1:29:A:SER:H	1:198:A:THR:HG1	5	0.46	0.24	0.37
(4,669)	1:29:A:SER:H	1:31:A:VAL:H	5	0.46	0.24	0.37
(1,120)	1:259:A:PHE:H	1:257:A:ALA:HB2	5	0.43	0.55	0.16
(1,120)	1:259:A:PHE:H	1:257:A:ALA:HB1	5	0.43	0.55	0.16
(4,1082)	1:251:A:LYS:H	1:251:A:LYS:HB3	5	0.33	0.19	0.29
(4,1082)	1:251:A:LYS:H	1:250:A:LEU:HB3	5	0.33	0.19	0.29
(4,1082)	1:251:A:LYS:H	1:251:A:LYS:HB2	5	0.33	0.19	0.29
(4,1200)	1:251:A:LYS:H	1:250:A:LEU:HB3	5	0.32	0.11	0.36
(4,1200)	1:251:A:LYS:H	1:251:A:LYS:HG2	5	0.32	0.11	0.36
(4,1200)	1:251:A:LYS:H	1:250:A:LEU:HB2	5	0.32	0.11	0.36
(4,43)	1:95:A:PHE:H	1:95:A:PHE:HB3	5	0.32	0.13	0.27
(4,43)	1:96:A:HIS:H	1:95:A:PHE:HB3	5	0.32	0.13	0.27
(4,1192)	1:251:A:LYS:H	1:250:A:LEU:HB3	5	0.31	0.11	0.35
(4,1192)	1:251:A:LYS:H	1:251:A:LYS:HG2	5	0.31	0.11	0.35
(4,1192)	1:251:A:LYS:H	1:250:A:LEU:HB2	5	0.31	0.11	0.35
(4,90)	1:33:A:ILE:H	1:108:A:THR:HB	5	0.31	0.15	0.27
(4,90)	1:112:A:LYS:H	1:108:A:THR:HB	5	0.31	0.15	0.27
(4,90)	1:233:A:GLU:H	1:168:A:THR:HB	5	0.31	0.15	0.27
(1,113)	1:104:A:GLY:H	1:103:A:GLN:HB3	5	0.3	0.16	0.24
(1,113)	1:104:A:GLY:H	1:103:A:GLN:HB2	5	0.3	0.16	0.24
(4,1212)	1:205:A:CYS:H	1:203:A:LEU:HB2	5	0.28	0.17	0.21
(4,1212)	1:205:A:CYS:H	1:206:A:VAL:HG23	5	0.28	0.17	0.21
(4,1212)	1:176:A:THR:H	1:176:A:THR:HG22	5	0.28	0.17	0.21
(4,436)	1:86:A:GLY:HA3	1:126:A:LYS:HG2	5	0.27	0.17	0.17
(4,436)	1:82:A:GLY:HA3	1:45:A:LYS:HG2	5	0.27	0.17	0.17
(4,436)	1:63:A:GLY:HA2	1:169:A:LYS:HG2	5	0.27	0.17	0.17
(4,436)	1:63:A:GLY:HA2	1:169:A:LYS:HG3	5	0.27	0.17	0.17
(4,1213)	1:239:A:LEU:H	1:239:A:LEU:HB2	5	0.24	0.07	0.27
(4,1213)	1:211:A:LEU:H	1:211:A:LEU:HG	5	0.24	0.07	0.27
(4,1213)	1:239:A:LEU:H	1:239:A:LEU:HB3	5	0.24	0.07	0.27
(4,1213)	1:256:A:LYS:H	1:256:A:LYS:HG3	5	0.24	0.07	0.27
(4,1213)	1:256:A:LYS:H	1:256:A:LYS:HG2	5	0.24	0.07	0.27
(4,1110)	1:23:A:ALA:H	1:23:A:ALA:HB1	5	0.23	0.11	0.17
(4,1110)	1:77:A:ALA:H	1:76:A:LYS:HB2	5	0.23	0.11	0.17
(4,1110)	1:77:A:ALA:H	1:76:A:LYS:HB3	5	0.23	0.11	0.17
(4,1110)	1:90:A:LEU:H	1:90:A:LEU:HB2	5	0.23	0.11	0.17

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,1185)	1:45:A:LYS:H	1:45:A:LYS:HG3	5	0.21	0.05	0.19
(4,1185)	1:126:A:LYS:H	1:126:A:LYS:HB2	5	0.21	0.05	0.19
(4,618)	1:56:A:SER:H	1:58:A:ARG:H	5	0.21	0.07	0.18
(4,618)	1:245:A:ARG:H	1:247:A:ALA:H	5	0.21	0.07	0.18
(4,1164)	1:167:A:LYS:H	1:167:A:LYS:HB3	5	0.2	0.1	0.16
(4,1164)	1:167:A:LYS:H	1:167:A:LYS:HB2	5	0.2	0.1	0.16
(4,1164)	1:197:A:LEU:H	1:197:A:LEU:HB2	5	0.2	0.1	0.16
(4,620)	1:37:A:THR:H	1:36:A:HIS:H	5	0.19	0.07	0.21
(4,909)	1:70:A:PHE:H	1:70:A:PHE:HB2	5	0.19	0.07	0.15
(4,909)	1:32:A:ASP:H	1:31:A:VAL:HA	5	0.19	0.07	0.15
(4,909)	1:190:A:TYR:H	1:258:A:SER:HB3	5	0.19	0.07	0.15
(4,909)	1:48:A:SER:H	1:48:A:SER:HB2	5	0.19	0.07	0.15
(1,14)	1:140:A:LEU:H	1:139:A:GLY:HA3	5	0.19	0.03	0.19
(4,1111)	1:181:A:ARG:H	1:181:A:ARG:HG3	5	0.18	0.05	0.18
(4,1111)	1:254:A:GLN:H	1:253:A:ARG:HB3	5	0.18	0.05	0.18
(4,1111)	1:197:A:LEU:H	1:197:A:LEU:HB2	5	0.18	0.05	0.18
(4,1058)	1:248:A:GLN:H	1:248:A:GLN:HB3	5	0.18	0.05	0.19
(4,1058)	1:52:A:ASP:H	1:52:A:ASP:HB2	5	0.18	0.05	0.19
(4,1058)	1:233:A:GLU:H	1:233:A:GLU:HG3	5	0.18	0.05	0.19
(4,1058)	1:248:A:GLN:H	1:248:A:GLN:HG2	5	0.18	0.05	0.19
(4,1058)	1:27:A:ARG:H	1:27:A:ARG:HG3	5	0.18	0.05	0.19
(4,1101)	1:181:A:ARG:H	1:181:A:ARG:HG3	5	0.17	0.03	0.18
(4,1101)	1:254:A:GLN:H	1:253:A:ARG:HB3	5	0.17	0.03	0.18
(4,1101)	1:220:A:GLU:H	1:220:A:GLU:HB2	5	0.17	0.03	0.18
(4,263)	1:244:A:TRP:HA	1:244:A:TRP:H	5	0.16	0.03	0.18
(4,263)	1:243:A:ASN:HA	1:244:A:TRP:H	5	0.16	0.03	0.18
(4,569)	1:127:A:TYR:H	1:126:A:LYS:H	5	0.16	0.06	0.11
(4,614)	1:19:A:ASP:H	1:20:A:PHE:H	5	0.15	0.04	0.13
(4,614)	1:160:A:VAL:H	1:161:A:ASP:H	5	0.15	0.04	0.13
(1,93)	1:150:A:GLY:H	1:218:A:SER:HA	4	2.11	0.43	1.92
(3,15)	1:243:A:ASN:H	1:97:A:TRP:H	4	1.53	1.18	1.51
(3,206)	1:100:A:LEU:H	1:103:A:GLN:H	4	1.5	0.85	1.65
(4,1337)	1:91:A:ILE:H	1:91:A:ILE:HD11	4	1.39	0.66	1.36
(4,1337)	1:91:A:ILE:H	1:91:A:ILE:HD13	4	1.39	0.66	1.36
(1,40)	1:203:A:LEU:H	1:202:A:LEU:HB3	4	1.07	0.19	1.06
(1,40)	1:203:A:LEU:H	1:202:A:LEU:HB2	4	1.07	0.19	1.06
(4,268)	1:203:A:LEU:H	1:203:A:LEU:HG	4	1.05	0.86	1.1
(4,268)	1:184:A:LEU:H	1:184:A:LEU:HG	4	1.05	0.86	1.1
(1,110)	1:198:A:THR:H	1:197:A:LEU:HB3	4	0.91	0.07	0.9
(1,110)	1:198:A:THR:H	1:197:A:LEU:HB2	4	0.91	0.07	0.9
(4,21)	1:123:A:TRP:H	1:89:A:ARG:HB3	4	0.84	0.57	0.66
(4,21)	1:118:A:LEU:H	1:147:A:LEU:HG	4	0.84	0.57	0.66

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,21)	1:123:A:TRP:H	1:89:A:ARG:HB2	4	0.84	0.57	0.66
(2,12)	1:107:A:HIS:HA	1:31:A:VAL:H	4	0.83	0.14	0.85
(4,401)	1:196:A:SER:HB3	1:204:A:GLU:HB3	4	0.76	0.36	0.76
(4,401)	1:196:A:SER:HB3	1:197:A:LEU:HG	4	0.76	0.36	0.76
(4,401)	1:203:A:LEU:HB2	1:196:A:SER:HB3	4	0.76	0.36	0.76
(4,401)	1:78:A:VAL:HB	1:87:A:THR:HB	4	0.76	0.36	0.76
(4,312)	1:255:A:ILE:HD12	1:255:A:ILE:HA	4	0.7	0.37	0.74
(4,312)	1:209:A:ILE:HD13	1:209:A:ILE:HA	4	0.7	0.37	0.74
(4,312)	1:209:A:ILE:HD12	1:209:A:ILE:HA	4	0.7	0.37	0.74
(4,168)	1:164:A:ASP:H	1:163:A:LEU:HB3	4	0.66	0.35	0.74
(4,168)	1:45:A:LYS:H	1:44:A:LEU:HB3	4	0.66	0.35	0.74
(4,168)	1:212:A:LYS:H	1:211:A:LEU:HB3	4	0.66	0.35	0.74
(4,234)	1:206:A:VAL:H	1:22:A:ILE:HD11	4	0.66	0.24	0.66
(4,234)	1:24:A:LYS:H	1:22:A:ILE:HD12	4	0.66	0.24	0.66
(4,234)	1:206:A:VAL:H	1:22:A:ILE:HD12	4	0.66	0.24	0.66
(1,71)	1:77:A:ALA:HB2	1:51:A:TYR:HA	4	0.66	0.83	0.18
(1,71)	1:77:A:ALA:HB1	1:51:A:TYR:HA	4	0.66	0.83	0.18
(1,71)	1:77:A:ALA:HB3	1:51:A:TYR:HA	4	0.66	0.83	0.18
(4,1217)	1:197:A:LEU:H	1:197:A:LEU:HG	4	0.63	0.34	0.53
(4,1217)	1:74:A:GLN:H	1:76:A:LYS:HD3	4	0.63	0.34	0.53
(4,609)	1:242:A:ASP:H	1:243:A:ASN:H	4	0.54	0.74	0.12
(1,59)	1:240:A:MET:HA	1:230:A:PHE:HB2	4	0.52	0.26	0.57
(4,442)	1:86:A:GLY:HA3	1:126:A:LYS:HG2	4	0.51	0.18	0.56
(4,442)	1:63:A:GLY:HA2	1:169:A:LYS:HG2	4	0.51	0.18	0.56
(4,442)	1:63:A:GLY:HA2	1:169:A:LYS:HG3	4	0.51	0.18	0.56
(4,442)	1:86:A:GLY:HA2	1:126:A:LYS:HD2	4	0.51	0.18	0.56
(2,16)	1:82:A:GLY:H	1:45:A:LYS:H	4	0.48	0.14	0.53
(4,1201)	1:172:A:SER:H	1:166:A:ILE:HG22	4	0.47	0.46	0.24
(4,1201)	1:172:A:SER:H	1:171:A:LYS:HD2	4	0.47	0.46	0.24
(4,1201)	1:172:A:SER:H	1:166:A:ILE:HG23	4	0.47	0.46	0.24
(4,1201)	1:172:A:SER:H	1:166:A:ILE:HG21	4	0.47	0.46	0.24
(4,24)	1:55:A:THR:H	1:76:A:LYS:HD2	4	0.46	0.24	0.5
(4,24)	1:55:A:THR:H	1:76:A:LYS:HD3	4	0.46	0.24	0.5
(4,1209)	1:172:A:SER:H	1:166:A:ILE:HG22	4	0.46	0.46	0.24
(4,1209)	1:172:A:SER:H	1:171:A:LYS:HD2	4	0.46	0.46	0.24
(4,1209)	1:172:A:SER:H	1:166:A:ILE:HG23	4	0.46	0.46	0.24
(4,1209)	1:172:A:SER:H	1:166:A:ILE:HG21	4	0.46	0.46	0.24
(4,409)	1:192:A:THR:HG21	1:257:A:ALA:HA	4	0.4	0.19	0.4
(4,409)	1:41:A:ASP:HA	1:41:A:ASP:HB3	4	0.4	0.19	0.4
(4,409)	1:192:A:THR:HG22	1:257:A:ALA:HA	4	0.4	0.19	0.4
(1,22)	1:156:A:LEU:H	1:153:A:LYS:HD2	4	0.34	0.17	0.36
(4,965)	1:253:A:ARG:H	1:252:A:ASN:HB2	4	0.32	0.21	0.22

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,965)	1:54:A:ALA:H	1:53:A:GLN:HB2	4	0.32	0.21	0.22
(4,965)	1:253:A:ARG:H	1:252:A:ASN:HB3	4	0.32	0.21	0.22
(4,1222)	1:223:A:LEU:H	1:223:A:LEU:HB2	4	0.31	0.01	0.31
(4,1222)	1:89:A:ARG:H	1:89:A:ARG:HB3	4	0.31	0.01	0.31
(4,1286)	1:87:A:THR:H	1:87:A:THR:HG22	4	0.3	0.24	0.17
(4,1286)	1:78:A:VAL:H	1:78:A:VAL:HG23	4	0.3	0.24	0.17
(4,1286)	1:258:A:SER:H	1:257:A:ALA:HB3	4	0.3	0.24	0.17
(1,60)	1:51:A:TYR:HB3	1:51:A:TYR:HA	4	0.3	0.0	0.3
(4,1287)	1:87:A:THR:H	1:87:A:THR:HG22	4	0.3	0.24	0.16
(4,1287)	1:78:A:VAL:H	1:78:A:VAL:HG23	4	0.3	0.24	0.16
(4,1287)	1:258:A:SER:H	1:257:A:ALA:HB3	4	0.3	0.24	0.16
(4,988)	1:205:A:CYS:H	1:205:A:CYS:HB3	4	0.28	0.16	0.26
(4,988)	1:116:A:ALA:H	1:114:A:TYR:HB3	4	0.28	0.16	0.26
(4,1024)	1:22:A:ILE:H	1:20:A:PHE:HB2	4	0.28	0.12	0.29
(4,1024)	1:22:A:ILE:H	1:20:A:PHE:HB3	4	0.28	0.12	0.29
(4,1048)	1:176:A:THR:H	1:175:A:PHE:HB2	4	0.28	0.16	0.23
(4,1048)	1:103:A:GLN:H	1:103:A:GLN:HG2	4	0.28	0.16	0.23
(4,1048)	1:103:A:GLN:H	1:100:A:LEU:HB3	4	0.28	0.16	0.23
(4,81)	1:55:A:THR:H	1:76:A:LYS:HG3	4	0.26	0.08	0.28
(4,213)	1:167:A:LYS:H	1:167:A:LYS:HB3	4	0.26	0.08	0.26
(4,213)	1:135:A:GLN:H	1:135:A:GLN:HG3	4	0.26	0.08	0.26
(4,213)	1:167:A:LYS:HB2	1:168:A:THR:H	4	0.26	0.08	0.26
(4,213)	1:167:A:LYS:HB3	1:168:A:THR:H	4	0.26	0.08	0.26
(4,1066)	1:224:A:LYS:H	1:224:A:LYS:HG3	4	0.25	0.05	0.25
(4,1066)	1:224:A:LYS:H	1:224:A:LYS:HG2	4	0.25	0.05	0.25
(4,1066)	1:135:A:GLN:H	1:135:A:GLN:HG2	4	0.25	0.05	0.25
(4,1066)	1:24:A:LYS:H	1:24:A:LYS:HB2	4	0.25	0.05	0.25
(4,974)	1:40:A:TYR:H	1:40:A:TYR:HB3	4	0.25	0.11	0.21
(4,974)	1:238:A:GLU:H	1:229:A:ASN:HB3	4	0.25	0.11	0.21
(4,864)	1:221:A:GLN:H	1:218:A:SER:HB3	4	0.24	0.0	0.24
(4,864)	1:167:A:LYS:H	1:167:A:LYS:HA	4	0.24	0.0	0.24
(4,1141)	1:20:A:PHE:H	1:19:A:ASP:HB2	4	0.23	0.05	0.23
(4,1141)	1:129:A:ASP:H	1:132:A:LYS:HB2	4	0.23	0.05	0.23
(4,1141)	1:164:A:ASP:H	1:163:A:LEU:HB3	4	0.23	0.05	0.23
(4,970)	1:88:A:TYR:H	1:88:A:TYR:HB2	4	0.23	0.1	0.18
(4,970)	1:88:A:TYR:H	1:88:A:TYR:HB3	4	0.23	0.1	0.18
(4,972)	1:18:A:LYS:H	1:17:A:HIS:HB3	4	0.22	0.05	0.2
(4,972)	1:100:A:LEU:H	1:99:A:SER:HB3	4	0.22	0.05	0.2
(4,972)	1:253:A:ARG:H	1:252:A:ASN:HB3	4	0.22	0.05	0.2
(4,96)	1:140:A:LEU:H	1:205:A:CYS:HB2	4	0.22	0.11	0.18
(4,96)	1:53:A:GLN:H	1:53:A:GLN:HB3	4	0.22	0.11	0.18
(4,96)	1:94:A:HIS:H	1:94:A:HIS:HB3	4	0.22	0.11	0.18

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,96)	1:140:A:LEU:H	1:205:A:CYS:HB3	4	0.22	0.11	0.18
(4,218)	1:169:A:LYS:H	1:169:A:LYS:HB2	4	0.16	0.05	0.15
(4,218)	1:224:A:LYS:H	1:224:A:LYS:HB2	4	0.16	0.05	0.15
(4,211)	1:206:A:VAL:H	1:206:A:VAL:HB	4	0.16	0.03	0.15
(4,924)	1:129:A:ASP:H	1:128:A:GLY:HA3	4	0.15	0.02	0.15
(4,924)	1:183:A:LEU:H	1:182:A:GLY:HA3	4	0.15	0.02	0.15
(4,924)	1:129:A:ASP:H	1:129:A:ASP:HA	4	0.15	0.02	0.15
(4,1036)	1:158:A:LYS:H	1:158:A:LYS:HB2	4	0.15	0.05	0.14
(4,1036)	1:158:A:LYS:H	1:158:A:LYS:HB3	4	0.15	0.05	0.14
(4,317)	1:209:A:ILE:HG21	1:209:A:ILE:HA	4	0.14	0.02	0.14
(4,317)	1:54:A:ALA:HB3	1:54:A:ALA:HA	4	0.14	0.02	0.14
(4,317)	1:166:A:ILE:HG22	1:166:A:ILE:HA	4	0.14	0.02	0.14
(4,317)	1:192:A:THR:HG23	1:192:A:THR:HB	4	0.14	0.02	0.14
(4,1057)	1:260:A:LYS:H	1:260:A:LYS:HB2	4	0.12	0.02	0.12
(4,1057)	1:204:A:GLU:H	1:204:A:GLU:HB2	4	0.12	0.02	0.12
(4,1057)	1:209:A:ILE:H	1:209:A:ILE:HB	4	0.12	0.02	0.12
(1,29)	1:163:A:LEU:HA	1:163:A:LEU:H	4	0.12	0.0	0.12
(4,305)	1:130:A:PHE:HB2	1:130:A:PHE:HA	4	0.12	0.0	0.12
(4,305)	1:110:A:ASP:HB3	1:110:A:ASP:HA	4	0.12	0.0	0.12
(4,305)	1:130:A:PHE:HB3	1:130:A:PHE:HA	4	0.12	0.0	0.12
(4,995)	1:124:A:ASN:H	1:124:A:ASN:HB2	4	0.12	0.0	0.12
(4,995)	1:178:A:PHE:H	1:178:A:PHE:HB3	4	0.12	0.0	0.12
(4,995)	1:70:A:PHE:H	1:70:A:PHE:HB2	4	0.12	0.0	0.12
(4,995)	1:229:A:ASN:H	1:229:A:ASN:HB2	4	0.12	0.0	0.12
(1,44)	1:91:A:ILE:HD12	1:122:A:HIS:HA	3	1.89	2.4	0.24
(1,44)	1:91:A:ILE:HD11	1:122:A:HIS:HA	3	1.89	2.4	0.24
(4,1245)	1:172:A:SER:H	1:166:A:ILE:HG21	3	1.64	0.47	1.73
(4,1245)	1:172:A:SER:H	1:166:A:ILE:HG22	3	1.64	0.47	1.73
(4,1245)	1:93:A:PHE:H	1:68:A:VAL:HG21	3	1.64	0.47	1.73
(4,1295)	1:123:A:TRP:H	1:91:A:ILE:HD11	3	1.44	0.37	1.2
(4,1295)	1:123:A:TRP:H	1:91:A:ILE:HD13	3	1.44	0.37	1.2
(4,1295)	1:148:A:LYS:H	1:148:A:LYS:HG2	3	1.44	0.37	1.2
(4,259)	1:242:A:ASP:H	1:241:A:VAL:HB	3	1.33	0.05	1.33
(3,47)	1:60:A:LEU:H	1:67:A:ASN:H	3	1.2	0.79	0.93
(3,12)	1:218:A:SER:H	1:150:A:GLY:H	3	1.11	0.69	1.55
(4,1063)	1:99:A:SER:H	1:241:A:VAL:HB	3	1.0	0.43	1.28
(4,1063)	1:8:A:GLY:H	1:7:A:TYR:HB3	3	1.0	0.43	1.28
(4,239)	1:135:A:GLN:H	1:139:A:GLY:HA3	3	0.95	0.61	1.06
(4,1177)	1:78:A:VAL:H	1:77:A:ALA:HB1	3	0.87	0.29	0.69
(4,1177)	1:78:A:VAL:H	1:77:A:ALA:HB2	3	0.87	0.29	0.69
(4,1177)	1:78:A:VAL:H	1:77:A:ALA:HB3	3	0.87	0.29	0.69
(1,32)	1:167:A:LYS:HB2	1:168:A:THR:H	3	0.84	0.14	0.84

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,1088)	1:232:A:GLY:H	1:235:A:GLU:HG3	3	0.78	0.41	0.72
(4,1088)	1:232:A:GLY:H	1:235:A:GLU:HG2	3	0.78	0.41	0.72
(4,1088)	1:232:A:GLY:H	1:169:A:LYS:HB2	3	0.78	0.41	0.72
(4,1334)	1:82:A:GLY:H	1:84:A:LEU:HD21	3	0.77	0.31	0.59
(4,1334)	1:82:A:GLY:H	1:84:A:LEU:HD23	3	0.77	0.31	0.59
(4,1334)	1:226:A:ARG:H	1:163:A:LEU:HD21	3	0.77	0.31	0.59
(1,109)	1:146:A:PHE:H	1:146:A:PHE:HB3	3	0.73	0.23	0.75
(1,109)	1:146:A:PHE:H	1:146:A:PHE:HB2	3	0.73	0.23	0.75
(1,21)	1:37:A:THR:H	1:37:A:THR:HB	3	0.73	0.01	0.73
(4,387)	1:22:A:ILE:HD11	1:28:A:GLN:HB2	3	0.72	0.47	0.79
(4,387)	1:22:A:ILE:HD11	1:20:A:PHE:HB3	3	0.72	0.47	0.79
(4,387)	1:22:A:ILE:HD12	1:28:A:GLN:HB2	3	0.72	0.47	0.79
(4,1326)	1:212:A:LYS:H	1:211:A:LEU:HD22	3	0.72	0.34	0.88
(4,1326)	1:212:A:LYS:H	1:211:A:LEU:HD23	3	0.72	0.34	0.88
(4,381)	1:40:A:TYR:HB3	1:260:A:LYS:HA	3	0.69	0.76	0.18
(4,381)	1:260:A:LYS:HA	1:259:A:PHE:HB3	3	0.69	0.76	0.18
(4,392)	1:64:A:HIS:HB2	1:169:A:LYS:HB2	3	0.68	0.27	0.8
(4,392)	1:61:A:ASN:HB3	1:64:A:HIS:HB3	3	0.68	0.27	0.8
(1,20)	1:197:A:LEU:H	1:197:A:LEU:HB2	3	0.63	0.17	0.69
(3,13)	1:207:A:THR:H	1:195:A:GLY:H	3	0.53	0.39	0.33
(1,26)	1:156:A:LEU:H	1:156:A:LEU:HB2	3	0.49	0.37	0.33
(1,26)	1:156:A:LEU:H	1:156:A:LEU:HB3	3	0.49	0.37	0.33
(4,1250)	1:163:A:LEU:H	1:162:A:VAL:HG21	3	0.48	0.45	0.16
(4,1250)	1:169:A:LYS:H	1:169:A:LYS:HG3	3	0.48	0.45	0.16
(4,1250)	1:163:A:LEU:H	1:162:A:VAL:HG23	3	0.48	0.45	0.16
(4,209)	1:82:A:GLY:H	1:47:A:LEU:HB3	3	0.47	0.38	0.25
(4,209)	1:199:A:THR:H	1:197:A:LEU:HB2	3	0.47	0.38	0.25
(4,209)	1:82:A:GLY:H	1:47:A:LEU:HB2	3	0.47	0.38	0.25
(4,1248)	1:22:A:ILE:H	1:22:A:ILE:HD12	3	0.44	0.37	0.23
(4,1248)	1:22:A:ILE:H	1:22:A:ILE:HD11	3	0.44	0.37	0.23
(4,495)	1:94:A:HIS:H	1:119:A:HIS:H	3	0.37	0.17	0.3
(4,495)	1:116:A:ALA:H	1:147:A:LEU:H	3	0.37	0.17	0.3
(4,475)	1:73:A:SER:H	1:72:A:ASP:H	3	0.34	0.06	0.31
(4,475)	1:219:A:SER:H	1:150:A:GLY:H	3	0.34	0.06	0.31
(4,36)	1:85:A:ASP:H	1:85:A:ASP:HB3	3	0.32	0.15	0.27
(4,36)	1:67:A:ASN:H	1:66:A:PHE:HB2	3	0.32	0.15	0.27
(1,45)	1:225:A:PHE:HB2	1:222:A:VAL:HA	3	0.32	0.07	0.27
(1,45)	1:225:A:PHE:HB3	1:222:A:VAL:HA	3	0.32	0.07	0.27
(4,703)	1:204:A:GLU:H	1:203:A:LEU:HA	3	0.32	0.08	0.35
(4,703)	1:112:A:LYS:H	1:112:A:LYS:HA	3	0.32	0.08	0.35
(4,896)	1:160:A:VAL:H	1:160:A:VAL:HA	3	0.31	0.02	0.32
(4,896)	1:159:A:VAL:H	1:159:A:VAL:HA	3	0.31	0.02	0.32

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,1265)	1:176:A:THR:H	1:176:A:THR:HG22	3	0.27	0.18	0.19
(4,1265)	1:205:A:CYS:H	1:206:A:VAL:HG23	3	0.27	0.18	0.19
(4,841)	1:161:A:ASP:H	1:161:A:ASP:HA	3	0.26	0.06	0.26
(4,841)	1:29:A:SER:H	1:28:A:GLN:HA	3	0.26	0.06	0.26
(4,841)	1:167:A:LYS:H	1:167:A:LYS:HA	3	0.26	0.06	0.26
(4,1094)	1:37:A:THR:H	1:34:A:ASP:HB3	3	0.24	0.07	0.26
(4,1106)	1:90:A:LEU:H	1:90:A:LEU:HB2	3	0.24	0.1	0.26
(4,1106)	1:77:A:ALA:H	1:76:A:LYS:HB3	3	0.24	0.1	0.26
(4,1106)	1:23:A:ALA:H	1:23:A:ALA:HB1	3	0.24	0.1	0.26
(4,34)	1:59:A:ILE:H	1:166:A:ILE:HG23	3	0.23	0.14	0.14
(4,34)	1:170:A:GLY:H	1:166:A:ILE:HG23	3	0.23	0.14	0.14
(4,34)	1:59:A:ILE:H	1:166:A:ILE:HG21	3	0.23	0.14	0.14
(4,715)	1:98:A:GLY:H	1:97:A:TRP:HA	3	0.21	0.06	0.17
(4,715)	1:98:A:GLY:H	1:98:A:GLY:HA3	3	0.21	0.06	0.17
(4,1009)	1:62:A:ASN:H	1:61:A:ASN:HB3	3	0.19	0.07	0.24
(4,1115)	1:158:A:LYS:H	1:158:A:LYS:HB2	3	0.19	0.03	0.19
(4,1115)	1:158:A:LYS:H	1:158:A:LYS:HB3	3	0.19	0.03	0.19
(4,145)	1:218:A:SER:H	1:221:A:GLN:HG3	3	0.19	0.07	0.17
(4,145)	1:149:A:VAL:H	1:148:A:LYS:HB2	3	0.19	0.07	0.17
(4,1053)	1:37:A:THR:H	1:34:A:ASP:HB3	3	0.18	0.05	0.19
(4,1053)	1:86:A:GLY:H	1:84:A:LEU:HB2	3	0.18	0.05	0.19
(4,931)	1:85:A:ASP:H	1:85:A:ASP:HB2	3	0.16	0.02	0.18
(4,931)	1:85:A:ASP:H	1:85:A:ASP:HB3	3	0.16	0.02	0.18
(4,1090)	1:197:A:LEU:H	1:197:A:LEU:HB2	3	0.16	0.05	0.17
(4,1090)	1:167:A:LYS:H	1:167:A:LYS:HB2	3	0.16	0.05	0.17
(4,1122)	1:224:A:LYS:H	1:224:A:LYS:HG3	3	0.16	0.02	0.18
(4,1122)	1:135:A:GLN:H	1:135:A:GLN:HB2	3	0.16	0.02	0.18
(4,1122)	1:24:A:LYS:H	1:24:A:LYS:HB2	3	0.16	0.02	0.18
(4,1078)	1:221:A:GLN:H	1:221:A:GLN:HB3	3	0.16	0.02	0.16
(4,1078)	1:28:A:GLN:H	1:28:A:GLN:HB3	3	0.16	0.02	0.16
(4,22)	1:110:A:ASP:H	1:109:A:VAL:HB	3	0.15	0.04	0.15
(1,118)	1:45:A:LYS:H	1:45:A:LYS:HG3	3	0.14	0.02	0.14
(4,865)	1:87:A:THR:H	1:86:A:GLY:HA2	3	0.14	0.03	0.16
(4,865)	1:258:A:SER:H	1:258:A:SER:HB3	3	0.14	0.03	0.16
(4,138)	1:133:A:ALA:H	1:133:A:ALA:HB2	3	0.14	0.03	0.16
(4,138)	1:210:A:VAL:H	1:209:A:ILE:HG21	3	0.14	0.03	0.16
(4,138)	1:133:A:ALA:H	1:133:A:ALA:HB3	3	0.14	0.03	0.16
(4,1103)	1:218:A:SER:H	1:221:A:GLN:HB2	3	0.14	0.04	0.11
(4,1103)	1:218:A:SER:H	1:221:A:GLN:HB3	3	0.14	0.04	0.11
(4,1034)	1:57:A:LEU:H	1:57:A:LEU:HB3	3	0.13	0.02	0.12
(4,1034)	1:230:A:PHE:H	1:229:A:ASN:HB3	3	0.13	0.02	0.12
(4,1034)	1:158:A:LYS:H	1:158:A:LYS:HB3	3	0.13	0.02	0.12

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,1089)	1:228:A:LEU:H	1:228:A:LEU:HG	3	0.13	0.01	0.13
(4,1089)	1:221:A:GLN:H	1:221:A:GLN:HG2	3	0.13	0.01	0.13
(4,1089)	1:228:A:LEU:H	1:228:A:LEU:HB2	3	0.13	0.01	0.13
(4,1020)	1:161:A:ASP:H	1:161:A:ASP:HB2	3	0.13	0.02	0.12
(4,1020)	1:230:A:PHE:H	1:230:A:PHE:HB2	3	0.13	0.02	0.12
(4,969)	1:244:A:TRP:H	1:244:A:TRP:HB3	3	0.12	0.01	0.12
(4,1014)	1:52:A:ASP:H	1:52:A:ASP:HB2	3	0.12	0.02	0.12
(4,1014)	1:174:A:ASP:H	1:174:A:ASP:HB3	3	0.12	0.02	0.12
(4,1023)	1:62:A:ASN:H	1:61:A:ASN:HB3	3	0.11	0.0	0.11
(4,303)	1:254:A:GLN:HB2	1:254:A:GLN:HA	3	0.11	0.01	0.11
(4,303)	1:254:A:GLN:HB3	1:254:A:GLN:HA	3	0.11	0.01	0.11
(4,303)	1:203:A:LEU:HB3	1:203:A:LEU:HA	3	0.11	0.01	0.11
(4,1079)	1:164:A:ASP:H	1:164:A:ASP:HB2	3	0.11	0.01	0.11
(4,1079)	1:28:A:GLN:H	1:28:A:GLN:HB3	3	0.11	0.01	0.11
(3,227)	1:149:A:VAL:H	1:115:A:ALA:H	2	3.51	0.83	3.51
(3,93)	1:115:A:ALA:H	1:149:A:VAL:H	2	3.31	0.83	3.31
(3,85)	1:115:A:ALA:H	1:149:A:VAL:H	2	3.21	0.83	3.21
(3,83)	1:111:A:LYS:H	1:33:A:ILE:H	2	1.88	1.69	1.88
(3,14)	1:147:A:LEU:H	1:117:A:GLU:H	2	1.8	1.42	1.8
(4,661)	1:198:A:THR:H	1:198:A:THR:HG1	2	1.52	0.03	1.52
(4,1215)	1:86:A:GLY:H	1:84:A:LEU:HG	2	1.2	0.74	1.2
(4,1215)	1:86:A:GLY:H	1:80:A:LYS:HD3	2	1.2	0.74	1.2
(3,80)	1:110:A:ASP:H	1:33:A:ILE:H	2	0.86	0.58	0.86
(1,134)	1:121:A:VAL:H	1:91:A:ILE:HD13	2	0.83	0.38	0.83
(1,134)	1:121:A:VAL:H	1:91:A:ILE:HD11	2	0.83	0.38	0.83
(4,384)	1:22:A:ILE:HD11	1:28:A:GLN:HB2	2	0.74	0.24	0.74
(4,384)	1:22:A:ILE:HD12	1:28:A:GLN:HB2	2	0.74	0.24	0.74
(4,1281)	1:163:A:LEU:H	1:163:A:LEU:HD23	2	0.66	0.27	0.66
(4,1281)	1:212:A:LYS:H	1:211:A:LEU:HD23	2	0.66	0.27	0.66
(4,667)	1:53:A:GLN:H	1:51:A:TYR:HA	2	0.6	0.32	0.6
(4,667)	1:251:A:LYS:H	1:252:A:ASN:H	2	0.6	0.32	0.6
(4,990)	1:253:A:ARG:H	1:253:A:ARG:HD3	2	0.6	0.36	0.6
(4,990)	1:253:A:ARG:H	1:252:A:ASN:HB3	2	0.6	0.36	0.6
(1,9)	1:173:A:ALA:H	1:172:A:SER:HB3	2	0.57	0.04	0.57
(1,52)	1:166:A:ILE:HD13	1:163:A:LEU:HA	2	0.54	0.38	0.54
(4,1328)	1:108:A:THR:H	1:33:A:ILE:HD13	2	0.51	0.27	0.51
(4,1328)	1:105:A:SER:H	1:113:A:LYS:HG2	2	0.51	0.27	0.51
(4,1095)	1:232:A:GLY:H	1:235:A:GLU:HG3	2	0.49	0.21	0.49
(4,1095)	1:232:A:GLY:H	1:235:A:GLU:HG2	2	0.49	0.21	0.49
(4,1338)	1:161:A:ASP:H	1:163:A:LEU:HD22	2	0.49	0.25	0.49
(4,1338)	1:217:A:VAL:H	1:149:A:VAL:HG22	2	0.49	0.25	0.49
(3,176)	1:129:A:ASP:H	1:133:A:ALA:H	2	0.46	0.07	0.46

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,444)	1:255:A:ILE:HG21	1:193:A:TYR:HB2	2	0.46	0.01	0.46
(4,456)	1:110:A:ASP:HB3	1:109:A:VAL:HG21	2	0.43	0.07	0.43
(4,456)	1:169:A:LYS:HG3	1:61:A:ASN:HB2	2	0.43	0.07	0.43
(4,1072)	1:66:A:PHE:H	1:66:A:PHE:HB3	2	0.43	0.16	0.43
(4,1072)	1:103:A:GLN:H	1:103:A:GLN:HG2	2	0.43	0.16	0.43
(3,48)	1:210:A:VAL:H	1:191:A:TRP:H	2	0.41	0.25	0.41
(3,81)	1:191:A:TRP:H	1:210:A:VAL:H	2	0.41	0.25	0.41
(4,241)	1:253:A:ARG:H	1:253:A:ARG:HD3	2	0.39	0.26	0.39
(4,241)	1:57:A:LEU:HB2	1:58:A:ARG:H	2	0.39	0.26	0.39
(4,222)	1:205:A:CYS:H	1:203:A:LEU:HB3	2	0.38	0.26	0.38
(4,939)	1:119:A:HIS:H	1:118:A:LEU:HB3	2	0.38	0.01	0.38
(4,529)	1:116:A:ALA:H	1:147:A:LEU:H	2	0.34	0.15	0.34
(4,345)	1:172:A:SER:HB3	1:174:A:ASP:HA	2	0.33	0.22	0.33
(4,345)	1:172:A:SER:HB2	1:174:A:ASP:HA	2	0.33	0.22	0.33
(4,809)	1:197:A:LEU:H	1:197:A:LEU:HA	2	0.32	0.02	0.32
(4,809)	1:167:A:LYS:H	1:167:A:LYS:HA	2	0.32	0.02	0.32
(4,1251)	1:176:A:THR:H	1:176:A:THR:HG22	2	0.3	0.16	0.3
(4,1251)	1:205:A:CYS:H	1:206:A:VAL:HG23	2	0.3	0.16	0.3
(1,51)	1:114:A:TYR:HB2	1:105:A:SER:HB2	2	0.28	0.16	0.28
(1,51)	1:114:A:TYR:HB2	1:105:A:SER:HB3	2	0.28	0.16	0.28
(4,183)	1:260:A:LYS:H	1:259:A:PHE:HA	2	0.28	0.06	0.28
(4,673)	1:191:A:TRP:H	1:191:A:TRP:HA	2	0.28	0.01	0.28
(4,1064)	1:155:A:GLY:H	1:153:A:LYS:HB3	2	0.28	0.06	0.28
(4,116)	1:87:A:THR:H	1:87:A:THR:HB	2	0.27	0.02	0.27
(4,116)	1:112:A:LYS:H	1:108:A:THR:HB	2	0.27	0.02	0.27
(4,1314)	1:55:A:THR:H	1:76:A:LYS:HG2	2	0.26	0.13	0.26
(4,1314)	1:55:A:THR:H	1:76:A:LYS:HG3	2	0.26	0.13	0.26
(4,206)	1:139:A:GLY:H	1:140:A:LEU:HB3	2	0.26	0.09	0.26
(4,206)	1:140:A:LEU:HB2	1:142:A:VAL:H	2	0.26	0.09	0.26
(4,281)	1:91:A:ILE:HD12	1:123:A:TRP:HA	2	0.26	0.05	0.26
(4,281)	1:91:A:ILE:HD11	1:123:A:TRP:HA	2	0.26	0.05	0.26
(4,878)	1:9:A:LYS:H	1:8:A:GLY:HA3	2	0.25	0.02	0.25
(4,878)	1:7:A:TYR:H	1:7:A:TYR:HB2	2	0.25	0.02	0.25
(4,115)	1:204:A:GLU:H	1:22:A:ILE:HD12	2	0.24	0.05	0.24
(4,115)	1:22:A:ILE:H	1:22:A:ILE:HD12	2	0.24	0.05	0.24
(4,1071)	1:103:A:GLN:H	1:103:A:GLN:HG2	2	0.22	0.11	0.22
(4,1071)	1:103:A:GLN:H	1:100:A:LEU:HB3	2	0.22	0.11	0.22
(4,799)	1:87:A:THR:H	1:87:A:THR:HB	2	0.22	0.05	0.22
(4,2)	1:245:A:ARG:HG2	1:245:A:ARG:H	2	0.22	0.02	0.22
(4,574)	1:127:A:TYR:H	1:126:A:LYS:H	2	0.22	0.04	0.22
(3,112)	1:129:A:ASP:H	1:131:A:GLY:H	2	0.22	0.1	0.22
(3,55)	1:156:A:LEU:H	1:158:A:LYS:H	2	0.21	0.11	0.21

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,84)	1:103:A:GLN:H	1:102:A:GLY:H	2	0.2	0.08	0.2
(4,508)	1:231:A:ASN:H	1:230:A:PHE:H	2	0.2	0.01	0.2
(4,655)	1:97:A:TRP:H	1:242:A:ASP:H	2	0.2	0.05	0.2
(4,655)	1:97:A:TRP:H	1:244:A:TRP:H	2	0.2	0.05	0.2
(4,688)	1:204:A:GLU:H	1:203:A:LEU:HA	2	0.2	0.02	0.2
(4,688)	1:207:A:THR:H	1:207:A:THR:HA	2	0.2	0.02	0.2
(4,800)	1:167:A:LYS:H	1:166:A:ILE:HA	2	0.19	0.0	0.19
(4,920)	1:56:A:SER:H	1:56:A:SER:HB3	2	0.19	0.09	0.19
(4,920)	1:56:A:SER:H	1:56:A:SER:HB2	2	0.19	0.09	0.19
(4,1237)	1:76:A:LYS:H	1:76:A:LYS:HG3	2	0.18	0.04	0.18
(4,1237)	1:76:A:LYS:H	1:76:A:LYS:HG2	2	0.18	0.04	0.18
(4,39)	1:37:A:THR:HG23	1:255:A:ILE:H	2	0.18	0.06	0.18
(4,39)	1:63:A:GLY:H	1:169:A:LYS:HG2	2	0.18	0.06	0.18
(4,894)	1:131:A:GLY:H	1:131:A:GLY:HA2	2	0.18	0.02	0.18
(4,894)	1:232:A:GLY:H	1:232:A:GLY:HA2	2	0.18	0.02	0.18
(3,61)	1:161:A:ASP:H	1:158:A:LYS:H	2	0.17	0.05	0.17
(3,35)	1:222:A:VAL:H	1:219:A:SER:H	2	0.16	0.0	0.16
(3,270)	1:219:A:SER:H	1:222:A:VAL:H	2	0.16	0.0	0.16
(4,37)	1:37:A:THR:HG23	1:255:A:ILE:H	2	0.16	0.06	0.16
(4,37)	1:63:A:GLY:H	1:169:A:LYS:HG2	2	0.16	0.06	0.16
(4,553)	1:28:A:GLN:H	1:27:A:ARG:H	2	0.16	0.01	0.16
(4,106)	1:196:A:SER:H	1:196:A:SER:HB3	2	0.16	0.05	0.16
(4,106)	1:87:A:THR:H	1:87:A:THR:HB	2	0.16	0.05	0.16
(4,122)	1:52:A:ASP:H	1:51:A:TYR:HA	2	0.15	0.0	0.15
(4,122)	1:86:A:GLY:H	1:85:A:ASP:HA	2	0.15	0.0	0.15
(4,144)	1:103:A:GLN:H	1:100:A:LEU:HB2	2	0.15	0.03	0.15
(4,144)	1:88:A:TYR:H	1:79:A:LEU:HB2	2	0.15	0.03	0.15
(4,712)	1:124:A:ASN:H	1:123:A:TRP:HA	2	0.14	0.02	0.14
(4,1280)	1:68:A:VAL:H	1:68:A:VAL:HG21	2	0.13	0.01	0.13
(4,1280)	1:114:A:TYR:H	1:113:A:LYS:HG2	2	0.13	0.01	0.13
(4,855)	1:57:A:LEU:H	1:56:A:SER:HA	2	0.12	0.0	0.12
(4,855)	1:230:A:PHE:H	1:229:A:ASN:HA	2	0.12	0.0	0.12
(4,1033)	1:119:A:HIS:H	1:119:A:HIS:HB2	2	0.12	0.01	0.12
(4,1033)	1:153:A:LYS:H	1:153:A:LYS:HB3	2	0.12	0.01	0.12
(4,1269)	1:162:A:VAL:H	1:162:A:VAL:HG22	2	0.12	0.02	0.12
(4,1269)	1:160:A:VAL:H	1:160:A:VAL:HG21	2	0.12	0.02	0.12
(1,18)	1:240:A:MET:H	1:240:A:MET:HA	2	0.12	0.0	0.12
(4,481)	1:28:A:GLN:H	1:27:A:ARG:H	2	0.12	0.0	0.12
(4,613)	1:74:A:GLN:H	1:75:A:ASP:H	2	0.12	0.0	0.12
(4,613)	1:222:A:VAL:H	1:223:A:LEU:H	2	0.12	0.0	0.12
(4,1220)	1:133:A:ALA:H	1:133:A:ALA:HB3	2	0.12	0.0	0.12
(4,83)	1:234:A:GLY:H	1:233:A:GLU:HA	2	0.11	0.0	0.11

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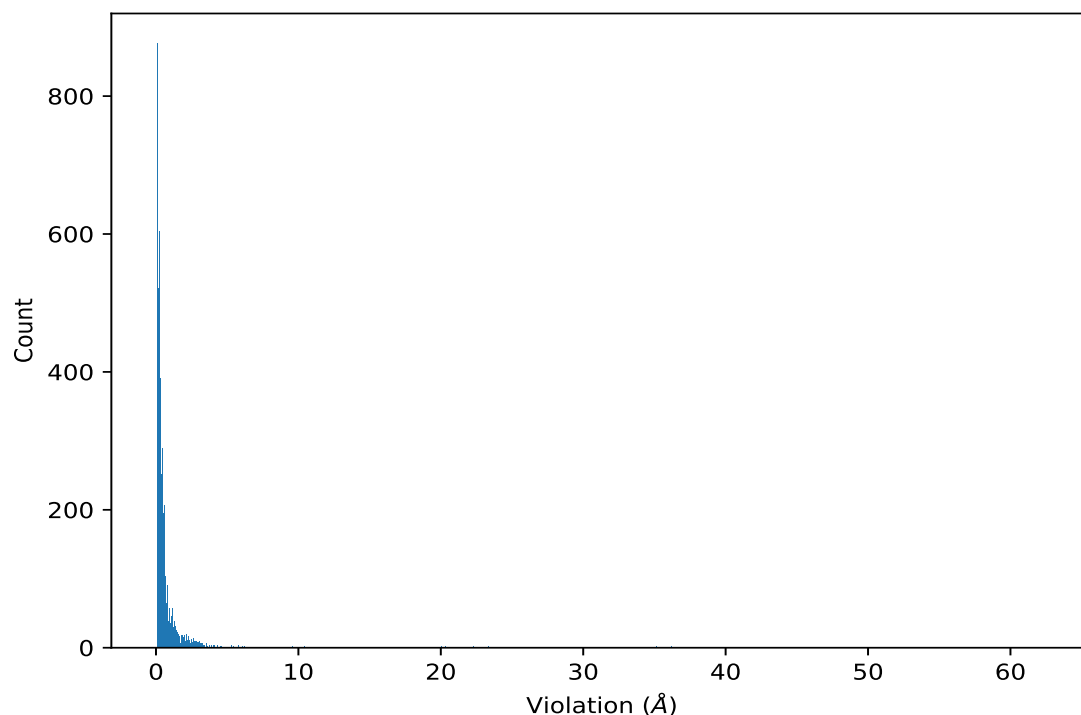
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(4,83)	1:57:A:LEU:H	1:56:A:SER:HA	2	0.11	0.0	0.11
(4,610)	1:74:A:GLN:H	1:75:A:ASP:H	2	0.11	0.0	0.11
(4,610)	1:222:A:VAL:H	1:223:A:LEU:H	2	0.11	0.0	0.11
(4,954)	1:161:A:ASP:H	1:161:A:ASP:HB2	2	0.11	0.0	0.11

¹Number of violated models, ²Standard deviation

9.5 All violated distance restraints [i](#)

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

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



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

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

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,304)	1:7:A:TYR:H	1:168:A:THR:H	1	62.69
(3,304)	1:7:A:TYR:H	1:168:A:THR:H	18	60.92
(3,304)	1:7:A:TYR:H	1:168:A:THR:H	4	56.2
(3,304)	1:7:A:TYR:H	1:168:A:THR:H	2	55.14
(3,304)	1:7:A:TYR:H	1:168:A:THR:H	20	54.01
(3,304)	1:7:A:TYR:H	1:168:A:THR:H	7	53.6
(3,304)	1:7:A:TYR:H	1:168:A:THR:H	10	53.22
(3,304)	1:7:A:TYR:H	1:168:A:THR:H	14	52.81
(3,304)	1:7:A:TYR:H	1:168:A:THR:H	12	52.33
(3,304)	1:7:A:TYR:H	1:168:A:THR:H	5	51.93
(3,304)	1:7:A:TYR:H	1:168:A:THR:H	3	51.42
(3,304)	1:7:A:TYR:H	1:168:A:THR:H	9	50.87
(3,304)	1:7:A:TYR:H	1:168:A:THR:H	8	47.82
(3,304)	1:7:A:TYR:H	1:168:A:THR:H	11	39.7
(3,304)	1:7:A:TYR:H	1:168:A:THR:H	15	39.66
(3,304)	1:7:A:TYR:H	1:168:A:THR:H	17	39.04
(3,304)	1:7:A:TYR:H	1:168:A:THR:H	13	38.39
(3,303)	1:86:A:GLY:H	1:168:A:THR:H	12	38.3
(3,303)	1:86:A:GLY:H	1:168:A:THR:H	10	37.41
(3,303)	1:86:A:GLY:H	1:168:A:THR:H	7	36.38
(3,303)	1:86:A:GLY:H	1:168:A:THR:H	18	36.19
(3,303)	1:86:A:GLY:H	1:168:A:THR:H	5	36.16
(3,303)	1:86:A:GLY:H	1:168:A:THR:H	11	36.06
(3,303)	1:86:A:GLY:H	1:168:A:THR:H	9	35.95
(3,303)	1:86:A:GLY:H	1:168:A:THR:H	19	35.93
(3,304)	1:7:A:TYR:H	1:168:A:THR:H	16	35.56
(3,303)	1:86:A:GLY:H	1:168:A:THR:H	1	35.39
(3,303)	1:86:A:GLY:H	1:168:A:THR:H	2	35.14
(3,303)	1:86:A:GLY:H	1:168:A:THR:H	4	35.11
(3,303)	1:86:A:GLY:H	1:168:A:THR:H	6	34.88
(3,303)	1:86:A:GLY:H	1:168:A:THR:H	8	34.69
(3,303)	1:86:A:GLY:H	1:168:A:THR:H	3	34.34
(3,303)	1:86:A:GLY:H	1:168:A:THR:H	14	34.15
(3,303)	1:86:A:GLY:H	1:168:A:THR:H	13	33.99
(3,303)	1:86:A:GLY:H	1:168:A:THR:H	16	33.6
(3,303)	1:86:A:GLY:H	1:168:A:THR:H	15	32.37
(3,303)	1:86:A:GLY:H	1:168:A:THR:H	20	32.18
(3,303)	1:86:A:GLY:H	1:168:A:THR:H	17	31.88
(3,304)	1:7:A:TYR:H	1:168:A:THR:H	19	31.65
(3,321)	1:127:A:TYR:H	1:184:A:LEU:H	6	25.21
(3,321)	1:127:A:TYR:H	1:184:A:LEU:H	12	24.07
(3,321)	1:127:A:TYR:H	1:184:A:LEU:H	16	23.74
(3,321)	1:127:A:TYR:H	1:184:A:LEU:H	19	23.33

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,304)	1:7:A:TYR:H	1:168:A:THR:H	6	23.32
(3,321)	1:127:A:TYR:H	1:184:A:LEU:H	2	23.19
(3,321)	1:127:A:TYR:H	1:184:A:LEU:H	11	23.11
(3,321)	1:127:A:TYR:H	1:184:A:LEU:H	15	22.3
(3,321)	1:127:A:TYR:H	1:184:A:LEU:H	10	22.27
(3,321)	1:127:A:TYR:H	1:184:A:LEU:H	18	22.26
(3,321)	1:127:A:TYR:H	1:184:A:LEU:H	7	21.91
(3,321)	1:127:A:TYR:H	1:184:A:LEU:H	14	21.87
(3,321)	1:127:A:TYR:H	1:184:A:LEU:H	8	21.51
(3,321)	1:127:A:TYR:H	1:184:A:LEU:H	17	21.14
(3,321)	1:127:A:TYR:H	1:184:A:LEU:H	13	20.98
(3,321)	1:127:A:TYR:H	1:184:A:LEU:H	1	20.42
(3,321)	1:127:A:TYR:H	1:184:A:LEU:H	3	20.34
(3,321)	1:127:A:TYR:H	1:184:A:LEU:H	5	20.3
(3,321)	1:127:A:TYR:H	1:184:A:LEU:H	4	20.09
(3,321)	1:127:A:TYR:H	1:184:A:LEU:H	20	20.05
(3,321)	1:127:A:TYR:H	1:184:A:LEU:H	9	19.24
(1,36)	1:203:A:LEU:H	1:22:A:ILE:HD12	17	18.95
(3,301)	1:63:A:GLY:H	1:227:A:LYS:H	20	12.11
(3,301)	1:63:A:GLY:H	1:227:A:LYS:H	17	11.53
(3,301)	1:63:A:GLY:H	1:227:A:LYS:H	18	11.34
(3,301)	1:63:A:GLY:H	1:227:A:LYS:H	10	10.94
(3,301)	1:63:A:GLY:H	1:227:A:LYS:H	14	10.88
(3,301)	1:63:A:GLY:H	1:227:A:LYS:H	1	10.81
(3,301)	1:63:A:GLY:H	1:227:A:LYS:H	2	10.77
(3,301)	1:63:A:GLY:H	1:227:A:LYS:H	16	10.64
(3,301)	1:63:A:GLY:H	1:227:A:LYS:H	9	10.53
(3,301)	1:63:A:GLY:H	1:227:A:LYS:H	4	10.44
(3,301)	1:63:A:GLY:H	1:227:A:LYS:H	19	10.41
(3,301)	1:63:A:GLY:H	1:227:A:LYS:H	7	10.3
(3,301)	1:63:A:GLY:H	1:227:A:LYS:H	5	10.28
(3,301)	1:63:A:GLY:H	1:227:A:LYS:H	15	10.2
(3,301)	1:63:A:GLY:H	1:227:A:LYS:H	12	10.04
(3,301)	1:63:A:GLY:H	1:227:A:LYS:H	3	9.7
(3,301)	1:63:A:GLY:H	1:227:A:LYS:H	11	9.59
(3,301)	1:63:A:GLY:H	1:227:A:LYS:H	8	9.56
(3,301)	1:63:A:GLY:H	1:227:A:LYS:H	13	9.16
(3,301)	1:63:A:GLY:H	1:227:A:LYS:H	6	8.85
(3,76)	1:227:A:LYS:H	1:240:A:MET:H	12	8.45
(3,76)	1:227:A:LYS:H	1:240:A:MET:H	19	7.51
(3,261)	1:240:A:MET:H	1:228:A:LEU:H	12	7.47
(3,76)	1:227:A:LYS:H	1:240:A:MET:H	11	7.33

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,264)	1:240:A:MET:H	1:228:A:LEU:H	12	7.17
(3,76)	1:227:A:LYS:H	1:240:A:MET:H	18	7.0
(1,76)	1:115:A:ALA:HB2	1:149:A:VAL:HG21	4	6.97
(3,261)	1:240:A:MET:H	1:228:A:LEU:H	18	6.71
(3,60)	1:29:A:SER:H	1:196:A:SER:H	14	6.54
(3,264)	1:240:A:MET:H	1:228:A:LEU:H	18	6.41
(1,77)	1:224:A:LYS:HB2	1:163:A:LEU:HD22	3	6.24
(3,76)	1:227:A:LYS:H	1:240:A:MET:H	10	6.2
(3,155)	1:169:A:LYS:H	1:231:A:ASN:H	17	6.09
(3,261)	1:240:A:MET:H	1:228:A:LEU:H	11	6.08
(4,1304)	1:177:A:ASN:H	1:162:A:VAL:HG21	8	5.96
(1,42)	1:116:A:ALA:HB3	1:97:A:TRP:HA	8	5.84
(3,264)	1:240:A:MET:H	1:228:A:LEU:H	11	5.78
(3,261)	1:240:A:MET:H	1:228:A:LEU:H	19	5.76
(3,261)	1:240:A:MET:H	1:228:A:LEU:H	10	5.75
(1,77)	1:224:A:LYS:HB2	1:163:A:LEU:HD23	5	5.61
(3,226)	1:231:A:ASN:H	1:169:A:LYS:H	17	5.59
(3,264)	1:240:A:MET:H	1:228:A:LEU:H	19	5.46
(3,264)	1:240:A:MET:H	1:228:A:LEU:H	10	5.45
(3,7)	1:56:A:SER:H	1:177:A:ASN:H	17	5.41
(1,44)	1:91:A:ILE:HD11	1:122:A:HIS:HA	6	5.29
(3,98)	1:12:A:GLY:H	1:7:A:TYR:H	9	5.28
(3,98)	1:12:A:GLY:H	1:7:A:TYR:H	1	5.27
(3,11)	1:177:A:ASN:H	1:56:A:SER:H	17	5.21
(3,98)	1:12:A:GLY:H	1:7:A:TYR:H	10	5.15
(3,60)	1:29:A:SER:H	1:196:A:SER:H	17	4.99
(3,60)	1:29:A:SER:H	1:196:A:SER:H	8	4.89
(1,56)	1:255:A:ILE:HD13	1:193:A:TYR:HB2	3	4.74
(3,98)	1:12:A:GLY:H	1:7:A:TYR:H	6	4.63
(3,98)	1:12:A:GLY:H	1:7:A:TYR:H	15	4.58
(3,155)	1:169:A:LYS:H	1:231:A:ASN:H	19	4.57
(3,98)	1:12:A:GLY:H	1:7:A:TYR:H	5	4.5
(3,59)	1:197:A:LEU:H	1:204:A:GLU:H	4	4.5
(3,98)	1:12:A:GLY:H	1:7:A:TYR:H	13	4.47
(3,76)	1:227:A:LYS:H	1:240:A:MET:H	7	4.43
(3,227)	1:149:A:VAL:H	1:115:A:ALA:H	4	4.34
(3,320)	1:97:A:TRP:H	1:244:A:TRP:H	18	4.33
(4,1271)	1:231:A:ASN:H	1:169:A:LYS:HG2	17	4.31
(3,98)	1:12:A:GLY:H	1:7:A:TYR:H	2	4.28
(1,36)	1:203:A:LEU:H	1:22:A:ILE:HD11	13	4.24
(3,98)	1:12:A:GLY:H	1:7:A:TYR:H	3	4.15
(3,93)	1:115:A:ALA:H	1:149:A:VAL:H	4	4.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,76)	1:227:A:LYS:H	1:240:A:MET:H	2	4.1
(1,77)	1:224:A:LYS:HB3	1:163:A:LEU:HD22	12	4.09
(3,226)	1:231:A:ASN:H	1:169:A:LYS:H	19	4.07
(1,56)	1:255:A:ILE:HD13	1:193:A:TYR:HB2	18	4.06
(3,85)	1:115:A:ALA:H	1:149:A:VAL:H	4	4.04
(1,6)	1:169:A:LYS:HB3	1:63:A:GLY:H	10	4.02
(3,126)	1:56:A:SER:H	1:178:A:PHE:H	17	4.0
(3,10)	1:178:A:PHE:H	1:56:A:SER:H	17	4.0
(3,7)	1:56:A:SER:H	1:177:A:ASN:H	10	3.94
(3,251)	1:242:A:ASP:H	1:100:A:LEU:H	1	3.93
(4,72)	1:229:A:ASN:H	1:163:A:LEU:HD22	2	3.91
(4,61)	1:229:A:ASN:H	1:163:A:LEU:HD22	2	3.91
(3,261)	1:240:A:MET:H	1:228:A:LEU:H	7	3.89
(4,273)	1:113:A:LYS:HD3	1:97:A:TRP:HA	18	3.85
(3,158)	1:57:A:LEU:H	1:70:A:PHE:H	12	3.83
(1,56)	1:255:A:ILE:HD11	1:193:A:TYR:HB2	4	3.77
(3,98)	1:12:A:GLY:H	1:7:A:TYR:H	17	3.75
(3,11)	1:177:A:ASN:H	1:56:A:SER:H	10	3.74
(3,7)	1:56:A:SER:H	1:177:A:ASN:H	7	3.74
(1,76)	1:115:A:ALA:HB2	1:149:A:VAL:HG21	9	3.73
(3,231)	1:191:A:TRP:H	1:212:A:LYS:H	15	3.7
(3,210)	1:197:A:LEU:H	1:205:A:CYS:H	4	3.61
(1,56)	1:255:A:ILE:HD13	1:193:A:TYR:HB2	5	3.61
(3,264)	1:240:A:MET:H	1:228:A:LEU:H	7	3.59
(3,83)	1:111:A:LYS:H	1:33:A:ILE:H	18	3.57
(1,121)	1:93:A:PHE:H	1:68:A:VAL:HG23	8	3.56
(3,11)	1:177:A:ASN:H	1:56:A:SER:H	7	3.54
(3,284)	1:48:A:SER:H	1:82:A:GLY:H	1	3.51
(3,166)	1:205:A:CYS:H	1:197:A:LEU:H	4	3.51
(3,251)	1:242:A:ASP:H	1:100:A:LEU:H	16	3.5
(3,249)	1:191:A:TRP:H	1:212:A:LYS:H	15	3.5
(3,245)	1:191:A:TRP:H	1:212:A:LYS:H	15	3.5
(4,1270)	1:93:A:PHE:H	1:68:A:VAL:HG23	8	3.48
(3,58)	1:70:A:PHE:H	1:57:A:LEU:H	12	3.43
(3,222)	1:197:A:LEU:H	1:205:A:CYS:H	4	3.41
(3,163)	1:205:A:CYS:H	1:197:A:LEU:H	4	3.41
(3,160)	1:205:A:CYS:H	1:197:A:LEU:H	4	3.41
(3,76)	1:227:A:LYS:H	1:240:A:MET:H	13	3.4
(1,47)	1:240:A:MET:HA	1:230:A:PHE:HA	7	3.37
(3,7)	1:56:A:SER:H	1:177:A:ASN:H	19	3.36
(3,314)	1:229:A:ASN:H	1:168:A:THR:H	17	3.32
(4,468)	1:76:A:LYS:HG3	1:51:A:TYR:HA	15	3.31

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,251)	1:242:A:ASP:H	1:100:A:LEU:H	12	3.31
(1,121)	1:93:A:PHE:H	1:68:A:VAL:HG22	18	3.31
(4,416)	1:23:A:ALA:HB2	1:17:A:HIS:HB2	13	3.3
(3,181)	1:153:A:LYS:H	1:157:A:GLN:H	6	3.3
(3,120)	1:248:A:GLN:H	1:32:A:ASP:H	14	3.3
(4,273)	1:113:A:LYS:HD3	1:244:A:TRP:HA	14	3.29
(4,398)	1:123:A:TRP:HB3	1:140:A:LEU:HB3	20	3.27
(3,251)	1:242:A:ASP:H	1:100:A:LEU:H	7	3.26
(3,181)	1:153:A:LYS:H	1:157:A:GLN:H	9	3.26
(4,1270)	1:93:A:PHE:H	1:68:A:VAL:HG22	18	3.24
(3,126)	1:56:A:SER:H	1:178:A:PHE:H	10	3.23
(3,10)	1:178:A:PHE:H	1:56:A:SER:H	10	3.23
(3,14)	1:147:A:LEU:H	1:117:A:GLU:H	12	3.21
(4,72)	1:158:A:LYS:H	1:163:A:LEU:HD23	14	3.2
(4,61)	1:158:A:LYS:H	1:163:A:LEU:HD23	14	3.2
(3,11)	1:177:A:ASN:H	1:56:A:SER:H	19	3.16
(1,47)	1:240:A:MET:HA	1:230:A:PHE:HA	10	3.16
(4,1304)	1:177:A:ASN:H	1:57:A:LEU:HD23	13	3.14
(3,126)	1:56:A:SER:H	1:178:A:PHE:H	19	3.14
(3,76)	1:227:A:LYS:H	1:240:A:MET:H	5	3.14
(3,10)	1:178:A:PHE:H	1:56:A:SER:H	19	3.14
(4,180)	1:228:A:LEU:H	1:240:A:MET:HA	19	3.12
(3,302)	1:229:A:ASN:H	1:168:A:THR:H	17	3.12
(3,103)	1:82:A:GLY:H	1:48:A:SER:H	1	3.11
(3,181)	1:153:A:LYS:H	1:157:A:GLN:H	1	3.09
(3,255)	1:147:A:LEU:H	1:115:A:ALA:H	12	3.08
(4,1259)	1:93:A:PHE:H	1:68:A:VAL:HG22	18	3.06
(4,72)	1:229:A:ASN:H	1:163:A:LEU:HD22	13	3.05
(4,61)	1:229:A:ASN:H	1:163:A:LEU:HD22	13	3.05
(3,237)	1:189:A:ASP:H	1:212:A:LYS:H	15	3.04
(1,121)	1:93:A:PHE:H	1:68:A:VAL:HG23	6	3.04
(3,59)	1:197:A:LEU:H	1:204:A:GLU:H	3	3.03
(4,1271)	1:231:A:ASN:H	1:169:A:LYS:HG2	19	3.02
(3,261)	1:240:A:MET:H	1:228:A:LEU:H	5	3.02
(4,72)	1:59:A:ILE:H	1:163:A:LEU:HD21	3	3.0
(4,61)	1:59:A:ILE:H	1:163:A:LEU:HD21	3	3.0
(1,75)	1:172:A:SER:HB3	1:60:A:LEU:HD13	19	3.0
(3,181)	1:153:A:LYS:H	1:157:A:GLN:H	10	2.99
(3,98)	1:12:A:GLY:H	1:7:A:TYR:H	14	2.99
(3,251)	1:242:A:ASP:H	1:100:A:LEU:H	5	2.98
(3,181)	1:153:A:LYS:H	1:157:A:GLN:H	14	2.98
(3,320)	1:97:A:TRP:H	1:244:A:TRP:H	10	2.97

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,17)	1:169:A:LYS:H	1:63:A:GLY:H	10	2.97
(4,1270)	1:93:A:PHE:H	1:68:A:VAL:HG23	6	2.96
(3,110)	1:12:A:GLY:H	1:8:A:GLY:H	10	2.96
(3,181)	1:153:A:LYS:H	1:157:A:GLN:H	2	2.94
(3,314)	1:229:A:ASN:H	1:168:A:THR:H	2	2.93
(3,282)	1:202:A:LEU:H	1:199:A:THR:H	3	2.93
(3,126)	1:56:A:SER:H	1:178:A:PHE:H	7	2.93
(3,10)	1:178:A:PHE:H	1:56:A:SER:H	7	2.93
(4,1304)	1:177:A:ASN:H	1:57:A:LEU:HD23	20	2.91
(4,180)	1:98:A:GLY:H	1:240:A:MET:HA	15	2.91
(1,123)	1:63:A:GLY:H	1:169:A:LYS:HG2	10	2.91
(3,181)	1:153:A:LYS:H	1:157:A:GLN:H	8	2.89
(4,72)	1:229:A:ASN:H	1:163:A:LEU:HD21	16	2.88
(4,61)	1:229:A:ASN:H	1:163:A:LEU:HD21	16	2.88
(3,37)	1:206:A:VAL:H	1:140:A:LEU:H	18	2.87
(3,115)	1:12:A:GLY:H	1:8:A:GLY:H	10	2.86
(1,75)	1:172:A:SER:HB3	1:60:A:LEU:HD11	16	2.86
(3,261)	1:240:A:MET:H	1:228:A:LEU:H	2	2.84
(1,93)	1:150:A:GLY:H	1:218:A:SER:HA	12	2.84
(4,72)	1:158:A:LYS:H	1:163:A:LEU:HD21	11	2.83
(4,61)	1:158:A:LYS:H	1:163:A:LEU:HD21	11	2.83
(3,261)	1:240:A:MET:H	1:228:A:LEU:H	13	2.83
(3,158)	1:57:A:LEU:H	1:70:A:PHE:H	17	2.82
(3,67)	1:169:A:LYS:H	1:229:A:ASN:H	17	2.82
(3,7)	1:56:A:SER:H	1:177:A:ASN:H	11	2.82
(3,15)	1:243:A:ASN:H	1:97:A:TRP:H	18	2.81
(3,60)	1:29:A:SER:H	1:196:A:SER:H	12	2.79
(4,1259)	1:93:A:PHE:H	1:68:A:VAL:HG23	6	2.78
(3,120)	1:248:A:GLN:H	1:32:A:ASP:H	6	2.78
(4,72)	1:229:A:ASN:H	1:163:A:LEU:HD22	18	2.77
(4,61)	1:229:A:ASN:H	1:163:A:LEU:HD22	18	2.77
(3,234)	1:8:A:GLY:H	1:12:A:GLY:H	10	2.76
(3,126)	1:56:A:SER:H	1:178:A:PHE:H	11	2.75
(3,98)	1:12:A:GLY:H	1:7:A:TYR:H	16	2.75
(3,10)	1:178:A:PHE:H	1:56:A:SER:H	11	2.75
(3,325)	1:197:A:LEU:H	1:203:A:LEU:H	3	2.73
(3,302)	1:229:A:ASN:H	1:168:A:THR:H	2	2.73
(3,76)	1:227:A:LYS:H	1:240:A:MET:H	9	2.73
(4,1259)	1:234:A:GLY:H	1:168:A:THR:HG21	8	2.72
(3,264)	1:240:A:MET:H	1:228:A:LEU:H	5	2.72
(3,237)	1:189:A:ASP:H	1:212:A:LYS:H	6	2.71
(3,237)	1:189:A:ASP:H	1:212:A:LYS:H	14	2.71

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,72)	1:158:A:LYS:H	1:163:A:LEU:HD23	10	2.7
(4,61)	1:158:A:LYS:H	1:163:A:LEU:HD23	10	2.7
(3,227)	1:149:A:VAL:H	1:115:A:ALA:H	9	2.68
(1,123)	1:63:A:GLY:H	1:169:A:LYS:HG2	7	2.68
(3,181)	1:153:A:LYS:H	1:157:A:GLN:H	7	2.65
(1,75)	1:172:A:SER:HB2	1:60:A:LEU:HD11	18	2.65
(4,72)	1:158:A:LYS:H	1:163:A:LEU:HD23	4	2.63
(4,72)	1:229:A:ASN:H	1:163:A:LEU:HD22	17	2.63
(4,61)	1:158:A:LYS:H	1:163:A:LEU:HD23	4	2.63
(4,61)	1:229:A:ASN:H	1:163:A:LEU:HD22	17	2.63
(3,282)	1:202:A:LEU:H	1:199:A:THR:H	14	2.63
(3,98)	1:12:A:GLY:H	1:7:A:TYR:H	7	2.63
(3,120)	1:248:A:GLN:H	1:32:A:ASP:H	12	2.62
(3,15)	1:243:A:ASN:H	1:97:A:TRP:H	8	2.62
(3,11)	1:177:A:ASN:H	1:56:A:SER:H	11	2.62
(3,173)	1:57:A:LEU:H	1:175:A:PHE:H	19	2.61
(1,56)	1:255:A:ILE:HD13	1:193:A:TYR:HB2	20	2.61
(3,98)	1:12:A:GLY:H	1:7:A:TYR:H	4	2.6
(3,237)	1:189:A:ASP:H	1:212:A:LYS:H	13	2.59
(3,286)	1:70:A:PHE:H	1:92:A:GLN:H	18	2.58
(4,72)	1:158:A:LYS:H	1:163:A:LEU:HD22	19	2.57
(4,61)	1:158:A:LYS:H	1:163:A:LEU:HD22	19	2.57
(3,271)	1:140:A:LEU:H	1:206:A:VAL:H	18	2.57
(4,72)	1:229:A:ASN:H	1:163:A:LEU:HD22	1	2.56
(4,61)	1:229:A:ASN:H	1:163:A:LEU:HD22	1	2.56
(1,75)	1:172:A:SER:HB2	1:60:A:LEU:HD11	2	2.56
(3,76)	1:227:A:LYS:H	1:240:A:MET:H	14	2.55
(1,42)	1:116:A:ALA:HB2	1:97:A:TRP:HA	10	2.55
(3,264)	1:240:A:MET:H	1:228:A:LEU:H	2	2.54
(3,264)	1:240:A:MET:H	1:228:A:LEU:H	13	2.53
(4,1304)	1:177:A:ASN:H	1:57:A:LEU:HD21	16	2.52
(4,1266)	1:66:A:PHE:H	1:169:A:LYS:HG2	11	2.51
(4,1339)	1:93:A:PHE:H	1:91:A:ILE:HD12	4	2.5
(4,72)	1:158:A:LYS:H	1:163:A:LEU:HD21	9	2.49
(4,61)	1:158:A:LYS:H	1:163:A:LEU:HD21	9	2.49
(3,93)	1:115:A:ALA:H	1:149:A:VAL:H	9	2.48
(1,36)	1:203:A:LEU:H	1:22:A:ILE:HD13	19	2.48
(4,1258)	1:202:A:LEU:H	1:202:A:LEU:HD21	6	2.47
(4,180)	1:228:A:LEU:H	1:240:A:MET:HA	3	2.47
(3,314)	1:229:A:ASN:H	1:168:A:THR:H	19	2.46
(3,37)	1:206:A:VAL:H	1:140:A:LEU:H	6	2.46
(3,290)	1:196:A:SER:H	1:206:A:VAL:H	4	2.45

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,252)	1:196:A:SER:H	1:206:A:VAL:H	4	2.45
(1,121)	1:93:A:PHE:H	1:68:A:VAL:HG23	9	2.45
(1,47)	1:240:A:MET:HA	1:230:A:PHE:HA	12	2.45
(3,37)	1:206:A:VAL:H	1:140:A:LEU:H	14	2.44
(3,231)	1:191:A:TRP:H	1:212:A:LYS:H	11	2.43
(3,181)	1:153:A:LYS:H	1:157:A:GLN:H	11	2.43
(3,164)	1:203:A:LEU:H	1:197:A:LEU:H	3	2.43
(3,58)	1:70:A:PHE:H	1:57:A:LEU:H	17	2.42
(2,20)	1:229:A:ASN:H	1:168:A:THR:H	17	2.42
(4,180)	1:228:A:LEU:H	1:240:A:MET:HA	9	2.41
(4,1304)	1:177:A:ASN:H	1:57:A:LEU:HD22	9	2.4
(3,60)	1:29:A:SER:H	1:196:A:SER:H	10	2.4
(3,59)	1:197:A:LEU:H	1:204:A:GLU:H	14	2.4
(3,76)	1:227:A:LYS:H	1:240:A:MET:H	8	2.39
(1,121)	1:93:A:PHE:H	1:68:A:VAL:HG21	11	2.39
(3,85)	1:115:A:ALA:H	1:149:A:VAL:H	9	2.38
(3,76)	1:227:A:LYS:H	1:240:A:MET:H	15	2.38
(3,325)	1:197:A:LEU:H	1:203:A:LEU:H	14	2.36
(1,56)	1:255:A:ILE:HD12	1:193:A:TYR:HB2	11	2.36
(3,237)	1:189:A:ASP:H	1:212:A:LYS:H	4	2.35
(3,206)	1:100:A:LEU:H	1:103:A:GLN:H	10	2.35
(3,290)	1:196:A:SER:H	1:206:A:VAL:H	12	2.34
(3,252)	1:196:A:SER:H	1:206:A:VAL:H	12	2.34
(3,76)	1:227:A:LYS:H	1:240:A:MET:H	4	2.34
(4,1270)	1:94:A:HIS:H	1:121:A:VAL:HG23	9	2.33
(1,36)	1:203:A:LEU:H	1:22:A:ILE:HD11	14	2.33
(4,1270)	1:93:A:PHE:H	1:68:A:VAL:HG21	11	2.32
(3,150)	1:206:A:VAL:H	1:197:A:LEU:H	4	2.32
(3,181)	1:153:A:LYS:H	1:157:A:GLN:H	4	2.31
(3,37)	1:206:A:VAL:H	1:140:A:LEU:H	2	2.31
(1,123)	1:63:A:GLY:H	1:169:A:LYS:HG2	19	2.31
(4,1337)	1:91:A:ILE:H	1:91:A:ILE:HD11	6	2.3
(1,123)	1:63:A:GLY:H	1:169:A:LYS:HG3	18	2.3
(4,1304)	1:177:A:ASN:H	1:57:A:LEU:HD23	6	2.29
(3,251)	1:242:A:ASP:H	1:100:A:LEU:H	19	2.29
(3,37)	1:206:A:VAL:H	1:140:A:LEU:H	13	2.29
(1,128)	1:81:A:GLY:H	1:84:A:LEU:HD23	19	2.29
(4,180)	1:228:A:LEU:H	1:240:A:MET:HA	14	2.28
(3,110)	1:12:A:GLY:H	1:8:A:GLY:H	2	2.28
(3,47)	1:60:A:LEU:H	1:67:A:ASN:H	19	2.28
(3,173)	1:57:A:LEU:H	1:175:A:PHE:H	12	2.27
(1,126)	1:78:A:VAL:H	1:78:A:VAL:HG22	12	2.27

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,78)	1:117:A:GLU:H	1:96:A:HIS:H	8	2.27
(1,64)	1:60:A:LEU:HB3	1:172:A:SER:HB3	8	2.27
(3,302)	1:229:A:ASN:H	1:168:A:THR:H	19	2.26
(3,282)	1:202:A:LEU:H	1:199:A:THR:H	4	2.26
(3,206)	1:100:A:LEU:H	1:103:A:GLN:H	18	2.26
(1,75)	1:172:A:SER:HB3	1:60:A:LEU:HD11	20	2.25
(3,249)	1:191:A:TRP:H	1:212:A:LYS:H	11	2.23
(3,245)	1:191:A:TRP:H	1:212:A:LYS:H	11	2.23
(1,128)	1:81:A:GLY:H	1:84:A:LEU:HD21	2	2.23
(1,128)	1:81:A:GLY:H	1:84:A:LEU:HD21	14	2.23
(4,190)	1:134:A:VAL:H	1:123:A:TRP:HB3	10	2.22
(3,114)	1:241:A:VAL:H	1:243:A:ASN:H	8	2.21
(3,98)	1:12:A:GLY:H	1:7:A:TYR:H	12	2.21
(3,251)	1:242:A:ASP:H	1:100:A:LEU:H	2	2.2
(3,76)	1:227:A:LYS:H	1:240:A:MET:H	1	2.2
(1,128)	1:81:A:GLY:H	1:84:A:LEU:HD23	20	2.2
(1,126)	1:78:A:VAL:H	1:78:A:VAL:HG23	11	2.2
(4,1260)	1:25:A:GLY:H	1:23:A:ALA:HB1	19	2.19
(4,1259)	1:93:A:PHE:H	1:68:A:VAL:HG23	9	2.19
(3,115)	1:12:A:GLY:H	1:8:A:GLY:H	2	2.18
(1,75)	1:172:A:SER:HB3	1:60:A:LEU:HD13	8	2.18
(1,47)	1:240:A:MET:HA	1:230:A:PHE:HA	18	2.17
(4,1245)	1:93:A:PHE:H	1:68:A:VAL:HG21	11	2.16
(4,180)	1:98:A:GLY:H	1:240:A:MET:HA	5	2.16
(3,271)	1:140:A:LEU:H	1:206:A:VAL:H	6	2.16
(3,37)	1:206:A:VAL:H	1:140:A:LEU:H	12	2.16
(1,128)	1:81:A:GLY:H	1:84:A:LEU:HD21	8	2.16
(4,1266)	1:66:A:PHE:H	1:68:A:VAL:HG21	7	2.15
(4,654)	1:199:A:THR:H	1:196:A:SER:H	3	2.15
(4,180)	1:228:A:LEU:H	1:240:A:MET:HA	17	2.15
(1,126)	1:78:A:VAL:H	1:78:A:VAL:HG22	1	2.15
(1,126)	1:78:A:VAL:H	1:78:A:VAL:HG23	18	2.15
(1,123)	1:63:A:GLY:H	1:169:A:LYS:HG3	14	2.15
(4,1259)	1:93:A:PHE:H	1:68:A:VAL:HG21	11	2.14
(4,72)	1:229:A:ASN:H	1:163:A:LEU:HD23	6	2.14
(4,61)	1:229:A:ASN:H	1:163:A:LEU:HD23	6	2.14
(3,320)	1:97:A:TRP:H	1:244:A:TRP:H	12	2.14
(3,271)	1:140:A:LEU:H	1:206:A:VAL:H	14	2.14
(3,181)	1:153:A:LYS:H	1:157:A:GLN:H	15	2.14
(3,76)	1:227:A:LYS:H	1:240:A:MET:H	20	2.14
(1,126)	1:78:A:VAL:H	1:78:A:VAL:HG21	8	2.14
(1,126)	1:78:A:VAL:H	1:78:A:VAL:HG23	2	2.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,64)	1:60:A:LEU:HB3	1:172:A:SER:HB3	16	2.13
(3,181)	1:153:A:LYS:H	1:157:A:GLN:H	13	2.12
(1,126)	1:78:A:VAL:H	1:78:A:VAL:HG22	16	2.12
(3,231)	1:191:A:TRP:H	1:212:A:LYS:H	12	2.11
(1,126)	1:78:A:VAL:H	1:78:A:VAL:HG23	6	2.11
(1,121)	1:93:A:PHE:H	1:68:A:VAL:HG21	13	2.11
(1,126)	1:78:A:VAL:H	1:78:A:VAL:HG23	4	2.1
(1,123)	1:63:A:GLY:H	1:169:A:LYS:HG3	1	2.1
(1,71)	1:77:A:ALA:HB1	1:51:A:TYR:HA	15	2.1
(1,47)	1:240:A:MET:HA	1:230:A:PHE:HA	5	2.1
(3,325)	1:197:A:LEU:H	1:203:A:LEU:H	4	2.09
(3,237)	1:189:A:ASP:H	1:212:A:LYS:H	2	2.09
(3,231)	1:191:A:TRP:H	1:212:A:LYS:H	13	2.09
(3,210)	1:197:A:LEU:H	1:205:A:CYS:H	12	2.09
(1,128)	1:81:A:GLY:H	1:84:A:LEU:HD23	3	2.09
(3,234)	1:8:A:GLY:H	1:12:A:GLY:H	2	2.08
(3,76)	1:227:A:LYS:H	1:240:A:MET:H	16	2.08
(1,126)	1:78:A:VAL:H	1:78:A:VAL:HG23	15	2.08
(3,150)	1:206:A:VAL:H	1:197:A:LEU:H	17	2.07
(3,164)	1:203:A:LEU:H	1:197:A:LEU:H	14	2.06
(4,72)	1:229:A:ASN:H	1:163:A:LEU:HD23	8	2.05
(4,61)	1:229:A:ASN:H	1:163:A:LEU:HD23	8	2.05
(4,180)	1:98:A:GLY:H	1:240:A:MET:HA	1	2.04
(4,180)	1:228:A:LEU:H	1:240:A:MET:HA	20	2.04
(3,98)	1:12:A:GLY:H	1:7:A:TYR:H	19	2.04
(1,93)	1:150:A:GLY:H	1:218:A:SER:HA	9	2.04
(4,1270)	1:93:A:PHE:H	1:68:A:VAL:HG21	13	2.03
(4,180)	1:98:A:GLY:H	1:240:A:MET:HA	8	2.03
(2,20)	1:229:A:ASN:H	1:168:A:THR:H	2	2.03
(4,1304)	1:177:A:ASN:H	1:57:A:LEU:HD21	14	2.02
(4,180)	1:169:A:LYS:H	1:240:A:MET:HA	13	2.02
(3,251)	1:242:A:ASP:H	1:100:A:LEU:H	8	2.02
(3,60)	1:29:A:SER:H	1:196:A:SER:H	6	2.02
(4,264)	1:77:A:ALA:HB1	1:51:A:TYR:HA	15	2.01
(3,271)	1:140:A:LEU:H	1:206:A:VAL:H	2	2.01
(3,150)	1:206:A:VAL:H	1:197:A:LEU:H	12	2.01
(3,314)	1:229:A:ASN:H	1:168:A:THR:H	10	2.0
(1,122)	1:226:A:ARG:H	1:226:A:ARG:HG3	5	2.0
(4,1339)	1:93:A:PHE:H	1:91:A:ILE:HD12	9	1.99
(4,66)	1:23:A:ALA:H	1:22:A:ILE:HD11	13	1.99
(4,66)	1:23:A:ALA:H	1:22:A:ILE:HD13	14	1.99
(3,271)	1:140:A:LEU:H	1:206:A:VAL:H	13	1.99

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,181)	1:153:A:LYS:H	1:157:A:GLN:H	5	1.99
(3,166)	1:205:A:CYS:H	1:197:A:LEU:H	12	1.99
(3,181)	1:153:A:LYS:H	1:157:A:GLN:H	19	1.98
(3,37)	1:206:A:VAL:H	1:140:A:LEU:H	10	1.97
(1,64)	1:60:A:LEU:HB3	1:172:A:SER:HB3	4	1.97
(4,1295)	1:148:A:LYS:H	1:148:A:LYS:HG2	15	1.96
(4,1129)	1:111:A:LYS:H	1:33:A:ILE:HB	8	1.96
(3,284)	1:48:A:SER:H	1:82:A:GLY:H	14	1.96
(1,64)	1:60:A:LEU:HB3	1:172:A:SER:HB3	2	1.96
(4,1258)	1:123:A:TRP:H	1:91:A:ILE:HG13	13	1.95
(4,72)	1:229:A:ASN:H	1:163:A:LEU:HD21	15	1.95
(4,61)	1:229:A:ASN:H	1:163:A:LEU:HD21	15	1.95
(4,1215)	1:86:A:GLY:H	1:84:A:LEU:HG	16	1.94
(3,251)	1:242:A:ASP:H	1:100:A:LEU:H	11	1.94
(3,181)	1:153:A:LYS:H	1:157:A:GLN:H	3	1.93
(1,123)	1:63:A:GLY:H	1:169:A:LYS:HG2	2	1.93
(4,268)	1:184:A:LEU:H	1:184:A:LEU:HG	2	1.92
(4,66)	1:23:A:ALA:H	1:22:A:ILE:HD12	6	1.92
(3,181)	1:153:A:LYS:H	1:157:A:GLN:H	20	1.92
(3,110)	1:12:A:GLY:H	1:8:A:GLY:H	9	1.92
(4,6)	1:113:A:LYS:HG3	1:107:A:HIS:H	18	1.91
(3,249)	1:191:A:TRP:H	1:212:A:LYS:H	12	1.91
(3,245)	1:191:A:TRP:H	1:212:A:LYS:H	12	1.91
(1,38)	1:77:A:ALA:HA	1:51:A:TYR:HA	15	1.91
(4,268)	1:184:A:LEU:H	1:184:A:LEU:HG	9	1.9
(3,76)	1:227:A:LYS:H	1:240:A:MET:H	3	1.9
(3,249)	1:191:A:TRP:H	1:212:A:LYS:H	13	1.89
(3,245)	1:191:A:TRP:H	1:212:A:LYS:H	13	1.89
(3,222)	1:197:A:LEU:H	1:205:A:CYS:H	12	1.89
(3,163)	1:205:A:CYS:H	1:197:A:LEU:H	12	1.89
(3,160)	1:205:A:CYS:H	1:197:A:LEU:H	12	1.89
(3,150)	1:206:A:VAL:H	1:197:A:LEU:H	19	1.88
(4,467)	1:95:A:PHE:HB3	1:118:A:LEU:HD23	19	1.87
(3,290)	1:196:A:SER:H	1:206:A:VAL:H	3	1.87
(3,252)	1:196:A:SER:H	1:206:A:VAL:H	3	1.87
(3,181)	1:153:A:LYS:H	1:157:A:GLN:H	16	1.87
(3,155)	1:169:A:LYS:H	1:231:A:ASN:H	2	1.87
(3,271)	1:140:A:LEU:H	1:206:A:VAL:H	12	1.86
(3,181)	1:153:A:LYS:H	1:157:A:GLN:H	12	1.86
(3,98)	1:12:A:GLY:H	1:7:A:TYR:H	20	1.86
(4,1259)	1:93:A:PHE:H	1:68:A:VAL:HG21	13	1.85
(3,261)	1:240:A:MET:H	1:228:A:LEU:H	15	1.85

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,356)	1:153:A:LYS:HD3	1:158:A:LYS:HE2	1	1.84
(4,275)	1:243:A:ASN:HB3	1:244:A:TRP:HA	12	1.84
(1,42)	1:116:A:ALA:HB2	1:97:A:TRP:HA	12	1.84
(4,609)	1:242:A:ASP:H	1:243:A:ASN:H	8	1.83
(4,180)	1:228:A:LEU:H	1:240:A:MET:HA	16	1.83
(3,115)	1:12:A:GLY:H	1:8:A:GLY:H	9	1.82
(1,100)	1:245:A:ARG:H	1:244:A:TRP:HB3	8	1.82
(4,180)	1:228:A:LEU:H	1:240:A:MET:HA	6	1.81
(4,88)	1:210:A:VAL:H	1:192:A:THR:HB	19	1.81
(3,323)	1:181:A:ARG:H	1:184:A:LEU:H	19	1.81
(3,237)	1:189:A:ASP:H	1:212:A:LYS:H	19	1.81
(3,110)	1:12:A:GLY:H	1:8:A:GLY:H	12	1.81
(1,123)	1:63:A:GLY:H	1:169:A:LYS:HG3	4	1.81
(4,275)	1:243:A:ASN:HB2	1:244:A:TRP:HA	5	1.8
(4,204)	1:253:A:ARG:H	1:253:A:ARG:HG3	8	1.8
(4,72)	1:229:A:ASN:H	1:163:A:LEU:HD22	7	1.8
(4,61)	1:229:A:ASN:H	1:163:A:LEU:HD22	7	1.8
(3,302)	1:229:A:ASN:H	1:168:A:THR:H	10	1.8
(4,356)	1:153:A:LYS:HD3	1:159:A:VAL:HA	19	1.79
(3,164)	1:203:A:LEU:H	1:197:A:LEU:H	4	1.79
(1,93)	1:150:A:GLY:H	1:218:A:SER:HA	4	1.79
(4,21)	1:123:A:TRP:H	1:89:A:ARG:HB3	12	1.78
(3,286)	1:70:A:PHE:H	1:92:A:GLN:H	6	1.78
(3,110)	1:12:A:GLY:H	1:8:A:GLY:H	7	1.78
(1,93)	1:150:A:GLY:H	1:218:A:SER:HA	20	1.78
(4,381)	1:260:A:LYS:HA	1:259:A:PHE:HB3	14	1.77
(4,332)	1:22:A:ILE:HD11	1:22:A:ILE:HA	11	1.75
(4,88)	1:71:A:ASP:H	1:55:A:THR:HB	11	1.75
(3,37)	1:206:A:VAL:H	1:140:A:LEU:H	11	1.74
(4,1245)	1:172:A:SER:H	1:166:A:ILE:HG22	18	1.73
(3,234)	1:8:A:GLY:H	1:12:A:GLY:H	9	1.72
(3,37)	1:206:A:VAL:H	1:140:A:LEU:H	16	1.72
(3,115)	1:12:A:GLY:H	1:8:A:GLY:H	12	1.71
(1,123)	1:63:A:GLY:H	1:169:A:LYS:HG3	9	1.71
(4,1316)	1:205:A:CYS:H	1:206:A:VAL:HG23	7	1.7
(3,261)	1:240:A:MET:H	1:228:A:LEU:H	1	1.7
(3,284)	1:48:A:SER:H	1:82:A:GLY:H	8	1.69
(1,132)	1:135:A:GLN:H	1:134:A:VAL:HG22	12	1.69
(4,15)	1:255:A:ILE:HG12	1:35:A:THR:H	4	1.68
(3,115)	1:12:A:GLY:H	1:8:A:GLY:H	7	1.68
(3,37)	1:206:A:VAL:H	1:140:A:LEU:H	15	1.68
(4,254)	1:135:A:GLN:H	1:133:A:ALA:HB2	15	1.67

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,180)	1:228:A:LEU:H	1:240:A:MET:HA	4	1.67
(3,271)	1:140:A:LEU:H	1:206:A:VAL:H	10	1.67
(4,1337)	1:91:A:ILE:H	1:91:A:ILE:HD11	14	1.65
(4,66)	1:23:A:ALA:H	1:22:A:ILE:HD11	19	1.65
(3,12)	1:218:A:SER:H	1:150:A:GLY:H	12	1.65
(4,239)	1:135:A:GLN:H	1:139:A:GLY:HA3	17	1.64
(3,286)	1:70:A:PHE:H	1:92:A:GLN:H	17	1.64
(3,98)	1:12:A:GLY:H	1:7:A:TYR:H	8	1.64
(4,72)	1:229:A:ASN:H	1:163:A:LEU:HD23	12	1.63
(4,61)	1:229:A:ASN:H	1:163:A:LEU:HD23	12	1.63
(3,110)	1:12:A:GLY:H	1:8:A:GLY:H	1	1.63
(1,78)	1:117:A:GLU:H	1:96:A:HIS:H	20	1.63
(4,1321)	1:205:A:CYS:H	1:206:A:VAL:HG23	7	1.62
(3,290)	1:196:A:SER:H	1:206:A:VAL:H	17	1.62
(3,252)	1:196:A:SER:H	1:206:A:VAL:H	17	1.62
(3,261)	1:240:A:MET:H	1:228:A:LEU:H	9	1.61
(3,234)	1:8:A:GLY:H	1:12:A:GLY:H	12	1.61
(3,255)	1:147:A:LEU:H	1:115:A:ALA:H	15	1.6
(4,356)	1:153:A:LYS:HD2	1:159:A:VAL:HA	20	1.59
(3,251)	1:242:A:ASP:H	1:100:A:LEU:H	18	1.59
(3,98)	1:12:A:GLY:H	1:7:A:TYR:H	11	1.59
(3,37)	1:206:A:VAL:H	1:140:A:LEU:H	3	1.59
(4,328)	1:240:A:MET:HA	1:239:A:LEU:HA	10	1.58
(3,234)	1:8:A:GLY:H	1:12:A:GLY:H	7	1.58
(1,100)	1:245:A:ARG:H	1:244:A:TRP:HB2	19	1.58
(4,66)	1:23:A:ALA:H	1:22:A:ILE:HD11	17	1.57
(4,328)	1:240:A:MET:HA	1:239:A:LEU:HA	7	1.56
(4,32)	1:211:A:LEU:HG	1:144:A:GLY:H	13	1.56
(3,110)	1:12:A:GLY:H	1:8:A:GLY:H	6	1.56
(3,103)	1:82:A:GLY:H	1:48:A:SER:H	14	1.56
(2,20)	1:229:A:ASN:H	1:168:A:THR:H	19	1.56
(4,661)	1:198:A:THR:H	1:198:A:THR:HG1	2	1.55
(4,163)	1:231:A:ASN:H	1:240:A:MET:HA	10	1.55
(4,147)	1:231:A:ASN:H	1:240:A:MET:HA	10	1.55
(3,314)	1:229:A:ASN:H	1:168:A:THR:H	7	1.55
(3,264)	1:240:A:MET:H	1:228:A:LEU:H	15	1.55
(3,12)	1:218:A:SER:H	1:150:A:GLY:H	4	1.55
(3,7)	1:56:A:SER:H	1:177:A:ASN:H	15	1.55
(4,72)	1:229:A:ASN:H	1:163:A:LEU:HD21	5	1.54
(4,61)	1:229:A:ASN:H	1:163:A:LEU:HD21	5	1.54
(3,59)	1:197:A:LEU:H	1:204:A:GLU:H	12	1.54
(3,37)	1:206:A:VAL:H	1:140:A:LEU:H	20	1.54

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,7)	1:56:A:SER:H	1:177:A:ASN:H	12	1.54
(1,120)	1:259:A:PHE:H	1:257:A:ALA:HB2	14	1.54
(4,1123)	1:172:A:SER:H	1:171:A:LYS:HB3	14	1.53
(4,519)	1:152:A:ALA:H	1:151:A:SER:H	13	1.53
(3,115)	1:12:A:GLY:H	1:8:A:GLY:H	1	1.53
(3,76)	1:227:A:LYS:H	1:240:A:MET:H	6	1.53
(3,286)	1:70:A:PHE:H	1:92:A:GLN:H	20	1.52
(3,17)	1:169:A:LYS:H	1:63:A:GLY:H	7	1.52
(4,467)	1:86:A:GLY:HA3	1:84:A:LEU:HD21	4	1.51
(3,125)	1:245:A:ARG:H	1:106:A:GLU:H	12	1.51
(1,78)	1:117:A:GLU:H	1:96:A:HIS:H	14	1.51
(4,661)	1:198:A:THR:H	1:198:A:THR:HG1	19	1.5
(4,519)	1:50:A:SER:H	1:49:A:VAL:H	11	1.5
(4,519)	1:50:A:SER:H	1:49:A:VAL:H	19	1.5
(4,328)	1:240:A:MET:HA	1:239:A:LEU:HA	5	1.5
(4,266)	1:244:A:TRP:H	1:241:A:VAL:HG23	17	1.5
(4,180)	1:98:A:GLY:H	1:240:A:MET:HA	2	1.5
(3,141)	1:87:A:THR:H	1:125:A:THR:H	6	1.5
(4,6)	1:113:A:LYS:HG3	1:245:A:ARG:H	2	1.49
(3,284)	1:48:A:SER:H	1:82:A:GLY:H	10	1.49
(1,75)	1:172:A:SER:HB2	1:60:A:LEU:HD11	14	1.49
(4,1258)	1:123:A:TRP:H	1:91:A:ILE:HG12	19	1.48
(4,463)	1:174:A:ASP:HA	1:176:A:THR:HG22	8	1.48
(4,266)	1:244:A:TRP:H	1:241:A:VAL:HG21	7	1.48
(4,328)	1:240:A:MET:HA	1:239:A:LEU:HA	12	1.47
(3,314)	1:229:A:ASN:H	1:168:A:THR:H	20	1.47
(4,519)	1:230:A:PHE:H	1:239:A:LEU:H	9	1.46
(4,470)	1:170:A:GLY:H	1:63:A:GLY:H	11	1.46
(4,328)	1:240:A:MET:HA	1:239:A:LEU:HA	18	1.46
(3,314)	1:229:A:ASN:H	1:168:A:THR:H	9	1.46
(3,115)	1:12:A:GLY:H	1:8:A:GLY:H	6	1.46
(4,1253)	1:198:A:THR:H	1:199:A:THR:HG22	14	1.45
(4,1176)	1:234:A:GLY:H	1:233:A:GLU:HB3	19	1.45
(4,1091)	1:81:A:GLY:H	1:80:A:LYS:HB3	12	1.45
(3,322)	1:108:A:THR:H	1:31:A:VAL:H	10	1.45
(3,37)	1:206:A:VAL:H	1:140:A:LEU:H	8	1.45
(3,17)	1:169:A:LYS:H	1:63:A:GLY:H	18	1.45
(4,1279)	1:250:A:LEU:H	1:250:A:LEU:HD22	12	1.44
(4,180)	1:98:A:GLY:H	1:240:A:MET:HA	11	1.44
(3,271)	1:140:A:LEU:H	1:206:A:VAL:H	11	1.44
(3,80)	1:110:A:ASP:H	1:33:A:ILE:H	18	1.44
(1,100)	1:245:A:ARG:H	1:244:A:TRP:HB3	20	1.44

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,282)	1:202:A:LEU:H	1:199:A:THR:H	8	1.43
(3,234)	1:8:A:GLY:H	1:12:A:GLY:H	1	1.43
(3,181)	1:153:A:LYS:H	1:157:A:GLN:H	18	1.43
(1,47)	1:240:A:MET:HA	1:230:A:PHE:HA	15	1.43
(4,1205)	1:198:A:THR:H	1:199:A:THR:HG23	2	1.42
(4,382)	1:75:A:ASP:HB2	1:74:A:GLN:HB3	14	1.42
(3,320)	1:97:A:TRP:H	1:244:A:TRP:H	9	1.42
(3,271)	1:140:A:LEU:H	1:206:A:VAL:H	16	1.42
(3,255)	1:147:A:LEU:H	1:115:A:ALA:H	5	1.42
(3,237)	1:189:A:ASP:H	1:212:A:LYS:H	16	1.42
(3,210)	1:197:A:LEU:H	1:205:A:CYS:H	3	1.42
(3,110)	1:12:A:GLY:H	1:8:A:GLY:H	17	1.42
(3,37)	1:206:A:VAL:H	1:140:A:LEU:H	9	1.42
(1,6)	1:169:A:LYS:HB3	1:63:A:GLY:H	12	1.42
(3,255)	1:147:A:LEU:H	1:115:A:ALA:H	6	1.41
(4,1006)	1:141:A:ALA:H	1:123:A:TRP:HB3	18	1.4
(4,551)	1:205:A:CYS:H	1:204:A:GLU:H	3	1.4
(4,253)	1:135:A:GLN:H	1:127:A:TYR:HB2	13	1.4
(3,264)	1:240:A:MET:H	1:228:A:LEU:H	1	1.4
(4,1176)	1:234:A:GLY:H	1:233:A:GLU:HB3	7	1.39
(4,467)	1:82:A:GLY:HA3	1:47:A:LEU:HD23	9	1.39
(4,466)	1:243:A:ASN:HB2	1:241:A:VAL:HG21	3	1.39
(4,259)	1:242:A:ASP:H	1:241:A:VAL:HB	11	1.39
(4,190)	1:92:A:GLN:H	1:123:A:TRP:HB3	3	1.38
(3,322)	1:108:A:THR:H	1:31:A:VAL:H	1	1.38
(3,271)	1:140:A:LEU:H	1:206:A:VAL:H	15	1.38
(3,79)	1:192:A:THR:H	1:256:A:LYS:H	15	1.38
(3,9)	1:256:A:LYS:H	1:192:A:THR:H	15	1.38
(4,1325)	1:59:A:ILE:H	1:166:A:ILE:HD11	10	1.37
(3,226)	1:231:A:ASN:H	1:169:A:LYS:H	2	1.37
(1,25)	1:169:A:LYS:H	1:168:A:THR:HB	7	1.37
(1,7)	1:59:A:ILE:H	1:166:A:ILE:HD11	10	1.37
(4,1076)	1:234:A:GLY:H	1:233:A:GLU:HB2	12	1.36
(4,399)	1:50:A:SER:HA	1:78:A:VAL:HB	15	1.36
(3,237)	1:189:A:ASP:H	1:212:A:LYS:H	20	1.36
(3,234)	1:8:A:GLY:H	1:12:A:GLY:H	6	1.36
(3,126)	1:56:A:SER:H	1:178:A:PHE:H	15	1.36
(3,60)	1:29:A:SER:H	1:196:A:SER:H	13	1.36
(3,10)	1:178:A:PHE:H	1:56:A:SER:H	15	1.36
(4,1253)	1:198:A:THR:H	1:199:A:THR:HG21	3	1.35
(4,1091)	1:81:A:GLY:H	1:80:A:LYS:HB3	1	1.35
(4,32)	1:211:A:LEU:HG	1:144:A:GLY:H	12	1.35

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,323)	1:181:A:ARG:H	1:184:A:LEU:H	10	1.35
(3,302)	1:229:A:ASN:H	1:168:A:THR:H	7	1.35
(3,11)	1:177:A:ASN:H	1:56:A:SER:H	15	1.35
(1,40)	1:203:A:LEU:H	1:202:A:LEU:HB3	12	1.35
(4,467)	1:78:A:VAL:HG22	1:80:A:LYS:HE3	13	1.34
(4,15)	1:192:A:THR:H	1:255:A:ILE:HG13	15	1.34
(3,155)	1:169:A:LYS:H	1:231:A:ASN:H	16	1.34
(3,11)	1:177:A:ASN:H	1:56:A:SER:H	12	1.34
(4,1271)	1:231:A:ASN:H	1:168:A:THR:HG22	16	1.33
(4,1063)	1:8:A:GLY:H	1:7:A:TYR:HB3	18	1.33
(4,266)	1:244:A:TRP:H	1:241:A:VAL:HG21	3	1.33
(4,259)	1:242:A:ASP:H	1:241:A:VAL:HB	18	1.33
(3,286)	1:70:A:PHE:H	1:92:A:GLN:H	16	1.33
(3,261)	1:240:A:MET:H	1:228:A:LEU:H	8	1.33
(3,210)	1:197:A:LEU:H	1:205:A:CYS:H	14	1.33
(4,1176)	1:234:A:GLY:H	1:233:A:GLU:HB3	4	1.32
(4,266)	1:166:A:ILE:HD13	1:168:A:THR:H	15	1.32
(3,210)	1:197:A:LEU:H	1:205:A:CYS:H	17	1.32
(3,166)	1:205:A:CYS:H	1:197:A:LEU:H	3	1.32
(3,115)	1:12:A:GLY:H	1:8:A:GLY:H	17	1.32
(3,97)	1:54:A:ALA:H	1:52:A:ASP:H	15	1.32
(1,100)	1:245:A:ARG:H	1:244:A:TRP:HB2	13	1.32
(4,1091)	1:81:A:GLY:H	1:80:A:LYS:HB3	7	1.31
(4,1088)	1:232:A:GLY:H	1:169:A:LYS:HB2	15	1.31
(4,519)	1:50:A:SER:H	1:49:A:VAL:H	2	1.31
(4,466)	1:243:A:ASN:HB2	1:241:A:VAL:HG23	17	1.31
(4,163)	1:231:A:ASN:H	1:240:A:MET:HA	5	1.31
(3,264)	1:240:A:MET:H	1:228:A:LEU:H	9	1.31
(4,1253)	1:198:A:THR:H	1:199:A:THR:HG21	18	1.3
(4,378)	1:22:A:ILE:HD11	1:28:A:GLN:HB2	16	1.3
(3,323)	1:181:A:ARG:H	1:184:A:LEU:H	11	1.3
(3,290)	1:196:A:SER:H	1:206:A:VAL:H	2	1.3
(3,252)	1:196:A:SER:H	1:206:A:VAL:H	2	1.3
(3,76)	1:227:A:LYS:H	1:240:A:MET:H	17	1.3
(3,37)	1:206:A:VAL:H	1:140:A:LEU:H	1	1.3
(3,37)	1:206:A:VAL:H	1:140:A:LEU:H	4	1.3
(4,1253)	1:198:A:THR:H	1:199:A:THR:HG21	6	1.29
(4,1205)	1:198:A:THR:H	1:199:A:THR:HG22	10	1.29
(4,540)	1:89:A:ARG:H	1:123:A:TRP:H	7	1.29
(4,328)	1:240:A:MET:HA	1:230:A:PHE:HA	15	1.29
(4,273)	1:113:A:LYS:HD2	1:244:A:TRP:HA	7	1.29
(3,286)	1:70:A:PHE:H	1:92:A:GLN:H	11	1.29

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,284)	1:48:A:SER:H	1:82:A:GLY:H	9	1.29
(3,271)	1:140:A:LEU:H	1:206:A:VAL:H	3	1.29
(3,255)	1:147:A:LEU:H	1:115:A:ALA:H	11	1.29
(3,200)	1:112:A:LYS:H	1:109:A:VAL:H	18	1.29
(3,139)	1:109:A:VAL:H	1:112:A:LYS:H	18	1.29
(3,110)	1:12:A:GLY:H	1:8:A:GLY:H	4	1.29
(3,103)	1:82:A:GLY:H	1:48:A:SER:H	8	1.29
(3,37)	1:206:A:VAL:H	1:140:A:LEU:H	17	1.29
(4,1177)	1:78:A:VAL:H	1:77:A:ALA:HB2	19	1.28
(4,1063)	1:99:A:SER:H	1:241:A:VAL:HB	17	1.28
(4,468)	1:76:A:LYS:HG3	1:51:A:TYR:HA	8	1.28
(4,468)	1:76:A:LYS:HG3	1:51:A:TYR:HA	11	1.28
(4,382)	1:89:A:ARG:HD2	1:75:A:ASP:HB2	6	1.28
(3,92)	1:55:A:THR:H	1:77:A:ALA:H	19	1.28
(4,1224)	1:229:A:ASN:H	1:228:A:LEU:HD23	10	1.27
(4,666)	1:226:A:ARG:H	1:222:A:VAL:H	14	1.27
(4,273)	1:113:A:LYS:HD3	1:244:A:TRP:HA	6	1.27
(3,302)	1:229:A:ASN:H	1:168:A:THR:H	20	1.27
(4,371)	1:22:A:ILE:HB	1:20:A:PHE:HB2	1	1.26
(4,356)	1:153:A:LYS:HD3	1:224:A:LYS:HE2	13	1.26
(4,259)	1:242:A:ASP:H	1:241:A:VAL:HB	12	1.26
(3,325)	1:197:A:LEU:H	1:203:A:LEU:H	8	1.26
(3,302)	1:229:A:ASN:H	1:168:A:THR:H	9	1.26
(3,284)	1:48:A:SER:H	1:82:A:GLY:H	19	1.26
(3,237)	1:189:A:ASP:H	1:212:A:LYS:H	18	1.26
(4,1209)	1:172:A:SER:H	1:166:A:ILE:HG21	9	1.25
(4,1201)	1:172:A:SER:H	1:166:A:ILE:HG21	9	1.25
(4,1129)	1:195:A:GLY:H	1:204:A:GLU:HG3	11	1.25
(4,469)	1:140:A:LEU:HB2	1:91:A:ILE:HD12	2	1.25
(4,401)	1:196:A:SER:HB3	1:197:A:LEU:HG	2	1.25
(4,387)	1:22:A:ILE:HD11	1:28:A:GLN:HB2	16	1.25
(3,314)	1:229:A:ASN:H	1:168:A:THR:H	18	1.25
(4,1325)	1:59:A:ILE:H	1:166:A:ILE:HD12	12	1.24
(4,1176)	1:234:A:GLY:H	1:233:A:GLU:HB3	11	1.24
(4,519)	1:152:A:ALA:H	1:151:A:SER:H	17	1.24
(4,468)	1:76:A:LYS:HG3	1:51:A:TYR:HA	12	1.24
(4,273)	1:226:A:ARG:HG2	1:97:A:TRP:HA	17	1.24
(4,266)	1:244:A:TRP:H	1:241:A:VAL:HG21	6	1.24
(3,271)	1:140:A:LEU:H	1:206:A:VAL:H	20	1.24
(3,155)	1:169:A:LYS:H	1:231:A:ASN:H	20	1.24
(3,110)	1:12:A:GLY:H	1:8:A:GLY:H	15	1.24
(1,7)	1:59:A:ILE:H	1:166:A:ILE:HD12	12	1.24

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1178)	1:177:A:ASN:H	1:176:A:THR:HG21	19	1.23
(3,322)	1:108:A:THR:H	1:31:A:VAL:H	15	1.23
(3,166)	1:205:A:CYS:H	1:197:A:LEU:H	14	1.23
(3,141)	1:87:A:THR:H	1:125:A:THR:H	14	1.23
(3,59)	1:197:A:LEU:H	1:204:A:GLU:H	5	1.23
(3,37)	1:206:A:VAL:H	1:140:A:LEU:H	19	1.23
(4,469)	1:140:A:LEU:HB3	1:134:A:VAL:HG23	18	1.22
(3,234)	1:8:A:GLY:H	1:12:A:GLY:H	17	1.22
(3,222)	1:197:A:LEU:H	1:205:A:CYS:H	3	1.22
(3,166)	1:205:A:CYS:H	1:197:A:LEU:H	17	1.22
(3,163)	1:205:A:CYS:H	1:197:A:LEU:H	3	1.22
(3,160)	1:205:A:CYS:H	1:197:A:LEU:H	3	1.22
(3,17)	1:169:A:LYS:H	1:63:A:GLY:H	12	1.22
(4,1308)	1:212:A:LYS:H	1:211:A:LEU:HD23	7	1.21
(4,156)	1:157:A:GLN:H	1:158:A:LYS:HG2	5	1.21
(4,150)	1:164:A:ASP:H	1:163:A:LEU:HG	5	1.21
(3,290)	1:196:A:SER:H	1:206:A:VAL:H	18	1.21
(3,252)	1:196:A:SER:H	1:206:A:VAL:H	18	1.21
(3,23)	1:138:A:ASP:H	1:140:A:LEU:H	7	1.21
(1,134)	1:121:A:VAL:H	1:91:A:ILE:HD13	11	1.21
(4,1334)	1:82:A:GLY:H	1:84:A:LEU:HD23	20	1.2
(4,1295)	1:123:A:TRP:H	1:91:A:ILE:HD11	9	1.2
(4,466)	1:243:A:ASN:HB2	1:241:A:VAL:HG21	6	1.2
(4,190)	1:130:A:PHE:H	1:123:A:TRP:HB3	9	1.2
(4,1091)	1:81:A:GLY:H	1:80:A:LYS:HB3	3	1.19
(4,466)	1:243:A:ASN:HB2	1:241:A:VAL:HG21	19	1.19
(3,115)	1:12:A:GLY:H	1:8:A:GLY:H	4	1.19
(4,478)	1:190:A:TYR:H	1:258:A:SER:H	1	1.18
(4,393)	1:63:A:GLY:HA2	1:169:A:LYS:HB2	5	1.18
(4,312)	1:209:A:ILE:HD12	1:209:A:ILE:HA	13	1.18
(3,251)	1:242:A:ASP:H	1:100:A:LEU:H	15	1.18
(3,158)	1:57:A:LEU:H	1:70:A:PHE:H	13	1.18
(3,155)	1:169:A:LYS:H	1:231:A:ASN:H	10	1.18
(4,1295)	1:123:A:TRP:H	1:91:A:ILE:HD13	10	1.17
(4,1217)	1:197:A:LEU:H	1:197:A:LEU:HG	6	1.17
(4,399)	1:50:A:SER:HA	1:52:A:ASP:HB3	13	1.17
(4,15)	1:255:A:ILE:HG12	1:35:A:THR:H	18	1.17
(3,322)	1:108:A:THR:H	1:31:A:VAL:H	17	1.17
(3,306)	1:156:A:LEU:H	1:159:A:VAL:H	18	1.17
(3,237)	1:189:A:ASP:H	1:212:A:LYS:H	1	1.17
(3,237)	1:189:A:ASP:H	1:212:A:LYS:H	12	1.17
(4,478)	1:190:A:TYR:H	1:258:A:SER:H	10	1.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,150)	1:164:A:ASP:H	1:163:A:LEU:HG	2	1.16
(4,1325)	1:59:A:ILE:H	1:166:A:ILE:HD13	7	1.15
(4,42)	1:38:A:ALA:HA	1:255:A:ILE:H	6	1.15
(3,290)	1:196:A:SER:H	1:206:A:VAL:H	1	1.15
(3,271)	1:140:A:LEU:H	1:206:A:VAL:H	8	1.15
(3,252)	1:196:A:SER:H	1:206:A:VAL:H	1	1.15
(3,141)	1:87:A:THR:H	1:125:A:THR:H	13	1.15
(3,79)	1:192:A:THR:H	1:256:A:LYS:H	8	1.15
(3,9)	1:256:A:LYS:H	1:192:A:THR:H	8	1.15
(1,7)	1:59:A:ILE:H	1:166:A:ILE:HD13	7	1.15
(4,1266)	1:66:A:PHE:H	1:169:A:LYS:HG2	19	1.14
(4,1091)	1:81:A:GLY:H	1:80:A:LYS:HB3	18	1.14
(4,666)	1:226:A:ARG:H	1:222:A:VAL:H	15	1.14
(4,386)	1:232:A:GLY:HA2	1:229:A:ASN:HB2	1	1.14
(3,115)	1:12:A:GLY:H	1:8:A:GLY:H	15	1.14
(1,40)	1:203:A:LEU:H	1:202:A:LEU:HB3	11	1.14
(4,1249)	1:169:A:LYS:H	1:169:A:LYS:HG3	20	1.13
(4,163)	1:231:A:ASN:H	1:240:A:MET:HA	12	1.13
(4,156)	1:223:A:LEU:H	1:224:A:LYS:HG2	20	1.13
(4,147)	1:231:A:ASN:H	1:240:A:MET:HA	12	1.13
(3,320)	1:97:A:TRP:H	1:244:A:TRP:H	1	1.13
(3,284)	1:48:A:SER:H	1:82:A:GLY:H	5	1.13
(3,222)	1:197:A:LEU:H	1:205:A:CYS:H	14	1.13
(3,163)	1:205:A:CYS:H	1:197:A:LEU:H	14	1.13
(3,160)	1:205:A:CYS:H	1:197:A:LEU:H	14	1.13
(3,92)	1:55:A:THR:H	1:77:A:ALA:H	13	1.13
(4,1250)	1:169:A:LYS:H	1:169:A:LYS:HG3	20	1.12
(4,654)	1:199:A:THR:H	1:196:A:SER:H	14	1.12
(4,478)	1:243:A:ASN:H	1:97:A:TRP:H	13	1.12
(4,469)	1:140:A:LEU:HB2	1:91:A:ILE:HD13	10	1.12
(4,466)	1:243:A:ASN:HB2	1:241:A:VAL:HG21	8	1.12
(4,466)	1:243:A:ASN:HB2	1:241:A:VAL:HG22	13	1.12
(4,386)	1:235:A:GLU:HG2	1:234:A:GLY:HA3	5	1.12
(4,15)	1:255:A:ILE:HG12	1:35:A:THR:H	3	1.12
(3,284)	1:48:A:SER:H	1:82:A:GLY:H	17	1.12
(3,271)	1:140:A:LEU:H	1:206:A:VAL:H	9	1.12
(3,255)	1:147:A:LEU:H	1:115:A:ALA:H	16	1.12
(3,222)	1:197:A:LEU:H	1:205:A:CYS:H	17	1.12
(3,163)	1:205:A:CYS:H	1:197:A:LEU:H	17	1.12
(3,160)	1:205:A:CYS:H	1:197:A:LEU:H	17	1.12
(3,17)	1:169:A:LYS:H	1:63:A:GLY:H	19	1.12
(1,106)	1:226:A:ARG:H	1:225:A:PHE:HB2	14	1.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1309)	1:169:A:LYS:H	1:169:A:LYS:HG3	13	1.11
(4,1224)	1:229:A:ASN:H	1:168:A:THR:HG21	15	1.11
(4,1218)	1:78:A:VAL:H	1:77:A:ALA:HB1	18	1.11
(4,150)	1:164:A:ASP:H	1:163:A:LEU:HG	18	1.11
(3,325)	1:197:A:LEU:H	1:203:A:LEU:H	13	1.11
(3,314)	1:229:A:ASN:H	1:168:A:THR:H	1	1.11
(3,286)	1:70:A:PHE:H	1:92:A:GLN:H	15	1.11
(3,17)	1:169:A:LYS:H	1:63:A:GLY:H	1	1.11
(4,1325)	1:59:A:ILE:H	1:166:A:ILE:HD12	14	1.1
(4,650)	1:19:A:ASP:H	1:14:A:GLU:H	3	1.1
(4,467)	1:82:A:GLY:HA3	1:44:A:LEU:HD23	7	1.1
(4,266)	1:166:A:ILE:HD12	1:168:A:THR:H	19	1.1
(3,237)	1:189:A:ASP:H	1:212:A:LYS:H	11	1.1
(3,155)	1:169:A:LYS:H	1:231:A:ASN:H	9	1.1
(2,20)	1:229:A:ASN:H	1:168:A:THR:H	10	1.1
(1,7)	1:59:A:ILE:H	1:166:A:ILE:HD12	14	1.1
(4,156)	1:223:A:LEU:H	1:224:A:LYS:HG2	1	1.09
(4,150)	1:223:A:LEU:H	1:224:A:LYS:HG2	20	1.09
(3,314)	1:229:A:ASN:H	1:168:A:THR:H	16	1.09
(3,286)	1:70:A:PHE:H	1:92:A:GLN:H	8	1.09
(3,234)	1:8:A:GLY:H	1:12:A:GLY:H	4	1.09
(3,114)	1:241:A:VAL:H	1:243:A:ASN:H	1	1.09
(3,103)	1:82:A:GLY:H	1:48:A:SER:H	10	1.09
(4,1337)	1:91:A:ILE:H	1:91:A:ILE:HD11	8	1.08
(4,1198)	1:22:A:ILE:H	1:22:A:ILE:HD13	9	1.08
(4,478)	1:32:A:ASP:H	1:250:A:LEU:H	12	1.08
(4,466)	1:243:A:ASN:HB2	1:241:A:VAL:HG21	4	1.08
(3,282)	1:202:A:LEU:H	1:199:A:THR:H	10	1.08
(3,237)	1:189:A:ASP:H	1:212:A:LYS:H	3	1.08
(3,17)	1:169:A:LYS:H	1:63:A:GLY:H	5	1.08
(3,13)	1:207:A:THR:H	1:195:A:GLY:H	12	1.08
(4,419)	1:203:A:LEU:HB3	1:205:A:CYS:HB3	16	1.07
(4,168)	1:164:A:ASP:H	1:163:A:LEU:HB3	19	1.07
(3,306)	1:156:A:LEU:H	1:159:A:VAL:H	4	1.07
(3,306)	1:156:A:LEU:H	1:159:A:VAL:H	6	1.07
(3,290)	1:196:A:SER:H	1:206:A:VAL:H	14	1.07
(3,286)	1:70:A:PHE:H	1:92:A:GLN:H	1	1.07
(3,252)	1:196:A:SER:H	1:206:A:VAL:H	14	1.07
(3,231)	1:191:A:TRP:H	1:212:A:LYS:H	14	1.07
(3,114)	1:241:A:VAL:H	1:243:A:ASN:H	11	1.07
(4,1308)	1:212:A:LYS:H	1:211:A:LEU:HD23	5	1.06
(4,1266)	1:66:A:PHE:H	1:169:A:LYS:HG3	18	1.06

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1228)	1:152:A:ALA:H	1:152:A:ALA:HB3	7	1.06
(4,1006)	1:141:A:ALA:H	1:123:A:TRP:HB3	15	1.06
(4,356)	1:153:A:LYS:HD2	1:158:A:LYS:HE2	2	1.06
(4,239)	1:135:A:GLN:H	1:139:A:GLY:HA3	20	1.06
(4,190)	1:92:A:GLN:H	1:123:A:TRP:HB3	4	1.06
(4,150)	1:223:A:LEU:H	1:224:A:LYS:HG2	1	1.06
(3,290)	1:196:A:SER:H	1:206:A:VAL:H	19	1.06
(3,252)	1:196:A:SER:H	1:206:A:VAL:H	19	1.06
(3,114)	1:241:A:VAL:H	1:243:A:ASN:H	19	1.06
(3,79)	1:192:A:THR:H	1:256:A:LYS:H	18	1.06
(3,9)	1:256:A:LYS:H	1:192:A:THR:H	18	1.06
(4,1253)	1:198:A:THR:H	1:199:A:THR:HG23	8	1.05
(4,1218)	1:78:A:VAL:H	1:77:A:ALA:HB2	4	1.05
(4,1022)	1:112:A:LYS:H	1:111:A:LYS:HB2	18	1.05
(4,273)	1:113:A:LYS:HD3	1:244:A:TRP:HA	15	1.05
(3,302)	1:229:A:ASN:H	1:168:A:THR:H	18	1.05
(3,290)	1:196:A:SER:H	1:206:A:VAL:H	11	1.05
(3,252)	1:196:A:SER:H	1:206:A:VAL:H	11	1.05
(3,110)	1:12:A:GLY:H	1:8:A:GLY:H	14	1.05
(3,60)	1:29:A:SER:H	1:196:A:SER:H	19	1.05
(4,1198)	1:22:A:ILE:H	1:22:A:ILE:HD13	5	1.04
(4,156)	1:164:A:ASP:H	1:163:A:LEU:HG	13	1.04
(3,314)	1:229:A:ASN:H	1:168:A:THR:H	4	1.04
(3,284)	1:48:A:SER:H	1:82:A:GLY:H	11	1.04
(3,282)	1:202:A:LEU:H	1:199:A:THR:H	15	1.04
(3,234)	1:8:A:GLY:H	1:12:A:GLY:H	15	1.04
(3,206)	1:100:A:LEU:H	1:103:A:GLN:H	8	1.04
(4,1326)	1:212:A:LYS:H	1:211:A:LEU:HD23	7	1.03
(4,1218)	1:78:A:VAL:H	1:77:A:ALA:HB2	2	1.03
(4,1021)	1:112:A:LYS:H	1:111:A:LYS:HB2	18	1.03
(4,1006)	1:79:A:LEU:H	1:88:A:TYR:HB2	7	1.03
(4,467)	1:95:A:PHE:HB3	1:118:A:LEU:HD23	5	1.03
(4,150)	1:223:A:LEU:H	1:224:A:LYS:HG2	16	1.03
(3,264)	1:240:A:MET:H	1:228:A:LEU:H	8	1.03
(1,56)	1:255:A:ILE:HD13	1:193:A:TYR:HB2	17	1.03
(1,36)	1:203:A:LEU:H	1:22:A:ILE:HD13	6	1.03
(4,1245)	1:172:A:SER:H	1:166:A:ILE:HG21	9	1.02
(4,1198)	1:157:A:GLN:H	1:153:A:LYS:HG2	11	1.02
(4,398)	1:130:A:PHE:HB3	1:123:A:TRP:HB2	14	1.02
(4,386)	1:26:A:GLU:HG2	1:25:A:GLY:HA3	3	1.02
(1,110)	1:198:A:THR:H	1:197:A:LEU:HB2	13	1.02
(4,1253)	1:198:A:THR:H	1:199:A:THR:HG21	17	1.01

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1205)	1:198:A:THR:H	1:199:A:THR:HG21	17	1.01
(4,234)	1:24:A:LYS:H	1:22:A:ILE:HD12	11	1.01
(4,156)	1:157:A:GLN:H	1:158:A:LYS:HG2	16	1.01
(3,17)	1:169:A:LYS:H	1:63:A:GLY:H	9	1.01
(2,12)	1:107:A:HIS:HA	1:31:A:VAL:H	15	1.01
(2,8)	1:54:A:ALA:H	1:51:A:TYR:HA	15	1.01
(1,32)	1:167:A:LYS:HB2	1:168:A:THR:H	8	1.01
(4,1022)	1:112:A:LYS:H	1:110:A:ASP:HB3	1	1.0
(4,466)	1:33:A:ILE:HD12	1:106:A:GLU:HG2	14	1.0
(4,209)	1:82:A:GLY:H	1:47:A:LEU:HB3	8	1.0
(4,150)	1:164:A:ASP:H	1:163:A:LEU:HG	13	1.0
(3,271)	1:140:A:LEU:H	1:206:A:VAL:H	1	1.0
(3,271)	1:140:A:LEU:H	1:206:A:VAL:H	4	1.0
(1,26)	1:156:A:LEU:H	1:156:A:LEU:HB2	12	1.0
(4,1198)	1:22:A:ILE:H	1:22:A:ILE:HD11	7	0.99
(4,156)	1:164:A:ASP:H	1:163:A:LEU:HG	12	0.99
(3,271)	1:140:A:LEU:H	1:206:A:VAL:H	17	0.99
(3,114)	1:241:A:VAL:H	1:243:A:ASN:H	2	0.99
(1,109)	1:146:A:PHE:H	1:146:A:PHE:HB2	12	0.99
(4,1021)	1:112:A:LYS:H	1:110:A:ASP:HB3	1	0.98
(4,1006)	1:79:A:LEU:H	1:88:A:TYR:HB2	8	0.98
(4,386)	1:235:A:GLU:HG2	1:234:A:GLY:HA3	7	0.98
(4,384)	1:22:A:ILE:HD11	1:28:A:GLN:HB2	16	0.98
(4,156)	1:157:A:GLN:H	1:158:A:LYS:HG2	18	0.98
(3,320)	1:97:A:TRP:H	1:244:A:TRP:H	2	0.98
(3,286)	1:70:A:PHE:H	1:92:A:GLN:H	3	0.98
(3,237)	1:189:A:ASP:H	1:212:A:LYS:H	17	0.98
(3,150)	1:206:A:VAL:H	1:197:A:LEU:H	3	0.98
(3,17)	1:169:A:LYS:H	1:63:A:GLY:H	4	0.98
(4,1022)	1:112:A:LYS:H	1:110:A:ASP:HB3	8	0.97
(4,423)	1:169:A:LYS:HD3	1:169:A:LYS:HE2	11	0.97
(4,423)	1:251:A:LYS:HD2	1:251:A:LYS:HE3	17	0.97
(4,156)	1:164:A:ASP:H	1:163:A:LEU:HG	6	0.97
(4,156)	1:164:A:ASP:H	1:163:A:LEU:HG	15	0.97
(3,261)	1:240:A:MET:H	1:228:A:LEU:H	4	0.97
(3,255)	1:147:A:LEU:H	1:115:A:ALA:H	17	0.97
(1,40)	1:203:A:LEU:H	1:202:A:LEU:HB2	4	0.97
(4,1248)	1:22:A:ILE:H	1:22:A:ILE:HD11	7	0.96
(4,990)	1:253:A:ARG:H	1:253:A:ARG:HD3	1	0.96
(4,468)	1:76:A:LYS:HG3	1:51:A:TYR:HA	16	0.96
(4,190)	1:92:A:GLN:H	1:123:A:TRP:HB3	8	0.96
(4,156)	1:157:A:GLN:H	1:158:A:LYS:HG3	2	0.96

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,156)	1:223:A:LEU:H	1:224:A:LYS:HG2	17	0.96
(3,286)	1:70:A:PHE:H	1:92:A:GLN:H	14	0.96
(3,173)	1:57:A:LEU:H	1:175:A:PHE:H	17	0.96
(3,164)	1:203:A:LEU:H	1:197:A:LEU:H	8	0.96
(4,1021)	1:112:A:LYS:H	1:110:A:ASP:HB3	8	0.95
(4,540)	1:71:A:ASP:H	1:55:A:THR:H	13	0.95
(4,423)	1:76:A:LYS:HD2	1:76:A:LYS:HE2	7	0.95
(4,423)	1:169:A:LYS:HD2	1:169:A:LYS:HE3	8	0.95
(4,423)	1:158:A:LYS:HD3	1:158:A:LYS:HE2	14	0.95
(4,150)	1:164:A:ASP:H	1:163:A:LEU:HG	12	0.95
(3,325)	1:197:A:LEU:H	1:203:A:LEU:H	15	0.95
(3,231)	1:191:A:TRP:H	1:212:A:LYS:H	19	0.95
(3,115)	1:12:A:GLY:H	1:8:A:GLY:H	14	0.95
(1,64)	1:60:A:LEU:HB2	1:172:A:SER:HB2	5	0.95
(4,1325)	1:59:A:ILE:H	1:166:A:ILE:HD12	2	0.94
(4,478)	1:32:A:ASP:H	1:250:A:LEU:H	20	0.94
(4,466)	1:33:A:ILE:HD13	1:106:A:GLU:HG2	15	0.94
(3,150)	1:206:A:VAL:H	1:197:A:LEU:H	6	0.94
(3,17)	1:169:A:LYS:H	1:63:A:GLY:H	14	0.94
(1,123)	1:63:A:GLY:H	1:169:A:LYS:HG3	20	0.94
(1,7)	1:59:A:ILE:H	1:166:A:ILE:HD12	2	0.94
(4,1281)	1:212:A:LYS:H	1:211:A:LEU:HD23	20	0.93
(4,667)	1:53:A:GLN:H	1:51:A:TYR:HA	17	0.93
(4,399)	1:50:A:SER:HA	1:52:A:ASP:HB3	7	0.93
(4,399)	1:50:A:SER:HA	1:52:A:ASP:HB3	20	0.93
(4,392)	1:61:A:ASN:HB3	1:64:A:HIS:HB3	10	0.93
(4,360)	1:89:A:ARG:HD2	1:125:A:THR:HB	6	0.93
(4,275)	1:117:A:GLU:HB3	1:146:A:PHE:HA	14	0.93
(4,253)	1:135:A:GLN:H	1:127:A:TYR:HB2	12	0.93
(4,150)	1:164:A:ASP:H	1:163:A:LEU:HG	6	0.93
(4,150)	1:164:A:ASP:H	1:163:A:LEU:HG	15	0.93
(3,271)	1:140:A:LEU:H	1:206:A:VAL:H	19	0.93
(3,141)	1:87:A:THR:H	1:125:A:THR:H	20	0.93
(3,92)	1:55:A:THR:H	1:77:A:ALA:H	4	0.93
(3,60)	1:29:A:SER:H	1:196:A:SER:H	5	0.93
(3,47)	1:60:A:LEU:H	1:67:A:ASN:H	12	0.93
(4,1253)	1:198:A:THR:H	1:199:A:THR:HG23	9	0.92
(4,626)	1:245:A:ARG:H	1:247:A:ALA:H	1	0.92
(4,253)	1:135:A:GLN:H	1:127:A:TYR:HB3	5	0.92
(4,150)	1:223:A:LEU:H	1:224:A:LYS:HG2	17	0.92
(4,15)	1:255:A:ILE:HG12	1:35:A:THR:H	5	0.92
(3,120)	1:248:A:GLN:H	1:32:A:ASP:H	15	0.92

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,17)	1:169:A:LYS:H	1:63:A:GLY:H	6	0.92
(1,52)	1:166:A:ILE:HD13	1:163:A:LEU:HA	9	0.92
(4,1021)	1:112:A:LYS:H	1:110:A:ASP:HB2	13	0.91
(4,519)	1:152:A:ALA:H	1:151:A:SER:H	15	0.91
(4,463)	1:174:A:ASP:HA	1:176:A:THR:HG23	7	0.91
(4,419)	1:205:A:CYS:HB2	1:134:A:VAL:HB	19	0.91
(3,302)	1:229:A:ASN:H	1:168:A:THR:H	1	0.91
(3,150)	1:206:A:VAL:H	1:197:A:LEU:H	11	0.91
(3,121)	1:80:A:LYS:H	1:48:A:SER:H	1	0.91
(3,71)	1:138:A:ASP:H	1:140:A:LEU:H	7	0.91
(3,17)	1:169:A:LYS:H	1:63:A:GLY:H	13	0.91
(3,17)	1:169:A:LYS:H	1:63:A:GLY:H	16	0.91
(4,1289)	1:203:A:LEU:H	1:203:A:LEU:HD22	14	0.9
(4,540)	1:97:A:TRP:H	1:98:A:GLY:H	17	0.9
(4,540)	1:97:A:TRP:H	1:98:A:GLY:H	20	0.9
(4,468)	1:76:A:LYS:HG3	1:51:A:TYR:HA	6	0.9
(3,282)	1:202:A:LEU:H	1:199:A:THR:H	11	0.9
(3,17)	1:169:A:LYS:H	1:63:A:GLY:H	2	0.9
(1,110)	1:198:A:THR:H	1:197:A:LEU:HB3	20	0.9
(4,1321)	1:205:A:CYS:H	1:206:A:VAL:HG23	14	0.89
(4,1261)	1:152:A:ALA:H	1:152:A:ALA:HB3	7	0.89
(4,1249)	1:169:A:LYS:H	1:169:A:LYS:HG3	14	0.89
(4,386)	1:26:A:GLU:HG3	1:25:A:GLY:HA2	4	0.89
(4,266)	1:166:A:ILE:HD11	1:168:A:THR:H	14	0.89
(4,253)	1:61:A:ASN:HB2	1:168:A:THR:H	14	0.89
(3,302)	1:229:A:ASN:H	1:168:A:THR:H	16	0.89
(3,141)	1:87:A:THR:H	1:125:A:THR:H	3	0.89
(3,103)	1:82:A:GLY:H	1:48:A:SER:H	9	0.89
(1,110)	1:198:A:THR:H	1:197:A:LEU:HB3	9	0.89
(4,1326)	1:212:A:LYS:H	1:211:A:LEU:HD23	5	0.88
(4,1309)	1:212:A:LYS:H	1:211:A:LEU:HD23	20	0.88
(4,519)	1:152:A:ALA:H	1:151:A:SER:H	6	0.88
(4,266)	1:166:A:ILE:HD13	1:168:A:THR:H	4	0.88
(4,260)	1:203:A:LEU:H	1:203:A:LEU:HB3	5	0.88
(2,12)	1:107:A:HIS:HA	1:31:A:VAL:H	1	0.88
(1,8)	1:95:A:PHE:H	1:95:A:PHE:HB2	1	0.88
(4,1339)	1:116:A:ALA:H	1:149:A:VAL:HG22	14	0.87
(4,1249)	1:169:A:LYS:H	1:169:A:LYS:HG3	15	0.87
(4,519)	1:152:A:ALA:H	1:151:A:SER:H	14	0.87
(4,386)	1:235:A:GLU:HG3	1:234:A:GLY:HA3	10	0.87
(4,382)	1:75:A:ASP:HB2	1:74:A:GLN:HB3	7	0.87
(4,371)	1:22:A:ILE:HB	1:20:A:PHE:HB2	11	0.87

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,255)	1:147:A:LEU:H	1:115:A:ALA:H	3	0.87
(3,249)	1:191:A:TRP:H	1:212:A:LYS:H	14	0.87
(3,245)	1:191:A:TRP:H	1:212:A:LYS:H	14	0.87
(3,155)	1:169:A:LYS:H	1:231:A:ASN:H	7	0.87
(3,59)	1:197:A:LEU:H	1:204:A:GLU:H	1	0.87
(1,6)	1:169:A:LYS:HB3	1:63:A:GLY:H	16	0.87
(4,1224)	1:123:A:TRP:H	1:91:A:ILE:HG12	11	0.86
(4,1006)	1:79:A:LEU:H	1:88:A:TYR:HB2	1	0.86
(4,469)	1:140:A:LEU:HB2	1:91:A:ILE:HD12	5	0.86
(4,401)	1:196:A:SER:HB3	1:204:A:GLU:HB3	1	0.86
(4,399)	1:50:A:SER:HA	1:52:A:ASP:HB3	1	0.86
(4,386)	1:235:A:GLU:HG2	1:234:A:GLY:HA3	20	0.86
(4,64)	1:229:A:ASN:H	1:228:A:LEU:HB3	20	0.86
(3,284)	1:48:A:SER:H	1:82:A:GLY:H	2	0.86
(3,103)	1:82:A:GLY:H	1:48:A:SER:H	19	0.86
(3,92)	1:55:A:THR:H	1:77:A:ALA:H	18	0.86
(4,423)	1:158:A:LYS:HG2	1:158:A:LYS:HE2	5	0.85
(4,423)	1:39:A:LYS:HD3	1:39:A:LYS:HE2	6	0.85
(4,266)	1:166:A:ILE:HD13	1:168:A:THR:H	20	0.85
(4,190)	1:130:A:PHE:H	1:123:A:TRP:HB3	16	0.85
(3,234)	1:8:A:GLY:H	1:12:A:GLY:H	14	0.85
(1,8)	1:95:A:PHE:H	1:95:A:PHE:HB2	12	0.85
(1,8)	1:95:A:PHE:H	1:95:A:PHE:HB2	17	0.85
(4,1027)	1:165:A:SER:H	1:164:A:ASP:HB3	10	0.84
(4,1006)	1:79:A:LEU:H	1:88:A:TYR:HB2	10	0.84
(4,371)	1:22:A:ILE:HB	1:20:A:PHE:HB3	5	0.84
(4,363)	1:80:A:LYS:HD3	1:80:A:LYS:HE2	9	0.84
(3,323)	1:181:A:ARG:H	1:184:A:LEU:H	17	0.84
(3,302)	1:229:A:ASN:H	1:168:A:THR:H	4	0.84
(3,286)	1:70:A:PHE:H	1:92:A:GLN:H	13	0.84
(3,231)	1:191:A:TRP:H	1:212:A:LYS:H	18	0.84
(3,226)	1:231:A:ASN:H	1:169:A:LYS:H	16	0.84
(3,114)	1:241:A:VAL:H	1:243:A:ASN:H	5	0.84
(3,114)	1:241:A:VAL:H	1:243:A:ASN:H	9	0.84
(3,110)	1:12:A:GLY:H	1:8:A:GLY:H	20	0.84
(1,32)	1:167:A:LYS:HB2	1:168:A:THR:H	18	0.84
(1,8)	1:95:A:PHE:H	1:95:A:PHE:HB2	3	0.84
(4,1205)	1:198:A:THR:H	1:199:A:THR:HG22	16	0.83
(4,1022)	1:193:A:TYR:H	1:208:A:TRP:HB3	17	0.83
(4,669)	1:29:A:SER:H	1:31:A:VAL:H	20	0.83
(4,668)	1:29:A:SER:H	1:31:A:VAL:H	20	0.83
(4,378)	1:22:A:ILE:HD12	1:28:A:GLN:HB2	18	0.83

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,363)	1:158:A:LYS:HD2	1:158:A:LYS:HE3	2	0.83
(4,363)	1:169:A:LYS:HD3	1:169:A:LYS:HE2	11	0.83
(4,363)	1:251:A:LYS:HD2	1:251:A:LYS:HE3	17	0.83
(4,251)	1:259:A:PHE:H	1:40:A:TYR:HB2	9	0.83
(4,58)	1:61:A:ASN:H	1:61:A:ASN:HB3	10	0.83
(3,305)	1:166:A:ILE:H	1:168:A:THR:H	3	0.83
(3,155)	1:169:A:LYS:H	1:231:A:ASN:H	4	0.83
(3,141)	1:87:A:THR:H	1:125:A:THR:H	7	0.83
(1,110)	1:198:A:THR:H	1:197:A:LEU:HB3	18	0.83
(1,59)	1:240:A:MET:HA	1:230:A:PHE:HB2	8	0.83
(1,40)	1:203:A:LEU:H	1:202:A:LEU:HB2	3	0.83
(4,1021)	1:193:A:TYR:H	1:208:A:TRP:HB3	17	0.82
(4,467)	1:80:A:LYS:HE2	1:47:A:LEU:HD23	6	0.82
(4,363)	1:169:A:LYS:HD2	1:169:A:LYS:HE2	3	0.82
(4,363)	1:158:A:LYS:HD3	1:158:A:LYS:HE2	12	0.82
(4,363)	1:251:A:LYS:HD2	1:251:A:LYS:HE2	15	0.82
(4,363)	1:167:A:LYS:HD3	1:167:A:LYS:HE2	18	0.82
(4,363)	1:169:A:LYS:HD2	1:169:A:LYS:HE3	19	0.82
(4,356)	1:153:A:LYS:HD3	1:224:A:LYS:HE2	9	0.82
(3,306)	1:156:A:LEU:H	1:159:A:VAL:H	2	0.82
(3,261)	1:240:A:MET:H	1:228:A:LEU:H	3	0.82
(2,12)	1:107:A:HIS:HA	1:31:A:VAL:H	10	0.82
(1,128)	1:81:A:GLY:H	1:84:A:LEU:HD23	12	0.82
(4,1257)	1:78:A:VAL:H	1:77:A:ALA:HB2	15	0.81
(4,1253)	1:198:A:THR:H	1:199:A:THR:HG21	19	0.81
(4,487)	1:48:A:SER:H	1:80:A:LYS:H	13	0.81
(4,398)	1:123:A:TRP:HB3	1:140:A:LEU:HB3	17	0.81
(4,386)	1:26:A:GLU:HG2	1:25:A:GLY:HA2	16	0.81
(4,363)	1:76:A:LYS:HD2	1:76:A:LYS:HE2	7	0.81
(4,363)	1:169:A:LYS:HD2	1:169:A:LYS:HE3	8	0.81
(4,363)	1:80:A:LYS:HD3	1:80:A:LYS:HE2	13	0.81
(4,363)	1:158:A:LYS:HD3	1:158:A:LYS:HE2	14	0.81
(4,312)	1:209:A:ILE:HD13	1:209:A:ILE:HA	20	0.81
(4,97)	1:204:A:GLU:H	1:202:A:LEU:HA	9	0.81
(3,282)	1:202:A:LEU:H	1:199:A:THR:H	20	0.81
(3,164)	1:203:A:LEU:H	1:197:A:LEU:H	13	0.81
(3,60)	1:29:A:SER:H	1:196:A:SER:H	20	0.81
(1,20)	1:197:A:LEU:H	1:197:A:LEU:HB2	10	0.81
(1,8)	1:95:A:PHE:H	1:95:A:PHE:HB2	19	0.81
(4,1266)	1:66:A:PHE:H	1:68:A:VAL:HG22	10	0.8
(4,773)	1:135:A:GLN:H	1:135:A:GLN:HA	1	0.8
(4,773)	1:135:A:GLN:H	1:135:A:GLN:HA	3	0.8

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,773)	1:135:A:GLN:H	1:135:A:GLN:HA	4	0.8
(4,773)	1:135:A:GLN:H	1:135:A:GLN:HA	5	0.8
(4,773)	1:24:A:LYS:H	1:24:A:LYS:HA	8	0.8
(4,773)	1:222:A:VAL:H	1:222:A:VAL:HA	13	0.8
(4,773)	1:135:A:GLN:H	1:135:A:GLN:HA	14	0.8
(4,773)	1:135:A:GLN:H	1:135:A:GLN:HA	15	0.8
(4,773)	1:135:A:GLN:H	1:135:A:GLN:HA	16	0.8
(4,773)	1:224:A:LYS:H	1:224:A:LYS:HA	17	0.8
(4,487)	1:152:A:ALA:H	1:151:A:SER:H	10	0.8
(4,399)	1:50:A:SER:HA	1:52:A:ASP:HB3	16	0.8
(4,392)	1:61:A:ASN:HB3	1:64:A:HIS:HB3	17	0.8
(4,374)	1:127:A:TYR:HB3	1:133:A:ALA:HA	8	0.8
(4,363)	1:169:A:LYS:HD2	1:169:A:LYS:HE3	16	0.8
(4,363)	1:167:A:LYS:HD3	1:167:A:LYS:HE2	20	0.8
(4,185)	1:142:A:VAL:H	1:209:A:ILE:HD12	9	0.8
(4,21)	1:123:A:TRP:H	1:89:A:ARG:HB3	5	0.8
(3,306)	1:156:A:LEU:H	1:159:A:VAL:H	16	0.8
(3,282)	1:202:A:LEU:H	1:199:A:THR:H	1	0.8
(3,120)	1:248:A:GLN:H	1:32:A:ASP:H	17	0.8
(3,110)	1:12:A:GLY:H	1:8:A:GLY:H	16	0.8
(3,79)	1:192:A:THR:H	1:256:A:LYS:H	3	0.8
(3,9)	1:256:A:LYS:H	1:192:A:THR:H	3	0.8
(4,1316)	1:205:A:CYS:H	1:206:A:VAL:HG21	6	0.79
(4,1006)	1:141:A:ALA:H	1:122:A:HIS:HB2	16	0.79
(4,773)	1:24:A:LYS:H	1:24:A:LYS:HA	2	0.79
(4,773)	1:135:A:GLN:H	1:135:A:GLN:HA	9	0.79
(4,773)	1:24:A:LYS:H	1:24:A:LYS:HA	10	0.79
(4,773)	1:24:A:LYS:H	1:24:A:LYS:HA	11	0.79
(4,773)	1:24:A:LYS:H	1:24:A:LYS:HA	12	0.79
(4,773)	1:135:A:GLN:H	1:135:A:GLN:HA	18	0.79
(4,773)	1:24:A:LYS:H	1:24:A:LYS:HA	19	0.79
(4,773)	1:24:A:LYS:H	1:24:A:LYS:HA	20	0.79
(4,469)	1:140:A:LEU:HB3	1:134:A:VAL:HG22	6	0.79
(4,387)	1:22:A:ILE:HD12	1:28:A:GLN:HB2	18	0.79
(4,386)	1:26:A:GLU:HG2	1:25:A:GLY:HA2	11	0.79
(4,363)	1:167:A:LYS:HD2	1:167:A:LYS:HE3	10	0.79
(4,273)	1:113:A:LYS:HD3	1:244:A:TRP:HA	1	0.79
(4,185)	1:142:A:VAL:H	1:209:A:ILE:HD12	12	0.79
(4,168)	1:45:A:LYS:H	1:44:A:LEU:HB3	3	0.79
(4,163)	1:231:A:ASN:H	1:240:A:MET:HA	18	0.79
(4,147)	1:231:A:ASN:H	1:240:A:MET:HA	18	0.79
(4,1328)	1:108:A:THR:H	1:33:A:ILE:HD13	18	0.78

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,371)	1:22:A:ILE:HB	1:20:A:PHE:HB2	16	0.78
(4,293)	1:32:A:ASP:HB2	1:32:A:ASP:HA	1	0.78
(4,293)	1:66:A:PHE:HB2	1:66:A:PHE:HA	6	0.78
(4,97)	1:23:A:ALA:H	1:202:A:LEU:HA	10	0.78
(4,72)	1:229:A:ASN:H	1:163:A:LEU:HD23	20	0.78
(4,61)	1:229:A:ASN:H	1:163:A:LEU:HD23	20	0.78
(3,231)	1:191:A:TRP:H	1:212:A:LYS:H	16	0.78
(3,155)	1:169:A:LYS:H	1:231:A:ASN:H	11	0.78
(3,126)	1:56:A:SER:H	1:178:A:PHE:H	12	0.78
(3,58)	1:70:A:PHE:H	1:57:A:LEU:H	13	0.78
(3,17)	1:169:A:LYS:H	1:63:A:GLY:H	8	0.78
(3,10)	1:178:A:PHE:H	1:56:A:SER:H	12	0.78
(1,106)	1:226:A:ARG:H	1:225:A:PHE:HB2	15	0.78
(1,8)	1:95:A:PHE:H	1:95:A:PHE:HB2	9	0.78
(4,1153)	1:78:A:VAL:H	1:77:A:ALA:HB1	20	0.77
(4,1022)	1:76:A:LYS:H	1:74:A:GLN:HB2	13	0.77
(4,773)	1:224:A:LYS:H	1:224:A:LYS:HA	7	0.77
(4,470)	1:219:A:SER:H	1:150:A:GLY:H	6	0.77
(4,405)	1:49:A:VAL:HA	1:49:A:VAL:HB	20	0.77
(4,399)	1:50:A:SER:HA	1:53:A:GLN:HG2	3	0.77
(4,363)	1:158:A:LYS:HD2	1:158:A:LYS:HE3	5	0.77
(4,293)	1:85:A:ASP:HB3	1:85:A:ASP:HA	3	0.77
(4,293)	1:41:A:ASP:HB2	1:41:A:ASP:HA	11	0.77
(3,261)	1:240:A:MET:H	1:228:A:LEU:H	14	0.77
(3,261)	1:240:A:MET:H	1:228:A:LEU:H	20	0.77
(3,17)	1:169:A:LYS:H	1:63:A:GLY:H	11	0.77
(4,1257)	1:78:A:VAL:H	1:77:A:ALA:HB2	4	0.76
(4,1218)	1:78:A:VAL:H	1:77:A:ALA:HB3	16	0.76
(4,1022)	1:112:A:LYS:H	1:110:A:ASP:HB3	5	0.76
(4,540)	1:89:A:ARG:H	1:123:A:TRP:H	2	0.76
(4,463)	1:174:A:ASP:HA	1:176:A:THR:HG22	3	0.76
(4,405)	1:159:A:VAL:HA	1:159:A:VAL:HB	11	0.76
(4,386)	1:26:A:GLU:HG3	1:25:A:GLY:HA3	2	0.76
(4,293)	1:66:A:PHE:HB3	1:66:A:PHE:HA	7	0.76
(4,293)	1:66:A:PHE:HB3	1:66:A:PHE:HA	9	0.76
(4,293)	1:174:A:ASP:HB3	1:174:A:ASP:HA	13	0.76
(4,293)	1:231:A:ASN:HB2	1:231:A:ASN:HA	14	0.76
(4,293)	1:259:A:PHE:HB2	1:259:A:PHE:HA	17	0.76
(4,163)	1:231:A:ASN:H	1:240:A:MET:HA	7	0.76
(3,306)	1:156:A:LEU:H	1:159:A:VAL:H	3	0.76
(4,1321)	1:205:A:CYS:H	1:206:A:VAL:HG23	16	0.75
(4,1253)	1:198:A:THR:H	1:199:A:THR:HG21	20	0.75

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1225)	1:64:A:HIS:H	1:169:A:LYS:HG2	1	0.75
(4,1021)	1:112:A:LYS:H	1:110:A:ASP:HB3	5	0.75
(4,666)	1:226:A:ARG:H	1:222:A:VAL:H	8	0.75
(4,666)	1:226:A:ARG:H	1:222:A:VAL:H	18	0.75
(4,399)	1:50:A:SER:HA	1:52:A:ASP:HB3	12	0.75
(4,382)	1:193:A:TYR:HB3	1:208:A:TRP:HB3	8	0.75
(4,363)	1:251:A:LYS:HD2	1:251:A:LYS:HE3	1	0.75
(4,293)	1:66:A:PHE:HB3	1:66:A:PHE:HA	2	0.75
(4,253)	1:135:A:GLN:H	1:127:A:TYR:HB3	8	0.75
(4,156)	1:164:A:ASP:H	1:163:A:LEU:HG	7	0.75
(3,249)	1:191:A:TRP:H	1:212:A:LYS:H	19	0.75
(3,245)	1:191:A:TRP:H	1:212:A:LYS:H	19	0.75
(1,109)	1:146:A:PHE:H	1:146:A:PHE:HB2	5	0.75
(1,28)	1:241:A:VAL:H	1:240:A:MET:HA	12	0.75
(4,1338)	1:217:A:VAL:H	1:149:A:VAL:HG22	20	0.74
(4,1279)	1:145:A:ILE:H	1:118:A:LEU:HG	19	0.74
(4,1257)	1:78:A:VAL:H	1:77:A:ALA:HB2	2	0.74
(4,626)	1:245:A:ARG:H	1:105:A:SER:H	15	0.74
(4,540)	1:89:A:ARG:H	1:123:A:TRP:H	1	0.74
(4,540)	1:243:A:ASN:H	1:97:A:TRP:H	19	0.74
(4,293)	1:179:A:ASP:HB3	1:179:A:ASP:HA	4	0.74
(4,293)	1:259:A:PHE:HB2	1:259:A:PHE:HA	8	0.74
(4,147)	1:243:A:ASN:H	1:240:A:MET:HA	5	0.74
(4,24)	1:55:A:THR:H	1:76:A:LYS:HD3	5	0.74
(3,320)	1:97:A:TRP:H	1:244:A:TRP:H	20	0.74
(3,286)	1:70:A:PHE:H	1:92:A:GLN:H	10	0.74
(3,226)	1:231:A:ASN:H	1:169:A:LYS:H	20	0.74
(3,210)	1:197:A:LEU:H	1:205:A:CYS:H	8	0.74
(3,173)	1:57:A:LEU:H	1:175:A:PHE:H	15	0.74
(3,115)	1:12:A:GLY:H	1:8:A:GLY:H	20	0.74
(1,79)	1:68:A:VAL:H	1:93:A:PHE:H	12	0.74
(1,21)	1:37:A:THR:H	1:37:A:THR:HB	8	0.74
(4,1249)	1:169:A:LYS:H	1:169:A:LYS:HG3	2	0.73
(4,1153)	1:96:A:HIS:H	1:116:A:ALA:HB3	2	0.73
(4,1102)	1:170:A:GLY:H	1:169:A:LYS:HB3	6	0.73
(4,1086)	1:25:A:GLY:H	1:24:A:LYS:HB2	5	0.73
(4,1021)	1:133:A:ALA:H	1:127:A:TYR:HB3	15	0.73
(4,386)	1:235:A:GLU:HG3	1:234:A:GLY:HA3	9	0.73
(4,363)	1:76:A:LYS:HD2	1:76:A:LYS:HE3	4	0.73
(4,293)	1:179:A:ASP:HB3	1:179:A:ASP:HA	10	0.73
(4,293)	1:66:A:PHE:HB3	1:66:A:PHE:HA	15	0.73
(4,293)	1:66:A:PHE:HB3	1:66:A:PHE:HA	16	0.73

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,293)	1:179:A:ASP:HB3	1:179:A:ASP:HA	19	0.73
(3,306)	1:156:A:LEU:H	1:159:A:VAL:H	14	0.73
(3,305)	1:166:A:ILE:H	1:168:A:THR:H	16	0.73
(3,103)	1:82:A:GLY:H	1:48:A:SER:H	5	0.73
(3,23)	1:138:A:ASP:H	1:140:A:LEU:H	3	0.73
(3,17)	1:169:A:LYS:H	1:63:A:GLY:H	3	0.73
(1,21)	1:37:A:THR:H	1:37:A:THR:HB	19	0.73
(4,1287)	1:258:A:SER:H	1:257:A:ALA:HB3	15	0.72
(4,1286)	1:258:A:SER:H	1:257:A:ALA:HB3	15	0.72
(4,1088)	1:232:A:GLY:H	1:235:A:GLU:HG2	11	0.72
(4,1003)	1:76:A:LYS:H	1:76:A:LYS:HE2	1	0.72
(4,650)	1:19:A:ASP:H	1:14:A:GLU:H	14	0.72
(4,626)	1:245:A:ARG:H	1:247:A:ALA:H	10	0.72
(4,399)	1:50:A:SER:HA	1:52:A:ASP:HB3	4	0.72
(4,399)	1:50:A:SER:HA	1:52:A:ASP:HB3	9	0.72
(4,399)	1:50:A:SER:HA	1:52:A:ASP:HB3	17	0.72
(4,150)	1:164:A:ASP:H	1:163:A:LEU:HG	7	0.72
(4,66)	1:202:A:LEU:H	1:22:A:ILE:HD11	8	0.72
(3,323)	1:181:A:ARG:H	1:184:A:LEU:H	15	0.72
(3,314)	1:229:A:ASN:H	1:168:A:THR:H	11	0.72
(3,306)	1:156:A:LEU:H	1:159:A:VAL:H	5	0.72
(3,306)	1:156:A:LEU:H	1:159:A:VAL:H	7	0.72
(3,305)	1:166:A:ILE:H	1:168:A:THR:H	12	0.72
(3,305)	1:166:A:ILE:H	1:168:A:THR:H	19	0.72
(3,103)	1:82:A:GLY:H	1:48:A:SER:H	17	0.72
(4,1321)	1:205:A:CYS:H	1:206:A:VAL:HG23	1	0.71
(4,1321)	1:205:A:CYS:H	1:206:A:VAL:HG21	6	0.71
(4,540)	1:89:A:ARG:H	1:123:A:TRP:H	8	0.71
(4,519)	1:152:A:ALA:H	1:151:A:SER:H	10	0.71
(4,363)	1:39:A:LYS:HD3	1:39:A:LYS:HE2	6	0.71
(4,332)	1:22:A:ILE:HD11	1:204:A:GLU:HA	5	0.71
(4,293)	1:66:A:PHE:HB3	1:66:A:PHE:HA	18	0.71
(4,190)	1:133:A:ALA:H	1:123:A:TRP:HB3	18	0.71
(4,42)	1:38:A:ALA:HA	1:255:A:ILE:H	15	0.71
(3,92)	1:55:A:THR:H	1:77:A:ALA:H	1	0.71
(1,21)	1:37:A:THR:H	1:37:A:THR:HB	6	0.71
(1,6)	1:169:A:LYS:HB3	1:63:A:GLY:H	5	0.71
(4,1095)	1:232:A:GLY:H	1:235:A:GLU:HG2	11	0.7
(4,393)	1:63:A:GLY:HA2	1:169:A:LYS:HB2	1	0.7
(4,374)	1:127:A:TYR:HB3	1:133:A:ALA:HA	7	0.7
(4,371)	1:146:A:PHE:HB3	1:114:A:TYR:HB2	6	0.7
(4,356)	1:153:A:LYS:HD2	1:158:A:LYS:HE2	5	0.7

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,293)	1:179:A:ASP:HB3	1:179:A:ASP:HA	20	0.7
(4,273)	1:113:A:LYS:HD3	1:244:A:TRP:HA	13	0.7
(4,201)	1:156:A:LEU:H	1:156:A:LEU:HB2	12	0.7
(4,168)	1:212:A:LYS:H	1:211:A:LEU:HB3	4	0.7
(3,314)	1:229:A:ASN:H	1:168:A:THR:H	14	0.7
(3,158)	1:57:A:LEU:H	1:70:A:PHE:H	2	0.7
(3,125)	1:245:A:ARG:H	1:106:A:GLU:H	14	0.7
(3,115)	1:12:A:GLY:H	1:8:A:GLY:H	16	0.7
(3,114)	1:241:A:VAL:H	1:243:A:ASN:H	12	0.7
(1,75)	1:172:A:SER:HB3	1:60:A:LEU:HD13	11	0.7
(4,1321)	1:205:A:CYS:H	1:206:A:VAL:HG22	18	0.69
(4,1177)	1:78:A:VAL:H	1:77:A:ALA:HB1	10	0.69
(4,454)	1:50:A:SER:HB3	1:78:A:VAL:HG23	3	0.69
(4,442)	1:86:A:GLY:HA2	1:126:A:LYS:HD2	7	0.69
(4,393)	1:232:A:GLY:HA2	1:169:A:LYS:HB2	16	0.69
(4,97)	1:204:A:GLU:H	1:202:A:LEU:HA	19	0.69
(3,323)	1:181:A:ARG:H	1:184:A:LEU:H	7	0.69
(3,286)	1:70:A:PHE:H	1:92:A:GLN:H	12	0.69
(3,110)	1:12:A:GLY:H	1:8:A:GLY:H	5	0.69
(3,79)	1:192:A:THR:H	1:256:A:LYS:H	7	0.69
(3,17)	1:169:A:LYS:H	1:63:A:GLY:H	20	0.69
(3,9)	1:256:A:LYS:H	1:192:A:THR:H	7	0.69
(1,28)	1:241:A:VAL:H	1:240:A:MET:HA	8	0.69
(1,20)	1:197:A:LEU:H	1:197:A:LEU:HB2	13	0.69
(4,1289)	1:203:A:LEU:H	1:203:A:LEU:HD22	6	0.68
(4,1129)	1:195:A:GLY:H	1:207:A:THR:HG22	15	0.68
(4,1082)	1:251:A:LYS:H	1:250:A:LEU:HB3	8	0.68
(4,1022)	1:133:A:ALA:H	1:127:A:TYR:HB3	10	0.68
(4,487)	1:152:A:ALA:H	1:151:A:SER:H	20	0.68
(4,470)	1:219:A:SER:H	1:150:A:GLY:H	8	0.68
(3,306)	1:156:A:LEU:H	1:159:A:VAL:H	8	0.68
(3,306)	1:156:A:LEU:H	1:159:A:VAL:H	13	0.68
(3,305)	1:166:A:ILE:H	1:168:A:THR:H	11	0.68
(3,286)	1:70:A:PHE:H	1:92:A:GLN:H	5	0.68
(3,226)	1:231:A:ASN:H	1:169:A:LYS:H	10	0.68
(3,158)	1:57:A:LEU:H	1:70:A:PHE:H	14	0.68
(1,114)	1:66:A:PHE:H	1:65:A:ALA:HB1	9	0.68
(1,28)	1:241:A:VAL:H	1:240:A:MET:HA	18	0.68
(4,1321)	1:205:A:CYS:H	1:206:A:VAL:HG21	5	0.67
(4,1274)	1:126:A:LYS:H	1:125:A:THR:HG22	8	0.67
(4,1128)	1:251:A:LYS:H	1:250:A:LEU:HB3	17	0.67
(4,1021)	1:133:A:ALA:H	1:127:A:TYR:HB3	10	0.67

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,965)	1:54:A:ALA:H	1:53:A:GLN:HB2	1	0.67
(4,469)	1:140:A:LEU:HB3	1:134:A:VAL:HG23	11	0.67
(4,469)	1:140:A:LEU:HB3	1:134:A:VAL:HG22	15	0.67
(4,409)	1:41:A:ASP:HA	1:41:A:ASP:HB3	15	0.67
(4,273)	1:113:A:LYS:HD3	1:244:A:TRP:HA	10	0.67
(4,260)	1:203:A:LEU:H	1:203:A:LEU:HB2	17	0.67
(4,234)	1:206:A:VAL:H	1:22:A:ILE:HD12	12	0.67
(4,97)	1:204:A:GLU:H	1:202:A:LEU:HA	14	0.67
(3,314)	1:229:A:ASN:H	1:168:A:THR:H	3	0.67
(3,264)	1:240:A:MET:H	1:228:A:LEU:H	4	0.67
(3,261)	1:240:A:MET:H	1:228:A:LEU:H	16	0.67
(3,210)	1:197:A:LEU:H	1:205:A:CYS:H	1	0.67
(3,141)	1:87:A:THR:H	1:125:A:THR:H	4	0.67
(3,114)	1:241:A:VAL:H	1:243:A:ASN:H	4	0.67
(3,92)	1:55:A:THR:H	1:77:A:ALA:H	3	0.67
(3,28)	1:61:A:ASN:H	1:170:A:GLY:H	10	0.67
(1,100)	1:245:A:ARG:H	1:244:A:TRP:HB2	2	0.67
(1,78)	1:117:A:GLU:H	1:96:A:HIS:H	10	0.67
(4,1006)	1:141:A:ALA:H	1:122:A:HIS:HB3	6	0.66
(4,989)	1:41:A:ASP:H	1:40:A:TYR:HB2	19	0.66
(4,466)	1:33:A:ILE:HD13	1:106:A:GLU:HG2	20	0.66
(4,446)	1:22:A:ILE:HG22	1:22:A:ILE:HA	17	0.66
(4,401)	1:78:A:VAL:HB	1:87:A:THR:HB	7	0.66
(4,312)	1:255:A:ILE:HD12	1:255:A:ILE:HA	18	0.66
(4,234)	1:206:A:VAL:H	1:22:A:ILE:HD11	9	0.66
(4,156)	1:164:A:ASP:H	1:163:A:LEU:HG	8	0.66
(4,42)	1:38:A:ALA:HA	1:255:A:ILE:H	16	0.66
(3,306)	1:156:A:LEU:H	1:159:A:VAL:H	19	0.66
(3,282)	1:202:A:LEU:H	1:199:A:THR:H	6	0.66
(3,261)	1:240:A:MET:H	1:228:A:LEU:H	6	0.66
(3,158)	1:57:A:LEU:H	1:70:A:PHE:H	4	0.66
(3,120)	1:248:A:GLN:H	1:32:A:ASP:H	18	0.66
(3,81)	1:191:A:TRP:H	1:210:A:VAL:H	13	0.66
(3,48)	1:210:A:VAL:H	1:191:A:TRP:H	13	0.66
(1,59)	1:240:A:MET:HA	1:230:A:PHE:HB2	10	0.66
(1,32)	1:167:A:LYS:HB2	1:168:A:THR:H	13	0.66
(4,1217)	1:197:A:LEU:H	1:197:A:LEU:HG	10	0.65
(4,1178)	1:177:A:ASN:H	1:176:A:THR:HG22	14	0.65
(4,1177)	1:78:A:VAL:H	1:77:A:ALA:HB3	7	0.65
(4,669)	1:29:A:SER:H	1:31:A:VAL:H	11	0.65
(4,668)	1:29:A:SER:H	1:31:A:VAL:H	11	0.65
(4,463)	1:174:A:ASP:HA	1:176:A:THR:HG21	2	0.65

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,463)	1:174:A:ASP:HA	1:176:A:THR:HG21	11	0.65
(4,423)	1:39:A:LYS:HE3	1:39:A:LYS:HB3	10	0.65
(4,423)	1:167:A:LYS:HE3	1:167:A:LYS:HB3	18	0.65
(4,241)	1:253:A:ARG:H	1:253:A:ARG:HD3	17	0.65
(4,88)	1:210:A:VAL:H	1:192:A:THR:HB	7	0.65
(4,42)	1:38:A:ALA:HA	1:255:A:ILE:H	19	0.65
(4,24)	1:55:A:THR:H	1:76:A:LYS:HD2	16	0.65
(3,282)	1:202:A:LEU:H	1:199:A:THR:H	12	0.65
(3,255)	1:147:A:LEU:H	1:115:A:ALA:H	1	0.65
(3,164)	1:203:A:LEU:H	1:197:A:LEU:H	15	0.65
(3,158)	1:57:A:LEU:H	1:70:A:PHE:H	19	0.65
(3,23)	1:138:A:ASP:H	1:140:A:LEU:H	1	0.65
(2,20)	1:229:A:ASN:H	1:168:A:THR:H	7	0.65
(1,100)	1:245:A:ARG:H	1:244:A:TRP:HB2	18	0.65
(4,1322)	1:203:A:LEU:H	1:203:A:LEU:HD22	14	0.64
(4,1298)	1:82:A:GLY:H	1:47:A:LEU:HD21	10	0.64
(4,1253)	1:198:A:THR:H	1:199:A:THR:HG23	15	0.64
(4,1225)	1:166:A:ILE:H	1:166:A:ILE:HG21	8	0.64
(4,1128)	1:251:A:LYS:H	1:251:A:LYS:HG2	8	0.64
(4,1003)	1:133:A:ALA:H	1:127:A:TYR:HB3	10	0.64
(4,989)	1:41:A:ASP:H	1:41:A:ASP:HB2	10	0.64
(4,836)	1:28:A:GLN:H	1:28:A:GLN:HA	8	0.64
(4,664)	1:54:A:ALA:H	1:51:A:TYR:HA	1	0.64
(4,540)	1:147:A:LEU:H	1:148:A:LYS:H	14	0.64
(4,412)	1:233:A:GLU:HA	1:233:A:GLU:HB2	10	0.64
(4,411)	1:212:A:LYS:HA	1:212:A:LYS:HB2	10	0.64
(4,356)	1:153:A:LYS:HD3	1:158:A:LYS:HE3	3	0.64
(4,222)	1:205:A:CYS:H	1:203:A:LEU:HB3	6	0.64
(4,163)	1:231:A:ASN:H	1:240:A:MET:HA	15	0.64
(4,147)	1:231:A:ASN:H	1:240:A:MET:HA	15	0.64
(3,305)	1:166:A:ILE:H	1:168:A:THR:H	6	0.64
(3,249)	1:191:A:TRP:H	1:212:A:LYS:H	18	0.64
(3,245)	1:191:A:TRP:H	1:212:A:LYS:H	18	0.64
(3,234)	1:8:A:GLY:H	1:12:A:GLY:H	20	0.64
(3,166)	1:205:A:CYS:H	1:197:A:LEU:H	8	0.64
(3,114)	1:241:A:VAL:H	1:243:A:ASN:H	13	0.64
(3,114)	1:241:A:VAL:H	1:243:A:ASN:H	16	0.64
(3,103)	1:82:A:GLY:H	1:48:A:SER:H	11	0.64
(1,28)	1:241:A:VAL:H	1:240:A:MET:HA	13	0.64
(4,1325)	1:59:A:ILE:H	1:166:A:ILE:HD11	1	0.63
(4,1266)	1:66:A:PHE:H	1:169:A:LYS:HG3	17	0.63
(4,1086)	1:25:A:GLY:H	1:24:A:LYS:HB2	11	0.63

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,836)	1:28:A:GLN:H	1:28:A:GLN:HA	5	0.63
(4,664)	1:54:A:ALA:H	1:51:A:TYR:HA	16	0.63
(4,466)	1:243:A:ASN:HB2	1:241:A:VAL:HG21	7	0.63
(4,419)	1:205:A:CYS:HB2	1:140:A:LEU:HG	15	0.63
(4,374)	1:127:A:TYR:HB3	1:133:A:ALA:HA	16	0.63
(4,150)	1:164:A:ASP:H	1:163:A:LEU:HG	8	0.63
(4,118)	1:164:A:ASP:H	1:163:A:LEU:HA	12	0.63
(4,118)	1:164:A:ASP:H	1:163:A:LEU:HA	13	0.63
(4,4)	1:146:A:PHE:H	1:147:A:LEU:HB2	4	0.63
(3,210)	1:197:A:LEU:H	1:205:A:CYS:H	10	0.63
(3,158)	1:57:A:LEU:H	1:70:A:PHE:H	9	0.63
(3,120)	1:248:A:GLN:H	1:32:A:ASP:H	4	0.63
(1,7)	1:59:A:ILE:H	1:166:A:ILE:HD11	1	0.63
(4,1322)	1:203:A:LEU:H	1:22:A:ILE:HD12	2	0.62
(4,1274)	1:126:A:LYS:H	1:125:A:THR:HG21	3	0.62
(4,1212)	1:205:A:CYS:H	1:206:A:VAL:HG23	19	0.62
(4,1022)	1:260:A:LYS:H	1:259:A:PHE:HB3	7	0.62
(4,1022)	1:133:A:ALA:H	1:127:A:TYR:HB3	16	0.62
(4,1003)	1:126:A:LYS:H	1:124:A:ASN:HB3	19	0.62
(4,879)	1:228:A:LEU:H	1:228:A:LEU:HA	2	0.62
(4,879)	1:228:A:LEU:H	1:228:A:LEU:HA	7	0.62
(4,805)	1:28:A:GLN:H	1:28:A:GLN:HA	8	0.62
(4,801)	1:28:A:GLN:H	1:28:A:GLN:HA	8	0.62
(4,666)	1:226:A:ARG:H	1:222:A:VAL:H	20	0.62
(4,411)	1:26:A:GLU:HA	1:26:A:GLU:HB2	7	0.62
(4,408)	1:206:A:VAL:HB	1:206:A:VAL:HA	12	0.62
(4,379)	1:169:A:LYS:HG3	1:61:A:ASN:HB2	6	0.62
(4,260)	1:203:A:LEU:H	1:203:A:LEU:HB3	10	0.62
(4,162)	1:105:A:SER:H	1:113:A:LYS:HD3	17	0.62
(4,118)	1:164:A:ASP:H	1:163:A:LEU:HA	7	0.62
(4,97)	1:161:A:ASP:H	1:163:A:LEU:HA	2	0.62
(4,42)	1:38:A:ALA:HA	1:255:A:ILE:H	7	0.62
(3,305)	1:166:A:ILE:H	1:168:A:THR:H	2	0.62
(3,98)	1:12:A:GLY:H	1:7:A:TYR:H	18	0.62
(4,1316)	1:165:A:SER:H	1:166:A:ILE:HD11	14	0.61
(4,1021)	1:260:A:LYS:H	1:259:A:PHE:HB3	7	0.61
(4,1021)	1:133:A:ALA:H	1:127:A:TYR:HB3	16	0.61
(4,879)	1:228:A:LEU:H	1:228:A:LEU:HA	11	0.61
(4,836)	1:166:A:ILE:H	1:165:A:SER:HB3	4	0.61
(4,495)	1:116:A:ALA:H	1:147:A:LEU:H	14	0.61
(4,470)	1:219:A:SER:H	1:150:A:GLY:H	10	0.61
(4,469)	1:140:A:LEU:HB3	1:91:A:ILE:HD12	17	0.61

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,442)	1:63:A:GLY:HA2	1:169:A:LYS:HG3	5	0.61
(4,423)	1:39:A:LYS:HE3	1:39:A:LYS:HB3	15	0.61
(4,412)	1:233:A:GLU:HA	1:233:A:GLU:HB2	1	0.61
(4,412)	1:26:A:GLU:HA	1:26:A:GLU:HB2	7	0.61
(4,182)	1:165:A:SER:H	1:163:A:LEU:HA	8	0.61
(4,118)	1:164:A:ASP:H	1:163:A:LEU:HA	6	0.61
(3,306)	1:156:A:LEU:H	1:159:A:VAL:H	10	0.61
(3,305)	1:166:A:ILE:H	1:168:A:THR:H	1	0.61
(3,141)	1:87:A:THR:H	1:125:A:THR:H	17	0.61
(2,12)	1:107:A:HIS:HA	1:31:A:VAL:H	17	0.61
(1,28)	1:241:A:VAL:H	1:240:A:MET:HA	2	0.61
(1,9)	1:173:A:ALA:H	1:172:A:SER:HB3	17	0.61
(4,1321)	1:205:A:CYS:H	1:203:A:LEU:HD22	2	0.6
(4,1289)	1:203:A:LEU:H	1:22:A:ILE:HG23	2	0.6
(4,1153)	1:78:A:VAL:H	1:77:A:ALA:HB3	17	0.6
(4,962)	1:166:A:ILE:H	1:163:A:LEU:HA	20	0.6
(4,805)	1:28:A:GLN:H	1:28:A:GLN:HA	5	0.6
(4,801)	1:28:A:GLN:H	1:28:A:GLN:HA	5	0.6
(4,722)	1:64:A:HIS:H	1:64:A:HIS:HA	17	0.6
(4,540)	1:97:A:TRP:H	1:98:A:GLY:H	6	0.6
(4,469)	1:140:A:LEU:HB3	1:134:A:VAL:HG21	7	0.6
(4,423)	1:39:A:LYS:HE2	1:39:A:LYS:HB2	1	0.6
(4,423)	1:39:A:LYS:HE2	1:39:A:LYS:HB3	2	0.6
(4,423)	1:39:A:LYS:HE3	1:39:A:LYS:HB3	16	0.6
(4,411)	1:212:A:LYS:HA	1:212:A:LYS:HB2	1	0.6
(4,389)	1:164:A:ASP:HB2	1:164:A:ASP:HA	14	0.6
(4,252)	1:40:A:TYR:HB3	1:259:A:PHE:H	9	0.6
(4,190)	1:130:A:PHE:H	1:123:A:TRP:HB3	15	0.6
(3,320)	1:97:A:TRP:H	1:244:A:TRP:H	8	0.6
(3,305)	1:166:A:ILE:H	1:168:A:THR:H	9	0.6
(3,234)	1:8:A:GLY:H	1:12:A:GLY:H	16	0.6
(3,226)	1:231:A:ASN:H	1:169:A:LYS:H	9	0.6
(3,173)	1:57:A:LEU:H	1:175:A:PHE:H	14	0.6
(3,79)	1:192:A:THR:H	1:256:A:LYS:H	4	0.6
(3,9)	1:256:A:LYS:H	1:192:A:THR:H	4	0.6
(4,1334)	1:226:A:ARG:H	1:163:A:LEU:HD21	15	0.59
(4,1129)	1:195:A:GLY:H	1:207:A:THR:HG22	2	0.59
(4,1072)	1:66:A:PHE:H	1:66:A:PHE:HB3	10	0.59
(4,1060)	1:260:A:LYS:H	1:260:A:LYS:HB2	7	0.59
(4,1003)	1:133:A:ALA:H	1:127:A:TYR:HB3	16	0.59
(4,948)	1:166:A:ILE:H	1:163:A:LEU:HA	18	0.59
(4,805)	1:166:A:ILE:H	1:165:A:SER:HB3	4	0.59

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,664)	1:54:A:ALA:H	1:51:A:TYR:HA	5	0.59
(4,446)	1:37:A:THR:HA	1:37:A:THR:HG22	19	0.59
(4,436)	1:86:A:GLY:HA3	1:126:A:LYS:HG2	1	0.59
(4,423)	1:39:A:LYS:HE2	1:39:A:LYS:HB2	4	0.59
(4,423)	1:39:A:LYS:HE2	1:39:A:LYS:HB2	13	0.59
(4,419)	1:94:A:HIS:HB2	1:65:A:ALA:HB1	2	0.59
(4,412)	1:226:A:ARG:HA	1:226:A:ARG:HB3	15	0.59
(4,411)	1:250:A:LEU:HB3	1:250:A:LEU:HA	12	0.59
(4,411)	1:226:A:ARG:HA	1:226:A:ARG:HB3	15	0.59
(4,411)	1:233:A:GLU:HA	1:233:A:GLU:HB2	17	0.59
(4,389)	1:93:A:PHE:HB2	1:93:A:PHE:HA	3	0.59
(4,389)	1:190:A:TYR:HB3	1:190:A:TYR:HA	5	0.59
(4,389)	1:117:A:GLU:HB3	1:117:A:GLU:HA	15	0.59
(4,389)	1:117:A:GLU:HB3	1:117:A:GLU:HA	17	0.59
(4,389)	1:174:A:ASP:HB3	1:174:A:ASP:HA	18	0.59
(4,374)	1:127:A:TYR:HB3	1:133:A:ALA:HA	11	0.59
(4,371)	1:146:A:PHE:HB3	1:114:A:TYR:HB3	10	0.59
(4,132)	1:93:A:PHE:H	1:93:A:PHE:HB3	6	0.59
(4,118)	1:165:A:SER:H	1:163:A:LEU:HA	15	0.59
(3,306)	1:156:A:LEU:H	1:159:A:VAL:H	15	0.59
(3,173)	1:57:A:LEU:H	1:175:A:PHE:H	7	0.59
(3,115)	1:12:A:GLY:H	1:8:A:GLY:H	5	0.59
(3,114)	1:241:A:VAL:H	1:243:A:ASN:H	10	0.59
(3,92)	1:55:A:THR:H	1:77:A:ALA:H	7	0.59
(3,60)	1:29:A:SER:H	1:196:A:SER:H	7	0.59
(2,16)	1:82:A:GLY:H	1:45:A:LYS:H	13	0.59
(1,76)	1:115:A:ALA:HB1	1:149:A:VAL:HG23	16	0.59
(4,1321)	1:205:A:CYS:H	1:206:A:VAL:HG21	4	0.58
(4,1274)	1:126:A:LYS:H	1:125:A:THR:HG21	4	0.58
(4,1128)	1:251:A:LYS:H	1:250:A:LEU:HB3	3	0.58
(4,948)	1:166:A:ILE:H	1:163:A:LEU:HA	1	0.58
(4,879)	1:228:A:LEU:H	1:228:A:LEU:HA	9	0.58
(4,654)	1:199:A:THR:H	1:196:A:SER:H	4	0.58
(4,650)	1:199:A:THR:H	1:196:A:SER:H	4	0.58
(4,519)	1:152:A:ALA:H	1:151:A:SER:H	20	0.58
(4,469)	1:140:A:LEU:HB3	1:134:A:VAL:HG23	19	0.58
(4,463)	1:174:A:ASP:HA	1:176:A:THR:HG23	5	0.58
(4,445)	1:76:A:LYS:HB3	1:76:A:LYS:HG3	9	0.58
(4,445)	1:76:A:LYS:HB2	1:76:A:LYS:HG3	15	0.58
(4,423)	1:39:A:LYS:HE3	1:39:A:LYS:HB2	3	0.58
(4,423)	1:39:A:LYS:HE2	1:39:A:LYS:HB3	9	0.58
(4,423)	1:39:A:LYS:HE3	1:39:A:LYS:HB3	20	0.58

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,418)	1:163:A:LEU:HB2	1:163:A:LEU:HA	14	0.58
(4,412)	1:250:A:LEU:HB2	1:250:A:LEU:HA	2	0.58
(4,412)	1:250:A:LEU:HB3	1:250:A:LEU:HA	12	0.58
(4,412)	1:233:A:GLU:HA	1:233:A:GLU:HB2	17	0.58
(4,411)	1:250:A:LEU:HB2	1:250:A:LEU:HA	2	0.58
(4,393)	1:232:A:GLY:HA3	1:169:A:LYS:HB2	20	0.58
(4,389)	1:117:A:GLU:HB2	1:117:A:GLU:HA	4	0.58
(4,389)	1:190:A:TYR:HB3	1:190:A:TYR:HA	6	0.58
(4,97)	1:161:A:ASP:H	1:163:A:LEU:HA	1	0.58
(3,306)	1:156:A:LEU:H	1:159:A:VAL:H	11	0.58
(3,306)	1:156:A:LEU:H	1:159:A:VAL:H	20	0.58
(3,305)	1:166:A:ILE:H	1:168:A:THR:H	15	0.58
(3,249)	1:191:A:TRP:H	1:212:A:LYS:H	16	0.58
(3,245)	1:191:A:TRP:H	1:212:A:LYS:H	16	0.58
(3,23)	1:138:A:ASP:H	1:140:A:LEU:H	5	0.58
(2,16)	1:82:A:GLY:H	1:45:A:LYS:H	16	0.58
(1,7)	1:59:A:ILE:H	1:166:A:ILE:HD12	11	0.58
(4,1293)	1:153:A:LYS:H	1:152:A:ALA:HB1	8	0.57
(4,1225)	1:64:A:HIS:H	1:169:A:LYS:HG2	9	0.57
(4,1102)	1:170:A:GLY:H	1:169:A:LYS:HB3	11	0.57
(4,1006)	1:79:A:LEU:H	1:88:A:TYR:HB2	2	0.57
(4,968)	1:129:A:ASP:H	1:127:A:TYR:HB2	12	0.57
(4,879)	1:247:A:ALA:H	1:247:A:ALA:HA	10	0.57
(4,870)	1:258:A:SER:H	1:258:A:SER:HA	14	0.57
(4,666)	1:226:A:ARG:H	1:222:A:VAL:H	19	0.57
(4,519)	1:152:A:ALA:H	1:151:A:SER:H	5	0.57
(4,487)	1:152:A:ALA:H	1:151:A:SER:H	3	0.57
(4,454)	1:49:A:VAL:HG22	1:49:A:VAL:HA	18	0.57
(4,445)	1:260:A:LYS:HB2	1:260:A:LYS:HG3	8	0.57
(4,445)	1:109:A:VAL:HB	1:109:A:VAL:HG21	18	0.57
(4,445)	1:76:A:LYS:HB3	1:76:A:LYS:HG2	20	0.57
(4,439)	1:260:A:LYS:HA	1:260:A:LYS:HG3	13	0.57
(4,418)	1:163:A:LEU:HB2	1:163:A:LEU:HA	4	0.57
(4,414)	1:226:A:ARG:HA	1:226:A:ARG:HB2	14	0.57
(4,412)	1:26:A:GLU:HA	1:26:A:GLU:HB3	6	0.57
(4,412)	1:226:A:ARG:HA	1:226:A:ARG:HB2	14	0.57
(4,412)	1:26:A:GLU:HA	1:26:A:GLU:HB3	16	0.57
(4,412)	1:233:A:GLU:HA	1:233:A:GLU:HB2	18	0.57
(4,411)	1:26:A:GLU:HA	1:26:A:GLU:HB3	6	0.57
(4,411)	1:226:A:ARG:HA	1:226:A:ARG:HB2	14	0.57
(4,411)	1:26:A:GLU:HA	1:26:A:GLU:HB3	16	0.57
(4,411)	1:233:A:GLU:HA	1:233:A:GLU:HB2	18	0.57

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,411)	1:26:A:GLU:HA	1:26:A:GLU:HB3	19	0.57
(4,408)	1:134:A:VAL:HA	1:134:A:VAL:HB	17	0.57
(4,389)	1:117:A:GLU:HB2	1:117:A:GLU:HA	7	0.57
(4,389)	1:174:A:ASP:HB3	1:174:A:ASP:HA	10	0.57
(4,389)	1:190:A:TYR:HB3	1:190:A:TYR:HA	16	0.57
(4,260)	1:203:A:LEU:H	1:203:A:LEU:HB3	12	0.57
(4,179)	1:20:A:PHE:H	1:19:A:ASP:HB3	12	0.57
(4,156)	1:164:A:ASP:H	1:163:A:LEU:HG	9	0.57
(4,132)	1:93:A:PHE:H	1:93:A:PHE:HB3	4	0.57
(4,90)	1:33:A:ILE:H	1:108:A:THR:HB	19	0.57
(3,166)	1:205:A:CYS:H	1:197:A:LEU:H	1	0.57
(3,150)	1:206:A:VAL:H	1:197:A:LEU:H	8	0.57
(2,20)	1:229:A:ASN:H	1:168:A:THR:H	20	0.57
(1,132)	1:135:A:GLN:H	1:134:A:VAL:HG22	11	0.57
(4,1288)	1:135:A:GLN:H	1:134:A:VAL:HG22	18	0.56
(4,1266)	1:66:A:PHE:H	1:169:A:LYS:HG3	12	0.56
(4,1257)	1:78:A:VAL:H	1:77:A:ALA:HB1	11	0.56
(4,1243)	1:247:A:ALA:H	1:247:A:ALA:HB2	4	0.56
(4,1189)	1:34:A:ASP:H	1:255:A:ILE:HG21	13	0.56
(4,1129)	1:111:A:LYS:H	1:108:A:THR:HG22	12	0.56
(4,879)	1:228:A:LEU:H	1:228:A:LEU:HA	13	0.56
(4,801)	1:156:A:LEU:H	1:156:A:LEU:HA	4	0.56
(4,789)	1:106:A:GLU:H	1:105:A:SER:HA	20	0.56
(4,463)	1:174:A:ASP:HA	1:176:A:THR:HG22	1	0.56
(4,458)	1:169:A:LYS:HB3	1:169:A:LYS:HG2	5	0.56
(4,454)	1:87:A:THR:HA	1:87:A:THR:HG22	1	0.56
(4,445)	1:260:A:LYS:HB2	1:260:A:LYS:HG3	4	0.56
(4,445)	1:76:A:LYS:HB3	1:76:A:LYS:HG2	7	0.56
(4,445)	1:76:A:LYS:HB2	1:76:A:LYS:HG3	11	0.56
(4,445)	1:76:A:LYS:HB2	1:76:A:LYS:HG3	12	0.56
(4,445)	1:76:A:LYS:HB3	1:76:A:LYS:HG2	14	0.56
(4,445)	1:109:A:VAL:HB	1:109:A:VAL:HG21	16	0.56
(4,445)	1:76:A:LYS:HB3	1:76:A:LYS:HG2	17	0.56
(4,419)	1:203:A:LEU:HB3	1:205:A:CYS:HB2	7	0.56
(4,412)	1:26:A:GLU:HA	1:26:A:GLU:HB3	19	0.56
(4,408)	1:134:A:VAL:HA	1:134:A:VAL:HB	1	0.56
(4,408)	1:134:A:VAL:HA	1:134:A:VAL:HB	4	0.56
(4,408)	1:134:A:VAL:HA	1:134:A:VAL:HB	7	0.56
(4,408)	1:134:A:VAL:HA	1:134:A:VAL:HB	15	0.56
(4,389)	1:117:A:GLU:HB2	1:117:A:GLU:HA	13	0.56
(4,252)	1:259:A:PHE:H	1:40:A:TYR:HB2	5	0.56
(4,251)	1:259:A:PHE:H	1:40:A:TYR:HB2	5	0.56

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,219)	1:134:A:VAL:H	1:134:A:VAL:HA	5	0.56
(4,132)	1:93:A:PHE:H	1:93:A:PHE:HB3	12	0.56
(4,132)	1:93:A:PHE:H	1:93:A:PHE:HB3	16	0.56
(3,286)	1:70:A:PHE:H	1:92:A:GLN:H	2	0.56
(3,282)	1:202:A:LEU:H	1:199:A:THR:H	7	0.56
(3,218)	1:257:A:ALA:H	1:41:A:ASP:H	10	0.56
(2,20)	1:229:A:ASN:H	1:168:A:THR:H	9	0.56
(1,28)	1:241:A:VAL:H	1:240:A:MET:HA	11	0.56
(4,1266)	1:66:A:PHE:H	1:169:A:LYS:HG3	8	0.55
(4,1242)	1:247:A:ALA:H	1:247:A:ALA:HB3	1	0.55
(4,1226)	1:258:A:SER:H	1:257:A:ALA:HB3	15	0.55
(4,1153)	1:78:A:VAL:H	1:77:A:ALA:HB1	10	0.55
(4,1086)	1:25:A:GLY:H	1:24:A:LYS:HB3	6	0.55
(4,1086)	1:25:A:GLY:H	1:24:A:LYS:HB3	17	0.55
(4,1051)	1:57:A:LEU:H	1:57:A:LEU:HB2	4	0.55
(4,1021)	1:193:A:TYR:H	1:208:A:TRP:HB3	20	0.55
(4,1003)	1:126:A:LYS:H	1:124:A:ASN:HB3	17	0.55
(4,948)	1:64:A:HIS:H	1:63:A:GLY:HA3	19	0.55
(4,879)	1:228:A:LEU:H	1:228:A:LEU:HA	19	0.55
(4,836)	1:166:A:ILE:H	1:165:A:SER:HB3	16	0.55
(4,772)	1:164:A:ASP:H	1:164:A:ASP:HA	16	0.55
(4,445)	1:241:A:VAL:HB	1:241:A:VAL:HG21	2	0.55
(4,408)	1:80:A:LYS:HB2	1:87:A:THR:HA	5	0.55
(4,408)	1:134:A:VAL:HA	1:134:A:VAL:HB	8	0.55
(4,408)	1:134:A:VAL:HA	1:134:A:VAL:HB	13	0.55
(4,408)	1:134:A:VAL:HA	1:134:A:VAL:HB	18	0.55
(4,408)	1:134:A:VAL:HA	1:134:A:VAL:HB	20	0.55
(4,406)	1:149:A:VAL:HA	1:149:A:VAL:HB	14	0.55
(4,389)	1:190:A:TYR:HB3	1:190:A:TYR:HA	1	0.55
(4,389)	1:117:A:GLU:HB3	1:117:A:GLU:HA	9	0.55
(4,389)	1:117:A:GLU:HB2	1:117:A:GLU:HA	11	0.55
(4,386)	1:232:A:GLY:HA2	1:229:A:ASN:HB2	14	0.55
(4,345)	1:172:A:SER:HB3	1:174:A:ASP:HA	17	0.55
(4,219)	1:134:A:VAL:H	1:134:A:VAL:HA	10	0.55
(4,132)	1:93:A:PHE:H	1:93:A:PHE:HB3	11	0.55
(4,132)	1:93:A:PHE:H	1:93:A:PHE:HB3	14	0.55
(4,118)	1:165:A:SER:H	1:163:A:LEU:HA	8	0.55
(4,105)	1:61:A:ASN:H	1:61:A:ASN:HB3	2	0.55
(3,320)	1:97:A:TRP:H	1:244:A:TRP:H	4	0.55
(3,320)	1:97:A:TRP:H	1:244:A:TRP:H	15	0.55
(3,305)	1:166:A:ILE:H	1:168:A:THR:H	18	0.55
(3,282)	1:202:A:LEU:H	1:199:A:THR:H	2	0.55

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,282)	1:202:A:LEU:H	1:199:A:THR:H	5	0.55
(3,158)	1:57:A:LEU:H	1:70:A:PHE:H	3	0.55
(3,110)	1:12:A:GLY:H	1:8:A:GLY:H	11	0.55
(3,110)	1:12:A:GLY:H	1:8:A:GLY:H	19	0.55
(3,67)	1:169:A:LYS:H	1:229:A:ASN:H	20	0.55
(3,23)	1:138:A:ASP:H	1:140:A:LEU:H	2	0.55
(1,132)	1:135:A:GLN:H	1:134:A:VAL:HG22	5	0.55
(1,78)	1:117:A:GLU:H	1:96:A:HIS:H	4	0.55
(1,28)	1:241:A:VAL:H	1:240:A:MET:HA	9	0.55
(4,1289)	1:203:A:LEU:H	1:22:A:ILE:HD12	16	0.54
(4,1261)	1:216:A:SER:H	1:147:A:LEU:HD22	16	0.54
(4,1176)	1:93:A:PHE:H	1:68:A:VAL:HB	10	0.54
(4,1006)	1:79:A:LEU:H	1:88:A:TYR:HB2	17	0.54
(4,963)	1:121:A:VAL:H	1:122:A:HIS:HB2	8	0.54
(4,963)	1:121:A:VAL:H	1:122:A:HIS:HB2	20	0.54
(4,772)	1:164:A:ASP:H	1:164:A:ASP:HA	15	0.54
(4,519)	1:152:A:ALA:H	1:151:A:SER:H	8	0.54
(4,458)	1:169:A:LYS:HB3	1:169:A:LYS:HG2	12	0.54
(4,458)	1:169:A:LYS:HB3	1:169:A:LYS:HG2	16	0.54
(4,454)	1:49:A:VAL:HG22	1:49:A:VAL:HA	2	0.54
(4,454)	1:87:A:THR:HA	1:87:A:THR:HG22	4	0.54
(4,454)	1:37:A:THR:HA	1:37:A:THR:HG23	8	0.54
(4,439)	1:260:A:LYS:HA	1:260:A:LYS:HG3	2	0.54
(4,418)	1:163:A:LEU:HB2	1:163:A:LEU:HA	13	0.54
(4,414)	1:260:A:LYS:HA	1:260:A:LYS:HB3	4	0.54
(4,414)	1:163:A:LEU:HB2	1:163:A:LEU:HA	8	0.54
(4,408)	1:134:A:VAL:HA	1:134:A:VAL:HB	3	0.54
(4,408)	1:134:A:VAL:HA	1:134:A:VAL:HB	6	0.54
(4,408)	1:134:A:VAL:HA	1:134:A:VAL:HB	16	0.54
(4,406)	1:133:A:ALA:HB1	1:130:A:PHE:HA	16	0.54
(4,406)	1:133:A:ALA:HB1	1:130:A:PHE:HA	18	0.54
(4,389)	1:117:A:GLU:HB3	1:117:A:GLU:HA	12	0.54
(4,389)	1:190:A:TYR:HB3	1:190:A:TYR:HA	19	0.54
(4,389)	1:117:A:GLU:HB2	1:117:A:GLU:HA	20	0.54
(4,374)	1:127:A:TYR:HB3	1:133:A:ALA:HA	4	0.54
(4,219)	1:134:A:VAL:H	1:134:A:VAL:HA	3	0.54
(4,215)	1:242:A:ASP:H	1:241:A:VAL:HA	9	0.54
(4,118)	1:165:A:SER:H	1:163:A:LEU:HA	18	0.54
(4,13)	1:56:A:SER:H	1:76:A:LYS:HG2	18	0.54
(3,320)	1:97:A:TRP:H	1:244:A:TRP:H	17	0.54
(3,222)	1:197:A:LEU:H	1:205:A:CYS:H	8	0.54
(3,173)	1:57:A:LEU:H	1:175:A:PHE:H	10	0.54

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,163)	1:205:A:CYS:H	1:197:A:LEU:H	8	0.54
(3,160)	1:205:A:CYS:H	1:197:A:LEU:H	8	0.54
(3,17)	1:169:A:LYS:H	1:63:A:GLY:H	15	0.54
(1,100)	1:245:A:ARG:H	1:244:A:TRP:HB2	14	0.54
(1,22)	1:156:A:LEU:H	1:153:A:LYS:HD2	4	0.54
(1,6)	1:169:A:LYS:HB3	1:63:A:GLY:H	18	0.54
(4,1243)	1:247:A:ALA:H	1:247:A:ALA:HB1	16	0.53
(4,1225)	1:64:A:HIS:H	1:169:A:LYS:HG2	2	0.53
(4,1205)	1:198:A:THR:H	1:199:A:THR:HG22	5	0.53
(4,1189)	1:34:A:ASP:H	1:37:A:THR:HG23	14	0.53
(4,1189)	1:34:A:ASP:H	1:37:A:THR:HG23	15	0.53
(4,1138)	1:238:A:GLU:H	1:238:A:GLU:HB3	16	0.53
(4,845)	1:151:A:SER:H	1:150:A:GLY:HA2	2	0.53
(4,789)	1:36:A:HIS:H	1:35:A:THR:HB	10	0.53
(4,789)	1:178:A:PHE:H	1:177:A:ASN:HA	15	0.53
(4,772)	1:158:A:LYS:H	1:158:A:LYS:HA	6	0.53
(4,445)	1:76:A:LYS:HB2	1:76:A:LYS:HG3	6	0.53
(4,439)	1:22:A:ILE:HG22	1:202:A:LEU:HA	11	0.53
(4,422)	1:119:A:HIS:HA	1:119:A:HIS:HB3	15	0.53
(4,418)	1:163:A:LEU:HB2	1:163:A:LEU:HA	8	0.53
(4,414)	1:163:A:LEU:HB2	1:163:A:LEU:HA	12	0.53
(4,414)	1:250:A:LEU:HB3	1:250:A:LEU:HA	13	0.53
(4,411)	1:250:A:LEU:HB3	1:250:A:LEU:HA	13	0.53
(4,408)	1:134:A:VAL:HA	1:134:A:VAL:HB	10	0.53
(4,408)	1:134:A:VAL:HA	1:134:A:VAL:HB	11	0.53
(4,219)	1:134:A:VAL:H	1:134:A:VAL:HA	4	0.53
(4,219)	1:105:A:SER:H	1:105:A:SER:HB3	15	0.53
(4,219)	1:134:A:VAL:H	1:134:A:VAL:HA	18	0.53
(4,215)	1:242:A:ASP:H	1:241:A:VAL:HA	13	0.53
(4,150)	1:164:A:ASP:H	1:163:A:LEU:HG	9	0.53
(4,132)	1:93:A:PHE:H	1:93:A:PHE:HB3	5	0.53
(4,118)	1:165:A:SER:H	1:163:A:LEU:HA	17	0.53
(4,97)	1:161:A:ASP:H	1:163:A:LEU:HA	5	0.53
(4,43)	1:95:A:PHE:H	1:95:A:PHE:HB3	19	0.53
(3,176)	1:129:A:ASP:H	1:133:A:ALA:H	13	0.53
(3,166)	1:205:A:CYS:H	1:197:A:LEU:H	10	0.53
(3,37)	1:206:A:VAL:H	1:140:A:LEU:H	5	0.53
(1,106)	1:226:A:ARG:H	1:225:A:PHE:HB3	5	0.53
(1,9)	1:173:A:ALA:H	1:172:A:SER:HB3	18	0.53
(1,6)	1:169:A:LYS:HB3	1:63:A:GLY:H	7	0.53
(4,1337)	1:91:A:ILE:H	1:91:A:ILE:HD13	11	0.52
(4,1279)	1:49:A:VAL:H	1:49:A:VAL:HG21	20	0.52

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1274)	1:126:A:LYS:H	1:125:A:THR:HG23	13	0.52
(4,1264)	1:90:A:LEU:H	1:89:A:ARG:HG2	13	0.52
(4,1243)	1:247:A:ALA:H	1:247:A:ALA:HB2	3	0.52
(4,1228)	1:152:A:ALA:H	1:152:A:ALA:HB2	1	0.52
(4,1227)	1:23:A:ALA:H	1:23:A:ALA:HB3	1	0.52
(4,962)	1:129:A:ASP:H	1:127:A:TYR:HB3	12	0.52
(4,879)	1:247:A:ALA:H	1:247:A:ALA:HA	1	0.52
(4,879)	1:228:A:LEU:H	1:228:A:LEU:HA	5	0.52
(4,879)	1:228:A:LEU:H	1:228:A:LEU:HA	15	0.52
(4,879)	1:228:A:LEU:H	1:228:A:LEU:HA	17	0.52
(4,805)	1:166:A:ILE:H	1:165:A:SER:HB3	16	0.52
(4,801)	1:166:A:ILE:H	1:165:A:SER:HB3	16	0.52
(4,772)	1:158:A:LYS:H	1:158:A:LYS:HA	18	0.52
(4,664)	1:54:A:ALA:H	1:51:A:TYR:HA	4	0.52
(4,460)	1:169:A:LYS:HA	1:169:A:LYS:HG3	7	0.52
(4,458)	1:169:A:LYS:HB3	1:169:A:LYS:HG2	8	0.52
(4,446)	1:22:A:ILE:HD12	1:22:A:ILE:HA	3	0.52
(4,446)	1:22:A:ILE:HG22	1:22:A:ILE:HA	5	0.52
(4,445)	1:76:A:LYS:HB3	1:76:A:LYS:HG2	1	0.52
(4,445)	1:76:A:LYS:HB2	1:76:A:LYS:HG3	10	0.52
(4,445)	1:76:A:LYS:HB2	1:76:A:LYS:HG3	13	0.52
(4,442)	1:86:A:GLY:HA3	1:126:A:LYS:HG2	1	0.52
(4,439)	1:260:A:LYS:HA	1:260:A:LYS:HG3	15	0.52
(4,418)	1:163:A:LEU:HB2	1:163:A:LEU:HA	12	0.52
(4,412)	1:250:A:LEU:HB3	1:250:A:LEU:HA	13	0.52
(4,412)	1:23:A:ALA:HB1	1:17:A:HIS:HA	20	0.52
(4,411)	1:23:A:ALA:HB1	1:17:A:HIS:HA	20	0.52
(4,371)	1:146:A:PHE:HB3	1:114:A:TYR:HB3	14	0.52
(4,215)	1:242:A:ASP:H	1:241:A:VAL:HA	4	0.52
(4,215)	1:242:A:ASP:H	1:241:A:VAL:HA	15	0.52
(4,182)	1:165:A:SER:H	1:163:A:LEU:HA	5	0.52
(4,132)	1:93:A:PHE:H	1:93:A:PHE:HB3	1	0.52
(4,36)	1:85:A:ASP:H	1:85:A:ASP:HB3	20	0.52
(3,305)	1:166:A:ILE:H	1:168:A:THR:H	4	0.52
(3,305)	1:166:A:ILE:H	1:168:A:THR:H	7	0.52
(3,302)	1:229:A:ASN:H	1:168:A:THR:H	11	0.52
(3,282)	1:202:A:LEU:H	1:199:A:THR:H	13	0.52
(3,264)	1:240:A:MET:H	1:228:A:LEU:H	3	0.52
(1,128)	1:81:A:GLY:H	1:84:A:LEU:HD21	9	0.52
(1,113)	1:104:A:GLY:H	1:103:A:GLN:HB3	18	0.52
(1,106)	1:226:A:ARG:H	1:225:A:PHE:HB2	11	0.52
(4,1334)	1:82:A:GLY:H	1:84:A:LEU:HD21	19	0.51

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1265)	1:205:A:CYS:H	1:206:A:VAL:HG23	19	0.51
(4,1243)	1:247:A:ALA:H	1:247:A:ALA:HB3	20	0.51
(4,1153)	1:78:A:VAL:H	1:77:A:ALA:HB3	7	0.51
(4,1123)	1:218:A:SER:H	1:221:A:GLN:HB3	12	0.51
(4,1048)	1:176:A:THR:H	1:175:A:PHE:HB2	10	0.51
(4,963)	1:121:A:VAL:H	1:122:A:HIS:HB2	3	0.51
(4,879)	1:228:A:LEU:H	1:228:A:LEU:HA	4	0.51
(4,852)	1:160:A:VAL:H	1:160:A:VAL:HA	10	0.51
(4,852)	1:160:A:VAL:H	1:160:A:VAL:HA	19	0.51
(4,664)	1:54:A:ALA:H	1:51:A:TYR:HA	11	0.51
(4,458)	1:126:A:LYS:HB2	1:126:A:LYS:HG3	10	0.51
(4,446)	1:22:A:ILE:HG21	1:22:A:ILE:HA	12	0.51
(4,445)	1:76:A:LYS:HB3	1:76:A:LYS:HG2	5	0.51
(4,423)	1:167:A:LYS:HE2	1:167:A:LYS:HB3	12	0.51
(4,412)	1:23:A:ALA:HB2	1:17:A:HIS:HA	11	0.51
(4,411)	1:23:A:ALA:HB2	1:17:A:HIS:HA	11	0.51
(4,384)	1:22:A:ILE:HD12	1:28:A:GLN:HB2	18	0.51
(4,370)	1:132:A:LYS:HG3	1:132:A:LYS:HE3	8	0.51
(4,370)	1:132:A:LYS:HG2	1:132:A:LYS:HE2	17	0.51
(4,260)	1:203:A:LEU:H	1:203:A:LEU:HB3	15	0.51
(4,215)	1:242:A:ASP:H	1:241:A:VAL:HA	20	0.51
(4,204)	1:100:A:LEU:H	1:100:A:LEU:HG	5	0.51
(4,132)	1:93:A:PHE:H	1:93:A:PHE:HB3	15	0.51
(4,132)	1:93:A:PHE:H	1:93:A:PHE:HB3	18	0.51
(4,118)	1:165:A:SER:H	1:163:A:LEU:HA	2	0.51
(4,118)	1:165:A:SER:H	1:163:A:LEU:HA	4	0.51
(4,21)	1:123:A:TRP:H	1:89:A:ARG:HB2	4	0.51
(3,325)	1:197:A:LEU:H	1:203:A:LEU:H	12	0.51
(3,286)	1:70:A:PHE:H	1:92:A:GLN:H	9	0.51
(3,158)	1:57:A:LEU:H	1:70:A:PHE:H	18	0.51
(3,155)	1:169:A:LYS:H	1:231:A:ASN:H	13	0.51
(4,1316)	1:165:A:SER:H	1:166:A:ILE:HD13	20	0.5
(4,1289)	1:203:A:LEU:H	1:203:A:LEU:HD23	13	0.5
(4,1274)	1:126:A:LYS:H	1:125:A:THR:HG21	6	0.5
(4,1243)	1:247:A:ALA:H	1:247:A:ALA:HB3	8	0.5
(4,1243)	1:247:A:ALA:H	1:247:A:ALA:HB1	14	0.5
(4,1243)	1:247:A:ALA:H	1:247:A:ALA:HB2	19	0.5
(4,1223)	1:152:A:ALA:H	1:152:A:ALA:HB2	1	0.5
(4,1205)	1:198:A:THR:H	1:199:A:THR:HG21	12	0.5
(4,1166)	1:116:A:ALA:H	1:115:A:ALA:HB2	9	0.5
(4,1147)	1:231:A:ASN:H	1:169:A:LYS:HD3	6	0.5
(4,1138)	1:40:A:TYR:H	1:39:A:LYS:HB3	10	0.5

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1022)	1:112:A:LYS:H	1:110:A:ASP:HB2	2	0.5
(4,852)	1:160:A:VAL:H	1:160:A:VAL:HA	1	0.5
(4,852)	1:160:A:VAL:H	1:160:A:VAL:HA	9	0.5
(4,852)	1:160:A:VAL:H	1:160:A:VAL:HA	11	0.5
(4,836)	1:166:A:ILE:H	1:165:A:SER:HB3	11	0.5
(4,733)	1:222:A:VAL:H	1:222:A:VAL:HA	15	0.5
(4,666)	1:226:A:ARG:H	1:222:A:VAL:H	4	0.5
(4,540)	1:243:A:ASN:H	1:97:A:TRP:H	11	0.5
(4,458)	1:169:A:LYS:HB3	1:169:A:LYS:HG2	13	0.5
(4,458)	1:169:A:LYS:HB3	1:169:A:LYS:HG2	15	0.5
(4,458)	1:169:A:LYS:HB3	1:169:A:LYS:HG2	20	0.5
(4,457)	1:78:A:VAL:HB	1:78:A:VAL:HG23	16	0.5
(4,456)	1:110:A:ASP:HB3	1:109:A:VAL:HG21	11	0.5
(4,454)	1:87:A:THR:HA	1:87:A:THR:HG21	11	0.5
(4,454)	1:49:A:VAL:HG21	1:49:A:VAL:HA	16	0.5
(4,414)	1:163:A:LEU:HB2	1:163:A:LEU:HA	6	0.5
(4,414)	1:163:A:LEU:HB2	1:163:A:LEU:HA	7	0.5
(4,414)	1:163:A:LEU:HB2	1:163:A:LEU:HA	18	0.5
(4,397)	1:159:A:VAL:HA	1:159:A:VAL:HB	3	0.5
(4,397)	1:159:A:VAL:HA	1:159:A:VAL:HB	11	0.5
(4,397)	1:159:A:VAL:HA	1:159:A:VAL:HB	14	0.5
(4,397)	1:159:A:VAL:HA	1:159:A:VAL:HB	20	0.5
(4,371)	1:146:A:PHE:HB3	1:114:A:TYR:HB2	7	0.5
(4,370)	1:132:A:LYS:HG3	1:132:A:LYS:HE3	4	0.5
(4,293)	1:229:A:ASN:HB2	1:168:A:THR:HA	5	0.5
(4,232)	1:259:A:PHE:H	1:259:A:PHE:HB3	6	0.5
(4,182)	1:166:A:ILE:H	1:163:A:LEU:HA	13	0.5
(4,118)	1:165:A:SER:H	1:163:A:LEU:HA	1	0.5
(3,320)	1:97:A:TRP:H	1:244:A:TRP:H	19	0.5
(3,305)	1:166:A:ILE:H	1:168:A:THR:H	10	0.5
(3,302)	1:229:A:ASN:H	1:168:A:THR:H	14	0.5
(3,286)	1:70:A:PHE:H	1:92:A:GLN:H	7	0.5
(3,261)	1:240:A:MET:H	1:228:A:LEU:H	17	0.5
(1,100)	1:245:A:ARG:H	1:244:A:TRP:HB2	1	0.5
(1,77)	1:224:A:LYS:HB2	1:163:A:LEU:HD22	18	0.5
(1,42)	1:116:A:ALA:HB1	1:97:A:TRP:HA	18	0.5
(4,1321)	1:205:A:CYS:H	1:206:A:VAL:HG21	20	0.49
(4,1316)	1:165:A:SER:H	1:166:A:ILE:HD13	18	0.49
(4,1274)	1:126:A:LYS:H	1:125:A:THR:HG22	16	0.49
(4,1227)	1:23:A:ALA:H	1:23:A:ALA:HB3	3	0.49
(4,1227)	1:65:A:ALA:H	1:65:A:ALA:HB3	15	0.49
(4,1214)	1:89:A:ARG:H	1:89:A:ARG:HB2	11	0.49

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1129)	1:111:A:LYS:H	1:108:A:THR:HG22	9	0.49
(4,1027)	1:103:A:GLN:H	1:103:A:GLN:HG2	18	0.49
(4,1021)	1:112:A:LYS:H	1:110:A:ASP:HB2	2	0.49
(4,1003)	1:126:A:LYS:H	1:124:A:ASN:HB3	5	0.49
(4,988)	1:205:A:CYS:H	1:205:A:CYS:HB3	8	0.49
(4,879)	1:100:A:LEU:H	1:99:A:SER:HB3	14	0.49
(4,529)	1:116:A:ALA:H	1:147:A:LEU:H	14	0.49
(4,487)	1:48:A:SER:H	1:80:A:LYS:H	8	0.49
(4,463)	1:174:A:ASP:HA	1:57:A:LEU:HD21	17	0.49
(4,458)	1:169:A:LYS:HB3	1:169:A:LYS:HG2	3	0.49
(4,458)	1:89:A:ARG:HB2	1:89:A:ARG:HG3	9	0.49
(4,458)	1:169:A:LYS:HB3	1:169:A:LYS:HG2	18	0.49
(4,457)	1:202:A:LEU:HB2	1:202:A:LEU:HD23	4	0.49
(4,457)	1:78:A:VAL:HB	1:78:A:VAL:HG23	8	0.49
(4,454)	1:37:A:THR:HA	1:37:A:THR:HG22	6	0.49
(4,446)	1:22:A:ILE:HG23	1:22:A:ILE:HA	11	0.49
(4,423)	1:39:A:LYS:HE3	1:39:A:LYS:HB2	19	0.49
(4,418)	1:163:A:LEU:HB2	1:163:A:LEU:HA	6	0.49
(4,418)	1:163:A:LEU:HB2	1:163:A:LEU:HA	7	0.49
(4,418)	1:163:A:LEU:HB2	1:163:A:LEU:HA	18	0.49
(4,414)	1:163:A:LEU:HB2	1:163:A:LEU:HA	3	0.49
(4,414)	1:163:A:LEU:HB2	1:163:A:LEU:HA	5	0.49
(4,408)	1:206:A:VAL:HB	1:206:A:VAL:HA	9	0.49
(4,389)	1:127:A:TYR:HA	1:127:A:TYR:HB3	2	0.49
(4,389)	1:93:A:PHE:HB2	1:93:A:PHE:HA	8	0.49
(4,380)	1:259:A:PHE:HB2	1:259:A:PHE:HA	9	0.49
(4,374)	1:127:A:TYR:HB3	1:133:A:ALA:HA	1	0.49
(4,370)	1:111:A:LYS:HG3	1:111:A:LYS:HE2	9	0.49
(4,190)	1:127:A:TYR:H	1:123:A:TRP:HB3	2	0.49
(4,190)	1:133:A:ALA:H	1:123:A:TRP:HB3	5	0.49
(4,185)	1:92:A:GLN:H	1:91:A:ILE:HD12	1	0.49
(4,185)	1:142:A:VAL:H	1:209:A:ILE:HD12	2	0.49
(4,165)	1:260:A:LYS:H	1:260:A:LYS:HA	16	0.49
(4,157)	1:207:A:THR:H	1:207:A:THR:HB	8	0.49
(3,290)	1:196:A:SER:H	1:206:A:VAL:H	6	0.49
(3,286)	1:70:A:PHE:H	1:92:A:GLN:H	4	0.49
(3,252)	1:196:A:SER:H	1:206:A:VAL:H	6	0.49
(3,234)	1:8:A:GLY:H	1:12:A:GLY:H	5	0.49
(3,120)	1:248:A:GLN:H	1:32:A:ASP:H	16	0.49
(3,4)	1:110:A:ASP:H	1:35:A:THR:H	18	0.49
(2,16)	1:82:A:GLY:H	1:45:A:LYS:H	6	0.49
(1,132)	1:135:A:GLN:H	1:134:A:VAL:HG22	10	0.49

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,64)	1:60:A:LEU:HB2	1:172:A:SER:HB2	1	0.49
(1,59)	1:240:A:MET:HA	1:230:A:PHE:HB2	7	0.49
(1,42)	1:116:A:ALA:HB2	1:97:A:TRP:HA	15	0.49
(4,1318)	1:49:A:VAL:H	1:49:A:VAL:HG22	11	0.48
(4,1293)	1:153:A:LYS:H	1:152:A:ALA:HB2	11	0.48
(4,1214)	1:89:A:ARG:H	1:89:A:ARG:HB3	3	0.48
(4,1128)	1:251:A:LYS:H	1:250:A:LEU:HB2	19	0.48
(4,989)	1:41:A:ASP:H	1:41:A:ASP:HB2	20	0.48
(4,980)	1:191:A:TRP:H	1:190:A:TYR:HB3	3	0.48
(4,879)	1:228:A:LEU:H	1:228:A:LEU:HA	6	0.48
(4,879)	1:228:A:LEU:H	1:228:A:LEU:HA	20	0.48
(4,862)	1:78:A:VAL:H	1:50:A:SER:HB2	1	0.48
(4,852)	1:160:A:VAL:H	1:160:A:VAL:HA	13	0.48
(4,852)	1:160:A:VAL:H	1:160:A:VAL:HA	20	0.48
(4,845)	1:151:A:SER:H	1:151:A:SER:HB2	13	0.48
(4,836)	1:166:A:ILE:H	1:163:A:LEU:HA	9	0.48
(4,828)	1:160:A:VAL:H	1:160:A:VAL:HA	13	0.48
(4,805)	1:129:A:ASP:H	1:128:A:GLY:HA3	9	0.48
(4,801)	1:129:A:ASP:H	1:128:A:GLY:HA3	9	0.48
(4,733)	1:24:A:LYS:H	1:24:A:LYS:HA	3	0.48
(4,733)	1:92:A:GLN:H	1:92:A:GLN:HA	4	0.48
(4,733)	1:127:A:TYR:H	1:127:A:TYR:HA	16	0.48
(4,733)	1:92:A:GLN:H	1:92:A:GLN:HA	17	0.48
(4,469)	1:140:A:LEU:HB2	1:91:A:ILE:HD12	16	0.48
(4,458)	1:169:A:LYS:HB3	1:169:A:LYS:HG2	4	0.48
(4,457)	1:78:A:VAL:HB	1:78:A:VAL:HG21	1	0.48
(4,457)	1:80:A:LYS:HB2	1:80:A:LYS:HG3	11	0.48
(4,454)	1:87:A:THR:HA	1:87:A:THR:HG21	15	0.48
(4,451)	1:203:A:LEU:HB3	1:203:A:LEU:HD22	8	0.48
(4,451)	1:183:A:LEU:HB2	1:183:A:LEU:HD21	12	0.48
(4,446)	1:37:A:THR:HA	1:37:A:THR:HG23	7	0.48
(4,446)	1:22:A:ILE:HD11	1:22:A:ILE:HA	15	0.48
(4,439)	1:260:A:LYS:HA	1:260:A:LYS:HG3	6	0.48
(4,439)	1:260:A:LYS:HA	1:260:A:LYS:HG2	20	0.48
(4,418)	1:163:A:LEU:HB2	1:163:A:LEU:HA	3	0.48
(4,418)	1:163:A:LEU:HB2	1:163:A:LEU:HA	5	0.48
(4,414)	1:163:A:LEU:HB2	1:163:A:LEU:HA	1	0.48
(4,414)	1:163:A:LEU:HB2	1:163:A:LEU:HA	2	0.48
(4,414)	1:163:A:LEU:HB2	1:163:A:LEU:HA	10	0.48
(4,414)	1:163:A:LEU:HB2	1:163:A:LEU:HA	11	0.48
(4,414)	1:163:A:LEU:HB2	1:163:A:LEU:HA	15	0.48
(4,414)	1:163:A:LEU:HB2	1:163:A:LEU:HA	19	0.48

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,406)	1:149:A:VAL:HA	1:149:A:VAL:HB	5	0.48
(4,406)	1:133:A:ALA:HB1	1:130:A:PHE:HA	8	0.48
(4,406)	1:133:A:ALA:HB1	1:130:A:PHE:HA	12	0.48
(4,406)	1:133:A:ALA:HB1	1:130:A:PHE:HA	20	0.48
(4,380)	1:245:A:ARG:HA	1:245:A:ARG:HB3	18	0.48
(4,370)	1:111:A:LYS:HG3	1:111:A:LYS:HE2	15	0.48
(4,370)	1:158:A:LYS:HG2	1:158:A:LYS:HE2	16	0.48
(4,232)	1:259:A:PHE:H	1:259:A:PHE:HB3	5	0.48
(4,182)	1:165:A:SER:H	1:163:A:LEU:HA	19	0.48
(4,118)	1:165:A:SER:H	1:163:A:LEU:HA	16	0.48
(4,118)	1:165:A:SER:H	1:163:A:LEU:HA	20	0.48
(3,323)	1:181:A:ARG:H	1:184:A:LEU:H	12	0.48
(3,306)	1:156:A:LEU:H	1:159:A:VAL:H	1	0.48
(3,305)	1:166:A:ILE:H	1:168:A:THR:H	14	0.48
(1,64)	1:60:A:LEU:HB2	1:172:A:SER:HB3	9	0.48
(1,56)	1:255:A:ILE:HD13	1:193:A:TYR:HB2	10	0.48
(4,1266)	1:66:A:PHE:H	1:169:A:LYS:HG3	15	0.47
(4,1251)	1:205:A:CYS:H	1:206:A:VAL:HG23	19	0.47
(4,1214)	1:89:A:ARG:H	1:89:A:ARG:HG3	8	0.47
(4,1214)	1:89:A:ARG:H	1:89:A:ARG:HB2	14	0.47
(4,1138)	1:40:A:TYR:H	1:39:A:LYS:HB3	15	0.47
(4,1134)	1:136:A:GLN:H	1:136:A:GLN:HB2	10	0.47
(4,1129)	1:195:A:GLY:H	1:207:A:THR:HG22	16	0.47
(4,1022)	1:112:A:LYS:H	1:110:A:ASP:HB3	6	0.47
(4,1022)	1:193:A:TYR:H	1:208:A:TRP:HB2	11	0.47
(4,1006)	1:79:A:LEU:H	1:88:A:TYR:HB2	19	0.47
(4,879)	1:100:A:LEU:H	1:99:A:SER:HB2	8	0.47
(4,879)	1:100:A:LEU:H	1:99:A:SER:HB2	18	0.47
(4,828)	1:135:A:GLN:H	1:135:A:GLN:HA	1	0.47
(4,805)	1:166:A:ILE:H	1:165:A:SER:HB3	11	0.47
(4,801)	1:166:A:ILE:H	1:165:A:SER:HB3	11	0.47
(4,789)	1:178:A:PHE:H	1:177:A:ASN:HA	14	0.47
(4,733)	1:24:A:LYS:H	1:24:A:LYS:HA	5	0.47
(4,733)	1:222:A:VAL:H	1:222:A:VAL:HA	6	0.47
(4,733)	1:24:A:LYS:H	1:24:A:LYS:HA	7	0.47
(4,733)	1:24:A:LYS:H	1:24:A:LYS:HA	9	0.47
(4,733)	1:222:A:VAL:H	1:222:A:VAL:HA	13	0.47
(4,733)	1:222:A:VAL:H	1:222:A:VAL:HA	14	0.47
(4,666)	1:226:A:ARG:H	1:222:A:VAL:H	13	0.47
(4,624)	1:103:A:GLN:H	1:102:A:GLY:H	10	0.47
(4,519)	1:152:A:ALA:H	1:151:A:SER:H	3	0.47
(4,478)	1:32:A:ASP:H	1:250:A:LEU:H	3	0.47

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,458)	1:169:A:LYS:HB3	1:169:A:LYS:HG2	1	0.47
(4,457)	1:78:A:VAL:HB	1:78:A:VAL:HG22	2	0.47
(4,457)	1:78:A:VAL:HB	1:78:A:VAL:HG21	20	0.47
(4,454)	1:49:A:VAL:HG23	1:49:A:VAL:HA	14	0.47
(4,451)	1:223:A:LEU:HB2	1:223:A:LEU:HG	4	0.47
(4,451)	1:203:A:LEU:HB3	1:203:A:LEU:HD23	5	0.47
(4,451)	1:250:A:LEU:HB3	1:250:A:LEU:HD23	7	0.47
(4,445)	1:76:A:LYS:HB3	1:76:A:LYS:HD3	19	0.47
(4,444)	1:255:A:ILE:HG21	1:193:A:TYR:HB2	11	0.47
(4,418)	1:163:A:LEU:HB2	1:163:A:LEU:HA	1	0.47
(4,418)	1:163:A:LEU:HB2	1:163:A:LEU:HA	2	0.47
(4,418)	1:163:A:LEU:HB2	1:163:A:LEU:HA	10	0.47
(4,418)	1:163:A:LEU:HB2	1:163:A:LEU:HA	11	0.47
(4,418)	1:163:A:LEU:HB2	1:163:A:LEU:HA	19	0.47
(4,414)	1:163:A:LEU:HB2	1:163:A:LEU:HA	16	0.47
(4,414)	1:163:A:LEU:HB2	1:163:A:LEU:HA	20	0.47
(4,380)	1:122:A:HIS:HB2	1:122:A:HIS:HA	11	0.47
(4,380)	1:74:A:GLN:HA	1:74:A:GLN:HB3	12	0.47
(4,380)	1:245:A:ARG:HA	1:245:A:ARG:HB3	13	0.47
(4,380)	1:122:A:HIS:HB3	1:122:A:HIS:HA	14	0.47
(4,380)	1:100:A:LEU:HB3	1:100:A:LEU:HA	16	0.47
(4,380)	1:100:A:LEU:HB3	1:100:A:LEU:HA	20	0.47
(4,374)	1:124:A:ASN:HB3	1:133:A:ALA:HA	14	0.47
(4,370)	1:251:A:LYS:HG3	1:251:A:LYS:HE2	3	0.47
(4,266)	1:166:A:ILE:HD11	1:168:A:THR:H	8	0.47
(4,251)	1:259:A:PHE:H	1:40:A:TYR:HB2	13	0.47
(4,231)	1:135:A:GLN:H	1:135:A:GLN:HB2	16	0.47
(4,219)	1:105:A:SER:H	1:105:A:SER:HB3	8	0.47
(4,215)	1:242:A:ASP:H	1:241:A:VAL:HA	3	0.47
(4,132)	1:93:A:PHE:H	1:93:A:PHE:HB3	20	0.47
(3,305)	1:166:A:ILE:H	1:168:A:THR:H	13	0.47
(3,302)	1:229:A:ASN:H	1:168:A:THR:H	3	0.47
(3,264)	1:240:A:MET:H	1:228:A:LEU:H	14	0.47
(3,264)	1:240:A:MET:H	1:228:A:LEU:H	20	0.47
(3,222)	1:197:A:LEU:H	1:205:A:CYS:H	1	0.47
(3,163)	1:205:A:CYS:H	1:197:A:LEU:H	1	0.47
(3,160)	1:205:A:CYS:H	1:197:A:LEU:H	1	0.47
(3,150)	1:206:A:VAL:H	1:197:A:LEU:H	1	0.47
(3,120)	1:248:A:GLN:H	1:32:A:ASP:H	5	0.47
(3,114)	1:241:A:VAL:H	1:243:A:ASN:H	18	0.47
(3,37)	1:206:A:VAL:H	1:140:A:LEU:H	7	0.47
(3,7)	1:56:A:SER:H	1:177:A:ASN:H	14	0.47

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,106)	1:226:A:ARG:H	1:225:A:PHE:HB2	20	0.47
(1,79)	1:68:A:VAL:H	1:93:A:PHE:H	19	0.47
(1,76)	1:115:A:ALA:HB1	1:149:A:VAL:HG23	3	0.47
(4,1227)	1:23:A:ALA:H	1:23:A:ALA:HB2	2	0.46
(4,1227)	1:23:A:ALA:H	1:23:A:ALA:HB2	5	0.46
(4,1227)	1:23:A:ALA:H	1:23:A:ALA:HB1	6	0.46
(4,1227)	1:23:A:ALA:H	1:23:A:ALA:HB1	13	0.46
(4,1215)	1:86:A:GLY:H	1:80:A:LYS:HD3	19	0.46
(4,1051)	1:57:A:LEU:H	1:57:A:LEU:HB3	15	0.46
(4,1022)	1:133:A:ALA:H	1:127:A:TYR:HB3	4	0.46
(4,1021)	1:112:A:LYS:H	1:110:A:ASP:HB3	6	0.46
(4,1021)	1:193:A:TYR:H	1:208:A:TRP:HB2	11	0.46
(4,998)	1:175:A:PHE:H	1:175:A:PHE:HB3	18	0.46
(4,957)	1:191:A:TRP:H	1:191:A:TRP:HB3	12	0.46
(4,948)	1:166:A:ILE:H	1:163:A:LEU:HA	20	0.46
(4,879)	1:228:A:LEU:H	1:228:A:LEU:HA	3	0.46
(4,852)	1:160:A:VAL:H	1:160:A:VAL:HA	5	0.46
(4,828)	1:227:A:LYS:H	1:227:A:LYS:HA	5	0.46
(4,828)	1:24:A:LYS:H	1:24:A:LYS:HA	10	0.46
(4,733)	1:24:A:LYS:H	1:24:A:LYS:HA	1	0.46
(4,733)	1:24:A:LYS:H	1:24:A:LYS:HA	8	0.46
(4,733)	1:19:A:ASP:H	1:19:A:ASP:HA	18	0.46
(4,666)	1:226:A:ARG:H	1:222:A:VAL:H	5	0.46
(4,458)	1:169:A:LYS:HB3	1:169:A:LYS:HG2	14	0.46
(4,457)	1:80:A:LYS:HB3	1:80:A:LYS:HG2	6	0.46
(4,457)	1:202:A:LEU:HB3	1:202:A:LEU:HD22	12	0.46
(4,457)	1:78:A:VAL:HB	1:78:A:VAL:HG22	14	0.46
(4,457)	1:202:A:LEU:HB3	1:202:A:LEU:HD23	15	0.46
(4,418)	1:163:A:LEU:HB2	1:163:A:LEU:HA	15	0.46
(4,418)	1:163:A:LEU:HB2	1:163:A:LEU:HA	16	0.46
(4,418)	1:163:A:LEU:HB2	1:163:A:LEU:HA	20	0.46
(4,380)	1:122:A:HIS:HB3	1:122:A:HIS:HA	2	0.46
(4,380)	1:122:A:HIS:HB3	1:122:A:HIS:HA	7	0.46
(4,374)	1:124:A:ASN:HB2	1:133:A:ALA:HA	5	0.46
(4,370)	1:251:A:LYS:HG3	1:251:A:LYS:HE2	7	0.46
(4,370)	1:158:A:LYS:HG2	1:158:A:LYS:HE3	10	0.46
(4,370)	1:158:A:LYS:HG2	1:158:A:LYS:HE3	12	0.46
(4,370)	1:111:A:LYS:HG3	1:111:A:LYS:HE2	13	0.46
(4,370)	1:45:A:LYS:HG3	1:45:A:LYS:HE2	18	0.46
(4,370)	1:158:A:LYS:HG3	1:158:A:LYS:HE2	19	0.46
(4,370)	1:111:A:LYS:HG3	1:111:A:LYS:HE2	20	0.46
(4,260)	1:203:A:LEU:H	1:203:A:LEU:HB3	1	0.46

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,232)	1:66:A:PHE:H	1:66:A:PHE:HB2	3	0.46
(4,182)	1:165:A:SER:H	1:163:A:LEU:HA	14	0.46
(4,132)	1:93:A:PHE:H	1:93:A:PHE:HB3	7	0.46
(4,118)	1:165:A:SER:H	1:163:A:LEU:HA	5	0.46
(4,100)	1:141:A:ALA:H	1:140:A:LEU:HB2	12	0.46
(4,13)	1:56:A:SER:H	1:76:A:LYS:HG2	2	0.46
(3,194)	1:257:A:ALA:H	1:41:A:ASP:H	10	0.46
(3,103)	1:82:A:GLY:H	1:48:A:SER:H	2	0.46
(3,92)	1:55:A:THR:H	1:77:A:ALA:H	2	0.46
(3,89)	1:41:A:ASP:H	1:257:A:ALA:H	10	0.46
(1,113)	1:104:A:GLY:H	1:103:A:GLN:HB3	20	0.46
(1,64)	1:60:A:LEU:HB2	1:172:A:SER:HB3	10	0.46
(1,22)	1:156:A:LEU:H	1:153:A:LYS:HD2	15	0.46
(4,1316)	1:165:A:SER:H	1:166:A:ILE:HD13	16	0.45
(4,1257)	1:78:A:VAL:H	1:77:A:ALA:HB2	6	0.45
(4,1253)	1:198:A:THR:H	1:199:A:THR:HG23	4	0.45
(4,1205)	1:198:A:THR:H	1:199:A:THR:HG23	4	0.45
(4,1202)	1:198:A:THR:H	1:199:A:THR:HG23	4	0.45
(4,1189)	1:34:A:ASP:H	1:255:A:ILE:HG22	1	0.45
(4,1021)	1:133:A:ALA:H	1:127:A:TYR:HB3	4	0.45
(4,998)	1:175:A:PHE:H	1:175:A:PHE:HB3	2	0.45
(4,998)	1:175:A:PHE:H	1:175:A:PHE:HB3	12	0.45
(4,879)	1:100:A:LEU:H	1:99:A:SER:HB3	16	0.45
(4,828)	1:160:A:VAL:H	1:160:A:VAL:HA	18	0.45
(4,733)	1:24:A:LYS:H	1:24:A:LYS:HA	2	0.45
(4,733)	1:24:A:LYS:H	1:24:A:LYS:HA	10	0.45
(4,733)	1:24:A:LYS:H	1:24:A:LYS:HA	11	0.45
(4,733)	1:24:A:LYS:H	1:24:A:LYS:HA	12	0.45
(4,733)	1:24:A:LYS:H	1:24:A:LYS:HA	19	0.45
(4,733)	1:24:A:LYS:H	1:24:A:LYS:HA	20	0.45
(4,723)	1:222:A:VAL:H	1:222:A:VAL:HA	15	0.45
(4,666)	1:226:A:ARG:H	1:222:A:VAL:H	11	0.45
(4,463)	1:174:A:ASP:HA	1:176:A:THR:HG23	4	0.45
(4,463)	1:174:A:ASP:HA	1:176:A:THR:HG22	6	0.45
(4,458)	1:169:A:LYS:HB3	1:169:A:LYS:HG2	11	0.45
(4,458)	1:169:A:LYS:HB3	1:169:A:LYS:HG2	17	0.45
(4,457)	1:78:A:VAL:HB	1:78:A:VAL:HG23	5	0.45
(4,457)	1:78:A:VAL:HB	1:78:A:VAL:HG22	17	0.45
(4,457)	1:78:A:VAL:HB	1:78:A:VAL:HG22	19	0.45
(4,454)	1:49:A:VAL:HG21	1:49:A:VAL:HA	12	0.45
(4,451)	1:223:A:LEU:HB3	1:223:A:LEU:HD22	17	0.45
(4,446)	1:68:A:VAL:HA	1:68:A:VAL:HG22	8	0.45

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,446)	1:22:A:ILE:HG22	1:22:A:ILE:HA	9	0.45
(4,444)	1:255:A:ILE:HG21	1:193:A:TYR:HB2	3	0.45
(4,421)	1:147:A:LEU:HA	1:147:A:LEU:HB3	7	0.45
(4,414)	1:163:A:LEU:HB2	1:163:A:LEU:HA	17	0.45
(4,386)	1:25:A:GLY:HA2	1:28:A:GLN:HB2	6	0.45
(4,380)	1:259:A:PHE:HB2	1:259:A:PHE:HA	8	0.45
(4,371)	1:146:A:PHE:HB3	1:114:A:TYR:HB3	2	0.45
(4,335)	1:22:A:ILE:HG21	1:22:A:ILE:HA	3	0.45
(4,275)	1:117:A:GLU:HB2	1:146:A:PHE:HA	20	0.45
(4,232)	1:259:A:PHE:H	1:259:A:PHE:HB3	2	0.45
(4,224)	1:160:A:VAL:H	1:160:A:VAL:HA	18	0.45
(4,132)	1:93:A:PHE:H	1:93:A:PHE:HB3	13	0.45
(4,48)	1:117:A:GLU:H	1:117:A:GLU:HB3	4	0.45
(4,42)	1:38:A:ALA:HA	1:255:A:ILE:H	5	0.45
(3,325)	1:197:A:LEU:H	1:203:A:LEU:H	10	0.45
(3,173)	1:57:A:LEU:H	1:175:A:PHE:H	20	0.45
(3,115)	1:12:A:GLY:H	1:8:A:GLY:H	11	0.45
(3,115)	1:12:A:GLY:H	1:8:A:GLY:H	19	0.45
(3,79)	1:192:A:THR:H	1:256:A:LYS:H	13	0.45
(3,9)	1:256:A:LYS:H	1:192:A:THR:H	13	0.45
(1,134)	1:121:A:VAL:H	1:91:A:ILE:HD11	6	0.45
(1,78)	1:117:A:GLU:H	1:96:A:HIS:H	13	0.45
(1,76)	1:115:A:ALA:HB3	1:149:A:VAL:HG22	14	0.45
(4,1316)	1:165:A:SER:H	1:166:A:ILE:HD13	1	0.44
(4,1258)	1:202:A:LEU:H	1:22:A:ILE:HD12	5	0.44
(4,1253)	1:99:A:SER:H	1:241:A:VAL:HG21	12	0.44
(4,1219)	1:203:A:LEU:H	1:203:A:LEU:HB3	2	0.44
(4,1214)	1:233:A:GLU:H	1:233:A:GLU:HB3	5	0.44
(4,1202)	1:99:A:SER:H	1:241:A:VAL:HG21	12	0.44
(4,1200)	1:251:A:LYS:H	1:250:A:LEU:HB3	17	0.44
(4,1189)	1:34:A:ASP:H	1:37:A:THR:HG22	17	0.44
(4,1189)	1:34:A:ASP:H	1:255:A:ILE:HG22	19	0.44
(4,1129)	1:195:A:GLY:H	1:207:A:THR:HG21	5	0.44
(4,1022)	1:193:A:TYR:H	1:208:A:TRP:HB3	19	0.44
(4,998)	1:112:A:LYS:H	1:110:A:ASP:HB3	6	0.44
(4,962)	1:129:A:ASP:H	1:127:A:TYR:HB2	6	0.44
(4,957)	1:191:A:TRP:H	1:191:A:TRP:HB3	3	0.44
(4,879)	1:100:A:LEU:H	1:99:A:SER:HB3	12	0.44
(4,852)	1:160:A:VAL:H	1:160:A:VAL:HA	7	0.44
(4,852)	1:160:A:VAL:H	1:160:A:VAL:HA	12	0.44
(4,852)	1:160:A:VAL:H	1:160:A:VAL:HA	14	0.44
(4,852)	1:160:A:VAL:H	1:160:A:VAL:HA	18	0.44

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,828)	1:160:A:VAL:H	1:160:A:VAL:HA	12	0.44
(4,666)	1:226:A:ARG:H	1:222:A:VAL:H	17	0.44
(4,468)	1:76:A:LYS:HG2	1:51:A:TYR:HA	1	0.44
(4,460)	1:99:A:SER:HA	1:241:A:VAL:HG23	5	0.44
(4,458)	1:169:A:LYS:HB3	1:169:A:LYS:HG2	2	0.44
(4,457)	1:80:A:LYS:HB3	1:80:A:LYS:HG2	3	0.44
(4,457)	1:202:A:LEU:HB3	1:202:A:LEU:HD23	13	0.44
(4,451)	1:250:A:LEU:HB2	1:250:A:LEU:HD21	6	0.44
(4,451)	1:250:A:LEU:HB3	1:250:A:LEU:HD22	11	0.44
(4,451)	1:223:A:LEU:HB3	1:223:A:LEU:HD22	14	0.44
(4,451)	1:239:A:LEU:HB3	1:239:A:LEU:HD22	18	0.44
(4,439)	1:260:A:LYS:HA	1:260:A:LYS:HG2	3	0.44
(4,421)	1:167:A:LYS:HA	1:167:A:LYS:HG3	6	0.44
(4,418)	1:163:A:LEU:HB2	1:163:A:LEU:HA	17	0.44
(4,406)	1:133:A:ALA:HB3	1:130:A:PHE:HA	4	0.44
(4,380)	1:100:A:LEU:HB3	1:100:A:LEU:HA	3	0.44
(4,380)	1:122:A:HIS:HB3	1:122:A:HIS:HA	15	0.44
(4,371)	1:22:A:ILE:HB	1:20:A:PHE:HB3	9	0.44
(4,273)	1:113:A:LYS:HD3	1:244:A:TRP:HA	11	0.44
(4,232)	1:34:A:ASP:H	1:34:A:ASP:HB2	4	0.44
(4,232)	1:34:A:ASP:H	1:34:A:ASP:HB2	16	0.44
(4,231)	1:135:A:GLN:H	1:135:A:GLN:HB2	10	0.44
(4,224)	1:160:A:VAL:H	1:160:A:VAL:HA	3	0.44
(4,224)	1:159:A:VAL:H	1:159:A:VAL:HA	5	0.44
(4,204)	1:183:A:LEU:H	1:183:A:LEU:HG	14	0.44
(4,204)	1:100:A:LEU:H	1:100:A:LEU:HG	16	0.44
(4,180)	1:98:A:GLY:H	1:240:A:MET:HA	18	0.44
(3,305)	1:166:A:ILE:H	1:168:A:THR:H	17	0.44
(3,286)	1:70:A:PHE:H	1:92:A:GLN:H	19	0.44
(3,282)	1:202:A:LEU:H	1:199:A:THR:H	18	0.44
(3,125)	1:245:A:ARG:H	1:106:A:GLU:H	1	0.44
(3,23)	1:138:A:ASP:H	1:140:A:LEU:H	9	0.44
(1,109)	1:146:A:PHE:H	1:146:A:PHE:HB3	18	0.44
(1,64)	1:60:A:LEU:HB2	1:172:A:SER:HB3	11	0.44
(1,51)	1:114:A:TYR:HB2	1:105:A:SER:HB2	3	0.44
(4,1316)	1:205:A:CYS:H	1:206:A:VAL:HG23	15	0.43
(4,1228)	1:152:A:ALA:H	1:152:A:ALA:HB3	5	0.43
(4,1227)	1:257:A:ALA:H	1:257:A:ALA:HB3	12	0.43
(4,1214)	1:89:A:ARG:H	1:89:A:ARG:HB2	20	0.43
(4,1192)	1:251:A:LYS:H	1:250:A:LEU:HB3	17	0.43
(4,1176)	1:234:A:GLY:H	1:233:A:GLU:HB3	12	0.43
(4,1051)	1:57:A:LEU:H	1:57:A:LEU:HB3	7	0.43

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1051)	1:57:A:LEU:H	1:57:A:LEU:HB3	10	0.43
(4,1021)	1:193:A:TYR:H	1:208:A:TRP:HB3	19	0.43
(4,1005)	1:175:A:PHE:H	1:175:A:PHE:HB3	12	0.43
(4,1003)	1:133:A:ALA:H	1:127:A:TYR:HB3	4	0.43
(4,857)	1:135:A:GLN:H	1:135:A:GLN:HA	13	0.43
(4,857)	1:135:A:GLN:H	1:135:A:GLN:HA	20	0.43
(4,852)	1:160:A:VAL:H	1:160:A:VAL:HA	3	0.43
(4,852)	1:160:A:VAL:H	1:160:A:VAL:HA	6	0.43
(4,852)	1:160:A:VAL:H	1:160:A:VAL:HA	16	0.43
(4,852)	1:160:A:VAL:H	1:160:A:VAL:HA	17	0.43
(4,828)	1:160:A:VAL:H	1:160:A:VAL:HA	16	0.43
(4,828)	1:205:A:CYS:H	1:205:A:CYS:HA	17	0.43
(4,705)	1:64:A:HIS:H	1:64:A:HIS:HA	19	0.43
(4,666)	1:226:A:ARG:H	1:222:A:VAL:H	1	0.43
(4,451)	1:239:A:LEU:HB3	1:239:A:LEU:HD23	3	0.43
(4,412)	1:23:A:ALA:HB1	1:17:A:HIS:HA	9	0.43
(4,411)	1:23:A:ALA:HB1	1:17:A:HIS:HA	9	0.43
(4,409)	1:192:A:THR:HG22	1:257:A:ALA:HA	7	0.43
(4,380)	1:74:A:GLN:HA	1:74:A:GLN:HB3	4	0.43
(4,380)	1:74:A:GLN:HA	1:74:A:GLN:HB3	6	0.43
(4,380)	1:100:A:LEU:HB3	1:100:A:LEU:HA	17	0.43
(4,371)	1:146:A:PHE:HB3	1:114:A:TYR:HB2	4	0.43
(4,365)	1:259:A:PHE:HB2	1:259:A:PHE:HA	4	0.43
(4,365)	1:122:A:HIS:HB2	1:122:A:HIS:HA	6	0.43
(4,365)	1:85:A:ASP:HB2	1:85:A:ASP:HA	16	0.43
(4,252)	1:40:A:TYR:HB3	1:259:A:PHE:H	13	0.43
(4,232)	1:34:A:ASP:H	1:34:A:ASP:HB2	1	0.43
(4,232)	1:34:A:ASP:H	1:34:A:ASP:HB2	10	0.43
(4,232)	1:34:A:ASP:H	1:34:A:ASP:HB2	20	0.43
(4,224)	1:159:A:VAL:H	1:159:A:VAL:HA	13	0.43
(4,219)	1:105:A:SER:H	1:105:A:SER:HB3	12	0.43
(4,215)	1:242:A:ASP:H	1:241:A:VAL:HA	14	0.43
(4,182)	1:166:A:ILE:H	1:163:A:LEU:HA	7	0.43
(4,132)	1:93:A:PHE:H	1:93:A:PHE:HB3	10	0.43
(4,118)	1:165:A:SER:H	1:163:A:LEU:HA	19	0.43
(4,88)	1:210:A:VAL:H	1:192:A:THR:HB	17	0.43
(4,87)	1:234:A:GLY:H	1:233:A:GLU:HB2	1	0.43
(4,34)	1:59:A:ILE:H	1:166:A:ILE:HG23	13	0.43
(3,290)	1:196:A:SER:H	1:206:A:VAL:H	16	0.43
(3,284)	1:48:A:SER:H	1:82:A:GLY:H	4	0.43
(3,252)	1:196:A:SER:H	1:206:A:VAL:H	16	0.43
(3,222)	1:197:A:LEU:H	1:205:A:CYS:H	10	0.43

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,163)	1:205:A:CYS:H	1:197:A:LEU:H	10	0.43
(3,160)	1:205:A:CYS:H	1:197:A:LEU:H	10	0.43
(3,79)	1:192:A:THR:H	1:256:A:LYS:H	10	0.43
(3,71)	1:138:A:ASP:H	1:140:A:LEU:H	3	0.43
(3,17)	1:169:A:LYS:H	1:63:A:GLY:H	17	0.43
(3,9)	1:256:A:LYS:H	1:192:A:THR:H	10	0.43
(1,106)	1:226:A:ARG:H	1:225:A:PHE:HB2	10	0.43
(1,106)	1:226:A:ARG:H	1:225:A:PHE:HB2	13	0.43
(1,47)	1:240:A:MET:HA	1:230:A:PHE:HA	3	0.43
(1,28)	1:241:A:VAL:H	1:240:A:MET:HA	1	0.43
(4,1322)	1:203:A:LEU:H	1:203:A:LEU:HD22	6	0.42
(4,1308)	1:212:A:LYS:H	1:211:A:LEU:HD22	8	0.42
(4,1279)	1:211:A:LEU:H	1:211:A:LEU:HG	5	0.42
(4,1243)	1:247:A:ALA:H	1:247:A:ALA:HB2	15	0.42
(4,1200)	1:251:A:LYS:H	1:251:A:LYS:HG2	8	0.42
(4,1147)	1:231:A:ASN:H	1:169:A:LYS:HD3	1	0.42
(4,1123)	1:218:A:SER:H	1:221:A:GLN:HB2	11	0.42
(4,1083)	1:237:A:GLU:H	1:237:A:GLU:HB2	18	0.42
(4,1022)	1:133:A:ALA:H	1:127:A:TYR:HB3	3	0.42
(4,1012)	1:18:A:LYS:H	1:17:A:HIS:HB2	16	0.42
(4,974)	1:40:A:TYR:H	1:40:A:TYR:HB3	17	0.42
(4,857)	1:135:A:GLN:H	1:135:A:GLN:HA	6	0.42
(4,852)	1:160:A:VAL:H	1:160:A:VAL:HA	4	0.42
(4,828)	1:160:A:VAL:H	1:160:A:VAL:HA	4	0.42
(4,723)	1:227:A:LYS:H	1:227:A:LYS:HA	4	0.42
(4,723)	1:24:A:LYS:H	1:24:A:LYS:HA	7	0.42
(4,723)	1:222:A:VAL:H	1:222:A:VAL:HA	13	0.42
(4,475)	1:73:A:SER:H	1:72:A:ASP:H	18	0.42
(4,460)	1:169:A:LYS:HA	1:169:A:LYS:HG2	10	0.42
(4,457)	1:80:A:LYS:HB2	1:80:A:LYS:HG3	18	0.42
(4,451)	1:183:A:LEU:HB3	1:183:A:LEU:HD21	13	0.42
(4,451)	1:183:A:LEU:HB3	1:183:A:LEU:HD23	20	0.42
(4,450)	1:147:A:LEU:HA	1:147:A:LEU:HD22	17	0.42
(4,445)	1:76:A:LYS:HB2	1:76:A:LYS:HD2	3	0.42
(4,421)	1:181:A:ARG:HA	1:181:A:ARG:HB3	15	0.42
(4,411)	1:23:A:ALA:HB2	1:17:A:HIS:HA	5	0.42
(4,393)	1:63:A:GLY:HA2	1:169:A:LYS:HB2	13	0.42
(4,380)	1:74:A:GLN:HA	1:74:A:GLN:HB3	1	0.42
(4,380)	1:122:A:HIS:HB3	1:122:A:HIS:HA	5	0.42
(4,380)	1:122:A:HIS:HB3	1:122:A:HIS:HA	19	0.42
(4,371)	1:22:A:ILE:HB	1:20:A:PHE:HB3	12	0.42
(4,365)	1:259:A:PHE:HB2	1:259:A:PHE:HA	18	0.42

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,232)	1:34:A:ASP:H	1:34:A:ASP:HB2	9	0.42
(4,232)	1:259:A:PHE:H	1:259:A:PHE:HB3	18	0.42
(4,231)	1:226:A:ARG:H	1:226:A:ARG:HB2	5	0.42
(4,224)	1:159:A:VAL:H	1:159:A:VAL:HA	1	0.42
(4,224)	1:159:A:VAL:H	1:159:A:VAL:HA	19	0.42
(4,215)	1:242:A:ASP:H	1:241:A:VAL:HA	17	0.42
(4,189)	1:37:A:THR:H	1:34:A:ASP:HB2	3	0.42
(4,165)	1:260:A:LYS:H	1:260:A:LYS:HA	17	0.42
(1,114)	1:66:A:PHE:H	1:65:A:ALA:HB1	13	0.42
(1,49)	1:224:A:LYS:HG2	1:224:A:LYS:HA	17	0.42
(4,1289)	1:203:A:LEU:H	1:22:A:ILE:HD13	7	0.41
(4,1228)	1:152:A:ALA:H	1:152:A:ALA:HB2	18	0.41
(4,1223)	1:152:A:ALA:H	1:152:A:ALA:HB3	5	0.41
(4,1223)	1:152:A:ALA:H	1:152:A:ALA:HB1	19	0.41
(4,1217)	1:74:A:GLN:H	1:76:A:LYS:HD3	20	0.41
(4,1214)	1:89:A:ARG:H	1:89:A:ARG:HB2	4	0.41
(4,1192)	1:251:A:LYS:H	1:251:A:LYS:HG2	8	0.41
(4,1114)	1:84:A:LEU:H	1:84:A:LEU:HB3	6	0.41
(4,998)	1:175:A:PHE:H	1:174:A:ASP:HB3	4	0.41
(4,989)	1:179:A:ASP:H	1:179:A:ASP:HB3	15	0.41
(4,857)	1:224:A:LYS:H	1:224:A:LYS:HA	8	0.41
(4,852)	1:160:A:VAL:H	1:160:A:VAL:HA	15	0.41
(4,828)	1:205:A:CYS:H	1:205:A:CYS:HA	7	0.41
(4,828)	1:160:A:VAL:H	1:160:A:VAL:HA	15	0.41
(4,789)	1:9:A:LYS:H	1:8:A:GLY:HA2	1	0.41
(4,789)	1:106:A:GLU:H	1:105:A:SER:HA	3	0.41
(4,723)	1:24:A:LYS:H	1:24:A:LYS:HA	1	0.41
(4,723)	1:227:A:LYS:H	1:227:A:LYS:HA	3	0.41
(4,723)	1:227:A:LYS:H	1:227:A:LYS:HA	17	0.41
(4,723)	1:19:A:ASP:H	1:19:A:ASP:HA	18	0.41
(4,469)	1:140:A:LEU:HB3	1:134:A:VAL:HG23	1	0.41
(4,451)	1:183:A:LEU:HB3	1:183:A:LEU:HD22	9	0.41
(4,421)	1:167:A:LYS:HA	1:167:A:LYS:HB2	2	0.41
(4,421)	1:181:A:ARG:HA	1:181:A:ARG:HB3	3	0.41
(4,421)	1:167:A:LYS:HA	1:167:A:LYS:HB2	4	0.41
(4,421)	1:147:A:LEU:HA	1:147:A:LEU:HB3	5	0.41
(4,421)	1:167:A:LYS:HA	1:167:A:LYS:HB2	12	0.41
(4,414)	1:163:A:LEU:HB2	1:163:A:LEU:HA	9	0.41
(4,412)	1:23:A:ALA:HB2	1:17:A:HIS:HA	5	0.41
(4,406)	1:133:A:ALA:HB3	1:130:A:PHE:HA	17	0.41
(4,365)	1:85:A:ASP:HB3	1:85:A:ASP:HA	3	0.41
(4,365)	1:259:A:PHE:HB2	1:259:A:PHE:HA	9	0.41

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,365)	1:53:A:GLN:HB3	1:53:A:GLN:HA	12	0.41
(4,365)	1:259:A:PHE:HB2	1:259:A:PHE:HA	13	0.41
(4,224)	1:160:A:VAL:H	1:160:A:VAL:HA	15	0.41
(4,202)	1:37:A:THR:H	1:34:A:ASP:HB2	3	0.41
(4,202)	1:34:A:ASP:H	1:34:A:ASP:HB2	16	0.41
(4,189)	1:34:A:ASP:H	1:34:A:ASP:HB2	1	0.41
(4,189)	1:74:A:GLN:H	1:76:A:LYS:HE3	16	0.41
(4,182)	1:166:A:ILE:H	1:163:A:LEU:HA	18	0.41
(4,167)	1:32:A:ASP:H	1:32:A:ASP:HB3	1	0.41
(4,165)	1:260:A:LYS:H	1:260:A:LYS:HA	19	0.41
(4,132)	1:93:A:PHE:H	1:93:A:PHE:HB3	2	0.41
(4,132)	1:93:A:PHE:H	1:93:A:PHE:HB3	9	0.41
(4,118)	1:165:A:SER:H	1:163:A:LEU:HA	9	0.41
(4,118)	1:165:A:SER:H	1:163:A:LEU:HA	14	0.41
(4,100)	1:141:A:ALA:H	1:140:A:LEU:HB2	13	0.41
(4,43)	1:95:A:PHE:H	1:95:A:PHE:HB3	9	0.41
(4,42)	1:38:A:ALA:HA	1:255:A:ILE:H	10	0.41
(3,158)	1:57:A:LEU:H	1:70:A:PHE:H	16	0.41
(3,67)	1:169:A:LYS:H	1:229:A:ASN:H	7	0.41
(3,67)	1:169:A:LYS:H	1:229:A:ASN:H	19	0.41
(1,114)	1:66:A:PHE:H	1:65:A:ALA:HB2	1	0.41
(1,103)	1:118:A:LEU:H	1:118:A:LEU:HB3	4	0.41
(1,45)	1:225:A:PHE:HB3	1:222:A:VAL:HA	12	0.41
(4,1316)	1:165:A:SER:H	1:166:A:ILE:HD13	4	0.4
(4,1242)	1:247:A:ALA:H	1:247:A:ALA:HB3	10	0.4
(4,1227)	1:90:A:LEU:H	1:90:A:LEU:HB2	4	0.4
(4,1172)	1:239:A:LEU:H	1:239:A:LEU:HB3	12	0.4
(4,1110)	1:23:A:ALA:H	1:23:A:ALA:HB1	13	0.4
(4,1051)	1:57:A:LEU:H	1:57:A:LEU:HB2	19	0.4
(4,1021)	1:133:A:ALA:H	1:127:A:TYR:HB3	3	0.4
(4,1006)	1:79:A:LEU:H	1:88:A:TYR:HB2	14	0.4
(4,1005)	1:175:A:PHE:H	1:174:A:ASP:HB3	4	0.4
(4,970)	1:88:A:TYR:H	1:88:A:TYR:HB3	6	0.4
(4,964)	1:52:A:ASP:H	1:52:A:ASP:HB2	18	0.4
(4,857)	1:135:A:GLN:H	1:135:A:GLN:HA	2	0.4
(4,857)	1:135:A:GLN:H	1:135:A:GLN:HA	3	0.4
(4,857)	1:135:A:GLN:H	1:135:A:GLN:HA	4	0.4
(4,857)	1:241:A:VAL:H	1:241:A:VAL:HA	5	0.4
(4,857)	1:135:A:GLN:H	1:135:A:GLN:HA	9	0.4
(4,857)	1:135:A:GLN:H	1:135:A:GLN:HA	11	0.4
(4,857)	1:135:A:GLN:H	1:135:A:GLN:HA	12	0.4
(4,857)	1:135:A:GLN:H	1:135:A:GLN:HA	14	0.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,857)	1:135:A:GLN:H	1:135:A:GLN:HA	15	0.4
(4,857)	1:135:A:GLN:H	1:135:A:GLN:HA	16	0.4
(4,857)	1:224:A:LYS:H	1:224:A:LYS:HA	17	0.4
(4,857)	1:135:A:GLN:H	1:135:A:GLN:HA	18	0.4
(4,857)	1:135:A:GLN:H	1:135:A:GLN:HA	19	0.4
(4,852)	1:160:A:VAL:H	1:160:A:VAL:HA	2	0.4
(4,852)	1:160:A:VAL:H	1:160:A:VAL:HA	8	0.4
(4,828)	1:160:A:VAL:H	1:160:A:VAL:HA	8	0.4
(4,828)	1:205:A:CYS:H	1:205:A:CYS:HA	9	0.4
(4,723)	1:227:A:LYS:H	1:227:A:LYS:HA	2	0.4
(4,723)	1:227:A:LYS:H	1:227:A:LYS:HA	5	0.4
(4,723)	1:227:A:LYS:H	1:227:A:LYS:HA	6	0.4
(4,723)	1:227:A:LYS:H	1:227:A:LYS:HA	8	0.4
(4,723)	1:227:A:LYS:H	1:227:A:LYS:HA	9	0.4
(4,723)	1:24:A:LYS:H	1:24:A:LYS:HA	10	0.4
(4,723)	1:24:A:LYS:H	1:24:A:LYS:HA	11	0.4
(4,723)	1:227:A:LYS:H	1:227:A:LYS:HA	12	0.4
(4,723)	1:227:A:LYS:H	1:227:A:LYS:HA	16	0.4
(4,723)	1:24:A:LYS:H	1:24:A:LYS:HA	20	0.4
(4,705)	1:64:A:HIS:H	1:64:A:HIS:HA	7	0.4
(4,664)	1:54:A:ALA:H	1:51:A:TYR:HA	13	0.4
(4,654)	1:199:A:THR:H	1:202:A:LEU:H	11	0.4
(4,650)	1:199:A:THR:H	1:202:A:LEU:H	11	0.4
(4,460)	1:169:A:LYS:HA	1:169:A:LYS:HG3	3	0.4
(4,458)	1:212:A:LYS:HB2	1:212:A:LYS:HG3	19	0.4
(4,451)	1:239:A:LEU:HB3	1:239:A:LEU:HD22	16	0.4
(4,437)	1:35:A:THR:HG23	1:35:A:THR:HB	1	0.4
(4,437)	1:199:A:THR:HB	1:199:A:THR:HG21	4	0.4
(4,437)	1:199:A:THR:HB	1:199:A:THR:HG23	6	0.4
(4,437)	1:199:A:THR:HB	1:199:A:THR:HG21	8	0.4
(4,437)	1:35:A:THR:HG21	1:35:A:THR:HB	11	0.4
(4,437)	1:199:A:THR:HB	1:199:A:THR:HG22	19	0.4
(4,421)	1:181:A:ARG:HA	1:181:A:ARG:HB3	1	0.4
(4,421)	1:147:A:LEU:HA	1:147:A:LEU:HB3	16	0.4
(4,419)	1:94:A:HIS:HB2	1:65:A:ALA:HB3	8	0.4
(4,419)	1:203:A:LEU:HB2	1:205:A:CYS:HB3	14	0.4
(4,418)	1:163:A:LEU:HB2	1:163:A:LEU:HA	9	0.4
(4,380)	1:100:A:LEU:HB3	1:100:A:LEU:HA	10	0.4
(4,365)	1:85:A:ASP:HB3	1:85:A:ASP:HA	10	0.4
(4,365)	1:122:A:HIS:HB2	1:122:A:HIS:HA	11	0.4
(4,365)	1:122:A:HIS:HB3	1:122:A:HIS:HA	14	0.4
(4,365)	1:259:A:PHE:HB2	1:259:A:PHE:HA	17	0.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,365)	1:32:A:ASP:HB2	1:32:A:ASP:HA	20	0.4
(4,224)	1:160:A:VAL:H	1:160:A:VAL:HA	8	0.4
(4,215)	1:242:A:ASP:H	1:241:A:VAL:HA	6	0.4
(4,204)	1:100:A:LEU:H	1:100:A:LEU:HG	4	0.4
(4,189)	1:34:A:ASP:H	1:34:A:ASP:HB2	9	0.4
(4,182)	1:166:A:ILE:H	1:163:A:LEU:HA	1	0.4
(4,182)	1:166:A:ILE:H	1:163:A:LEU:HA	2	0.4
(4,165)	1:260:A:LYS:H	1:260:A:LYS:HA	15	0.4
(3,318)	1:171:A:LYS:H	1:168:A:THR:H	3	0.4
(3,306)	1:156:A:LEU:H	1:159:A:VAL:H	9	0.4
(3,255)	1:147:A:LEU:H	1:115:A:ALA:H	9	0.4
(3,251)	1:242:A:ASP:H	1:100:A:LEU:H	10	0.4
(3,125)	1:245:A:ARG:H	1:106:A:GLU:H	8	0.4
(3,47)	1:60:A:LEU:H	1:67:A:ASN:H	13	0.4
(3,15)	1:243:A:ASN:H	1:97:A:TRP:H	10	0.4
(1,132)	1:135:A:GLN:H	1:134:A:VAL:HG22	9	0.4
(1,76)	1:115:A:ALA:HB2	1:149:A:VAL:HG23	18	0.4
(1,20)	1:197:A:LEU:H	1:197:A:LEU:HB2	8	0.4
(4,1325)	1:59:A:ILE:H	1:166:A:ILE:HD13	19	0.39
(4,1314)	1:55:A:THR:H	1:76:A:LYS:HG3	13	0.39
(4,1281)	1:163:A:LEU:H	1:163:A:LEU:HD23	4	0.39
(4,1228)	1:152:A:ALA:H	1:152:A:ALA:HB1	14	0.39
(4,1225)	1:164:A:ASP:H	1:163:A:LEU:HG	11	0.39
(4,1223)	1:152:A:ALA:H	1:152:A:ALA:HB2	18	0.39
(4,1160)	1:135:A:GLN:H	1:135:A:GLN:HB2	6	0.39
(4,1160)	1:224:A:LYS:H	1:224:A:LYS:HG3	9	0.39
(4,1147)	1:99:A:SER:H	1:100:A:LEU:HG	17	0.39
(4,1139)	1:211:A:LEU:H	1:211:A:LEU:HB2	19	0.39
(4,1125)	1:223:A:LEU:H	1:223:A:LEU:HB2	20	0.39
(4,1121)	1:9:A:LYS:H	1:9:A:LYS:HB2	16	0.39
(4,1114)	1:223:A:LEU:H	1:223:A:LEU:HB2	5	0.39
(4,1063)	1:8:A:GLY:H	1:7:A:TYR:HB3	7	0.39
(4,1024)	1:22:A:ILE:H	1:20:A:PHE:HB3	10	0.39
(4,1024)	1:22:A:ILE:H	1:20:A:PHE:HB2	16	0.39
(4,1016)	1:43:A:SER:H	1:41:A:ASP:HB3	16	0.39
(4,989)	1:179:A:ASP:H	1:179:A:ASP:HB3	11	0.39
(4,983)	1:119:A:HIS:H	1:119:A:HIS:HB2	8	0.39
(4,983)	1:68:A:VAL:H	1:67:A:ASN:HB3	15	0.39
(4,723)	1:227:A:LYS:H	1:227:A:LYS:HA	14	0.39
(4,723)	1:227:A:LYS:H	1:227:A:LYS:HA	19	0.39
(4,705)	1:64:A:HIS:H	1:64:A:HIS:HA	4	0.39
(4,703)	1:112:A:LYS:H	1:112:A:LYS:HA	12	0.39

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,666)	1:226:A:ARG:H	1:222:A:VAL:H	9	0.39
(4,557)	1:162:A:VAL:H	1:161:A:ASP:H	15	0.39
(4,463)	1:174:A:ASP:HA	1:176:A:THR:HG23	12	0.39
(4,458)	1:169:A:LYS:HB3	1:169:A:LYS:HG2	7	0.39
(4,451)	1:183:A:LEU:HB3	1:183:A:LEU:HD23	19	0.39
(4,437)	1:199:A:THR:HB	1:199:A:THR:HG22	12	0.39
(4,437)	1:199:A:THR:HB	1:199:A:THR:HG22	13	0.39
(4,437)	1:199:A:THR:HB	1:199:A:THR:HG23	14	0.39
(4,437)	1:35:A:THR:HG22	1:35:A:THR:HB	18	0.39
(4,437)	1:35:A:THR:HG22	1:35:A:THR:HB	20	0.39
(4,421)	1:181:A:ARG:HA	1:181:A:ARG:HB3	14	0.39
(4,421)	1:167:A:LYS:HA	1:167:A:LYS:HG3	20	0.39
(4,379)	1:260:A:LYS:HG3	1:260:A:LYS:HE2	12	0.39
(4,371)	1:146:A:PHE:HB3	1:114:A:TYR:HB2	13	0.39
(4,365)	1:122:A:HIS:HB3	1:122:A:HIS:HA	2	0.39
(4,365)	1:122:A:HIS:HB3	1:122:A:HIS:HA	7	0.39
(4,232)	1:259:A:PHE:H	1:259:A:PHE:HB3	8	0.39
(4,224)	1:159:A:VAL:H	1:159:A:VAL:HA	10	0.39
(4,204)	1:100:A:LEU:H	1:100:A:LEU:HG	13	0.39
(4,202)	1:34:A:ASP:H	1:34:A:ASP:HB2	1	0.39
(4,202)	1:34:A:ASP:H	1:34:A:ASP:HB2	20	0.39
(4,165)	1:260:A:LYS:H	1:260:A:LYS:HA	8	0.39
(4,165)	1:260:A:LYS:H	1:260:A:LYS:HA	12	0.39
(4,96)	1:140:A:LEU:H	1:205:A:CYS:HB3	15	0.39
(4,87)	1:181:A:ARG:H	1:181:A:ARG:HB2	16	0.39
(3,204)	1:9:A:LYS:H	1:12:A:GLY:H	10	0.39
(3,195)	1:9:A:LYS:H	1:12:A:GLY:H	10	0.39
(3,176)	1:129:A:ASP:H	1:133:A:ALA:H	12	0.39
(3,110)	1:12:A:GLY:H	1:8:A:GLY:H	13	0.39
(3,79)	1:192:A:THR:H	1:256:A:LYS:H	12	0.39
(3,9)	1:256:A:LYS:H	1:192:A:THR:H	12	0.39
(1,7)	1:59:A:ILE:H	1:166:A:ILE:HD13	19	0.39
(4,1264)	1:204:A:GLU:H	1:22:A:ILE:HD13	3	0.38
(4,1227)	1:90:A:LEU:H	1:90:A:LEU:HB2	7	0.38
(4,1227)	1:91:A:ILE:H	1:91:A:ILE:HG13	8	0.38
(4,1227)	1:23:A:ALA:H	1:22:A:ILE:HG22	16	0.38
(4,1227)	1:90:A:LEU:H	1:90:A:LEU:HB2	19	0.38
(4,1214)	1:233:A:GLU:H	1:233:A:GLU:HB3	6	0.38
(4,1172)	1:239:A:LEU:H	1:239:A:LEU:HB3	15	0.38
(4,1164)	1:167:A:LYS:H	1:167:A:LYS:HB3	13	0.38
(4,1160)	1:224:A:LYS:H	1:224:A:LYS:HB2	14	0.38
(4,1135)	1:221:A:GLN:H	1:221:A:GLN:HB3	18	0.38

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1129)	1:195:A:GLY:H	1:207:A:THR:HG22	18	0.38
(4,1102)	1:140:A:LEU:H	1:140:A:LEU:HB3	3	0.38
(4,1003)	1:133:A:ALA:H	1:127:A:TYR:HB3	3	0.38
(4,1003)	1:126:A:LYS:H	1:124:A:ASN:HB3	13	0.38
(4,951)	1:252:A:ASN:H	1:252:A:ASN:HB3	12	0.38
(4,939)	1:119:A:HIS:H	1:118:A:LEU:HB3	17	0.38
(4,903)	1:49:A:VAL:H	1:49:A:VAL:HA	3	0.38
(4,903)	1:49:A:VAL:H	1:49:A:VAL:HA	14	0.38
(4,903)	1:49:A:VAL:H	1:49:A:VAL:HA	20	0.38
(4,857)	1:241:A:VAL:H	1:241:A:VAL:HA	1	0.38
(4,828)	1:205:A:CYS:H	1:204:A:GLU:HA	14	0.38
(4,789)	1:9:A:LYS:H	1:8:A:GLY:HA2	19	0.38
(4,742)	1:71:A:ASP:H	1:70:A:PHE:HA	19	0.38
(4,705)	1:29:A:SER:H	1:29:A:SER:HA	12	0.38
(4,705)	1:29:A:SER:H	1:29:A:SER:HA	16	0.38
(4,677)	1:173:A:ALA:H	1:173:A:ALA:HA	3	0.38
(4,460)	1:169:A:LYS:HA	1:169:A:LYS:HG3	18	0.38
(4,458)	1:224:A:LYS:HB2	1:224:A:LYS:HD3	6	0.38
(4,451)	1:183:A:LEU:HB3	1:183:A:LEU:HD23	10	0.38
(4,451)	1:203:A:LEU:HB3	1:203:A:LEU:HD22	15	0.38
(4,439)	1:260:A:LYS:HA	1:260:A:LYS:HG2	12	0.38
(4,437)	1:35:A:THR:HG22	1:35:A:THR:HB	2	0.38
(4,437)	1:199:A:THR:HB	1:199:A:THR:HG21	3	0.38
(4,437)	1:35:A:THR:HG23	1:35:A:THR:HB	5	0.38
(4,437)	1:35:A:THR:HG23	1:35:A:THR:HB	7	0.38
(4,437)	1:35:A:THR:HG23	1:35:A:THR:HB	15	0.38
(4,437)	1:35:A:THR:HG23	1:35:A:THR:HB	16	0.38
(4,437)	1:35:A:THR:HG23	1:35:A:THR:HB	17	0.38
(4,421)	1:167:A:LYS:HA	1:167:A:LYS:HB3	8	0.38
(4,421)	1:167:A:LYS:HA	1:167:A:LYS:HB3	18	0.38
(4,421)	1:181:A:ARG:HA	1:181:A:ARG:HB3	19	0.38
(4,408)	1:219:A:SER:HA	1:222:A:VAL:HB	14	0.38
(4,382)	1:193:A:TYR:HB3	1:208:A:TRP:HB3	15	0.38
(4,379)	1:260:A:LYS:HG3	1:260:A:LYS:HE2	3	0.38
(4,371)	1:22:A:ILE:HB	1:20:A:PHE:HB3	3	0.38
(4,365)	1:122:A:HIS:HB3	1:122:A:HIS:HA	1	0.38
(4,365)	1:259:A:PHE:HB2	1:259:A:PHE:HA	8	0.38
(4,273)	1:113:A:LYS:HD3	1:244:A:TRP:HA	4	0.38
(4,232)	1:34:A:ASP:H	1:34:A:ASP:HB2	13	0.38
(4,232)	1:34:A:ASP:H	1:34:A:ASP:HB2	14	0.38
(4,231)	1:226:A:ARG:H	1:226:A:ARG:HB2	12	0.38
(4,215)	1:242:A:ASP:H	1:241:A:VAL:HA	8	0.38

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,213)	1:167:A:LYS:H	1:167:A:LYS:HB3	18	0.38
(4,202)	1:34:A:ASP:H	1:34:A:ASP:HB2	9	0.38
(4,189)	1:37:A:THR:H	1:34:A:ASP:HB2	4	0.38
(4,182)	1:165:A:SER:H	1:163:A:LEU:HA	10	0.38
(4,165)	1:260:A:LYS:H	1:260:A:LYS:HA	6	0.38
(4,97)	1:204:A:GLU:H	1:202:A:LEU:HA	16	0.38
(3,323)	1:181:A:ARG:H	1:184:A:LEU:H	16	0.38
(3,305)	1:166:A:ILE:H	1:168:A:THR:H	5	0.38
(3,282)	1:202:A:LEU:H	1:199:A:THR:H	17	0.38
(3,120)	1:248:A:GLN:H	1:32:A:ASP:H	2	0.38
(3,79)	1:192:A:THR:H	1:256:A:LYS:H	2	0.38
(3,14)	1:147:A:LEU:H	1:117:A:GLU:H	4	0.38
(3,9)	1:256:A:LYS:H	1:192:A:THR:H	2	0.38
(1,100)	1:245:A:ARG:H	1:244:A:TRP:HB2	11	0.38
(1,73)	1:134:A:VAL:HG23	1:131:A:GLY:HA2	19	0.38
(4,1228)	1:152:A:ALA:H	1:152:A:ALA:HB3	17	0.37
(4,1225)	1:164:A:ASP:H	1:163:A:LEU:HG	10	0.37
(4,1214)	1:248:A:GLN:H	1:247:A:ALA:HB1	18	0.37
(4,1205)	1:231:A:ASN:H	1:169:A:LYS:HD3	1	0.37
(4,1191)	1:9:A:LYS:H	1:9:A:LYS:HB3	10	0.37
(4,1129)	1:195:A:GLY:H	1:207:A:THR:HG22	3	0.37
(4,1128)	1:251:A:LYS:H	1:250:A:LEU:HB3	18	0.37
(4,1125)	1:248:A:GLN:H	1:248:A:GLN:HB3	5	0.37
(4,1121)	1:48:A:SER:H	1:47:A:LEU:HB2	18	0.37
(4,1083)	1:69:A:GLU:H	1:69:A:GLU:HB2	7	0.37
(4,1075)	1:164:A:ASP:H	1:164:A:ASP:HB2	8	0.37
(4,1006)	1:79:A:LEU:H	1:88:A:TYR:HB2	5	0.37
(4,988)	1:205:A:CYS:H	1:205:A:CYS:HB3	19	0.37
(4,957)	1:191:A:TRP:H	1:191:A:TRP:HB3	11	0.37
(4,947)	1:129:A:ASP:H	1:127:A:TYR:HB2	15	0.37
(4,939)	1:119:A:HIS:H	1:118:A:LEU:HB3	18	0.37
(4,922)	1:119:A:HIS:H	1:118:A:LEU:HB3	2	0.37
(4,903)	1:49:A:VAL:H	1:49:A:VAL:HA	19	0.37
(4,857)	1:224:A:LYS:H	1:224:A:LYS:HA	7	0.37
(4,836)	1:166:A:ILE:H	1:165:A:SER:HB3	6	0.37
(4,705)	1:64:A:HIS:H	1:64:A:HIS:HA	6	0.37
(4,677)	1:173:A:ALA:H	1:173:A:ALA:HA	15	0.37
(4,669)	1:29:A:SER:H	1:198:A:THR:HG1	5	0.37
(4,668)	1:29:A:SER:H	1:198:A:THR:HG1	5	0.37
(4,666)	1:226:A:ARG:H	1:222:A:VAL:H	10	0.37
(4,664)	1:54:A:ALA:H	1:51:A:TYR:HA	8	0.37
(4,451)	1:203:A:LEU:HB3	1:203:A:LEU:HD21	1	0.37

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,437)	1:35:A:THR:HG22	1:35:A:THR:HB	9	0.37
(4,412)	1:23:A:ALA:HB1	1:17:A:HIS:HA	8	0.37
(4,411)	1:23:A:ALA:HB1	1:17:A:HIS:HA	8	0.37
(4,409)	1:192:A:THR:HG21	1:257:A:ALA:HA	17	0.37
(4,379)	1:260:A:LYS:HG3	1:260:A:LYS:HE3	2	0.37
(4,379)	1:260:A:LYS:HG3	1:260:A:LYS:HE2	5	0.37
(4,379)	1:260:A:LYS:HG3	1:260:A:LYS:HE2	20	0.37
(4,374)	1:127:A:TYR:HB3	1:133:A:ALA:HA	9	0.37
(4,356)	1:153:A:LYS:HD2	1:224:A:LYS:HE3	7	0.37
(4,332)	1:22:A:ILE:HD12	1:204:A:GLU:HA	4	0.37
(4,238)	1:92:A:GLN:H	1:92:A:GLN:HA	3	0.37
(4,232)	1:34:A:ASP:H	1:34:A:ASP:HB2	11	0.37
(4,232)	1:34:A:ASP:H	1:34:A:ASP:HB2	19	0.37
(4,202)	1:37:A:THR:H	1:34:A:ASP:HB2	4	0.37
(4,165)	1:260:A:LYS:H	1:260:A:LYS:HA	10	0.37
(4,132)	1:93:A:PHE:H	1:93:A:PHE:HB3	17	0.37
(4,118)	1:165:A:SER:H	1:163:A:LEU:HA	11	0.37
(4,112)	1:181:A:ARG:H	1:181:A:ARG:HA	15	0.37
(4,112)	1:181:A:ARG:H	1:181:A:ARG:HA	17	0.37
(4,112)	1:73:A:SER:H	1:73:A:SER:HA	20	0.37
(3,264)	1:240:A:MET:H	1:228:A:LEU:H	16	0.37
(3,226)	1:231:A:ASN:H	1:169:A:LYS:H	7	0.37
(3,210)	1:197:A:LEU:H	1:205:A:CYS:H	19	0.37
(3,173)	1:57:A:LEU:H	1:175:A:PHE:H	11	0.37
(2,24)	1:118:A:LEU:H	1:147:A:LEU:HG	12	0.37
(2,2)	1:97:A:TRP:H	1:241:A:VAL:HA	18	0.37
(1,132)	1:135:A:GLN:H	1:134:A:VAL:HG22	19	0.37
(1,106)	1:226:A:ARG:H	1:225:A:PHE:HB3	19	0.37
(1,78)	1:117:A:GLU:H	1:96:A:HIS:H	19	0.37
(1,73)	1:134:A:VAL:HG21	1:131:A:GLY:HA2	3	0.37
(1,57)	1:33:A:ILE:HD12	1:107:A:HIS:HB3	10	0.37
(4,1266)	1:66:A:PHE:H	1:169:A:LYS:HG3	5	0.36
(4,1214)	1:89:A:ARG:H	1:89:A:ARG:HG2	9	0.36
(4,1200)	1:251:A:LYS:H	1:250:A:LEU:HB3	3	0.36
(4,1173)	1:223:A:LEU:H	1:223:A:LEU:HB2	5	0.36
(4,1172)	1:256:A:LYS:H	1:256:A:LYS:HG3	19	0.36
(4,1168)	1:152:A:ALA:H	1:152:A:ALA:HB3	5	0.36
(4,1139)	1:211:A:LEU:H	1:211:A:LEU:HB2	5	0.36
(4,1138)	1:238:A:GLU:H	1:238:A:GLU:HB2	7	0.36
(4,1129)	1:195:A:GLY:H	1:207:A:THR:HG23	1	0.36
(4,1125)	1:233:A:GLU:H	1:233:A:GLU:HB3	6	0.36
(4,1121)	1:106:A:GLU:H	1:106:A:GLU:HB2	3	0.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1121)	1:106:A:GLU:H	1:106:A:GLU:HB3	20	0.36
(4,1107)	1:106:A:GLU:H	1:106:A:GLU:HB3	20	0.36
(4,1075)	1:28:A:GLN:H	1:28:A:GLN:HB3	20	0.36
(4,1055)	1:100:A:LEU:H	1:100:A:LEU:HB3	7	0.36
(4,1055)	1:18:A:LYS:H	1:18:A:LYS:HB2	14	0.36
(4,1051)	1:26:A:GLU:H	1:26:A:GLU:HB2	13	0.36
(4,998)	1:175:A:PHE:H	1:175:A:PHE:HB3	1	0.36
(4,998)	1:175:A:PHE:H	1:175:A:PHE:HB3	13	0.36
(4,962)	1:129:A:ASP:H	1:127:A:TYR:HB3	15	0.36
(4,915)	1:252:A:ASN:H	1:252:A:ASN:HB3	12	0.36
(4,903)	1:49:A:VAL:H	1:49:A:VAL:HA	15	0.36
(4,903)	1:49:A:VAL:H	1:49:A:VAL:HA	16	0.36
(4,903)	1:49:A:VAL:H	1:49:A:VAL:HA	17	0.36
(4,903)	1:49:A:VAL:H	1:49:A:VAL:HA	18	0.36
(4,857)	1:241:A:VAL:H	1:241:A:VAL:HA	10	0.36
(4,828)	1:205:A:CYS:H	1:205:A:CYS:HA	2	0.36
(4,828)	1:205:A:CYS:H	1:204:A:GLU:HA	19	0.36
(4,828)	1:205:A:CYS:H	1:204:A:GLU:HA	20	0.36
(4,699)	1:176:A:THR:H	1:176:A:THR:HA	1	0.36
(4,699)	1:176:A:THR:H	1:176:A:THR:HA	2	0.36
(4,699)	1:176:A:THR:H	1:176:A:THR:HA	3	0.36
(4,699)	1:176:A:THR:H	1:176:A:THR:HA	5	0.36
(4,699)	1:176:A:THR:H	1:176:A:THR:HA	16	0.36
(4,699)	1:176:A:THR:H	1:176:A:THR:HA	18	0.36
(4,677)	1:39:A:LYS:H	1:39:A:LYS:HA	12	0.36
(4,677)	1:173:A:ALA:H	1:173:A:ALA:HA	17	0.36
(4,677)	1:173:A:ALA:H	1:173:A:ALA:HA	19	0.36
(4,664)	1:54:A:ALA:H	1:51:A:TYR:HA	14	0.36
(4,557)	1:222:A:VAL:H	1:221:A:GLN:H	18	0.36
(4,456)	1:169:A:LYS:HG3	1:61:A:ASN:HB2	3	0.36
(4,421)	1:181:A:ARG:HA	1:181:A:ARG:HB3	10	0.36
(4,379)	1:260:A:LYS:HG2	1:260:A:LYS:HE2	1	0.36
(4,379)	1:260:A:LYS:HG2	1:260:A:LYS:HE3	8	0.36
(4,374)	1:127:A:TYR:HB3	1:133:A:ALA:HA	15	0.36
(4,370)	1:45:A:LYS:HG2	1:45:A:LYS:HE2	11	0.36
(4,365)	1:53:A:GLN:HB3	1:53:A:GLN:HA	15	0.36
(4,238)	1:92:A:GLN:H	1:92:A:GLN:HA	1	0.36
(4,238)	1:222:A:VAL:H	1:222:A:VAL:HA	9	0.36
(4,238)	1:222:A:VAL:H	1:222:A:VAL:HA	15	0.36
(4,189)	1:34:A:ASP:H	1:34:A:ASP:HB2	13	0.36
(4,185)	1:142:A:VAL:H	1:209:A:ILE:HD12	16	0.36
(4,167)	1:179:A:ASP:H	1:179:A:ASP:HB2	2	0.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,165)	1:260:A:LYS:H	1:260:A:LYS:HA	1	0.36
(4,165)	1:260:A:LYS:H	1:260:A:LYS:HA	2	0.36
(4,132)	1:93:A:PHE:H	1:93:A:PHE:HB3	3	0.36
(4,118)	1:165:A:SER:H	1:163:A:LEU:HA	3	0.36
(4,112)	1:73:A:SER:H	1:73:A:SER:HA	9	0.36
(4,112)	1:73:A:SER:H	1:73:A:SER:HA	19	0.36
(4,97)	1:161:A:ASP:H	1:163:A:LEU:HA	7	0.36
(4,81)	1:55:A:THR:H	1:76:A:LYS:HG3	18	0.36
(4,48)	1:202:A:LEU:H	1:202:A:LEU:HB3	7	0.36
(3,264)	1:240:A:MET:H	1:228:A:LEU:H	6	0.36
(3,237)	1:189:A:ASP:H	1:212:A:LYS:H	10	0.36
(3,205)	1:124:A:ASN:H	1:127:A:TYR:H	3	0.36
(3,141)	1:87:A:THR:H	1:125:A:THR:H	18	0.36
(3,79)	1:192:A:THR:H	1:256:A:LYS:H	11	0.36
(3,59)	1:197:A:LEU:H	1:204:A:GLU:H	8	0.36
(3,9)	1:256:A:LYS:H	1:192:A:THR:H	11	0.36
(1,123)	1:63:A:GLY:H	1:169:A:LYS:HG2	13	0.36
(1,106)	1:226:A:ARG:H	1:225:A:PHE:HB2	8	0.36
(4,1321)	1:205:A:CYS:H	1:206:A:VAL:HG23	15	0.35
(4,1316)	1:205:A:CYS:H	1:206:A:VAL:HG22	10	0.35
(4,1316)	1:165:A:SER:H	1:166:A:ILE:HD12	19	0.35
(4,1261)	1:152:A:ALA:H	1:152:A:ALA:HB2	1	0.35
(4,1242)	1:247:A:ALA:H	1:247:A:ALA:HB1	14	0.35
(4,1242)	1:247:A:ALA:H	1:247:A:ALA:HB3	20	0.35
(4,1228)	1:152:A:ALA:H	1:152:A:ALA:HB2	13	0.35
(4,1223)	1:152:A:ALA:H	1:152:A:ALA:HB3	17	0.35
(4,1218)	1:172:A:SER:H	1:171:A:LYS:HD2	1	0.35
(4,1192)	1:251:A:LYS:H	1:250:A:LEU:HB3	3	0.35
(4,1173)	1:233:A:GLU:H	1:233:A:GLU:HB3	6	0.35
(4,1125)	1:248:A:GLN:H	1:248:A:GLN:HB2	10	0.35
(4,1102)	1:140:A:LEU:H	1:140:A:LEU:HG	15	0.35
(4,1091)	1:81:A:GLY:H	1:80:A:LYS:HB3	9	0.35
(4,1086)	1:98:A:GLY:H	1:116:A:ALA:HB3	20	0.35
(4,1082)	1:251:A:LYS:H	1:251:A:LYS:HB2	13	0.35
(4,1075)	1:164:A:ASP:H	1:164:A:ASP:HB2	5	0.35
(4,1075)	1:164:A:ASP:H	1:164:A:ASP:HB2	11	0.35
(4,1075)	1:164:A:ASP:H	1:164:A:ASP:HB2	16	0.35
(4,1051)	1:26:A:GLU:H	1:26:A:GLU:HB3	8	0.35
(4,980)	1:191:A:TRP:H	1:191:A:TRP:HB2	14	0.35
(4,975)	1:133:A:ALA:H	1:133:A:ALA:HA	1	0.35
(4,975)	1:133:A:ALA:H	1:133:A:ALA:HA	19	0.35
(4,948)	1:129:A:ASP:H	1:127:A:TYR:HB2	15	0.35

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,948)	1:166:A:ILE:H	1:163:A:LEU:HA	16	0.35
(4,923)	1:243:A:ASN:H	1:243:A:ASN:HB3	18	0.35
(4,922)	1:119:A:HIS:H	1:118:A:LEU:HB3	17	0.35
(4,880)	1:224:A:LYS:H	1:224:A:LYS:HA	14	0.35
(4,805)	1:166:A:ILE:H	1:165:A:SER:HB3	6	0.35
(4,789)	1:9:A:LYS:H	1:8:A:GLY:HA2	9	0.35
(4,705)	1:29:A:SER:H	1:29:A:SER:HA	10	0.35
(4,703)	1:204:A:GLU:H	1:203:A:LEU:HA	11	0.35
(4,699)	1:176:A:THR:H	1:176:A:THR:HA	4	0.35
(4,699)	1:176:A:THR:H	1:176:A:THR:HA	6	0.35
(4,699)	1:176:A:THR:H	1:176:A:THR:HA	8	0.35
(4,699)	1:176:A:THR:H	1:176:A:THR:HA	9	0.35
(4,699)	1:176:A:THR:H	1:176:A:THR:HA	13	0.35
(4,699)	1:176:A:THR:H	1:176:A:THR:HA	14	0.35
(4,699)	1:176:A:THR:H	1:176:A:THR:HA	20	0.35
(4,421)	1:158:A:LYS:HA	1:158:A:LYS:HG3	9	0.35
(4,421)	1:147:A:LEU:HA	1:147:A:LEU:HB3	11	0.35
(4,421)	1:147:A:LEU:HA	1:147:A:LEU:HB3	17	0.35
(4,386)	1:235:A:GLU:HG3	1:232:A:GLY:HA3	18	0.35
(4,379)	1:260:A:LYS:HG2	1:260:A:LYS:HE3	11	0.35
(4,370)	1:45:A:LYS:HG2	1:45:A:LYS:HE2	2	0.35
(4,365)	1:122:A:HIS:HB3	1:122:A:HIS:HA	5	0.35
(4,365)	1:122:A:HIS:HB3	1:122:A:HIS:HA	19	0.35
(4,260)	1:203:A:LEU:H	1:203:A:LEU:HB3	2	0.35
(4,260)	1:203:A:LEU:H	1:203:A:LEU:HB2	9	0.35
(4,238)	1:222:A:VAL:H	1:222:A:VAL:HA	5	0.35
(4,238)	1:92:A:GLN:H	1:92:A:GLN:HA	7	0.35
(4,238)	1:92:A:GLN:H	1:92:A:GLN:HA	10	0.35
(4,238)	1:92:A:GLN:H	1:92:A:GLN:HA	11	0.35
(4,238)	1:222:A:VAL:H	1:222:A:VAL:HA	16	0.35
(4,232)	1:34:A:ASP:H	1:34:A:ASP:HB2	17	0.35
(4,206)	1:140:A:LEU:HB2	1:142:A:VAL:H	3	0.35
(4,204)	1:100:A:LEU:H	1:100:A:LEU:HG	12	0.35
(4,189)	1:34:A:ASP:H	1:34:A:ASP:HB2	11	0.35
(4,189)	1:37:A:THR:H	1:34:A:ASP:HB3	19	0.35
(4,165)	1:260:A:LYS:H	1:260:A:LYS:HA	4	0.35
(4,165)	1:166:A:ILE:H	1:163:A:LEU:HA	9	0.35
(4,165)	1:260:A:LYS:H	1:260:A:LYS:HA	11	0.35
(4,165)	1:260:A:LYS:H	1:260:A:LYS:HA	13	0.35
(4,112)	1:73:A:SER:H	1:73:A:SER:HA	1	0.35
(4,112)	1:73:A:SER:H	1:73:A:SER:HA	8	0.35
(3,318)	1:171:A:LYS:H	1:168:A:THR:H	7	0.35

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,314)	1:229:A:ASN:H	1:168:A:THR:H	5	0.35
(3,234)	1:8:A:GLY:H	1:12:A:GLY:H	11	0.35
(3,234)	1:8:A:GLY:H	1:12:A:GLY:H	19	0.35
(3,158)	1:57:A:LEU:H	1:70:A:PHE:H	6	0.35
(3,71)	1:138:A:ASP:H	1:140:A:LEU:H	1	0.35
(2,20)	1:229:A:ASN:H	1:168:A:THR:H	18	0.35
(1,132)	1:135:A:GLN:H	1:134:A:VAL:HG23	3	0.35
(1,106)	1:226:A:ARG:H	1:225:A:PHE:HB2	1	0.35
(4,1316)	1:165:A:SER:H	1:166:A:ILE:HD11	2	0.34
(4,1293)	1:153:A:LYS:H	1:152:A:ALA:HB1	16	0.34
(4,1293)	1:23:A:ALA:H	1:22:A:ILE:HG22	18	0.34
(4,1257)	1:78:A:VAL:H	1:77:A:ALA:HB3	1	0.34
(4,1228)	1:152:A:ALA:H	1:152:A:ALA:HB3	8	0.34
(4,1227)	1:90:A:LEU:H	1:90:A:LEU:HB3	20	0.34
(4,1202)	1:99:A:SER:H	1:100:A:LEU:HG	17	0.34
(4,1178)	1:177:A:ASN:H	1:55:A:THR:HG21	2	0.34
(4,1172)	1:141:A:ALA:H	1:140:A:LEU:HB2	5	0.34
(4,1152)	1:205:A:CYS:H	1:203:A:LEU:HB3	19	0.34
(4,1139)	1:239:A:LEU:H	1:239:A:LEU:HB2	10	0.34
(4,1106)	1:23:A:ALA:H	1:23:A:ALA:HB1	13	0.34
(4,1083)	1:248:A:GLN:H	1:248:A:GLN:HG2	11	0.34
(4,1075)	1:28:A:GLN:H	1:28:A:GLN:HB2	6	0.34
(4,1055)	1:18:A:LYS:H	1:18:A:LYS:HB2	10	0.34
(4,1055)	1:100:A:LEU:H	1:100:A:LEU:HB2	11	0.34
(4,1005)	1:175:A:PHE:H	1:175:A:PHE:HB3	1	0.34
(4,1005)	1:175:A:PHE:H	1:175:A:PHE:HB3	13	0.34
(4,983)	1:119:A:HIS:H	1:119:A:HIS:HB2	1	0.34
(4,975)	1:133:A:ALA:H	1:133:A:ALA:HA	10	0.34
(4,975)	1:133:A:ALA:H	1:133:A:ALA:HA	13	0.34
(4,948)	1:166:A:ILE:H	1:163:A:LEU:HA	17	0.34
(4,903)	1:49:A:VAL:H	1:49:A:VAL:HA	5	0.34
(4,903)	1:49:A:VAL:H	1:49:A:VAL:HA	9	0.34
(4,880)	1:224:A:LYS:H	1:224:A:LYS:HA	2	0.34
(4,869)	1:129:A:ASP:H	1:129:A:ASP:HA	8	0.34
(4,869)	1:129:A:ASP:H	1:129:A:ASP:HA	14	0.34
(4,862)	1:218:A:SER:H	1:218:A:SER:HB3	15	0.34
(4,856)	1:167:A:LYS:H	1:167:A:LYS:HA	13	0.34
(4,809)	1:197:A:LEU:H	1:197:A:LEU:HA	16	0.34
(4,801)	1:166:A:ILE:H	1:165:A:SER:HB3	6	0.34
(4,742)	1:71:A:ASP:H	1:70:A:PHE:HA	4	0.34
(4,742)	1:71:A:ASP:H	1:70:A:PHE:HA	9	0.34
(4,705)	1:29:A:SER:H	1:29:A:SER:HA	8	0.34

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,705)	1:64:A:HIS:H	1:64:A:HIS:HA	20	0.34
(4,699)	1:176:A:THR:H	1:176:A:THR:HA	15	0.34
(4,677)	1:173:A:ALA:H	1:173:A:ALA:HA	6	0.34
(4,677)	1:173:A:ALA:H	1:173:A:ALA:HA	10	0.34
(4,666)	1:226:A:ARG:H	1:222:A:VAL:H	7	0.34
(4,572)	1:227:A:LYS:H	1:228:A:LEU:H	10	0.34
(4,457)	1:78:A:VAL:HB	1:87:A:THR:HG22	9	0.34
(4,450)	1:147:A:LEU:HA	1:147:A:LEU:HD23	11	0.34
(4,446)	1:22:A:ILE:HG22	1:22:A:ILE:HA	6	0.34
(4,438)	1:255:A:ILE:HG21	1:255:A:ILE:HA	5	0.34
(4,438)	1:255:A:ILE:HA	1:255:A:ILE:HG13	17	0.34
(4,421)	1:167:A:LYS:HA	1:167:A:LYS:HB3	13	0.34
(4,396)	1:67:A:ASN:HB2	1:67:A:ASN:HA	11	0.34
(4,379)	1:140:A:LEU:HD21	1:130:A:PHE:HB2	7	0.34
(4,370)	1:45:A:LYS:HG3	1:45:A:LYS:HE3	6	0.34
(4,238)	1:92:A:GLN:H	1:92:A:GLN:HA	2	0.34
(4,238)	1:92:A:GLN:H	1:92:A:GLN:HA	4	0.34
(4,238)	1:222:A:VAL:H	1:222:A:VAL:HA	6	0.34
(4,238)	1:92:A:GLN:H	1:92:A:GLN:HA	12	0.34
(4,238)	1:92:A:GLN:H	1:92:A:GLN:HA	17	0.34
(4,238)	1:222:A:VAL:H	1:222:A:VAL:HA	18	0.34
(4,238)	1:92:A:GLN:H	1:92:A:GLN:HA	20	0.34
(4,231)	1:169:A:LYS:H	1:169:A:LYS:HD2	7	0.34
(4,208)	1:45:A:LYS:H	1:44:A:LEU:HA	1	0.34
(4,202)	1:34:A:ASP:H	1:34:A:ASP:HB2	11	0.34
(4,202)	1:34:A:ASP:H	1:34:A:ASP:HB2	13	0.34
(4,167)	1:32:A:ASP:H	1:32:A:ASP:HB2	10	0.34
(4,165)	1:260:A:LYS:H	1:260:A:LYS:HA	3	0.34
(4,165)	1:260:A:LYS:H	1:260:A:LYS:HA	18	0.34
(4,165)	1:260:A:LYS:H	1:260:A:LYS:HA	20	0.34
(4,112)	1:181:A:ARG:H	1:181:A:ARG:HA	18	0.34
(4,90)	1:233:A:GLU:H	1:168:A:THR:HB	20	0.34
(4,24)	1:55:A:THR:H	1:76:A:LYS:HD2	12	0.34
(3,323)	1:181:A:ARG:H	1:184:A:LEU:H	18	0.34
(3,318)	1:171:A:LYS:H	1:168:A:THR:H	19	0.34
(3,114)	1:241:A:VAL:H	1:243:A:ASN:H	17	0.34
(1,106)	1:226:A:ARG:H	1:225:A:PHE:HB3	4	0.34
(1,106)	1:226:A:ARG:H	1:225:A:PHE:HB2	6	0.34
(1,105)	1:6:A:GLY:H	1:6:A:GLY:HA3	1	0.34
(1,105)	1:6:A:GLY:H	1:6:A:GLY:HA3	2	0.34
(1,105)	1:6:A:GLY:H	1:6:A:GLY:HA3	6	0.34
(1,105)	1:6:A:GLY:H	1:6:A:GLY:HA3	10	0.34

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,105)	1:6:A:GLY:H	1:6:A:GLY:HA3	11	0.34
(1,105)	1:6:A:GLY:H	1:6:A:GLY:HA3	13	0.34
(1,76)	1:115:A:ALA:HB3	1:149:A:VAL:HG21	5	0.34
(4,1325)	1:59:A:ILE:H	1:166:A:ILE:HD11	13	0.33
(4,1309)	1:163:A:LEU:H	1:163:A:LEU:HD23	4	0.33
(4,1243)	1:163:A:LEU:H	1:162:A:VAL:HG21	11	0.33
(4,1213)	1:239:A:LEU:H	1:239:A:LEU:HB3	12	0.33
(4,1201)	1:172:A:SER:H	1:171:A:LYS:HD2	1	0.33
(4,1189)	1:34:A:ASP:H	1:37:A:THR:HG21	16	0.33
(4,1178)	1:177:A:ASN:H	1:176:A:THR:HG23	11	0.33
(4,1178)	1:177:A:ASN:H	1:176:A:THR:HG22	12	0.33
(4,1134)	1:197:A:LEU:H	1:197:A:LEU:HB2	12	0.33
(4,1114)	1:84:A:LEU:H	1:84:A:LEU:HB2	14	0.33
(4,1109)	1:133:A:ALA:H	1:133:A:ALA:HB3	12	0.33
(4,1075)	1:28:A:GLN:H	1:28:A:GLN:HB3	1	0.33
(4,1075)	1:28:A:GLN:H	1:28:A:GLN:HB2	3	0.33
(4,1075)	1:164:A:ASP:H	1:164:A:ASP:HB2	15	0.33
(4,1075)	1:164:A:ASP:H	1:164:A:ASP:HB2	19	0.33
(4,1071)	1:103:A:GLN:H	1:103:A:GLN:HG2	18	0.33
(4,1064)	1:155:A:GLY:H	1:153:A:LYS:HB3	11	0.33
(4,1055)	1:100:A:LEU:H	1:100:A:LEU:HB3	9	0.33
(4,1048)	1:103:A:GLN:H	1:103:A:GLN:HG2	18	0.33
(4,1012)	1:253:A:ARG:H	1:252:A:ASN:HB3	7	0.33
(4,1007)	1:122:A:HIS:H	1:122:A:HIS:HB2	8	0.33
(4,1006)	1:141:A:ALA:H	1:122:A:HIS:HB2	3	0.33
(4,993)	1:159:A:VAL:H	1:159:A:VAL:HB	8	0.33
(4,896)	1:159:A:VAL:H	1:159:A:VAL:HA	20	0.33
(4,874)	1:247:A:ALA:H	1:247:A:ALA:HA	15	0.33
(4,869)	1:129:A:ASP:H	1:129:A:ASP:HA	2	0.33
(4,869)	1:129:A:ASP:H	1:129:A:ASP:HA	5	0.33
(4,841)	1:161:A:ASP:H	1:161:A:ASP:HA	16	0.33
(4,775)	1:106:A:GLU:H	1:105:A:SER:HA	12	0.33
(4,742)	1:71:A:ASP:H	1:70:A:PHE:HA	5	0.33
(4,705)	1:64:A:HIS:H	1:64:A:HIS:HA	2	0.33
(4,705)	1:64:A:HIS:H	1:64:A:HIS:HA	17	0.33
(4,699)	1:176:A:THR:H	1:176:A:THR:HA	7	0.33
(4,699)	1:176:A:THR:H	1:176:A:THR:HA	11	0.33
(4,699)	1:176:A:THR:H	1:176:A:THR:HA	19	0.33
(4,677)	1:173:A:ALA:H	1:173:A:ALA:HA	11	0.33
(4,677)	1:173:A:ALA:H	1:173:A:ALA:HA	13	0.33
(4,677)	1:173:A:ALA:H	1:173:A:ALA:HA	14	0.33
(4,666)	1:226:A:ARG:H	1:222:A:VAL:H	2	0.33

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,557)	1:160:A:VAL:H	1:161:A:ASP:H	19	0.33
(4,478)	1:243:A:ASN:H	1:97:A:TRP:H	16	0.33
(4,460)	1:99:A:SER:HA	1:241:A:VAL:HG23	9	0.33
(4,449)	1:160:A:VAL:HA	1:160:A:VAL:HG21	3	0.33
(4,446)	1:22:A:ILE:HD11	1:22:A:ILE:HA	13	0.33
(4,438)	1:255:A:ILE:HA	1:255:A:ILE:HG13	4	0.33
(4,435)	1:160:A:VAL:HA	1:160:A:VAL:HG21	4	0.33
(4,416)	1:23:A:ALA:HB1	1:16:A:TRP:HB2	6	0.33
(4,396)	1:67:A:ASN:HB3	1:67:A:ASN:HA	13	0.33
(4,371)	1:22:A:ILE:HB	1:20:A:PHE:HB3	17	0.33
(4,238)	1:222:A:VAL:H	1:222:A:VAL:HA	8	0.33
(4,238)	1:222:A:VAL:H	1:222:A:VAL:HA	13	0.33
(4,238)	1:222:A:VAL:H	1:222:A:VAL:HA	14	0.33
(4,232)	1:34:A:ASP:H	1:34:A:ASP:HB2	15	0.33
(4,224)	1:259:A:PHE:H	1:258:A:SER:HB3	4	0.33
(4,215)	1:242:A:ASP:H	1:241:A:VAL:HA	7	0.33
(4,205)	1:54:A:ALA:H	1:54:A:ALA:HB3	14	0.33
(4,202)	1:37:A:THR:H	1:34:A:ASP:HB3	19	0.33
(4,189)	1:34:A:ASP:H	1:34:A:ASP:HB2	17	0.33
(4,183)	1:260:A:LYS:H	1:259:A:PHE:HA	14	0.33
(4,167)	1:32:A:ASP:H	1:32:A:ASP:HB2	4	0.33
(4,167)	1:32:A:ASP:H	1:32:A:ASP:HB3	7	0.33
(4,167)	1:32:A:ASP:H	1:32:A:ASP:HB3	11	0.33
(4,167)	1:32:A:ASP:H	1:32:A:ASP:HB3	19	0.33
(4,165)	1:260:A:LYS:H	1:260:A:LYS:HA	5	0.33
(4,112)	1:181:A:ARG:H	1:181:A:ARG:HA	10	0.33
(4,74)	1:256:A:LYS:H	1:256:A:LYS:HB3	16	0.33
(4,13)	1:63:A:GLY:H	1:60:A:LEU:HD13	17	0.33
(4,12)	1:34:A:ASP:HB3	1:35:A:THR:H	10	0.33
(3,255)	1:147:A:LEU:H	1:115:A:ALA:H	18	0.33
(3,226)	1:231:A:ASN:H	1:169:A:LYS:H	4	0.33
(3,206)	1:100:A:LEU:H	1:103:A:GLN:H	6	0.33
(3,120)	1:248:A:GLN:H	1:32:A:ASP:H	20	0.33
(3,114)	1:241:A:VAL:H	1:243:A:ASN:H	3	0.33
(3,100)	1:183:A:LEU:H	1:181:A:ARG:H	19	0.33
(3,66)	1:82:A:GLY:H	1:47:A:LEU:H	1	0.33
(3,13)	1:207:A:THR:H	1:195:A:GLY:H	2	0.33
(1,132)	1:135:A:GLN:H	1:134:A:VAL:HG21	15	0.33
(1,106)	1:226:A:ARG:H	1:225:A:PHE:HB2	7	0.33
(1,106)	1:226:A:ARG:H	1:225:A:PHE:HB2	17	0.33
(1,105)	1:6:A:GLY:H	1:6:A:GLY:HA3	14	0.33
(1,78)	1:117:A:GLU:H	1:96:A:HIS:H	9	0.33

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,38)	1:77:A:ALA:HA	1:51:A:TYR:HA	2	0.33
(1,26)	1:156:A:LEU:H	1:156:A:LEU:HB3	14	0.33
(1,7)	1:59:A:ILE:H	1:166:A:ILE:HD11	13	0.33
(4,1321)	1:205:A:CYS:H	1:206:A:VAL:HG23	19	0.32
(4,1242)	1:247:A:ALA:H	1:247:A:ALA:HB1	11	0.32
(4,1227)	1:91:A:ILE:H	1:91:A:ILE:HG13	17	0.32
(4,1223)	1:152:A:ALA:H	1:152:A:ALA:HB3	8	0.32
(4,1222)	1:223:A:LEU:H	1:223:A:LEU:HB2	8	0.32
(4,1222)	1:223:A:LEU:H	1:223:A:LEU:HB2	14	0.32
(4,1209)	1:172:A:SER:H	1:171:A:LYS:HD2	1	0.32
(4,1173)	1:89:A:ARG:H	1:89:A:ARG:HG2	9	0.32
(4,1173)	1:27:A:ARG:H	1:27:A:ARG:HG3	18	0.32
(4,1165)	1:103:A:GLN:H	1:103:A:GLN:HB2	17	0.32
(4,1139)	1:211:A:LEU:H	1:211:A:LEU:HB2	12	0.32
(4,1139)	1:256:A:LYS:H	1:256:A:LYS:HG3	18	0.32
(4,1125)	1:171:A:LYS:H	1:171:A:LYS:HB2	18	0.32
(4,1121)	1:9:A:LYS:H	1:9:A:LYS:HB2	12	0.32
(4,1114)	1:84:A:LEU:H	1:84:A:LEU:HB2	20	0.32
(4,1110)	1:90:A:LEU:H	1:90:A:LEU:HB2	19	0.32
(4,1109)	1:133:A:ALA:H	1:133:A:ALA:HB3	7	0.32
(4,1107)	1:229:A:ASN:H	1:228:A:LEU:HB3	18	0.32
(4,1102)	1:140:A:LEU:H	1:140:A:LEU:HG	4	0.32
(4,1094)	1:37:A:THR:H	1:34:A:ASP:HB3	16	0.32
(4,1066)	1:224:A:LYS:H	1:224:A:LYS:HG3	9	0.32
(4,1051)	1:26:A:GLU:H	1:26:A:GLU:HG2	6	0.32
(4,1051)	1:170:A:GLY:H	1:61:A:ASN:HB3	16	0.32
(4,999)	1:122:A:HIS:H	1:122:A:HIS:HB2	8	0.32
(4,975)	1:133:A:ALA:H	1:133:A:ALA:HA	16	0.32
(4,975)	1:133:A:ALA:H	1:133:A:ALA:HA	17	0.32
(4,962)	1:166:A:ILE:H	1:163:A:LEU:HA	3	0.32
(4,896)	1:160:A:VAL:H	1:160:A:VAL:HA	17	0.32
(4,880)	1:224:A:LYS:H	1:224:A:LYS:HA	4	0.32
(4,880)	1:224:A:LYS:H	1:224:A:LYS:HA	8	0.32
(4,836)	1:129:A:ASP:H	1:128:A:GLY:HA3	19	0.32
(4,789)	1:106:A:GLU:H	1:105:A:SER:HA	2	0.32
(4,758)	1:259:A:PHE:H	1:259:A:PHE:HA	19	0.32
(4,705)	1:64:A:HIS:H	1:64:A:HIS:HA	14	0.32
(4,677)	1:173:A:ALA:H	1:173:A:ALA:HA	1	0.32
(4,677)	1:173:A:ALA:H	1:173:A:ALA:HA	7	0.32
(4,677)	1:173:A:ALA:H	1:173:A:ALA:HA	18	0.32
(4,460)	1:224:A:LYS:HA	1:227:A:LYS:HG2	13	0.32
(4,449)	1:159:A:VAL:HA	1:159:A:VAL:HG21	14	0.32

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,449)	1:159:A:VAL:HA	1:159:A:VAL:HG21	20	0.32
(4,437)	1:199:A:THR:HB	1:199:A:THR:HG22	10	0.32
(4,398)	1:123:A:TRP:HB3	1:140:A:LEU:HB3	2	0.32
(4,396)	1:67:A:ASN:HB3	1:67:A:ASN:HA	2	0.32
(4,396)	1:153:A:LYS:HA	1:153:A:LYS:HB2	3	0.32
(4,396)	1:148:A:LYS:HB3	1:148:A:LYS:HA	7	0.32
(4,396)	1:67:A:ASN:HB3	1:67:A:ASN:HA	14	0.32
(4,396)	1:153:A:LYS:HA	1:153:A:LYS:HB3	20	0.32
(4,379)	1:260:A:LYS:HG2	1:260:A:LYS:HE2	13	0.32
(4,238)	1:66:A:PHE:H	1:66:A:PHE:HA	19	0.32
(4,234)	1:206:A:VAL:H	1:22:A:ILE:HD11	5	0.32
(4,208)	1:45:A:LYS:H	1:44:A:LEU:HA	20	0.32
(4,189)	1:37:A:THR:H	1:34:A:ASP:HB2	18	0.32
(4,182)	1:166:A:ILE:H	1:163:A:LEU:HA	4	0.32
(4,167)	1:32:A:ASP:H	1:32:A:ASP:HB2	6	0.32
(4,167)	1:32:A:ASP:H	1:32:A:ASP:HB2	15	0.32
(4,166)	1:76:A:LYS:H	1:76:A:LYS:HD2	17	0.32
(4,118)	1:165:A:SER:H	1:163:A:LEU:HA	10	0.32
(4,112)	1:73:A:SER:H	1:73:A:SER:HA	14	0.32
(4,88)	1:210:A:VAL:H	1:192:A:THR:HB	20	0.32
(4,87)	1:233:A:GLU:H	1:233:A:GLU:HB2	4	0.32
(4,87)	1:233:A:GLU:H	1:233:A:GLU:HB3	6	0.32
(4,48)	1:202:A:LEU:H	1:202:A:LEU:HB3	2	0.32
(4,12)	1:34:A:ASP:HB3	1:35:A:THR:H	15	0.32
(3,210)	1:197:A:LEU:H	1:205:A:CYS:H	5	0.32
(3,205)	1:124:A:ASN:H	1:127:A:TYR:H	14	0.32
(3,55)	1:156:A:LEU:H	1:158:A:LYS:H	10	0.32
(3,23)	1:138:A:ASP:H	1:140:A:LEU:H	16	0.32
(1,123)	1:63:A:GLY:H	1:169:A:LYS:HG2	11	0.32
(1,105)	1:6:A:GLY:H	1:6:A:GLY:HA3	5	0.32
(1,105)	1:6:A:GLY:H	1:6:A:GLY:HA3	8	0.32
(1,73)	1:134:A:VAL:HG22	1:131:A:GLY:HA2	12	0.32
(1,25)	1:169:A:LYS:H	1:168:A:THR:HB	2	0.32
(4,1139)	1:211:A:LEU:H	1:211:A:LEU:HB2	15	0.31
(4,1138)	1:40:A:TYR:H	1:39:A:LYS:HG3	11	0.31
(4,1129)	1:111:A:LYS:H	1:108:A:THR:HG21	19	0.31
(4,1114)	1:22:A:ILE:H	1:22:A:ILE:HB	17	0.31
(4,1083)	1:248:A:GLN:H	1:248:A:GLN:HG2	13	0.31
(4,1075)	1:164:A:ASP:H	1:164:A:ASP:HB3	9	0.31
(4,1055)	1:253:A:ARG:H	1:253:A:ARG:HB2	18	0.31
(4,1051)	1:57:A:LEU:H	1:57:A:LEU:HB2	2	0.31
(4,998)	1:175:A:PHE:H	1:175:A:PHE:HB3	16	0.31

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,993)	1:127:A:TYR:H	1:127:A:TYR:HB2	11	0.31
(4,975)	1:133:A:ALA:H	1:133:A:ALA:HA	3	0.31
(4,975)	1:133:A:ALA:H	1:133:A:ALA:HA	5	0.31
(4,948)	1:129:A:ASP:H	1:127:A:TYR:HB2	6	0.31
(4,948)	1:64:A:HIS:H	1:62:A:ASN:HB2	12	0.31
(4,862)	1:43:A:SER:H	1:43:A:SER:HB3	20	0.31
(4,845)	1:151:A:SER:H	1:150:A:GLY:HA2	11	0.31
(4,836)	1:166:A:ILE:H	1:165:A:SER:HB3	12	0.31
(4,817)	1:205:A:CYS:H	1:205:A:CYS:HA	12	0.31
(4,809)	1:167:A:LYS:H	1:167:A:LYS:HA	4	0.31
(4,789)	1:106:A:GLU:H	1:105:A:SER:HA	11	0.31
(4,758)	1:252:A:ASN:H	1:252:A:ASN:HA	11	0.31
(4,758)	1:252:A:ASN:H	1:251:A:LYS:HA	18	0.31
(4,699)	1:176:A:THR:H	1:176:A:THR:HA	17	0.31
(4,677)	1:173:A:ALA:H	1:173:A:ALA:HA	8	0.31
(4,664)	1:54:A:ALA:H	1:51:A:TYR:HA	3	0.31
(4,654)	1:199:A:THR:H	1:202:A:LEU:H	20	0.31
(4,650)	1:199:A:THR:H	1:202:A:LEU:H	20	0.31
(4,628)	1:181:A:ARG:H	1:182:A:GLY:H	14	0.31
(4,626)	1:245:A:ARG:H	1:105:A:SER:H	12	0.31
(4,618)	1:56:A:SER:H	1:58:A:ARG:H	15	0.31
(4,557)	1:222:A:VAL:H	1:223:A:LEU:H	5	0.31
(4,557)	1:222:A:VAL:H	1:221:A:GLN:H	6	0.31
(4,557)	1:162:A:VAL:H	1:161:A:ASP:H	20	0.31
(4,540)	1:89:A:ARG:H	1:123:A:TRP:H	10	0.31
(4,475)	1:73:A:SER:H	1:72:A:ASP:H	20	0.31
(4,451)	1:250:A:LEU:HB3	1:250:A:LEU:HD23	2	0.31
(4,435)	1:159:A:VAL:HA	1:159:A:VAL:HG23	1	0.31
(4,433)	1:173:A:ALA:HA	1:173:A:ALA:HB3	1	0.31
(4,433)	1:173:A:ALA:HA	1:173:A:ALA:HB1	2	0.31
(4,433)	1:173:A:ALA:HA	1:173:A:ALA:HB2	4	0.31
(4,433)	1:173:A:ALA:HA	1:173:A:ALA:HB2	6	0.31
(4,433)	1:173:A:ALA:HA	1:173:A:ALA:HB3	8	0.31
(4,433)	1:173:A:ALA:HA	1:173:A:ALA:HB2	9	0.31
(4,433)	1:173:A:ALA:HA	1:173:A:ALA:HB1	18	0.31
(4,406)	1:133:A:ALA:HB2	1:130:A:PHE:HA	7	0.31
(4,392)	1:64:A:HIS:HB2	1:169:A:LYS:HB2	16	0.31
(4,382)	1:193:A:TYR:HB3	1:208:A:TRP:HB2	3	0.31
(4,379)	1:260:A:LYS:HG3	1:260:A:LYS:HE3	14	0.31
(4,379)	1:260:A:LYS:HG2	1:260:A:LYS:HE3	16	0.31
(4,379)	1:260:A:LYS:HG2	1:260:A:LYS:HE3	18	0.31
(4,379)	1:260:A:LYS:HG3	1:260:A:LYS:HE3	19	0.31

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,374)	1:127:A:TYR:HB3	1:133:A:ALA:HA	2	0.31
(4,370)	1:251:A:LYS:HG2	1:251:A:LYS:HE2	1	0.31
(4,281)	1:91:A:ILE:HD12	1:123:A:TRP:HA	18	0.31
(4,252)	1:259:A:PHE:H	1:40:A:TYR:HB2	18	0.31
(4,251)	1:259:A:PHE:H	1:40:A:TYR:HB2	18	0.31
(4,245)	1:228:A:LEU:H	1:228:A:LEU:HA	2	0.31
(4,245)	1:228:A:LEU:H	1:228:A:LEU:HA	7	0.31
(4,245)	1:228:A:LEU:H	1:228:A:LEU:HA	11	0.31
(4,232)	1:179:A:ASP:HB3	1:182:A:GLY:H	7	0.31
(4,202)	1:34:A:ASP:H	1:34:A:ASP:HB2	17	0.31
(4,112)	1:73:A:SER:H	1:73:A:SER:HA	2	0.31
(4,112)	1:73:A:SER:H	1:73:A:SER:HA	7	0.31
(4,87)	1:181:A:ARG:H	1:181:A:ARG:HB2	5	0.31
(4,87)	1:233:A:GLU:H	1:233:A:GLU:HB2	12	0.31
(4,80)	1:240:A:MET:H	1:240:A:MET:HB3	8	0.31
(4,12)	1:34:A:ASP:HB3	1:35:A:THR:H	7	0.31
(4,12)	1:34:A:ASP:HB3	1:35:A:THR:H	11	0.31
(4,12)	1:34:A:ASP:HB3	1:35:A:THR:H	17	0.31
(4,12)	1:34:A:ASP:HB3	1:35:A:THR:H	19	0.31
(3,314)	1:229:A:ASN:H	1:168:A:THR:H	12	0.31
(3,290)	1:196:A:SER:H	1:206:A:VAL:H	9	0.31
(3,252)	1:196:A:SER:H	1:206:A:VAL:H	9	0.31
(3,150)	1:206:A:VAL:H	1:197:A:LEU:H	18	0.31
(3,114)	1:241:A:VAL:H	1:243:A:ASN:H	20	0.31
(3,112)	1:129:A:ASP:H	1:131:A:GLY:H	8	0.31
(3,79)	1:192:A:THR:H	1:256:A:LYS:H	16	0.31
(3,9)	1:256:A:LYS:H	1:192:A:THR:H	16	0.31
(3,7)	1:56:A:SER:H	1:177:A:ASN:H	3	0.31
(1,105)	1:6:A:GLY:H	1:6:A:GLY:HA3	20	0.31
(1,79)	1:68:A:VAL:H	1:93:A:PHE:H	11	0.31
(1,60)	1:51:A:TYR:HB3	1:51:A:TYR:HA	11	0.31
(4,1243)	1:163:A:LEU:H	1:162:A:VAL:HG21	10	0.3
(4,1222)	1:223:A:LEU:H	1:223:A:LEU:HB2	20	0.3
(4,1217)	1:197:A:LEU:H	1:197:A:LEU:HG	12	0.3
(4,1214)	1:80:A:LYS:H	1:80:A:LYS:HG2	7	0.3
(4,1213)	1:256:A:LYS:H	1:256:A:LYS:HG3	19	0.3
(4,1178)	1:177:A:ASN:H	1:176:A:THR:HG22	15	0.3
(4,1172)	1:239:A:LEU:H	1:239:A:LEU:HB2	10	0.3
(4,1162)	1:133:A:ALA:H	1:133:A:ALA:HB3	12	0.3
(4,1139)	1:256:A:LYS:H	1:256:A:LYS:HB2	14	0.3
(4,1138)	1:238:A:GLU:H	1:238:A:GLU:HB2	8	0.3
(4,1128)	1:251:A:LYS:H	1:250:A:LEU:HB3	11	0.3

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1114)	1:84:A:LEU:H	1:84:A:LEU:HB3	2	0.3
(4,1114)	1:223:A:LEU:H	1:223:A:LEU:HB2	11	0.3
(4,1109)	1:204:A:GLU:H	1:204:A:GLU:HB2	3	0.3
(4,1109)	1:133:A:ALA:H	1:133:A:ALA:HB1	17	0.3
(4,1107)	1:229:A:ASN:H	1:228:A:LEU:HB2	3	0.3
(4,1102)	1:26:A:GLU:H	1:26:A:GLU:HB2	17	0.3
(4,1088)	1:232:A:GLY:H	1:235:A:GLU:HG3	19	0.3
(4,1075)	1:164:A:ASP:H	1:164:A:ASP:HB2	10	0.3
(4,1055)	1:100:A:LEU:H	1:100:A:LEU:HB2	5	0.3
(4,1025)	1:164:A:ASP:H	1:164:A:ASP:HB3	20	0.3
(4,980)	1:191:A:TRP:H	1:191:A:TRP:HB2	15	0.3
(4,975)	1:133:A:ALA:H	1:133:A:ALA:HA	4	0.3
(4,972)	1:253:A:ARG:H	1:252:A:ASN:HB3	7	0.3
(4,964)	1:174:A:ASP:H	1:174:A:ASP:HB3	5	0.3
(4,923)	1:243:A:ASN:H	1:243:A:ASN:HB2	8	0.3
(4,903)	1:49:A:VAL:H	1:49:A:VAL:HA	2	0.3
(4,901)	1:167:A:LYS:H	1:167:A:LYS:HA	13	0.3
(4,880)	1:241:A:VAL:H	1:241:A:VAL:HA	5	0.3
(4,836)	1:166:A:ILE:H	1:165:A:SER:HB2	15	0.3
(4,817)	1:103:A:GLN:H	1:103:A:GLN:HA	10	0.3
(4,817)	1:205:A:CYS:H	1:205:A:CYS:HA	18	0.3
(4,758)	1:259:A:PHE:H	1:259:A:PHE:HA	7	0.3
(4,742)	1:71:A:ASP:H	1:70:A:PHE:HA	17	0.3
(4,722)	1:57:A:LEU:H	1:56:A:SER:HA	11	0.3
(4,705)	1:64:A:HIS:H	1:64:A:HIS:HA	1	0.3
(4,705)	1:64:A:HIS:H	1:64:A:HIS:HA	5	0.3
(4,705)	1:64:A:HIS:H	1:64:A:HIS:HA	13	0.3
(4,705)	1:64:A:HIS:H	1:64:A:HIS:HA	15	0.3
(4,705)	1:64:A:HIS:H	1:64:A:HIS:HA	18	0.3
(4,677)	1:173:A:ALA:H	1:173:A:ALA:HA	4	0.3
(4,677)	1:173:A:ALA:H	1:173:A:ALA:HA	9	0.3
(4,677)	1:173:A:ALA:H	1:173:A:ALA:HA	16	0.3
(4,654)	1:199:A:THR:H	1:202:A:LEU:H	1	0.3
(4,650)	1:199:A:THR:H	1:202:A:LEU:H	1	0.3
(4,624)	1:159:A:VAL:H	1:160:A:VAL:H	18	0.3
(4,572)	1:222:A:VAL:H	1:221:A:GLN:H	19	0.3
(4,557)	1:222:A:VAL:H	1:221:A:GLN:H	13	0.3
(4,540)	1:89:A:ARG:H	1:123:A:TRP:H	15	0.3
(4,495)	1:116:A:ALA:H	1:147:A:LEU:H	20	0.3
(4,469)	1:140:A:LEU:HB3	1:134:A:VAL:HG21	14	0.3
(4,463)	1:174:A:ASP:HA	1:176:A:THR:HG22	10	0.3
(4,446)	1:22:A:ILE:HD12	1:22:A:ILE:HA	10	0.3

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,446)	1:22:A:ILE:HD12	1:22:A:ILE:HA	18	0.3
(4,436)	1:63:A:GLY:HA2	1:169:A:LYS:HG2	13	0.3
(4,435)	1:35:A:THR:HG23	1:35:A:THR:HA	14	0.3
(4,433)	1:173:A:ALA:HA	1:173:A:ALA:HB1	3	0.3
(4,433)	1:173:A:ALA:HA	1:173:A:ALA:HB2	7	0.3
(4,433)	1:173:A:ALA:HA	1:173:A:ALA:HB3	10	0.3
(4,433)	1:173:A:ALA:HA	1:173:A:ALA:HB1	11	0.3
(4,433)	1:173:A:ALA:HA	1:173:A:ALA:HB3	12	0.3
(4,433)	1:173:A:ALA:HA	1:173:A:ALA:HB3	13	0.3
(4,433)	1:173:A:ALA:HA	1:173:A:ALA:HB1	16	0.3
(4,433)	1:173:A:ALA:HA	1:173:A:ALA:HB2	17	0.3
(4,379)	1:260:A:LYS:HG3	1:260:A:LYS:HE3	9	0.3
(4,335)	1:22:A:ILE:HG22	1:22:A:ILE:HA	17	0.3
(4,258)	1:242:A:ASP:H	1:97:A:TRP:HB2	5	0.3
(4,245)	1:228:A:LEU:H	1:228:A:LEU:HA	18	0.3
(4,237)	1:166:A:ILE:H	1:166:A:ILE:HA	17	0.3
(4,219)	1:105:A:SER:H	1:105:A:SER:HB3	1	0.3
(4,219)	1:44:A:LEU:H	1:43:A:SER:HB3	9	0.3
(4,202)	1:37:A:THR:H	1:34:A:ASP:HB2	18	0.3
(4,189)	1:37:A:THR:H	1:34:A:ASP:HB3	10	0.3
(4,167)	1:32:A:ASP:H	1:32:A:ASP:HB2	13	0.3
(4,167)	1:32:A:ASP:H	1:32:A:ASP:HB2	16	0.3
(4,112)	1:73:A:SER:H	1:73:A:SER:HA	3	0.3
(4,112)	1:73:A:SER:H	1:73:A:SER:HA	12	0.3
(4,112)	1:73:A:SER:H	1:73:A:SER:HA	16	0.3
(4,100)	1:141:A:ALA:H	1:140:A:LEU:HB2	10	0.3
(4,81)	1:55:A:THR:H	1:76:A:LYS:HG3	2	0.3
(4,80)	1:93:A:PHE:H	1:92:A:GLN:HB2	2	0.3
(4,6)	1:113:A:LYS:HG3	1:107:A:HIS:H	8	0.3
(3,255)	1:147:A:LEU:H	1:115:A:ALA:H	4	0.3
(3,210)	1:197:A:LEU:H	1:205:A:CYS:H	13	0.3
(3,202)	1:111:A:LYS:H	1:109:A:VAL:H	18	0.3
(3,158)	1:57:A:LEU:H	1:70:A:PHE:H	10	0.3
(3,110)	1:12:A:GLY:H	1:8:A:GLY:H	3	0.3
(3,58)	1:70:A:PHE:H	1:57:A:LEU:H	2	0.3
(3,15)	1:243:A:ASN:H	1:97:A:TRP:H	12	0.3
(1,131)	1:55:A:THR:H	1:76:A:LYS:HG3	13	0.3
(1,114)	1:66:A:PHE:H	1:65:A:ALA:HB3	14	0.3
(1,105)	1:6:A:GLY:H	1:6:A:GLY:HA3	3	0.3
(1,60)	1:51:A:TYR:HB3	1:51:A:TYR:HA	2	0.3
(1,60)	1:51:A:TYR:HB3	1:51:A:TYR:HA	10	0.3
(1,60)	1:51:A:TYR:HB3	1:51:A:TYR:HA	14	0.3

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1299)	1:79:A:LEU:H	1:78:A:VAL:HG23	6	0.29
(4,1223)	1:152:A:ALA:H	1:152:A:ALA:HB1	2	0.29
(4,1222)	1:89:A:ARG:H	1:89:A:ARG:HB3	19	0.29
(4,1214)	1:50:A:SER:H	1:78:A:VAL:HG23	19	0.29
(4,1168)	1:229:A:ASN:H	1:228:A:LEU:HB3	1	0.29
(4,1147)	1:231:A:ASN:H	1:169:A:LYS:HD3	18	0.29
(4,1141)	1:20:A:PHE:H	1:19:A:ASP:HB2	16	0.29
(4,1091)	1:81:A:GLY:H	1:80:A:LYS:HB3	8	0.29
(4,1082)	1:251:A:LYS:H	1:251:A:LYS:HB3	2	0.29
(4,1075)	1:164:A:ASP:H	1:164:A:ASP:HB2	13	0.29
(4,1027)	1:103:A:GLN:H	1:103:A:GLN:HG2	4	0.29
(4,1027)	1:103:A:GLN:H	1:100:A:LEU:HB3	6	0.29
(4,1025)	1:164:A:ASP:H	1:164:A:ASP:HB2	8	0.29
(4,1025)	1:164:A:ASP:H	1:164:A:ASP:HB3	14	0.29
(4,1016)	1:43:A:SER:H	1:41:A:ASP:HB3	14	0.29
(4,998)	1:175:A:PHE:H	1:174:A:ASP:HB2	5	0.29
(4,993)	1:127:A:TYR:H	1:127:A:TYR:HB2	13	0.29
(4,933)	1:129:A:ASP:H	1:129:A:ASP:HA	18	0.29
(4,933)	1:129:A:ASP:H	1:129:A:ASP:HA	19	0.29
(4,909)	1:48:A:SER:H	1:48:A:SER:HB2	20	0.29
(4,874)	1:247:A:ALA:H	1:247:A:ALA:HA	3	0.29
(4,874)	1:247:A:ALA:H	1:247:A:ALA:HA	5	0.29
(4,874)	1:247:A:ALA:H	1:247:A:ALA:HA	17	0.29
(4,874)	1:84:A:LEU:H	1:84:A:LEU:HA	19	0.29
(4,869)	1:166:A:ILE:H	1:165:A:SER:HB3	4	0.29
(4,862)	1:218:A:SER:H	1:218:A:SER:HB2	14	0.29
(4,836)	1:166:A:ILE:H	1:165:A:SER:HB3	3	0.29
(4,805)	1:166:A:ILE:H	1:165:A:SER:HB3	12	0.29
(4,805)	1:129:A:ASP:H	1:128:A:GLY:HA3	19	0.29
(4,801)	1:129:A:ASP:H	1:128:A:GLY:HA3	19	0.29
(4,775)	1:148:A:LYS:H	1:147:A:LEU:HA	14	0.29
(4,758)	1:252:A:ASN:H	1:252:A:ASN:HA	3	0.29
(4,758)	1:252:A:ASN:H	1:252:A:ASN:HA	17	0.29
(4,715)	1:98:A:GLY:H	1:98:A:GLY:HA3	18	0.29
(4,705)	1:64:A:HIS:H	1:64:A:HIS:HA	3	0.29
(4,705)	1:64:A:HIS:H	1:64:A:HIS:HA	11	0.29
(4,699)	1:176:A:THR:H	1:176:A:THR:HA	12	0.29
(4,626)	1:245:A:ARG:H	1:247:A:ALA:H	14	0.29
(4,620)	1:37:A:THR:H	1:36:A:HIS:H	14	0.29
(4,618)	1:56:A:SER:H	1:58:A:ARG:H	1	0.29
(4,572)	1:222:A:VAL:H	1:221:A:GLN:H	5	0.29
(4,454)	1:50:A:SER:HB3	1:78:A:VAL:HG23	19	0.29

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,449)	1:159:A:VAL:HA	1:159:A:VAL:HG23	1	0.29
(4,449)	1:160:A:VAL:HA	1:160:A:VAL:HG21	2	0.29
(4,449)	1:160:A:VAL:HA	1:160:A:VAL:HG21	12	0.29
(4,449)	1:160:A:VAL:HA	1:160:A:VAL:HG21	13	0.29
(4,449)	1:159:A:VAL:HA	1:159:A:VAL:HG23	16	0.29
(4,435)	1:35:A:THR:HG22	1:35:A:THR:HA	7	0.29
(4,435)	1:35:A:THR:HG23	1:35:A:THR:HA	11	0.29
(4,433)	1:173:A:ALA:HA	1:173:A:ALA:HB3	5	0.29
(4,433)	1:173:A:ALA:HA	1:173:A:ALA:HB3	20	0.29
(4,396)	1:67:A:ASN:HB3	1:67:A:ASN:HA	8	0.29
(4,396)	1:148:A:LYS:HB3	1:148:A:LYS:HA	12	0.29
(4,396)	1:153:A:LYS:HA	1:153:A:LYS:HB2	15	0.29
(4,371)	1:22:A:ILE:HB	1:20:A:PHE:HB3	8	0.29
(4,328)	1:240:A:MET:HA	1:230:A:PHE:HA	3	0.29
(4,268)	1:203:A:LEU:H	1:203:A:LEU:HG	18	0.29
(4,253)	1:135:A:GLN:H	1:127:A:TYR:HB3	16	0.29
(4,252)	1:259:A:PHE:H	1:40:A:TYR:HB2	20	0.29
(4,231)	1:169:A:LYS:H	1:169:A:LYS:HD2	13	0.29
(4,219)	1:105:A:SER:H	1:105:A:SER:HB3	19	0.29
(4,202)	1:37:A:THR:H	1:34:A:ASP:HB3	10	0.29
(4,167)	1:179:A:ASP:H	1:179:A:ASP:HB2	18	0.29
(4,132)	1:93:A:PHE:H	1:93:A:PHE:HB3	19	0.29
(4,116)	1:87:A:THR:H	1:87:A:THR:HB	16	0.29
(4,115)	1:204:A:GLU:H	1:22:A:ILE:HD12	12	0.29
(4,114)	1:256:A:LYS:H	1:255:A:ILE:HG13	7	0.29
(4,112)	1:147:A:LEU:H	1:147:A:LEU:HA	4	0.29
(4,112)	1:73:A:SER:H	1:73:A:SER:HA	6	0.29
(4,100)	1:141:A:ALA:H	1:140:A:LEU:HB2	14	0.29
(4,87)	1:55:A:THR:H	1:76:A:LYS:HD3	3	0.29
(4,87)	1:233:A:GLU:H	1:233:A:GLU:HB2	15	0.29
(4,48)	1:202:A:LEU:H	1:202:A:LEU:HB2	1	0.29
(4,32)	1:121:A:VAL:H	1:90:A:LEU:HG	14	0.29
(4,21)	1:118:A:LEU:H	1:147:A:LEU:HG	20	0.29
(4,12)	1:34:A:ASP:HB3	1:35:A:THR:H	12	0.29
(3,290)	1:196:A:SER:H	1:206:A:VAL:H	7	0.29
(3,252)	1:196:A:SER:H	1:206:A:VAL:H	7	0.29
(3,115)	1:12:A:GLY:H	1:8:A:GLY:H	13	0.29
(3,60)	1:29:A:SER:H	1:196:A:SER:H	2	0.29
(1,123)	1:63:A:GLY:H	1:169:A:LYS:HG2	8	0.29
(1,79)	1:68:A:VAL:H	1:93:A:PHE:H	17	0.29
(1,49)	1:224:A:LYS:HG2	1:224:A:LYS:HA	16	0.29
(4,1322)	1:203:A:LEU:H	1:22:A:ILE:HD12	16	0.28

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1292)	1:79:A:LEU:H	1:78:A:VAL:HG23	6	0.28
(4,1257)	1:251:A:LYS:H	1:251:A:LYS:HG3	18	0.28
(4,1228)	1:147:A:LEU:H	1:147:A:LEU:HG	6	0.28
(4,1228)	1:152:A:ALA:H	1:152:A:ALA:HB2	9	0.28
(4,1224)	1:123:A:TRP:H	1:89:A:ARG:HB2	9	0.28
(4,1185)	1:45:A:LYS:H	1:45:A:LYS:HG3	9	0.28
(4,1172)	1:256:A:LYS:H	1:256:A:LYS:HG3	18	0.28
(4,1139)	1:239:A:LEU:H	1:239:A:LEU:HB2	2	0.28
(4,1139)	1:141:A:ALA:H	1:140:A:LEU:HB2	7	0.28
(4,1128)	1:251:A:LYS:H	1:250:A:LEU:HB3	7	0.28
(4,1126)	1:228:A:LEU:H	1:228:A:LEU:HB2	11	0.28
(4,1125)	1:80:A:LYS:H	1:80:A:LYS:HG2	7	0.28
(4,1114)	1:84:A:LEU:H	1:84:A:LEU:HB3	9	0.28
(4,1114)	1:84:A:LEU:H	1:84:A:LEU:HB3	10	0.28
(4,1109)	1:133:A:ALA:H	1:133:A:ALA:HB3	2	0.28
(4,1102)	1:26:A:GLU:H	1:26:A:GLU:HB2	13	0.28
(4,1095)	1:232:A:GLY:H	1:235:A:GLU:HG3	19	0.28
(4,1075)	1:164:A:ASP:H	1:164:A:ASP:HB2	7	0.28
(4,1075)	1:28:A:GLN:H	1:28:A:GLN:HB2	17	0.28
(4,1055)	1:253:A:ARG:H	1:253:A:ARG:HB3	16	0.28
(4,1055)	1:18:A:LYS:H	1:18:A:LYS:HB2	17	0.28
(4,1051)	1:57:A:LEU:H	1:57:A:LEU:HB2	12	0.28
(4,1051)	1:26:A:GLU:H	1:26:A:GLU:HB2	18	0.28
(4,1025)	1:164:A:ASP:H	1:164:A:ASP:HB2	1	0.28
(4,1012)	1:253:A:ARG:H	1:252:A:ASN:HB2	14	0.28
(4,962)	1:129:A:ASP:H	1:129:A:ASP:HB3	19	0.28
(4,933)	1:129:A:ASP:H	1:129:A:ASP:HA	1	0.28
(4,933)	1:129:A:ASP:H	1:129:A:ASP:HA	4	0.28
(4,933)	1:129:A:ASP:H	1:129:A:ASP:HA	10	0.28
(4,933)	1:129:A:ASP:H	1:129:A:ASP:HA	16	0.28
(4,933)	1:129:A:ASP:H	1:129:A:ASP:HA	17	0.28
(4,933)	1:129:A:ASP:H	1:129:A:ASP:HA	20	0.28
(4,920)	1:56:A:SER:H	1:56:A:SER:HB2	12	0.28
(4,896)	1:160:A:VAL:H	1:160:A:VAL:HA	2	0.28
(4,874)	1:84:A:LEU:H	1:84:A:LEU:HA	6	0.28
(4,862)	1:43:A:SER:H	1:43:A:SER:HB3	7	0.28
(4,862)	1:43:A:SER:H	1:43:A:SER:HB3	9	0.28
(4,856)	1:167:A:LYS:H	1:167:A:LYS:HA	12	0.28
(4,836)	1:166:A:ILE:H	1:165:A:SER:HB3	13	0.28
(4,835)	1:229:A:ASN:H	1:228:A:LEU:HA	3	0.28
(4,835)	1:229:A:ASN:H	1:228:A:LEU:HA	19	0.28
(4,832)	1:253:A:ARG:H	1:253:A:ARG:HA	13	0.28

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,817)	1:103:A:GLN:H	1:103:A:GLN:HA	1	0.28
(4,758)	1:252:A:ASN:H	1:252:A:ASN:HA	4	0.28
(4,742)	1:71:A:ASP:H	1:70:A:PHE:HA	6	0.28
(4,705)	1:64:A:HIS:H	1:64:A:HIS:HA	9	0.28
(4,699)	1:176:A:THR:H	1:176:A:THR:HA	10	0.28
(4,677)	1:173:A:ALA:H	1:173:A:ALA:HA	2	0.28
(4,677)	1:173:A:ALA:H	1:173:A:ALA:HA	5	0.28
(4,677)	1:173:A:ALA:H	1:173:A:ALA:HA	20	0.28
(4,673)	1:191:A:TRP:H	1:191:A:TRP:HA	15	0.28
(4,667)	1:251:A:LYS:H	1:252:A:ASN:H	14	0.28
(4,654)	1:162:A:VAL:H	1:174:A:ASP:H	15	0.28
(4,650)	1:162:A:VAL:H	1:174:A:ASP:H	15	0.28
(4,572)	1:227:A:LYS:H	1:228:A:LEU:H	7	0.28
(4,572)	1:135:A:GLN:H	1:136:A:GLN:H	8	0.28
(4,557)	1:222:A:VAL:H	1:223:A:LEU:H	10	0.28
(4,557)	1:222:A:VAL:H	1:221:A:GLN:H	14	0.28
(4,519)	1:152:A:ALA:H	1:151:A:SER:H	18	0.28
(4,475)	1:219:A:SER:H	1:150:A:GLY:H	15	0.28
(4,452)	1:205:A:CYS:HB2	1:203:A:LEU:HD21	5	0.28
(4,449)	1:160:A:VAL:HA	1:160:A:VAL:HG22	7	0.28
(4,449)	1:159:A:VAL:HA	1:159:A:VAL:HG22	11	0.28
(4,449)	1:160:A:VAL:HA	1:160:A:VAL:HG23	15	0.28
(4,447)	1:147:A:LEU:HA	1:147:A:LEU:HD22	17	0.28
(4,446)	1:22:A:ILE:HD13	1:22:A:ILE:HA	14	0.28
(4,435)	1:35:A:THR:HG23	1:35:A:THR:HA	13	0.28
(4,435)	1:35:A:THR:HG22	1:35:A:THR:HA	15	0.28
(4,435)	1:35:A:THR:HG21	1:35:A:THR:HA	20	0.28
(4,433)	1:173:A:ALA:HA	1:173:A:ALA:HB1	15	0.28
(4,433)	1:173:A:ALA:HA	1:173:A:ALA:HB2	19	0.28
(4,396)	1:138:A:ASP:HB3	1:138:A:ASP:HA	9	0.28
(4,396)	1:153:A:LYS:HA	1:153:A:LYS:HB2	10	0.28
(4,375)	1:114:A:TYR:HB2	1:105:A:SER:HB2	3	0.28
(4,371)	1:146:A:PHE:HB2	1:114:A:TYR:HB3	18	0.28
(4,324)	1:178:A:PHE:HB2	1:178:A:PHE:HA	16	0.28
(4,293)	1:229:A:ASN:HB2	1:168:A:THR:HA	12	0.28
(4,275)	1:117:A:GLU:HB2	1:146:A:PHE:HA	4	0.28
(4,245)	1:228:A:LEU:H	1:228:A:LEU:HA	9	0.28
(4,245)	1:228:A:LEU:H	1:228:A:LEU:HA	10	0.28
(4,205)	1:54:A:ALA:H	1:54:A:ALA:HB1	9	0.28
(4,205)	1:115:A:ALA:H	1:115:A:ALA:HB3	17	0.28
(4,204)	1:100:A:LEU:H	1:100:A:LEU:HG	6	0.28
(4,189)	1:37:A:THR:H	1:34:A:ASP:HB2	2	0.28

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,189)	1:37:A:THR:H	1:34:A:ASP:HB3	8	0.28
(4,182)	1:166:A:ILE:H	1:163:A:LEU:HA	12	0.28
(4,182)	1:166:A:ILE:H	1:163:A:LEU:HA	20	0.28
(4,167)	1:179:A:ASP:H	1:179:A:ASP:HB2	9	0.28
(4,167)	1:32:A:ASP:H	1:32:A:ASP:HB3	17	0.28
(4,145)	1:149:A:VAL:H	1:148:A:LYS:HB2	4	0.28
(4,119)	1:174:A:ASP:H	1:174:A:ASP:HB2	19	0.28
(4,112)	1:73:A:SER:H	1:73:A:SER:HA	11	0.28
(4,112)	1:73:A:SER:H	1:73:A:SER:HA	13	0.28
(4,100)	1:141:A:ALA:H	1:140:A:LEU:HB2	15	0.28
(4,12)	1:178:A:PHE:HB3	1:56:A:SER:H	18	0.28
(3,226)	1:231:A:ASN:H	1:169:A:LYS:H	11	0.28
(3,173)	1:57:A:LEU:H	1:175:A:PHE:H	2	0.28
(3,173)	1:57:A:LEU:H	1:175:A:PHE:H	3	0.28
(3,141)	1:87:A:THR:H	1:125:A:THR:H	5	0.28
(3,80)	1:110:A:ASP:H	1:33:A:ILE:H	20	0.28
(3,71)	1:138:A:ASP:H	1:140:A:LEU:H	5	0.28
(3,67)	1:169:A:LYS:H	1:229:A:ASN:H	3	0.28
(3,60)	1:29:A:SER:H	1:196:A:SER:H	11	0.28
(3,58)	1:70:A:PHE:H	1:57:A:LEU:H	14	0.28
(1,132)	1:135:A:GLN:H	1:134:A:VAL:HG23	13	0.28
(1,105)	1:6:A:GLY:H	1:6:A:GLY:HA3	17	0.28
(1,84)	1:103:A:GLN:H	1:102:A:GLY:H	10	0.28
(1,38)	1:77:A:ALA:HA	1:51:A:TYR:HA	11	0.28
(1,25)	1:169:A:LYS:H	1:168:A:THR:HB	9	0.28
(4,1339)	1:116:A:ALA:H	1:149:A:VAL:HG21	5	0.27
(4,1339)	1:116:A:ALA:H	1:149:A:VAL:HG23	16	0.27
(4,1321)	1:205:A:CYS:H	1:206:A:VAL:HG22	10	0.27
(4,1316)	1:205:A:CYS:H	1:206:A:VAL:HG22	8	0.27
(4,1309)	1:212:A:LYS:H	1:211:A:LEU:HD22	8	0.27
(4,1284)	1:125:A:THR:H	1:125:A:THR:HG21	14	0.27
(4,1283)	1:152:A:ALA:H	1:152:A:ALA:HB3	17	0.27
(4,1213)	1:211:A:LEU:H	1:211:A:LEU:HG	5	0.27
(4,1168)	1:190:A:TYR:H	1:189:A:ASP:HB3	17	0.27
(4,1162)	1:204:A:GLU:H	1:204:A:GLU:HB2	3	0.27
(4,1160)	1:224:A:LYS:H	1:224:A:LYS:HG3	10	0.27
(4,1139)	1:239:A:LEU:H	1:239:A:LEU:HB2	3	0.27
(4,1139)	1:256:A:LYS:H	1:256:A:LYS:HG2	20	0.27
(4,1126)	1:228:A:LEU:H	1:228:A:LEU:HB2	9	0.27
(4,1126)	1:228:A:LEU:H	1:228:A:LEU:HB2	10	0.27
(4,1121)	1:147:A:LEU:H	1:146:A:PHE:HB3	8	0.27
(4,1114)	1:22:A:ILE:H	1:22:A:ILE:HB	19	0.27

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1109)	1:133:A:ALA:H	1:133:A:ALA:HB3	14	0.27
(4,1102)	1:26:A:GLU:H	1:26:A:GLU:HB3	1	0.27
(4,1102)	1:140:A:LEU:H	1:140:A:LEU:HG	2	0.27
(4,1102)	1:26:A:GLU:H	1:26:A:GLU:HB3	8	0.27
(4,1102)	1:140:A:LEU:H	1:140:A:LEU:HG	10	0.27
(4,1102)	1:26:A:GLU:H	1:26:A:GLU:HB2	12	0.27
(4,1072)	1:103:A:GLN:H	1:103:A:GLN:HG2	18	0.27
(4,1066)	1:24:A:LYS:H	1:24:A:LYS:HB2	14	0.27
(4,1055)	1:100:A:LEU:H	1:100:A:LEU:HB2	4	0.27
(4,1025)	1:164:A:ASP:H	1:164:A:ASP:HB2	4	0.27
(4,1025)	1:164:A:ASP:H	1:164:A:ASP:HB2	5	0.27
(4,1025)	1:164:A:ASP:H	1:164:A:ASP:HB2	11	0.27
(4,1025)	1:164:A:ASP:H	1:164:A:ASP:HB2	16	0.27
(4,1022)	1:76:A:LYS:H	1:74:A:GLN:HB2	15	0.27
(4,980)	1:191:A:TRP:H	1:191:A:TRP:HB2	1	0.27
(4,962)	1:129:A:ASP:H	1:129:A:ASP:HB2	4	0.27
(4,948)	1:129:A:ASP:H	1:127:A:TYR:HB2	4	0.27
(4,948)	1:64:A:HIS:H	1:62:A:ASN:HB2	10	0.27
(4,933)	1:129:A:ASP:H	1:129:A:ASP:HA	12	0.27
(4,923)	1:7:A:TYR:H	1:7:A:TYR:HB2	1	0.27
(4,923)	1:243:A:ASN:H	1:243:A:ASN:HB2	4	0.27
(4,878)	1:9:A:LYS:H	1:8:A:GLY:HA3	13	0.27
(4,862)	1:43:A:SER:H	1:43:A:SER:HB3	6	0.27
(4,862)	1:78:A:VAL:H	1:50:A:SER:HB2	10	0.27
(4,862)	1:43:A:SER:H	1:43:A:SER:HB3	12	0.27
(4,856)	1:167:A:LYS:H	1:167:A:LYS:HA	5	0.27
(4,856)	1:167:A:LYS:H	1:167:A:LYS:HA	14	0.27
(4,856)	1:221:A:GLN:H	1:218:A:SER:HB3	17	0.27
(4,856)	1:167:A:LYS:H	1:167:A:LYS:HA	18	0.27
(4,835)	1:229:A:ASN:H	1:228:A:LEU:HA	10	0.27
(4,817)	1:205:A:CYS:H	1:205:A:CYS:HA	16	0.27
(4,805)	1:166:A:ILE:H	1:165:A:SER:HB3	3	0.27
(4,805)	1:166:A:ILE:H	1:165:A:SER:HB2	15	0.27
(4,801)	1:166:A:ILE:H	1:165:A:SER:HB2	15	0.27
(4,799)	1:87:A:THR:H	1:87:A:THR:HB	6	0.27
(4,758)	1:252:A:ASN:H	1:252:A:ASN:HA	20	0.27
(4,753)	1:172:A:SER:H	1:171:A:LYS:HA	8	0.27
(4,753)	1:172:A:SER:H	1:171:A:LYS:HA	13	0.27
(4,742)	1:71:A:ASP:H	1:70:A:PHE:HA	20	0.27
(4,704)	1:16:A:TRP:H	1:16:A:TRP:HA	9	0.27
(4,673)	1:191:A:TRP:H	1:191:A:TRP:HA	14	0.27
(4,572)	1:159:A:VAL:H	1:160:A:VAL:H	2	0.27

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,569)	1:127:A:TYR:H	1:126:A:LYS:H	2	0.27
(4,557)	1:162:A:VAL:H	1:161:A:ASP:H	8	0.27
(4,557)	1:222:A:VAL:H	1:221:A:GLN:H	16	0.27
(4,455)	1:219:A:SER:HA	1:222:A:VAL:HG21	15	0.27
(4,453)	1:209:A:ILE:HG12	1:209:A:ILE:HG13	1	0.27
(4,453)	1:209:A:ILE:HG12	1:209:A:ILE:HG13	2	0.27
(4,453)	1:209:A:ILE:HG12	1:209:A:ILE:HG13	3	0.27
(4,453)	1:209:A:ILE:HG12	1:209:A:ILE:HG13	4	0.27
(4,453)	1:209:A:ILE:HG12	1:209:A:ILE:HG13	5	0.27
(4,453)	1:209:A:ILE:HG12	1:209:A:ILE:HG13	6	0.27
(4,453)	1:209:A:ILE:HG12	1:209:A:ILE:HG13	7	0.27
(4,453)	1:209:A:ILE:HG12	1:209:A:ILE:HG13	8	0.27
(4,453)	1:209:A:ILE:HG12	1:209:A:ILE:HG13	9	0.27
(4,453)	1:209:A:ILE:HG12	1:209:A:ILE:HG13	10	0.27
(4,453)	1:209:A:ILE:HG12	1:209:A:ILE:HG13	11	0.27
(4,453)	1:209:A:ILE:HG12	1:209:A:ILE:HG13	12	0.27
(4,453)	1:209:A:ILE:HG12	1:209:A:ILE:HG13	13	0.27
(4,453)	1:209:A:ILE:HG12	1:209:A:ILE:HG13	14	0.27
(4,453)	1:209:A:ILE:HG12	1:209:A:ILE:HG13	15	0.27
(4,453)	1:209:A:ILE:HG12	1:209:A:ILE:HG13	16	0.27
(4,453)	1:209:A:ILE:HG12	1:209:A:ILE:HG13	18	0.27
(4,453)	1:209:A:ILE:HG12	1:209:A:ILE:HG13	19	0.27
(4,453)	1:209:A:ILE:HG12	1:209:A:ILE:HG13	20	0.27
(4,438)	1:22:A:ILE:HD12	1:22:A:ILE:HA	18	0.27
(4,435)	1:160:A:VAL:HA	1:160:A:VAL:HG23	8	0.27
(4,416)	1:24:A:LYS:HG3	1:17:A:HIS:HB3	19	0.27
(4,397)	1:159:A:VAL:HA	1:162:A:VAL:HB	4	0.27
(4,396)	1:67:A:ASN:HB3	1:67:A:ASN:HA	6	0.27
(4,396)	1:153:A:LYS:HA	1:153:A:LYS:HB2	16	0.27
(4,324)	1:67:A:ASN:HB3	1:67:A:ASN:HA	2	0.27
(4,245)	1:228:A:LEU:H	1:228:A:LEU:HA	8	0.27
(4,219)	1:105:A:SER:H	1:105:A:SER:HB2	11	0.27
(4,219)	1:105:A:SER:H	1:105:A:SER:HB3	13	0.27
(4,213)	1:167:A:LYS:HB2	1:168:A:THR:H	11	0.27
(4,208)	1:45:A:LYS:H	1:44:A:LEU:HA	8	0.27
(4,208)	1:45:A:LYS:H	1:44:A:LEU:HA	14	0.27
(4,205)	1:54:A:ALA:H	1:54:A:ALA:HB2	8	0.27
(4,205)	1:66:A:PHE:H	1:65:A:ALA:HB2	15	0.27
(4,205)	1:54:A:ALA:H	1:54:A:ALA:HB2	20	0.27
(4,204)	1:253:A:ARG:H	1:253:A:ARG:HG2	19	0.27
(4,202)	1:37:A:THR:H	1:34:A:ASP:HB2	2	0.27
(4,202)	1:37:A:THR:H	1:34:A:ASP:HB3	8	0.27

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,189)	1:162:A:VAL:H	1:161:A:ASP:HB2	7	0.27
(4,119)	1:232:A:GLY:H	1:231:A:ASN:HB3	2	0.27
(4,114)	1:89:A:ARG:H	1:89:A:ARG:HG2	9	0.27
(4,114)	1:27:A:ARG:H	1:27:A:ARG:HG3	18	0.27
(4,90)	1:112:A:LYS:H	1:108:A:THR:HB	17	0.27
(4,43)	1:95:A:PHE:H	1:95:A:PHE:HB3	1	0.27
(4,36)	1:85:A:ASP:H	1:85:A:ASP:HB3	8	0.27
(3,305)	1:166:A:ILE:H	1:168:A:THR:H	20	0.27
(3,205)	1:124:A:ASN:H	1:127:A:TYR:H	12	0.27
(3,166)	1:205:A:CYS:H	1:197:A:LEU:H	19	0.27
(3,11)	1:177:A:ASN:H	1:56:A:SER:H	14	0.27
(1,129)	1:114:A:TYR:H	1:113:A:LYS:HG2	12	0.27
(1,105)	1:6:A:GLY:H	1:6:A:GLY:HA3	16	0.27
(1,100)	1:245:A:ARG:H	1:244:A:TRP:HB2	5	0.27
(1,100)	1:245:A:ARG:H	1:244:A:TRP:HB2	17	0.27
(1,45)	1:225:A:PHE:HB2	1:222:A:VAL:HA	8	0.27
(1,45)	1:225:A:PHE:HB2	1:222:A:VAL:HA	17	0.27
(1,42)	1:116:A:ALA:HB3	1:97:A:TRP:HA	14	0.27
(4,1299)	1:91:A:ILE:H	1:91:A:ILE:HD13	5	0.26
(4,1282)	1:152:A:ALA:H	1:152:A:ALA:HB3	17	0.26
(4,1261)	1:152:A:ALA:H	1:152:A:ALA:HB3	5	0.26
(4,1261)	1:152:A:ALA:H	1:152:A:ALA:HB3	6	0.26
(4,1261)	1:152:A:ALA:H	1:152:A:ALA:HB1	19	0.26
(4,1242)	1:247:A:ALA:H	1:247:A:ALA:HB2	15	0.26
(4,1223)	1:147:A:LEU:H	1:147:A:LEU:HG	6	0.26
(4,1223)	1:152:A:ALA:H	1:152:A:ALA:HB2	9	0.26
(4,1223)	1:124:A:ASN:H	1:133:A:ALA:HB3	13	0.26
(4,1185)	1:126:A:LYS:H	1:126:A:LYS:HB2	8	0.26
(4,1173)	1:80:A:LYS:H	1:80:A:LYS:HG2	7	0.26
(4,1160)	1:224:A:LYS:H	1:224:A:LYS:HG2	15	0.26
(4,1147)	1:231:A:ASN:H	1:169:A:LYS:HD3	14	0.26
(4,1141)	1:129:A:ASP:H	1:132:A:LYS:HB2	17	0.26
(4,1139)	1:256:A:LYS:H	1:256:A:LYS:HG3	13	0.26
(4,1138)	1:238:A:GLU:H	1:238:A:GLU:HB2	1	0.26
(4,1128)	1:251:A:LYS:H	1:250:A:LEU:HB3	15	0.26
(4,1114)	1:84:A:LEU:H	1:84:A:LEU:HB3	7	0.26
(4,1114)	1:84:A:LEU:H	1:84:A:LEU:HB3	18	0.26
(4,1109)	1:209:A:ILE:H	1:209:A:ILE:HB	5	0.26
(4,1109)	1:204:A:GLU:H	1:204:A:GLU:HB2	15	0.26
(4,1107)	1:147:A:LEU:H	1:146:A:PHE:HB3	8	0.26
(4,1106)	1:90:A:LEU:H	1:90:A:LEU:HB2	19	0.26
(4,1094)	1:37:A:THR:H	1:34:A:ASP:HB3	9	0.26

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1059)	1:229:A:ASN:H	1:228:A:LEU:HB3	18	0.26
(4,1055)	1:18:A:LYS:H	1:18:A:LYS:HB2	1	0.26
(4,1055)	1:18:A:LYS:H	1:18:A:LYS:HB2	2	0.26
(4,1055)	1:18:A:LYS:H	1:18:A:LYS:HB2	6	0.26
(4,1027)	1:103:A:GLN:H	1:100:A:LEU:HB2	14	0.26
(4,1025)	1:28:A:GLN:H	1:28:A:GLN:HB2	6	0.26
(4,1025)	1:164:A:ASP:H	1:164:A:ASP:HB2	15	0.26
(4,974)	1:238:A:GLU:H	1:229:A:ASN:HB3	2	0.26
(4,962)	1:129:A:ASP:H	1:129:A:ASP:HB2	11	0.26
(4,962)	1:129:A:ASP:H	1:129:A:ASP:HB3	18	0.26
(4,880)	1:166:A:ILE:H	1:165:A:SER:HB3	16	0.26
(4,874)	1:84:A:LEU:H	1:84:A:LEU:HA	7	0.26
(4,874)	1:84:A:LEU:H	1:84:A:LEU:HA	11	0.26
(4,874)	1:84:A:LEU:H	1:84:A:LEU:HA	16	0.26
(4,874)	1:84:A:LEU:H	1:84:A:LEU:HA	20	0.26
(4,862)	1:78:A:VAL:H	1:50:A:SER:HB2	17	0.26
(4,841)	1:167:A:LYS:H	1:167:A:LYS:HA	4	0.26
(4,835)	1:229:A:ASN:H	1:228:A:LEU:HA	1	0.26
(4,835)	1:229:A:ASN:H	1:228:A:LEU:HA	2	0.26
(4,801)	1:166:A:ILE:H	1:165:A:SER:HB3	3	0.26
(4,767)	1:229:A:ASN:H	1:228:A:LEU:HA	17	0.26
(4,762)	1:93:A:PHE:H	1:93:A:PHE:HA	8	0.26
(4,753)	1:172:A:SER:H	1:171:A:LYS:HA	3	0.26
(4,753)	1:172:A:SER:H	1:171:A:LYS:HA	9	0.26
(4,753)	1:172:A:SER:H	1:171:A:LYS:HA	18	0.26
(4,742)	1:71:A:ASP:H	1:70:A:PHE:HA	16	0.26
(4,669)	1:29:A:SER:H	1:31:A:VAL:H	19	0.26
(4,668)	1:29:A:SER:H	1:31:A:VAL:H	19	0.26
(4,574)	1:127:A:TYR:H	1:126:A:LYS:H	2	0.26
(4,572)	1:159:A:VAL:H	1:160:A:VAL:H	9	0.26
(4,557)	1:222:A:VAL:H	1:221:A:GLN:H	11	0.26
(4,453)	1:209:A:ILE:HG12	1:209:A:ILE:HG13	17	0.26
(4,449)	1:160:A:VAL:HA	1:160:A:VAL:HG23	8	0.26
(4,449)	1:159:A:VAL:HA	1:159:A:VAL:HG21	17	0.26
(4,438)	1:22:A:ILE:HD13	1:22:A:ILE:HA	14	0.26
(4,435)	1:35:A:THR:HG22	1:35:A:THR:HA	16	0.26
(4,405)	1:49:A:VAL:HA	1:49:A:VAL:HB	13	0.26
(4,404)	1:134:A:VAL:HA	1:134:A:VAL:HB	13	0.26
(4,396)	1:148:A:LYS:HB3	1:148:A:LYS:HA	4	0.26
(4,396)	1:67:A:ASN:HB3	1:67:A:ASN:HA	17	0.26
(4,396)	1:153:A:LYS:HA	1:153:A:LYS:HB2	18	0.26
(4,379)	1:260:A:LYS:HG2	1:260:A:LYS:HE3	4	0.26

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,379)	1:169:A:LYS:HG3	1:61:A:ASN:HB2	15	0.26
(4,330)	1:152:A:ALA:HB3	1:152:A:ALA:HA	13	0.26
(4,324)	1:67:A:ASN:HB3	1:67:A:ASN:HA	4	0.26
(4,324)	1:60:A:LEU:HB2	1:60:A:LEU:HA	13	0.26
(4,245)	1:228:A:LEU:H	1:228:A:LEU:HA	1	0.26
(4,245)	1:228:A:LEU:H	1:228:A:LEU:HA	14	0.26
(4,224)	1:259:A:PHE:H	1:258:A:SER:HB3	7	0.26
(4,224)	1:259:A:PHE:H	1:258:A:SER:HB3	11	0.26
(4,213)	1:167:A:LYS:HB3	1:168:A:THR:H	12	0.26
(4,208)	1:45:A:LYS:H	1:44:A:LEU:HA	10	0.26
(4,205)	1:54:A:ALA:H	1:54:A:ALA:HB3	19	0.26
(4,87)	1:91:A:ILE:H	1:91:A:ILE:HG13	8	0.26
(4,81)	1:55:A:THR:H	1:76:A:LYS:HG3	19	0.26
(4,80)	1:119:A:HIS:H	1:119:A:HIS:HB2	19	0.26
(4,66)	1:204:A:GLU:H	1:22:A:ILE:HD12	12	0.26
(4,15)	1:192:A:THR:H	1:255:A:ILE:HG12	20	0.26
(4,6)	1:113:A:LYS:HG3	1:107:A:HIS:H	20	0.26
(3,318)	1:171:A:LYS:H	1:168:A:THR:H	13	0.26
(3,290)	1:196:A:SER:H	1:206:A:VAL:H	5	0.26
(3,282)	1:202:A:LEU:H	1:199:A:THR:H	16	0.26
(3,252)	1:196:A:SER:H	1:206:A:VAL:H	5	0.26
(3,158)	1:57:A:LEU:H	1:70:A:PHE:H	8	0.26
(3,67)	1:169:A:LYS:H	1:229:A:ASN:H	2	0.26
(3,58)	1:70:A:PHE:H	1:57:A:LEU:H	4	0.26
(1,123)	1:63:A:GLY:H	1:169:A:LYS:HG2	15	0.26
(1,73)	1:134:A:VAL:HG21	1:131:A:GLY:HA2	17	0.26
(1,22)	1:156:A:LEU:H	1:153:A:LYS:HD2	16	0.26
(4,1316)	1:205:A:CYS:H	1:206:A:VAL:HG23	11	0.25
(4,1299)	1:23:A:ALA:H	1:22:A:ILE:HG22	18	0.25
(4,1292)	1:91:A:ILE:H	1:91:A:ILE:HD13	5	0.25
(4,1283)	1:148:A:LYS:H	1:148:A:LYS:HG3	5	0.25
(4,1283)	1:152:A:ALA:H	1:152:A:ALA:HB2	13	0.25
(4,1225)	1:164:A:ASP:H	1:163:A:LEU:HG	19	0.25
(4,1200)	1:251:A:LYS:H	1:250:A:LEU:HB2	19	0.25
(4,1195)	1:228:A:LEU:H	1:228:A:LEU:HB2	11	0.25
(4,1189)	1:34:A:ASP:H	1:37:A:THR:HG22	9	0.25
(4,1176)	1:93:A:PHE:H	1:68:A:VAL:HB	20	0.25
(4,1174)	1:148:A:LYS:H	1:148:A:LYS:HG3	5	0.25
(4,1174)	1:152:A:ALA:H	1:152:A:ALA:HB2	13	0.25
(4,1172)	1:256:A:LYS:H	1:256:A:LYS:HB2	14	0.25
(4,1162)	1:133:A:ALA:H	1:133:A:ALA:HB3	2	0.25
(4,1160)	1:224:A:LYS:H	1:224:A:LYS:HG2	1	0.25

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1147)	1:231:A:ASN:H	1:169:A:LYS:HD3	8	0.25
(4,1135)	1:221:A:GLN:H	1:221:A:GLN:HB2	4	0.25
(4,1125)	1:22:A:ILE:H	1:22:A:ILE:HB	8	0.25
(4,1125)	1:233:A:GLU:H	1:233:A:GLU:HG3	12	0.25
(4,1114)	1:171:A:LYS:H	1:171:A:LYS:HB2	1	0.25
(4,1114)	1:22:A:ILE:H	1:22:A:ILE:HB	8	0.25
(4,1114)	1:84:A:LEU:H	1:84:A:LEU:HB2	16	0.25
(4,1109)	1:133:A:ALA:H	1:133:A:ALA:HB3	4	0.25
(4,1109)	1:133:A:ALA:H	1:133:A:ALA:HB1	8	0.25
(4,1109)	1:133:A:ALA:H	1:133:A:ALA:HB1	13	0.25
(4,1109)	1:133:A:ALA:H	1:133:A:ALA:HB1	18	0.25
(4,1083)	1:248:A:GLN:H	1:248:A:GLN:HG2	10	0.25
(4,1075)	1:164:A:ASP:H	1:163:A:LEU:HG	14	0.25
(4,1059)	1:229:A:ASN:H	1:228:A:LEU:HB3	12	0.25
(4,1059)	1:229:A:ASN:H	1:228:A:LEU:HB3	16	0.25
(4,1055)	1:18:A:LYS:H	1:18:A:LYS:HB2	12	0.25
(4,1025)	1:28:A:GLN:H	1:28:A:GLN:HB2	3	0.25
(4,1025)	1:164:A:ASP:H	1:164:A:ASP:HB2	19	0.25
(4,1016)	1:43:A:SER:H	1:41:A:ASP:HB3	3	0.25
(4,998)	1:175:A:PHE:H	1:175:A:PHE:HB2	20	0.25
(4,993)	1:205:A:CYS:H	1:205:A:CYS:HB2	1	0.25
(4,980)	1:191:A:TRP:H	1:191:A:TRP:HB3	13	0.25
(4,968)	1:129:A:ASP:H	1:129:A:ASP:HB3	18	0.25
(4,933)	1:129:A:ASP:H	1:129:A:ASP:HA	15	0.25
(4,922)	1:122:A:HIS:H	1:122:A:HIS:HB2	13	0.25
(4,874)	1:84:A:LEU:H	1:84:A:LEU:HA	9	0.25
(4,874)	1:84:A:LEU:H	1:84:A:LEU:HA	13	0.25
(4,864)	1:167:A:LYS:H	1:167:A:LYS:HA	12	0.25
(4,862)	1:78:A:VAL:H	1:50:A:SER:HB2	13	0.25
(4,849)	1:99:A:SER:H	1:99:A:SER:HA	13	0.25
(4,836)	1:129:A:ASP:H	1:128:A:GLY:HA3	20	0.25
(4,835)	1:229:A:ASN:H	1:228:A:LEU:HA	11	0.25
(4,835)	1:229:A:ASN:H	1:228:A:LEU:HA	14	0.25
(4,832)	1:247:A:ALA:H	1:247:A:ALA:HA	8	0.25
(4,832)	1:253:A:ARG:H	1:253:A:ARG:HA	18	0.25
(4,817)	1:103:A:GLN:H	1:103:A:GLN:HA	5	0.25
(4,817)	1:103:A:GLN:H	1:103:A:GLN:HA	8	0.25
(4,817)	1:103:A:GLN:H	1:103:A:GLN:HA	15	0.25
(4,805)	1:166:A:ILE:H	1:165:A:SER:HB3	13	0.25
(4,801)	1:166:A:ILE:H	1:165:A:SER:HB3	13	0.25
(4,758)	1:252:A:ASN:H	1:252:A:ASN:HA	15	0.25
(4,753)	1:172:A:SER:H	1:171:A:LYS:HA	1	0.25

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,753)	1:172:A:SER:H	1:171:A:LYS:HA	4	0.25
(4,753)	1:172:A:SER:H	1:171:A:LYS:HA	5	0.25
(4,704)	1:16:A:TRP:H	1:16:A:TRP:HA	2	0.25
(4,655)	1:97:A:TRP:H	1:244:A:TRP:H	15	0.25
(4,620)	1:37:A:THR:H	1:36:A:HIS:H	7	0.25
(4,557)	1:222:A:VAL:H	1:223:A:LEU:H	9	0.25
(4,557)	1:222:A:VAL:H	1:223:A:LEU:H	17	0.25
(4,457)	1:78:A:VAL:HB	1:87:A:THR:HG22	10	0.25
(4,446)	1:22:A:ILE:HG22	1:22:A:ILE:HA	20	0.25
(4,439)	1:22:A:ILE:HG22	1:202:A:LEU:HA	4	0.25
(4,412)	1:23:A:ALA:HB3	1:17:A:HIS:HA	3	0.25
(4,411)	1:23:A:ALA:HB3	1:17:A:HIS:HA	3	0.25
(4,404)	1:49:A:VAL:HA	1:49:A:VAL:HB	4	0.25
(4,404)	1:159:A:VAL:HA	1:159:A:VAL:HB	18	0.25
(4,404)	1:134:A:VAL:HA	1:134:A:VAL:HB	20	0.25
(4,401)	1:203:A:LEU:HB2	1:196:A:SER:HB3	19	0.25
(4,397)	1:163:A:LEU:HB3	1:160:A:VAL:HA	2	0.25
(4,330)	1:152:A:ALA:HB3	1:152:A:ALA:HA	12	0.25
(4,324)	1:67:A:ASN:HB3	1:67:A:ASN:HA	8	0.25
(4,324)	1:230:A:PHE:HB3	1:230:A:PHE:HA	14	0.25
(4,324)	1:230:A:PHE:HB2	1:230:A:PHE:HA	15	0.25
(4,245)	1:228:A:LEU:H	1:228:A:LEU:HA	13	0.25
(4,245)	1:228:A:LEU:H	1:228:A:LEU:HA	19	0.25
(4,219)	1:105:A:SER:H	1:105:A:SER:HB3	7	0.25
(4,218)	1:224:A:LYS:H	1:224:A:LYS:HB2	10	0.25
(4,209)	1:82:A:GLY:H	1:47:A:LEU:HB2	10	0.25
(4,205)	1:54:A:ALA:H	1:54:A:ALA:HB2	7	0.25
(4,205)	1:54:A:ALA:H	1:54:A:ALA:HB3	16	0.25
(4,204)	1:100:A:LEU:H	1:100:A:LEU:HG	20	0.25
(4,202)	1:162:A:VAL:H	1:161:A:ASP:HB2	7	0.25
(4,189)	1:37:A:THR:H	1:34:A:ASP:HB2	6	0.25
(4,185)	1:22:A:ILE:H	1:22:A:ILE:HD13	14	0.25
(4,182)	1:166:A:ILE:H	1:163:A:LEU:HA	6	0.25
(4,167)	1:32:A:ASP:H	1:32:A:ASP:HB3	20	0.25
(4,119)	1:229:A:ASN:H	1:229:A:ASN:HB2	11	0.25
(4,116)	1:112:A:LYS:H	1:108:A:THR:HB	17	0.25
(3,322)	1:108:A:THR:H	1:31:A:VAL:H	20	0.25
(3,314)	1:229:A:ASN:H	1:168:A:THR:H	15	0.25
(3,237)	1:189:A:ASP:H	1:212:A:LYS:H	5	0.25
(3,210)	1:197:A:LEU:H	1:205:A:CYS:H	6	0.25
(3,92)	1:55:A:THR:H	1:77:A:ALA:H	9	0.25
(3,92)	1:55:A:THR:H	1:77:A:ALA:H	14	0.25

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,71)	1:138:A:ASP:H	1:140:A:LEU:H	2	0.25
(3,58)	1:70:A:PHE:H	1:57:A:LEU:H	19	0.25
(1,105)	1:6:A:GLY:H	1:6:A:GLY:HA3	4	0.25
(1,105)	1:6:A:GLY:H	1:6:A:GLY:HA3	7	0.25
(1,38)	1:77:A:ALA:HA	1:51:A:TYR:HA	3	0.25
(4,1338)	1:161:A:ASP:H	1:163:A:LEU:HD22	12	0.24
(4,1328)	1:105:A:SER:H	1:113:A:LYS:HG2	5	0.24
(4,1326)	1:212:A:LYS:H	1:211:A:LEU:HD22	8	0.24
(4,1322)	1:203:A:LEU:H	1:203:A:LEU:HD23	13	0.24
(4,1292)	1:23:A:ALA:H	1:22:A:ILE:HG22	18	0.24
(4,1282)	1:148:A:LYS:H	1:148:A:LYS:HG3	5	0.24
(4,1282)	1:152:A:ALA:H	1:152:A:ALA:HB2	13	0.24
(4,1228)	1:152:A:ALA:H	1:152:A:ALA:HB3	15	0.24
(4,1212)	1:205:A:CYS:H	1:203:A:LEU:HB2	10	0.24
(4,1195)	1:228:A:LEU:H	1:228:A:LEU:HB2	9	0.24
(4,1195)	1:228:A:LEU:H	1:228:A:LEU:HB2	10	0.24
(4,1192)	1:251:A:LYS:H	1:250:A:LEU:HB2	19	0.24
(4,1172)	1:239:A:LEU:H	1:239:A:LEU:HB2	2	0.24
(4,1172)	1:141:A:ALA:H	1:140:A:LEU:HB2	7	0.24
(4,1164)	1:167:A:LYS:H	1:167:A:LYS:HB3	8	0.24
(4,1162)	1:133:A:ALA:H	1:133:A:ALA:HB3	14	0.24
(4,1147)	1:99:A:SER:H	1:100:A:LEU:HG	10	0.24
(4,1128)	1:251:A:LYS:H	1:250:A:LEU:HB2	10	0.24
(4,1121)	1:147:A:LEU:H	1:146:A:PHE:HB3	10	0.24
(4,1111)	1:181:A:ARG:H	1:181:A:ARG:HG3	20	0.24
(4,1109)	1:133:A:ALA:H	1:133:A:ALA:HB1	1	0.24
(4,1109)	1:209:A:ILE:H	1:209:A:ILE:HB	6	0.24
(4,1109)	1:133:A:ALA:H	1:133:A:ALA:HB3	11	0.24
(4,1107)	1:147:A:LEU:H	1:146:A:PHE:HB3	10	0.24
(4,1084)	1:259:A:PHE:H	1:259:A:PHE:HB2	16	0.24
(4,1075)	1:28:A:GLN:H	1:28:A:GLN:HB2	12	0.24
(4,1059)	1:124:A:ASN:H	1:124:A:ASN:HB3	20	0.24
(4,1058)	1:248:A:GLN:H	1:248:A:GLN:HB3	6	0.24
(4,1053)	1:37:A:THR:H	1:34:A:ASP:HB3	14	0.24
(4,1051)	1:57:A:LEU:H	1:57:A:LEU:HB2	5	0.24
(4,1009)	1:62:A:ASN:H	1:61:A:ASN:HB3	5	0.24
(4,1009)	1:62:A:ASN:H	1:61:A:ASN:HB3	10	0.24
(4,998)	1:175:A:PHE:H	1:175:A:PHE:HB3	14	0.24
(4,994)	1:37:A:THR:H	1:34:A:ASP:HB3	14	0.24
(4,990)	1:253:A:ARG:H	1:252:A:ASN:HB3	7	0.24
(4,968)	1:129:A:ASP:H	1:129:A:ASP:HB2	11	0.24
(4,965)	1:253:A:ARG:H	1:252:A:ASN:HB3	7	0.24

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,963)	1:121:A:VAL:H	1:122:A:HIS:HB2	12	0.24
(4,909)	1:70:A:PHE:H	1:70:A:PHE:HB2	7	0.24
(4,901)	1:167:A:LYS:H	1:167:A:LYS:HA	12	0.24
(4,901)	1:221:A:GLN:H	1:218:A:SER:HB3	17	0.24
(4,874)	1:84:A:LEU:H	1:84:A:LEU:HA	4	0.24
(4,874)	1:84:A:LEU:H	1:84:A:LEU:HA	12	0.24
(4,864)	1:167:A:LYS:H	1:167:A:LYS:HA	14	0.24
(4,864)	1:221:A:GLN:H	1:218:A:SER:HB3	17	0.24
(4,864)	1:167:A:LYS:H	1:167:A:LYS:HA	18	0.24
(4,849)	1:116:A:ALA:H	1:116:A:ALA:HA	19	0.24
(4,835)	1:229:A:ASN:H	1:228:A:LEU:HA	20	0.24
(4,832)	1:247:A:ALA:H	1:247:A:ALA:HA	14	0.24
(4,832)	1:247:A:ALA:H	1:247:A:ALA:HA	16	0.24
(4,832)	1:253:A:ARG:H	1:253:A:ARG:HA	19	0.24
(4,817)	1:103:A:GLN:H	1:103:A:GLN:HA	4	0.24
(4,789)	1:106:A:GLU:H	1:105:A:SER:HA	6	0.24
(4,762)	1:93:A:PHE:H	1:93:A:PHE:HA	10	0.24
(4,762)	1:93:A:PHE:H	1:93:A:PHE:HA	17	0.24
(4,624)	1:103:A:GLN:H	1:102:A:GLY:H	6	0.24
(4,572)	1:222:A:VAL:H	1:221:A:GLN:H	6	0.24
(4,557)	1:222:A:VAL:H	1:221:A:GLN:H	12	0.24
(4,468)	1:51:A:TYR:HA	1:78:A:VAL:HG23	14	0.24
(4,466)	1:106:A:GLU:HG3	1:113:A:LYS:HD3	9	0.24
(4,460)	1:224:A:LYS:HA	1:224:A:LYS:HD3	15	0.24
(4,457)	1:78:A:VAL:HB	1:87:A:THR:HG22	7	0.24
(4,446)	1:221:A:GLN:HA	1:160:A:VAL:HG21	4	0.24
(4,435)	1:35:A:THR:HG21	1:35:A:THR:HA	2	0.24
(4,435)	1:35:A:THR:HG22	1:35:A:THR:HA	3	0.24
(4,435)	1:35:A:THR:HG21	1:35:A:THR:HA	9	0.24
(4,435)	1:159:A:VAL:HA	1:159:A:VAL:HG21	19	0.24
(4,431)	1:108:A:THR:HG21	1:108:A:THR:HB	18	0.24
(4,396)	1:67:A:ASN:HB3	1:67:A:ASN:HA	1	0.24
(4,396)	1:148:A:LYS:HB3	1:148:A:LYS:HA	5	0.24
(4,374)	1:127:A:TYR:HB3	1:133:A:ALA:HA	18	0.24
(4,371)	1:146:A:PHE:HB3	1:114:A:TYR:HB3	20	0.24
(4,330)	1:192:A:THR:HG21	1:192:A:THR:HB	6	0.24
(4,330)	1:247:A:ALA:HB2	1:247:A:ALA:HA	7	0.24
(4,330)	1:247:A:ALA:HB3	1:247:A:ALA:HA	17	0.24
(4,330)	1:54:A:ALA:HB3	1:54:A:ALA:HA	18	0.24
(4,324)	1:60:A:LEU:HB2	1:60:A:LEU:HA	5	0.24
(4,324)	1:60:A:LEU:HB2	1:60:A:LEU:HA	10	0.24
(4,324)	1:60:A:LEU:HB2	1:60:A:LEU:HA	12	0.24

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,300)	1:209:A:ILE:HD13	1:209:A:ILE:HA	6	0.24
(4,258)	1:252:A:ASN:H	1:252:A:ASN:HB3	9	0.24
(4,252)	1:259:A:PHE:H	1:40:A:TYR:HB2	3	0.24
(4,251)	1:259:A:PHE:H	1:40:A:TYR:HB2	3	0.24
(4,236)	1:82:A:GLY:H	1:82:A:GLY:HA3	7	0.24
(4,205)	1:66:A:PHE:H	1:65:A:ALA:HB3	4	0.24
(4,205)	1:54:A:ALA:H	1:54:A:ALA:HB2	10	0.24
(4,189)	1:37:A:THR:H	1:34:A:ASP:HB3	15	0.24
(4,185)	1:22:A:ILE:H	1:22:A:ILE:HD12	6	0.24
(4,167)	1:32:A:ASP:H	1:32:A:ASP:HB2	3	0.24
(4,87)	1:256:A:LYS:H	1:256:A:LYS:HD2	2	0.24
(4,87)	1:55:A:THR:H	1:76:A:LYS:HD3	13	0.24
(4,87)	1:91:A:ILE:H	1:91:A:ILE:HG13	20	0.24
(4,71)	1:61:A:ASN:H	1:60:A:LEU:HD11	19	0.24
(4,39)	1:37:A:THR:HG23	1:255:A:ILE:H	20	0.24
(4,32)	1:191:A:TRP:H	1:211:A:LEU:HG	20	0.24
(4,2)	1:245:A:ARG:HG2	1:245:A:ARG:H	4	0.24
(3,255)	1:147:A:LEU:H	1:115:A:ALA:H	19	0.24
(3,184)	1:43:A:SER:H	1:41:A:ASP:H	18	0.24
(2,16)	1:82:A:GLY:H	1:45:A:LYS:H	18	0.24
(1,113)	1:104:A:GLY:H	1:103:A:GLN:HB2	13	0.24
(1,79)	1:68:A:VAL:H	1:93:A:PHE:H	9	0.24
(1,78)	1:117:A:GLU:H	1:96:A:HIS:H	7	0.24
(1,73)	1:134:A:VAL:HG22	1:131:A:GLY:HA2	15	0.24
(1,64)	1:60:A:LEU:HB2	1:172:A:SER:HB3	3	0.24
(1,44)	1:91:A:ILE:HD12	1:122:A:HIS:HA	11	0.24
(4,1316)	1:165:A:SER:H	1:166:A:ILE:HD12	5	0.23
(4,1283)	1:152:A:ALA:H	1:152:A:ALA:HB3	11	0.23
(4,1283)	1:152:A:ALA:H	1:152:A:ALA:HB2	12	0.23
(4,1282)	1:152:A:ALA:H	1:152:A:ALA:HB2	12	0.23
(4,1271)	1:231:A:ASN:H	1:169:A:LYS:HG2	20	0.23
(4,1261)	1:152:A:ALA:H	1:152:A:ALA:HB1	14	0.23
(4,1257)	1:251:A:LYS:H	1:251:A:LYS:HG2	16	0.23
(4,1248)	1:22:A:ILE:H	1:22:A:ILE:HD12	20	0.23
(4,1227)	1:23:A:ALA:H	1:22:A:ILE:HG22	18	0.23
(4,1173)	1:22:A:ILE:H	1:22:A:ILE:HB	8	0.23
(4,1172)	1:239:A:LEU:H	1:239:A:LEU:HB2	3	0.23
(4,1172)	1:256:A:LYS:H	1:256:A:LYS:HG2	20	0.23
(4,1162)	1:209:A:ILE:H	1:209:A:ILE:HB	5	0.23
(4,1162)	1:47:A:LEU:H	1:47:A:LEU:HB3	15	0.23
(4,1135)	1:221:A:GLN:H	1:221:A:GLN:HB3	12	0.23
(4,1135)	1:221:A:GLN:H	1:221:A:GLN:HB3	16	0.23

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1126)	1:228:A:LEU:H	1:228:A:LEU:HG	16	0.23
(4,1126)	1:18:A:LYS:H	1:18:A:LYS:HG2	20	0.23
(4,1125)	1:149:A:VAL:H	1:148:A:LYS:HB2	16	0.23
(4,1115)	1:158:A:LYS:H	1:158:A:LYS:HB3	19	0.23
(4,1114)	1:84:A:LEU:H	1:84:A:LEU:HB3	12	0.23
(4,1109)	1:133:A:ALA:H	1:133:A:ALA:HB1	16	0.23
(4,1083)	1:237:A:GLU:H	1:237:A:GLU:HG2	12	0.23
(4,1066)	1:135:A:GLN:H	1:135:A:GLN:HG2	6	0.23
(4,1055)	1:18:A:LYS:H	1:18:A:LYS:HB2	3	0.23
(4,1054)	1:131:A:GLY:H	1:129:A:ASP:HB2	20	0.23
(4,1036)	1:158:A:LYS:H	1:158:A:LYS:HB2	8	0.23
(4,1027)	1:103:A:GLN:H	1:100:A:LEU:HB2	13	0.23
(4,1025)	1:164:A:ASP:H	1:164:A:ASP:HB3	9	0.23
(4,1016)	1:43:A:SER:H	1:41:A:ASP:HB3	1	0.23
(4,1005)	1:175:A:PHE:H	1:175:A:PHE:HB3	14	0.23
(4,1005)	1:175:A:PHE:H	1:175:A:PHE:HB2	20	0.23
(4,998)	1:175:A:PHE:H	1:175:A:PHE:HB3	3	0.23
(4,993)	1:127:A:TYR:H	1:127:A:TYR:HB2	6	0.23
(4,993)	1:127:A:TYR:H	1:127:A:TYR:HB2	14	0.23
(4,993)	1:127:A:TYR:H	1:127:A:TYR:HB2	15	0.23
(4,993)	1:127:A:TYR:H	1:127:A:TYR:HB2	19	0.23
(4,993)	1:127:A:TYR:H	1:127:A:TYR:HB3	20	0.23
(4,983)	1:119:A:HIS:H	1:119:A:HIS:HB2	2	0.23
(4,962)	1:129:A:ASP:H	1:129:A:ASP:HB2	1	0.23
(4,962)	1:129:A:ASP:H	1:129:A:ASP:HB2	16	0.23
(4,962)	1:129:A:ASP:H	1:129:A:ASP:HB2	17	0.23
(4,922)	1:65:A:ALA:H	1:62:A:ASN:HB3	1	0.23
(4,901)	1:167:A:LYS:H	1:167:A:LYS:HA	5	0.23
(4,901)	1:167:A:LYS:H	1:167:A:LYS:HA	14	0.23
(4,901)	1:167:A:LYS:H	1:167:A:LYS:HA	18	0.23
(4,898)	1:49:A:VAL:H	1:49:A:VAL:HA	20	0.23
(4,878)	1:7:A:TYR:H	1:7:A:TYR:HB2	14	0.23
(4,874)	1:84:A:LEU:H	1:84:A:LEU:HA	10	0.23
(4,862)	1:78:A:VAL:H	1:50:A:SER:HB2	11	0.23
(4,845)	1:151:A:SER:H	1:150:A:GLY:HA2	7	0.23
(4,835)	1:106:A:GLU:H	1:105:A:SER:HA	6	0.23
(4,817)	1:103:A:GLN:H	1:103:A:GLN:HA	13	0.23
(4,781)	1:25:A:GLY:H	1:25:A:GLY:HA3	12	0.23
(4,762)	1:93:A:PHE:H	1:93:A:PHE:HA	2	0.23
(4,762)	1:93:A:PHE:H	1:93:A:PHE:HA	3	0.23
(4,762)	1:93:A:PHE:H	1:93:A:PHE:HA	13	0.23
(4,762)	1:93:A:PHE:H	1:93:A:PHE:HA	15	0.23

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,762)	1:93:A:PHE:H	1:93:A:PHE:HA	19	0.23
(4,758)	1:252:A:ASN:H	1:252:A:ASN:HA	6	0.23
(4,753)	1:172:A:SER:H	1:171:A:LYS:HA	16	0.23
(4,742)	1:71:A:ASP:H	1:70:A:PHE:HA	1	0.23
(4,722)	1:57:A:LEU:H	1:56:A:SER:HA	16	0.23
(4,572)	1:227:A:LYS:H	1:228:A:LEU:H	13	0.23
(4,572)	1:135:A:GLN:H	1:136:A:GLN:H	17	0.23
(4,557)	1:222:A:VAL:H	1:221:A:GLN:H	3	0.23
(4,557)	1:222:A:VAL:H	1:223:A:LEU:H	7	0.23
(4,487)	1:48:A:SER:H	1:47:A:LEU:H	15	0.23
(4,466)	1:243:A:ASN:HB2	1:241:A:VAL:HG21	5	0.23
(4,450)	1:147:A:LEU:HA	1:147:A:LEU:HD22	1	0.23
(4,450)	1:147:A:LEU:HA	1:147:A:LEU:HD23	10	0.23
(4,449)	1:159:A:VAL:HA	1:159:A:VAL:HG21	19	0.23
(4,446)	1:22:A:ILE:HD11	1:22:A:ILE:HA	2	0.23
(4,431)	1:192:A:THR:HG22	1:192:A:THR:HB	13	0.23
(4,406)	1:133:A:ALA:HB3	1:130:A:PHE:HA	11	0.23
(4,405)	1:49:A:VAL:HA	1:49:A:VAL:HB	4	0.23
(4,405)	1:159:A:VAL:HA	1:159:A:VAL:HB	18	0.23
(4,404)	1:134:A:VAL:HA	1:134:A:VAL:HB	11	0.23
(4,369)	1:94:A:HIS:HB3	1:94:A:HIS:HA	1	0.23
(4,369)	1:94:A:HIS:HB3	1:94:A:HIS:HA	12	0.23
(4,369)	1:94:A:HIS:HB3	1:94:A:HIS:HA	13	0.23
(4,369)	1:94:A:HIS:HB3	1:94:A:HIS:HA	17	0.23
(4,369)	1:94:A:HIS:HB2	1:94:A:HIS:HA	19	0.23
(4,332)	1:22:A:ILE:HD12	1:22:A:ILE:HA	17	0.23
(4,330)	1:152:A:ALA:HB2	1:152:A:ALA:HA	2	0.23
(4,324)	1:230:A:PHE:HB2	1:230:A:PHE:HA	3	0.23
(4,324)	1:67:A:ASN:HB3	1:67:A:ASN:HA	6	0.23
(4,324)	1:60:A:LEU:HB2	1:60:A:LEU:HA	7	0.23
(4,324)	1:60:A:LEU:HB2	1:60:A:LEU:HA	9	0.23
(4,324)	1:60:A:LEU:HB3	1:60:A:LEU:HA	18	0.23
(4,252)	1:259:A:PHE:H	1:40:A:TYR:HB2	10	0.23
(4,251)	1:259:A:PHE:H	1:40:A:TYR:HB2	10	0.23
(4,237)	1:167:A:LYS:H	1:166:A:ILE:HA	6	0.23
(4,224)	1:44:A:LEU:H	1:43:A:SER:HB3	16	0.23
(4,219)	1:44:A:LEU:H	1:43:A:SER:HB3	6	0.23
(4,205)	1:54:A:ALA:H	1:54:A:ALA:HB1	1	0.23
(4,205)	1:54:A:ALA:H	1:54:A:ALA:HB1	13	0.23
(4,202)	1:37:A:THR:H	1:34:A:ASP:HB2	6	0.23
(4,202)	1:37:A:THR:H	1:34:A:ASP:HB3	15	0.23
(4,191)	1:160:A:VAL:H	1:160:A:VAL:HG23	10	0.23

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,157)	1:207:A:THR:H	1:207:A:THR:HB	1	0.23
(4,119)	1:161:A:ASP:H	1:161:A:ASP:HB3	6	0.23
(4,119)	1:231:A:ASN:H	1:229:A:ASN:HB3	15	0.23
(4,100)	1:141:A:ALA:H	1:140:A:LEU:HB2	2	0.23
(4,90)	1:112:A:LYS:H	1:108:A:THR:HB	11	0.23
(4,80)	1:119:A:HIS:H	1:119:A:HIS:HB2	6	0.23
(4,13)	1:113:A:LYS:HG2	1:245:A:ARG:H	4	0.23
(4,12)	1:178:A:PHE:HB3	1:56:A:SER:H	14	0.23
(3,271)	1:140:A:LEU:H	1:206:A:VAL:H	5	0.23
(3,210)	1:197:A:LEU:H	1:205:A:CYS:H	18	0.23
(3,205)	1:124:A:ASN:H	1:127:A:TYR:H	10	0.23
(3,141)	1:87:A:THR:H	1:125:A:THR:H	12	0.23
(3,58)	1:70:A:PHE:H	1:57:A:LEU:H	9	0.23
(4,1308)	1:212:A:LYS:H	1:212:A:LYS:HG2	19	0.22
(4,1293)	1:91:A:ILE:H	1:91:A:ILE:HD13	7	0.22
(4,1289)	1:203:A:LEU:H	1:22:A:ILE:HD12	5	0.22
(4,1283)	1:152:A:ALA:H	1:152:A:ALA:HB3	4	0.22
(4,1282)	1:152:A:ALA:H	1:152:A:ALA:HB3	11	0.22
(4,1257)	1:251:A:LYS:H	1:251:A:LYS:HG2	8	0.22
(4,1243)	1:247:A:ALA:H	1:247:A:ALA:HB3	2	0.22
(4,1237)	1:76:A:LYS:H	1:76:A:LYS:HG3	1	0.22
(4,1223)	1:152:A:ALA:H	1:152:A:ALA:HB3	15	0.22
(4,1172)	1:256:A:LYS:H	1:256:A:LYS:HG3	13	0.22
(4,1168)	1:147:A:LEU:H	1:147:A:LEU:HG	6	0.22
(4,1168)	1:152:A:ALA:H	1:152:A:ALA:HB2	9	0.22
(4,1162)	1:133:A:ALA:H	1:133:A:ALA:HB1	18	0.22
(4,1162)	1:47:A:LEU:H	1:47:A:LEU:HB3	19	0.22
(4,1134)	1:253:A:ARG:H	1:253:A:ARG:HB2	8	0.22
(4,1128)	1:251:A:LYS:H	1:250:A:LEU:HB2	9	0.22
(4,1109)	1:133:A:ALA:H	1:133:A:ALA:HB2	9	0.22
(4,1102)	1:26:A:GLU:H	1:26:A:GLU:HB2	20	0.22
(4,1090)	1:167:A:LYS:H	1:167:A:LYS:HB2	12	0.22
(4,1083)	1:248:A:GLN:H	1:248:A:GLN:HG3	16	0.22
(4,1083)	1:237:A:GLU:H	1:237:A:GLU:HG2	20	0.22
(4,1075)	1:164:A:ASP:H	1:164:A:ASP:HB2	2	0.22
(4,1064)	1:155:A:GLY:H	1:153:A:LYS:HB3	19	0.22
(4,1055)	1:100:A:LEU:H	1:100:A:LEU:HB2	8	0.22
(4,1055)	1:253:A:ARG:H	1:253:A:ARG:HB2	19	0.22
(4,1055)	1:18:A:LYS:H	1:18:A:LYS:HB2	20	0.22
(4,1051)	1:57:A:LEU:H	1:57:A:LEU:HB2	17	0.22
(4,1041)	1:153:A:LYS:H	1:153:A:LYS:HB2	2	0.22
(4,1025)	1:164:A:ASP:H	1:164:A:ASP:HB2	10	0.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1025)	1:164:A:ASP:H	1:164:A:ASP:HB2	13	0.22
(4,1005)	1:175:A:PHE:H	1:175:A:PHE:HB3	3	0.22
(4,998)	1:175:A:PHE:H	1:175:A:PHE:HB2	8	0.22
(4,997)	1:231:A:ASN:H	1:231:A:ASN:HB3	13	0.22
(4,983)	1:119:A:HIS:H	1:119:A:HIS:HB2	18	0.22
(4,972)	1:100:A:LEU:H	1:99:A:SER:HB3	14	0.22
(4,968)	1:129:A:ASP:H	1:129:A:ASP:HB2	1	0.22
(4,933)	1:166:A:ILE:H	1:163:A:LEU:HA	3	0.22
(4,898)	1:49:A:VAL:H	1:49:A:VAL:HA	3	0.22
(4,898)	1:49:A:VAL:H	1:49:A:VAL:HA	14	0.22
(4,874)	1:84:A:LEU:H	1:84:A:LEU:HA	1	0.22
(4,869)	1:166:A:ILE:H	1:165:A:SER:HB3	16	0.22
(4,849)	1:198:A:THR:H	1:197:A:LEU:HA	4	0.22
(4,849)	1:198:A:THR:H	1:198:A:THR:HA	8	0.22
(4,832)	1:253:A:ARG:H	1:253:A:ARG:HA	4	0.22
(4,823)	1:184:A:LEU:H	1:181:A:ARG:HA	8	0.22
(4,817)	1:103:A:GLN:H	1:103:A:GLN:HA	6	0.22
(4,805)	1:129:A:ASP:H	1:128:A:GLY:HA3	20	0.22
(4,801)	1:129:A:ASP:H	1:128:A:GLY:HA3	20	0.22
(4,762)	1:93:A:PHE:H	1:93:A:PHE:HA	20	0.22
(4,758)	1:252:A:ASN:H	1:252:A:ASN:HA	13	0.22
(4,753)	1:172:A:SER:H	1:171:A:LYS:HA	6	0.22
(4,736)	1:127:A:TYR:H	1:127:A:TYR:HA	15	0.22
(4,704)	1:16:A:TRP:H	1:16:A:TRP:HA	19	0.22
(4,704)	1:16:A:TRP:H	1:16:A:TRP:HA	20	0.22
(4,688)	1:207:A:THR:H	1:207:A:THR:HA	12	0.22
(4,670)	1:39:A:LYS:H	1:39:A:LYS:HA	10	0.22
(4,670)	1:39:A:LYS:H	1:39:A:LYS:HA	11	0.22
(4,572)	1:227:A:LYS:H	1:228:A:LEU:H	1	0.22
(4,572)	1:222:A:VAL:H	1:221:A:GLN:H	14	0.22
(4,557)	1:222:A:VAL:H	1:223:A:LEU:H	4	0.22
(4,467)	1:82:A:GLY:HA3	1:44:A:LEU:HD23	8	0.22
(4,467)	1:80:A:LYS:HE2	1:84:A:LEU:HD22	14	0.22
(4,442)	1:63:A:GLY:HA2	1:169:A:LYS:HG2	15	0.22
(4,438)	1:22:A:ILE:HG22	1:22:A:ILE:HA	20	0.22
(4,435)	1:35:A:THR:HG21	1:35:A:THR:HA	6	0.22
(4,435)	1:35:A:THR:HG21	1:35:A:THR:HA	12	0.22
(4,435)	1:35:A:THR:HG22	1:35:A:THR:HA	17	0.22
(4,431)	1:192:A:THR:HG22	1:192:A:THR:HB	2	0.22
(4,431)	1:55:A:THR:HB	1:55:A:THR:HG22	3	0.22
(4,431)	1:192:A:THR:HG21	1:192:A:THR:HB	4	0.22
(4,431)	1:192:A:THR:HG21	1:192:A:THR:HB	5	0.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,431)	1:192:A:THR:HG23	1:192:A:THR:HB	10	0.22
(4,431)	1:192:A:THR:HG21	1:192:A:THR:HB	11	0.22
(4,431)	1:108:A:THR:HG23	1:108:A:THR:HB	15	0.22
(4,419)	1:205:A:CYS:HB2	1:140:A:LEU:HB2	17	0.22
(4,416)	1:23:A:ALA:HB3	1:16:A:TRP:HB3	15	0.22
(4,396)	1:67:A:ASN:HB3	1:67:A:ASN:HA	19	0.22
(4,335)	1:49:A:VAL:HG22	1:49:A:VAL:HA	15	0.22
(4,335)	1:49:A:VAL:HG21	1:49:A:VAL:HA	19	0.22
(4,330)	1:192:A:THR:HG21	1:192:A:THR:HB	19	0.22
(4,324)	1:67:A:ASN:HB3	1:67:A:ASN:HA	17	0.22
(4,245)	1:228:A:LEU:H	1:228:A:LEU:HA	15	0.22
(4,245)	1:228:A:LEU:H	1:228:A:LEU:HA	16	0.22
(4,245)	1:228:A:LEU:H	1:228:A:LEU:HA	17	0.22
(4,208)	1:45:A:LYS:H	1:44:A:LEU:HA	2	0.22
(4,207)	1:159:A:VAL:H	1:159:A:VAL:HA	4	0.22
(4,207)	1:159:A:VAL:H	1:159:A:VAL:HA	18	0.22
(4,205)	1:54:A:ALA:H	1:54:A:ALA:HB3	2	0.22
(4,183)	1:260:A:LYS:H	1:259:A:PHE:HA	20	0.22
(4,167)	1:32:A:ASP:H	1:32:A:ASP:HB3	5	0.22
(4,119)	1:70:A:PHE:H	1:70:A:PHE:HB2	7	0.22
(4,96)	1:94:A:HIS:H	1:94:A:HIS:HB3	14	0.22
(4,80)	1:240:A:MET:H	1:240:A:MET:HB3	3	0.22
(4,43)	1:96:A:HIS:H	1:95:A:PHE:HB3	5	0.22
(4,37)	1:37:A:THR:HG23	1:255:A:ILE:H	20	0.22
(3,320)	1:97:A:TRP:H	1:244:A:TRP:H	14	0.22
(3,282)	1:202:A:LEU:H	1:199:A:THR:H	19	0.22
(3,173)	1:57:A:LEU:H	1:175:A:PHE:H	5	0.22
(3,173)	1:57:A:LEU:H	1:175:A:PHE:H	9	0.22
(3,166)	1:205:A:CYS:H	1:197:A:LEU:H	5	0.22
(3,61)	1:161:A:ASP:H	1:158:A:LYS:H	12	0.22
(3,59)	1:197:A:LEU:H	1:204:A:GLU:H	10	0.22
(3,41)	1:156:A:LEU:H	1:158:A:LYS:H	10	0.22
(1,123)	1:63:A:GLY:H	1:169:A:LYS:HG3	5	0.22
(1,77)	1:224:A:LYS:HB3	1:163:A:LEU:HD21	13	0.22
(1,49)	1:224:A:LYS:HG2	1:224:A:LYS:HA	1	0.22
(1,49)	1:224:A:LYS:HG2	1:224:A:LYS:HA	20	0.22
(4,1293)	1:153:A:LYS:H	1:152:A:ALA:HB1	6	0.21
(4,1293)	1:91:A:ILE:H	1:91:A:ILE:HD12	13	0.21
(4,1289)	1:203:A:LEU:H	1:22:A:ILE:HD13	20	0.21
(4,1282)	1:152:A:ALA:H	1:152:A:ALA:HB3	4	0.21
(4,1261)	1:152:A:ALA:H	1:152:A:ALA:HB3	17	0.21
(4,1254)	1:206:A:VAL:H	1:206:A:VAL:HG23	7	0.21

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1234)	1:87:A:THR:H	1:126:A:LYS:HG3	10	0.21
(4,1228)	1:152:A:ALA:H	1:152:A:ALA:HB1	10	0.21
(4,1212)	1:205:A:CYS:H	1:206:A:VAL:HG23	12	0.21
(4,1205)	1:231:A:ASN:H	1:169:A:LYS:HD3	14	0.21
(4,1202)	1:231:A:ASN:H	1:169:A:LYS:HD3	14	0.21
(4,1168)	1:124:A:ASN:H	1:133:A:ALA:HB3	13	0.21
(4,1168)	1:190:A:TYR:H	1:189:A:ASP:HB3	18	0.21
(4,1135)	1:28:A:GLN:H	1:28:A:GLN:HB3	20	0.21
(4,1128)	1:251:A:LYS:H	1:250:A:LEU:HB3	5	0.21
(4,1128)	1:251:A:LYS:H	1:250:A:LEU:HB2	6	0.21
(4,1127)	1:183:A:LEU:H	1:183:A:LEU:HB2	20	0.21
(4,1102)	1:26:A:GLU:H	1:26:A:GLU:HB2	18	0.21
(4,1091)	1:81:A:GLY:H	1:84:A:LEU:HB3	4	0.21
(4,1058)	1:52:A:ASP:H	1:52:A:ASP:HB2	7	0.21
(4,1027)	1:103:A:GLN:H	1:103:A:GLN:HG2	8	0.21
(4,1012)	1:18:A:LYS:H	1:17:A:HIS:HB3	8	0.21
(4,1007)	1:119:A:HIS:H	1:119:A:HIS:HB2	3	0.21
(4,1002)	1:231:A:ASN:H	1:231:A:ASN:HB3	13	0.21
(4,993)	1:205:A:CYS:H	1:205:A:CYS:HB2	4	0.21
(4,993)	1:205:A:CYS:H	1:205:A:CYS:HB2	9	0.21
(4,987)	1:244:A:TRP:H	1:244:A:TRP:HB3	11	0.21
(4,898)	1:49:A:VAL:H	1:49:A:VAL:HA	17	0.21
(4,880)	1:166:A:ILE:H	1:165:A:SER:HB3	11	0.21
(4,874)	1:84:A:LEU:H	1:84:A:LEU:HA	2	0.21
(4,874)	1:84:A:LEU:H	1:84:A:LEU:HA	8	0.21
(4,874)	1:84:A:LEU:H	1:84:A:LEU:HA	18	0.21
(4,849)	1:198:A:THR:H	1:198:A:THR:HA	10	0.21
(4,832)	1:247:A:ALA:H	1:247:A:ALA:HA	1	0.21
(4,817)	1:205:A:CYS:H	1:205:A:CYS:HA	17	0.21
(4,789)	1:9:A:LYS:H	1:8:A:GLY:HA2	12	0.21
(4,767)	1:71:A:ASP:H	1:70:A:PHE:HA	11	0.21
(4,762)	1:93:A:PHE:H	1:93:A:PHE:HA	18	0.21
(4,758)	1:252:A:ASN:H	1:252:A:ASN:HA	10	0.21
(4,758)	1:252:A:ASN:H	1:252:A:ASN:HA	12	0.21
(4,742)	1:71:A:ASP:H	1:70:A:PHE:HA	2	0.21
(4,736)	1:127:A:TYR:H	1:127:A:TYR:HA	9	0.21
(4,704)	1:16:A:TRP:H	1:16:A:TRP:HA	17	0.21
(4,703)	1:204:A:GLU:H	1:203:A:LEU:HA	13	0.21
(4,670)	1:39:A:LYS:H	1:39:A:LYS:HA	2	0.21
(4,670)	1:39:A:LYS:H	1:39:A:LYS:HA	19	0.21
(4,662)	1:51:A:TYR:H	1:51:A:TYR:HA	12	0.21
(4,662)	1:51:A:TYR:H	1:51:A:TYR:HA	16	0.21

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,620)	1:37:A:THR:H	1:36:A:HIS:H	9	0.21
(4,614)	1:19:A:ASP:H	1:20:A:PHE:H	5	0.21
(4,572)	1:159:A:VAL:H	1:160:A:VAL:H	4	0.21
(4,572)	1:222:A:VAL:H	1:221:A:GLN:H	16	0.21
(4,572)	1:159:A:VAL:H	1:160:A:VAL:H	18	0.21
(4,557)	1:222:A:VAL:H	1:223:A:LEU:H	1	0.21
(4,508)	1:231:A:ASN:H	1:230:A:PHE:H	13	0.21
(4,460)	1:223:A:LEU:HA	1:226:A:ARG:HG2	6	0.21
(4,449)	1:159:A:VAL:HA	1:159:A:VAL:HG23	6	0.21
(4,438)	1:133:A:ALA:HB3	1:130:A:PHE:HA	11	0.21
(4,431)	1:55:A:THR:HB	1:55:A:THR:HG23	7	0.21
(4,431)	1:55:A:THR:HB	1:55:A:THR:HG23	8	0.21
(4,431)	1:55:A:THR:HB	1:55:A:THR:HG22	16	0.21
(4,404)	1:49:A:VAL:HA	1:49:A:VAL:HB	1	0.21
(4,404)	1:49:A:VAL:HA	1:49:A:VAL:HB	14	0.21
(4,404)	1:160:A:VAL:HA	1:160:A:VAL:HB	19	0.21
(4,398)	1:123:A:TRP:HB3	1:140:A:LEU:HB3	19	0.21
(4,382)	1:193:A:TYR:HB3	1:208:A:TRP:HB3	13	0.21
(4,369)	1:94:A:HIS:HB3	1:94:A:HIS:HA	3	0.21
(4,369)	1:94:A:HIS:HB3	1:94:A:HIS:HA	4	0.21
(4,369)	1:94:A:HIS:HB3	1:94:A:HIS:HA	6	0.21
(4,369)	1:94:A:HIS:HB3	1:94:A:HIS:HA	8	0.21
(4,369)	1:94:A:HIS:HB3	1:94:A:HIS:HA	9	0.21
(4,369)	1:94:A:HIS:HB3	1:94:A:HIS:HA	10	0.21
(4,369)	1:20:A:PHE:HB3	1:20:A:PHE:HA	16	0.21
(4,369)	1:94:A:HIS:HB3	1:94:A:HIS:HA	20	0.21
(4,258)	1:252:A:ASN:H	1:252:A:ASN:HB3	2	0.21
(4,251)	1:259:A:PHE:H	1:40:A:TYR:HB2	2	0.21
(4,245)	1:228:A:LEU:H	1:228:A:LEU:HA	4	0.21
(4,245)	1:228:A:LEU:H	1:228:A:LEU:HA	5	0.21
(4,219)	1:44:A:LEU:H	1:43:A:SER:HB3	2	0.21
(4,219)	1:44:A:LEU:H	1:43:A:SER:HB3	17	0.21
(4,219)	1:44:A:LEU:H	1:43:A:SER:HB3	20	0.21
(4,208)	1:45:A:LYS:H	1:44:A:LEU:HA	18	0.21
(4,207)	1:159:A:VAL:H	1:159:A:VAL:HA	9	0.21
(4,207)	1:159:A:VAL:H	1:159:A:VAL:HA	14	0.21
(4,205)	1:54:A:ALA:H	1:54:A:ALA:HB1	12	0.21
(4,204)	1:183:A:LEU:H	1:183:A:LEU:HG	7	0.21
(4,200)	1:108:A:THR:H	1:107:A:HIS:HA	14	0.21
(4,191)	1:160:A:VAL:H	1:160:A:VAL:HG21	16	0.21
(4,119)	1:179:A:ASP:H	1:179:A:ASP:HB2	3	0.21
(4,119)	1:36:A:HIS:H	1:34:A:ASP:HB3	4	0.21

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,119)	1:229:A:ASN:H	1:229:A:ASN:HB2	13	0.21
(4,6)	1:113:A:LYS:HG3	1:107:A:HIS:H	13	0.21
(3,205)	1:124:A:ASN:H	1:127:A:TYR:H	2	0.21
(3,205)	1:124:A:ASN:H	1:127:A:TYR:H	5	0.21
(3,164)	1:203:A:LEU:H	1:197:A:LEU:H	12	0.21
(3,79)	1:192:A:THR:H	1:256:A:LYS:H	6	0.21
(3,9)	1:256:A:LYS:H	1:192:A:THR:H	6	0.21
(2,20)	1:229:A:ASN:H	1:168:A:THR:H	1	0.21
(1,123)	1:63:A:GLY:H	1:169:A:LYS:HG3	6	0.21
(1,120)	1:259:A:PHE:H	1:257:A:ALA:HB1	11	0.21
(1,114)	1:66:A:PHE:H	1:65:A:ALA:HB3	20	0.21
(1,103)	1:118:A:LEU:H	1:118:A:LEU:HB3	16	0.21
(1,79)	1:68:A:VAL:H	1:93:A:PHE:H	1	0.21
(1,71)	1:77:A:ALA:HB2	1:51:A:TYR:HA	2	0.21
(1,49)	1:224:A:LYS:HG2	1:224:A:LYS:HA	15	0.21
(1,42)	1:116:A:ALA:HB1	1:97:A:TRP:HA	3	0.21
(1,38)	1:77:A:ALA:HA	1:51:A:TYR:HA	14	0.21
(1,14)	1:140:A:LEU:H	1:139:A:GLY:HA3	12	0.21
(1,14)	1:140:A:LEU:H	1:139:A:GLY:HA3	14	0.21
(1,6)	1:169:A:LYS:HB3	1:63:A:GLY:H	14	0.21
(4,1293)	1:213:A:GLU:H	1:212:A:LYS:HG3	2	0.2
(4,1268)	1:210:A:VAL:H	1:209:A:ILE:HG22	15	0.2
(4,1249)	1:163:A:LEU:H	1:162:A:VAL:HG21	11	0.2
(4,1243)	1:163:A:LEU:H	1:162:A:VAL:HG23	1	0.2
(4,1228)	1:147:A:LEU:H	1:147:A:LEU:HG	12	0.2
(4,1225)	1:129:A:ASP:H	1:132:A:LYS:HG3	18	0.2
(4,1205)	1:231:A:ASN:H	1:169:A:LYS:HD3	8	0.2
(4,1202)	1:231:A:ASN:H	1:169:A:LYS:HD3	8	0.2
(4,1202)	1:99:A:SER:H	1:100:A:LEU:HG	10	0.2
(4,1198)	1:189:A:ASP:H	1:188:A:LEU:HB3	12	0.2
(4,1195)	1:228:A:LEU:H	1:228:A:LEU:HG	16	0.2
(4,1195)	1:18:A:LYS:H	1:18:A:LYS:HG2	20	0.2
(4,1162)	1:209:A:ILE:H	1:209:A:ILE:HB	6	0.2
(4,1162)	1:47:A:LEU:H	1:47:A:LEU:HB3	7	0.2
(4,1162)	1:133:A:ALA:H	1:133:A:ALA:HB1	10	0.2
(4,1162)	1:209:A:ILE:H	1:209:A:ILE:HG12	13	0.2
(4,1162)	1:133:A:ALA:H	1:133:A:ALA:HB1	16	0.2
(4,1158)	1:223:A:LEU:H	1:223:A:LEU:HB2	5	0.2
(4,1141)	1:164:A:ASP:H	1:163:A:LEU:HB3	7	0.2
(4,1134)	1:197:A:LEU:H	1:197:A:LEU:HB2	20	0.2
(4,1128)	1:251:A:LYS:H	1:250:A:LEU:HB2	16	0.2
(4,1111)	1:197:A:LEU:H	1:197:A:LEU:HB2	18	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1103)	1:218:A:SER:H	1:221:A:GLN:HB2	17	0.2
(4,1086)	1:86:A:GLY:H	1:84:A:LEU:HB2	10	0.2
(4,1083)	1:248:A:GLN:H	1:248:A:GLN:HG3	8	0.2
(4,1082)	1:251:A:LYS:H	1:250:A:LEU:HB3	17	0.2
(4,1060)	1:260:A:LYS:H	1:260:A:LYS:HB2	18	0.2
(4,1059)	1:147:A:LEU:H	1:146:A:PHE:HB3	8	0.2
(4,1051)	1:57:A:LEU:H	1:57:A:LEU:HB2	3	0.2
(4,1041)	1:240:A:MET:H	1:240:A:MET:HB3	17	0.2
(4,1025)	1:164:A:ASP:H	1:164:A:ASP:HB2	7	0.2
(4,1025)	1:28:A:GLN:H	1:28:A:GLN:HB2	17	0.2
(4,1007)	1:119:A:HIS:H	1:119:A:HIS:HB2	17	0.2
(4,1005)	1:175:A:PHE:H	1:175:A:PHE:HB2	8	0.2
(4,999)	1:119:A:HIS:H	1:119:A:HIS:HB2	17	0.2
(4,993)	1:127:A:TYR:H	1:127:A:TYR:HB2	3	0.2
(4,993)	1:127:A:TYR:H	1:127:A:TYR:HB2	18	0.2
(4,987)	1:244:A:TRP:H	1:244:A:TRP:HB3	1	0.2
(4,983)	1:119:A:HIS:H	1:119:A:HIS:HB2	17	0.2
(4,903)	1:49:A:VAL:H	1:48:A:SER:HB3	13	0.2
(4,898)	1:49:A:VAL:H	1:49:A:VAL:HA	15	0.2
(4,898)	1:49:A:VAL:H	1:49:A:VAL:HA	16	0.2
(4,898)	1:49:A:VAL:H	1:49:A:VAL:HA	18	0.2
(4,874)	1:84:A:LEU:H	1:84:A:LEU:HA	14	0.2
(4,870)	1:258:A:SER:H	1:258:A:SER:HB3	1	0.2
(4,870)	1:78:A:VAL:H	1:50:A:SER:HB2	20	0.2
(4,862)	1:78:A:VAL:H	1:50:A:SER:HB3	2	0.2
(4,835)	1:9:A:LYS:H	1:8:A:GLY:HA2	12	0.2
(4,835)	1:152:A:ALA:H	1:218:A:SER:HB2	17	0.2
(4,832)	1:253:A:ARG:H	1:253:A:ARG:HA	5	0.2
(4,772)	1:87:A:THR:H	1:86:A:GLY:HA2	13	0.2
(4,768)	1:16:A:TRP:H	1:16:A:TRP:HA	9	0.2
(4,762)	1:93:A:PHE:H	1:93:A:PHE:HA	6	0.2
(4,762)	1:93:A:PHE:H	1:93:A:PHE:HA	7	0.2
(4,762)	1:93:A:PHE:H	1:93:A:PHE:HA	12	0.2
(4,762)	1:93:A:PHE:H	1:93:A:PHE:HA	14	0.2
(4,758)	1:252:A:ASN:H	1:252:A:ASN:HA	2	0.2
(4,758)	1:252:A:ASN:H	1:252:A:ASN:HA	5	0.2
(4,758)	1:252:A:ASN:H	1:252:A:ASN:HA	8	0.2
(4,736)	1:43:A:SER:H	1:43:A:SER:HA	12	0.2
(4,736)	1:127:A:TYR:H	1:127:A:TYR:HA	17	0.2
(4,736)	1:127:A:TYR:H	1:127:A:TYR:HA	18	0.2
(4,722)	1:57:A:LEU:H	1:56:A:SER:HA	4	0.2
(4,722)	1:57:A:LEU:H	1:56:A:SER:HA	5	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,704)	1:16:A:TRP:H	1:16:A:TRP:HA	14	0.2
(4,702)	1:121:A:VAL:H	1:121:A:VAL:HA	2	0.2
(4,702)	1:121:A:VAL:H	1:121:A:VAL:HA	4	0.2
(4,702)	1:121:A:VAL:H	1:121:A:VAL:HA	12	0.2
(4,702)	1:121:A:VAL:H	1:121:A:VAL:HA	13	0.2
(4,702)	1:121:A:VAL:H	1:121:A:VAL:HA	14	0.2
(4,702)	1:121:A:VAL:H	1:121:A:VAL:HA	19	0.2
(4,662)	1:51:A:TYR:H	1:51:A:TYR:HA	7	0.2
(4,662)	1:51:A:TYR:H	1:51:A:TYR:HA	20	0.2
(4,628)	1:221:A:GLN:H	1:220:A:GLU:H	16	0.2
(4,611)	1:19:A:ASP:H	1:20:A:PHE:H	1	0.2
(4,611)	1:19:A:ASP:H	1:20:A:PHE:H	5	0.2
(4,495)	1:94:A:HIS:H	1:119:A:HIS:H	9	0.2
(4,470)	1:170:A:GLY:H	1:63:A:GLY:H	12	0.2
(4,470)	1:219:A:SER:H	1:150:A:GLY:H	19	0.2
(4,450)	1:147:A:LEU:HA	1:147:A:LEU:HD22	16	0.2
(4,435)	1:159:A:VAL:HA	1:159:A:VAL:HG21	10	0.2
(4,435)	1:159:A:VAL:HA	1:159:A:VAL:HG23	18	0.2
(4,431)	1:192:A:THR:HG23	1:192:A:THR:HB	1	0.2
(4,431)	1:192:A:THR:HG21	1:192:A:THR:HB	6	0.2
(4,431)	1:192:A:THR:HG22	1:192:A:THR:HB	17	0.2
(4,431)	1:192:A:THR:HG22	1:192:A:THR:HB	20	0.2
(4,419)	1:205:A:CYS:HB3	1:140:A:LEU:HG	1	0.2
(4,410)	1:35:A:THR:HG22	1:35:A:THR:HA	1	0.2
(4,405)	1:49:A:VAL:HA	1:49:A:VAL:HB	1	0.2
(4,405)	1:49:A:VAL:HA	1:49:A:VAL:HB	14	0.2
(4,405)	1:160:A:VAL:HA	1:160:A:VAL:HB	19	0.2
(4,386)	1:232:A:GLY:HA2	1:229:A:ASN:HB2	17	0.2
(4,369)	1:94:A:HIS:HB3	1:94:A:HIS:HA	7	0.2
(4,369)	1:94:A:HIS:HB3	1:94:A:HIS:HA	11	0.2
(4,369)	1:231:A:ASN:HB2	1:231:A:ASN:HA	14	0.2
(4,335)	1:134:A:VAL:HG23	1:131:A:GLY:HA2	4	0.2
(4,332)	1:22:A:ILE:HD13	1:22:A:ILE:HA	8	0.2
(4,330)	1:247:A:ALA:HB2	1:247:A:ALA:HA	1	0.2
(4,330)	1:152:A:ALA:HB2	1:152:A:ALA:HA	10	0.2
(4,330)	1:152:A:ALA:HB1	1:152:A:ALA:HA	15	0.2
(4,324)	1:67:A:ASN:HB3	1:67:A:ASN:HA	1	0.2
(4,324)	1:230:A:PHE:HB3	1:230:A:PHE:HA	11	0.2
(4,281)	1:91:A:ILE:HD11	1:123:A:TRP:HA	5	0.2
(4,263)	1:244:A:TRP:HA	1:244:A:TRP:H	6	0.2
(4,224)	1:44:A:LEU:H	1:43:A:SER:HB3	9	0.2
(4,219)	1:105:A:SER:H	1:105:A:SER:HB3	14	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,211)	1:206:A:VAL:H	1:206:A:VAL:HB	3	0.2
(4,207)	1:159:A:VAL:H	1:159:A:VAL:HA	2	0.2
(4,207)	1:159:A:VAL:H	1:159:A:VAL:HA	11	0.2
(4,207)	1:159:A:VAL:H	1:159:A:VAL:HA	15	0.2
(4,207)	1:159:A:VAL:H	1:159:A:VAL:HA	16	0.2
(4,205)	1:54:A:ALA:H	1:54:A:ALA:HB3	5	0.2
(4,191)	1:160:A:VAL:H	1:160:A:VAL:HG21	17	0.2
(4,119)	1:32:A:ASP:H	1:32:A:ASP:HB3	20	0.2
(4,114)	1:61:A:ASN:H	1:60:A:LEU:HG	15	0.2
(4,106)	1:196:A:SER:H	1:196:A:SER:HB3	17	0.2
(4,48)	1:26:A:GLU:H	1:26:A:GLU:HG3	18	0.2
(4,42)	1:38:A:ALA:HA	1:255:A:ILE:H	1	0.2
(4,22)	1:110:A:ASP:H	1:109:A:VAL:HB	10	0.2
(4,2)	1:245:A:ARG:HG2	1:245:A:ARG:H	12	0.2
(3,264)	1:240:A:MET:H	1:228:A:LEU:H	17	0.2
(3,173)	1:57:A:LEU:H	1:175:A:PHE:H	1	0.2
(3,166)	1:205:A:CYS:H	1:197:A:LEU:H	13	0.2
(3,158)	1:57:A:LEU:H	1:70:A:PHE:H	5	0.2
(3,115)	1:12:A:GLY:H	1:8:A:GLY:H	3	0.2
(3,114)	1:241:A:VAL:H	1:243:A:ASN:H	7	0.2
(3,59)	1:197:A:LEU:H	1:204:A:GLU:H	6	0.2
(3,36)	1:28:A:GLN:H	1:26:A:GLU:H	10	0.2
(1,121)	1:93:A:PHE:H	1:68:A:VAL:HG21	10	0.2
(1,106)	1:226:A:ARG:H	1:225:A:PHE:HB3	12	0.2
(1,99)	1:238:A:GLU:H	1:237:A:GLU:HA	11	0.2
(1,47)	1:240:A:MET:HA	1:230:A:PHE:HA	20	0.2
(1,42)	1:116:A:ALA:HB1	1:97:A:TRP:HA	13	0.2
(4,1321)	1:205:A:CYS:H	1:206:A:VAL:HG22	8	0.19
(4,1293)	1:91:A:ILE:H	1:91:A:ILE:HD12	19	0.19
(4,1289)	1:203:A:LEU:H	1:22:A:ILE:HD13	18	0.19
(4,1268)	1:204:A:GLU:H	1:22:A:ILE:HD12	7	0.19
(4,1265)	1:176:A:THR:H	1:176:A:THR:HG22	10	0.19
(4,1214)	1:248:A:GLN:H	1:247:A:ALA:HB3	13	0.19
(4,1185)	1:126:A:LYS:H	1:126:A:LYS:HB2	14	0.19
(4,1178)	1:177:A:ASN:H	1:176:A:THR:HG22	7	0.19
(4,1178)	1:177:A:ASN:H	1:55:A:THR:HG22	18	0.19
(4,1174)	1:9:A:LYS:H	1:9:A:LYS:HB2	17	0.19
(4,1146)	1:227:A:LYS:H	1:227:A:LYS:HB2	15	0.19
(4,1139)	1:256:A:LYS:H	1:256:A:LYS:HG3	1	0.19
(4,1135)	1:221:A:GLN:H	1:221:A:GLN:HB2	5	0.19
(4,1135)	1:221:A:GLN:H	1:221:A:GLN:HB3	7	0.19
(4,1135)	1:221:A:GLN:H	1:221:A:GLN:HB2	11	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1126)	1:228:A:LEU:H	1:228:A:LEU:HG	12	0.19
(4,1121)	1:48:A:SER:H	1:47:A:LEU:HB3	1	0.19
(4,1115)	1:158:A:LYS:H	1:158:A:LYS:HB3	7	0.19
(4,1114)	1:22:A:ILE:H	1:22:A:ILE:HB	3	0.19
(4,1107)	1:48:A:SER:H	1:47:A:LEU:HB3	1	0.19
(4,1102)	1:26:A:GLU:H	1:26:A:GLU:HB2	5	0.19
(4,1101)	1:220:A:GLU:H	1:220:A:GLU:HB2	18	0.19
(4,1101)	1:220:A:GLU:H	1:220:A:GLU:HB2	20	0.19
(4,1083)	1:237:A:GLU:H	1:237:A:GLU:HG3	6	0.19
(4,1060)	1:260:A:LYS:H	1:260:A:LYS:HB3	4	0.19
(4,1060)	1:260:A:LYS:H	1:260:A:LYS:HB3	11	0.19
(4,1058)	1:27:A:ARG:H	1:27:A:ARG:HG3	18	0.19
(4,1053)	1:86:A:GLY:H	1:84:A:LEU:HB2	9	0.19
(4,1024)	1:22:A:ILE:H	1:20:A:PHE:HB3	12	0.19
(4,1007)	1:85:A:ASP:H	1:85:A:ASP:HB2	1	0.19
(4,987)	1:244:A:TRP:H	1:244:A:TRP:HB3	18	0.19
(4,965)	1:253:A:ARG:H	1:252:A:ASN:HB3	13	0.19
(4,962)	1:166:A:ILE:H	1:163:A:LEU:HA	9	0.19
(4,948)	1:166:A:ILE:H	1:163:A:LEU:HA	3	0.19
(4,933)	1:129:A:ASP:H	1:127:A:TYR:HB2	11	0.19
(4,922)	1:65:A:ALA:H	1:62:A:ASN:HB2	9	0.19
(4,898)	1:49:A:VAL:H	1:49:A:VAL:HA	9	0.19
(4,894)	1:232:A:GLY:H	1:232:A:GLY:HA2	14	0.19
(4,880)	1:166:A:ILE:H	1:163:A:LEU:HA	9	0.19
(4,870)	1:258:A:SER:H	1:258:A:SER:HB3	6	0.19
(4,870)	1:78:A:VAL:H	1:50:A:SER:HB3	16	0.19
(4,842)	1:8:A:GLY:H	1:8:A:GLY:HA3	19	0.19
(4,841)	1:29:A:SER:H	1:28:A:GLN:HA	18	0.19
(4,823)	1:184:A:LEU:H	1:184:A:LEU:HA	15	0.19
(4,800)	1:167:A:LYS:H	1:166:A:ILE:HA	4	0.19
(4,800)	1:167:A:LYS:H	1:166:A:ILE:HA	16	0.19
(4,789)	1:9:A:LYS:H	1:8:A:GLY:HA2	8	0.19
(4,789)	1:106:A:GLU:H	1:105:A:SER:HA	13	0.19
(4,762)	1:93:A:PHE:H	1:93:A:PHE:HA	1	0.19
(4,762)	1:93:A:PHE:H	1:93:A:PHE:HA	9	0.19
(4,762)	1:93:A:PHE:H	1:93:A:PHE:HA	11	0.19
(4,758)	1:252:A:ASN:H	1:252:A:ASN:HA	9	0.19
(4,736)	1:43:A:SER:H	1:43:A:SER:HA	1	0.19
(4,736)	1:43:A:SER:H	1:43:A:SER:HA	2	0.19
(4,736)	1:43:A:SER:H	1:43:A:SER:HA	3	0.19
(4,736)	1:43:A:SER:H	1:43:A:SER:HA	6	0.19
(4,736)	1:218:A:SER:H	1:218:A:SER:HA	8	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,722)	1:57:A:LEU:H	1:56:A:SER:HA	1	0.19
(4,702)	1:121:A:VAL:H	1:121:A:VAL:HA	7	0.19
(4,702)	1:121:A:VAL:H	1:121:A:VAL:HA	11	0.19
(4,702)	1:121:A:VAL:H	1:121:A:VAL:HA	15	0.19
(4,702)	1:121:A:VAL:H	1:121:A:VAL:HA	17	0.19
(4,702)	1:121:A:VAL:H	1:121:A:VAL:HA	18	0.19
(4,662)	1:51:A:TYR:H	1:51:A:TYR:HA	3	0.19
(4,662)	1:51:A:TYR:H	1:51:A:TYR:HA	6	0.19
(4,612)	1:24:A:LYS:H	1:23:A:ALA:H	7	0.19
(4,572)	1:222:A:VAL:H	1:221:A:GLN:H	11	0.19
(4,557)	1:222:A:VAL:H	1:223:A:LEU:H	2	0.19
(4,540)	1:89:A:ARG:H	1:123:A:TRP:H	5	0.19
(4,529)	1:116:A:ALA:H	1:147:A:LEU:H	20	0.19
(4,508)	1:231:A:ASN:H	1:230:A:PHE:H	9	0.19
(4,469)	1:140:A:LEU:HB3	1:91:A:ILE:HD13	20	0.19
(4,467)	1:78:A:VAL:HG21	1:80:A:LYS:HE3	10	0.19
(4,460)	1:224:A:LYS:HA	1:224:A:LYS:HD3	17	0.19
(4,449)	1:159:A:VAL:HA	1:159:A:VAL:HG21	10	0.19
(4,431)	1:192:A:THR:HG23	1:192:A:THR:HB	9	0.19
(4,416)	1:23:A:ALA:HB1	1:17:A:HIS:HB3	9	0.19
(4,406)	1:133:A:ALA:HB1	1:130:A:PHE:HA	10	0.19
(4,404)	1:49:A:VAL:HA	1:49:A:VAL:HB	3	0.19
(4,404)	1:160:A:VAL:HA	1:160:A:VAL:HB	9	0.19
(4,395)	1:35:A:THR:HB	1:34:A:ASP:HB3	6	0.19
(4,369)	1:94:A:HIS:HB3	1:94:A:HIS:HA	2	0.19
(4,369)	1:94:A:HIS:HB3	1:94:A:HIS:HA	5	0.19
(4,353)	1:209:A:ILE:HD11	1:207:A:THR:HB	5	0.19
(4,330)	1:192:A:THR:HG23	1:192:A:THR:HB	14	0.19
(4,327)	1:148:A:LYS:HB3	1:148:A:LYS:HA	14	0.19
(4,327)	1:148:A:LYS:HB3	1:148:A:LYS:HA	18	0.19
(4,266)	1:166:A:ILE:HD11	1:168:A:THR:H	9	0.19
(4,258)	1:252:A:ASN:H	1:252:A:ASN:HB2	1	0.19
(4,245)	1:228:A:LEU:H	1:228:A:LEU:HA	12	0.19
(4,242)	1:57:A:LEU:HB2	1:58:A:ARG:H	3	0.19
(4,242)	1:129:A:ASP:H	1:129:A:ASP:HB2	17	0.19
(4,219)	1:105:A:SER:H	1:105:A:SER:HB2	16	0.19
(4,208)	1:45:A:LYS:H	1:44:A:LEU:HA	9	0.19
(4,207)	1:159:A:VAL:H	1:159:A:VAL:HA	6	0.19
(4,204)	1:34:A:ASP:H	1:255:A:ILE:HG13	11	0.19
(4,204)	1:183:A:LEU:H	1:183:A:LEU:HG	15	0.19
(4,200)	1:108:A:THR:H	1:107:A:HIS:HA	6	0.19
(4,200)	1:108:A:THR:H	1:107:A:HIS:HA	17	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,191)	1:159:A:VAL:H	1:159:A:VAL:HG22	12	0.19
(4,189)	1:162:A:VAL:H	1:161:A:ASP:HB3	5	0.19
(4,182)	1:166:A:ILE:H	1:163:A:LEU:HA	15	0.19
(4,167)	1:32:A:ASP:H	1:32:A:ASP:HB2	8	0.19
(4,157)	1:207:A:THR:H	1:207:A:THR:HB	11	0.19
(4,119)	1:174:A:ASP:H	1:174:A:ASP:HB2	9	0.19
(4,87)	1:91:A:ILE:H	1:91:A:ILE:HG13	17	0.19
(4,12)	1:178:A:PHE:HB2	1:56:A:SER:H	8	0.19
(3,318)	1:171:A:LYS:H	1:168:A:THR:H	1	0.19
(3,234)	1:8:A:GLY:H	1:12:A:GLY:H	13	0.19
(3,150)	1:206:A:VAL:H	1:197:A:LEU:H	10	0.19
(3,24)	1:258:A:SER:H	1:191:A:TRP:H	14	0.19
(2,20)	1:229:A:ASN:H	1:168:A:THR:H	16	0.19
(1,132)	1:135:A:GLN:H	1:134:A:VAL:HG21	6	0.19
(1,83)	1:37:A:THR:H	1:38:A:ALA:H	9	0.19
(1,78)	1:117:A:GLU:H	1:96:A:HIS:H	5	0.19
(1,38)	1:77:A:ALA:HA	1:51:A:TYR:HA	18	0.19
(1,38)	1:77:A:ALA:HA	1:51:A:TYR:HA	19	0.19
(1,14)	1:140:A:LEU:H	1:139:A:GLY:HA3	13	0.19
(4,1299)	1:91:A:ILE:H	1:91:A:ILE:HD13	3	0.18
(4,1283)	1:152:A:ALA:H	1:152:A:ALA:HB2	9	0.18
(4,1264)	1:204:A:GLU:H	1:22:A:ILE:HD13	10	0.18
(4,1264)	1:210:A:VAL:H	1:209:A:ILE:HG23	20	0.18
(4,1261)	1:152:A:ALA:H	1:152:A:ALA:HB2	13	0.18
(4,1243)	1:247:A:ALA:H	1:247:A:ALA:HB2	9	0.18
(4,1228)	1:152:A:ALA:H	1:152:A:ALA:HB1	3	0.18
(4,1227)	1:91:A:ILE:H	1:91:A:ILE:HG12	9	0.18
(4,1212)	1:176:A:THR:H	1:176:A:THR:HG22	20	0.18
(4,1191)	1:9:A:LYS:H	1:9:A:LYS:HB3	13	0.18
(4,1191)	1:9:A:LYS:H	1:9:A:LYS:HB2	20	0.18
(4,1187)	1:140:A:LEU:H	1:140:A:LEU:HG	10	0.18
(4,1186)	1:9:A:LYS:H	1:9:A:LYS:HB3	3	0.18
(4,1174)	1:152:A:ALA:H	1:152:A:ALA:HB2	9	0.18
(4,1169)	1:252:A:ASN:H	1:250:A:LEU:HG	18	0.18
(4,1162)	1:133:A:ALA:H	1:133:A:ALA:HB2	9	0.18
(4,1139)	1:211:A:LEU:H	1:211:A:LEU:HB2	8	0.18
(4,1139)	1:209:A:ILE:H	1:209:A:ILE:HG12	11	0.18
(4,1133)	1:93:A:PHE:H	1:92:A:GLN:HB2	20	0.18
(4,1129)	1:195:A:GLY:H	1:207:A:THR:HG23	20	0.18
(4,1126)	1:228:A:LEU:H	1:228:A:LEU:HB2	2	0.18
(4,1126)	1:228:A:LEU:H	1:228:A:LEU:HB2	6	0.18
(4,1122)	1:135:A:GLN:H	1:135:A:GLN:HB2	6	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1122)	1:224:A:LYS:H	1:224:A:LYS:HG3	9	0.18
(4,1111)	1:181:A:ARG:H	1:181:A:ARG:HG3	12	0.18
(4,1109)	1:204:A:GLU:H	1:203:A:LEU:HB2	10	0.18
(4,1109)	1:133:A:ALA:H	1:133:A:ALA:HB1	20	0.18
(4,1101)	1:181:A:ARG:H	1:181:A:ARG:HG3	12	0.18
(4,1083)	1:248:A:GLN:H	1:248:A:GLN:HG2	4	0.18
(4,1078)	1:221:A:GLN:H	1:221:A:GLN:HB3	16	0.18
(4,1075)	1:164:A:ASP:H	1:164:A:ASP:HB2	18	0.18
(4,1066)	1:224:A:LYS:H	1:224:A:LYS:HG2	15	0.18
(4,1060)	1:260:A:LYS:H	1:260:A:LYS:HB2	5	0.18
(4,1027)	1:103:A:GLN:H	1:103:A:GLN:HG2	2	0.18
(4,1027)	1:103:A:GLN:H	1:100:A:LEU:HB3	9	0.18
(4,1008)	1:37:A:THR:H	1:34:A:ASP:HB3	14	0.18
(4,999)	1:85:A:ASP:H	1:85:A:ASP:HB2	1	0.18
(4,993)	1:205:A:CYS:H	1:205:A:CYS:HB2	2	0.18
(4,972)	1:100:A:LEU:H	1:99:A:SER:HB3	16	0.18
(4,970)	1:88:A:TYR:H	1:88:A:TYR:HB2	5	0.18
(4,968)	1:166:A:ILE:H	1:163:A:LEU:HA	9	0.18
(4,957)	1:191:A:TRP:H	1:191:A:TRP:HB3	2	0.18
(4,933)	1:129:A:ASP:H	1:129:A:ASP:HA	6	0.18
(4,931)	1:85:A:ASP:H	1:85:A:ASP:HB3	11	0.18
(4,931)	1:85:A:ASP:H	1:85:A:ASP:HB2	17	0.18
(4,924)	1:129:A:ASP:H	1:129:A:ASP:HA	12	0.18
(4,898)	1:49:A:VAL:H	1:49:A:VAL:HA	5	0.18
(4,870)	1:258:A:SER:H	1:258:A:SER:HB3	3	0.18
(4,870)	1:258:A:SER:H	1:258:A:SER:HB3	7	0.18
(4,867)	1:189:A:ASP:H	1:189:A:ASP:HA	12	0.18
(4,867)	1:157:A:GLN:H	1:157:A:GLN:HA	14	0.18
(4,867)	1:157:A:GLN:H	1:157:A:GLN:HA	17	0.18
(4,849)	1:198:A:THR:H	1:197:A:LEU:HA	6	0.18
(4,836)	1:129:A:ASP:H	1:128:A:GLY:HA3	18	0.18
(4,835)	1:9:A:LYS:H	1:8:A:GLY:HA2	8	0.18
(4,835)	1:106:A:GLU:H	1:105:A:SER:HA	13	0.18
(4,817)	1:205:A:CYS:H	1:205:A:CYS:HA	7	0.18
(4,768)	1:16:A:TRP:H	1:16:A:TRP:HA	2	0.18
(4,762)	1:93:A:PHE:H	1:93:A:PHE:HA	4	0.18
(4,762)	1:93:A:PHE:H	1:93:A:PHE:HA	5	0.18
(4,762)	1:93:A:PHE:H	1:93:A:PHE:HA	16	0.18
(4,727)	1:147:A:LEU:H	1:146:A:PHE:HA	4	0.18
(4,722)	1:57:A:LEU:H	1:56:A:SER:HA	18	0.18
(4,711)	1:51:A:TYR:H	1:50:A:SER:HA	20	0.18
(4,702)	1:121:A:VAL:H	1:121:A:VAL:HA	8	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,702)	1:121:A:VAL:H	1:121:A:VAL:HA	16	0.18
(4,683)	1:138:A:ASP:H	1:138:A:ASP:HA	9	0.18
(4,669)	1:29:A:SER:H	1:31:A:VAL:H	6	0.18
(4,668)	1:29:A:SER:H	1:31:A:VAL:H	6	0.18
(4,662)	1:51:A:TYR:H	1:51:A:TYR:HA	4	0.18
(4,628)	1:181:A:ARG:H	1:182:A:GLY:H	5	0.18
(4,626)	1:245:A:ARG:H	1:247:A:ALA:H	18	0.18
(4,618)	1:245:A:ARG:H	1:247:A:ALA:H	18	0.18
(4,614)	1:19:A:ASP:H	1:20:A:PHE:H	18	0.18
(4,572)	1:222:A:VAL:H	1:221:A:GLN:H	12	0.18
(4,569)	1:127:A:TYR:H	1:126:A:LYS:H	14	0.18
(4,460)	1:224:A:LYS:HA	1:224:A:LYS:HD3	16	0.18
(4,449)	1:159:A:VAL:HA	1:159:A:VAL:HG23	18	0.18
(4,446)	1:22:A:ILE:HD12	1:22:A:ILE:HA	1	0.18
(4,419)	1:205:A:CYS:HB3	1:140:A:LEU:HG	4	0.18
(4,405)	1:49:A:VAL:HA	1:49:A:VAL:HB	3	0.18
(4,405)	1:160:A:VAL:HA	1:160:A:VAL:HB	9	0.18
(4,397)	1:163:A:LEU:HB3	1:160:A:VAL:HA	13	0.18
(4,381)	1:40:A:TYR:HB3	1:260:A:LYS:HA	17	0.18
(4,370)	1:132:A:LYS:HG2	1:129:A:ASP:HB2	5	0.18
(4,369)	1:94:A:HIS:HB3	1:94:A:HIS:HA	18	0.18
(4,330)	1:23:A:ALA:HB2	1:17:A:HIS:HA	11	0.18
(4,327)	1:148:A:LYS:HB3	1:148:A:LYS:HA	3	0.18
(4,327)	1:117:A:GLU:HB3	1:117:A:GLU:HA	15	0.18
(4,324)	1:67:A:ASN:HB3	1:67:A:ASN:HA	19	0.18
(4,266)	1:244:A:TRP:H	1:241:A:VAL:HG22	16	0.18
(4,263)	1:244:A:TRP:HA	1:244:A:TRP:H	2	0.18
(4,263)	1:243:A:ASN:HA	1:244:A:TRP:H	3	0.18
(4,245)	1:228:A:LEU:H	1:228:A:LEU:HA	6	0.18
(4,245)	1:228:A:LEU:H	1:228:A:LEU:HA	20	0.18
(4,207)	1:159:A:VAL:H	1:159:A:VAL:HA	3	0.18
(4,207)	1:159:A:VAL:H	1:159:A:VAL:HA	8	0.18
(4,204)	1:253:A:ARG:H	1:253:A:ARG:HG2	1	0.18
(4,202)	1:162:A:VAL:H	1:161:A:ASP:HB3	5	0.18
(4,200)	1:108:A:THR:H	1:107:A:HIS:HA	18	0.18
(4,191)	1:159:A:VAL:H	1:159:A:VAL:HG23	7	0.18
(4,191)	1:160:A:VAL:H	1:160:A:VAL:HG22	8	0.18
(4,182)	1:166:A:ILE:H	1:163:A:LEU:HA	11	0.18
(4,157)	1:207:A:THR:H	1:207:A:THR:HB	20	0.18
(4,119)	1:231:A:ASN:H	1:229:A:ASN:HB3	14	0.18
(4,115)	1:22:A:ILE:H	1:22:A:ILE:HD12	20	0.18
(4,80)	1:93:A:PHE:H	1:92:A:GLN:HB2	1	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,323)	1:181:A:ARG:H	1:184:A:LEU:H	13	0.18
(3,306)	1:156:A:LEU:H	1:159:A:VAL:H	17	0.18
(3,231)	1:191:A:TRP:H	1:212:A:LYS:H	3	0.18
(3,231)	1:191:A:TRP:H	1:212:A:LYS:H	20	0.18
(3,150)	1:206:A:VAL:H	1:197:A:LEU:H	13	0.18
(3,114)	1:241:A:VAL:H	1:243:A:ASN:H	15	0.18
(3,83)	1:111:A:LYS:H	1:33:A:ILE:H	15	0.18
(3,13)	1:207:A:THR:H	1:195:A:GLY:H	4	0.18
(1,73)	1:134:A:VAL:HG22	1:131:A:GLY:HA2	2	0.18
(1,69)	1:87:A:THR:HB	1:87:A:THR:HG22	6	0.18
(1,69)	1:87:A:THR:HB	1:87:A:THR:HG23	8	0.18
(1,69)	1:87:A:THR:HB	1:87:A:THR:HG22	11	0.18
(1,69)	1:87:A:THR:HB	1:87:A:THR:HG23	14	0.18
(1,69)	1:87:A:THR:HB	1:87:A:THR:HG22	17	0.18
(1,69)	1:87:A:THR:HB	1:87:A:THR:HG21	18	0.18
(1,69)	1:87:A:THR:HB	1:87:A:THR:HG22	19	0.18
(1,14)	1:140:A:LEU:H	1:139:A:GLY:HA3	18	0.18
(1,10)	1:55:A:THR:H	1:55:A:THR:HB	18	0.18
(4,1329)	1:219:A:SER:H	1:149:A:VAL:HG21	13	0.17
(4,1321)	1:205:A:CYS:H	1:206:A:VAL:HG23	11	0.17
(4,1292)	1:91:A:ILE:H	1:91:A:ILE:HD13	3	0.17
(4,1289)	1:203:A:LEU:H	1:22:A:ILE:HD13	4	0.17
(4,1286)	1:87:A:THR:H	1:87:A:THR:HG22	8	0.17
(4,1286)	1:78:A:VAL:H	1:78:A:VAL:HG23	10	0.17
(4,1282)	1:152:A:ALA:H	1:152:A:ALA:HB2	9	0.17
(4,1268)	1:204:A:GLU:H	1:22:A:ILE:HD13	10	0.17
(4,1268)	1:210:A:VAL:H	1:209:A:ILE:HG23	20	0.17
(4,1261)	1:152:A:ALA:H	1:152:A:ALA:HB3	8	0.17
(4,1261)	1:152:A:ALA:H	1:152:A:ALA:HB2	12	0.17
(4,1249)	1:163:A:LEU:H	1:162:A:VAL:HG21	10	0.17
(4,1242)	1:247:A:ALA:H	1:247:A:ALA:HB3	12	0.17
(4,1228)	1:84:A:LEU:H	1:84:A:LEU:HG	19	0.17
(4,1228)	1:152:A:ALA:H	1:152:A:ALA:HB1	20	0.17
(4,1218)	1:172:A:SER:H	1:166:A:ILE:HG23	6	0.17
(4,1218)	1:172:A:SER:H	1:166:A:ILE:HG22	8	0.17
(4,1212)	1:176:A:THR:H	1:176:A:THR:HG22	13	0.17
(4,1198)	1:22:A:ILE:H	1:22:A:ILE:HD12	10	0.17
(4,1189)	1:34:A:ASP:H	1:37:A:THR:HG21	20	0.17
(4,1186)	1:117:A:GLU:H	1:116:A:ALA:HB3	2	0.17
(4,1185)	1:45:A:LYS:H	1:45:A:LYS:HG3	2	0.17
(4,1185)	1:126:A:LYS:H	1:126:A:LYS:HB2	17	0.17
(4,1178)	1:177:A:ASN:H	1:176:A:THR:HG21	10	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1173)	1:22:A:ILE:H	1:22:A:ILE:HB	3	0.17
(4,1168)	1:152:A:ALA:H	1:152:A:ALA:HB3	15	0.17
(4,1141)	1:164:A:ASP:H	1:163:A:LEU:HB3	12	0.17
(4,1134)	1:197:A:LEU:H	1:197:A:LEU:HB3	6	0.17
(4,1130)	1:133:A:ALA:H	1:133:A:ALA:HB3	7	0.17
(4,1128)	1:251:A:LYS:H	1:250:A:LEU:HB3	1	0.17
(4,1128)	1:251:A:LYS:H	1:250:A:LEU:HB2	4	0.17
(4,1128)	1:251:A:LYS:H	1:250:A:LEU:HB2	20	0.17
(4,1127)	1:197:A:LEU:H	1:197:A:LEU:HB2	11	0.17
(4,1123)	1:218:A:SER:H	1:221:A:GLN:HB2	17	0.17
(4,1113)	1:117:A:GLU:H	1:116:A:ALA:HB2	3	0.17
(4,1111)	1:181:A:ARG:H	1:181:A:ARG:HG3	6	0.17
(4,1110)	1:77:A:ALA:H	1:76:A:LYS:HB3	20	0.17
(4,1102)	1:57:A:LEU:H	1:57:A:LEU:HG	19	0.17
(4,1101)	1:181:A:ARG:H	1:181:A:ARG:HG3	6	0.17
(4,1090)	1:197:A:LEU:H	1:197:A:LEU:HB2	20	0.17
(4,1086)	1:86:A:GLY:H	1:84:A:LEU:HB2	1	0.17
(4,1083)	1:233:A:GLU:H	1:233:A:GLU:HG2	17	0.17
(4,1083)	1:237:A:GLU:H	1:237:A:GLU:HG3	19	0.17
(4,1059)	1:147:A:LEU:H	1:146:A:PHE:HB3	10	0.17
(4,1041)	1:60:A:LEU:H	1:60:A:LEU:HB3	1	0.17
(4,1041)	1:153:A:LYS:H	1:153:A:LYS:HB3	8	0.17
(4,1041)	1:119:A:HIS:H	1:119:A:HIS:HB2	19	0.17
(4,1022)	1:76:A:LYS:H	1:74:A:GLN:HB2	20	0.17
(4,1007)	1:85:A:ASP:H	1:85:A:ASP:HB2	15	0.17
(4,1006)	1:79:A:LEU:H	1:88:A:TYR:HB2	20	0.17
(4,993)	1:127:A:TYR:H	1:127:A:TYR:HB3	17	0.17
(4,981)	1:164:A:ASP:H	1:164:A:ASP:HB3	20	0.17
(4,975)	1:126:A:LYS:H	1:124:A:ASN:HB2	20	0.17
(4,972)	1:18:A:LYS:H	1:17:A:HIS:HB3	8	0.17
(4,970)	1:88:A:TYR:H	1:88:A:TYR:HB2	2	0.17
(4,968)	1:241:A:VAL:H	1:240:A:MET:HA	20	0.17
(4,965)	1:253:A:ARG:H	1:252:A:ASN:HB2	8	0.17
(4,923)	1:243:A:ASN:H	1:243:A:ASN:HB2	13	0.17
(4,903)	1:49:A:VAL:H	1:48:A:SER:HB2	6	0.17
(4,903)	1:49:A:VAL:H	1:48:A:SER:HB3	12	0.17
(4,869)	1:166:A:ILE:H	1:165:A:SER:HB3	11	0.17
(4,867)	1:157:A:GLN:H	1:157:A:GLN:HA	2	0.17
(4,865)	1:258:A:SER:H	1:258:A:SER:HB3	6	0.17
(4,836)	1:129:A:ASP:H	1:128:A:GLY:HA3	17	0.17
(4,823)	1:184:A:LEU:H	1:184:A:LEU:HA	11	0.17
(4,817)	1:205:A:CYS:H	1:205:A:CYS:HA	9	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,799)	1:87:A:THR:H	1:87:A:THR:HB	18	0.17
(4,789)	1:152:A:ALA:H	1:152:A:ALA:HA	7	0.17
(4,789)	1:7:A:TYR:H	1:7:A:TYR:HA	17	0.17
(4,767)	1:70:A:PHE:H	1:69:A:GLU:HA	16	0.17
(4,758)	1:252:A:ASN:H	1:252:A:ASN:HA	14	0.17
(4,742)	1:71:A:ASP:H	1:70:A:PHE:HA	11	0.17
(4,736)	1:43:A:SER:H	1:43:A:SER:HA	20	0.17
(4,722)	1:57:A:LEU:H	1:56:A:SER:HA	8	0.17
(4,715)	1:98:A:GLY:H	1:97:A:TRP:HA	9	0.17
(4,702)	1:121:A:VAL:H	1:121:A:VAL:HA	1	0.17
(4,702)	1:121:A:VAL:H	1:121:A:VAL:HA	3	0.17
(4,702)	1:121:A:VAL:H	1:121:A:VAL:HA	5	0.17
(4,702)	1:121:A:VAL:H	1:121:A:VAL:HA	6	0.17
(4,702)	1:121:A:VAL:H	1:121:A:VAL:HA	10	0.17
(4,702)	1:121:A:VAL:H	1:121:A:VAL:HA	20	0.17
(4,688)	1:204:A:GLU:H	1:203:A:LEU:HA	11	0.17
(4,683)	1:92:A:GLN:H	1:92:A:GLN:HA	5	0.17
(4,662)	1:51:A:TYR:H	1:51:A:TYR:HA	5	0.17
(4,662)	1:51:A:TYR:H	1:51:A:TYR:HA	19	0.17
(4,611)	1:163:A:LEU:H	1:164:A:ASP:H	8	0.17
(4,611)	1:19:A:ASP:H	1:20:A:PHE:H	18	0.17
(4,574)	1:127:A:TYR:H	1:126:A:LYS:H	14	0.17
(4,559)	1:156:A:LEU:H	1:155:A:GLY:H	17	0.17
(4,553)	1:28:A:GLN:H	1:27:A:ARG:H	7	0.17
(4,470)	1:219:A:SER:H	1:150:A:GLY:H	15	0.17
(4,463)	1:174:A:ASP:HA	1:176:A:THR:HG22	16	0.17
(4,462)	1:159:A:VAL:HA	1:159:A:VAL:HG21	14	0.17
(4,438)	1:255:A:ILE:HD13	1:255:A:ILE:HA	8	0.17
(4,438)	1:133:A:ALA:HB1	1:130:A:PHE:HA	10	0.17
(4,436)	1:63:A:GLY:HA2	1:169:A:LYS:HG3	16	0.17
(4,431)	1:192:A:THR:HG21	1:192:A:THR:HB	19	0.17
(4,410)	1:35:A:THR:HG23	1:35:A:THR:HA	5	0.17
(4,410)	1:35:A:THR:HG23	1:35:A:THR:HA	14	0.17
(4,408)	1:80:A:LYS:HB2	1:87:A:THR:HA	19	0.17
(4,403)	1:123:A:TRP:HB2	1:140:A:LEU:HB3	12	0.17
(4,335)	1:22:A:ILE:HG22	1:22:A:ILE:HA	7	0.17
(4,330)	1:152:A:ALA:HB2	1:152:A:ALA:HA	20	0.17
(4,273)	1:113:A:LYS:HD2	1:244:A:TRP:HA	2	0.17
(4,258)	1:252:A:ASN:H	1:252:A:ASN:HB3	6	0.17
(4,208)	1:45:A:LYS:H	1:44:A:LEU:HA	11	0.17
(4,205)	1:54:A:ALA:H	1:54:A:ALA:HB2	18	0.17
(4,200)	1:108:A:THR:H	1:107:A:HIS:HA	5	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,196)	1:205:A:CYS:H	1:22:A:ILE:HD11	11	0.17
(4,191)	1:160:A:VAL:H	1:160:A:VAL:HG23	3	0.17
(4,191)	1:160:A:VAL:H	1:160:A:VAL:HG23	4	0.17
(4,191)	1:159:A:VAL:H	1:159:A:VAL:HG21	13	0.17
(4,191)	1:160:A:VAL:H	1:160:A:VAL:HG22	19	0.17
(4,145)	1:149:A:VAL:H	1:148:A:LYS:HB2	7	0.17
(4,144)	1:103:A:GLN:H	1:100:A:LEU:HB2	2	0.17
(4,121)	1:22:A:ILE:H	1:22:A:ILE:HD12	20	0.17
(4,119)	1:229:A:ASN:H	1:229:A:ASN:HB2	8	0.17
(4,119)	1:232:A:GLY:H	1:231:A:ASN:HB3	18	0.17
(4,114)	1:254:A:GLN:H	1:253:A:ARG:HG3	5	0.17
(4,114)	1:61:A:ASN:H	1:60:A:LEU:HG	6	0.17
(4,48)	1:202:A:LEU:H	1:202:A:LEU:HB2	8	0.17
(4,43)	1:95:A:PHE:H	1:95:A:PHE:HB3	17	0.17
(4,15)	1:192:A:THR:H	1:255:A:ILE:HG13	17	0.17
(4,13)	1:63:A:GLY:H	1:60:A:LEU:HD13	12	0.17
(3,271)	1:140:A:LEU:H	1:206:A:VAL:H	7	0.17
(3,222)	1:197:A:LEU:H	1:205:A:CYS:H	19	0.17
(3,205)	1:124:A:ASN:H	1:127:A:TYR:H	13	0.17
(3,163)	1:205:A:CYS:H	1:197:A:LEU:H	19	0.17
(3,160)	1:205:A:CYS:H	1:197:A:LEU:H	19	0.17
(3,141)	1:87:A:THR:H	1:125:A:THR:H	19	0.17
(3,59)	1:197:A:LEU:H	1:204:A:GLU:H	15	0.17
(1,118)	1:45:A:LYS:H	1:45:A:LYS:HG3	8	0.17
(1,114)	1:66:A:PHE:H	1:65:A:ALA:HB1	2	0.17
(1,103)	1:118:A:LEU:H	1:118:A:LEU:HB3	11	0.17
(1,79)	1:68:A:VAL:H	1:93:A:PHE:H	5	0.17
(1,79)	1:68:A:VAL:H	1:93:A:PHE:H	7	0.17
(1,69)	1:87:A:THR:HB	1:87:A:THR:HG21	5	0.17
(1,69)	1:87:A:THR:HB	1:87:A:THR:HG22	7	0.17
(1,69)	1:87:A:THR:HB	1:87:A:THR:HG22	9	0.17
(1,69)	1:87:A:THR:HB	1:87:A:THR:HG21	12	0.17
(4,1309)	1:163:A:LEU:H	1:162:A:VAL:HG23	7	0.16
(4,1293)	1:91:A:ILE:H	1:91:A:ILE:HD11	12	0.16
(4,1289)	1:203:A:LEU:H	1:22:A:ILE:HD12	9	0.16
(4,1287)	1:87:A:THR:H	1:87:A:THR:HG22	8	0.16
(4,1287)	1:78:A:VAL:H	1:78:A:VAL:HG23	10	0.16
(4,1287)	1:78:A:VAL:H	1:78:A:VAL:HG23	17	0.16
(4,1286)	1:78:A:VAL:H	1:78:A:VAL:HG23	17	0.16
(4,1279)	1:211:A:LEU:H	1:211:A:LEU:HG	7	0.16
(4,1271)	1:231:A:ASN:H	1:169:A:LYS:HG2	4	0.16
(4,1261)	1:152:A:ALA:H	1:152:A:ALA:HB3	11	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1250)	1:163:A:LEU:H	1:162:A:VAL:HG21	10	0.16
(4,1249)	1:163:A:LEU:H	1:162:A:VAL:HG23	7	0.16
(4,1249)	1:171:A:LYS:H	1:171:A:LYS:HG3	9	0.16
(4,1223)	1:152:A:ALA:H	1:152:A:ALA:HB1	3	0.16
(4,1213)	1:239:A:LEU:H	1:239:A:LEU:HB2	3	0.16
(4,1213)	1:256:A:LYS:H	1:256:A:LYS:HG2	20	0.16
(4,1195)	1:228:A:LEU:H	1:228:A:LEU:HG	12	0.16
(4,1191)	1:9:A:LYS:H	1:9:A:LYS:HB2	9	0.16
(4,1186)	1:9:A:LYS:H	1:9:A:LYS:HB3	5	0.16
(4,1172)	1:256:A:LYS:H	1:256:A:LYS:HG2	8	0.16
(4,1164)	1:167:A:LYS:H	1:167:A:LYS:HB2	12	0.16
(4,1146)	1:135:A:GLN:H	1:135:A:GLN:HB2	10	0.16
(4,1128)	1:251:A:LYS:H	1:250:A:LEU:HB2	12	0.16
(4,1123)	1:218:A:SER:H	1:221:A:GLN:HB3	15	0.16
(4,1097)	1:157:A:GLN:H	1:157:A:GLN:HB2	1	0.16
(4,1097)	1:157:A:GLN:H	1:157:A:GLN:HB3	5	0.16
(4,1086)	1:86:A:GLY:H	1:84:A:LEU:HB2	7	0.16
(4,1078)	1:28:A:GLN:H	1:28:A:GLN:HB3	20	0.16
(4,1051)	1:170:A:GLY:H	1:61:A:ASN:HB3	9	0.16
(4,1034)	1:158:A:LYS:H	1:158:A:LYS:HB3	6	0.16
(4,1025)	1:28:A:GLN:H	1:28:A:GLN:HB2	12	0.16
(4,1010)	1:174:A:ASP:H	1:174:A:ASP:HB2	6	0.16
(4,999)	1:85:A:ASP:H	1:85:A:ASP:HB2	15	0.16
(4,993)	1:127:A:TYR:H	1:127:A:TYR:HB2	16	0.16
(4,981)	1:164:A:ASP:H	1:164:A:ASP:HB2	8	0.16
(4,981)	1:164:A:ASP:H	1:164:A:ASP:HB3	14	0.16
(4,980)	1:191:A:TRP:H	1:191:A:TRP:HB2	6	0.16
(4,974)	1:40:A:TYR:H	1:40:A:TYR:HB3	4	0.16
(4,970)	1:88:A:TYR:H	1:88:A:TYR:HB2	4	0.16
(4,967)	1:17:A:HIS:H	1:17:A:HIS:HB3	2	0.16
(4,962)	1:129:A:ASP:H	1:129:A:ASP:HB2	10	0.16
(4,923)	1:7:A:TYR:H	1:7:A:TYR:HB2	16	0.16
(4,916)	1:129:A:ASP:H	1:129:A:ASP:HA	15	0.16
(4,903)	1:49:A:VAL:H	1:48:A:SER:HB3	7	0.16
(4,894)	1:131:A:GLY:H	1:131:A:GLY:HA2	17	0.16
(4,870)	1:78:A:VAL:H	1:50:A:SER:HB2	5	0.16
(4,867)	1:157:A:GLN:H	1:157:A:GLN:HA	6	0.16
(4,867)	1:157:A:GLN:H	1:157:A:GLN:HA	11	0.16
(4,865)	1:258:A:SER:H	1:258:A:SER:HB3	7	0.16
(4,837)	1:17:A:HIS:H	1:17:A:HIS:HA	14	0.16
(4,836)	1:129:A:ASP:H	1:128:A:GLY:HA3	10	0.16
(4,835)	1:152:A:ALA:H	1:152:A:ALA:HA	7	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,805)	1:129:A:ASP:H	1:128:A:GLY:HA3	18	0.16
(4,789)	1:147:A:LEU:H	1:147:A:LEU:HA	5	0.16
(4,789)	1:152:A:ALA:H	1:152:A:ALA:HA	16	0.16
(4,775)	1:148:A:LYS:H	1:147:A:LEU:HA	6	0.16
(4,736)	1:43:A:SER:H	1:43:A:SER:HA	4	0.16
(4,736)	1:43:A:SER:H	1:43:A:SER:HA	7	0.16
(4,736)	1:43:A:SER:H	1:43:A:SER:HA	11	0.16
(4,722)	1:57:A:LEU:H	1:56:A:SER:HA	10	0.16
(4,715)	1:98:A:GLY:H	1:97:A:TRP:HA	16	0.16
(4,712)	1:124:A:ASN:H	1:123:A:TRP:HA	7	0.16
(4,683)	1:92:A:GLN:H	1:92:A:GLN:HA	3	0.16
(4,683)	1:92:A:GLN:H	1:92:A:GLN:HA	13	0.16
(4,683)	1:92:A:GLN:H	1:92:A:GLN:HA	15	0.16
(4,654)	1:199:A:THR:H	1:202:A:LEU:H	6	0.16
(4,650)	1:199:A:THR:H	1:202:A:LEU:H	6	0.16
(4,628)	1:221:A:GLN:H	1:220:A:GLU:H	9	0.16
(4,628)	1:221:A:GLN:H	1:220:A:GLU:H	18	0.16
(4,572)	1:222:A:VAL:H	1:221:A:GLN:H	3	0.16
(4,507)	1:50:A:SER:H	1:78:A:VAL:H	10	0.16
(4,462)	1:159:A:VAL:HA	1:159:A:VAL:HG23	2	0.16
(4,450)	1:147:A:LEU:HA	1:147:A:LEU:HD21	20	0.16
(4,443)	1:106:A:GLU:HG2	1:245:A:ARG:HG2	1	0.16
(4,436)	1:86:A:GLY:HA3	1:126:A:LYS:HG2	20	0.16
(4,410)	1:35:A:THR:HG22	1:35:A:THR:HA	7	0.16
(4,397)	1:159:A:VAL:HA	1:162:A:VAL:HB	8	0.16
(4,382)	1:193:A:TYR:HB3	1:208:A:TRP:HB3	12	0.16
(4,371)	1:22:A:ILE:HB	1:20:A:PHE:HB3	19	0.16
(4,327)	1:117:A:GLU:HB2	1:117:A:GLU:HA	7	0.16
(4,317)	1:166:A:ILE:HG22	1:166:A:ILE:HA	12	0.16
(4,312)	1:209:A:ILE:HD12	1:209:A:ILE:HA	4	0.16
(4,283)	1:95:A:PHE:HB2	1:95:A:PHE:HA	2	0.16
(4,283)	1:95:A:PHE:HB2	1:95:A:PHE:HA	15	0.16
(4,283)	1:95:A:PHE:HB2	1:95:A:PHE:HA	18	0.16
(4,258)	1:242:A:ASP:H	1:242:A:ASP:HB3	10	0.16
(4,253)	1:135:A:GLN:H	1:127:A:TYR:HB2	17	0.16
(4,245)	1:228:A:LEU:H	1:228:A:LEU:HA	3	0.16
(4,239)	1:135:A:GLN:H	1:139:A:GLY:HA3	18	0.16
(4,237)	1:167:A:LYS:H	1:166:A:ILE:HA	7	0.16
(4,237)	1:167:A:LYS:H	1:166:A:ILE:HA	8	0.16
(4,237)	1:167:A:LYS:H	1:166:A:ILE:HA	15	0.16
(4,224)	1:259:A:PHE:H	1:258:A:SER:HB3	12	0.16
(4,218)	1:169:A:LYS:H	1:169:A:LYS:HB2	14	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,216)	1:130:A:PHE:H	1:130:A:PHE:HB3	3	0.16
(4,211)	1:206:A:VAL:H	1:206:A:VAL:HB	7	0.16
(4,209)	1:199:A:THR:H	1:197:A:LEU:HB2	2	0.16
(4,208)	1:45:A:LYS:H	1:44:A:LEU:HA	6	0.16
(4,208)	1:45:A:LYS:H	1:44:A:LEU:HA	12	0.16
(4,207)	1:159:A:VAL:H	1:159:A:VAL:HA	20	0.16
(4,206)	1:139:A:GLY:H	1:140:A:LEU:HB3	2	0.16
(4,200)	1:108:A:THR:H	1:107:A:HIS:HA	4	0.16
(4,200)	1:108:A:THR:H	1:107:A:HIS:HA	7	0.16
(4,191)	1:159:A:VAL:H	1:159:A:VAL:HG22	1	0.16
(4,191)	1:160:A:VAL:H	1:160:A:VAL:HG21	6	0.16
(4,191)	1:126:A:LYS:H	1:126:A:LYS:HG3	9	0.16
(4,191)	1:159:A:VAL:H	1:159:A:VAL:HG23	20	0.16
(4,185)	1:255:A:ILE:HD11	1:34:A:ASP:H	10	0.16
(4,182)	1:166:A:ILE:H	1:163:A:LEU:HA	16	0.16
(4,182)	1:166:A:ILE:H	1:163:A:LEU:HA	17	0.16
(4,173)	1:157:A:GLN:H	1:157:A:GLN:HA	17	0.16
(4,157)	1:207:A:THR:H	1:207:A:THR:HB	15	0.16
(4,157)	1:207:A:THR:H	1:207:A:THR:HB	16	0.16
(4,138)	1:133:A:ALA:H	1:133:A:ALA:HB2	3	0.16
(4,138)	1:133:A:ALA:H	1:133:A:ALA:HB3	7	0.16
(4,119)	1:231:A:ASN:H	1:229:A:ASN:HB3	5	0.16
(4,114)	1:61:A:ASN:H	1:60:A:LEU:HG	3	0.16
(4,114)	1:61:A:ASN:H	1:60:A:LEU:HG	13	0.16
(4,110)	1:77:A:ALA:H	1:77:A:ALA:HB1	7	0.16
(4,80)	1:93:A:PHE:H	1:92:A:GLN:HB2	11	0.16
(4,42)	1:38:A:ALA:HA	1:255:A:ILE:H	17	0.16
(4,36)	1:67:A:ASN:H	1:66:A:PHE:HB2	14	0.16
(4,6)	1:113:A:LYS:HG3	1:107:A:HIS:H	11	0.16
(3,270)	1:219:A:SER:H	1:222:A:VAL:H	1	0.16
(3,270)	1:219:A:SER:H	1:222:A:VAL:H	8	0.16
(3,251)	1:242:A:ASP:H	1:100:A:LEU:H	20	0.16
(3,81)	1:191:A:TRP:H	1:210:A:VAL:H	15	0.16
(3,48)	1:210:A:VAL:H	1:191:A:TRP:H	15	0.16
(3,35)	1:222:A:VAL:H	1:219:A:SER:H	1	0.16
(3,35)	1:222:A:VAL:H	1:219:A:SER:H	8	0.16
(1,132)	1:135:A:GLN:H	1:134:A:VAL:HG22	18	0.16
(1,120)	1:259:A:PHE:H	1:257:A:ALA:HB2	12	0.16
(1,103)	1:118:A:LEU:H	1:118:A:LEU:HB3	9	0.16
(1,71)	1:77:A:ALA:HB1	1:51:A:TYR:HA	19	0.16
(1,69)	1:87:A:THR:HB	1:87:A:THR:HG23	1	0.16
(1,69)	1:87:A:THR:HB	1:87:A:THR:HG23	4	0.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,69)	1:87:A:THR:HB	1:87:A:THR:HG21	10	0.16
(1,52)	1:166:A:ILE:HD13	1:163:A:LEU:HA	10	0.16
(1,6)	1:169:A:LYS:HB3	1:63:A:GLY:H	1	0.16
(4,1322)	1:203:A:LEU:H	1:22:A:ILE:HD13	7	0.15
(4,1304)	1:177:A:ASN:H	1:162:A:VAL:HG21	19	0.15
(4,1293)	1:213:A:GLU:H	1:212:A:LYS:HG3	17	0.15
(4,1274)	1:113:A:LYS:H	1:112:A:LYS:HG3	20	0.15
(4,1261)	1:152:A:ALA:H	1:152:A:ALA:HB3	4	0.15
(4,1250)	1:163:A:LEU:H	1:162:A:VAL:HG23	7	0.15
(4,1237)	1:76:A:LYS:H	1:76:A:LYS:HG2	12	0.15
(4,1223)	1:152:A:ALA:H	1:152:A:ALA:HB1	20	0.15
(4,1209)	1:172:A:SER:H	1:166:A:ILE:HG22	8	0.15
(4,1201)	1:172:A:SER:H	1:166:A:ILE:HG22	8	0.15
(4,1195)	1:228:A:LEU:H	1:228:A:LEU:HB2	2	0.15
(4,1195)	1:228:A:LEU:H	1:228:A:LEU:HB2	6	0.15
(4,1186)	1:9:A:LYS:H	1:9:A:LYS:HB2	11	0.15
(4,1172)	1:256:A:LYS:H	1:256:A:LYS:HG3	1	0.15
(4,1162)	1:133:A:ALA:H	1:133:A:ALA:HB1	20	0.15
(4,1146)	1:135:A:GLN:H	1:135:A:GLN:HB2	1	0.15
(4,1146)	1:227:A:LYS:H	1:227:A:LYS:HB2	9	0.15
(4,1138)	1:238:A:GLU:H	1:238:A:GLU:HB3	12	0.15
(4,1126)	1:228:A:LEU:H	1:228:A:LEU:HB2	5	0.15
(4,1115)	1:158:A:LYS:H	1:158:A:LYS:HB2	9	0.15
(4,1114)	1:22:A:ILE:H	1:22:A:ILE:HB	15	0.15
(4,1107)	1:147:A:LEU:H	1:147:A:LEU:HG	12	0.15
(4,1102)	1:140:A:LEU:H	1:140:A:LEU:HG	7	0.15
(4,1097)	1:237:A:GLU:H	1:237:A:GLU:HB3	9	0.15
(4,1097)	1:157:A:GLN:H	1:157:A:GLN:HB3	11	0.15
(4,1089)	1:228:A:LEU:H	1:228:A:LEU:HB2	20	0.15
(4,1080)	1:86:A:GLY:H	1:84:A:LEU:HB2	9	0.15
(4,1047)	1:129:A:ASP:H	1:129:A:ASP:HB3	14	0.15
(4,1036)	1:158:A:LYS:H	1:158:A:LYS:HB3	6	0.15
(4,1027)	1:103:A:GLN:H	1:100:A:LEU:HB2	20	0.15
(4,1025)	1:164:A:ASP:H	1:164:A:ASP:HB2	2	0.15
(4,1020)	1:161:A:ASP:H	1:161:A:ASP:HB2	11	0.15
(4,1007)	1:119:A:HIS:H	1:119:A:HIS:HB2	19	0.15
(4,999)	1:119:A:HIS:H	1:119:A:HIS:HB2	19	0.15
(4,988)	1:205:A:CYS:H	1:205:A:CYS:HB3	18	0.15
(4,983)	1:119:A:HIS:H	1:119:A:HIS:HB2	19	0.15
(4,981)	1:164:A:ASP:H	1:164:A:ASP:HB2	1	0.15
(4,981)	1:164:A:ASP:H	1:164:A:ASP:HB2	6	0.15
(4,981)	1:164:A:ASP:H	1:164:A:ASP:HB2	17	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,974)	1:40:A:TYR:H	1:40:A:TYR:HB3	14	0.15
(4,964)	1:52:A:ASP:H	1:52:A:ASP:HB2	11	0.15
(4,964)	1:52:A:ASP:H	1:52:A:ASP:HB2	17	0.15
(4,961)	1:130:A:PHE:H	1:130:A:PHE:HB2	2	0.15
(4,957)	1:191:A:TRP:H	1:191:A:TRP:HB3	18	0.15
(4,948)	1:129:A:ASP:H	1:127:A:TYR:HB2	11	0.15
(4,924)	1:183:A:LEU:H	1:182:A:GLY:HA3	4	0.15
(4,924)	1:129:A:ASP:H	1:129:A:ASP:HA	15	0.15
(4,909)	1:32:A:ASP:H	1:31:A:VAL:HA	14	0.15
(4,898)	1:49:A:VAL:H	1:49:A:VAL:HA	2	0.15
(4,870)	1:78:A:VAL:H	1:50:A:SER:HB2	10	0.15
(4,870)	1:258:A:SER:H	1:258:A:SER:HB3	12	0.15
(4,869)	1:166:A:ILE:H	1:163:A:LEU:HA	9	0.15
(4,867)	1:157:A:GLN:H	1:157:A:GLN:HA	8	0.15
(4,867)	1:157:A:GLN:H	1:157:A:GLN:HA	18	0.15
(4,867)	1:157:A:GLN:H	1:157:A:GLN:HA	19	0.15
(4,862)	1:78:A:VAL:H	1:50:A:SER:HB2	4	0.15
(4,835)	1:147:A:LEU:H	1:147:A:LEU:HA	5	0.15
(4,835)	1:152:A:ALA:H	1:151:A:SER:HB2	9	0.15
(4,835)	1:152:A:ALA:H	1:152:A:ALA:HA	16	0.15
(4,817)	1:205:A:CYS:H	1:204:A:GLU:HA	14	0.15
(4,816)	1:258:A:SER:H	1:257:A:ALA:HA	7	0.15
(4,805)	1:129:A:ASP:H	1:128:A:GLY:HA3	17	0.15
(4,801)	1:129:A:ASP:H	1:128:A:GLY:HA3	18	0.15
(4,789)	1:106:A:GLU:H	1:105:A:SER:HA	4	0.15
(4,775)	1:7:A:TYR:H	1:7:A:TYR:HA	17	0.15
(4,768)	1:16:A:TRP:H	1:16:A:TRP:HA	19	0.15
(4,767)	1:70:A:PHE:H	1:69:A:GLU:HA	1	0.15
(4,767)	1:70:A:PHE:H	1:69:A:GLU:HA	2	0.15
(4,767)	1:197:A:LEU:H	1:197:A:LEU:HA	13	0.15
(4,736)	1:43:A:SER:H	1:43:A:SER:HA	19	0.15
(4,702)	1:121:A:VAL:H	1:121:A:VAL:HA	9	0.15
(4,683)	1:92:A:GLN:H	1:92:A:GLN:HA	6	0.15
(4,683)	1:92:A:GLN:H	1:92:A:GLN:HA	16	0.15
(4,662)	1:51:A:TYR:H	1:51:A:TYR:HA	17	0.15
(4,654)	1:199:A:THR:H	1:202:A:LEU:H	12	0.15
(4,650)	1:199:A:THR:H	1:202:A:LEU:H	12	0.15
(4,628)	1:181:A:ARG:H	1:182:A:GLY:H	6	0.15
(4,624)	1:103:A:GLN:H	1:102:A:GLY:H	16	0.15
(4,618)	1:56:A:SER:H	1:58:A:ARG:H	10	0.15
(4,611)	1:19:A:ASP:H	1:20:A:PHE:H	4	0.15
(4,553)	1:28:A:GLN:H	1:27:A:ARG:H	20	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,540)	1:89:A:ARG:H	1:123:A:TRP:H	16	0.15
(4,487)	1:152:A:ALA:H	1:151:A:SER:H	1	0.15
(4,462)	1:159:A:VAL:HA	1:159:A:VAL:HG22	9	0.15
(4,462)	1:159:A:VAL:HA	1:159:A:VAL:HG22	13	0.15
(4,462)	1:159:A:VAL:HA	1:159:A:VAL:HG23	16	0.15
(4,450)	1:147:A:LEU:HA	1:147:A:LEU:HD21	2	0.15
(4,450)	1:147:A:LEU:HA	1:147:A:LEU:HD22	6	0.15
(4,450)	1:147:A:LEU:HA	1:147:A:LEU:HD22	13	0.15
(4,440)	1:106:A:GLU:HG2	1:245:A:ARG:HG2	1	0.15
(4,436)	1:82:A:GLY:HA3	1:45:A:LYS:HG2	5	0.15
(4,431)	1:192:A:THR:HG23	1:192:A:THR:HB	14	0.15
(4,416)	1:23:A:ALA:HB2	1:16:A:TRP:HB2	8	0.15
(4,410)	1:35:A:THR:HG23	1:35:A:THR:HA	13	0.15
(4,410)	1:35:A:THR:HG22	1:35:A:THR:HA	15	0.15
(4,410)	1:35:A:THR:HG21	1:35:A:THR:HA	20	0.15
(4,409)	1:41:A:ASP:HA	1:41:A:ASP:HB3	14	0.15
(4,406)	1:133:A:ALA:HB2	1:130:A:PHE:HA	9	0.15
(4,404)	1:49:A:VAL:HA	1:49:A:VAL:HB	2	0.15
(4,404)	1:189:A:ASP:HB3	1:258:A:SER:HB3	15	0.15
(4,378)	1:22:A:ILE:HD11	1:20:A:PHE:HB3	10	0.15
(4,374)	1:127:A:TYR:HB3	1:133:A:ALA:HA	19	0.15
(4,327)	1:148:A:LYS:HB3	1:148:A:LYS:HA	6	0.15
(4,327)	1:117:A:GLU:HB2	1:117:A:GLU:HA	13	0.15
(4,317)	1:54:A:ALA:HB3	1:54:A:ALA:HA	18	0.15
(4,283)	1:95:A:PHE:HB2	1:95:A:PHE:HA	4	0.15
(4,283)	1:95:A:PHE:HB2	1:95:A:PHE:HA	5	0.15
(4,283)	1:95:A:PHE:HB2	1:95:A:PHE:HA	6	0.15
(4,283)	1:95:A:PHE:HB2	1:95:A:PHE:HA	7	0.15
(4,283)	1:95:A:PHE:HB2	1:95:A:PHE:HA	8	0.15
(4,283)	1:95:A:PHE:HB2	1:95:A:PHE:HA	10	0.15
(4,283)	1:95:A:PHE:HB2	1:95:A:PHE:HA	13	0.15
(4,283)	1:95:A:PHE:HB2	1:95:A:PHE:HA	14	0.15
(4,283)	1:95:A:PHE:HB2	1:95:A:PHE:HA	16	0.15
(4,283)	1:95:A:PHE:HB2	1:95:A:PHE:HA	20	0.15
(4,263)	1:243:A:ASN:HA	1:244:A:TRP:H	18	0.15
(4,242)	1:57:A:LEU:HB2	1:58:A:ARG:H	5	0.15
(4,208)	1:45:A:LYS:H	1:44:A:LEU:HA	4	0.15
(4,207)	1:159:A:VAL:H	1:159:A:VAL:HA	5	0.15
(4,207)	1:159:A:VAL:H	1:159:A:VAL:HA	12	0.15
(4,207)	1:159:A:VAL:H	1:159:A:VAL:HA	17	0.15
(4,204)	1:253:A:ARG:H	1:253:A:ARG:HG2	18	0.15
(4,191)	1:160:A:VAL:H	1:160:A:VAL:HG23	2	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,191)	1:160:A:VAL:H	1:160:A:VAL:HG22	14	0.15
(4,191)	1:160:A:VAL:H	1:160:A:VAL:HG22	15	0.15
(4,177)	1:179:A:ASP:H	1:179:A:ASP:HA	6	0.15
(4,177)	1:179:A:ASP:H	1:179:A:ASP:HA	10	0.15
(4,177)	1:179:A:ASP:H	1:179:A:ASP:HA	13	0.15
(4,157)	1:207:A:THR:H	1:207:A:THR:HB	2	0.15
(4,157)	1:207:A:THR:H	1:207:A:THR:HB	13	0.15
(4,153)	1:61:A:ASN:H	1:60:A:LEU:HA	14	0.15
(4,148)	1:164:A:ASP:H	1:164:A:ASP:HB3	20	0.15
(4,122)	1:86:A:GLY:H	1:85:A:ASP:HA	10	0.15
(4,119)	1:231:A:ASN:H	1:229:A:ASN:HB3	1	0.15
(4,119)	1:70:A:PHE:H	1:70:A:PHE:HB2	12	0.15
(4,114)	1:250:A:LEU:H	1:250:A:LEU:HG	20	0.15
(4,96)	1:53:A:GLN:H	1:53:A:GLN:HB3	5	0.15
(4,80)	1:119:A:HIS:H	1:119:A:HIS:HB2	16	0.15
(4,62)	1:85:A:ASP:H	1:84:A:LEU:HA	11	0.15
(4,22)	1:110:A:ASP:H	1:109:A:VAL:HB	17	0.15
(3,302)	1:229:A:ASN:H	1:168:A:THR:H	5	0.15
(3,237)	1:189:A:ASP:H	1:212:A:LYS:H	7	0.15
(3,231)	1:191:A:TRP:H	1:212:A:LYS:H	9	0.15
(3,166)	1:205:A:CYS:H	1:197:A:LEU:H	6	0.15
(3,164)	1:203:A:LEU:H	1:197:A:LEU:H	10	0.15
(3,158)	1:57:A:LEU:H	1:70:A:PHE:H	1	0.15
(3,59)	1:197:A:LEU:H	1:204:A:GLU:H	9	0.15
(3,58)	1:70:A:PHE:H	1:57:A:LEU:H	3	0.15
(1,132)	1:135:A:GLN:H	1:134:A:VAL:HG22	1	0.15
(1,132)	1:135:A:GLN:H	1:134:A:VAL:HG22	4	0.15
(1,117)	1:156:A:LEU:H	1:153:A:LYS:HG3	20	0.15
(1,103)	1:118:A:LEU:H	1:118:A:LEU:HB2	5	0.15
(1,103)	1:118:A:LEU:H	1:118:A:LEU:HB3	13	0.15
(1,79)	1:68:A:VAL:H	1:93:A:PHE:H	13	0.15
(1,71)	1:77:A:ALA:HB3	1:51:A:TYR:HA	13	0.15
(1,69)	1:87:A:THR:HB	1:87:A:THR:HG22	15	0.15
(1,69)	1:87:A:THR:HB	1:87:A:THR:HG23	20	0.15
(1,26)	1:156:A:LEU:H	1:156:A:LEU:HB3	6	0.15
(1,10)	1:55:A:THR:H	1:55:A:THR:HB	4	0.15
(4,1307)	1:76:A:LYS:H	1:76:A:LYS:HG3	1	0.14
(4,1293)	1:91:A:ILE:H	1:91:A:ILE:HD11	10	0.14
(4,1283)	1:152:A:ALA:H	1:152:A:ALA:HB3	15	0.14
(4,1283)	1:148:A:LYS:H	1:148:A:LYS:HG2	16	0.14
(4,1282)	1:148:A:LYS:H	1:148:A:LYS:HG2	16	0.14
(4,1280)	1:114:A:TYR:H	1:113:A:LYS:HG2	15	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1261)	1:152:A:ALA:H	1:152:A:ALA:HB1	2	0.14
(4,1258)	1:202:A:LEU:H	1:22:A:ILE:HG23	12	0.14
(4,1251)	1:176:A:THR:H	1:176:A:THR:HG22	10	0.14
(4,1248)	1:22:A:ILE:H	1:22:A:ILE:HD12	10	0.14
(4,1227)	1:91:A:ILE:H	1:91:A:ILE:HG12	11	0.14
(4,1225)	1:166:A:ILE:H	1:166:A:ILE:HG22	7	0.14
(4,1225)	1:166:A:ILE:H	1:166:A:ILE:HG21	12	0.14
(4,1209)	1:172:A:SER:H	1:166:A:ILE:HG23	6	0.14
(4,1201)	1:172:A:SER:H	1:166:A:ILE:HG23	6	0.14
(4,1200)	1:251:A:LYS:H	1:250:A:LEU:HB3	18	0.14
(4,1186)	1:117:A:GLU:H	1:116:A:ALA:HB3	15	0.14
(4,1174)	1:152:A:ALA:H	1:152:A:ALA:HB3	15	0.14
(4,1168)	1:190:A:TYR:H	1:189:A:ASP:HB3	2	0.14
(4,1158)	1:147:A:LEU:H	1:147:A:LEU:HB2	6	0.14
(4,1158)	1:84:A:LEU:H	1:84:A:LEU:HB2	14	0.14
(4,1138)	1:238:A:GLU:H	1:238:A:GLU:HB3	2	0.14
(4,1135)	1:221:A:GLN:H	1:221:A:GLN:HB2	6	0.14
(4,1134)	1:197:A:LEU:H	1:197:A:LEU:HB2	11	0.14
(4,1127)	1:197:A:LEU:H	1:197:A:LEU:HB2	18	0.14
(4,1126)	1:228:A:LEU:H	1:228:A:LEU:HB2	8	0.14
(4,1123)	1:218:A:SER:H	1:221:A:GLN:HB2	19	0.14
(4,1097)	1:157:A:GLN:H	1:157:A:GLN:HB2	10	0.14
(4,1094)	1:37:A:THR:H	1:34:A:ASP:HB3	1	0.14
(4,1086)	1:86:A:GLY:H	1:84:A:LEU:HB2	9	0.14
(4,1078)	1:221:A:GLN:H	1:221:A:GLN:HB3	7	0.14
(4,1058)	1:248:A:GLN:H	1:248:A:GLN:HG2	13	0.14
(4,1057)	1:204:A:GLU:H	1:204:A:GLU:HB2	4	0.14
(4,1057)	1:209:A:ILE:H	1:209:A:ILE:HB	20	0.14
(4,1051)	1:26:A:GLU:H	1:26:A:GLU:HG3	20	0.14
(4,1041)	1:119:A:HIS:H	1:119:A:HIS:HB2	11	0.14
(4,1027)	1:103:A:GLN:H	1:103:A:GLN:HG3	15	0.14
(4,1016)	1:218:A:SER:H	1:221:A:GLN:HG3	8	0.14
(4,1014)	1:174:A:ASP:H	1:174:A:ASP:HB3	14	0.14
(4,1010)	1:174:A:ASP:H	1:174:A:ASP:HB3	14	0.14
(4,1010)	1:174:A:ASP:H	1:174:A:ASP:HB2	19	0.14
(4,993)	1:162:A:VAL:H	1:161:A:ASP:HB2	7	0.14
(4,989)	1:41:A:ASP:H	1:41:A:ASP:HB2	4	0.14
(4,989)	1:179:A:ASP:H	1:179:A:ASP:HB2	7	0.14
(4,989)	1:41:A:ASP:H	1:41:A:ASP:HB2	8	0.14
(4,981)	1:164:A:ASP:H	1:164:A:ASP:HB2	3	0.14
(4,981)	1:164:A:ASP:H	1:164:A:ASP:HB2	4	0.14
(4,981)	1:164:A:ASP:H	1:164:A:ASP:HB2	5	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,981)	1:164:A:ASP:H	1:164:A:ASP:HB2	11	0.14
(4,981)	1:164:A:ASP:H	1:164:A:ASP:HB2	16	0.14
(4,968)	1:129:A:ASP:H	1:129:A:ASP:HB2	10	0.14
(4,963)	1:121:A:VAL:H	1:122:A:HIS:HB2	4	0.14
(4,958)	1:37:A:THR:H	1:36:A:HIS:HB3	7	0.14
(4,923)	1:7:A:TYR:H	1:7:A:TYR:HB2	3	0.14
(4,923)	1:124:A:ASN:H	1:123:A:TRP:HB2	7	0.14
(4,909)	1:190:A:TYR:H	1:258:A:SER:HB3	13	0.14
(4,903)	1:49:A:VAL:H	1:48:A:SER:HB3	10	0.14
(4,870)	1:258:A:SER:H	1:258:A:SER:HB3	9	0.14
(4,870)	1:258:A:SER:H	1:258:A:SER:HB3	15	0.14
(4,870)	1:78:A:VAL:H	1:50:A:SER:HB2	17	0.14
(4,867)	1:157:A:GLN:H	1:157:A:GLN:HA	4	0.14
(4,867)	1:157:A:GLN:H	1:157:A:GLN:HA	5	0.14
(4,867)	1:157:A:GLN:H	1:157:A:GLN:HA	7	0.14
(4,867)	1:157:A:GLN:H	1:157:A:GLN:HA	9	0.14
(4,867)	1:157:A:GLN:H	1:157:A:GLN:HA	15	0.14
(4,867)	1:157:A:GLN:H	1:157:A:GLN:HA	16	0.14
(4,844)	1:33:A:ILE:H	1:33:A:ILE:HA	11	0.14
(4,835)	1:106:A:GLU:H	1:105:A:SER:HA	4	0.14
(4,832)	1:253:A:ARG:H	1:253:A:ARG:HA	17	0.14
(4,817)	1:205:A:CYS:H	1:205:A:CYS:HA	2	0.14
(4,805)	1:129:A:ASP:H	1:128:A:GLY:HA3	10	0.14
(4,801)	1:129:A:ASP:H	1:128:A:GLY:HA3	10	0.14
(4,801)	1:129:A:ASP:H	1:128:A:GLY:HA3	17	0.14
(4,775)	1:147:A:LEU:H	1:147:A:LEU:HA	5	0.14
(4,768)	1:16:A:TRP:H	1:16:A:TRP:HA	17	0.14
(4,767)	1:70:A:PHE:H	1:69:A:GLU:HA	19	0.14
(4,711)	1:122:A:HIS:H	1:121:A:VAL:HA	4	0.14
(4,683)	1:138:A:ASP:H	1:138:A:ASP:HA	1	0.14
(4,683)	1:92:A:GLN:H	1:92:A:GLN:HA	10	0.14
(4,683)	1:92:A:GLN:H	1:92:A:GLN:HA	14	0.14
(4,670)	1:52:A:ASP:H	1:51:A:TYR:HA	12	0.14
(4,655)	1:97:A:TRP:H	1:242:A:ASP:H	4	0.14
(4,624)	1:103:A:GLN:H	1:102:A:GLY:H	2	0.14
(4,624)	1:103:A:GLN:H	1:102:A:GLY:H	12	0.14
(4,572)	1:227:A:LYS:H	1:228:A:LEU:H	15	0.14
(4,467)	1:82:A:GLY:HA3	1:44:A:LEU:HD22	18	0.14
(4,462)	1:159:A:VAL:HA	1:159:A:VAL:HG22	11	0.14
(4,450)	1:147:A:LEU:HA	1:147:A:LEU:HD21	18	0.14
(4,410)	1:35:A:THR:HG21	1:35:A:THR:HA	18	0.14
(4,406)	1:133:A:ALA:HB1	1:130:A:PHE:HA	13	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,405)	1:189:A:ASP:HB3	1:258:A:SER:HB3	15	0.14
(4,404)	1:49:A:VAL:HA	1:49:A:VAL:HB	10	0.14
(4,378)	1:22:A:ILE:HD13	1:20:A:PHE:HB3	2	0.14
(4,327)	1:106:A:GLU:HG3	1:106:A:GLU:HA	1	0.14
(4,327)	1:148:A:LYS:HB3	1:148:A:LYS:HA	16	0.14
(4,324)	1:60:A:LEU:HB3	1:60:A:LEU:HA	20	0.14
(4,283)	1:95:A:PHE:HB2	1:95:A:PHE:HA	11	0.14
(4,253)	1:135:A:GLN:H	1:127:A:TYR:HB3	2	0.14
(4,232)	1:169:A:LYS:H	1:229:A:ASN:HB2	12	0.14
(4,213)	1:135:A:GLN:H	1:135:A:GLN:HG3	2	0.14
(4,211)	1:206:A:VAL:H	1:206:A:VAL:HB	20	0.14
(4,208)	1:45:A:LYS:H	1:44:A:LEU:HA	5	0.14
(4,207)	1:159:A:VAL:H	1:159:A:VAL:HA	7	0.14
(4,207)	1:159:A:VAL:H	1:159:A:VAL:HA	13	0.14
(4,204)	1:100:A:LEU:H	1:100:A:LEU:HG	3	0.14
(4,200)	1:108:A:THR:H	1:107:A:HIS:HA	19	0.14
(4,177)	1:41:A:ASP:H	1:41:A:ASP:HA	1	0.14
(4,177)	1:41:A:ASP:H	1:41:A:ASP:HA	2	0.14
(4,177)	1:41:A:ASP:H	1:41:A:ASP:HA	7	0.14
(4,177)	1:179:A:ASP:H	1:179:A:ASP:HA	12	0.14
(4,177)	1:41:A:ASP:H	1:41:A:ASP:HA	14	0.14
(4,177)	1:179:A:ASP:H	1:179:A:ASP:HA	16	0.14
(4,177)	1:41:A:ASP:H	1:41:A:ASP:HA	19	0.14
(4,177)	1:41:A:ASP:H	1:41:A:ASP:HA	20	0.14
(4,173)	1:157:A:GLN:H	1:157:A:GLN:HA	2	0.14
(4,157)	1:207:A:THR:H	1:207:A:THR:HB	19	0.14
(4,148)	1:164:A:ASP:H	1:164:A:ASP:HB2	6	0.14
(4,148)	1:164:A:ASP:H	1:164:A:ASP:HB3	14	0.14
(4,147)	1:243:A:ASN:H	1:240:A:MET:HA	7	0.14
(4,122)	1:52:A:ASP:H	1:51:A:TYR:HA	2	0.14
(4,104)	1:119:A:HIS:H	1:118:A:LEU:HB3	5	0.14
(4,81)	1:55:A:THR:H	1:76:A:LYS:HG3	4	0.14
(4,80)	1:119:A:HIS:H	1:119:A:HIS:HB2	10	0.14
(4,62)	1:211:A:LEU:H	1:210:A:VAL:HA	9	0.14
(4,62)	1:55:A:THR:H	1:54:A:ALA:HA	12	0.14
(4,62)	1:101:A:ASP:H	1:100:A:LEU:HA	18	0.14
(4,48)	1:148:A:LYS:H	1:148:A:LYS:HB3	15	0.14
(4,34)	1:170:A:GLY:H	1:166:A:ILE:HG23	14	0.14
(3,173)	1:57:A:LEU:H	1:175:A:PHE:H	18	0.14
(3,120)	1:248:A:GLN:H	1:32:A:ASP:H	1	0.14
(3,71)	1:138:A:ASP:H	1:140:A:LEU:H	9	0.14
(3,12)	1:218:A:SER:H	1:150:A:GLY:H	9	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,20)	1:229:A:ASN:H	1:168:A:THR:H	4	0.14
(1,123)	1:63:A:GLY:H	1:169:A:LYS:HG2	3	0.14
(1,120)	1:259:A:PHE:H	1:257:A:ALA:HB1	4	0.14
(1,118)	1:45:A:LYS:H	1:45:A:LYS:HG3	14	0.14
(1,113)	1:104:A:GLY:H	1:103:A:GLN:HB3	11	0.14
(1,106)	1:226:A:ARG:H	1:225:A:PHE:HB3	2	0.14
(1,103)	1:118:A:LEU:H	1:118:A:LEU:HB3	10	0.14
(1,83)	1:37:A:THR:H	1:38:A:ALA:H	17	0.14
(1,69)	1:87:A:THR:HB	1:87:A:THR:HG23	16	0.14
(1,44)	1:91:A:ILE:HD12	1:122:A:HIS:HA	1	0.14
(1,38)	1:77:A:ALA:HA	1:51:A:TYR:HA	10	0.14
(1,25)	1:169:A:LYS:H	1:168:A:THR:HB	5	0.14
(1,14)	1:140:A:LEU:H	1:139:A:GLY:HA3	17	0.14
(4,1316)	1:205:A:CYS:H	1:206:A:VAL:HG22	13	0.13
(4,1314)	1:55:A:THR:H	1:76:A:LYS:HG2	3	0.13
(4,1308)	1:189:A:ASP:H	1:188:A:LEU:HD23	4	0.13
(4,1299)	1:91:A:ILE:H	1:91:A:ILE:HD13	7	0.13
(4,1282)	1:152:A:ALA:H	1:152:A:ALA:HB3	15	0.13
(4,1274)	1:113:A:LYS:H	1:112:A:LYS:HG2	1	0.13
(4,1269)	1:160:A:VAL:H	1:160:A:VAL:HG21	18	0.13
(4,1264)	1:204:A:GLU:H	1:22:A:ILE:HD11	5	0.13
(4,1264)	1:210:A:VAL:H	1:209:A:ILE:HG22	18	0.13
(4,1228)	1:147:A:LEU:H	1:147:A:LEU:HG	4	0.13
(4,1192)	1:251:A:LYS:H	1:250:A:LEU:HB3	18	0.13
(4,1191)	1:9:A:LYS:H	1:9:A:LYS:HB2	12	0.13
(4,1186)	1:9:A:LYS:H	1:9:A:LYS:HB2	9	0.13
(4,1172)	1:209:A:ILE:H	1:209:A:ILE:HG12	11	0.13
(4,1160)	1:92:A:GLN:H	1:91:A:ILE:HB	20	0.13
(4,1147)	1:231:A:ASN:H	1:169:A:LYS:HB2	5	0.13
(4,1139)	1:209:A:ILE:H	1:209:A:ILE:HG12	17	0.13
(4,1130)	1:133:A:ALA:H	1:133:A:ALA:HB3	14	0.13
(4,1127)	1:167:A:LYS:H	1:167:A:LYS:HB2	6	0.13
(4,1127)	1:221:A:GLN:H	1:221:A:GLN:HB2	8	0.13
(4,1127)	1:183:A:LEU:H	1:183:A:LEU:HB2	12	0.13
(4,1127)	1:20:A:PHE:H	1:19:A:ASP:HB3	13	0.13
(4,1122)	1:24:A:LYS:H	1:24:A:LYS:HB2	14	0.13
(4,1110)	1:77:A:ALA:H	1:76:A:LYS:HB2	17	0.13
(4,1109)	1:204:A:GLU:H	1:203:A:LEU:HB3	19	0.13
(4,1102)	1:219:A:SER:H	1:149:A:VAL:HB	14	0.13
(4,1089)	1:228:A:LEU:H	1:228:A:LEU:HG	16	0.13
(4,1086)	1:86:A:GLY:H	1:84:A:LEU:HB2	3	0.13
(4,1060)	1:133:A:ALA:H	1:132:A:LYS:HB2	14	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1060)	1:260:A:LYS:H	1:260:A:LYS:HB2	20	0.13
(4,1056)	1:220:A:GLU:H	1:220:A:GLU:HB2	12	0.13
(4,1051)	1:26:A:GLU:H	1:26:A:GLU:HG2	11	0.13
(4,1048)	1:103:A:GLN:H	1:103:A:GLN:HG2	4	0.13
(4,1048)	1:103:A:GLN:H	1:100:A:LEU:HB3	6	0.13
(4,1041)	1:240:A:MET:H	1:240:A:MET:HB3	3	0.13
(4,1033)	1:119:A:HIS:H	1:119:A:HIS:HB2	17	0.13
(4,1024)	1:22:A:ILE:H	1:20:A:PHE:HB3	5	0.13
(4,1016)	1:43:A:SER:H	1:41:A:ASP:HB3	4	0.13
(4,1016)	1:218:A:SER:H	1:221:A:GLN:HB3	12	0.13
(4,1010)	1:52:A:ASP:H	1:52:A:ASP:HB2	3	0.13
(4,1007)	1:85:A:ASP:H	1:85:A:ASP:HB2	2	0.13
(4,1007)	1:119:A:HIS:H	1:119:A:HIS:HB2	6	0.13
(4,1007)	1:119:A:HIS:H	1:119:A:HIS:HB2	11	0.13
(4,1006)	1:79:A:LEU:H	1:88:A:TYR:HB2	9	0.13
(4,1003)	1:76:A:LYS:H	1:74:A:GLN:HB2	20	0.13
(4,999)	1:85:A:ASP:H	1:85:A:ASP:HB2	2	0.13
(4,987)	1:241:A:VAL:H	1:240:A:MET:HA	5	0.13
(4,969)	1:244:A:TRP:H	1:244:A:TRP:HB3	11	0.13
(4,963)	1:121:A:VAL:H	1:122:A:HIS:HB2	9	0.13
(4,931)	1:85:A:ASP:H	1:85:A:ASP:HB2	9	0.13
(4,924)	1:129:A:ASP:H	1:128:A:GLY:HA3	16	0.13
(4,923)	1:9:A:LYS:H	1:8:A:GLY:HA3	11	0.13
(4,880)	1:166:A:ILE:H	1:165:A:SER:HB3	7	0.13
(4,870)	1:78:A:VAL:H	1:50:A:SER:HB2	13	0.13
(4,867)	1:157:A:GLN:H	1:157:A:GLN:HA	1	0.13
(4,867)	1:157:A:GLN:H	1:157:A:GLN:HA	3	0.13
(4,867)	1:157:A:GLN:H	1:157:A:GLN:HA	10	0.13
(4,845)	1:151:A:SER:H	1:150:A:GLY:HA3	17	0.13
(4,838)	1:148:A:LYS:H	1:147:A:LEU:HA	14	0.13
(4,836)	1:129:A:ASP:H	1:128:A:GLY:HA3	1	0.13
(4,817)	1:205:A:CYS:H	1:204:A:GLU:HA	19	0.13
(4,817)	1:205:A:CYS:H	1:204:A:GLU:HA	20	0.13
(4,775)	1:106:A:GLU:H	1:105:A:SER:HA	4	0.13
(4,773)	1:92:A:GLN:H	1:91:A:ILE:HA	6	0.13
(4,768)	1:16:A:TRP:H	1:16:A:TRP:HA	1	0.13
(4,768)	1:16:A:TRP:H	1:16:A:TRP:HA	14	0.13
(4,768)	1:189:A:ASP:H	1:189:A:ASP:HA	20	0.13
(4,767)	1:190:A:TYR:H	1:189:A:ASP:HA	6	0.13
(4,736)	1:43:A:SER:H	1:43:A:SER:HA	10	0.13
(4,736)	1:43:A:SER:H	1:43:A:SER:HA	13	0.13
(4,736)	1:218:A:SER:H	1:218:A:SER:HA	14	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,736)	1:218:A:SER:H	1:218:A:SER:HA	16	0.13
(4,722)	1:57:A:LEU:H	1:56:A:SER:HA	15	0.13
(4,711)	1:51:A:TYR:H	1:50:A:SER:HA	3	0.13
(4,711)	1:122:A:HIS:H	1:121:A:VAL:HA	16	0.13
(4,683)	1:92:A:GLN:H	1:92:A:GLN:HA	2	0.13
(4,683)	1:92:A:GLN:H	1:92:A:GLN:HA	4	0.13
(4,683)	1:92:A:GLN:H	1:92:A:GLN:HA	7	0.13
(4,683)	1:92:A:GLN:H	1:92:A:GLN:HA	8	0.13
(4,683)	1:92:A:GLN:H	1:92:A:GLN:HA	11	0.13
(4,683)	1:92:A:GLN:H	1:92:A:GLN:HA	12	0.13
(4,683)	1:92:A:GLN:H	1:92:A:GLN:HA	17	0.13
(4,683)	1:92:A:GLN:H	1:92:A:GLN:HA	18	0.13
(4,683)	1:92:A:GLN:H	1:92:A:GLN:HA	19	0.13
(4,683)	1:92:A:GLN:H	1:92:A:GLN:HA	20	0.13
(4,670)	1:52:A:ASP:H	1:51:A:TYR:HA	4	0.13
(4,670)	1:52:A:ASP:H	1:51:A:TYR:HA	6	0.13
(4,618)	1:56:A:SER:H	1:58:A:ARG:H	14	0.13
(4,614)	1:19:A:ASP:H	1:20:A:PHE:H	16	0.13
(4,611)	1:19:A:ASP:H	1:20:A:PHE:H	11	0.13
(4,602)	1:37:A:THR:H	1:36:A:HIS:H	7	0.13
(4,460)	1:223:A:LEU:HA	1:223:A:LEU:HD23	8	0.13
(4,454)	1:50:A:SER:HB2	1:78:A:VAL:HG21	9	0.13
(4,450)	1:147:A:LEU:HA	1:147:A:LEU:HD22	3	0.13
(4,450)	1:147:A:LEU:HA	1:147:A:LEU:HD22	4	0.13
(4,450)	1:147:A:LEU:HA	1:147:A:LEU:HD23	5	0.13
(4,450)	1:147:A:LEU:HA	1:147:A:LEU:HD22	8	0.13
(4,446)	1:22:A:ILE:HD13	1:22:A:ILE:HA	16	0.13
(4,438)	1:133:A:ALA:HB2	1:130:A:PHE:HA	9	0.13
(4,435)	1:159:A:VAL:HA	1:159:A:VAL:HG23	5	0.13
(4,431)	1:55:A:THR:HB	1:55:A:THR:HG21	12	0.13
(4,416)	1:23:A:ALA:HB1	1:17:A:HIS:HB3	18	0.13
(4,405)	1:49:A:VAL:HA	1:49:A:VAL:HB	2	0.13
(4,405)	1:49:A:VAL:HA	1:49:A:VAL:HB	10	0.13
(4,393)	1:63:A:GLY:HA2	1:169:A:LYS:HB2	8	0.13
(4,386)	1:232:A:GLY:HA2	1:229:A:ASN:HB2	13	0.13
(4,371)	1:22:A:ILE:HB	1:20:A:PHE:HB2	15	0.13
(4,369)	1:20:A:PHE:HB3	1:20:A:PHE:HA	15	0.13
(4,327)	1:117:A:GLU:HB3	1:117:A:GLU:HA	12	0.13
(4,327)	1:221:A:GLN:HG2	1:221:A:GLN:HA	17	0.13
(4,327)	1:117:A:GLU:HB2	1:117:A:GLU:HA	20	0.13
(4,317)	1:209:A:ILE:HG21	1:209:A:ILE:HA	16	0.13
(4,241)	1:57:A:LEU:HB2	1:58:A:ARG:H	3	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,237)	1:167:A:LYS:H	1:166:A:ILE:HA	12	0.13
(4,224)	1:44:A:LEU:H	1:43:A:SER:HB3	6	0.13
(4,218)	1:169:A:LYS:H	1:169:A:LYS:HB2	15	0.13
(4,208)	1:45:A:LYS:H	1:44:A:LEU:HA	17	0.13
(4,207)	1:159:A:VAL:H	1:159:A:VAL:HA	1	0.13
(4,207)	1:159:A:VAL:H	1:159:A:VAL:HA	19	0.13
(4,173)	1:157:A:GLN:H	1:157:A:GLN:HA	6	0.13
(4,157)	1:207:A:THR:H	1:207:A:THR:HB	14	0.13
(4,148)	1:164:A:ASP:H	1:164:A:ASP:HB2	1	0.13
(4,62)	1:211:A:LEU:H	1:210:A:VAL:HA	1	0.13
(4,62)	1:257:A:ALA:H	1:256:A:LYS:HA	2	0.13
(4,62)	1:238:A:GLU:H	1:237:A:GLU:HA	4	0.13
(4,62)	1:254:A:GLN:HA	1:255:A:ILE:H	10	0.13
(4,62)	1:240:A:MET:H	1:239:A:LEU:HA	13	0.13
(4,62)	1:238:A:GLU:H	1:237:A:GLU:HA	15	0.13
(4,62)	1:240:A:MET:H	1:239:A:LEU:HA	16	0.13
(4,62)	1:123:A:TRP:H	1:122:A:HIS:HA	17	0.13
(4,62)	1:211:A:LEU:H	1:210:A:VAL:HA	19	0.13
(4,42)	1:38:A:ALA:HA	1:255:A:ILE:H	2	0.13
(4,24)	1:55:A:THR:H	1:76:A:LYS:HD2	6	0.13
(4,13)	1:63:A:GLY:H	1:60:A:LEU:HD11	13	0.13
(3,314)	1:229:A:ASN:H	1:168:A:THR:H	13	0.13
(3,166)	1:205:A:CYS:H	1:197:A:LEU:H	18	0.13
(3,105)	1:183:A:LEU:H	1:181:A:ARG:H	19	0.13
(3,92)	1:55:A:THR:H	1:77:A:ALA:H	10	0.13
(3,59)	1:197:A:LEU:H	1:204:A:GLU:H	7	0.13
(1,132)	1:135:A:GLN:H	1:134:A:VAL:HG21	2	0.13
(1,128)	1:81:A:GLY:H	1:84:A:LEU:HD21	15	0.13
(1,113)	1:104:A:GLY:H	1:103:A:GLN:HB2	12	0.13
(1,103)	1:118:A:LEU:H	1:118:A:LEU:HB3	7	0.13
(1,85)	1:162:A:VAL:H	1:161:A:ASP:H	5	0.13
(1,84)	1:103:A:GLN:H	1:102:A:GLY:H	18	0.13
(1,83)	1:37:A:THR:H	1:38:A:ALA:H	5	0.13
(1,83)	1:37:A:THR:H	1:38:A:ALA:H	6	0.13
(1,73)	1:134:A:VAL:HG22	1:131:A:GLY:HA2	6	0.13
(1,69)	1:87:A:THR:HB	1:87:A:THR:HG21	2	0.13
(1,69)	1:87:A:THR:HB	1:87:A:THR:HG23	3	0.13
(1,69)	1:87:A:THR:HB	1:87:A:THR:HG21	13	0.13
(1,49)	1:224:A:LYS:HG2	1:224:A:LYS:HA	2	0.13
(1,25)	1:169:A:LYS:H	1:168:A:THR:HB	3	0.13
(1,10)	1:55:A:THR:H	1:55:A:THR:HB	20	0.13
(1,6)	1:169:A:LYS:HB3	1:63:A:GLY:H	19	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1299)	1:91:A:ILE:H	1:91:A:ILE:HD12	13	0.12
(4,1292)	1:91:A:ILE:H	1:91:A:ILE:HD13	7	0.12
(4,1289)	1:203:A:LEU:H	1:203:A:LEU:HD22	19	0.12
(4,1280)	1:68:A:VAL:H	1:68:A:VAL:HG21	13	0.12
(4,1270)	1:93:A:PHE:H	1:68:A:VAL:HG21	10	0.12
(4,1268)	1:204:A:GLU:H	1:22:A:ILE:HD11	5	0.12
(4,1261)	1:152:A:ALA:H	1:152:A:ALA:HB2	9	0.12
(4,1225)	1:64:A:HIS:H	1:169:A:LYS:HG2	17	0.12
(4,1224)	1:148:A:LYS:H	1:148:A:LYS:HG3	12	0.12
(4,1220)	1:133:A:ALA:H	1:133:A:ALA:HB3	7	0.12
(4,1195)	1:228:A:LEU:H	1:228:A:LEU:HB2	5	0.12
(4,1191)	1:148:A:LYS:H	1:148:A:LYS:HG3	5	0.12
(4,1164)	1:167:A:LYS:H	1:167:A:LYS:HB2	10	0.12
(4,1158)	1:22:A:ILE:H	1:22:A:ILE:HB	17	0.12
(4,1151)	1:156:A:LEU:H	1:153:A:LYS:HG3	20	0.12
(4,1146)	1:135:A:GLN:H	1:135:A:GLN:HB2	6	0.12
(4,1138)	1:238:A:GLU:H	1:238:A:GLU:HB2	19	0.12
(4,1138)	1:238:A:GLU:H	1:238:A:GLU:HB2	20	0.12
(4,1126)	1:228:A:LEU:H	1:228:A:LEU:HG	14	0.12
(4,1121)	1:48:A:SER:H	1:47:A:LEU:HB3	17	0.12
(4,1107)	1:48:A:SER:H	1:47:A:LEU:HB3	17	0.12
(4,1102)	1:140:A:LEU:H	1:140:A:LEU:HG	9	0.12
(4,1097)	1:237:A:GLU:H	1:237:A:GLU:HB2	13	0.12
(4,1097)	1:237:A:GLU:H	1:237:A:GLU:HB2	19	0.12
(4,1091)	1:81:A:GLY:H	1:80:A:LYS:HB3	10	0.12
(4,1089)	1:221:A:GLN:H	1:221:A:GLN:HG2	11	0.12
(4,1086)	1:86:A:GLY:H	1:84:A:LEU:HB2	18	0.12
(4,1082)	1:251:A:LYS:H	1:250:A:LEU:HB3	3	0.12
(4,1079)	1:164:A:ASP:H	1:164:A:ASP:HB2	8	0.12
(4,1071)	1:103:A:GLN:H	1:100:A:LEU:HB3	6	0.12
(4,1053)	1:37:A:THR:H	1:34:A:ASP:HB3	1	0.12
(4,1051)	1:170:A:GLY:H	1:61:A:ASN:HB3	1	0.12
(4,1036)	1:158:A:LYS:H	1:158:A:LYS:HB3	5	0.12
(4,1034)	1:230:A:PHE:H	1:229:A:ASN:HB3	13	0.12
(4,1034)	1:57:A:LEU:H	1:57:A:LEU:HB3	20	0.12
(4,1023)	1:62:A:ASN:H	1:61:A:ASN:HB3	5	0.12
(4,1020)	1:161:A:ASP:H	1:161:A:ASP:HB2	18	0.12
(4,1014)	1:52:A:ASP:H	1:52:A:ASP:HB2	20	0.12
(4,1012)	1:18:A:LYS:H	1:17:A:HIS:HB2	1	0.12
(4,1012)	1:18:A:LYS:H	1:17:A:HIS:HB3	13	0.12
(4,1010)	1:27:A:ARG:H	1:27:A:ARG:HB2	18	0.12
(4,1010)	1:52:A:ASP:H	1:52:A:ASP:HB2	20	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1007)	1:85:A:ASP:H	1:85:A:ASP:HB2	18	0.12
(4,999)	1:65:A:ALA:H	1:62:A:ASN:HB2	3	0.12
(4,999)	1:119:A:HIS:H	1:119:A:HIS:HB2	6	0.12
(4,999)	1:119:A:HIS:H	1:119:A:HIS:HB2	11	0.12
(4,995)	1:70:A:PHE:H	1:70:A:PHE:HB2	4	0.12
(4,995)	1:178:A:PHE:H	1:178:A:PHE:HB3	10	0.12
(4,993)	1:127:A:TYR:H	1:127:A:TYR:HB2	10	0.12
(4,987)	1:244:A:TRP:H	1:244:A:TRP:HB3	9	0.12
(4,983)	1:65:A:ALA:H	1:62:A:ASN:HB2	3	0.12
(4,983)	1:119:A:HIS:H	1:119:A:HIS:HB2	6	0.12
(4,983)	1:119:A:HIS:H	1:119:A:HIS:HB2	11	0.12
(4,981)	1:164:A:ASP:H	1:164:A:ASP:HB2	12	0.12
(4,981)	1:164:A:ASP:H	1:164:A:ASP:HB2	15	0.12
(4,981)	1:164:A:ASP:H	1:164:A:ASP:HB2	19	0.12
(4,980)	1:191:A:TRP:H	1:191:A:TRP:HB2	8	0.12
(4,969)	1:244:A:TRP:H	1:244:A:TRP:HB3	1	0.12
(4,964)	1:52:A:ASP:H	1:52:A:ASP:HB2	2	0.12
(4,964)	1:174:A:ASP:H	1:174:A:ASP:HB2	6	0.12
(4,963)	1:121:A:VAL:H	1:122:A:HIS:HB2	16	0.12
(4,918)	1:119:A:HIS:H	1:118:A:LEU:HB3	2	0.12
(4,909)	1:32:A:ASP:H	1:31:A:VAL:HA	11	0.12
(4,867)	1:157:A:GLN:H	1:157:A:GLN:HA	20	0.12
(4,862)	1:78:A:VAL:H	1:50:A:SER:HB3	18	0.12
(4,855)	1:57:A:LEU:H	1:56:A:SER:HA	2	0.12
(4,855)	1:230:A:PHE:H	1:229:A:ASN:HA	6	0.12
(4,845)	1:151:A:SER:H	1:151:A:SER:HA	8	0.12
(4,845)	1:151:A:SER:H	1:151:A:SER:HA	10	0.12
(4,845)	1:151:A:SER:H	1:151:A:SER:HA	14	0.12
(4,845)	1:151:A:SER:H	1:151:A:SER:HA	15	0.12
(4,845)	1:151:A:SER:H	1:151:A:SER:HA	18	0.12
(4,845)	1:151:A:SER:H	1:151:A:SER:HA	20	0.12
(4,823)	1:184:A:LEU:H	1:184:A:LEU:HA	10	0.12
(4,767)	1:70:A:PHE:H	1:69:A:GLU:HA	4	0.12
(4,742)	1:197:A:LEU:H	1:197:A:LEU:HA	8	0.12
(4,742)	1:197:A:LEU:H	1:197:A:LEU:HA	10	0.12
(4,736)	1:43:A:SER:H	1:43:A:SER:HA	5	0.12
(4,722)	1:57:A:LEU:H	1:56:A:SER:HA	6	0.12
(4,711)	1:188:A:LEU:H	1:187:A:SER:HA	8	0.12
(4,711)	1:51:A:TYR:H	1:50:A:SER:HA	12	0.12
(4,711)	1:90:A:LEU:H	1:89:A:ARG:HA	13	0.12
(4,704)	1:189:A:ASP:H	1:188:A:LEU:HA	5	0.12
(4,690)	1:187:A:SER:H	1:187:A:SER:HA	18	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,670)	1:52:A:ASP:H	1:51:A:TYR:HA	5	0.12
(4,620)	1:37:A:THR:H	1:36:A:HIS:H	15	0.12
(4,614)	1:19:A:ASP:H	1:20:A:PHE:H	2	0.12
(4,613)	1:74:A:GLN:H	1:75:A:ASP:H	11	0.12
(4,611)	1:19:A:ASP:H	1:20:A:PHE:H	16	0.12
(4,609)	1:242:A:ASP:H	1:243:A:ASN:H	7	0.12
(4,609)	1:242:A:ASP:H	1:243:A:ASN:H	14	0.12
(4,481)	1:28:A:GLN:H	1:27:A:ARG:H	7	0.12
(4,462)	1:159:A:VAL:HA	1:159:A:VAL:HG21	17	0.12
(4,460)	1:224:A:LYS:HA	1:224:A:LYS:HD3	20	0.12
(4,450)	1:147:A:LEU:HA	1:147:A:LEU:HD21	12	0.12
(4,449)	1:159:A:VAL:HA	1:159:A:VAL:HG23	5	0.12
(4,438)	1:255:A:ILE:HD11	1:255:A:ILE:HA	7	0.12
(4,438)	1:133:A:ALA:HB1	1:130:A:PHE:HA	13	0.12
(4,410)	1:35:A:THR:HG22	1:35:A:THR:HA	16	0.12
(4,408)	1:48:A:SER:HB3	1:80:A:LYS:HD2	2	0.12
(4,406)	1:133:A:ALA:HB3	1:130:A:PHE:HA	2	0.12
(4,386)	1:232:A:GLY:HA2	1:229:A:ASN:HB2	8	0.12
(4,383)	1:23:A:ALA:HB1	1:16:A:TRP:HB2	19	0.12
(4,381)	1:40:A:TYR:HB3	1:260:A:LYS:HA	19	0.12
(4,378)	1:22:A:ILE:HD11	1:20:A:PHE:HB3	4	0.12
(4,378)	1:22:A:ILE:HD11	1:20:A:PHE:HB3	20	0.12
(4,335)	1:49:A:VAL:HG21	1:49:A:VAL:HA	12	0.12
(4,305)	1:130:A:PHE:HB3	1:130:A:PHE:HA	5	0.12
(4,305)	1:130:A:PHE:HB2	1:130:A:PHE:HA	8	0.12
(4,305)	1:110:A:ASP:HB3	1:110:A:ASP:HA	12	0.12
(4,303)	1:254:A:GLN:HB2	1:254:A:GLN:HA	16	0.12
(4,242)	1:57:A:LEU:HB3	1:58:A:ARG:H	14	0.12
(4,222)	1:205:A:CYS:H	1:203:A:LEU:HB3	2	0.12
(4,211)	1:206:A:VAL:H	1:206:A:VAL:HB	13	0.12
(4,208)	1:45:A:LYS:H	1:44:A:LEU:HA	13	0.12
(4,208)	1:45:A:LYS:H	1:44:A:LEU:HA	16	0.12
(4,205)	1:66:A:PHE:H	1:65:A:ALA:HB1	6	0.12
(4,200)	1:108:A:THR:H	1:107:A:HIS:HA	9	0.12
(4,200)	1:108:A:THR:H	1:107:A:HIS:HA	12	0.12
(4,185)	1:142:A:VAL:H	1:209:A:ILE:HD11	4	0.12
(4,177)	1:179:A:ASP:H	1:179:A:ASP:HA	4	0.12
(4,177)	1:179:A:ASP:H	1:179:A:ASP:HA	8	0.12
(4,173)	1:157:A:GLN:H	1:157:A:GLN:HA	7	0.12
(4,173)	1:157:A:GLN:H	1:157:A:GLN:HA	8	0.12
(4,173)	1:167:A:LYS:H	1:167:A:LYS:HA	11	0.12
(4,173)	1:167:A:LYS:H	1:167:A:LYS:HA	19	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,157)	1:207:A:THR:H	1:207:A:THR:HB	3	0.12
(4,157)	1:207:A:THR:H	1:207:A:THR:HB	4	0.12
(4,157)	1:207:A:THR:H	1:207:A:THR:HB	18	0.12
(4,148)	1:164:A:ASP:H	1:164:A:ASP:HB2	3	0.12
(4,148)	1:164:A:ASP:H	1:164:A:ASP:HB2	4	0.12
(4,148)	1:164:A:ASP:H	1:164:A:ASP:HB2	5	0.12
(4,148)	1:164:A:ASP:H	1:164:A:ASP:HB2	11	0.12
(4,144)	1:88:A:TYR:H	1:79:A:LEU:HB2	10	0.12
(4,90)	1:33:A:ILE:H	1:108:A:THR:HB	7	0.12
(4,80)	1:93:A:PHE:H	1:92:A:GLN:HB2	7	0.12
(4,80)	1:213:A:GLU:H	1:212:A:LYS:HB2	15	0.12
(4,62)	1:238:A:GLU:H	1:237:A:GLU:HA	3	0.12
(4,62)	1:254:A:GLN:HA	1:255:A:ILE:H	5	0.12
(4,62)	1:238:A:GLU:H	1:237:A:GLU:HA	6	0.12
(4,62)	1:211:A:LEU:H	1:210:A:VAL:HA	7	0.12
(4,62)	1:254:A:GLN:HA	1:255:A:ILE:H	8	0.12
(4,62)	1:85:A:ASP:H	1:84:A:LEU:HA	20	0.12
(4,48)	1:232:A:GLY:H	1:235:A:GLU:HG3	12	0.12
(4,39)	1:63:A:GLY:H	1:169:A:LYS:HG2	15	0.12
(4,13)	1:56:A:SER:H	1:76:A:LYS:HG3	10	0.12
(3,222)	1:197:A:LEU:H	1:205:A:CYS:H	5	0.12
(3,205)	1:124:A:ASN:H	1:127:A:TYR:H	9	0.12
(3,163)	1:205:A:CYS:H	1:197:A:LEU:H	5	0.12
(3,160)	1:205:A:CYS:H	1:197:A:LEU:H	5	0.12
(3,112)	1:129:A:ASP:H	1:131:A:GLY:H	5	0.12
(3,61)	1:161:A:ASP:H	1:158:A:LYS:H	8	0.12
(1,118)	1:45:A:LYS:H	1:45:A:LYS:HG3	17	0.12
(1,114)	1:66:A:PHE:H	1:65:A:ALA:HB3	12	0.12
(1,83)	1:37:A:THR:H	1:38:A:ALA:H	4	0.12
(1,83)	1:37:A:THR:H	1:38:A:ALA:H	14	0.12
(1,83)	1:37:A:THR:H	1:38:A:ALA:H	18	0.12
(1,78)	1:117:A:GLU:H	1:96:A:HIS:H	12	0.12
(1,78)	1:117:A:GLU:H	1:96:A:HIS:H	16	0.12
(1,64)	1:60:A:LEU:HB2	1:172:A:SER:HB3	13	0.12
(1,59)	1:240:A:MET:HA	1:230:A:PHE:HB2	5	0.12
(1,51)	1:114:A:TYR:HB2	1:105:A:SER:HB3	4	0.12
(1,29)	1:163:A:LEU:HA	1:163:A:LEU:H	3	0.12
(1,29)	1:163:A:LEU:HA	1:163:A:LEU:H	9	0.12
(1,29)	1:163:A:LEU:HA	1:163:A:LEU:H	15	0.12
(1,25)	1:169:A:LYS:H	1:168:A:THR:HB	18	0.12
(1,18)	1:240:A:MET:H	1:240:A:MET:HA	10	0.12
(1,10)	1:55:A:THR:H	1:55:A:THR:HB	7	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1299)	1:213:A:GLU:H	1:212:A:LYS:HG3	2	0.11
(4,1292)	1:91:A:ILE:H	1:91:A:ILE:HD12	13	0.11
(4,1264)	1:210:A:VAL:H	1:209:A:ILE:HG22	6	0.11
(4,1258)	1:202:A:LEU:H	1:22:A:ILE:HG22	1	0.11
(4,1258)	1:202:A:LEU:H	1:22:A:ILE:HG23	2	0.11
(4,1227)	1:91:A:ILE:H	1:91:A:ILE:HG12	10	0.11
(4,1225)	1:64:A:HIS:H	1:169:A:LYS:HG2	20	0.11
(4,1223)	1:147:A:LEU:H	1:147:A:LEU:HG	4	0.11
(4,1223)	1:124:A:ASN:H	1:133:A:ALA:HB2	12	0.11
(4,1220)	1:133:A:ALA:H	1:133:A:ALA:HB3	15	0.11
(4,1195)	1:228:A:LEU:H	1:228:A:LEU:HB2	8	0.11
(4,1191)	1:9:A:LYS:H	1:9:A:LYS:HB2	4	0.11
(4,1174)	1:152:A:ALA:H	1:152:A:ALA:HB1	10	0.11
(4,1164)	1:197:A:LEU:H	1:197:A:LEU:HB2	20	0.11
(4,1158)	1:84:A:LEU:H	1:84:A:LEU:HB3	2	0.11
(4,1158)	1:223:A:LEU:H	1:223:A:LEU:HB2	11	0.11
(4,1139)	1:256:A:LYS:H	1:256:A:LYS:HG3	9	0.11
(4,1130)	1:260:A:LYS:H	1:260:A:LYS:HB2	2	0.11
(4,1130)	1:260:A:LYS:H	1:260:A:LYS:HB2	15	0.11
(4,1130)	1:133:A:ALA:H	1:133:A:ALA:HB1	18	0.11
(4,1130)	1:260:A:LYS:H	1:260:A:LYS:HB2	19	0.11
(4,1127)	1:197:A:LEU:H	1:197:A:LEU:HG	1	0.11
(4,1125)	1:223:A:LEU:H	1:223:A:LEU:HB2	13	0.11
(4,1114)	1:223:A:LEU:H	1:223:A:LEU:HB2	13	0.11
(4,1112)	1:116:A:ALA:H	1:115:A:ALA:HB2	14	0.11
(4,1110)	1:77:A:ALA:H	1:76:A:LYS:HB3	18	0.11
(4,1108)	1:156:A:LEU:H	1:153:A:LYS:HG3	20	0.11
(4,1106)	1:77:A:ALA:H	1:76:A:LYS:HB3	20	0.11
(4,1103)	1:218:A:SER:H	1:221:A:GLN:HB2	2	0.11
(4,1103)	1:218:A:SER:H	1:221:A:GLN:HB3	7	0.11
(4,1097)	1:157:A:GLN:H	1:157:A:GLN:HB2	4	0.11
(4,1083)	1:237:A:GLU:H	1:237:A:GLU:HG2	5	0.11
(4,1079)	1:28:A:GLN:H	1:28:A:GLN:HB3	20	0.11
(4,1060)	1:260:A:LYS:H	1:260:A:LYS:HB2	3	0.11
(4,1041)	1:153:A:LYS:H	1:153:A:LYS:HB3	6	0.11
(4,1041)	1:119:A:HIS:H	1:119:A:HIS:HB2	13	0.11
(4,1036)	1:158:A:LYS:H	1:158:A:LYS:HB3	20	0.11
(4,1033)	1:153:A:LYS:H	1:153:A:LYS:HB3	3	0.11
(4,1025)	1:164:A:ASP:H	1:164:A:ASP:HB2	18	0.11
(4,1023)	1:62:A:ASN:H	1:61:A:ASN:HB3	10	0.11
(4,1023)	1:62:A:ASN:H	1:61:A:ASN:HB3	11	0.11
(4,1020)	1:230:A:PHE:H	1:230:A:PHE:HB2	20	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1010)	1:52:A:ASP:H	1:52:A:ASP:HB2	12	0.11
(4,999)	1:85:A:ASP:H	1:85:A:ASP:HB2	18	0.11
(4,998)	1:175:A:PHE:H	1:174:A:ASP:HB2	17	0.11
(4,995)	1:124:A:ASN:H	1:124:A:ASN:HB2	2	0.11
(4,995)	1:229:A:ASN:H	1:229:A:ASN:HB2	14	0.11
(4,987)	1:241:A:VAL:H	1:240:A:MET:HA	10	0.11
(4,980)	1:191:A:TRP:H	1:190:A:TYR:HB2	7	0.11
(4,971)	1:124:A:ASN:H	1:124:A:ASN:HB2	4	0.11
(4,969)	1:244:A:TRP:H	1:244:A:TRP:HB3	18	0.11
(4,964)	1:174:A:ASP:H	1:174:A:ASP:HB3	1	0.11
(4,957)	1:191:A:TRP:H	1:191:A:TRP:HB3	17	0.11
(4,956)	1:178:A:PHE:H	1:178:A:PHE:HB3	2	0.11
(4,955)	1:127:A:TYR:H	1:127:A:TYR:HB2	8	0.11
(4,954)	1:161:A:ASP:H	1:161:A:ASP:HB2	11	0.11
(4,928)	1:260:A:LYS:H	1:260:A:LYS:HA	8	0.11
(4,922)	1:188:A:LEU:H	1:187:A:SER:HB2	11	0.11
(4,922)	1:188:A:LEU:H	1:187:A:SER:HB3	18	0.11
(4,870)	1:78:A:VAL:H	1:50:A:SER:HB2	11	0.11
(4,862)	1:78:A:VAL:H	1:50:A:SER:HB2	8	0.11
(4,845)	1:151:A:SER:H	1:151:A:SER:HA	1	0.11
(4,845)	1:151:A:SER:H	1:151:A:SER:HA	6	0.11
(4,845)	1:151:A:SER:H	1:151:A:SER:HA	19	0.11
(4,823)	1:184:A:LEU:H	1:184:A:LEU:HA	6	0.11
(4,823)	1:184:A:LEU:H	1:184:A:LEU:HA	14	0.11
(4,823)	1:184:A:LEU:H	1:184:A:LEU:HA	17	0.11
(4,808)	1:109:A:VAL:H	1:108:A:THR:HA	5	0.11
(4,780)	1:230:A:PHE:H	1:229:A:ASN:HA	13	0.11
(4,775)	1:148:A:LYS:H	1:147:A:LEU:HA	15	0.11
(4,767)	1:70:A:PHE:H	1:69:A:GLU:HA	18	0.11
(4,742)	1:71:A:ASP:H	1:70:A:PHE:HA	3	0.11
(4,742)	1:71:A:ASP:H	1:70:A:PHE:HA	7	0.11
(4,742)	1:197:A:LEU:H	1:197:A:LEU:HA	13	0.11
(4,742)	1:197:A:LEU:H	1:196:A:SER:HA	15	0.11
(4,722)	1:57:A:LEU:H	1:56:A:SER:HA	2	0.11
(4,712)	1:124:A:ASN:H	1:123:A:TRP:HA	14	0.11
(4,641)	1:224:A:LYS:H	1:223:A:LEU:H	11	0.11
(4,628)	1:181:A:ARG:H	1:182:A:GLY:H	12	0.11
(4,613)	1:222:A:VAL:H	1:223:A:LEU:H	3	0.11
(4,611)	1:19:A:ASP:H	1:20:A:PHE:H	2	0.11
(4,610)	1:74:A:GLN:H	1:75:A:ASP:H	11	0.11
(4,569)	1:127:A:TYR:H	1:126:A:LYS:H	4	0.11
(4,569)	1:127:A:TYR:H	1:126:A:LYS:H	17	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,569)	1:127:A:TYR:H	1:126:A:LYS:H	20	0.11
(4,561)	1:74:A:GLN:H	1:73:A:SER:H	13	0.11
(4,531)	1:164:A:ASP:H	1:165:A:SER:H	3	0.11
(4,481)	1:28:A:GLN:H	1:27:A:ARG:H	20	0.11
(4,460)	1:224:A:LYS:HA	1:224:A:LYS:HD2	1	0.11
(4,450)	1:147:A:LEU:HA	1:147:A:LEU:HD22	9	0.11
(4,438)	1:22:A:ILE:HD13	1:22:A:ILE:HA	16	0.11
(4,419)	1:205:A:CYS:HB3	1:140:A:LEU:HG	12	0.11
(4,410)	1:35:A:THR:HG21	1:35:A:THR:HA	2	0.11
(4,410)	1:35:A:THR:HG22	1:35:A:THR:HA	3	0.11
(4,406)	1:133:A:ALA:HB1	1:130:A:PHE:HA	1	0.11
(4,387)	1:22:A:ILE:HD11	1:20:A:PHE:HB3	10	0.11
(4,345)	1:172:A:SER:HB2	1:174:A:ASP:HA	7	0.11
(4,335)	1:134:A:VAL:HG23	1:131:A:GLY:HA2	11	0.11
(4,332)	1:22:A:ILE:HD12	1:22:A:ILE:HA	19	0.11
(4,305)	1:130:A:PHE:HB3	1:130:A:PHE:HA	6	0.11
(4,303)	1:254:A:GLN:HB3	1:254:A:GLN:HA	11	0.11
(4,273)	1:113:A:LYS:HD2	1:244:A:TRP:HA	8	0.11
(4,242)	1:57:A:LEU:HB2	1:58:A:ARG:H	2	0.11
(4,242)	1:57:A:LEU:HB3	1:58:A:ARG:H	9	0.11
(4,237)	1:167:A:LYS:H	1:166:A:ILE:HA	20	0.11
(4,224)	1:44:A:LEU:H	1:43:A:SER:HB3	17	0.11
(4,224)	1:44:A:LEU:H	1:43:A:SER:HB3	20	0.11
(4,218)	1:169:A:LYS:H	1:169:A:LYS:HB2	1	0.11
(4,215)	1:242:A:ASP:H	1:241:A:VAL:HA	18	0.11
(4,205)	1:66:A:PHE:H	1:65:A:ALA:HB1	3	0.11
(4,200)	1:108:A:THR:H	1:107:A:HIS:HA	1	0.11
(4,200)	1:108:A:THR:H	1:107:A:HIS:HA	10	0.11
(4,194)	1:221:A:GLN:H	1:221:A:GLN:HB3	18	0.11
(4,180)	1:66:A:PHE:H	1:240:A:MET:HA	7	0.11
(4,177)	1:179:A:ASP:H	1:179:A:ASP:HA	11	0.11
(4,177)	1:179:A:ASP:H	1:179:A:ASP:HA	17	0.11
(4,173)	1:167:A:LYS:H	1:167:A:LYS:HA	9	0.11
(4,173)	1:167:A:LYS:H	1:167:A:LYS:HA	12	0.11
(4,173)	1:157:A:GLN:H	1:157:A:GLN:HA	15	0.11
(4,173)	1:157:A:GLN:H	1:157:A:GLN:HA	16	0.11
(4,157)	1:36:A:HIS:H	1:35:A:THR:HB	10	0.11
(4,157)	1:207:A:THR:H	1:207:A:THR:HB	17	0.11
(4,148)	1:164:A:ASP:H	1:164:A:ASP:HB2	12	0.11
(4,145)	1:218:A:SER:H	1:221:A:GLN:HG3	10	0.11
(4,106)	1:87:A:THR:H	1:87:A:THR:HB	3	0.11
(4,100)	1:141:A:ALA:H	1:140:A:LEU:HB2	1	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,83)	1:57:A:LEU:H	1:56:A:SER:HA	2	0.11
(4,83)	1:234:A:GLY:H	1:233:A:GLU:HA	16	0.11
(4,62)	1:85:A:ASP:H	1:84:A:LEU:HA	14	0.11
(4,34)	1:59:A:ILE:H	1:166:A:ILE:HG21	7	0.11
(3,318)	1:171:A:LYS:H	1:168:A:THR:H	20	0.11
(3,302)	1:229:A:ASN:H	1:168:A:THR:H	12	0.11
(3,125)	1:245:A:ARG:H	1:106:A:GLU:H	11	0.11
(3,120)	1:248:A:GLN:H	1:32:A:ASP:H	8	0.11
(3,58)	1:70:A:PHE:H	1:57:A:LEU:H	18	0.11
(3,11)	1:177:A:ASN:H	1:56:A:SER:H	3	0.11
(1,121)	1:93:A:PHE:H	1:68:A:VAL:HG21	3	0.11
(1,120)	1:259:A:PHE:H	1:257:A:ALA:HB2	3	0.11
(1,114)	1:66:A:PHE:H	1:65:A:ALA:HB3	5	0.11
(1,105)	1:6:A:GLY:H	1:6:A:GLY:HA3	19	0.11
(1,78)	1:117:A:GLU:H	1:96:A:HIS:H	6	0.11
(1,42)	1:116:A:ALA:HB1	1:97:A:TRP:HA	17	0.11
(1,38)	1:77:A:ALA:HA	1:51:A:TYR:HA	13	0.11
(1,29)	1:163:A:LEU:HA	1:163:A:LEU:H	8	0.11
(1,18)	1:240:A:MET:H	1:240:A:MET:HA	19	0.11
(1,10)	1:55:A:THR:H	1:55:A:THR:HB	9	0.11
(4,1283)	1:152:A:ALA:H	1:152:A:ALA:HB1	10	0.1
(4,1279)	1:211:A:LEU:H	1:211:A:LEU:HG	18	0.1
(4,1269)	1:162:A:VAL:H	1:162:A:VAL:HG22	10	0.1
(4,1268)	1:210:A:VAL:H	1:209:A:ILE:HG22	6	0.1
(4,1265)	1:205:A:CYS:H	1:206:A:VAL:HG23	12	0.1
(4,1243)	1:163:A:LEU:H	1:162:A:VAL:HG22	6	0.1
(4,1176)	1:234:A:GLY:H	1:233:A:GLU:HB2	5	0.1
(4,1176)	1:93:A:PHE:H	1:68:A:VAL:HB	15	0.1
(4,1176)	1:234:A:GLY:H	1:233:A:GLU:HB2	18	0.1
(4,1174)	1:147:A:LEU:H	1:147:A:LEU:HG	12	0.1
(4,1168)	1:152:A:ALA:H	1:152:A:ALA:HB1	20	0.1
(4,1146)	1:162:A:VAL:H	1:162:A:VAL:HB	14	0.1
(4,1144)	1:126:A:LYS:H	1:126:A:LYS:HB2	8	0.1
(4,1130)	1:133:A:ALA:H	1:133:A:ALA:HB3	4	0.1
(4,1130)	1:133:A:ALA:H	1:133:A:ALA:HB1	8	0.1
(4,1130)	1:133:A:ALA:H	1:133:A:ALA:HB1	13	0.1
(4,1111)	1:254:A:GLN:H	1:253:A:ARG:HB3	16	0.1
(4,1101)	1:254:A:GLN:H	1:253:A:ARG:HB3	16	0.1
(4,1097)	1:237:A:GLU:H	1:237:A:GLU:HB2	6	0.1
(4,1097)	1:237:A:GLU:H	1:237:A:GLU:HB2	18	0.1
(4,1090)	1:197:A:LEU:H	1:197:A:LEU:HB2	11	0.1
(4,1079)	1:164:A:ASP:H	1:164:A:ASP:HB2	16	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,1070)	1:218:A:SER:H	1:221:A:GLN:HB2	17	0.1
(4,1058)	1:233:A:GLU:H	1:233:A:GLU:HG3	12	0.1
(4,1057)	1:204:A:GLU:H	1:204:A:GLU:HB2	3	0.1
(4,1057)	1:260:A:LYS:H	1:260:A:LYS:HB2	8	0.1
(4,1041)	1:153:A:LYS:H	1:153:A:LYS:HB3	18	0.1
(4,1014)	1:52:A:ASP:H	1:52:A:ASP:HB2	12	0.1
(4,1011)	1:124:A:ASN:H	1:124:A:ASN:HB2	4	0.1
(4,1009)	1:62:A:ASN:H	1:61:A:ASN:HB3	3	0.1
(4,988)	1:116:A:ALA:H	1:114:A:TYR:HB3	3	0.1
(4,975)	1:126:A:LYS:H	1:124:A:ASN:HB3	8	0.1
(4,954)	1:161:A:ASP:H	1:161:A:ASP:HB2	10	0.1
(4,920)	1:56:A:SER:H	1:56:A:SER:HB3	18	0.1
(4,898)	1:256:A:LYS:H	1:193:A:TYR:HB2	19	0.1
(4,867)	1:157:A:GLN:H	1:157:A:GLN:HA	13	0.1
(4,865)	1:87:A:THR:H	1:86:A:GLY:HA2	13	0.1
(4,840)	1:57:A:LEU:H	1:56:A:SER:HA	1	0.1
(4,805)	1:129:A:ASP:H	1:128:A:GLY:HA3	1	0.1
(4,772)	1:87:A:THR:H	1:86:A:GLY:HA2	12	0.1
(4,769)	1:108:A:THR:H	1:107:A:HIS:HA	12	0.1
(4,763)	1:99:A:SER:H	1:98:A:GLY:HA2	6	0.1
(4,722)	1:57:A:LEU:H	1:56:A:SER:HA	20	0.1
(4,711)	1:122:A:HIS:H	1:121:A:VAL:HA	1	0.1
(4,670)	1:52:A:ASP:H	1:51:A:TYR:HA	3	0.1
(4,662)	1:241:A:VAL:H	1:240:A:MET:H	18	0.1
(4,620)	1:37:A:THR:H	1:36:A:HIS:H	20	0.1
(4,617)	1:226:A:ARG:H	1:225:A:PHE:H	18	0.1
(4,614)	1:160:A:VAL:H	1:161:A:ASP:H	11	0.1
(4,610)	1:222:A:VAL:H	1:223:A:LEU:H	3	0.1
(4,609)	1:242:A:ASP:H	1:243:A:ASN:H	17	0.1
(4,487)	1:48:A:SER:H	1:47:A:LEU:H	6	0.1
(4,450)	1:147:A:LEU:HA	1:147:A:LEU:HD21	7	0.1
(4,450)	1:147:A:LEU:HA	1:147:A:LEU:HD21	14	0.1
(4,438)	1:133:A:ALA:HB3	1:130:A:PHE:HA	2	0.1
(4,404)	1:163:A:LEU:HB3	1:160:A:VAL:HA	17	0.1
(4,374)	1:127:A:TYR:HB3	1:133:A:ALA:HA	3	0.1
(4,327)	1:148:A:LYS:HB3	1:148:A:LYS:HA	5	0.1
(4,325)	1:156:A:LEU:HB3	1:156:A:LEU:HA	19	0.1
(4,317)	1:192:A:THR:HG23	1:192:A:THR:HB	14	0.1
(4,303)	1:203:A:LEU:HB3	1:203:A:LEU:HA	4	0.1
(4,290)	1:199:A:THR:HB	1:199:A:THR:HA	11	0.1
(4,268)	1:203:A:LEU:H	1:203:A:LEU:HG	1	0.1
(4,263)	1:243:A:ASN:HA	1:244:A:TRP:H	5	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(4,253)	1:135:A:GLN:H	1:127:A:TYR:HB3	9	0.1
(4,242)	1:57:A:LEU:HB3	1:58:A:ARG:H	4	0.1
(4,224)	1:44:A:LEU:H	1:43:A:SER:HB3	2	0.1
(4,215)	1:242:A:ASP:H	1:241:A:VAL:HA	2	0.1
(4,208)	1:45:A:LYS:H	1:44:A:LEU:HA	19	0.1
(4,200)	1:108:A:THR:H	1:107:A:HIS:HA	20	0.1
(4,199)	1:224:A:LYS:H	1:223:A:LEU:HB3	10	0.1
(4,177)	1:179:A:ASP:H	1:179:A:ASP:HA	5	0.1
(4,173)	1:157:A:GLN:H	1:157:A:GLN:HA	3	0.1
(4,173)	1:167:A:LYS:H	1:167:A:LYS:HA	4	0.1
(4,173)	1:157:A:GLN:H	1:157:A:GLN:HA	10	0.1
(4,173)	1:167:A:LYS:H	1:167:A:LYS:HA	14	0.1
(4,168)	1:164:A:ASP:H	1:163:A:LEU:HB3	16	0.1
(4,157)	1:207:A:THR:H	1:207:A:THR:HB	5	0.1
(4,157)	1:207:A:THR:H	1:207:A:THR:HB	6	0.1
(4,157)	1:207:A:THR:H	1:207:A:THR:HB	9	0.1
(4,148)	1:164:A:ASP:H	1:164:A:ASP:HB2	15	0.1
(4,141)	1:158:A:LYS:H	1:158:A:LYS:HB3	17	0.1
(4,138)	1:210:A:VAL:H	1:209:A:ILE:HG21	5	0.1
(4,96)	1:140:A:LEU:H	1:205:A:CYS:HB2	8	0.1
(4,54)	1:51:A:TYR:H	1:51:A:TYR:HA	2	0.1
(4,37)	1:63:A:GLY:H	1:169:A:LYS:HG2	15	0.1
(4,32)	1:191:A:TRP:H	1:211:A:LEU:HG	3	0.1
(4,22)	1:110:A:ASP:H	1:109:A:VAL:HB	16	0.1
(4,13)	1:56:A:SER:H	1:76:A:LYS:HG3	16	0.1
(3,290)	1:196:A:SER:H	1:206:A:VAL:H	10	0.1
(3,252)	1:196:A:SER:H	1:206:A:VAL:H	10	0.1
(3,222)	1:197:A:LEU:H	1:205:A:CYS:H	13	0.1
(3,163)	1:205:A:CYS:H	1:197:A:LEU:H	13	0.1
(3,160)	1:205:A:CYS:H	1:197:A:LEU:H	13	0.1
(3,55)	1:156:A:LEU:H	1:158:A:LYS:H	13	0.1
(2,11)	1:259:A:PHE:H	1:191:A:TRP:HA	15	0.1
(1,100)	1:245:A:ARG:H	1:244:A:TRP:HB2	4	0.1
(1,83)	1:37:A:THR:H	1:38:A:ALA:H	20	0.1
(1,64)	1:60:A:LEU:HB2	1:172:A:SER:HB3	12	0.1
(1,42)	1:116:A:ALA:HB3	1:97:A:TRP:HA	5	0.1
(1,38)	1:77:A:ALA:HA	1:51:A:TYR:HA	8	0.1
(1,22)	1:156:A:LEU:H	1:153:A:LYS:HD2	18	0.1
(1,10)	1:55:A:THR:H	1:55:A:THR:HB	1	0.1

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

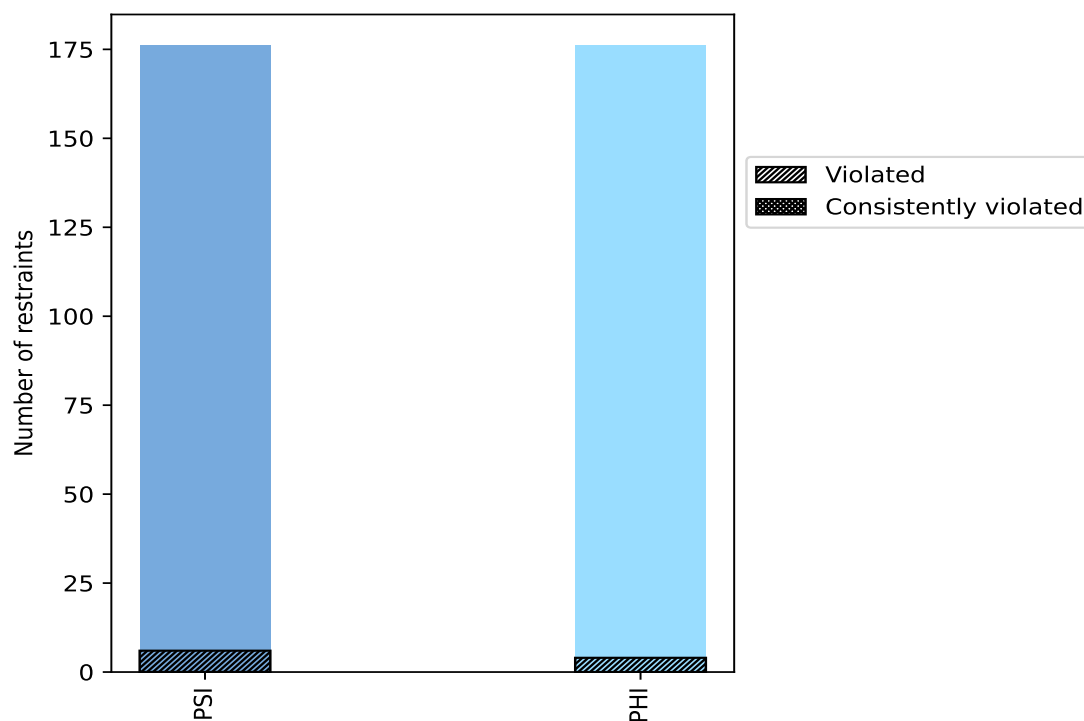
10.1 Summary of dihedral-angle violations [i](#)

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

Angle type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
PSI	176	50.0	6	3.4	1.7	0	0.0	0.0
PHI	176	50.0	4	2.3	1.1	0	0.0	0.0
Total	352	100.0	10	2.8	2.8	0	0.0	0.0

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

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



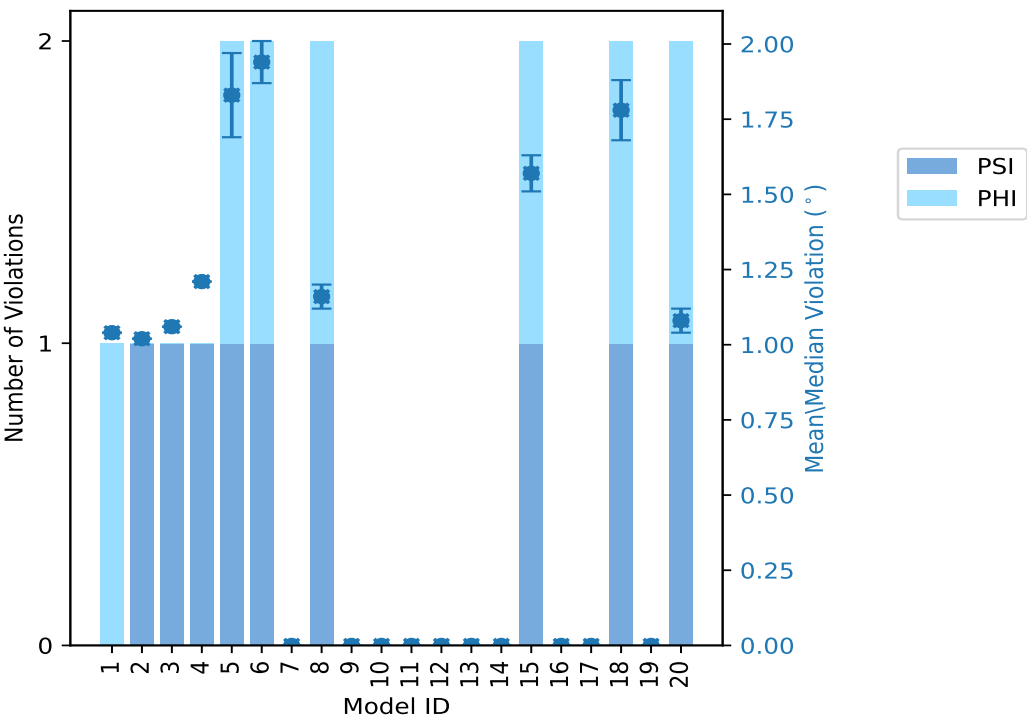
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

10.2 Dihedral-angle violation statistics for each model

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

Model ID	Number of violations			Mean (°)	Max (°)	SD (°)	Median (°)
	PSI	PHI	Total				
1	0	1	1	1.04	1.04	0.0	1.04
2	1	0	1	1.02	1.02	0.0	1.02
3	1	0	1	1.06	1.06	0.0	1.06
4	1	0	1	1.21	1.21	0.0	1.21
5	1	1	2	1.83	1.97	0.14	1.83
6	1	1	2	1.94	2.02	0.07	1.94
7	0	0	0	0.0	0.0	0.0	0.0
8	1	1	2	1.16	1.2	0.04	1.16
9	0	0	0	0.0	0.0	0.0	0.0
10	0	0	0	0.0	0.0	0.0	0.0
11	0	0	0	0.0	0.0	0.0	0.0
12	0	0	0	0.0	0.0	0.0	0.0
13	0	0	0	0.0	0.0	0.0	0.0
14	0	0	0	0.0	0.0	0.0	0.0
15	1	1	2	1.57	1.63	0.06	1.57
16	0	0	0	0.0	0.0	0.0	0.0
17	0	0	0	0.0	0.0	0.0	0.0
18	1	1	2	1.78	1.89	0.1	1.78
19	0	0	0	0.0	0.0	0.0	0.0
20	1	1	2	1.08	1.13	0.04	1.08

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



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

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

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

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

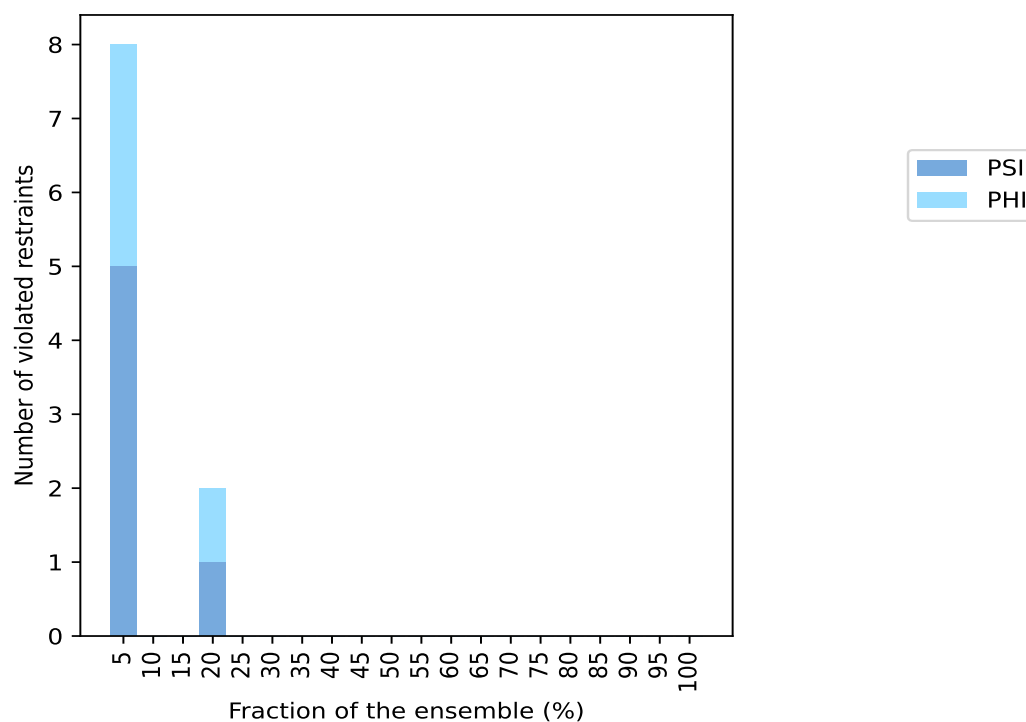
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Number of violated restraints			Fraction of the ensemble	
PSI	PHI	Total	Count ¹	%
0	0	0	12	60.0
0	0	0	13	65.0
0	0	0	14	70.0
0	0	0	15	75.0
0	0	0	16	80.0
0	0	0	17	85.0
0	0	0	18	90.0
0	0	0	19	95.0
0	0	0	20	100.0

¹ Number of models with violations

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

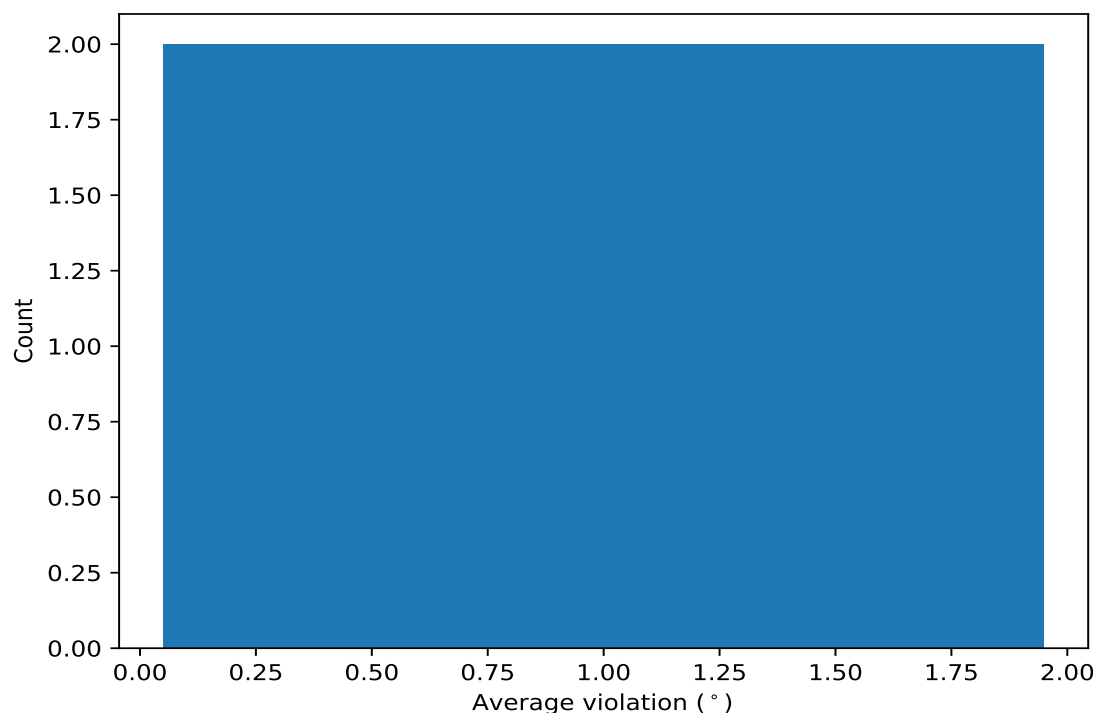


10.4 Most violated dihedral-angle restraints in the ensemble [i](#)

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.

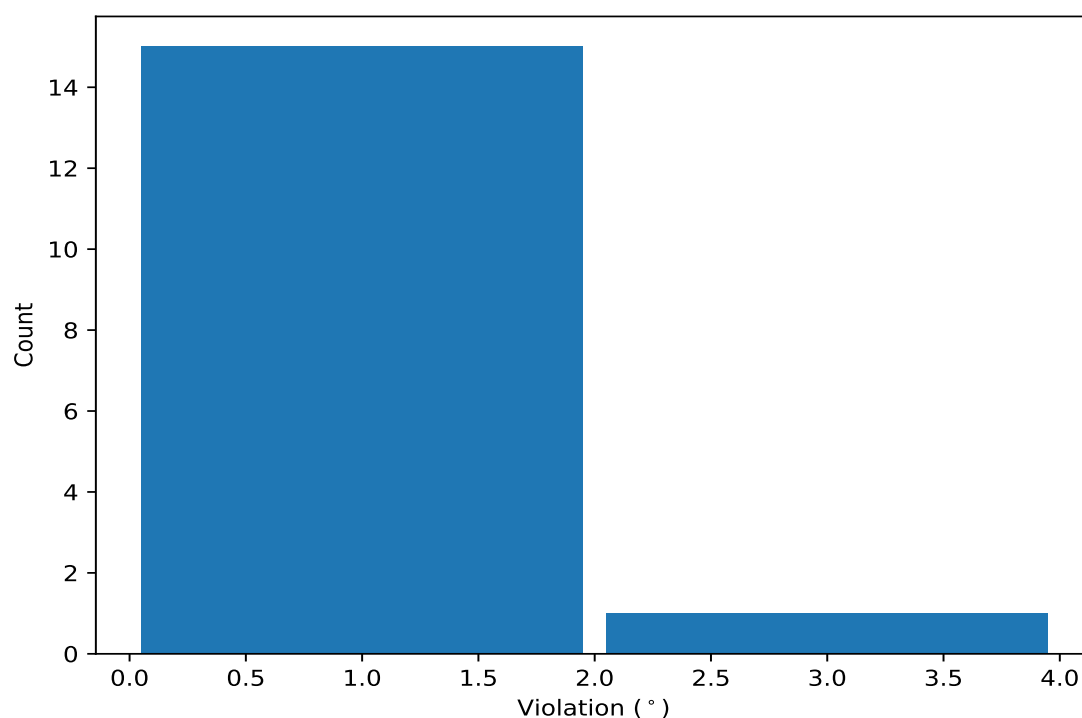
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,118)	1:94:A:HIS:N	1:94:A:HIS:CA	1:94:A:HIS:C	1:95:A:PHE:N	4	1.59	0.28	1.6
(1,119)	1:94:A:HIS:C	1:95:A:PHE:N	1:95:A:PHE:CA	1:95:A:PHE:C	4	1.58	0.29	1.66

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 (°)
(1,111)	1:89:A:ARG:C	1:90:A:LEU:N	1:90:A:LEU:CA	1:90:A:LEU:C	6	2.02
(1,118)	1:94:A:HIS:N	1:94:A:HIS:CA	1:94:A:HIS:C	1:95:A:PHE:N	5	1.97
(1,119)	1:94:A:HIS:C	1:95:A:PHE:N	1:95:A:PHE:CA	1:95:A:PHE:C	18	1.89
(1,110)	1:89:A:ARG:N	1:89:A:ARG:CA	1:89:A:ARG:C	1:90:A:LEU:N	6	1.87
(1,119)	1:94:A:HIS:C	1:95:A:PHE:N	1:95:A:PHE:CA	1:95:A:PHE:C	5	1.69
(1,118)	1:94:A:HIS:N	1:94:A:HIS:CA	1:94:A:HIS:C	1:95:A:PHE:N	18	1.68
(1,119)	1:94:A:HIS:C	1:95:A:PHE:N	1:95:A:PHE:CA	1:95:A:PHE:C	15	1.63
(1,118)	1:94:A:HIS:N	1:94:A:HIS:CA	1:94:A:HIS:C	1:95:A:PHE:N	15	1.51
(1,270)	1:200:A:PRO:N	1:200:A:PRO:CA	1:200:A:PRO:C	1:201:A:PRO:N	4	1.21
(1,118)	1:94:A:HIS:N	1:94:A:HIS:CA	1:94:A:HIS:C	1:95:A:PHE:N	8	1.2
(1,157)	1:126:A:LYS:C	1:127:A:TYR:N	1:127:A:TYR:CA	1:127:A:TYR:C	20	1.13
(1,119)	1:94:A:HIS:C	1:95:A:PHE:N	1:95:A:PHE:CA	1:95:A:PHE:C	8	1.11
(1,318)	1:233:A:GLU:N	1:233:A:GLU:CA	1:233:A:GLU:C	1:234:A:GLY:N	3	1.06
(1,333)	1:243:A:ASN:C	1:244:A:TRP:N	1:244:A:TRP:CA	1:244:A:TRP:C	1	1.04
(1,156)	1:126:A:LYS:N	1:126:A:LYS:CA	1:126:A:LYS:C	1:127:A:TYR:N	20	1.04
(1,154)	1:125:A:THR:N	1:125:A:THR:CA	1:125:A:THR:C	1:126:A:LYS:N	2	1.02