



Full wwPDB NMR Structure Validation Report ⓘ

Mar 18, 2026 – 12:31 AM UTC

PDB ID : 2N02 / pdb_00002n02
BMRB ID : 25513
Title : Solution structure of the A147T variant of the mitochondrial translocator protein (tspo) in complex with pk11195
Authors : Jaremko, M.; Jaremko, L.; Giller, K.; Becker, S.; Zweckstetter, M.
Deposited on : 2015-03-04

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)
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
BMRB Restraints Analysis : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

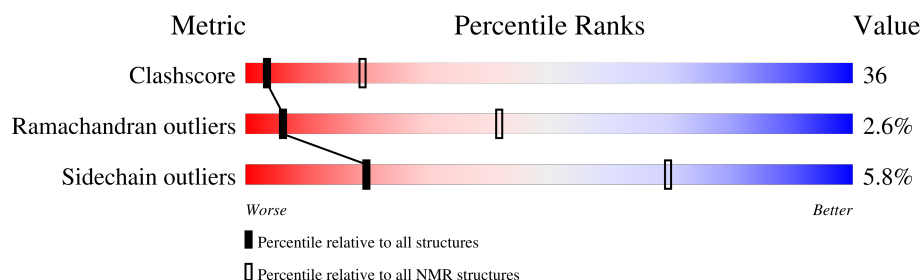
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 84%.

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	169	

2 Ensemble composition and analysis

This entry contains 20 models. Model 7 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:6-A:159 (154)	0.59	7

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

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

The models can be grouped into 3 clusters. No single-model clusters were found.

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

3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 2695 atoms, of which 1332 are hydrogens and 0 are deuteriums.

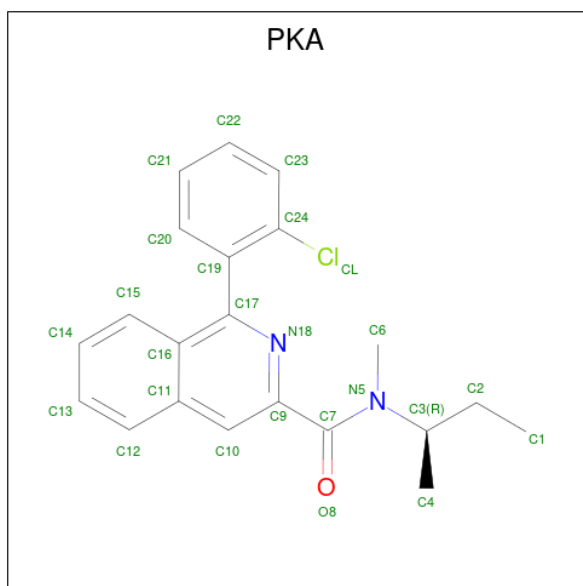
- Molecule 1 is a protein called Translocator protein.

Mol	Chain	Residues	Atoms						Trace
1	A	169	Total	C	H	N	O	S	0
			2649	889	1311	223	221	5	

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	147	THR	ALA	engineered mutation	UNP Q99M32

- Molecule 2 is N-[(2R)-butan-2-yl]-1-(2-chlorophenyl)-N-methylisoquinoline-3-carboxamide (CCD ID: PKA) (formula: C₂₁H₂₁ClN₂O).



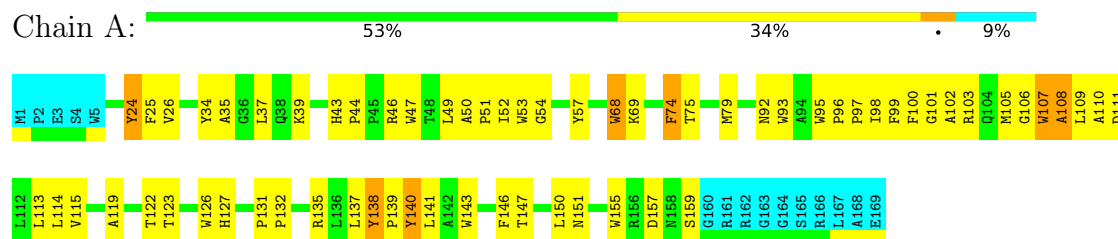
Mol	Chain	Residues	Atoms					
2	A	1	Total	C	Cl	H	N	O
			46	21	1	21	2	1

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

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

- Molecule 1: Translocator protein

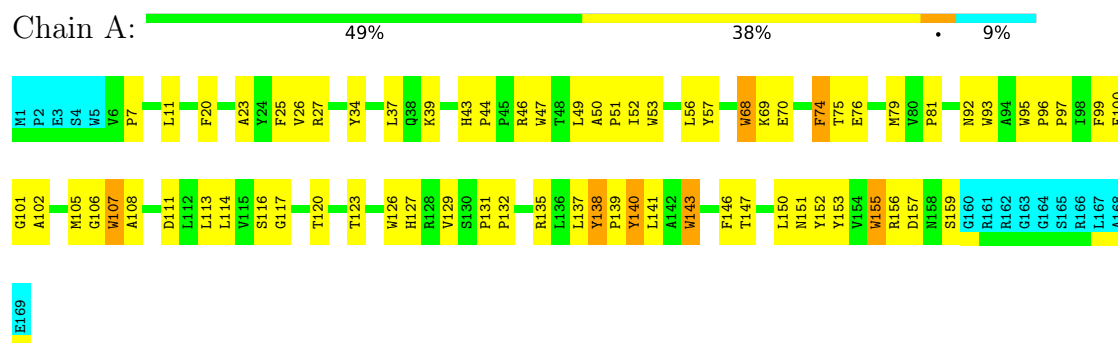


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

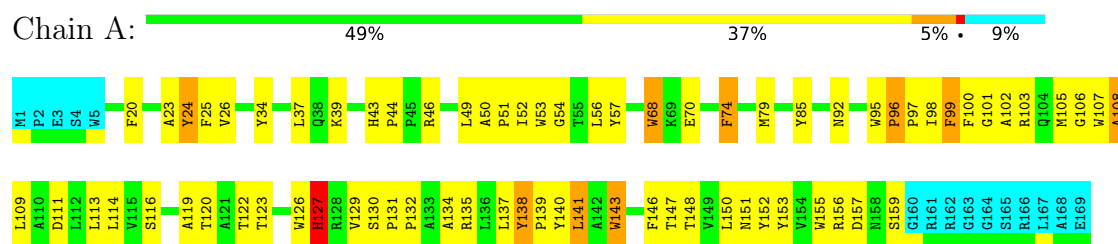
4.2.1 Score per residue for model 1

- Molecule 1: Translocator protein



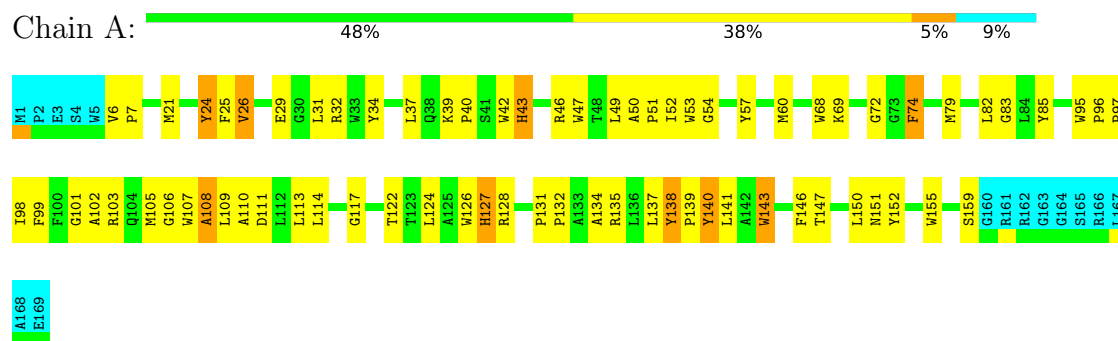
4.2.2 Score per residue for model 2

- Molecule 1: Translocator protein



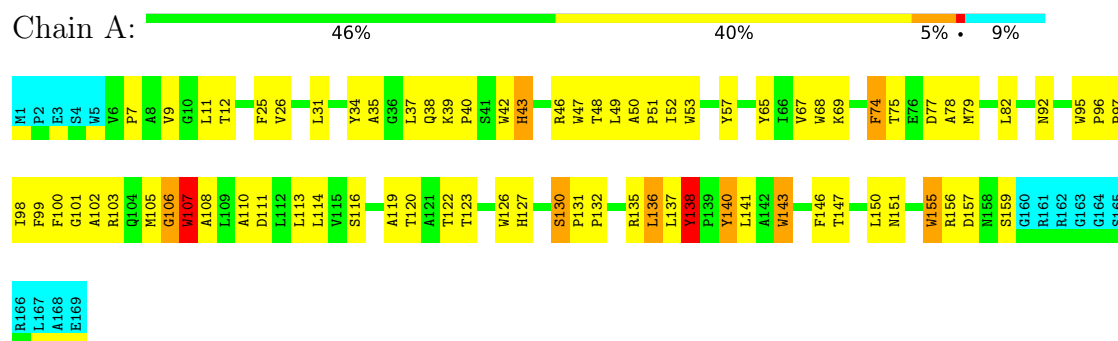
4.2.3 Score per residue for model 3

- Molecule 1: Translocator protein



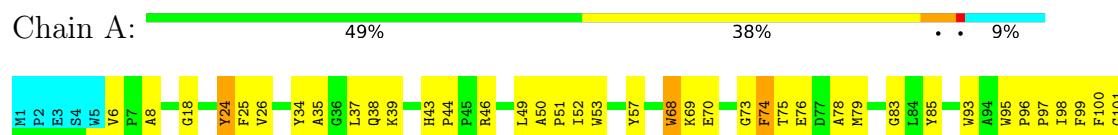
4.2.4 Score per residue for model 4

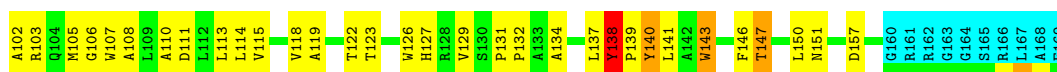
- Molecule 1: Translocator protein



4.2.5 Score per residue for model 5

- Molecule 1: Translocator protein

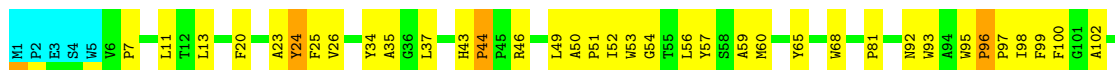




4.2.6 Score per residue for model 6

- Molecule 1: Translocator protein

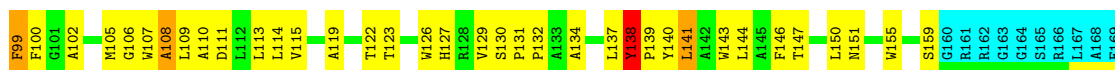
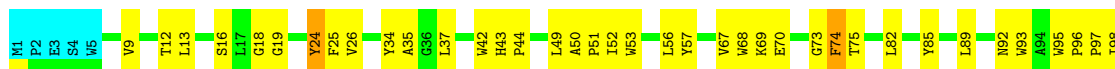
Chain A: 50% 37% 9%



4.2.7 Score per residue for model 7 (medoid)

- Molecule 1: Translocator protein

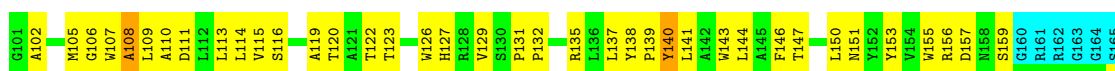
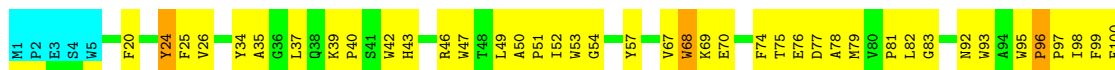
Chain A: 47% 40% 9%



4.2.8 Score per residue for model 8

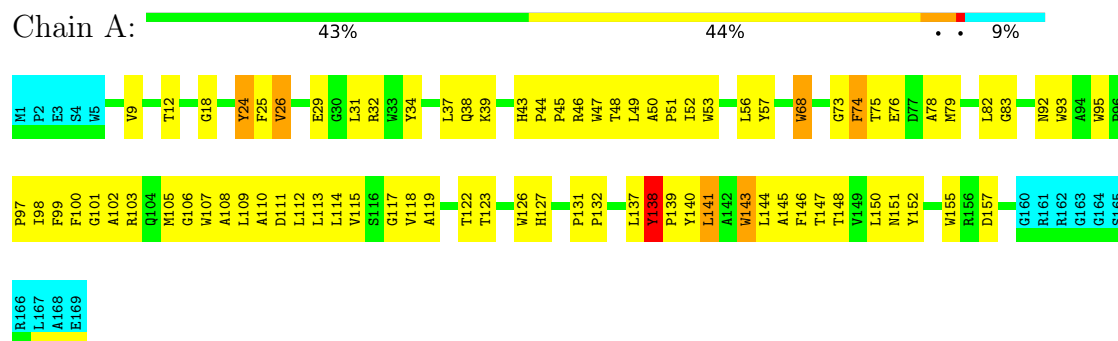
- Molecule 1: Translocator protein

Chain A: 44% 44% 9%



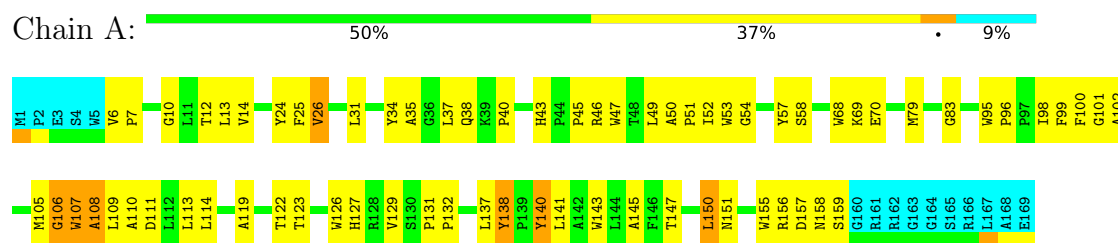
4.2.9 Score per residue for model 9

- Molecule 1: Translocator protein



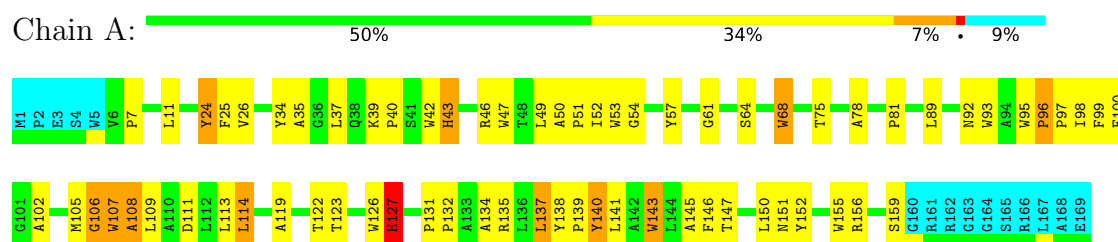
4.2.10 Score per residue for model 10

- Molecule 1: Translocator protein



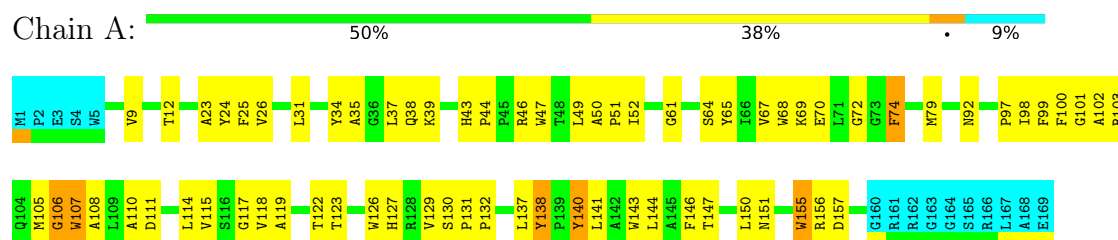
4.2.11 Score per residue for model 11

- Molecule 1: Translocator protein



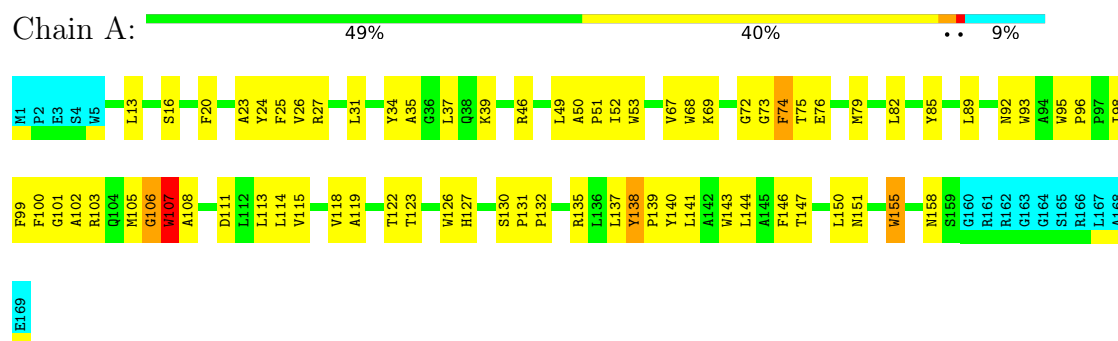
4.2.12 Score per residue for model 12

- Molecule 1: Translocator protein



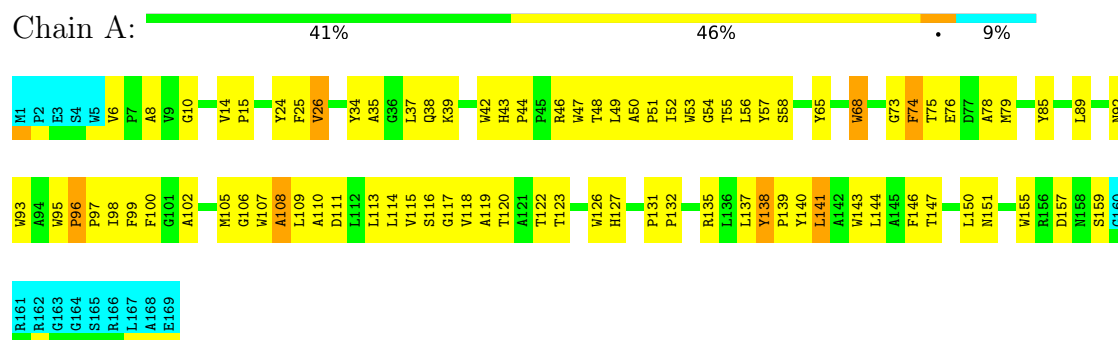
4.2.13 Score per residue for model 13

- Molecule 1: Translocator protein



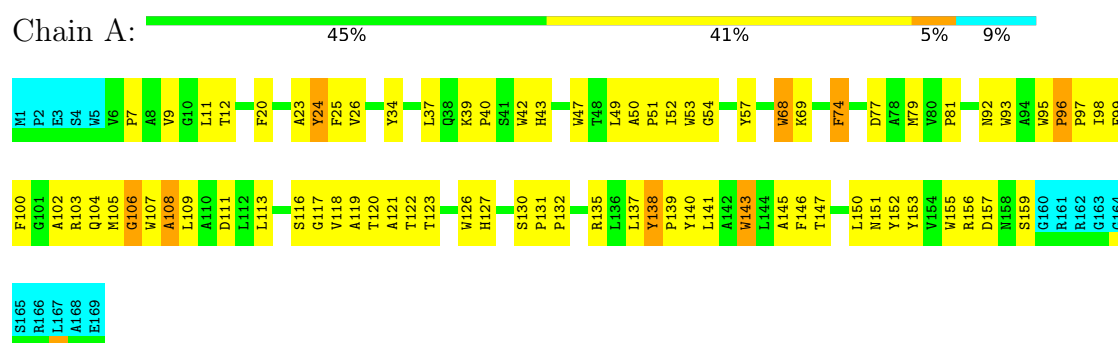
4.2.14 Score per residue for model 14

- Molecule 1: Translocator protein



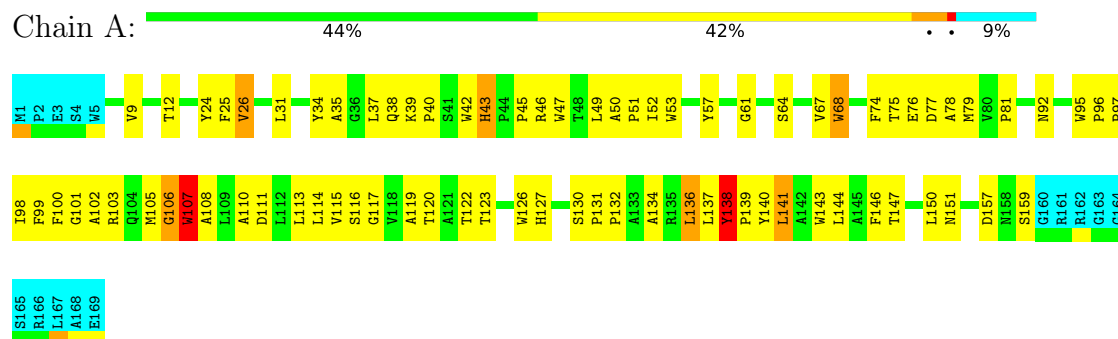
4.2.15 Score per residue for model 15

- Molecule 1: Translocator protein



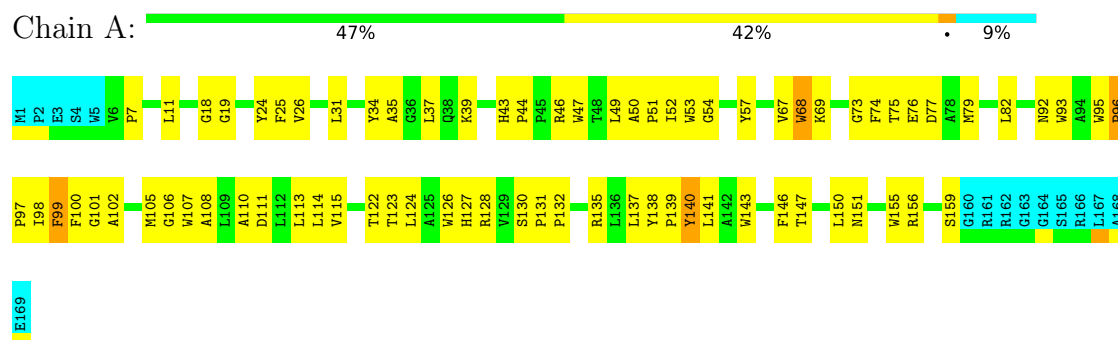
4.2.16 Score per residue for model 16

- Molecule 1: Translocator protein



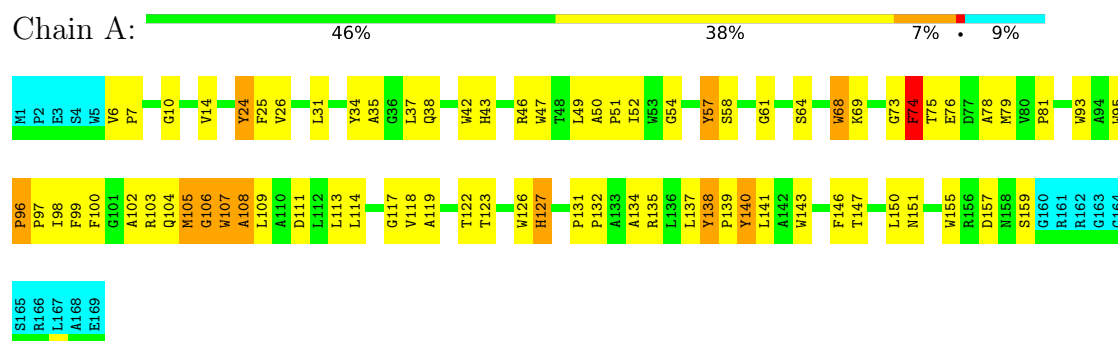
4.2.17 Score per residue for model 17

- Molecule 1: Translocator protein



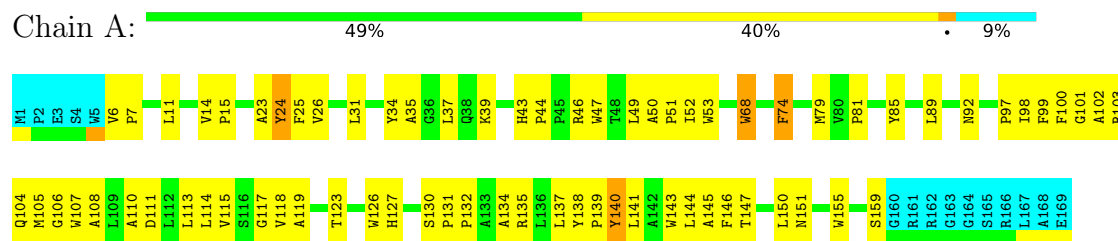
4.2.18 Score per residue for model 18

- Molecule 1: Translocator protein

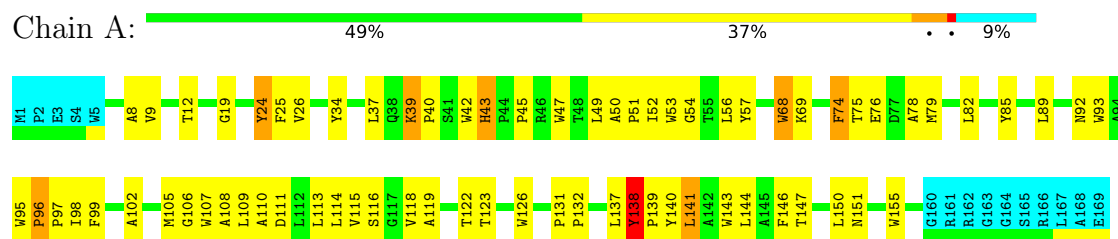


4.2.19 Score per residue for model 19

- Molecule 1: Translocator protein



- Molecule 1: Translocator protein



5 Refinement protocol and experimental data overview

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

Of the 105 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
CYANA 3.0	structure solution	
X-PLOR NIH	structure solution	
X-PLOR NIH	refinement	

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

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	2
Total number of shifts	2253
Number of shifts mapped to atoms	2253
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	84%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.64±0.01	0±0/1272 (0.0± 0.0%)	0.99±0.01	0±0/1753 (0.0± 0.0%)
All	All	0.64	0/25440 (0.0%)	0.99	4/35060 (0.0%)

There are no bond-length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	127	HIS	CA-CB-CG	-5.29	108.51	113.80	11	3
1	A	25	PHE	CA-CB-CG	-5.04	108.76	113.80	10	1

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	1220	1199	1197	87±9
2	A	25	21	21	6±2
All	All	24900	24400	24360	1764

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 36.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:49:LEU:O	1:A:52:ILE:HG23	0.93	1.64	7	20
1:A:150:LEU:HD12	1:A:150:LEU:O	0.87	1.70	10	1
1:A:98:ILE:O	1:A:102:ALA:HB2	0.82	1.75	16	9
1:A:52:ILE:HD12	1:A:143:TRP:HE1	0.82	1.33	20	1
1:A:136:LEU:C	1:A:136:LEU:HD13	0.80	2.01	4	1
1:A:113:LEU:C	1:A:113:LEU:HD23	0.79	2.03	8	14
1:A:43:HIS:NE2	1:A:150:LEU:HD13	0.77	1.94	10	1
1:A:123:THR:HG23	1:A:127:HIS:CD2	0.76	2.16	18	3
1:A:123:THR:HG23	1:A:127:HIS:CE1	0.74	2.17	19	4
1:A:141:LEU:C	1:A:141:LEU:HD13	0.74	2.08	8	5
1:A:108:ALA:HB2	1:A:155:TRP:CZ2	0.73	2.18	11	10
1:A:39:LYS:HZ1	2:A:201:PKA:H1C	0.73	1.42	9	1
1:A:146:PHE:CE2	1:A:150:LEU:HD22	0.73	2.19	17	17
1:A:105:MET:O	1:A:107:TRP:N	0.72	2.22	13	20
1:A:74:PHE:CD1	1:A:79:MET:SD	0.72	2.83	13	7
2:A:201:PKA:H3	2:A:201:PKA:N18	0.71	2.00	18	19
1:A:123:THR:HG23	1:A:127:HIS:ND1	0.71	1.99	5	4
1:A:52:ILE:HD12	1:A:143:TRP:NE1	0.71	2.00	20	8
1:A:34:TYR:CE1	1:A:39:LYS:NZ	0.70	2.60	12	3
1:A:34:TYR:CD1	1:A:39:LYS:NZ	0.70	2.59	5	3
1:A:43:HIS:CE1	1:A:46:ARG:NH1	0.70	2.60	5	1
1:A:143:TRP:CH2	1:A:147:THR:CG2	0.69	2.75	9	9
1:A:147:THR:HG22	1:A:151:ASN:HD21	0.69	1.47	16	4
1:A:39:LYS:HZ2	1:A:46:ARG:HH21	0.69	1.27	13	1
1:A:74:PHE:CE2	1:A:79:MET:SD	0.69	2.86	19	5
1:A:74:PHE:CD2	1:A:79:MET:SD	0.69	2.85	20	3
1:A:146:PHE:CZ	1:A:150:LEU:HD22	0.68	2.22	6	17
1:A:24:TYR:CD1	1:A:25:PHE:N	0.68	2.61	3	1
1:A:114:LEU:CD2	1:A:147:THR:HG21	0.67	2.18	3	10
1:A:19:GLY:N	1:A:93:TRP:CH2	0.67	2.62	7	3
1:A:39:LYS:NZ	1:A:46:ARG:NH2	0.67	2.42	3	6
1:A:39:LYS:HZ2	1:A:46:ARG:NH2	0.66	1.89	3	3
1:A:107:TRP:O	1:A:109:LEU:N	0.66	2.28	15	10
1:A:77:ASP:OD1	1:A:78:ALA:N	0.66	2.28	4	1
1:A:74:PHE:CE2	1:A:79:MET:HE3	0.66	2.25	14	3
1:A:39:LYS:NZ	2:A:201:PKA:H1C	0.66	2.05	20	3
1:A:143:TRP:CZ3	1:A:147:THR:OG1	0.66	2.49	12	10
1:A:74:PHE:CE1	1:A:79:MET:SD	0.66	2.89	2	5
1:A:39:LYS:NZ	1:A:46:ARG:CZ	0.66	2.59	14	4
1:A:122:THR:CG2	1:A:126:TRP:CE3	0.65	2.80	9	17
1:A:150:LEU:HD12	1:A:150:LEU:C	0.65	2.15	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:74:PHE:CZ	1:A:79:MET:HE3	0.65	2.25	5	1
1:A:56:LEU:HD21	1:A:143:TRP:CE3	0.65	2.26	20	1
1:A:43:HIS:NE2	1:A:46:ARG:NH1	0.65	2.45	5	1
1:A:105:MET:C	1:A:107:TRP:H	0.64	2.00	12	20
1:A:146:PHE:CZ	1:A:150:LEU:HD13	0.64	2.27	15	6
1:A:52:ILE:HD11	2:A:201:PKA:H12	0.64	1.69	20	4
1:A:107:TRP:CD1	1:A:155:TRP:HE1	0.64	2.11	6	5
1:A:39:LYS:HZ1	1:A:46:ARG:HE	0.64	1.33	3	2
1:A:43:HIS:ND1	1:A:43:HIS:C	0.64	2.55	8	4
1:A:95:TRP:O	1:A:97:PRO:N	0.63	2.31	16	13
1:A:143:TRP:CZ3	1:A:144:LEU:HD21	0.63	2.28	20	1
1:A:111:ASP:OD1	1:A:147:THR:HG22	0.63	1.94	20	2
1:A:137:LEU:O	1:A:139:PRO:N	0.63	2.31	9	11
1:A:52:ILE:HD12	1:A:143:TRP:CE2	0.62	2.28	8	18
1:A:114:LEU:HD23	1:A:147:THR:HG21	0.62	1.71	3	4
1:A:50:ALA:O	1:A:53:TRP:CE3	0.62	2.52	7	5
1:A:34:TYR:OH	1:A:107:TRP:CE3	0.62	2.53	1	11
1:A:39:LYS:NZ	1:A:46:ARG:HH21	0.62	1.91	13	3
1:A:26:VAL:HG21	2:A:201:PKA:H1B	0.61	1.69	9	2
1:A:141:LEU:O	1:A:141:LEU:HD13	0.61	1.95	9	6
1:A:147:THR:O	1:A:151:ASN:ND2	0.61	2.33	15	9
1:A:68:TRP:O	1:A:73:GLY:N	0.61	2.33	9	4
1:A:50:ALA:O	1:A:53:TRP:CZ3	0.61	2.53	14	4
1:A:143:TRP:O	1:A:143:TRP:CE3	0.61	2.54	1	17
1:A:31:LEU:CD2	1:A:46:ARG:CZ	0.61	2.79	13	8
1:A:68:TRP:CG	1:A:69:LYS:N	0.61	2.69	8	4
1:A:43:HIS:NE2	1:A:150:LEU:HD22	0.61	2.10	10	1
1:A:40:PRO:O	1:A:43:HIS:CE1	0.61	2.54	4	4
1:A:43:HIS:CE1	1:A:44:PRO:O	0.61	2.54	12	10
1:A:92:ASN:O	1:A:113:LEU:HD11	0.61	1.96	11	5
1:A:99:PHE:CG	1:A:100:PHE:N	0.61	2.69	16	17
1:A:43:HIS:O	1:A:43:HIS:ND1	0.61	2.34	15	5
1:A:113:LEU:HD23	1:A:114:LEU:N	0.60	2.11	5	7
1:A:147:THR:HG22	1:A:151:ASN:ND2	0.60	2.10	18	4
1:A:40:PRO:O	1:A:43:HIS:CD2	0.60	2.54	15	5
1:A:140:TYR:CD1	1:A:141:LEU:N	0.60	2.70	15	20
1:A:151:ASN:HD21	2:A:201:PKA:C21	0.60	2.09	10	2
1:A:127:HIS:CD2	1:A:134:ALA:HB2	0.60	2.31	6	8
1:A:155:TRP:O	1:A:159:SER:N	0.60	2.34	8	8
1:A:136:LEU:C	1:A:136:LEU:CD1	0.60	2.74	4	1
2:A:201:PKA:C15	2:A:201:PKA:CL	0.60	2.86	15	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:25:PHE:CZ	1:A:102:ALA:O	0.60	2.55	11	14
1:A:124:LEU:O	1:A:128:ARG:NE	0.60	2.34	3	1
1:A:99:PHE:C	1:A:99:PHE:CD1	0.60	2.80	16	3
1:A:107:TRP:CD1	1:A:108:ALA:N	0.60	2.69	5	15
1:A:43:HIS:NE2	1:A:44:PRO:O	0.60	2.34	14	2
1:A:95:TRP:CD1	1:A:113:LEU:HD11	0.59	2.32	18	3
1:A:52:ILE:CD1	1:A:143:TRP:CE2	0.59	2.85	12	13
1:A:111:ASP:CG	1:A:151:ASN:ND2	0.59	2.60	4	5
1:A:24:TYR:CD1	1:A:24:TYR:C	0.59	2.80	11	12
1:A:147:THR:HG22	1:A:151:ASN:OD1	0.59	1.98	12	1
1:A:68:TRP:C	1:A:68:TRP:CD1	0.59	2.81	9	9
1:A:34:TYR:O	1:A:37:LEU:N	0.59	2.36	6	17
1:A:107:TRP:CE3	2:A:201:PKA:C22	0.59	2.85	3	4
1:A:105:MET:C	1:A:107:TRP:N	0.59	2.60	12	20
1:A:107:TRP:CE3	2:A:201:PKA:C23	0.59	2.85	4	7
1:A:25:PHE:CE2	1:A:102:ALA:O	0.59	2.55	1	13
1:A:95:TRP:N	1:A:96:PRO:CD	0.59	2.66	20	11
1:A:141:LEU:HD13	1:A:141:LEU:O	0.59	1.98	13	5
1:A:26:VAL:HG21	2:A:201:PKA:H4B	0.59	1.75	10	3
1:A:34:TYR:OH	1:A:107:TRP:CZ3	0.59	2.55	16	2
1:A:38:GLN:N	1:A:157:ASP:OD2	0.58	2.36	5	6
1:A:39:LYS:HZ1	1:A:46:ARG:NE	0.58	1.95	3	1
1:A:101:GLY:O	1:A:102:ALA:HB3	0.58	1.98	17	3
1:A:114:LEU:HD21	1:A:147:THR:HG21	0.58	1.75	8	7
1:A:99:PHE:CD1	1:A:100:PHE:N	0.58	2.72	16	8
1:A:113:LEU:C	1:A:113:LEU:CD2	0.58	2.77	17	11
1:A:40:PRO:O	1:A:43:HIS:CG	0.58	2.57	11	2
1:A:95:TRP:C	1:A:95:TRP:CD1	0.58	2.82	10	2
1:A:137:LEU:C	1:A:139:PRO:CD	0.58	2.77	8	4
1:A:56:LEU:HD11	1:A:143:TRP:CD1	0.58	2.34	7	3
1:A:111:ASP:CB	1:A:151:ASN:OD1	0.58	2.52	20	3
1:A:137:LEU:O	1:A:140:TYR:N	0.57	2.36	12	5
1:A:43:HIS:C	1:A:43:HIS:HD1	0.57	2.08	8	3
1:A:93:TRP:O	1:A:96:PRO:CD	0.57	2.52	1	11
1:A:42:TRP:C	1:A:42:TRP:CD1	0.57	2.83	4	8
1:A:39:LYS:HZ1	1:A:46:ARG:CZ	0.57	2.10	14	1
1:A:137:LEU:O	1:A:138:TYR:C	0.57	2.47	9	16
1:A:135:ARG:O	1:A:138:TYR:CD2	0.57	2.58	8	13
1:A:73:GLY:O	1:A:75:THR:N	0.57	2.37	18	5
1:A:105:MET:O	1:A:105:MET:SD	0.57	2.63	5	2
1:A:146:PHE:CZ	1:A:150:LEU:HD12	0.57	2.34	16	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:143:TRP:CZ3	1:A:147:THR:HG23	0.57	2.34	1	4
1:A:39:LYS:HZ1	1:A:46:ARG:NH1	0.57	1.97	1	1
1:A:143:TRP:CH2	2:A:201:PKA:C10	0.57	2.86	15	11
1:A:111:ASP:O	1:A:115:VAL:HG23	0.57	1.98	20	4
1:A:68:TRP:CD2	1:A:68:TRP:C	0.56	2.84	8	4
1:A:29:GLU:OE1	1:A:32:ARG:NE	0.56	2.39	9	1
1:A:143:TRP:CZ3	1:A:147:THR:CG2	0.56	2.88	2	6
1:A:49:LEU:HD12	2:A:201:PKA:H6A	0.56	1.78	3	14
1:A:67:VAL:HG22	1:A:130:SER:OG	0.56	2.00	13	6
1:A:111:ASP:OD1	1:A:147:THR:CG2	0.56	2.54	20	3
1:A:39:LYS:NZ	1:A:46:ARG:HE	0.56	1.97	19	3
1:A:98:ILE:HG21	1:A:107:TRP:HA	0.56	1.78	11	7
1:A:39:LYS:NZ	1:A:46:ARG:NE	0.56	2.54	3	2
1:A:43:HIS:ND1	1:A:43:HIS:O	0.56	2.38	3	2
1:A:50:ALA:HB3	1:A:51:PRO:CD	0.55	2.31	5	18
1:A:107:TRP:C	1:A:109:LEU:N	0.55	2.64	15	11
1:A:152:TYR:CE1	1:A:156:ARG:NE	0.55	2.73	6	1
1:A:34:TYR:O	1:A:37:LEU:O	0.55	2.25	10	20
1:A:50:ALA:HB3	1:A:51:PRO:HD3	0.55	1.78	6	20
1:A:74:PHE:CE2	1:A:79:MET:HE1	0.55	2.36	16	1
1:A:43:HIS:CE1	1:A:46:ARG:HH12	0.55	2.18	5	1
1:A:111:ASP:CG	1:A:151:ASN:HD22	0.55	2.09	16	1
1:A:75:THR:CG2	1:A:77:ASP:OD1	0.55	2.54	4	1
1:A:43:HIS:NE2	2:A:201:PKA:H6B	0.55	2.17	1	4
1:A:98:ILE:O	1:A:102:ALA:CB	0.55	2.54	9	9
1:A:52:ILE:HD12	1:A:143:TRP:CD1	0.55	2.36	3	5
1:A:95:TRP:CD1	1:A:95:TRP:C	0.55	2.85	7	2
1:A:111:ASP:OD2	1:A:151:ASN:ND2	0.54	2.40	4	4
1:A:127:HIS:N	1:A:127:HIS:ND1	0.54	2.54	18	3
1:A:51:PRO:O	1:A:54:GLY:N	0.54	2.41	6	9
1:A:98:ILE:O	1:A:102:ALA:N	0.54	2.41	3	6
1:A:155:TRP:O	1:A:159:SER:O	0.54	2.25	8	2
1:A:57:TYR:C	1:A:57:TYR:CD1	0.54	2.82	8	1
1:A:25:PHE:CD1	1:A:102:ALA:HB3	0.54	2.38	3	1
1:A:156:ARG:O	1:A:159:SER:O	0.54	2.25	4	3
1:A:105:MET:SD	1:A:105:MET:C	0.54	2.90	5	1
1:A:92:ASN:O	1:A:113:LEU:CD1	0.53	2.56	8	7
1:A:105:MET:HE1	1:A:158:ASN:CB	0.53	2.33	13	1
1:A:99:PHE:CD1	1:A:99:PHE:C	0.53	2.86	14	1
1:A:131:PRO:N	1:A:132:PRO:CD	0.53	2.70	19	20
1:A:107:TRP:CD1	1:A:107:TRP:C	0.53	2.87	13	9

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:111:ASP:CG	1:A:151:ASN:OD1	0.53	2.52	20	12
1:A:141:LEU:C	1:A:141:LEU:CD1	0.53	2.80	18	9
1:A:75:THR:O	1:A:78:ALA:N	0.53	2.41	18	6
1:A:57:TYR:CG	1:A:58:SER:N	0.53	2.77	10	3
1:A:108:ALA:HB2	1:A:155:TRP:CH2	0.53	2.39	15	1
1:A:34:TYR:CE1	1:A:107:TRP:CH2	0.52	2.96	10	4
1:A:25:PHE:CD2	1:A:102:ALA:HB1	0.52	2.39	17	8
1:A:47:TRP:CD1	1:A:48:THR:N	0.52	2.77	14	3
1:A:40:PRO:CG	1:A:43:HIS:CE1	0.52	2.91	10	1
1:A:68:TRP:CE3	1:A:73:GLY:CA	0.52	2.93	5	3
1:A:49:LEU:O	1:A:50:ALA:C	0.52	2.53	14	20
1:A:140:TYR:CG	1:A:141:LEU:N	0.52	2.77	15	10
1:A:9:VAL:O	1:A:12:THR:HG22	0.52	2.05	20	7
1:A:54:GLY:O	1:A:57:TYR:CD2	0.52	2.63	10	2
1:A:54:GLY:O	1:A:57:TYR:CE2	0.52	2.63	10	2
1:A:101:GLY:C	1:A:103:ARG:H	0.52	2.13	9	9
1:A:143:TRP:CE3	1:A:144:LEU:HD21	0.52	2.40	20	1
1:A:92:ASN:OD1	1:A:113:LEU:HD11	0.52	2.05	8	1
1:A:43:HIS:CD2	1:A:150:LEU:HD22	0.52	2.40	10	1
1:A:70:GLU:OE1	1:A:129:VAL:O	0.51	2.27	7	7
1:A:126:TRP:CD1	1:A:126:TRP:N	0.51	2.77	7	11
1:A:98:ILE:HD13	1:A:107:TRP:HA	0.51	1.82	18	3
1:A:114:LEU:HD21	1:A:143:TRP:CZ2	0.51	2.40	9	5
1:A:147:THR:O	1:A:151:ASN:OD1	0.51	2.29	10	4
1:A:108:ALA:HB2	1:A:155:TRP:CE2	0.51	2.40	1	5
1:A:119:ALA:O	1:A:123:THR:OG1	0.51	2.28	5	17
1:A:47:TRP:C	1:A:47:TRP:CD1	0.51	2.89	4	5
1:A:103:ARG:CZ	1:A:104:GLN:NE2	0.51	2.73	15	2
1:A:31:LEU:CD2	1:A:46:ARG:HE	0.50	2.19	12	1
1:A:143:TRP:CH2	1:A:147:THR:OG1	0.50	2.62	13	1
1:A:49:LEU:O	1:A:52:ILE:CG2	0.50	2.52	20	15
1:A:60:MET:SD	1:A:85:TYR:OH	0.50	2.68	3	1
1:A:113:LEU:CD2	1:A:113:LEU:N	0.50	2.74	10	1
1:A:75:THR:O	1:A:76:GLU:C	0.50	2.54	9	10
1:A:73:GLY:O	1:A:78:ALA:HB3	0.50	2.06	14	2
1:A:43:HIS:NE2	2:A:201:PKA:C6	0.50	2.74	7	2
1:A:7:PRO:O	1:A:11:LEU:HD13	0.50	2.07	15	7
1:A:98:ILE:HD11	1:A:110:ALA:HB2	0.50	1.84	5	8
1:A:109:LEU:N	1:A:109:LEU:CD1	0.50	2.75	15	4
1:A:56:LEU:CD2	1:A:143:TRP:CE3	0.50	2.94	20	1
1:A:39:LYS:HZ2	1:A:46:ARG:CZ	0.49	2.19	17	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:153:TYR:O	1:A:157:ASP:CG	0.49	2.55	2	4
1:A:92:ASN:OD1	1:A:113:LEU:HD13	0.49	2.07	7	1
1:A:45:PRO:CB	1:A:47:TRP:NE1	0.49	2.75	16	1
1:A:47:TRP:CD1	1:A:47:TRP:C	0.49	2.90	14	4
1:A:147:THR:O	1:A:151:ASN:CG	0.49	2.55	9	9
1:A:53:TRP:O	1:A:57:TYR:CB	0.49	2.60	6	8
1:A:152:TYR:O	1:A:156:ARG:CB	0.49	2.60	1	1
1:A:111:ASP:OD2	1:A:151:ASN:OD1	0.49	2.29	8	9
1:A:107:TRP:CZ3	2:A:201:PKA:C23	0.49	2.95	8	2
1:A:152:TYR:CE2	1:A:156:ARG:NH1	0.49	2.81	11	1
1:A:23:ALA:HB1	1:A:46:ARG:NH2	0.49	2.23	6	2
1:A:110:ALA:O	1:A:114:LEU:CB	0.48	2.61	10	7
1:A:29:GLU:OE2	1:A:32:ARG:NH2	0.48	2.46	3	1
1:A:108:ALA:HB3	1:A:155:TRP:CZ2	0.48	2.43	9	2
1:A:23:ALA:HA	2:A:201:PKA:CL	0.48	2.45	15	5
1:A:34:TYR:O	1:A:35:ALA:C	0.48	2.56	12	14
1:A:75:THR:HG23	1:A:77:ASP:H	0.48	1.68	16	2
1:A:124:LEU:O	1:A:128:ARG:CG	0.48	2.62	17	1
1:A:110:ALA:HB3	2:A:201:PKA:C22	0.48	2.38	20	1
1:A:20:PHE:CZ	1:A:27:ARG:NH1	0.48	2.82	1	1
1:A:105:MET:O	1:A:105:MET:CG	0.48	2.62	20	13
1:A:107:TRP:O	1:A:108:ALA:C	0.48	2.57	11	6
1:A:47:TRP:O	1:A:51:PRO:CD	0.48	2.62	16	9
1:A:108:ALA:CB	1:A:155:TRP:CZ2	0.48	2.97	18	11
1:A:97:PRO:CD	1:A:109:LEU:HD23	0.47	2.39	15	1
1:A:15:PRO:HB3	1:A:89:LEU:HD21	0.47	1.83	14	1
1:A:101:GLY:C	1:A:103:ARG:N	0.47	2.71	9	9
1:A:143:TRP:C	1:A:143:TRP:CD2	0.47	2.91	9	2
1:A:107:TRP:C	1:A:109:LEU:H	0.47	2.18	15	4
1:A:150:LEU:C	1:A:150:LEU:CD1	0.47	2.82	10	1
1:A:61:GLY:O	1:A:64:SER:OG	0.47	2.29	11	4
1:A:119:ALA:O	1:A:123:THR:CB	0.47	2.62	2	12
1:A:115:VAL:HA	1:A:144:LEU:HD13	0.47	1.87	9	7
1:A:12:THR:OG1	1:A:57:TYR:O	0.47	2.30	10	1
1:A:108:ALA:HB2	1:A:155:TRP:NE1	0.47	2.25	12	1
1:A:74:PHE:CE2	1:A:79:MET:CE	0.47	2.98	16	1
1:A:143:TRP:CE3	1:A:147:THR:OG1	0.47	2.68	12	6
1:A:141:LEU:HD13	1:A:141:LEU:C	0.47	2.34	20	3
1:A:68:TRP:CD1	1:A:69:LYS:N	0.47	2.83	1	8
1:A:116:SER:O	1:A:120:THR:CB	0.47	2.62	16	3
1:A:122:THR:CG2	1:A:126:TRP:CD2	0.47	2.98	2	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:106:GLY:O	1:A:108:ALA:N	0.47	2.48	16	6
1:A:155:TRP:C	1:A:159:SER:O	0.47	2.58	8	1
1:A:95:TRP:CD1	1:A:96:PRO:N	0.47	2.83	14	1
1:A:117:GLY:O	1:A:121:ALA:HB3	0.47	2.09	15	1
1:A:37:LEU:HD13	1:A:105:MET:SD	0.46	2.49	14	1
1:A:143:TRP:CD2	1:A:143:TRP:C	0.46	2.93	2	5
1:A:39:LYS:HZ2	2:A:201:PKA:H1C	0.46	1.67	20	1
1:A:10:GLY:O	1:A:14:VAL:HG23	0.46	2.10	10	3
1:A:43:HIS:NE2	1:A:150:LEU:CD1	0.46	2.76	10	1
1:A:141:LEU:O	1:A:145:ALA:HB2	0.46	2.10	15	6
1:A:106:GLY:C	1:A:108:ALA:N	0.46	2.73	13	8
1:A:155:TRP:O	1:A:159:SER:OG	0.46	2.32	15	4
1:A:38:GLN:O	1:A:157:ASP:OD2	0.46	2.34	14	4
1:A:55:THR:CG2	1:A:56:LEU:N	0.46	2.79	14	1
1:A:39:LYS:HZ2	1:A:46:ARG:NE	0.46	2.07	14	1
1:A:101:GLY:O	1:A:102:ALA:CB	0.46	2.63	17	1
1:A:57:TYR:CE1	1:A:58:SER:OG	0.46	2.66	18	1
1:A:92:ASN:ND2	1:A:117:GLY:CA	0.46	2.79	12	3
1:A:138:TYR:CB	1:A:139:PRO:CD	0.46	2.94	3	8
1:A:65:TYR:O	1:A:68:TRP:CD1	0.46	2.69	6	2
1:A:18:GLY:C	1:A:93:TRP:CZ3	0.46	2.94	7	1
1:A:43:HIS:CD2	2:A:201:PKA:H6B	0.46	2.46	12	1
1:A:123:THR:O	1:A:127:HIS:CB	0.45	2.64	15	10
1:A:37:LEU:HD21	1:A:158:ASN:ND2	0.45	2.25	10	1
1:A:49:LEU:O	1:A:52:ILE:N	0.45	2.38	10	1
1:A:105:MET:O	1:A:107:TRP:CD1	0.45	2.70	15	1
1:A:122:THR:HG23	1:A:126:TRP:CD2	0.45	2.47	2	4
1:A:95:TRP:NE1	1:A:112:LEU:HD23	0.45	2.27	9	1
1:A:25:PHE:CD2	1:A:102:ALA:CB	0.45	2.99	14	2
1:A:103:ARG:NH1	1:A:104:GLN:NE2	0.45	2.65	18	1
1:A:53:TRP:O	1:A:57:TYR:N	0.45	2.49	20	11
1:A:137:LEU:O	1:A:139:PRO:CD	0.45	2.65	14	4
1:A:49:LEU:CD1	1:A:146:PHE:CE2	0.45	2.99	6	2
1:A:151:ASN:ND2	2:A:201:PKA:C21	0.45	2.79	10	2
1:A:21:MET:O	1:A:24:TYR:CD1	0.45	2.69	3	1
1:A:68:TRP:O	1:A:72:GLY:N	0.45	2.50	3	3
1:A:13:LEU:O	1:A:16:SER:OG	0.45	2.31	7	2
1:A:45:PRO:CB	1:A:47:TRP:CE2	0.45	3.00	9	3
1:A:50:ALA:CB	1:A:51:PRO:CD	0.45	2.95	5	12
1:A:143:TRP:O	1:A:147:THR:OG1	0.45	2.35	5	3
1:A:25:PHE:CE2	1:A:102:ALA:HB1	0.45	2.46	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:151:ASN:HD22	1:A:151:ASN:N	0.45	2.09	8	1
1:A:107:TRP:HE1	1:A:155:TRP:NE1	0.45	2.10	2	1
1:A:110:ALA:O	1:A:114:LEU:HD23	0.45	2.11	6	1
1:A:68:TRP:CD2	1:A:69:LYS:N	0.45	2.85	8	4
1:A:68:TRP:C	1:A:68:TRP:CE3	0.45	2.95	18	4
1:A:23:ALA:CA	2:A:201:PKA:CL	0.45	3.02	15	1
1:A:42:TRP:CD1	1:A:42:TRP:C	0.44	2.95	7	1
1:A:77:ASP:O	1:A:81:PRO:CD	0.44	2.64	15	2
1:A:143:TRP:CE3	1:A:144:LEU:CD2	0.44	2.99	20	1
1:A:95:TRP:CG	1:A:113:LEU:HD11	0.44	2.47	18	2
1:A:113:LEU:O	1:A:117:GLY:N	0.44	2.50	14	5
1:A:67:VAL:HG13	1:A:129:VAL:HG11	0.44	1.90	8	1
1:A:85:TYR:O	1:A:89:LEU:CB	0.44	2.66	20	5
1:A:122:THR:CG2	1:A:126:TRP:CZ3	0.44	3.00	11	3
1:A:12:THR:CG2	1:A:13:LEU:N	0.44	2.81	10	1
1:A:14:VAL:N	1:A:15:PRO:CD	0.44	2.80	19	1
1:A:148:THR:O	1:A:152:TYR:CD2	0.44	2.71	2	2
1:A:13:LEU:HD21	1:A:57:TYR:CE1	0.44	2.48	6	1
1:A:141:LEU:O	1:A:145:ALA:CB	0.44	2.66	11	3
1:A:42:TRP:NE1	1:A:146:PHE:CE1	0.44	2.85	18	1
1:A:107:TRP:NE1	1:A:155:TRP:NE1	0.44	2.66	2	2
1:A:51:PRO:O	1:A:52:ILE:C	0.44	2.61	3	8
1:A:126:TRP:N	1:A:126:TRP:CD1	0.43	2.86	13	3
1:A:144:LEU:O	1:A:147:THR:OG1	0.43	2.35	8	2
1:A:52:ILE:HD11	2:A:201:PKA:C12	0.43	2.43	7	3
1:A:116:SER:O	1:A:120:THR:OG1	0.43	2.30	16	5
1:A:103:ARG:HH11	1:A:104:GLN:NE2	0.43	2.12	18	1
1:A:20:PHE:O	1:A:24:TYR:CB	0.43	2.66	2	3
1:A:79:MET:O	1:A:83:GLY:N	0.43	2.51	10	5
1:A:98:ILE:O	1:A:99:PHE:C	0.43	2.61	6	8
1:A:59:ALA:O	1:A:136:LEU:HD21	0.43	2.13	6	1
1:A:95:TRP:N	1:A:96:PRO:HD3	0.43	2.29	18	4
1:A:107:TRP:NE1	1:A:155:TRP:HE1	0.43	2.11	7	1
1:A:39:LYS:NZ	2:A:201:PKA:C1	0.43	2.80	20	1
1:A:127:HIS:CD2	1:A:127:HIS:N	0.43	2.86	5	1
1:A:107:TRP:CD1	1:A:155:TRP:NE1	0.43	2.86	6	1
1:A:107:TRP:CE3	2:A:201:PKA:H22	0.43	2.48	15	1
1:A:65:TYR:CZ	1:A:69:LYS:CE	0.43	3.02	12	1
1:A:143:TRP:CH2	2:A:201:PKA:C11	0.43	3.02	15	1
2:A:201:PKA:N18	2:A:201:PKA:H3	0.43	2.29	20	1
1:A:82:LEU:HD12	1:A:82:LEU:N	0.43	2.28	13	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:68:TRP:CD2	1:A:73:GLY:HA2	0.43	2.49	14	3
1:A:107:TRP:CE3	1:A:108:ALA:HA	0.43	2.49	15	1
1:A:92:ASN:HD22	1:A:117:GLY:CA	0.43	2.27	1	1
1:A:127:HIS:CE1	1:A:134:ALA:HB2	0.43	2.48	2	1
1:A:127:HIS:CG	1:A:134:ALA:HB2	0.43	2.49	18	1
1:A:122:THR:HG23	1:A:126:TRP:CE3	0.42	2.49	8	3
1:A:138:TYR:N	1:A:139:PRO:CD	0.42	2.82	17	2
1:A:116:SER:O	1:A:120:THR:N	0.42	2.49	14	2
1:A:49:LEU:HD12	2:A:201:PKA:O8	0.42	2.15	17	1
1:A:99:PHE:CD2	1:A:100:PHE:N	0.42	2.88	19	2
1:A:43:HIS:CD2	1:A:44:PRO:O	0.42	2.72	14	1
1:A:113:LEU:HD23	1:A:113:LEU:O	0.42	2.14	1	2
1:A:57:TYR:CD1	1:A:57:TYR:C	0.42	2.98	14	1
1:A:40:PRO:O	1:A:43:HIS:NE2	0.42	2.51	16	1
1:A:111:ASP:OD1	1:A:115:VAL:HG23	0.42	2.15	5	1
1:A:107:TRP:CE2	1:A:155:TRP:NE1	0.42	2.88	15	1
1:A:74:PHE:CZ	1:A:79:MET:SD	0.42	3.13	16	1
1:A:151:ASN:N	1:A:151:ASN:ND2	0.42	2.68	8	1
1:A:92:ASN:O	1:A:113:LEU:HD12	0.42	2.14	13	1
1:A:73:GLY:O	1:A:78:ALA:CB	0.42	2.67	14	2
1:A:107:TRP:C	1:A:107:TRP:CD1	0.42	2.97	10	1
1:A:114:LEU:O	1:A:118:VAL:HG12	0.42	2.15	18	1
1:A:126:TRP:O	1:A:130:SER:N	0.42	2.44	15	2
1:A:77:ASP:OD1	1:A:77:ASP:C	0.42	2.61	4	1
1:A:115:VAL:HA	1:A:144:LEU:HD22	0.42	1.92	7	3
1:A:31:LEU:HD21	1:A:46:ARG:CZ	0.42	2.44	10	1
1:A:136:LEU:N	1:A:136:LEU:CD2	0.42	2.83	16	1
1:A:111:ASP:OD1	1:A:115:VAL:CG2	0.42	2.68	5	2
1:A:111:ASP:C	1:A:111:ASP:OD1	0.42	2.61	11	1
1:A:26:VAL:O	1:A:46:ARG:NH1	0.42	2.53	14	1
1:A:53:TRP:HE1	2:A:201:PKA:H13	0.41	1.74	19	2
1:A:18:GLY:CA	1:A:93:TRP:CZ2	0.41	3.03	9	2
2:A:201:PKA:N18	2:A:201:PKA:C3	0.41	2.81	15	2
1:A:103:ARG:CZ	1:A:104:GLN:HE21	0.41	2.27	19	1
1:A:109:LEU:N	1:A:109:LEU:HD12	0.41	2.29	15	1
1:A:140:TYR:CD1	1:A:140:TYR:C	0.41	2.97	19	1
1:A:56:LEU:N	1:A:56:LEU:HD12	0.41	2.30	1	1
1:A:40:PRO:O	1:A:43:HIS:ND1	0.41	2.53	4	1
1:A:20:PHE:O	1:A:24:TYR:N	0.41	2.54	15	1
1:A:68:TRP:CE3	1:A:73:GLY:HA2	0.41	2.49	17	1
1:A:68:TRP:CE3	1:A:68:TRP:O	0.41	2.74	18	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:137:LEU:C	1:A:139:PRO:HD2	0.41	2.40	11	1
1:A:151:ASN:N	1:A:151:ASN:HD22	0.41	2.13	14	1
1:A:127:HIS:CD2	1:A:134:ALA:CB	0.41	3.03	18	1
1:A:152:TYR:O	1:A:156:ARG:CG	0.41	2.69	2	2
1:A:92:ASN:OD1	1:A:113:LEU:HD22	0.41	2.15	7	1
1:A:27:ARG:O	1:A:31:LEU:HD11	0.41	2.16	13	1
1:A:6:VAL:N	1:A:7:PRO:HD2	0.41	2.31	10	3
1:A:26:VAL:CG2	2:A:201:PKA:H4B	0.41	2.44	10	1
1:A:89:LEU:O	1:A:93:TRP:CD1	0.41	2.73	11	1
1:A:50:ALA:N	1:A:51:PRO:HD2	0.41	2.31	19	4
1:A:111:ASP:O	1:A:115:VAL:CG2	0.41	2.69	20	1
1:A:95:TRP:O	1:A:96:PRO:C	0.41	2.64	2	2
1:A:92:ASN:OD1	1:A:113:LEU:CD1	0.41	2.69	8	1
1:A:85:TYR:CE1	1:A:122:THR:OG1	0.41	2.74	5	2
1:A:56:LEU:HB3	1:A:60:MET:HE3	0.41	1.92	6	1
1:A:111:ASP:OD1	1:A:111:ASP:O	0.41	2.39	18	1
1:A:82:LEU:N	1:A:82:LEU:HD12	0.41	2.31	20	1
1:A:56:LEU:HD12	1:A:56:LEU:N	0.40	2.31	2	1
1:A:49:LEU:CB	2:A:201:PKA:O8	0.40	2.69	14	1
1:A:18:GLY:C	1:A:93:TRP:CH2	0.40	2.99	17	1
1:A:111:ASP:OD1	1:A:111:ASP:C	0.40	2.61	18	1
1:A:57:TYR:CZ	1:A:58:SER:OG	0.40	2.75	10	1
1:A:20:PHE:CE1	1:A:53:TRP:CZ3	0.40	3.10	13	1
1:A:37:LEU:CD1	1:A:105:MET:SD	0.40	3.09	14	1
1:A:151:ASN:OD1	2:A:201:PKA:C21	0.40	2.69	16	1
1:A:13:LEU:CD2	1:A:57:TYR:CE1	0.40	3.05	6	1
1:A:134:ALA:HA	1:A:137:LEU:HD12	0.40	1.92	16	1
1:A:114:LEU:HD13	1:A:143:TRP:CZ2	0.40	2.51	20	1
1:A:31:LEU:HD22	1:A:46:ARG:CZ	0.40	2.46	19	1
1:A:103:ARG:CB	1:A:103:ARG:NH1	0.40	2.84	2	1
1:A:122:THR:HG23	1:A:126:TRP:CE2	0.40	2.51	2	1
1:A:152:TYR:CZ	1:A:156:ARG:NH1	0.40	2.89	11	1

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	154/169 (91%)	143±1 (93±1%)	7±2 (5±1%)	4±1 (3±1%)	6	42
All	All	3080/3380 (91%)	2852 (93%)	147 (5%)	81 (3%)	6	42

All 10 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	106	GLY	20
1	A	96	PRO	14
1	A	138	TYR	13
1	A	108	ALA	10
1	A	81	PRO	6
1	A	107	TRP	6
1	A	97	PRO	5
1	A	74	PHE	5
1	A	44	PRO	1
1	A	137	LEU	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	119/130 (92%)	112±2 (94±2%)	7±2 (6±2%)	20	69
All	All	2380/2600 (92%)	2243 (94%)	137 (6%)	20	69

All 23 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	26	VAL	20
1	A	24	TYR	16
1	A	68	TRP	13
1	A	74	PHE	12
1	A	140	TYR	12
1	A	143	TRP	9
1	A	138	TYR	8
1	A	118	VAL	8

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Mol	Chain	Res	Type	Models (Total)
1	A	141	LEU	6
1	A	107	TRP	5
1	A	99	PHE	5
1	A	43	HIS	5
1	A	155	TRP	4
1	A	127	HIS	3
1	A	130	SER	2
1	A	136	LEU	2
1	A	147	THR	1
1	A	150	LEU	1
1	A	114	LEU	1
1	A	57	TYR	1
1	A	105	MET	1
1	A	39	LYS	1
1	A	116	SER	1

6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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
2	PKA	A	201	-	27,27,27	1.72±0.05	3±0 (11±0%)

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
2	PKA	A	201	-	34,38,38	1.38±0.03	5±0 (13±1%)

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
2	PKA	A	201	-	-	0±0,18,18,18	0±0,3,3,3

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
2	A	201	PKA	C17-N18	6.38	1.40	1.32	1	20
2	A	201	PKA	C9-N18	3.99	1.40	1.34	9	20
2	A	201	PKA	C10-C9	3.26	1.40	1.37	17	20

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

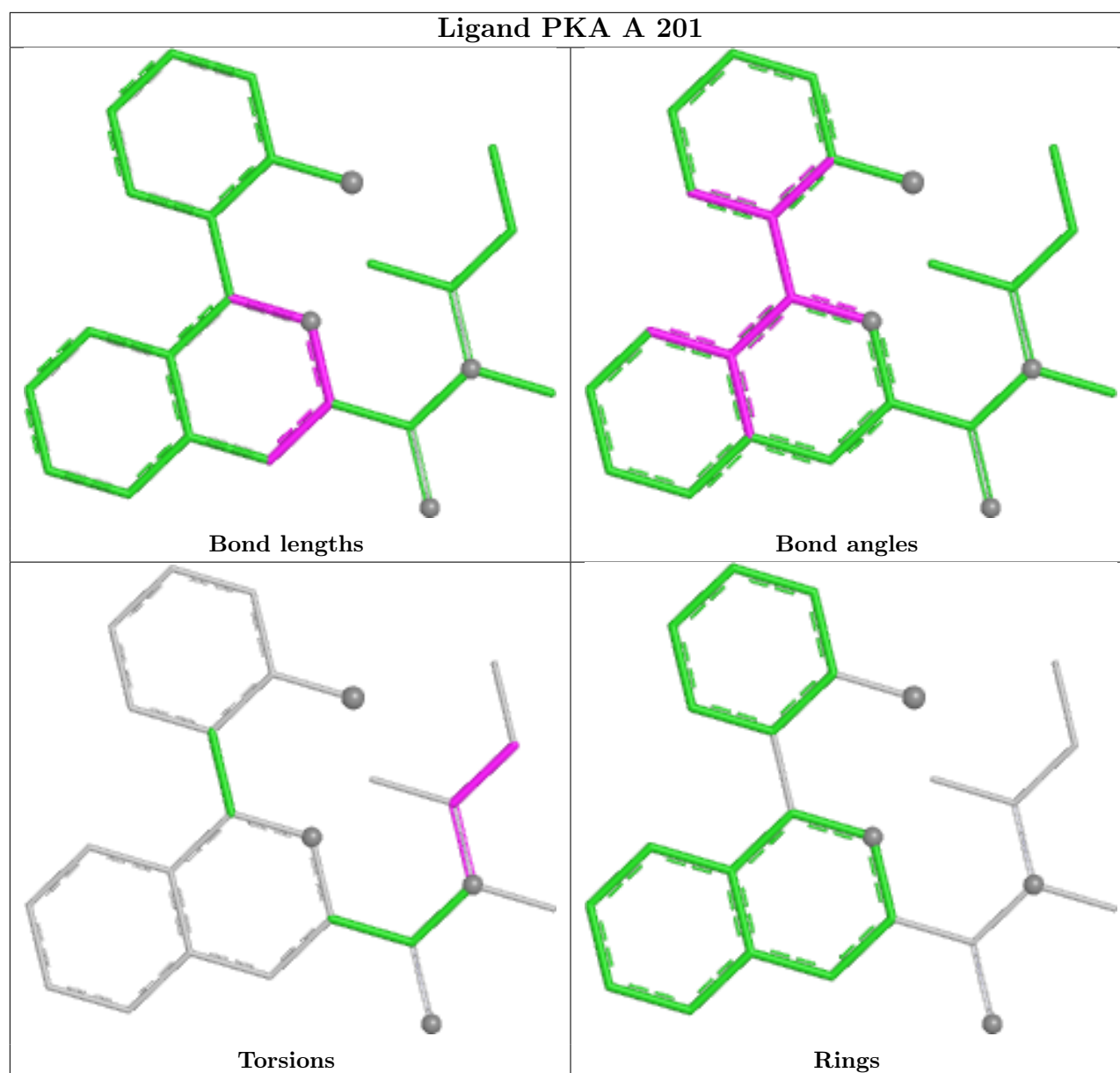
Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	A	201	PKA	C19-C17-N18	4.41	119.89	115.23	8	20
2	A	201	PKA	C17-C16-C11	4.22	120.00	117.60	12	20
2	A	201	PKA	C15-C16-C17	2.41	119.99	123.67	12	20
2	A	201	PKA	C20-C19-C24	2.33	120.22	117.60	3	20
2	A	201	PKA	C16-C17-N18	2.25	119.75	122.02	17	15

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 84% for the well-defined parts and 83% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_2*

7.1.1 Bookkeeping

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

Total number of shifts	316
Number of shifts mapped to atoms	316
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	168	-1.63 ± 0.15	Should be checked
$^{13}\text{C}_\beta$	148	0.33 ± 0.06	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	0	—	None (insufficient data)

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 14%, i.e. 289 atoms were assigned a chemical shift out of a possible 2120. 0 out of 33 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	153/763 (20%)	0/313 (0%)	153/308 (50%)	0/142 (0%)
Sidechain	136/1059 (13%)	0/709 (0%)	136/321 (42%)	0/29 (0%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	0/298 (0%)	0/144 (0%)	0/139 (0%)	0/15 (0%)
Overall	289/2120 (14%)	0/1166 (0%)	289/768 (38%)	0/186 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 14%, i.e. 316 atoms were assigned a chemical shift out of a possible 2321. 0 out of 34 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	168/839 (20%)	0/345 (0%)	168/338 (50%)	0/156 (0%)
Sidechain	148/1172 (13%)	0/781 (0%)	148/353 (42%)	0/38 (0%)
Aromatic	0/310 (0%)	0/150 (0%)	0/144 (0%)	0/16 (0%)
Overall	316/2321 (14%)	0/1276 (0%)	316/835 (38%)	0/210 (0%)

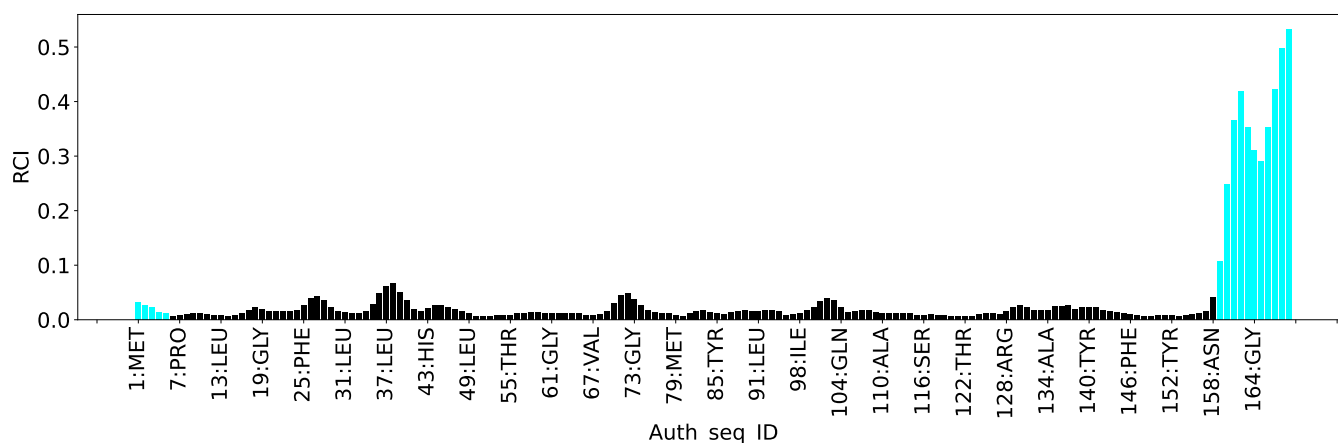
7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

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

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

Random coil index (RCI) for chain A:



7.2 Chemical shift list 2

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.2.1 Bookkeeping

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

Total number of shifts	1937
Number of shifts mapped to atoms	1937
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	22

7.2.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	168	-1.65 ± 0.13	Should be checked
$^{13}\text{C}_\beta$	148	0.24 ± 0.08	None needed (< 0.5 ppm)
$^{13}\text{C}'$	7	—	None (insufficient data)
^{15}N	152	0.69 ± 0.23	Should be applied

7.2.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 84%, i.e. 1789 atoms were assigned a chemical shift out of a possible 2120. 0 out of 33 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	608/763 (80%)	309/313 (99%)	160/308 (52%)	139/142 (98%)
Sidechain	975/1059 (92%)	669/709 (94%)	299/321 (93%)	7/29 (24%)
Aromatic	206/298 (69%)	103/144 (72%)	92/139 (66%)	11/15 (73%)
Overall	1789/2120 (84%)	1081/1166 (93%)	551/768 (72%)	157/186 (84%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 83%, i.e. 1936 atoms were assigned a chemical shift out of a possible 2321. 0 out of 34 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	665/839 (79%)	339/345 (98%)	175/338 (52%)	151/156 (97%)
Sidechain	1059/1172 (90%)	726/781 (93%)	326/353 (92%)	7/38 (18%)
Aromatic	212/310 (68%)	106/150 (71%)	94/144 (65%)	12/16 (75%)
Overall	1936/2321 (83%)	1171/1276 (92%)	595/835 (71%)	170/210 (81%)

7.2.4 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.

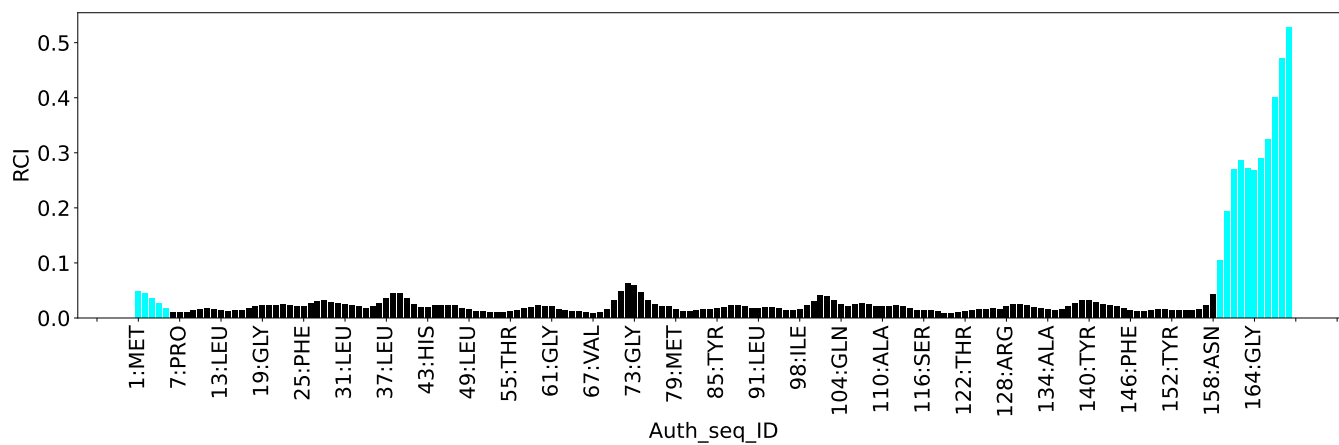
List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
2	A	156	ARG	NE	106.33	76.53 – 92.65	13.5
2	A	68	TRP	NE1	107.27	118.53 – 139.98	-10.2
2	A	53	TRP	NE1	107.52	118.53 – 139.98	-10.1
2	A	95	TRP	NE1	107.70	118.53 – 139.98	-10.1
2	A	107	TRP	NE1	108.36	118.53 – 139.98	-9.7
2	A	33	TRP	NE1	108.92	118.53 – 139.98	-9.5
2	A	5	TRP	NE1	109.30	118.53 – 139.98	-9.3
2	A	155	TRP	NE1	110.73	118.53 – 139.98	-8.6
2	A	42	TRP	NE1	111.22	118.53 – 139.98	-8.4
2	A	47	TRP	NE1	111.42	118.53 – 139.98	-8.3
2	A	63	GLY	HA3	1.28	2.08 – 5.71	-7.2
2	A	18	GLY	HA2	1.52	2.15 – 5.77	-6.8
2	A	52	ILE	HG21	-1.00	-0.56 – 2.11	-6.7
2	A	52	ILE	HG22	-1.00	-0.56 – 2.11	-6.7
2	A	52	ILE	HG23	-1.00	-0.56 – 2.11	-6.7
2	A	73	GLY	HA3	1.66	2.08 – 5.71	-6.2
2	A	40	PRO	HB2	-0.01	0.37 – 3.78	-6.1
2	A	48	THR	HG21	-0.12	0.08 – 2.19	-6.0
2	A	48	THR	HG22	-0.12	0.08 – 2.19	-6.0
2	A	48	THR	HG23	-0.12	0.08 – 2.19	-6.0
2	A	143	TRP	HZ2	5.62	5.71 – 8.86	-5.3
2	A	53	TRP	HZ2	5.65	5.71 – 8.86	-5.2

7.2.5 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	3353
Intra-residue ($ i-j =0$)	724
Sequential ($ i-j =1$)	631
Medium range ($ i-j >1$ and $ i-j <5$)	894
Long range ($ i-j \geq 5$)	923
Inter-chain	55
Hydrogen bond restraints	126
Disulfide bond restraints	0
Total dihedral-angle restraints	264
Number of unmapped restraints	0
Number of restraints per residue	21.3
Number of long range restraints per residue ¹	5.4

¹Long range hydrogen bonds and disulfide bonds are counted as long range restraints while calculating the number of long range restraints per residue

8.2 Residual restraint violations

This section provides the overview of the restraint violations analysis. The violations are binned as small, medium and large violations based on its absolute value. Average number of violations per model is calculated by dividing the total number of violations in each bin by the size of the ensemble.

8.2.1 Average number of distance violations per model

Distance violations less than 0.1 Å are not included in the calculation.

Bins (Å)	Average number of violations per model	Max (Å)
0.1-0.2 (Small)	1.6	0.19
0.2-0.5 (Medium)	5.7	0.5
>0.5 (Large)	42.3	4.21

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

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

Bins (°)	Average number of violations per model	Max (°)
1.0-10.0 (Small)	5.0	3.49
10.0-20.0 (Medium)	None	None
>20.0 (Large)	None	None

9 Distance violation analysis ⓘ

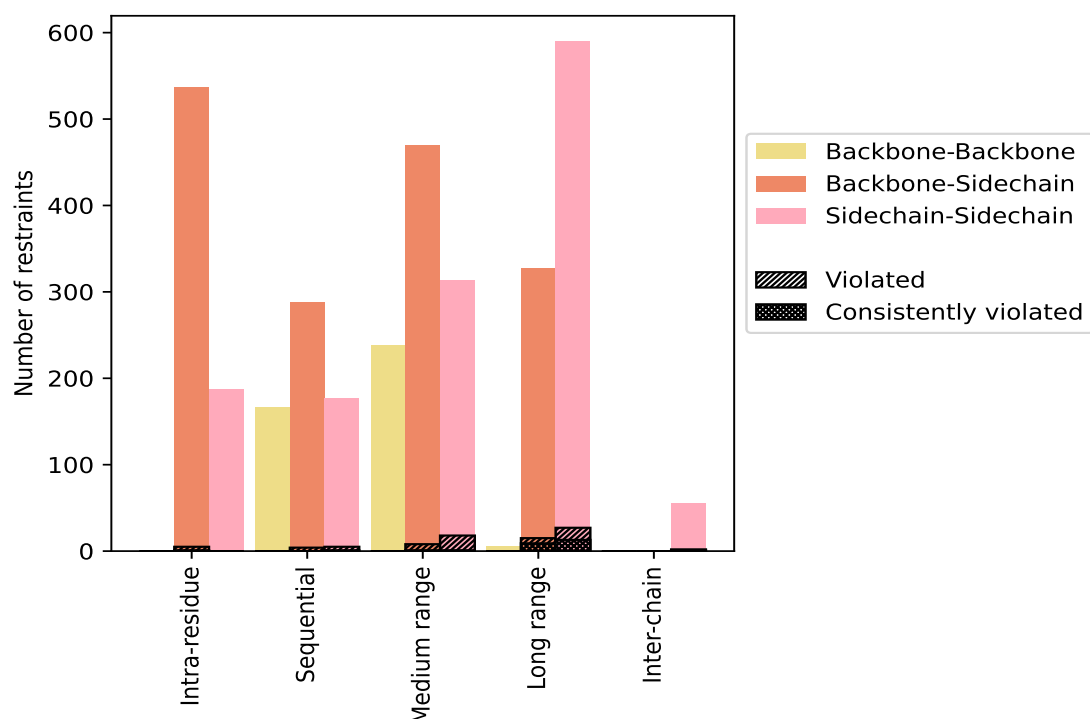
9.1 Summary of distance violations ⓘ

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 ($i-j =0$)	724	21.6	5	0.7	0.1	1	0.1	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	537	16.0	5	0.9	0.1	1	0.2	0.0
Sidechain-Sidechain	187	5.6	0	0.0	0.0	0	0.0	0.0
Sequential ($i-j =1$)	631	18.8	9	1.4	0.3	1	0.2	0.0
Backbone-Backbone	166	5.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	288	8.6	4	1.4	0.1	0	0.0	0.0
Sidechain-Sidechain	177	5.3	5	2.8	0.1	1	0.6	0.0
Medium range ($i-j >1$ & $i-j <5$)	894	26.7	26	2.9	0.8	2	0.2	0.1
Backbone-Backbone	238	7.1	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	343	10.2	8	2.3	0.2	1	0.3	0.0
Sidechain-Sidechain	313	9.3	18	5.8	0.5	1	0.3	0.0
Long range ($i-j \geq 5$)	923	27.5	42	4.6	1.3	22	2.4	0.7
Backbone-Backbone	6	0.2	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	327	9.8	15	4.6	0.4	9	2.8	0.3
Sidechain-Sidechain	590	17.6	27	4.6	0.8	13	2.2	0.4
Inter-chain	55	1.6	2	3.6	0.1	1	1.8	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	55	1.6	2	3.6	0.1	1	1.8	0.0
Hydrogen bond	126	3.8	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	3353	100.0	84	2.5	2.5	27	0.8	0.8
Backbone-Backbone	410	12.2	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	1621	48.3	32	2.0	1.0	11	0.7	0.3
Sidechain-Sidechain	1322	39.4	52	3.9	1.6	16	1.2	0.5

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	1	4	13	36	2	56	1.69	4.14	1.09	1.58
2	3	3	13	36	2	57	1.64	4.15	1.03	1.53
3	1	2	10	35	2	50	1.76	3.99	0.98	1.64
4	3	6	6	25	2	42	1.63	4.09	1.07	1.45
5	3	2	21	35	2	63	1.55	4.19	1.09	1.22
6	3	4	4	25	2	38	1.53	4.03	1.05	1.22
7	4	2	14	25	2	47	1.57	4.05	1.09	1.23
8	1	3	3	26	2	35	1.53	4.03	1.12	1.2
9	1	1	10	35	2	49	1.79	4.08	1.06	1.59
10	1	3	11	32	1	48	1.78	4.16	0.95	1.63

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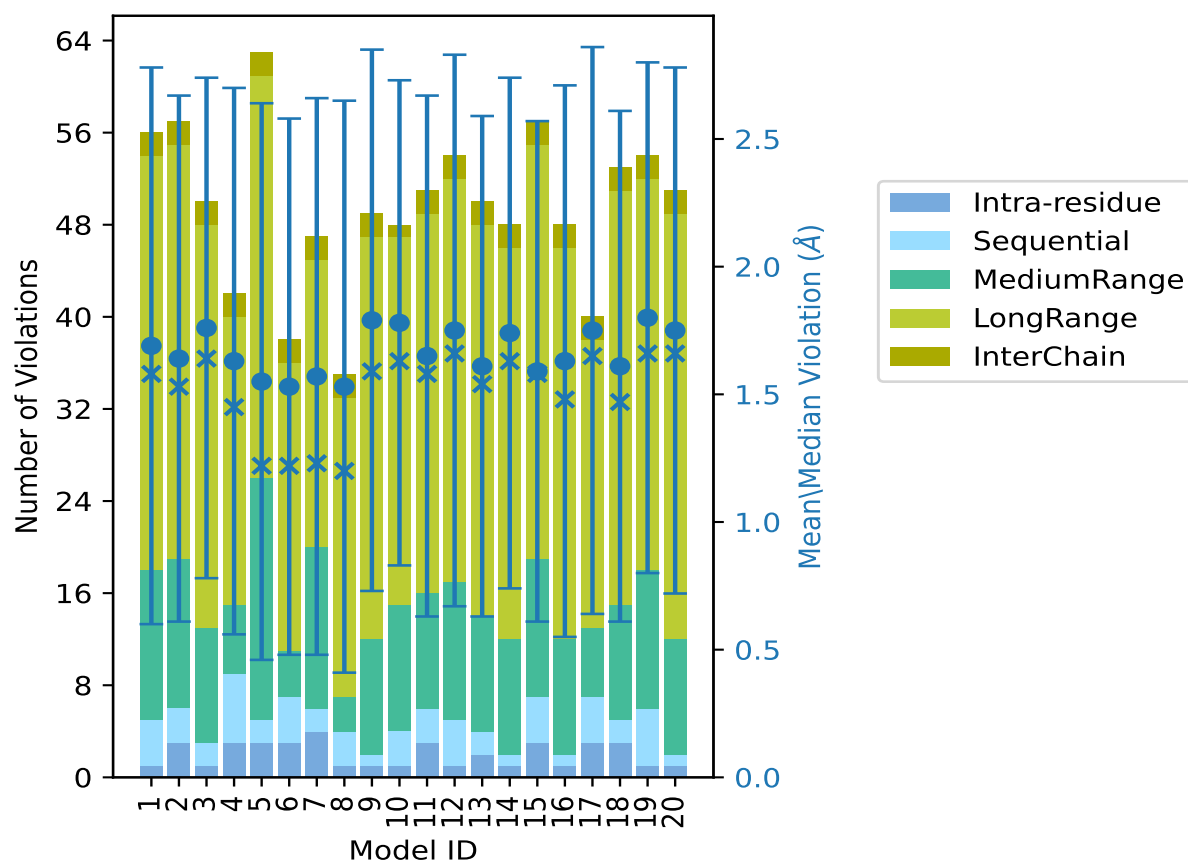
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD ⁶ (Å)	Median (Å)
	IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total				
11	3	3	10	33	2	51	1.65	4.11	1.02	1.58
12	1	4	12	35	2	54	1.75	4.13	1.08	1.66
13	2	2	10	34	2	50	1.61	3.87	0.98	1.54
14	1	1	10	34	2	48	1.74	4.21	1.0	1.63
15	3	4	12	36	2	57	1.59	3.9	0.98	1.58
16	1	1	10	34	2	48	1.63	4.14	1.08	1.48
17	3	4	6	25	2	40	1.75	4.12	1.11	1.65
18	3	2	10	36	2	53	1.61	4.0	1.0	1.47
19	1	5	12	34	2	54	1.8	4.13	1.0	1.66
20	1	1	10	37	2	51	1.75	4.15	1.03	1.66

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

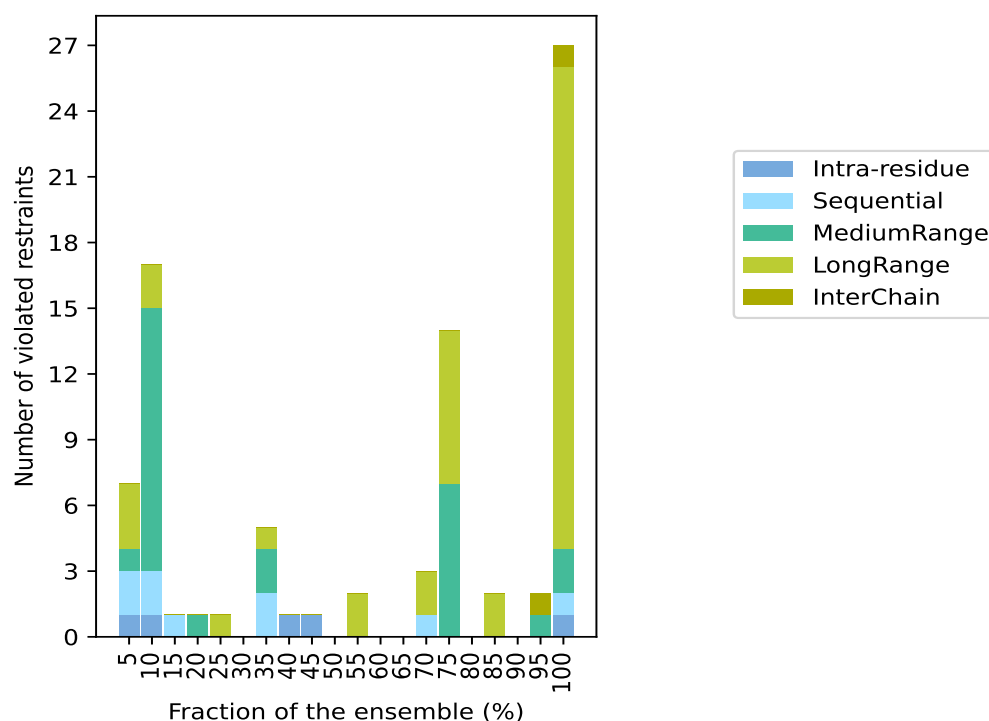
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 3143(IR:719, SQ:622, MR:868, LR:881, IC:53) restraints are 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	%
1	2	1	3	0	7	1	5.0
1	2	12	2	0	17	2	10.0
0	1	0	0	0	1	3	15.0
0	0	1	0	0	1	4	20.0
0	0	0	1	0	1	5	25.0
0	0	0	0	0	0	6	30.0
0	2	2	1	0	5	7	35.0
1	0	0	0	0	1	8	40.0
1	0	0	0	0	1	9	45.0
0	0	0	0	0	0	10	50.0
0	0	0	2	0	2	11	55.0
0	0	0	0	0	0	12	60.0
0	0	0	0	0	0	13	65.0
0	1	0	2	0	3	14	70.0
0	0	7	7	0	14	15	75.0
0	0	0	0	0	0	16	80.0
0	0	0	2	0	2	17	85.0
0	0	0	0	0	0	18	90.0
0	0	1	0	1	2	19	95.0
1	1	2	22	1	27	20	100.0

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

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

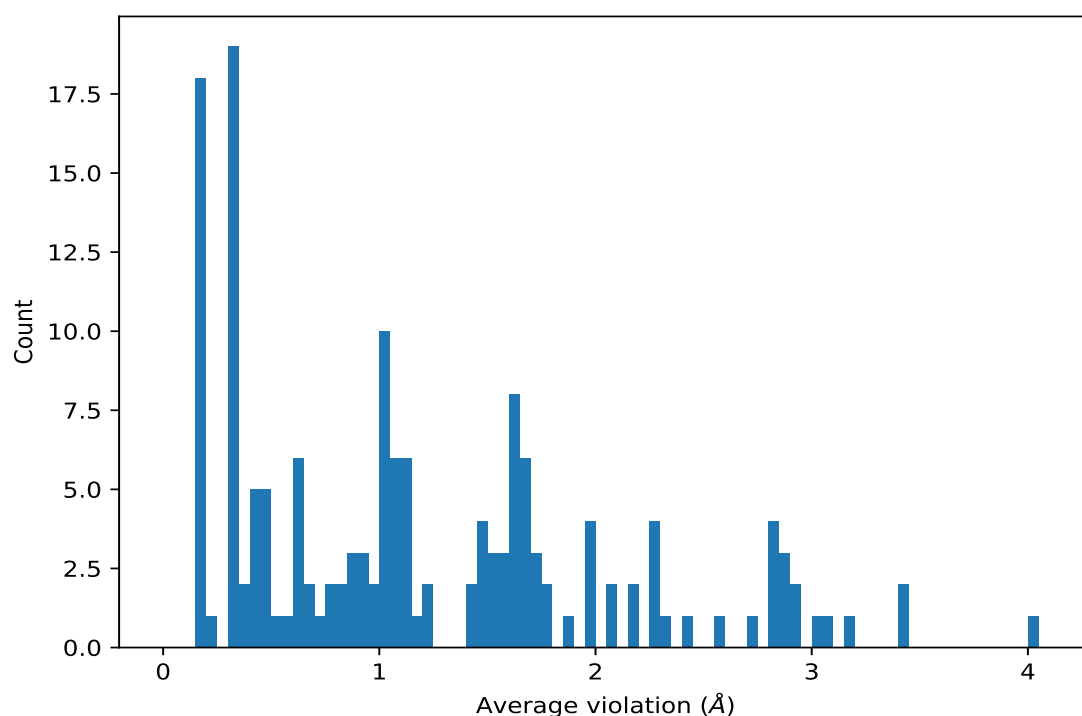
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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

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

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



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

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

Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,1329)	1:11:A:LEU:H	1:85:A:TYR:HE1	20	4.03	0.08	4.03
(1,1249)	1:12:A:THR:H	1:85:A:TYR:HD1	20	3.4	0.17	3.38
(1,1275)	1:62:A:TYR:HE1	1:136:A:LEU:HG	20	3.16	0.53	3.3
(1,1311)	1:62:A:TYR:HD1	1:133:A:ALA:HA	20	3.08	0.33	3.16
(1,1148)	1:11:A:LEU:HB2	1:85:A:TYR:HE1	20	3.02	0.15	3.03
(1,1348)	1:14:A:VAL:H	1:85:A:TYR:HE1	20	2.93	0.18	2.92
(1,1154)	1:12:A:THR:H	1:85:A:TYR:HE1	20	2.93	0.19	2.94
(1,1094)	1:25:A:PHE:HE1	1:105:A:MET:HA	20	2.71	0.16	2.72
(1,1066)	1:11:A:LEU:HA	1:85:A:TYR:HE1	20	2.57	0.12	2.58
(1,1142)	1:62:A:TYR:HD1	1:136:A:LEU:HG	20	2.25	0.47	2.38
(1,1357)	1:25:A:PHE:HD2	1:101:A:GLY:HA2	20	2.06	0.37	1.96
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG21	20	1.71	0.18	1.72
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG22	20	1.71	0.18	1.72
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG23	20	1.71	0.18	1.72
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG21	20	1.67	0.17	1.65
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG22	20	1.67	0.17	1.65

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG23	20	1.67	0.17	1.65
(1,1065)	1:118:A:VAL:HG21	1:140:A:TYR:HD1	20	1.65	0.21	1.66
(1,1065)	1:118:A:VAL:HG22	1:140:A:TYR:HD1	20	1.65	0.21	1.66
(1,1065)	1:118:A:VAL:HG23	1:140:A:TYR:HD1	20	1.65	0.21	1.66
(1,919)	1:11:A:LEU:HD21	1:85:A:TYR:HD1	20	1.63	0.15	1.63
(1,919)	1:11:A:LEU:HD22	1:85:A:TYR:HD1	20	1.63	0.15	1.63
(1,919)	1:11:A:LEU:HD23	1:85:A:TYR:HD1	20	1.63	0.15	1.63
(1,2764)	1:84:A:LEU:HD21	1:85:A:TYR:HD2	20	1.56	0.4	1.72
(1,2764)	1:84:A:LEU:HD22	1:85:A:TYR:HD2	20	1.56	0.4	1.72
(1,2764)	1:84:A:LEU:HD23	1:85:A:TYR:HD2	20	1.56	0.4	1.72
(1,981)	1:119:A:ALA:HB1	1:140:A:TYR:HD1	20	1.48	0.31	1.44
(1,981)	1:119:A:ALA:HB2	1:140:A:TYR:HD1	20	1.48	0.31	1.44
(1,981)	1:119:A:ALA:HB3	1:140:A:TYR:HD1	20	1.48	0.31	1.44
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB1	20	1.14	0.39	1.1
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB2	20	1.14	0.39	1.1
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB3	20	1.14	0.39	1.1
(1,1340)	1:11:A:LEU:HD21	1:85:A:TYR:HE1	20	1.08	0.14	1.1
(1,1340)	1:11:A:LEU:HD22	1:85:A:TYR:HE1	20	1.08	0.14	1.1
(1,1340)	1:11:A:LEU:HD23	1:85:A:TYR:HE1	20	1.08	0.14	1.1
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	20	1.02	0.12	1.02
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	20	1.02	0.12	1.02
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	20	1.02	0.12	1.02
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	20	1.02	0.12	1.02
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	20	1.02	0.12	1.02
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	20	1.02	0.12	1.02
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	20	1.01	0.39	1.0
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	20	1.01	0.39	1.0
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	20	1.01	0.39	1.0
(1,2128)	1:62:A:TYR:HE2	1:65:A:TYR:HB2	20	0.96	0.26	0.99
(1,2121)	1:140:A:TYR:HD2	1:142:A:ALA:H	20	0.91	0.16	0.9
(1,1144)	1:25:A:PHE:HD2	1:103:A:ARG:H	20	0.86	0.22	0.8
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD11	20	0.61	0.17	0.6
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD12	20	0.61	0.17	0.6
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD13	20	0.61	0.17	0.6
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD21	20	0.61	0.17	0.6
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD22	20	0.61	0.17	0.6
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD23	20	0.61	0.17	0.6
(1,685)	1:140:A:TYR:H	1:140:A:TYR:HE2	20	0.46	0.15	0.42
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	20	0.32	0.02	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	20	0.32	0.02	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	20	0.32	0.02	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	20	0.32	0.02	0.33

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	20	0.32	0.02	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	20	0.32	0.02	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	20	0.32	0.02	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	20	0.32	0.02	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	20	0.32	0.02	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	20	0.32	0.02	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	20	0.32	0.02	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	20	0.32	0.02	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	20	0.32	0.02	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	20	0.32	0.02	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	20	0.32	0.02	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	20	0.32	0.02	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	20	0.32	0.02	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	20	0.32	0.02	0.33
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD11	19	0.43	0.16	0.44
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD12	19	0.43	0.16	0.44
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD13	19	0.43	0.16	0.44
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	19	0.16	0.03	0.17
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	19	0.16	0.03	0.17
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	19	0.16	0.03	0.17
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	19	0.16	0.03	0.17
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	19	0.16	0.03	0.17
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	19	0.16	0.03	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	19	0.16	0.03	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	19	0.16	0.03	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	19	0.16	0.03	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	19	0.16	0.03	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	19	0.16	0.03	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	19	0.16	0.03	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	19	0.16	0.03	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	19	0.16	0.03	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	19	0.16	0.03	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	19	0.16	0.03	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	19	0.16	0.03	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	19	0.16	0.03	0.17
(1,1466)	1:85:A:TYR:HE2	1:118:A:VAL:HA	17	0.71	0.3	0.61
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	17	0.49	0.42	0.46
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	17	0.49	0.42	0.46
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	17	0.49	0.42	0.46
(1,1100)	1:34:A:TYR:HE2	1:154:A:VAL:HB	15	2.88	0.2	2.83
(1,2152)	1:34:A:TYR:HD2	1:37:A:LEU:HA	15	2.85	0.13	2.91
(1,1372)	1:34:A:TYR:HE2	1:39:A:LYS:HA	15	2.85	0.27	2.89

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Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG21	15	2.82	0.14	2.87
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG22	15	2.82	0.14	2.87
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG23	15	2.82	0.14	2.87
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG11	15	2.28	0.14	2.29
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG12	15	2.28	0.14	2.29
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG13	15	2.28	0.14	2.29
(1,975)	1:34:A:TYR:HE2	1:39:A:LYS:HG3	15	2.08	0.41	2.04
(1,1809)	1:31:A:LEU:HD21	1:34:A:TYR:HE1	15	1.96	0.13	1.91
(1,1809)	1:31:A:LEU:HD22	1:34:A:TYR:HE1	15	1.96	0.13	1.91
(1,1809)	1:31:A:LEU:HD23	1:34:A:TYR:HE1	15	1.96	0.13	1.91
(1,1090)	1:34:A:TYR:HD2	1:39:A:LYS:HB2	15	1.79	0.51	1.87
(1,2256)	1:34:A:TYR:HE2	1:37:A:LEU:HB3	15	1.6	0.23	1.65
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG11	15	1.53	0.15	1.54
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG12	15	1.53	0.15	1.54
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG13	15	1.53	0.15	1.54
(1,1976)	1:34:A:TYR:HD2	1:37:A:LEU:HB3	15	1.46	0.14	1.5
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD11	15	1.13	0.25	1.13
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD12	15	1.13	0.25	1.13
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD13	15	1.13	0.25	1.13
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD21	15	1.05	0.22	1.03
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD22	15	1.05	0.22	1.03
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD23	15	1.05	0.22	1.03
(1,2037)	1:34:A:TYR:HD2	1:37:A:LEU:H	15	0.79	0.12	0.82
(1,1240)	1:20:A:PHE:HE2	1:51:A:PRO:HA	14	3.42	1.35	4.11
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD21	14	1.63	0.81	1.96
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD22	14	1.63	0.81	1.96
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD23	14	1.63	0.81	1.96
(1,1371)	1:34:A:TYR:HD2	1:39:A:LYS:HG2	14	0.39	0.15	0.38
(1,1007)	1:34:A:TYR:HE2	1:39:A:LYS:HE2	11	1.15	0.63	1.02
(1,1343)	1:12:A:THR:HA	1:85:A:TYR:HE1	11	0.35	0.12	0.31
(1,277)	1:99:A:PHE:H	1:99:A:PHE:HD2	9	0.31	0.08	0.33
(1,624)	1:99:A:PHE:H	1:99:A:PHE:HE2	8	0.43	0.15	0.43
(1,1839)	1:65:A:TYR:HD1	1:69:A:LYS:HB2	7	2.84	0.28	2.86
(1,2640)	1:65:A:TYR:HD1	1:66:A:ILE:HG13	7	1.98	0.1	2.01
(1,2773)	1:65:A:TYR:HD1	1:66:A:ILE:HA	7	0.84	0.05	0.84
(1,1759)	1:65:A:TYR:HE1	1:69:A:LYS:HG2	7	0.81	0.27	0.78
(1,1082)	1:34:A:TYR:HD2	1:39:A:LYS:HG3	7	0.45	0.19	0.39
(1,1008)	1:34:A:TYR:HE2	1:39:A:LYS:HE3	5	0.97	0.57	0.94
(1,1845)	1:65:A:TYR:HE1	1:69:A:LYS:HE3	4	2.32	0.34	2.46
(1,2642)	1:140:A:TYR:HD2	1:141:A:LEU:H	3	0.22	0.11	0.17
(1,1867)	1:135:A:ARG:HG3	1:138:A:TYR:HE2	2	2.4	1.46	2.4
(1,1791)	1:135:A:ARG:HD2	1:138:A:TYR:HE2	2	2.16	0.08	2.16

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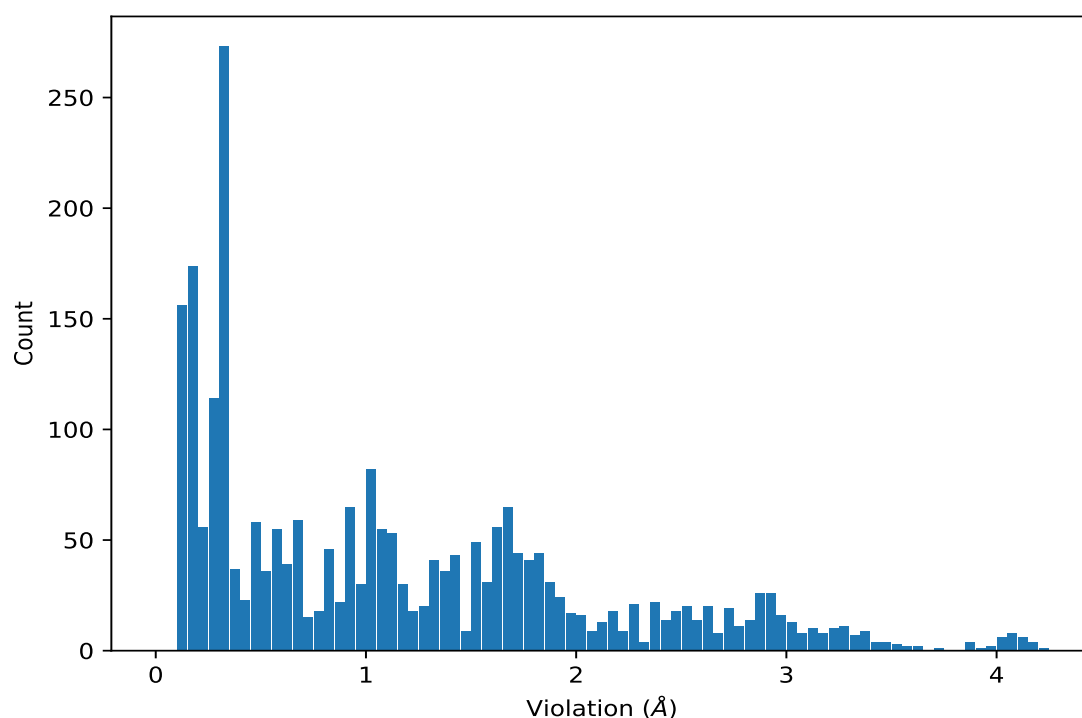
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(1,1791)	1:135:A:ARG:HD3	1:138:A:TYR:HE2	2	2.16	0.08	2.16
(1,1866)	1:135:A:ARG:HG2	1:138:A:TYR:HE2	2	1.88	0.32	1.88
(1,2900)	1:23:A:ALA:H	1:24:A:TYR:HD1	2	1.75	0.01	1.75
(1,1955)	1:135:A:ARG:HG3	1:138:A:TYR:HD2	2	1.62	1.48	1.62
(1,1788)	1:135:A:ARG:HG2	1:138:A:TYR:HD2	2	1.42	0.93	1.42
(1,1788)	1:135:A:ARG:HG3	1:138:A:TYR:HD2	2	1.42	0.93	1.42
(1,1748)	1:135:A:ARG:HG2	1:138:A:TYR:HE2	2	1.23	0.7	1.23
(1,1748)	1:135:A:ARG:HG3	1:138:A:TYR:HE2	2	1.23	0.7	1.23
(1,2440)	1:138:A:TYR:HD1	1:142:A:ALA:H	2	1.02	0.11	1.02
(1,1954)	1:135:A:ARG:HG2	1:138:A:TYR:HD2	2	0.94	0.8	0.94
(1,1921)	1:24:A:TYR:HD2	1:27:A:ARG:HD2	2	0.92	0.01	0.92
(1,2986)	1:24:A:TYR:HE1	1:25:A:PHE:HB2	2	0.87	0.11	0.87
(1,2075)	1:135:A:ARG:HA	1:138:A:TYR:HE2	2	0.86	0.05	0.86
(1,2437)	1:136:A:LEU:HA	1:138:A:TYR:HD2	2	0.75	0.11	0.75
(1,927)	1:34:A:TYR:HE2	1:39:A:LYS:HE2	2	0.65	0.1	0.65
(1,927)	1:34:A:TYR:HE2	1:39:A:LYS:HE3	2	0.65	0.1	0.65
(1,2035)	1:135:A:ARG:HA	1:138:A:TYR:HD2	2	0.56	0.02	0.56
(1,680)	1:138:A:TYR:H	1:138:A:TYR:HE2	2	0.54	0.02	0.54
(1,1359)	1:25:A:PHE:HD2	1:103:A:ARG:HA	2	0.44	0.11	0.44

¹Number of violated models, ²Standard deviation

9.5 All violated distance restraints [i](#)

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

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



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

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

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1240)	1:20:A:PHE:HE2	1:51:A:PRO:HA	14	4.21
(1,1240)	1:20:A:PHE:HE2	1:51:A:PRO:HA	5	4.19
(1,1329)	1:11:A:LEU:H	1:85:A:TYR:HE1	10	4.16
(1,1329)	1:11:A:LEU:H	1:85:A:TYR:HE1	2	4.15
(1,1240)	1:20:A:PHE:HE2	1:51:A:PRO:HA	20	4.15
(1,1329)	1:11:A:LEU:H	1:85:A:TYR:HE1	16	4.14
(1,1240)	1:20:A:PHE:HE2	1:51:A:PRO:HA	1	4.14
(1,1240)	1:20:A:PHE:HE2	1:51:A:PRO:HA	12	4.13
(1,1240)	1:20:A:PHE:HE2	1:51:A:PRO:HA	19	4.13
(1,1240)	1:20:A:PHE:HE2	1:51:A:PRO:HA	17	4.12
(1,1329)	1:11:A:LEU:H	1:85:A:TYR:HE1	11	4.11
(1,1329)	1:11:A:LEU:H	1:85:A:TYR:HE1	4	4.09
(1,1329)	1:11:A:LEU:H	1:85:A:TYR:HE1	5	4.09
(1,1240)	1:20:A:PHE:HE2	1:51:A:PRO:HA	16	4.09
(1,1240)	1:20:A:PHE:HE2	1:51:A:PRO:HA	9	4.08
(1,1329)	1:11:A:LEU:H	1:85:A:TYR:HE1	1	4.07

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1329)	1:11:A:LEU:H	1:85:A:TYR:HE1	12	4.07
(1,1240)	1:20:A:PHE:HE2	1:51:A:PRO:HA	4	4.07
(1,1329)	1:11:A:LEU:H	1:85:A:TYR:HE1	7	4.05
(1,1329)	1:11:A:LEU:H	1:85:A:TYR:HE1	6	4.03
(1,1329)	1:11:A:LEU:H	1:85:A:TYR:HE1	8	4.03
(1,1329)	1:11:A:LEU:H	1:85:A:TYR:HE1	9	4.01
(1,1329)	1:11:A:LEU:H	1:85:A:TYR:HE1	17	4.0
(1,1329)	1:11:A:LEU:H	1:85:A:TYR:HE1	18	4.0
(1,1329)	1:11:A:LEU:H	1:85:A:TYR:HE1	19	4.0
(1,1329)	1:11:A:LEU:H	1:85:A:TYR:HE1	3	3.99
(1,1240)	1:20:A:PHE:HE2	1:51:A:PRO:HA	3	3.95
(1,1329)	1:11:A:LEU:H	1:85:A:TYR:HE1	14	3.92
(1,1329)	1:11:A:LEU:H	1:85:A:TYR:HE1	15	3.9
(1,1329)	1:11:A:LEU:H	1:85:A:TYR:HE1	20	3.9
(1,1329)	1:11:A:LEU:H	1:85:A:TYR:HE1	13	3.87
(1,1867)	1:135:A:ARG:HG3	1:138:A:TYR:HE2	7	3.85
(1,1249)	1:12:A:THR:H	1:85:A:TYR:HD1	2	3.73
(1,1249)	1:12:A:THR:H	1:85:A:TYR:HD1	10	3.63
(1,1249)	1:12:A:THR:H	1:85:A:TYR:HD1	12	3.62
(1,1249)	1:12:A:THR:H	1:85:A:TYR:HD1	16	3.59
(1,1249)	1:12:A:THR:H	1:85:A:TYR:HD1	7	3.58
(1,1249)	1:12:A:THR:H	1:85:A:TYR:HD1	5	3.53
(1,1311)	1:62:A:TYR:HD1	1:133:A:ALA:HA	17	3.52
(1,1249)	1:12:A:THR:H	1:85:A:TYR:HD1	1	3.51
(1,1311)	1:62:A:TYR:HD1	1:133:A:ALA:HA	2	3.49
(1,1311)	1:62:A:TYR:HD1	1:133:A:ALA:HA	4	3.47
(1,1275)	1:62:A:TYR:HE1	1:136:A:LEU:HG	9	3.47
(1,1311)	1:62:A:TYR:HD1	1:133:A:ALA:HA	19	3.46
(1,1249)	1:12:A:THR:H	1:85:A:TYR:HD1	8	3.44
(1,1249)	1:12:A:THR:H	1:85:A:TYR:HD1	9	3.44
(1,1275)	1:62:A:TYR:HE1	1:136:A:LEU:HG	5	3.42
(1,1275)	1:62:A:TYR:HE1	1:136:A:LEU:HG	2	3.41
(1,1311)	1:62:A:TYR:HD1	1:133:A:ALA:HA	8	3.4
(1,1275)	1:62:A:TYR:HE1	1:136:A:LEU:HG	1	3.4
(1,1249)	1:12:A:THR:H	1:85:A:TYR:HD1	13	3.4
(1,1275)	1:62:A:TYR:HE1	1:136:A:LEU:HG	17	3.37
(1,1249)	1:12:A:THR:H	1:85:A:TYR:HD1	4	3.37
(1,1249)	1:12:A:THR:H	1:85:A:TYR:HD1	20	3.37
(1,1275)	1:62:A:TYR:HE1	1:136:A:LEU:HG	12	3.36
(1,1275)	1:62:A:TYR:HE1	1:136:A:LEU:HG	18	3.36
(1,1311)	1:62:A:TYR:HD1	1:133:A:ALA:HA	12	3.35
(1,1311)	1:62:A:TYR:HD1	1:133:A:ALA:HA	5	3.34

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1275)	1:62:A:TYR:HE1	1:136:A:LEU:HG	14	3.33
(1,1249)	1:12:A:THR:H	1:85:A:TYR:HD1	18	3.33
(1,1275)	1:62:A:TYR:HE1	1:136:A:LEU:HG	19	3.32
(1,1154)	1:12:A:THR:H	1:85:A:TYR:HE1	2	3.32
(1,1275)	1:62:A:TYR:HE1	1:136:A:LEU:HG	7	3.31
(1,1148)	1:11:A:LEU:HB2	1:85:A:TYR:HE1	2	3.31
(1,1311)	1:62:A:TYR:HD1	1:133:A:ALA:HA	9	3.3
(1,1275)	1:62:A:TYR:HE1	1:136:A:LEU:HG	6	3.3
(1,1275)	1:62:A:TYR:HE1	1:136:A:LEU:HG	8	3.3
(1,1275)	1:62:A:TYR:HE1	1:136:A:LEU:HG	10	3.3
(1,1275)	1:62:A:TYR:HE1	1:136:A:LEU:HG	11	3.29
(1,1249)	1:12:A:THR:H	1:85:A:TYR:HD1	11	3.29
(1,1249)	1:12:A:THR:H	1:85:A:TYR:HD1	19	3.29
(1,1275)	1:62:A:TYR:HE1	1:136:A:LEU:HG	15	3.27
(1,1148)	1:11:A:LEU:HB2	1:85:A:TYR:HE1	10	3.26
(1,1249)	1:12:A:THR:H	1:85:A:TYR:HD1	3	3.25
(1,1249)	1:12:A:THR:H	1:85:A:TYR:HD1	6	3.25
(1,1148)	1:11:A:LEU:HB2	1:85:A:TYR:HE1	16	3.24
(1,1100)	1:34:A:TYR:HE2	1:154:A:VAL:HB	13	3.24
(1,1372)	1:34:A:TYR:HE2	1:39:A:LYS:HA	20	3.23
(1,1275)	1:62:A:TYR:HE1	1:136:A:LEU:HG	20	3.23
(1,1249)	1:12:A:THR:H	1:85:A:TYR:HD1	17	3.23
(1,1311)	1:62:A:TYR:HD1	1:133:A:ALA:HA	11	3.22
(1,1275)	1:62:A:TYR:HE1	1:136:A:LEU:HG	3	3.22
(1,1100)	1:34:A:TYR:HE2	1:154:A:VAL:HB	12	3.22
(1,1148)	1:11:A:LEU:HB2	1:85:A:TYR:HE1	11	3.21
(1,1348)	1:14:A:VAL:H	1:85:A:TYR:HE1	10	3.2
(1,1275)	1:62:A:TYR:HE1	1:136:A:LEU:HG	13	3.19
(1,1154)	1:12:A:THR:H	1:85:A:TYR:HE1	12	3.19
(1,1372)	1:34:A:TYR:HE2	1:39:A:LYS:HA	9	3.18
(1,1249)	1:12:A:THR:H	1:85:A:TYR:HD1	15	3.17
(1,1154)	1:12:A:THR:H	1:85:A:TYR:HE1	7	3.17
(1,1348)	1:14:A:VAL:H	1:85:A:TYR:HE1	1	3.16
(1,1311)	1:62:A:TYR:HD1	1:133:A:ALA:HA	6	3.16
(1,1100)	1:34:A:TYR:HE2	1:154:A:VAL:HB	16	3.16
(1,1311)	1:62:A:TYR:HD1	1:133:A:ALA:HA	1	3.15
(1,1348)	1:14:A:VAL:H	1:85:A:TYR:HE1	12	3.14
(1,1154)	1:12:A:THR:H	1:85:A:TYR:HE1	10	3.14
(1,1348)	1:14:A:VAL:H	1:85:A:TYR:HE1	5	3.13
(1,1955)	1:135:A:ARG:HG3	1:138:A:TYR:HD2	7	3.11
(1,1839)	1:65:A:TYR:HD1	1:69:A:LYS:HB2	17	3.11
(1,1348)	1:14:A:VAL:H	1:85:A:TYR:HE1	8	3.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1372)	1:34:A:TYR:HE2	1:39:A:LYS:HA	15	3.1
(1,1154)	1:12:A:THR:H	1:85:A:TYR:HE1	16	3.1
(1,1148)	1:11:A:LEU:HB2	1:85:A:TYR:HE1	4	3.1
(1,1372)	1:34:A:TYR:HE2	1:39:A:LYS:HA	5	3.09
(1,1839)	1:65:A:TYR:HD1	1:69:A:LYS:HB2	1	3.07
(1,1372)	1:34:A:TYR:HE2	1:39:A:LYS:HA	2	3.07
(1,1348)	1:14:A:VAL:H	1:85:A:TYR:HE1	18	3.07
(1,1249)	1:12:A:THR:H	1:85:A:TYR:HD1	14	3.07
(1,1148)	1:11:A:LEU:HB2	1:85:A:TYR:HE1	6	3.07
(1,1839)	1:65:A:TYR:HD1	1:69:A:LYS:HB2	19	3.06
(1,1148)	1:11:A:LEU:HB2	1:85:A:TYR:HE1	19	3.06
(1,1154)	1:12:A:THR:H	1:85:A:TYR:HE1	9	3.05
(1,1348)	1:14:A:VAL:H	1:85:A:TYR:HE1	9	3.04
(1,1148)	1:11:A:LEU:HB2	1:85:A:TYR:HE1	1	3.04
(1,1372)	1:34:A:TYR:HE2	1:39:A:LYS:HA	3	3.03
(1,1148)	1:11:A:LEU:HB2	1:85:A:TYR:HE1	5	3.03
(1,1148)	1:11:A:LEU:HB2	1:85:A:TYR:HE1	7	3.03
(1,1148)	1:11:A:LEU:HB2	1:85:A:TYR:HE1	12	3.03
(1,1100)	1:34:A:TYR:HE2	1:154:A:VAL:HB	19	3.03
(1,2152)	1:34:A:TYR:HD2	1:37:A:LEU:HA	10	3.02
(1,1154)	1:12:A:THR:H	1:85:A:TYR:HE1	5	3.02
(1,1311)	1:62:A:TYR:HD1	1:133:A:ALA:HA	16	3.01
(1,1154)	1:12:A:THR:H	1:85:A:TYR:HE1	1	3.0
(1,1094)	1:25:A:PHE:HE1	1:105:A:MET:HA	18	3.0
(1,2152)	1:34:A:TYR:HD2	1:37:A:LEU:HA	14	2.99
(1,1148)	1:11:A:LEU:HB2	1:85:A:TYR:HE1	17	2.99
(1,1348)	1:14:A:VAL:H	1:85:A:TYR:HE1	6	2.98
(1,1154)	1:12:A:THR:H	1:85:A:TYR:HE1	13	2.98
(1,1100)	1:34:A:TYR:HE2	1:154:A:VAL:HB	15	2.98
(1,1094)	1:25:A:PHE:HE1	1:105:A:MET:HA	7	2.98
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG21	12	2.98
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG22	12	2.98
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG23	12	2.98
(1,2152)	1:34:A:TYR:HD2	1:37:A:LEU:HA	19	2.96
(1,1154)	1:12:A:THR:H	1:85:A:TYR:HE1	8	2.96
(1,1148)	1:11:A:LEU:HB2	1:85:A:TYR:HE1	18	2.96
(1,2152)	1:34:A:TYR:HD2	1:37:A:LEU:HA	20	2.95
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG21	16	2.95
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG22	16	2.95
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG23	16	2.95
(1,2152)	1:34:A:TYR:HD2	1:37:A:LEU:HA	11	2.94
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG21	13	2.94

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG22	13	2.94
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG23	13	2.94
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG21	19	2.94
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG22	19	2.94
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG23	19	2.94
(1,2152)	1:34:A:TYR:HD2	1:37:A:LEU:HA	18	2.93
(1,1348)	1:14:A:VAL:H	1:85:A:TYR:HE1	4	2.93
(1,1348)	1:14:A:VAL:H	1:85:A:TYR:HE1	11	2.93
(1,1311)	1:62:A:TYR:HD1	1:133:A:ALA:HA	14	2.93
(1,1154)	1:12:A:THR:H	1:85:A:TYR:HE1	20	2.93
(1,2152)	1:34:A:TYR:HD2	1:37:A:LEU:HA	5	2.92
(1,1372)	1:34:A:TYR:HE2	1:39:A:LYS:HA	1	2.92
(1,1348)	1:14:A:VAL:H	1:85:A:TYR:HE1	17	2.92
(1,1094)	1:25:A:PHE:HE1	1:105:A:MET:HA	20	2.92
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG21	14	2.92
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG22	14	2.92
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG23	14	2.92
(1,2152)	1:34:A:TYR:HD2	1:37:A:LEU:HA	9	2.91
(1,1348)	1:14:A:VAL:H	1:85:A:TYR:HE1	2	2.91
(1,1348)	1:14:A:VAL:H	1:85:A:TYR:HE1	3	2.91
(1,1148)	1:11:A:LEU:HB2	1:85:A:TYR:HE1	8	2.91
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG21	9	2.91
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG22	9	2.91
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG23	9	2.91
(1,1148)	1:11:A:LEU:HB2	1:85:A:TYR:HE1	9	2.9
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG21	15	2.9
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG22	15	2.9
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG23	15	2.9
(1,1372)	1:34:A:TYR:HE2	1:39:A:LYS:HA	11	2.89
(1,1311)	1:62:A:TYR:HD1	1:133:A:ALA:HA	7	2.89
(1,1348)	1:14:A:VAL:H	1:85:A:TYR:HE1	20	2.88
(1,1154)	1:12:A:THR:H	1:85:A:TYR:HE1	4	2.88
(1,1148)	1:11:A:LEU:HB2	1:85:A:TYR:HE1	3	2.87
(1,1100)	1:34:A:TYR:HE2	1:154:A:VAL:HB	5	2.87
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG21	18	2.87
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG22	18	2.87
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG23	18	2.87
(1,2152)	1:34:A:TYR:HD2	1:37:A:LEU:HA	2	2.86
(1,1839)	1:65:A:TYR:HD1	1:69:A:LYS:HB2	2	2.86
(1,1839)	1:65:A:TYR:HD1	1:69:A:LYS:HB2	12	2.86
(1,1348)	1:14:A:VAL:H	1:85:A:TYR:HE1	14	2.86
(1,1154)	1:12:A:THR:H	1:85:A:TYR:HE1	18	2.86

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1094)	1:25:A:PHE:HE1	1:105:A:MET:HA	17	2.86
(1,1348)	1:14:A:VAL:H	1:85:A:TYR:HE1	15	2.85
(1,1327)	1:9:A:VAL:HA	1:57:A:TYR:HE1	18	2.85
(1,1148)	1:11:A:LEU:HB2	1:85:A:TYR:HE1	13	2.85
(1,1148)	1:11:A:LEU:HB2	1:85:A:TYR:HE1	14	2.85
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG21	11	2.85
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG22	11	2.85
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG23	11	2.85
(1,2152)	1:34:A:TYR:HD2	1:37:A:LEU:HA	3	2.84
(1,2152)	1:34:A:TYR:HD2	1:37:A:LEU:HA	12	2.84
(1,1348)	1:14:A:VAL:H	1:85:A:TYR:HE1	7	2.84
(1,1100)	1:34:A:TYR:HE2	1:154:A:VAL:HB	3	2.84
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG21	5	2.84
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG22	5	2.84
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG23	5	2.84
(1,1148)	1:11:A:LEU:HB2	1:85:A:TYR:HE1	15	2.83
(1,1100)	1:34:A:TYR:HE2	1:154:A:VAL:HB	14	2.83
(1,1094)	1:25:A:PHE:HE1	1:105:A:MET:HA	6	2.83
(1,1372)	1:34:A:TYR:HE2	1:39:A:LYS:HA	14	2.82
(1,1372)	1:34:A:TYR:HE2	1:39:A:LYS:HA	19	2.82
(1,1100)	1:34:A:TYR:HE2	1:154:A:VAL:HB	11	2.81
(1,1094)	1:25:A:PHE:HE1	1:105:A:MET:HA	12	2.81
(1,1148)	1:11:A:LEU:HB2	1:85:A:TYR:HE1	20	2.8
(1,1154)	1:12:A:THR:H	1:85:A:TYR:HE1	11	2.79
(1,1100)	1:34:A:TYR:HE2	1:154:A:VAL:HB	9	2.79
(1,1154)	1:12:A:THR:H	1:85:A:TYR:HE1	19	2.78
(1,1100)	1:34:A:TYR:HE2	1:154:A:VAL:HB	18	2.77
(1,1094)	1:25:A:PHE:HE1	1:105:A:MET:HA	10	2.77
(1,1154)	1:12:A:THR:H	1:85:A:TYR:HE1	3	2.76
(1,1348)	1:14:A:VAL:H	1:85:A:TYR:HE1	13	2.75
(1,1311)	1:62:A:TYR:HD1	1:133:A:ALA:HA	10	2.75
(1,1154)	1:12:A:THR:H	1:85:A:TYR:HE1	6	2.75
(1,1100)	1:34:A:TYR:HE2	1:154:A:VAL:HB	20	2.75
(1,2152)	1:34:A:TYR:HD2	1:37:A:LEU:HA	16	2.74
(1,1094)	1:25:A:PHE:HE1	1:105:A:MET:HA	8	2.74
(1,1094)	1:25:A:PHE:HE1	1:105:A:MET:HA	11	2.74
(1,1094)	1:25:A:PHE:HE1	1:105:A:MET:HA	1	2.73
(1,1066)	1:11:A:LEU:HA	1:85:A:TYR:HE1	17	2.73
(1,1154)	1:12:A:THR:H	1:85:A:TYR:HE1	17	2.72
(1,1066)	1:11:A:LEU:HA	1:85:A:TYR:HE1	3	2.72
(1,1100)	1:34:A:TYR:HE2	1:154:A:VAL:HB	10	2.71
(1,1066)	1:11:A:LEU:HA	1:85:A:TYR:HE1	4	2.71

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1066)	1:11:A:LEU:HA	1:85:A:TYR:HE1	11	2.71
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG21	20	2.71
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG22	20	2.71
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG23	20	2.71
(1,1094)	1:25:A:PHE:HE1	1:105:A:MET:HA	5	2.7
(1,1066)	1:11:A:LEU:HA	1:85:A:TYR:HE1	15	2.7
(1,975)	1:34:A:TYR:HE2	1:39:A:LYS:HG3	15	2.7
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG21	3	2.7
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG22	3	2.7
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG23	3	2.7
(1,1311)	1:62:A:TYR:HD1	1:133:A:ALA:HA	18	2.69
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG21	2	2.69
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG22	2	2.69
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG23	2	2.69
(1,1311)	1:62:A:TYR:HD1	1:133:A:ALA:HA	15	2.68
(1,1372)	1:34:A:TYR:HE2	1:39:A:LYS:HA	12	2.67
(1,1094)	1:25:A:PHE:HE1	1:105:A:MET:HA	13	2.67
(1,1066)	1:11:A:LEU:HA	1:85:A:TYR:HE1	6	2.66
(1,2152)	1:34:A:TYR:HD2	1:37:A:LEU:HA	15	2.65
(1,1839)	1:65:A:TYR:HD1	1:69:A:LYS:HB2	15	2.65
(1,1066)	1:11:A:LEU:HA	1:85:A:TYR:HE1	8	2.65
(1,1100)	1:34:A:TYR:HE2	1:154:A:VAL:HB	1	2.64
(1,1094)	1:25:A:PHE:HE1	1:105:A:MET:HA	4	2.64
(1,2152)	1:34:A:TYR:HD2	1:37:A:LEU:HA	1	2.63
(1,2152)	1:34:A:TYR:HD2	1:37:A:LEU:HA	13	2.63
(1,1154)	1:12:A:THR:H	1:85:A:TYR:HE1	15	2.63
(1,1094)	1:25:A:PHE:HE1	1:105:A:MET:HA	19	2.63
(1,1066)	1:11:A:LEU:HA	1:85:A:TYR:HE1	14	2.63
(1,975)	1:34:A:TYR:HE2	1:39:A:LYS:HG3	1	2.63
(1,1845)	1:65:A:TYR:HE1	1:69:A:LYS:HE3	19	2.61
(1,1066)	1:11:A:LEU:HA	1:85:A:TYR:HE1	1	2.61
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG21	10	2.61
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG22	10	2.61
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG23	10	2.61
(1,1311)	1:62:A:TYR:HD1	1:133:A:ALA:HA	20	2.6
(1,1154)	1:12:A:THR:H	1:85:A:TYR:HE1	14	2.6
(1,1066)	1:11:A:LEU:HA	1:85:A:TYR:HE1	5	2.6
(1,975)	1:34:A:TYR:HE2	1:39:A:LYS:HG3	3	2.6
(1,1372)	1:34:A:TYR:HE2	1:39:A:LYS:HA	13	2.59
(1,1372)	1:34:A:TYR:HE2	1:39:A:LYS:HA	18	2.59
(1,1142)	1:62:A:TYR:HD1	1:136:A:LEU:HG	9	2.59
(1,1311)	1:62:A:TYR:HD1	1:133:A:ALA:HA	3	2.58

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1094)	1:25:A:PHE:HE1	1:105:A:MET:HA	16	2.58
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD21	11	2.57
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD22	11	2.57
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD23	11	2.57
(1,1348)	1:14:A:VAL:H	1:85:A:TYR:HE1	16	2.57
(1,1066)	1:11:A:LEU:HA	1:85:A:TYR:HE1	18	2.57
(1,1094)	1:25:A:PHE:HE1	1:105:A:MET:HA	14	2.56
(1,1066)	1:11:A:LEU:HA	1:85:A:TYR:HE1	16	2.56
(1,1066)	1:11:A:LEU:HA	1:85:A:TYR:HE1	19	2.56
(1,1007)	1:34:A:TYR:HE2	1:39:A:LYS:HE2	20	2.56
(1,1090)	1:34:A:TYR:HD2	1:39:A:LYS:HB2	1	2.55
(1,1311)	1:62:A:TYR:HD1	1:133:A:ALA:HA	13	2.54
(1,1100)	1:34:A:TYR:HE2	1:154:A:VAL:HB	2	2.54
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG11	13	2.54
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG12	13	2.54
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG13	13	2.54
(1,1357)	1:25:A:PHE:HD2	1:101:A:GLY:HA2	2	2.53
(1,1142)	1:62:A:TYR:HD1	1:136:A:LEU:HG	5	2.53
(1,1094)	1:25:A:PHE:HE1	1:105:A:MET:HA	15	2.53
(1,1066)	1:11:A:LEU:HA	1:85:A:TYR:HE1	9	2.53
(1,1066)	1:11:A:LEU:HA	1:85:A:TYR:HE1	10	2.53
(1,1142)	1:62:A:TYR:HD1	1:136:A:LEU:HG	2	2.52
(1,1094)	1:25:A:PHE:HE1	1:105:A:MET:HA	9	2.51
(1,981)	1:119:A:ALA:HB1	1:140:A:TYR:HD1	20	2.51
(1,981)	1:119:A:ALA:HB2	1:140:A:TYR:HD1	20	2.51
(1,981)	1:119:A:ALA:HB3	1:140:A:TYR:HD1	20	2.51
(1,1094)	1:25:A:PHE:HE1	1:105:A:MET:HA	3	2.5
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG21	1	2.5
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG22	1	2.5
(1,908)	1:34:A:TYR:HE2	1:154:A:VAL:HG23	1	2.5
(1,1357)	1:25:A:PHE:HD2	1:101:A:GLY:HA2	5	2.49
(1,1348)	1:14:A:VAL:H	1:85:A:TYR:HE1	19	2.49
(1,1142)	1:62:A:TYR:HD1	1:136:A:LEU:HG	1	2.49
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG11	12	2.49
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG12	12	2.49
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG13	12	2.49
(1,1357)	1:25:A:PHE:HD2	1:101:A:GLY:HA2	4	2.48
(1,1142)	1:62:A:TYR:HD1	1:136:A:LEU:HG	17	2.48
(1,1845)	1:65:A:TYR:HE1	1:69:A:LYS:HE3	17	2.47
(1,1357)	1:25:A:PHE:HD2	1:101:A:GLY:HA2	13	2.47
(1,1357)	1:25:A:PHE:HD2	1:101:A:GLY:HA2	12	2.46
(1,1142)	1:62:A:TYR:HD1	1:136:A:LEU:HG	18	2.46

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1066)	1:11:A:LEU:HA	1:85:A:TYR:HE1	12	2.46
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	4	2.46
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	4	2.46
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	4	2.46
(1,1142)	1:62:A:TYR:HD1	1:136:A:LEU:HG	12	2.45
(1,1090)	1:34:A:TYR:HD2	1:39:A:LYS:HB2	15	2.45
(1,1845)	1:65:A:TYR:HE1	1:69:A:LYS:HE3	1	2.44
(1,1357)	1:25:A:PHE:HD2	1:101:A:GLY:HA2	9	2.44
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG11	19	2.44
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG12	19	2.44
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG13	19	2.44
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD21	12	2.43
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD22	12	2.43
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD23	12	2.43
(1,1357)	1:25:A:PHE:HD2	1:101:A:GLY:HA2	3	2.43
(1,1142)	1:62:A:TYR:HD1	1:136:A:LEU:HG	19	2.43
(1,1094)	1:25:A:PHE:HE1	1:105:A:MET:HA	2	2.43
(1,1066)	1:11:A:LEU:HA	1:85:A:TYR:HE1	20	2.43
(1,1372)	1:34:A:TYR:HE2	1:39:A:LYS:HA	10	2.42
(1,1066)	1:11:A:LEU:HA	1:85:A:TYR:HE1	7	2.42
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD21	17	2.4
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD22	17	2.4
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD23	17	2.4
(1,1066)	1:11:A:LEU:HA	1:85:A:TYR:HE1	2	2.4
(1,975)	1:34:A:TYR:HE2	1:39:A:LYS:HG3	9	2.4
(1,975)	1:34:A:TYR:HE2	1:39:A:LYS:HG3	20	2.4
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG11	16	2.4
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG12	16	2.4
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG13	16	2.4
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD21	6	2.39
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD22	6	2.39
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD23	6	2.39
(1,1357)	1:25:A:PHE:HD2	1:101:A:GLY:HA2	16	2.39
(1,1142)	1:62:A:TYR:HD1	1:136:A:LEU:HG	14	2.39
(1,1142)	1:62:A:TYR:HD1	1:136:A:LEU:HG	8	2.38
(1,1142)	1:62:A:TYR:HD1	1:136:A:LEU:HG	11	2.38
(1,1142)	1:62:A:TYR:HD1	1:136:A:LEU:HG	6	2.37
(1,1357)	1:25:A:PHE:HD2	1:101:A:GLY:HA2	19	2.36
(1,1142)	1:62:A:TYR:HD1	1:136:A:LEU:HG	7	2.36
(1,1788)	1:135:A:ARG:HG2	1:138:A:TYR:HD2	7	2.35
(1,1788)	1:135:A:ARG:HG3	1:138:A:TYR:HD2	7	2.35
(1,1142)	1:62:A:TYR:HD1	1:136:A:LEU:HG	10	2.35

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1142)	1:62:A:TYR:HD1	1:136:A:LEU:HG	15	2.33
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG11	20	2.33
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG12	20	2.33
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG13	20	2.33
(1,1372)	1:34:A:TYR:HE2	1:39:A:LYS:HA	16	2.3
(1,1090)	1:34:A:TYR:HD2	1:39:A:LYS:HB2	3	2.3
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG11	18	2.3
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG12	18	2.3
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG13	18	2.3
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG11	9	2.29
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG12	9	2.29
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG13	9	2.29
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG11	11	2.29
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG12	11	2.29
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG13	11	2.29
(1,1142)	1:62:A:TYR:HD1	1:136:A:LEU:HG	20	2.27
(1,1066)	1:11:A:LEU:HA	1:85:A:TYR:HE1	13	2.27
(1,975)	1:34:A:TYR:HE2	1:39:A:LYS:HG3	2	2.27
(1,1839)	1:65:A:TYR:HD1	1:69:A:LYS:HB2	4	2.26
(1,1809)	1:31:A:LEU:HD21	1:34:A:TYR:HE1	5	2.25
(1,1809)	1:31:A:LEU:HD22	1:34:A:TYR:HE1	5	2.25
(1,1809)	1:31:A:LEU:HD23	1:34:A:TYR:HE1	5	2.25
(1,1791)	1:135:A:ARG:HD2	1:138:A:TYR:HE2	5	2.25
(1,1791)	1:135:A:ARG:HD3	1:138:A:TYR:HE2	5	2.25
(1,1142)	1:62:A:TYR:HD1	1:136:A:LEU:HG	3	2.25
(1,1142)	1:62:A:TYR:HD1	1:136:A:LEU:HG	13	2.24
(1,1090)	1:34:A:TYR:HD2	1:39:A:LYS:HB2	20	2.22
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG11	10	2.22
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG12	10	2.22
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG13	10	2.22
(1,1866)	1:135:A:ARG:HG2	1:138:A:TYR:HE2	7	2.21
(1,975)	1:34:A:TYR:HE2	1:39:A:LYS:HG3	5	2.21
(1,1891)	1:100:A:PHE:HD2	1:102:A:ALA:H	10	2.2
(1,1090)	1:34:A:TYR:HD2	1:39:A:LYS:HB2	9	2.2
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG11	15	2.19
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG12	15	2.19
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG13	15	2.19
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG11	5	2.17
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG12	5	2.17
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG13	5	2.17
(1,1809)	1:31:A:LEU:HD21	1:34:A:TYR:HE1	18	2.16
(1,1809)	1:31:A:LEU:HD22	1:34:A:TYR:HE1	18	2.16

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1809)	1:31:A:LEU:HD23	1:34:A:TYR:HE1	18	2.16
(1,1809)	1:31:A:LEU:HD21	1:34:A:TYR:HE1	9	2.15
(1,1809)	1:31:A:LEU:HD22	1:34:A:TYR:HE1	9	2.15
(1,1809)	1:31:A:LEU:HD23	1:34:A:TYR:HE1	9	2.15
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG11	2	2.15
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG12	2	2.15
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG13	2	2.15
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG11	14	2.15
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG12	14	2.15
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG13	14	2.15
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	16	2.12
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	16	2.12
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	16	2.12
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD21	4	2.11
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD22	4	2.11
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD23	4	2.11
(1,1275)	1:62:A:TYR:HE1	1:136:A:LEU:HG	4	2.11
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG21	1	2.11
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG22	1	2.11
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG23	1	2.11
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG11	3	2.11
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG12	3	2.11
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG13	3	2.11
(1,1791)	1:135:A:ARG:HD2	1:138:A:TYR:HE2	7	2.08
(1,1791)	1:135:A:ARG:HD3	1:138:A:TYR:HE2	7	2.08
(1,2640)	1:65:A:TYR:HD1	1:66:A:ILE:HG13	19	2.07
(1,1090)	1:34:A:TYR:HD2	1:39:A:LYS:HB2	2	2.07
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG11	1	2.07
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG12	1	2.07
(1,888)	1:34:A:TYR:HE2	1:154:A:VAL:HG13	1	2.07
(1,2640)	1:65:A:TYR:HD1	1:66:A:ILE:HG13	1	2.06
(1,2640)	1:65:A:TYR:HD1	1:66:A:ILE:HG13	17	2.06
(1,2674)	1:100:A:PHE:HD2	1:101:A:GLY:HA3	10	2.04
(1,1809)	1:31:A:LEU:HD21	1:34:A:TYR:HE1	12	2.04
(1,1809)	1:31:A:LEU:HD22	1:34:A:TYR:HE1	12	2.04
(1,1809)	1:31:A:LEU:HD23	1:34:A:TYR:HE1	12	2.04
(1,975)	1:34:A:TYR:HE2	1:39:A:LYS:HG3	19	2.04
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD21	3	2.02
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD22	3	2.02
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD23	3	2.02
(1,1065)	1:118:A:VAL:HG21	1:140:A:TYR:HD1	20	2.02
(1,1065)	1:118:A:VAL:HG22	1:140:A:TYR:HD1	20	2.02

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1065)	1:118:A:VAL:HG23	1:140:A:TYR:HD1	20	2.02
(1,975)	1:34:A:TYR:HE2	1:39:A:LYS:HG3	11	2.02
(1,2640)	1:65:A:TYR:HD1	1:66:A:ILE:HG13	2	2.01
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG21	1	2.01
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG22	1	2.01
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG23	1	2.01
(1,2640)	1:65:A:TYR:HD1	1:66:A:ILE:HG13	15	1.99
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD21	10	1.98
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD22	10	1.98
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD23	10	1.98
(1,1065)	1:118:A:VAL:HG21	1:140:A:TYR:HD1	9	1.98
(1,1065)	1:118:A:VAL:HG22	1:140:A:TYR:HD1	9	1.98
(1,1065)	1:118:A:VAL:HG23	1:140:A:TYR:HD1	9	1.98
(1,1809)	1:31:A:LEU:HD21	1:34:A:TYR:HE1	15	1.97
(1,1809)	1:31:A:LEU:HD22	1:34:A:TYR:HE1	15	1.97
(1,1809)	1:31:A:LEU:HD23	1:34:A:TYR:HE1	15	1.97
(1,1357)	1:25:A:PHE:HD2	1:101:A:GLY:HA2	1	1.97
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG21	17	1.97
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG22	17	1.97
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG23	17	1.97
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG21	17	1.96
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG22	17	1.96
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG23	17	1.96
(1,2256)	1:34:A:TYR:HE2	1:37:A:LEU:HB3	14	1.94
(1,1357)	1:25:A:PHE:HD2	1:101:A:GLY:HA2	8	1.94
(1,1357)	1:25:A:PHE:HD2	1:101:A:GLY:HA2	17	1.94
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD21	5	1.93
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD22	5	1.93
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD23	5	1.93
(1,1748)	1:135:A:ARG:HG2	1:138:A:TYR:HE2	7	1.93
(1,1748)	1:135:A:ARG:HG3	1:138:A:TYR:HE2	7	1.93
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD21	15	1.92
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD22	15	1.92
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD23	15	1.92
(1,1809)	1:31:A:LEU:HD21	1:34:A:TYR:HE1	10	1.92
(1,1809)	1:31:A:LEU:HD22	1:34:A:TYR:HE1	10	1.92
(1,1809)	1:31:A:LEU:HD23	1:34:A:TYR:HE1	10	1.92
(1,1809)	1:31:A:LEU:HD21	1:34:A:TYR:HE1	11	1.92
(1,1809)	1:31:A:LEU:HD22	1:34:A:TYR:HE1	11	1.92
(1,1809)	1:31:A:LEU:HD23	1:34:A:TYR:HE1	11	1.92
(1,1090)	1:34:A:TYR:HD2	1:39:A:LYS:HB2	5	1.92
(1,1809)	1:31:A:LEU:HD21	1:34:A:TYR:HE1	3	1.91

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1809)	1:31:A:LEU:HD22	1:34:A:TYR:HE1	3	1.91
(1,1809)	1:31:A:LEU:HD23	1:34:A:TYR:HE1	3	1.91
(1,1065)	1:118:A:VAL:HG21	1:140:A:TYR:HD1	13	1.91
(1,1065)	1:118:A:VAL:HG22	1:140:A:TYR:HD1	13	1.91
(1,1065)	1:118:A:VAL:HG23	1:140:A:TYR:HD1	13	1.91
(1,2640)	1:65:A:TYR:HD1	1:66:A:ILE:HG13	4	1.9
(1,1809)	1:31:A:LEU:HD21	1:34:A:TYR:HE1	2	1.9
(1,1809)	1:31:A:LEU:HD22	1:34:A:TYR:HE1	2	1.9
(1,1809)	1:31:A:LEU:HD23	1:34:A:TYR:HE1	2	1.9
(1,1809)	1:31:A:LEU:HD21	1:34:A:TYR:HE1	14	1.9
(1,1809)	1:31:A:LEU:HD22	1:34:A:TYR:HE1	14	1.9
(1,1809)	1:31:A:LEU:HD23	1:34:A:TYR:HE1	14	1.9
(1,2256)	1:34:A:TYR:HE2	1:37:A:LEU:HB3	10	1.89
(1,1809)	1:31:A:LEU:HD21	1:34:A:TYR:HE1	20	1.89
(1,1809)	1:31:A:LEU:HD22	1:34:A:TYR:HE1	20	1.89
(1,1809)	1:31:A:LEU:HD23	1:34:A:TYR:HE1	20	1.89
(1,1809)	1:31:A:LEU:HD21	1:34:A:TYR:HE1	16	1.88
(1,1809)	1:31:A:LEU:HD22	1:34:A:TYR:HE1	16	1.88
(1,1809)	1:31:A:LEU:HD23	1:34:A:TYR:HE1	16	1.88
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB1	3	1.88
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB2	3	1.88
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB3	3	1.88
(1,919)	1:11:A:LEU:HD21	1:85:A:TYR:HD1	2	1.88
(1,919)	1:11:A:LEU:HD22	1:85:A:TYR:HD1	2	1.88
(1,919)	1:11:A:LEU:HD23	1:85:A:TYR:HD1	2	1.88
(1,1090)	1:34:A:TYR:HD2	1:39:A:LYS:HB2	19	1.87
(1,1008)	1:34:A:TYR:HE2	1:39:A:LYS:HE3	15	1.86
(1,1809)	1:31:A:LEU:HD21	1:34:A:TYR:HE1	19	1.85
(1,1809)	1:31:A:LEU:HD22	1:34:A:TYR:HE1	19	1.85
(1,1809)	1:31:A:LEU:HD23	1:34:A:TYR:HE1	19	1.85
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG21	15	1.85
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG22	15	1.85
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG23	15	1.85
(1,981)	1:119:A:ALA:HB1	1:140:A:TYR:HD1	2	1.85
(1,981)	1:119:A:ALA:HB2	1:140:A:TYR:HD1	2	1.85
(1,981)	1:119:A:ALA:HB3	1:140:A:TYR:HD1	2	1.85
(1,1357)	1:25:A:PHE:HD2	1:101:A:GLY:HA2	7	1.84
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG21	14	1.84
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG22	14	1.84
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG23	14	1.84
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG21	14	1.84
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG22	14	1.84

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG23	14	1.84
(1,919)	1:11:A:LEU:HD21	1:85:A:TYR:HD1	11	1.84
(1,919)	1:11:A:LEU:HD22	1:85:A:TYR:HD1	11	1.84
(1,919)	1:11:A:LEU:HD23	1:85:A:TYR:HD1	11	1.84
(1,1357)	1:25:A:PHE:HD2	1:101:A:GLY:HA2	6	1.83
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG21	15	1.83
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG22	15	1.83
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG23	15	1.83
(1,1809)	1:31:A:LEU:HD21	1:34:A:TYR:HE1	1	1.82
(1,1809)	1:31:A:LEU:HD22	1:34:A:TYR:HE1	1	1.82
(1,1809)	1:31:A:LEU:HD23	1:34:A:TYR:HE1	1	1.82
(1,1065)	1:118:A:VAL:HG21	1:140:A:TYR:HD1	5	1.82
(1,1065)	1:118:A:VAL:HG22	1:140:A:TYR:HD1	5	1.82
(1,1065)	1:118:A:VAL:HG23	1:140:A:TYR:HD1	5	1.82
(1,975)	1:34:A:TYR:HE2	1:39:A:LYS:HG3	14	1.82
(1,919)	1:11:A:LEU:HD21	1:85:A:TYR:HD1	10	1.82
(1,919)	1:11:A:LEU:HD22	1:85:A:TYR:HD1	10	1.82
(1,919)	1:11:A:LEU:HD23	1:85:A:TYR:HD1	10	1.82
(1,1809)	1:31:A:LEU:HD21	1:34:A:TYR:HE1	13	1.81
(1,1809)	1:31:A:LEU:HD22	1:34:A:TYR:HE1	13	1.81
(1,1809)	1:31:A:LEU:HD23	1:34:A:TYR:HE1	13	1.81
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG21	16	1.81
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG22	16	1.81
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG23	16	1.81
(1,1065)	1:118:A:VAL:HG21	1:140:A:TYR:HD1	19	1.81
(1,1065)	1:118:A:VAL:HG22	1:140:A:TYR:HD1	19	1.81
(1,1065)	1:118:A:VAL:HG23	1:140:A:TYR:HD1	19	1.81
(1,975)	1:34:A:TYR:HE2	1:39:A:LYS:HG3	18	1.81
(1,2764)	1:84:A:LEU:HD21	1:85:A:TYR:HD2	4	1.8
(1,2764)	1:84:A:LEU:HD22	1:85:A:TYR:HD2	4	1.8
(1,2764)	1:84:A:LEU:HD23	1:85:A:TYR:HD2	4	1.8
(1,2764)	1:84:A:LEU:HD21	1:85:A:TYR:HD2	10	1.8
(1,2764)	1:84:A:LEU:HD22	1:85:A:TYR:HD2	10	1.8
(1,2764)	1:84:A:LEU:HD23	1:85:A:TYR:HD2	10	1.8
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG21	6	1.8
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG22	6	1.8
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG23	6	1.8
(1,1007)	1:34:A:TYR:HE2	1:39:A:LYS:HE2	1	1.8
(1,2256)	1:34:A:TYR:HE2	1:37:A:LEU:HB3	18	1.79
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG21	8	1.79
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG22	8	1.79
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG23	8	1.79

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG21	11	1.79
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG22	11	1.79
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG23	11	1.79
(1,919)	1:11:A:LEU:HD21	1:85:A:TYR:HD1	16	1.79
(1,919)	1:11:A:LEU:HD22	1:85:A:TYR:HD1	16	1.79
(1,919)	1:11:A:LEU:HD23	1:85:A:TYR:HD1	16	1.79
(1,2764)	1:84:A:LEU:HD21	1:85:A:TYR:HD2	1	1.78
(1,2764)	1:84:A:LEU:HD22	1:85:A:TYR:HD2	1	1.78
(1,2764)	1:84:A:LEU:HD23	1:85:A:TYR:HD2	1	1.78
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG21	11	1.78
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG22	11	1.78
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG23	11	1.78
(1,1065)	1:118:A:VAL:HG21	1:140:A:TYR:HD1	14	1.78
(1,1065)	1:118:A:VAL:HG22	1:140:A:TYR:HD1	14	1.78
(1,1065)	1:118:A:VAL:HG23	1:140:A:TYR:HD1	14	1.78
(1,2764)	1:84:A:LEU:HD21	1:85:A:TYR:HD2	7	1.77
(1,2764)	1:84:A:LEU:HD22	1:85:A:TYR:HD2	7	1.77
(1,2764)	1:84:A:LEU:HD23	1:85:A:TYR:HD2	7	1.77
(1,2764)	1:84:A:LEU:HD21	1:85:A:TYR:HD2	11	1.77
(1,2764)	1:84:A:LEU:HD22	1:85:A:TYR:HD2	11	1.77
(1,2764)	1:84:A:LEU:HD23	1:85:A:TYR:HD2	11	1.77
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG11	13	1.77
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG12	13	1.77
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG13	13	1.77
(1,2900)	1:23:A:ALA:H	1:24:A:TYR:HD1	4	1.76
(1,2640)	1:65:A:TYR:HD1	1:66:A:ILE:HG13	12	1.76
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG21	16	1.76
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG22	16	1.76
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG23	16	1.76
(1,1065)	1:118:A:VAL:HG21	1:140:A:TYR:HD1	15	1.76
(1,1065)	1:118:A:VAL:HG22	1:140:A:TYR:HD1	15	1.76
(1,1065)	1:118:A:VAL:HG23	1:140:A:TYR:HD1	15	1.76
(1,2764)	1:84:A:LEU:HD21	1:85:A:TYR:HD2	17	1.75
(1,2764)	1:84:A:LEU:HD22	1:85:A:TYR:HD2	17	1.75
(1,2764)	1:84:A:LEU:HD23	1:85:A:TYR:HD2	17	1.75
(1,2256)	1:34:A:TYR:HE2	1:37:A:LEU:HB3	12	1.75
(1,1090)	1:34:A:TYR:HD2	1:39:A:LYS:HB2	11	1.75
(1,2900)	1:23:A:ALA:H	1:24:A:TYR:HD1	6	1.74
(1,2764)	1:84:A:LEU:HD21	1:85:A:TYR:HD2	12	1.74
(1,2764)	1:84:A:LEU:HD22	1:85:A:TYR:HD2	12	1.74
(1,2764)	1:84:A:LEU:HD23	1:85:A:TYR:HD2	12	1.74
(1,1845)	1:65:A:TYR:HE1	1:69:A:LYS:HE3	2	1.74

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2764)	1:84:A:LEU:HD21	1:85:A:TYR:HD2	15	1.73
(1,2764)	1:84:A:LEU:HD22	1:85:A:TYR:HD2	15	1.73
(1,2764)	1:84:A:LEU:HD23	1:85:A:TYR:HD2	15	1.73
(1,1954)	1:135:A:ARG:HG2	1:138:A:TYR:HD2	7	1.73
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG21	4	1.73
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG22	4	1.73
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG23	4	1.73
(1,2764)	1:84:A:LEU:HD21	1:85:A:TYR:HD2	3	1.72
(1,2764)	1:84:A:LEU:HD22	1:85:A:TYR:HD2	3	1.72
(1,2764)	1:84:A:LEU:HD23	1:85:A:TYR:HD2	3	1.72
(1,2764)	1:84:A:LEU:HD21	1:85:A:TYR:HD2	6	1.72
(1,2764)	1:84:A:LEU:HD22	1:85:A:TYR:HD2	6	1.72
(1,2764)	1:84:A:LEU:HD23	1:85:A:TYR:HD2	6	1.72
(1,2764)	1:84:A:LEU:HD21	1:85:A:TYR:HD2	14	1.72
(1,2764)	1:84:A:LEU:HD22	1:85:A:TYR:HD2	14	1.72
(1,2764)	1:84:A:LEU:HD23	1:85:A:TYR:HD2	14	1.72
(1,2256)	1:34:A:TYR:HE2	1:37:A:LEU:HB3	5	1.72
(1,2256)	1:34:A:TYR:HE2	1:37:A:LEU:HB3	11	1.72
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG21	12	1.72
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG22	12	1.72
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG23	12	1.72
(1,1065)	1:118:A:VAL:HG21	1:140:A:TYR:HD1	12	1.72
(1,1065)	1:118:A:VAL:HG22	1:140:A:TYR:HD1	12	1.72
(1,1065)	1:118:A:VAL:HG23	1:140:A:TYR:HD1	12	1.72
(1,919)	1:11:A:LEU:HD21	1:85:A:TYR:HD1	3	1.72
(1,919)	1:11:A:LEU:HD22	1:85:A:TYR:HD1	3	1.72
(1,919)	1:11:A:LEU:HD23	1:85:A:TYR:HD1	3	1.72
(1,919)	1:11:A:LEU:HD21	1:85:A:TYR:HD1	8	1.72
(1,919)	1:11:A:LEU:HD22	1:85:A:TYR:HD1	8	1.72
(1,919)	1:11:A:LEU:HD23	1:85:A:TYR:HD1	8	1.72
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG21	20	1.71
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG22	20	1.71
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG23	20	1.71
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG21	20	1.71
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG22	20	1.71
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG23	20	1.71
(1,919)	1:11:A:LEU:HD21	1:85:A:TYR:HD1	6	1.71
(1,919)	1:11:A:LEU:HD22	1:85:A:TYR:HD1	6	1.71
(1,919)	1:11:A:LEU:HD23	1:85:A:TYR:HD1	6	1.71
(1,2764)	1:84:A:LEU:HD21	1:85:A:TYR:HD2	2	1.7
(1,2764)	1:84:A:LEU:HD22	1:85:A:TYR:HD2	2	1.7
(1,2764)	1:84:A:LEU:HD23	1:85:A:TYR:HD2	2	1.7

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2764)	1:84:A:LEU:HD21	1:85:A:TYR:HD2	18	1.7
(1,2764)	1:84:A:LEU:HD22	1:85:A:TYR:HD2	18	1.7
(1,2764)	1:84:A:LEU:HD23	1:85:A:TYR:HD2	18	1.7
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG21	7	1.7
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG22	7	1.7
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG23	7	1.7
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG21	13	1.7
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG22	13	1.7
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG23	13	1.7
(1,1065)	1:118:A:VAL:HG21	1:140:A:TYR:HD1	8	1.7
(1,1065)	1:118:A:VAL:HG22	1:140:A:TYR:HD1	8	1.7
(1,1065)	1:118:A:VAL:HG23	1:140:A:TYR:HD1	8	1.7
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB1	18	1.7
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB2	18	1.7
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB3	18	1.7
(1,919)	1:11:A:LEU:HD21	1:85:A:TYR:HD1	12	1.7
(1,919)	1:11:A:LEU:HD22	1:85:A:TYR:HD1	12	1.7
(1,919)	1:11:A:LEU:HD23	1:85:A:TYR:HD1	12	1.7
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG21	4	1.69
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG22	4	1.69
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG23	4	1.69
(1,975)	1:34:A:TYR:HE2	1:39:A:LYS:HG3	13	1.69
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG11	15	1.69
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG12	15	1.69
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG13	15	1.69
(1,2764)	1:84:A:LEU:HD21	1:85:A:TYR:HD2	9	1.68
(1,2764)	1:84:A:LEU:HD22	1:85:A:TYR:HD2	9	1.68
(1,2764)	1:84:A:LEU:HD23	1:85:A:TYR:HD2	9	1.68
(1,2764)	1:84:A:LEU:HD21	1:85:A:TYR:HD2	20	1.68
(1,2764)	1:84:A:LEU:HD22	1:85:A:TYR:HD2	20	1.68
(1,2764)	1:84:A:LEU:HD23	1:85:A:TYR:HD2	20	1.68
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG21	19	1.68
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG22	19	1.68
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG23	19	1.68
(1,975)	1:34:A:TYR:HE2	1:39:A:LYS:HG3	12	1.68
(1,919)	1:11:A:LEU:HD21	1:85:A:TYR:HD1	19	1.68
(1,919)	1:11:A:LEU:HD22	1:85:A:TYR:HD1	19	1.68
(1,919)	1:11:A:LEU:HD23	1:85:A:TYR:HD1	19	1.68
(1,1065)	1:118:A:VAL:HG21	1:140:A:TYR:HD1	17	1.67
(1,1065)	1:118:A:VAL:HG22	1:140:A:TYR:HD1	17	1.67
(1,1065)	1:118:A:VAL:HG23	1:140:A:TYR:HD1	17	1.67
(1,981)	1:119:A:ALA:HB1	1:140:A:TYR:HD1	3	1.67

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,981)	1:119:A:ALA:HB2	1:140:A:TYR:HD1	3	1.67
(1,981)	1:119:A:ALA:HB3	1:140:A:TYR:HD1	3	1.67
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG11	19	1.67
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG12	19	1.67
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG13	19	1.67
(1,2764)	1:84:A:LEU:HD21	1:85:A:TYR:HD2	13	1.66
(1,2764)	1:84:A:LEU:HD22	1:85:A:TYR:HD2	13	1.66
(1,2764)	1:84:A:LEU:HD23	1:85:A:TYR:HD2	13	1.66
(1,2256)	1:34:A:TYR:HE2	1:37:A:LEU:HB3	19	1.66
(1,1976)	1:34:A:TYR:HD2	1:37:A:LEU:HB3	10	1.66
(1,1357)	1:25:A:PHE:HD2	1:101:A:GLY:HA2	11	1.66
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG21	18	1.66
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG22	18	1.66
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG23	18	1.66
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG21	19	1.66
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG22	19	1.66
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG23	19	1.66
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG11	20	1.66
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG12	20	1.66
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG13	20	1.66
(1,2256)	1:34:A:TYR:HE2	1:37:A:LEU:HB3	9	1.65
(1,1357)	1:25:A:PHE:HD2	1:101:A:GLY:HA2	18	1.65
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG21	9	1.65
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG22	9	1.65
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG23	9	1.65
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG21	12	1.65
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG22	12	1.65
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG23	12	1.65
(1,1065)	1:118:A:VAL:HG21	1:140:A:TYR:HD1	2	1.65
(1,1065)	1:118:A:VAL:HG22	1:140:A:TYR:HD1	2	1.65
(1,1065)	1:118:A:VAL:HG23	1:140:A:TYR:HD1	2	1.65
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG21	8	1.64
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG22	8	1.64
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG23	8	1.64
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG21	13	1.64
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG22	13	1.64
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG23	13	1.64
(1,1065)	1:118:A:VAL:HG21	1:140:A:TYR:HD1	10	1.64
(1,1065)	1:118:A:VAL:HG22	1:140:A:TYR:HD1	10	1.64
(1,1065)	1:118:A:VAL:HG23	1:140:A:TYR:HD1	10	1.64
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG11	12	1.64
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG12	12	1.64

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG13	12	1.64
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG11	16	1.64
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG12	16	1.64
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG13	16	1.64
(1,919)	1:11:A:LEU:HD21	1:85:A:TYR:HD1	17	1.64
(1,919)	1:11:A:LEU:HD22	1:85:A:TYR:HD1	17	1.64
(1,919)	1:11:A:LEU:HD23	1:85:A:TYR:HD1	17	1.64
(1,2764)	1:84:A:LEU:HD21	1:85:A:TYR:HD2	19	1.63
(1,2764)	1:84:A:LEU:HD22	1:85:A:TYR:HD2	19	1.63
(1,2764)	1:84:A:LEU:HD23	1:85:A:TYR:HD2	19	1.63
(1,1976)	1:34:A:TYR:HD2	1:37:A:LEU:HB3	14	1.63
(1,919)	1:11:A:LEU:HD21	1:85:A:TYR:HD1	4	1.63
(1,919)	1:11:A:LEU:HD22	1:85:A:TYR:HD1	4	1.63
(1,919)	1:11:A:LEU:HD23	1:85:A:TYR:HD1	4	1.63
(1,919)	1:11:A:LEU:HD21	1:85:A:TYR:HD1	14	1.63
(1,919)	1:11:A:LEU:HD22	1:85:A:TYR:HD1	14	1.63
(1,919)	1:11:A:LEU:HD23	1:85:A:TYR:HD1	14	1.63
(1,2256)	1:34:A:TYR:HE2	1:37:A:LEU:HB3	16	1.62
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD11	10	1.62
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD12	10	1.62
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD13	10	1.62
(1,1240)	1:20:A:PHE:HE2	1:51:A:PRO:HA	13	1.62
(1,981)	1:119:A:ALA:HB1	1:140:A:TYR:HD1	14	1.62
(1,981)	1:119:A:ALA:HB2	1:140:A:TYR:HD1	14	1.62
(1,981)	1:119:A:ALA:HB3	1:140:A:TYR:HD1	14	1.62
(1,1357)	1:25:A:PHE:HD2	1:101:A:GLY:HA2	20	1.61
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG21	6	1.61
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG22	6	1.61
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG23	6	1.61
(1,1007)	1:34:A:TYR:HE2	1:39:A:LYS:HE2	3	1.61
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG11	1	1.61
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG12	1	1.61
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG13	1	1.61
(1,1357)	1:25:A:PHE:HD2	1:101:A:GLY:HA2	14	1.6
(1,1357)	1:25:A:PHE:HD2	1:101:A:GLY:HA2	15	1.59
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG21	7	1.59
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG22	7	1.59
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG23	7	1.59
(1,919)	1:11:A:LEU:HD21	1:85:A:TYR:HD1	5	1.59
(1,919)	1:11:A:LEU:HD22	1:85:A:TYR:HD1	5	1.59
(1,919)	1:11:A:LEU:HD23	1:85:A:TYR:HD1	5	1.59
(1,919)	1:11:A:LEU:HD21	1:85:A:TYR:HD1	9	1.59

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,919)	1:11:A:LEU:HD22	1:85:A:TYR:HD1	9	1.59
(1,919)	1:11:A:LEU:HD23	1:85:A:TYR:HD1	9	1.59
(1,1065)	1:118:A:VAL:HG21	1:140:A:TYR:HD1	11	1.58
(1,1065)	1:118:A:VAL:HG22	1:140:A:TYR:HD1	11	1.58
(1,1065)	1:118:A:VAL:HG23	1:140:A:TYR:HD1	11	1.58
(1,981)	1:119:A:ALA:HB1	1:140:A:TYR:HD1	15	1.58
(1,981)	1:119:A:ALA:HB2	1:140:A:TYR:HD1	15	1.58
(1,981)	1:119:A:ALA:HB3	1:140:A:TYR:HD1	15	1.58
(1,981)	1:119:A:ALA:HB1	1:140:A:TYR:HD1	16	1.58
(1,981)	1:119:A:ALA:HB2	1:140:A:TYR:HD1	16	1.58
(1,981)	1:119:A:ALA:HB3	1:140:A:TYR:HD1	16	1.58
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG21	18	1.57
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG22	18	1.57
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG23	18	1.57
(1,1866)	1:135:A:ARG:HG2	1:138:A:TYR:HE2	5	1.56
(1,981)	1:119:A:ALA:HB1	1:140:A:TYR:HD1	13	1.56
(1,981)	1:119:A:ALA:HB2	1:140:A:TYR:HD1	13	1.56
(1,981)	1:119:A:ALA:HB3	1:140:A:TYR:HD1	13	1.56
(1,975)	1:34:A:TYR:HE2	1:39:A:LYS:HG3	10	1.56
(1,1976)	1:34:A:TYR:HD2	1:37:A:LEU:HB3	18	1.55
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG21	9	1.55
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG22	9	1.55
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG23	9	1.55
(1,2256)	1:34:A:TYR:HE2	1:37:A:LEU:HB3	20	1.54
(1,1976)	1:34:A:TYR:HD2	1:37:A:LEU:HB3	5	1.54
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG21	2	1.54
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG22	2	1.54
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG23	2	1.54
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG21	2	1.54
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG22	2	1.54
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG23	2	1.54
(1,1065)	1:118:A:VAL:HG21	1:140:A:TYR:HD1	1	1.54
(1,1065)	1:118:A:VAL:HG22	1:140:A:TYR:HD1	1	1.54
(1,1065)	1:118:A:VAL:HG23	1:140:A:TYR:HD1	1	1.54
(1,981)	1:119:A:ALA:HB1	1:140:A:TYR:HD1	5	1.54
(1,981)	1:119:A:ALA:HB2	1:140:A:TYR:HD1	5	1.54
(1,981)	1:119:A:ALA:HB3	1:140:A:TYR:HD1	5	1.54
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG11	3	1.54
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG12	3	1.54
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG13	3	1.54
(1,2256)	1:34:A:TYR:HE2	1:37:A:LEU:HB3	2	1.53
(1,2256)	1:34:A:TYR:HE2	1:37:A:LEU:HB3	13	1.53

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG21	5	1.53
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG22	5	1.53
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG23	5	1.53
(1,1065)	1:118:A:VAL:HG21	1:140:A:TYR:HD1	7	1.53
(1,1065)	1:118:A:VAL:HG22	1:140:A:TYR:HD1	7	1.53
(1,1065)	1:118:A:VAL:HG23	1:140:A:TYR:HD1	7	1.53
(1,919)	1:11:A:LEU:HD21	1:85:A:TYR:HD1	7	1.53
(1,919)	1:11:A:LEU:HD22	1:85:A:TYR:HD1	7	1.53
(1,919)	1:11:A:LEU:HD23	1:85:A:TYR:HD1	7	1.53
(1,1976)	1:34:A:TYR:HD2	1:37:A:LEU:HB3	9	1.52
(1,1976)	1:34:A:TYR:HD2	1:37:A:LEU:HB3	11	1.52
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB1	17	1.52
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB2	17	1.52
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB3	17	1.52
(1,2128)	1:62:A:TYR:HE2	1:65:A:TYR:HB2	20	1.51
(1,1357)	1:25:A:PHE:HD2	1:101:A:GLY:HA2	10	1.51
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB1	15	1.51
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB2	15	1.51
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB3	15	1.51
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG11	9	1.51
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG12	9	1.51
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG13	9	1.51
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG11	11	1.51
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG12	11	1.51
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG13	11	1.51
(1,1976)	1:34:A:TYR:HD2	1:37:A:LEU:HB3	19	1.5
(1,1976)	1:34:A:TYR:HD2	1:37:A:LEU:HB3	20	1.5
(1,981)	1:119:A:ALA:HB1	1:140:A:TYR:HD1	4	1.5
(1,981)	1:119:A:ALA:HB2	1:140:A:TYR:HD1	4	1.5
(1,981)	1:119:A:ALA:HB3	1:140:A:TYR:HD1	4	1.5
(1,1090)	1:34:A:TYR:HD2	1:39:A:LYS:HB2	14	1.49
(1,1090)	1:34:A:TYR:HD2	1:39:A:LYS:HB2	18	1.49
(1,1065)	1:118:A:VAL:HG21	1:140:A:TYR:HD1	16	1.49
(1,1065)	1:118:A:VAL:HG22	1:140:A:TYR:HD1	16	1.49
(1,1065)	1:118:A:VAL:HG23	1:140:A:TYR:HD1	16	1.49
(1,1976)	1:34:A:TYR:HD2	1:37:A:LEU:HB3	16	1.48
(1,981)	1:119:A:ALA:HB1	1:140:A:TYR:HD1	18	1.47
(1,981)	1:119:A:ALA:HB2	1:140:A:TYR:HD1	18	1.47
(1,981)	1:119:A:ALA:HB3	1:140:A:TYR:HD1	18	1.47
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG21	10	1.45
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG22	10	1.45
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG23	10	1.45

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG21	10	1.45
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG22	10	1.45
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG23	10	1.45
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB1	13	1.45
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB2	13	1.45
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB3	13	1.45
(1,919)	1:11:A:LEU:HD21	1:85:A:TYR:HD1	13	1.45
(1,919)	1:11:A:LEU:HD22	1:85:A:TYR:HD1	13	1.45
(1,919)	1:11:A:LEU:HD23	1:85:A:TYR:HD1	13	1.45
(1,919)	1:11:A:LEU:HD21	1:85:A:TYR:HD1	15	1.45
(1,919)	1:11:A:LEU:HD22	1:85:A:TYR:HD1	15	1.45
(1,919)	1:11:A:LEU:HD23	1:85:A:TYR:HD1	15	1.45
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD21	10	1.44
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD22	10	1.44
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD23	10	1.44
(1,2128)	1:62:A:TYR:HE2	1:65:A:TYR:HB2	15	1.44
(1,1976)	1:34:A:TYR:HD2	1:37:A:LEU:HB3	12	1.44
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG21	5	1.44
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG22	5	1.44
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG23	5	1.44
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB1	10	1.44
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB2	10	1.44
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB3	10	1.44
(1,919)	1:11:A:LEU:HD21	1:85:A:TYR:HD1	18	1.44
(1,919)	1:11:A:LEU:HD22	1:85:A:TYR:HD1	18	1.44
(1,919)	1:11:A:LEU:HD23	1:85:A:TYR:HD1	18	1.44
(1,1090)	1:34:A:TYR:HD2	1:39:A:LYS:HB2	13	1.43
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD11	16	1.42
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD12	16	1.42
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD13	16	1.42
(1,1065)	1:118:A:VAL:HG21	1:140:A:TYR:HD1	6	1.42
(1,1065)	1:118:A:VAL:HG22	1:140:A:TYR:HD1	6	1.42
(1,1065)	1:118:A:VAL:HG23	1:140:A:TYR:HD1	6	1.42
(1,981)	1:119:A:ALA:HB1	1:140:A:TYR:HD1	9	1.42
(1,981)	1:119:A:ALA:HB2	1:140:A:TYR:HD1	9	1.42
(1,981)	1:119:A:ALA:HB3	1:140:A:TYR:HD1	9	1.42
(1,2256)	1:34:A:TYR:HE2	1:37:A:LEU:HB3	3	1.41
(1,919)	1:11:A:LEU:HD21	1:85:A:TYR:HD1	1	1.41
(1,919)	1:11:A:LEU:HD22	1:85:A:TYR:HD1	1	1.41
(1,919)	1:11:A:LEU:HD23	1:85:A:TYR:HD1	1	1.41
(1,1976)	1:34:A:TYR:HD2	1:37:A:LEU:HB3	2	1.4
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	4	1.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	4	1.4
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	4	1.4
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	4	1.4
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	4	1.4
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	4	1.4
(1,2128)	1:62:A:TYR:HE2	1:65:A:TYR:HB2	1	1.39
(1,981)	1:119:A:ALA:HB1	1:140:A:TYR:HD1	1	1.39
(1,981)	1:119:A:ALA:HB2	1:140:A:TYR:HD1	1	1.39
(1,981)	1:119:A:ALA:HB3	1:140:A:TYR:HD1	1	1.39
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG11	10	1.39
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG12	10	1.39
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG13	10	1.39
(1,1976)	1:34:A:TYR:HD2	1:37:A:LEU:HB3	3	1.38
(1,1976)	1:34:A:TYR:HD2	1:37:A:LEU:HB3	13	1.38
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD11	18	1.38
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD12	18	1.38
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD13	18	1.38
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG11	5	1.38
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG12	5	1.38
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG13	5	1.38
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG11	18	1.38
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG12	18	1.38
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG13	18	1.38
(1,1466)	1:85:A:TYR:HE2	1:118:A:VAL:HA	3	1.37
(1,1144)	1:25:A:PHE:HD2	1:103:A:ARG:H	3	1.37
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB1	8	1.37
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB2	8	1.37
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB3	8	1.37
(1,981)	1:119:A:ALA:HB1	1:140:A:TYR:HD1	17	1.37
(1,981)	1:119:A:ALA:HB2	1:140:A:TYR:HD1	17	1.37
(1,981)	1:119:A:ALA:HB3	1:140:A:TYR:HD1	17	1.37
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG11	2	1.35
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG12	2	1.35
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG13	2	1.35
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD11	14	1.34
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD12	14	1.34
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD13	14	1.34
(1,1340)	1:11:A:LEU:HD21	1:85:A:TYR:HE1	2	1.34
(1,1340)	1:11:A:LEU:HD22	1:85:A:TYR:HE1	2	1.34
(1,1340)	1:11:A:LEU:HD23	1:85:A:TYR:HE1	2	1.34
(1,1065)	1:118:A:VAL:HG21	1:140:A:TYR:HD1	3	1.33
(1,1065)	1:118:A:VAL:HG22	1:140:A:TYR:HD1	3	1.33

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1065)	1:118:A:VAL:HG23	1:140:A:TYR:HD1	3	1.33
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB1	11	1.33
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB2	11	1.33
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB3	11	1.33
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB1	20	1.33
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB2	20	1.33
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB3	20	1.33
(1,981)	1:119:A:ALA:HB1	1:140:A:TYR:HD1	12	1.33
(1,981)	1:119:A:ALA:HB2	1:140:A:TYR:HD1	12	1.33
(1,981)	1:119:A:ALA:HB3	1:140:A:TYR:HD1	12	1.33
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD21	18	1.32
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD22	18	1.32
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD23	18	1.32
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD11	13	1.31
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD12	13	1.31
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD13	13	1.31
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG21	3	1.31
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG22	3	1.31
(1,1201)	1:25:A:PHE:HE1	1:98:A:ILE:HG23	3	1.31
(1,919)	1:11:A:LEU:HD21	1:85:A:TYR:HD1	20	1.31
(1,919)	1:11:A:LEU:HD22	1:85:A:TYR:HD1	20	1.31
(1,919)	1:11:A:LEU:HD23	1:85:A:TYR:HD1	20	1.31
(1,2121)	1:140:A:TYR:HD2	1:142:A:ALA:H	19	1.3
(1,1065)	1:118:A:VAL:HG21	1:140:A:TYR:HD1	4	1.3
(1,1065)	1:118:A:VAL:HG22	1:140:A:TYR:HD1	4	1.3
(1,1065)	1:118:A:VAL:HG23	1:140:A:TYR:HD1	4	1.3
(1,1065)	1:118:A:VAL:HG21	1:140:A:TYR:HD1	18	1.3
(1,1065)	1:118:A:VAL:HG22	1:140:A:TYR:HD1	18	1.3
(1,1065)	1:118:A:VAL:HG23	1:140:A:TYR:HD1	18	1.3
(1,981)	1:119:A:ALA:HB1	1:140:A:TYR:HD1	19	1.3
(1,981)	1:119:A:ALA:HB2	1:140:A:TYR:HD1	19	1.3
(1,981)	1:119:A:ALA:HB3	1:140:A:TYR:HD1	19	1.3
(1,975)	1:34:A:TYR:HE2	1:39:A:LYS:HG3	16	1.3
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD21	14	1.29
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD22	14	1.29
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD23	14	1.29
(1,981)	1:119:A:ALA:HB1	1:140:A:TYR:HD1	6	1.29
(1,981)	1:119:A:ALA:HB2	1:140:A:TYR:HD1	6	1.29
(1,981)	1:119:A:ALA:HB3	1:140:A:TYR:HD1	6	1.29
(1,1340)	1:11:A:LEU:HD21	1:85:A:TYR:HE1	11	1.27
(1,1340)	1:11:A:LEU:HD22	1:85:A:TYR:HE1	11	1.27
(1,1340)	1:11:A:LEU:HD23	1:85:A:TYR:HE1	11	1.27

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1090)	1:34:A:TYR:HD2	1:39:A:LYS:HB2	12	1.26
(1,1007)	1:34:A:TYR:HE2	1:39:A:LYS:HE2	9	1.25
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD11	4	1.25
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD12	4	1.25
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD13	4	1.25
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD21	4	1.25
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD22	4	1.25
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD23	4	1.25
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG11	14	1.25
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG12	14	1.25
(1,929)	1:34:A:TYR:HD2	1:154:A:VAL:HG13	14	1.25
(1,1340)	1:11:A:LEU:HD21	1:85:A:TYR:HE1	10	1.23
(1,1340)	1:11:A:LEU:HD22	1:85:A:TYR:HE1	10	1.23
(1,1340)	1:11:A:LEU:HD23	1:85:A:TYR:HE1	10	1.23
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG21	3	1.23
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG22	3	1.23
(1,1216)	1:25:A:PHE:HD1	1:98:A:ILE:HG23	3	1.23
(1,981)	1:119:A:ALA:HB1	1:140:A:TYR:HD1	7	1.23
(1,981)	1:119:A:ALA:HB2	1:140:A:TYR:HD1	7	1.23
(1,981)	1:119:A:ALA:HB3	1:140:A:TYR:HD1	7	1.23
(1,981)	1:119:A:ALA:HB1	1:140:A:TYR:HD1	8	1.23
(1,981)	1:119:A:ALA:HB2	1:140:A:TYR:HD1	8	1.23
(1,981)	1:119:A:ALA:HB3	1:140:A:TYR:HD1	8	1.23
(1,1008)	1:34:A:TYR:HE2	1:39:A:LYS:HE3	5	1.22
(1,1759)	1:65:A:TYR:HE1	1:69:A:LYS:HG2	15	1.21
(1,1340)	1:11:A:LEU:HD21	1:85:A:TYR:HE1	16	1.21
(1,1340)	1:11:A:LEU:HD22	1:85:A:TYR:HE1	16	1.21
(1,1340)	1:11:A:LEU:HD23	1:85:A:TYR:HE1	16	1.21
(1,1007)	1:34:A:TYR:HE2	1:39:A:LYS:HE2	2	1.21
(1,1466)	1:85:A:TYR:HE2	1:118:A:VAL:HA	8	1.2
(1,1144)	1:25:A:PHE:HD2	1:103:A:ARG:H	2	1.2
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	18	1.2
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	18	1.2
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	18	1.2
(1,1340)	1:11:A:LEU:HD21	1:85:A:TYR:HE1	3	1.19
(1,1340)	1:11:A:LEU:HD22	1:85:A:TYR:HE1	3	1.19
(1,1340)	1:11:A:LEU:HD23	1:85:A:TYR:HE1	3	1.19
(1,1275)	1:62:A:TYR:HE1	1:136:A:LEU:HG	16	1.19
(1,2256)	1:34:A:TYR:HE2	1:37:A:LEU:HB3	15	1.18
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD11	19	1.18
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD12	19	1.18
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD13	19	1.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1059)	1:9:A:VAL:HG11	1:57:A:TYR:HE1	18	1.18
(1,1059)	1:9:A:VAL:HG12	1:57:A:TYR:HE1	18	1.18
(1,1059)	1:9:A:VAL:HG13	1:57:A:TYR:HE1	18	1.18
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD21	16	1.17
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD22	16	1.17
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD23	16	1.17
(1,1976)	1:34:A:TYR:HD2	1:37:A:LEU:HB3	15	1.17
(1,1340)	1:11:A:LEU:HD21	1:85:A:TYR:HE1	12	1.17
(1,1340)	1:11:A:LEU:HD22	1:85:A:TYR:HE1	12	1.17
(1,1340)	1:11:A:LEU:HD23	1:85:A:TYR:HE1	12	1.17
(1,981)	1:119:A:ALA:HB1	1:140:A:TYR:HD1	11	1.17
(1,981)	1:119:A:ALA:HB2	1:140:A:TYR:HD1	11	1.17
(1,981)	1:119:A:ALA:HB3	1:140:A:TYR:HD1	11	1.17
(1,1976)	1:34:A:TYR:HD2	1:37:A:LEU:HB3	1	1.16
(1,1340)	1:11:A:LEU:HD21	1:85:A:TYR:HE1	8	1.16
(1,1340)	1:11:A:LEU:HD22	1:85:A:TYR:HE1	8	1.16
(1,1340)	1:11:A:LEU:HD23	1:85:A:TYR:HE1	8	1.16
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD21	11	1.15
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD22	11	1.15
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD23	11	1.15
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD21	19	1.15
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD22	19	1.15
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD23	19	1.15
(1,1340)	1:11:A:LEU:HD21	1:85:A:TYR:HE1	6	1.15
(1,1340)	1:11:A:LEU:HD22	1:85:A:TYR:HE1	6	1.15
(1,1340)	1:11:A:LEU:HD23	1:85:A:TYR:HE1	6	1.15
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD21	19	1.14
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD22	19	1.14
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD23	19	1.14
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD11	5	1.14
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD12	5	1.14
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD13	5	1.14
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB1	14	1.14
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB2	14	1.14
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB3	14	1.14
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD11	11	1.13
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD12	11	1.13
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD13	11	1.13
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD11	12	1.13
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD12	12	1.13
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD13	12	1.13
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	9	1.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	9	1.13
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	9	1.13
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	9	1.13
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	9	1.13
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	9	1.13
(1,2440)	1:138:A:TYR:HD1	1:142:A:ALA:H	5	1.12
(1,1340)	1:11:A:LEU:HD21	1:85:A:TYR:HE1	19	1.12
(1,1340)	1:11:A:LEU:HD22	1:85:A:TYR:HE1	19	1.12
(1,1340)	1:11:A:LEU:HD23	1:85:A:TYR:HE1	19	1.12
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	9	1.12
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	9	1.12
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	9	1.12
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	17	1.11
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	17	1.11
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	17	1.11
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	17	1.11
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	17	1.11
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	17	1.11
(1,2121)	1:140:A:TYR:HD2	1:142:A:ALA:H	8	1.1
(1,1340)	1:11:A:LEU:HD21	1:85:A:TYR:HE1	14	1.1
(1,1340)	1:11:A:LEU:HD22	1:85:A:TYR:HE1	14	1.1
(1,1340)	1:11:A:LEU:HD23	1:85:A:TYR:HE1	14	1.1
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	2	1.1
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	2	1.1
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	2	1.1
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	2	1.1
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	2	1.1
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	2	1.1
(1,1340)	1:11:A:LEU:HD21	1:85:A:TYR:HE1	4	1.09
(1,1340)	1:11:A:LEU:HD22	1:85:A:TYR:HE1	4	1.09
(1,1340)	1:11:A:LEU:HD23	1:85:A:TYR:HE1	4	1.09
(1,1340)	1:11:A:LEU:HD21	1:85:A:TYR:HE1	9	1.09
(1,1340)	1:11:A:LEU:HD22	1:85:A:TYR:HE1	9	1.09
(1,1340)	1:11:A:LEU:HD23	1:85:A:TYR:HE1	9	1.09
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	5	1.09
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	5	1.09
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	5	1.09
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	5	1.09
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	5	1.09
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	5	1.09
(1,2256)	1:34:A:TYR:HE2	1:37:A:LEU:HB3	1	1.08
(1,2121)	1:140:A:TYR:HD2	1:142:A:ALA:H	11	1.08

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1340)	1:11:A:LEU:HD21	1:85:A:TYR:HE1	17	1.08
(1,1340)	1:11:A:LEU:HD22	1:85:A:TYR:HE1	17	1.08
(1,1340)	1:11:A:LEU:HD23	1:85:A:TYR:HE1	17	1.08
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	15	1.08
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	15	1.08
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	15	1.08
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD21	12	1.07
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD22	12	1.07
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD23	12	1.07
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB1	19	1.07
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB2	19	1.07
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB3	19	1.07
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	13	1.07
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	13	1.07
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	13	1.07
(1,2121)	1:140:A:TYR:HD2	1:142:A:ALA:H	13	1.06
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD11	9	1.06
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD12	9	1.06
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD13	9	1.06
(1,1328)	1:9:A:VAL:HG11	1:57:A:TYR:HD1	18	1.06
(1,1328)	1:9:A:VAL:HG12	1:57:A:TYR:HD1	18	1.06
(1,1328)	1:9:A:VAL:HG13	1:57:A:TYR:HD1	18	1.06
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB1	7	1.06
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB2	7	1.06
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB3	7	1.06
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	16	1.06
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	16	1.06
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	16	1.06
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	16	1.06
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	16	1.06
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	16	1.06
(1,2128)	1:62:A:TYR:HE2	1:65:A:TYR:HB2	13	1.05
(1,1466)	1:85:A:TYR:HE2	1:118:A:VAL:HA	18	1.05
(1,1144)	1:25:A:PHE:HD2	1:103:A:ARG:H	5	1.05
(1,1144)	1:25:A:PHE:HD2	1:103:A:ARG:H	9	1.05
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	19	1.05
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	19	1.05
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	19	1.05
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	19	1.05
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	19	1.05
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	19	1.05
(1,2121)	1:140:A:TYR:HD2	1:142:A:ALA:H	7	1.04

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD11	3	1.04
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD12	3	1.04
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD13	3	1.04
(1,1466)	1:85:A:TYR:HE2	1:118:A:VAL:HA	10	1.04
(1,1340)	1:11:A:LEU:HD21	1:85:A:TYR:HE1	7	1.04
(1,1340)	1:11:A:LEU:HD22	1:85:A:TYR:HE1	7	1.04
(1,1340)	1:11:A:LEU:HD23	1:85:A:TYR:HE1	7	1.04
(1,1144)	1:25:A:PHE:HD2	1:103:A:ARG:H	13	1.04
(1,1142)	1:62:A:TYR:HD1	1:136:A:LEU:HG	4	1.04
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	1	1.04
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	1	1.04
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	1	1.04
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	1	1.04
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	1	1.04
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	1	1.04
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	1	1.04
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	1	1.04
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	1	1.04
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	8	1.04
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	8	1.04
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	8	1.04
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	8	1.04
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	8	1.04
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	8	1.04
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	12	1.04
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	12	1.04
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	12	1.04
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	12	1.04
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	12	1.04
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	12	1.04
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD21	9	1.03
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD22	9	1.03
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD23	9	1.03
(1,2128)	1:62:A:TYR:HE2	1:65:A:TYR:HB2	10	1.03
(1,2128)	1:62:A:TYR:HE2	1:65:A:TYR:HB2	18	1.03
(1,2121)	1:140:A:TYR:HD2	1:142:A:ALA:H	10	1.03
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	7	1.03
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	7	1.03
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	7	1.03
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	14	1.03
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	14	1.03
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	14	1.03

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD21	13	1.02
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD22	13	1.02
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD23	13	1.02
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD21	20	1.02
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD22	20	1.02
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD23	20	1.02
(1,2128)	1:62:A:TYR:HE2	1:65:A:TYR:HB2	7	1.02
(1,2128)	1:62:A:TYR:HE2	1:65:A:TYR:HB2	9	1.02
(1,1759)	1:65:A:TYR:HE1	1:69:A:LYS:HG2	19	1.02
(1,1340)	1:11:A:LEU:HD21	1:85:A:TYR:HE1	5	1.02
(1,1340)	1:11:A:LEU:HD22	1:85:A:TYR:HE1	5	1.02
(1,1340)	1:11:A:LEU:HD23	1:85:A:TYR:HE1	5	1.02
(1,1007)	1:34:A:TYR:HE2	1:39:A:LYS:HE2	14	1.02
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD21	5	1.01
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD22	5	1.01
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD23	5	1.01
(1,1144)	1:25:A:PHE:HD2	1:103:A:ARG:H	4	1.01
(1,1144)	1:25:A:PHE:HD2	1:103:A:ARG:H	19	1.01
(1,1090)	1:34:A:TYR:HD2	1:39:A:LYS:HB2	10	1.01
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	3	1.01
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	3	1.01
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	3	1.01
(1,2128)	1:62:A:TYR:HE2	1:65:A:TYR:HB2	8	1.0
(1,2128)	1:62:A:TYR:HE2	1:65:A:TYR:HB2	14	1.0
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	2	1.0
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	2	1.0
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	2	1.0
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	11	1.0
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	11	1.0
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	11	1.0
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	11	1.0
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	11	1.0
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	11	1.0
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	18	1.0
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	18	1.0
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	18	1.0
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	18	1.0
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	18	1.0
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	18	1.0
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD11	20	0.99
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD12	20	0.99
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD13	20	0.99

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1466)	1:85:A:TYR:HE2	1:118:A:VAL:HA	11	0.99
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	10	0.99
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	10	0.99
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	10	0.99
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	20	0.99
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	20	0.99
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	20	0.99
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	6	0.99
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	6	0.99
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	6	0.99
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	6	0.99
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	6	0.99
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	6	0.99
(1,2986)	1:24:A:TYR:HE1	1:25:A:PHE:HB2	4	0.98
(1,2128)	1:62:A:TYR:HE2	1:65:A:TYR:HB2	2	0.98
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	5	0.97
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	5	0.97
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	5	0.97
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	17	0.97
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	17	0.97
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	17	0.97
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	14	0.96
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	14	0.96
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	14	0.96
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	14	0.96
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	14	0.96
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	14	0.96
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD21	3	0.95
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD22	3	0.95
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD23	3	0.95
(1,1144)	1:25:A:PHE:HD2	1:103:A:ARG:H	12	0.95
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	7	0.95
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	7	0.95
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	7	0.95
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	7	0.95
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	7	0.95
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	7	0.95
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD21	2	0.94
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD22	2	0.94
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD23	2	0.94
(1,2128)	1:62:A:TYR:HE2	1:65:A:TYR:HB2	3	0.94
(1,2121)	1:140:A:TYR:HD2	1:142:A:ALA:H	4	0.94

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2121)	1:140:A:TYR:HD2	1:142:A:ALA:H	17	0.94
(1,1867)	1:135:A:ARG:HG3	1:138:A:TYR:HE2	5	0.94
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD11	2	0.94
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD12	2	0.94
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD13	2	0.94
(1,1340)	1:11:A:LEU:HD21	1:85:A:TYR:HE1	13	0.94
(1,1340)	1:11:A:LEU:HD22	1:85:A:TYR:HE1	13	0.94
(1,1340)	1:11:A:LEU:HD23	1:85:A:TYR:HE1	13	0.94
(1,1008)	1:34:A:TYR:HE2	1:39:A:LYS:HE3	20	0.94
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB1	6	0.94
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB2	6	0.94
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB3	6	0.94
(1,981)	1:119:A:ALA:HB1	1:140:A:TYR:HD1	10	0.94
(1,981)	1:119:A:ALA:HB2	1:140:A:TYR:HD1	10	0.94
(1,981)	1:119:A:ALA:HB3	1:140:A:TYR:HD1	10	0.94
(1,2121)	1:140:A:TYR:HD2	1:142:A:ALA:H	6	0.93
(1,1921)	1:24:A:TYR:HD2	1:27:A:ARG:HD2	6	0.93
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	10	0.93
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	10	0.93
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	10	0.93
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	10	0.93
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	10	0.93
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	10	0.93
(1,2128)	1:62:A:TYR:HE2	1:65:A:TYR:HB2	19	0.92
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB1	2	0.92
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB2	2	0.92
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB3	2	0.92
(1,2773)	1:65:A:TYR:HD1	1:66:A:ILE:HA	19	0.91
(1,2440)	1:138:A:TYR:HD1	1:142:A:ALA:H	7	0.91
(1,2075)	1:135:A:ARG:HA	1:138:A:TYR:HE2	5	0.91
(1,2037)	1:34:A:TYR:HD2	1:37:A:LEU:H	10	0.91
(1,2037)	1:34:A:TYR:HD2	1:37:A:LEU:H	14	0.91
(1,2037)	1:34:A:TYR:HD2	1:37:A:LEU:H	19	0.91
(1,1921)	1:24:A:TYR:HD2	1:27:A:ARG:HD2	4	0.91
(1,1144)	1:25:A:PHE:HD2	1:103:A:ARG:H	16	0.91
(1,2121)	1:140:A:TYR:HD2	1:142:A:ALA:H	12	0.9
(1,1759)	1:65:A:TYR:HE1	1:69:A:LYS:HG2	17	0.9
(1,1340)	1:11:A:LEU:HD21	1:85:A:TYR:HE1	18	0.9
(1,1340)	1:11:A:LEU:HD22	1:85:A:TYR:HE1	18	0.9
(1,1340)	1:11:A:LEU:HD23	1:85:A:TYR:HE1	18	0.9
(1,1007)	1:34:A:TYR:HE2	1:39:A:LYS:HE2	19	0.9
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB1	12	0.9

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB2	12	0.9
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB3	12	0.9
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	15	0.9
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	15	0.9
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	15	0.9
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	15	0.9
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	15	0.9
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	15	0.9
(1,2121)	1:140:A:TYR:HD2	1:142:A:ALA:H	9	0.89
(1,2037)	1:34:A:TYR:HD2	1:37:A:LEU:H	20	0.89
(1,1340)	1:11:A:LEU:HD21	1:85:A:TYR:HE1	15	0.89
(1,1340)	1:11:A:LEU:HD22	1:85:A:TYR:HE1	15	0.89
(1,1340)	1:11:A:LEU:HD23	1:85:A:TYR:HE1	15	0.89
(1,2121)	1:140:A:TYR:HD2	1:142:A:ALA:H	1	0.88
(1,2121)	1:140:A:TYR:HD2	1:142:A:ALA:H	18	0.88
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB1	9	0.88
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB2	9	0.88
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB3	9	0.88
(1,2773)	1:65:A:TYR:HD1	1:66:A:ILE:HA	1	0.87
(1,2037)	1:34:A:TYR:HD2	1:37:A:LEU:H	11	0.87
(1,1144)	1:25:A:PHE:HD2	1:103:A:ARG:H	10	0.87
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB1	16	0.87
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB2	16	0.87
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB3	16	0.87
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	8	0.87
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	8	0.87
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	8	0.87
(1,2773)	1:65:A:TYR:HD1	1:66:A:ILE:HA	17	0.86
(1,2437)	1:136:A:LEU:HA	1:138:A:TYR:HD2	5	0.86
(1,1240)	1:20:A:PHE:HE2	1:51:A:PRO:HA	6	0.86
(1,2121)	1:140:A:TYR:HD2	1:142:A:ALA:H	14	0.85
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	20	0.85
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	20	0.85
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	20	0.85
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	20	0.85
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	20	0.85
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	20	0.85
(1,2773)	1:65:A:TYR:HD1	1:66:A:ILE:HA	2	0.84
(1,2128)	1:62:A:TYR:HE2	1:65:A:TYR:HB2	17	0.84
(1,2121)	1:140:A:TYR:HD2	1:142:A:ALA:H	16	0.84
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	12	0.84
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	12	0.84

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	12	0.84
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	3	0.84
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	3	0.84
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	3	0.84
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	3	0.84
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	3	0.84
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	3	0.84
(1,2773)	1:65:A:TYR:HD1	1:66:A:ILE:HA	4	0.83
(1,2037)	1:34:A:TYR:HD2	1:37:A:LEU:H	2	0.83
(1,1340)	1:11:A:LEU:HD21	1:85:A:TYR:HE1	1	0.83
(1,1340)	1:11:A:LEU:HD22	1:85:A:TYR:HE1	1	0.83
(1,1340)	1:11:A:LEU:HD23	1:85:A:TYR:HE1	1	0.83
(1,1090)	1:34:A:TYR:HD2	1:39:A:LYS:HB2	16	0.83
(1,1007)	1:34:A:TYR:HE2	1:39:A:LYS:HE2	15	0.83
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	19	0.83
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	19	0.83
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	19	0.83
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	13	0.83
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	13	0.83
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	13	0.83
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	13	0.83
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	13	0.83
(1,879)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	13	0.83
(1,2037)	1:34:A:TYR:HD2	1:37:A:LEU:H	5	0.82
(1,2037)	1:34:A:TYR:HD2	1:37:A:LEU:H	18	0.82
(1,1340)	1:11:A:LEU:HD21	1:85:A:TYR:HE1	20	0.81
(1,1340)	1:11:A:LEU:HD22	1:85:A:TYR:HE1	20	0.81
(1,1340)	1:11:A:LEU:HD23	1:85:A:TYR:HE1	20	0.81
(1,2075)	1:135:A:ARG:HA	1:138:A:TYR:HE2	7	0.8
(1,2037)	1:34:A:TYR:HD2	1:37:A:LEU:H	3	0.8
(1,2037)	1:34:A:TYR:HD2	1:37:A:LEU:H	9	0.8
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD11	20	0.8
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD12	20	0.8
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD13	20	0.8
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD21	8	0.79
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD22	8	0.79
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD23	8	0.79
(1,2128)	1:62:A:TYR:HE2	1:65:A:TYR:HB2	5	0.79
(1,2037)	1:34:A:TYR:HD2	1:37:A:LEU:H	12	0.79
(1,2773)	1:65:A:TYR:HD1	1:66:A:ILE:HA	15	0.78
(1,1759)	1:65:A:TYR:HE1	1:69:A:LYS:HG2	12	0.78
(1,2121)	1:140:A:TYR:HD2	1:142:A:ALA:H	2	0.77

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2121)	1:140:A:TYR:HD2	1:142:A:ALA:H	3	0.77
(1,1007)	1:34:A:TYR:HE2	1:39:A:LYS:HE2	11	0.77
(1,2986)	1:24:A:TYR:HE1	1:25:A:PHE:HB2	6	0.76
(1,2773)	1:65:A:TYR:HD1	1:66:A:ILE:HA	12	0.76
(1,1759)	1:65:A:TYR:HE1	1:69:A:LYS:HG2	1	0.75
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD11	1	0.75
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD12	1	0.75
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD13	1	0.75
(1,927)	1:34:A:TYR:HE2	1:39:A:LYS:HE2	20	0.75
(1,927)	1:34:A:TYR:HE2	1:39:A:LYS:HE3	20	0.75
(1,1759)	1:65:A:TYR:HE1	1:69:A:LYS:HG2	2	0.74
(1,1144)	1:25:A:PHE:HD2	1:103:A:ARG:H	8	0.74
(1,2128)	1:62:A:TYR:HE2	1:65:A:TYR:HB2	4	0.73
(1,1144)	1:25:A:PHE:HD2	1:103:A:ARG:H	11	0.73
(1,1144)	1:25:A:PHE:HD2	1:103:A:ARG:H	14	0.73
(1,1144)	1:25:A:PHE:HD2	1:103:A:ARG:H	15	0.73
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	11	0.73
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	11	0.73
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	11	0.73
(1,1466)	1:85:A:TYR:HE2	1:118:A:VAL:HA	19	0.72
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	6	0.72
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	6	0.72
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	6	0.72
(1,2121)	1:140:A:TYR:HD2	1:142:A:ALA:H	20	0.71
(1,1008)	1:34:A:TYR:HE2	1:39:A:LYS:HE3	12	0.71
(1,2128)	1:62:A:TYR:HE2	1:65:A:TYR:HB2	11	0.7
(1,1466)	1:85:A:TYR:HE2	1:118:A:VAL:HA	15	0.7
(1,1142)	1:62:A:TYR:HD1	1:136:A:LEU:HG	16	0.7
(1,1082)	1:34:A:TYR:HD2	1:39:A:LYS:HG3	15	0.7
(1,685)	1:140:A:TYR:H	1:140:A:TYR:HE2	12	0.7
(1,2128)	1:62:A:TYR:HE2	1:65:A:TYR:HB2	12	0.69
(1,2037)	1:34:A:TYR:HD2	1:37:A:LEU:H	15	0.69
(1,1144)	1:25:A:PHE:HD2	1:103:A:ARG:H	7	0.69
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB1	4	0.69
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB2	4	0.69
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB3	4	0.69
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD11	9	0.69
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD12	9	0.69
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD13	9	0.69
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD21	9	0.69
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD22	9	0.69
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD23	9	0.69

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2764)	1:84:A:LEU:HD21	1:85:A:TYR:HD2	5	0.68
(1,2764)	1:84:A:LEU:HD22	1:85:A:TYR:HD2	5	0.68
(1,2764)	1:84:A:LEU:HD23	1:85:A:TYR:HD2	5	0.68
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD11	2	0.68
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD12	2	0.68
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD13	2	0.68
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD21	2	0.68
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD22	2	0.68
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD23	2	0.68
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD11	2	0.67
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD12	2	0.67
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD13	2	0.67
(1,1144)	1:25:A:PHE:HD2	1:103:A:ARG:H	6	0.67
(1,1144)	1:25:A:PHE:HD2	1:103:A:ARG:H	20	0.67
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD11	5	0.67
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD12	5	0.67
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD13	5	0.67
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD21	5	0.67
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD22	5	0.67
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD23	5	0.67
(1,685)	1:140:A:TYR:H	1:140:A:TYR:HE2	19	0.67
(1,624)	1:99:A:PHE:H	1:99:A:PHE:HE2	7	0.67
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD21	1	0.66
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD22	1	0.66
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD23	1	0.66
(1,2121)	1:140:A:TYR:HD2	1:142:A:ALA:H	5	0.66
(1,2121)	1:140:A:TYR:HD2	1:142:A:ALA:H	15	0.66
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD11	17	0.66
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD12	17	0.66
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD13	17	0.66
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD21	17	0.66
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD22	17	0.66
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD23	17	0.66
(1,1144)	1:25:A:PHE:HD2	1:103:A:ARG:H	18	0.65
(1,1082)	1:34:A:TYR:HD2	1:39:A:LYS:HG3	1	0.65
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD11	1	0.65
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD12	1	0.65
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD13	1	0.65
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD21	1	0.65
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD22	1	0.65
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD23	1	0.65
(1,685)	1:140:A:TYR:H	1:140:A:TYR:HE2	6	0.65

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2437)	1:136:A:LEU:HA	1:138:A:TYR:HD2	7	0.64
(1,2037)	1:34:A:TYR:HD2	1:37:A:LEU:H	1	0.64
(1,2037)	1:34:A:TYR:HD2	1:37:A:LEU:H	16	0.64
(1,685)	1:140:A:TYR:H	1:140:A:TYR:HE2	8	0.64
(1,2128)	1:62:A:TYR:HE2	1:65:A:TYR:HB2	6	0.63
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD11	16	0.63
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD12	16	0.63
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD13	16	0.63
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD11	12	0.63
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD12	12	0.63
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD13	12	0.63
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD21	12	0.63
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD22	12	0.63
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD23	12	0.63
(1,685)	1:140:A:TYR:H	1:140:A:TYR:HE2	11	0.63
(1,685)	1:140:A:TYR:H	1:140:A:TYR:HE2	17	0.63
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD11	8	0.62
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD12	8	0.62
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD13	8	0.62
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD21	8	0.62
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD22	8	0.62
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD23	8	0.62
(1,1466)	1:85:A:TYR:HE2	1:118:A:VAL:HA	4	0.61
(1,1466)	1:85:A:TYR:HE2	1:118:A:VAL:HA	17	0.61
(1,1371)	1:34:A:TYR:HD2	1:39:A:LYS:HG2	9	0.61
(1,1343)	1:12:A:THR:HA	1:85:A:TYR:HE1	2	0.61
(1,1082)	1:34:A:TYR:HD2	1:39:A:LYS:HG3	3	0.61
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD11	18	0.61
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD12	18	0.61
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD13	18	0.61
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD21	18	0.61
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD22	18	0.61
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD23	18	0.61
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD11	19	0.61
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD12	19	0.61
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD13	19	0.61
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD21	19	0.61
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD22	19	0.61
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD23	19	0.61
(1,2764)	1:84:A:LEU:HD21	1:85:A:TYR:HD2	16	0.6
(1,2764)	1:84:A:LEU:HD22	1:85:A:TYR:HD2	16	0.6
(1,2764)	1:84:A:LEU:HD23	1:85:A:TYR:HD2	16	0.6

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2035)	1:135:A:ARG:HA	1:138:A:TYR:HD2	5	0.59
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD11	15	0.59
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD12	15	0.59
(1,1707)	1:34:A:TYR:HD2	1:37:A:LEU:HD13	15	0.59
(1,1371)	1:34:A:TYR:HD2	1:39:A:LYS:HG2	2	0.59
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD11	6	0.59
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD12	6	0.59
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD13	6	0.59
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD21	6	0.59
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD22	6	0.59
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD23	6	0.59
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD11	14	0.59
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD12	14	0.59
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD13	14	0.59
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD21	14	0.59
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD22	14	0.59
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD23	14	0.59
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD11	11	0.58
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD12	11	0.58
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD13	11	0.58
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD21	11	0.58
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD22	11	0.58
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD23	11	0.58
(1,2764)	1:84:A:LEU:HD21	1:85:A:TYR:HD2	8	0.57
(1,2764)	1:84:A:LEU:HD22	1:85:A:TYR:HD2	8	0.57
(1,2764)	1:84:A:LEU:HD23	1:85:A:TYR:HD2	8	0.57
(1,1466)	1:85:A:TYR:HE2	1:118:A:VAL:HA	20	0.57
(1,1371)	1:34:A:TYR:HD2	1:39:A:LYS:HG2	5	0.57
(1,1144)	1:25:A:PHE:HD2	1:103:A:ARG:H	1	0.57
(1,1007)	1:34:A:TYR:HE2	1:39:A:LYS:HE2	13	0.57
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD11	7	0.57
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD12	7	0.57
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD13	7	0.57
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD21	7	0.57
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD22	7	0.57
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD23	7	0.57
(1,624)	1:99:A:PHE:H	1:99:A:PHE:HE2	2	0.57
(1,1371)	1:34:A:TYR:HD2	1:39:A:LYS:HG2	20	0.56
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD11	10	0.56
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD12	10	0.56
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD13	10	0.56
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD21	10	0.56

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD22	10	0.56
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD23	10	0.56
(1,685)	1:140:A:TYR:H	1:140:A:TYR:HE2	10	0.56
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD21	15	0.55
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD22	15	0.55
(1,2255)	1:34:A:TYR:HD2	1:37:A:LEU:HD23	15	0.55
(1,1144)	1:25:A:PHE:HD2	1:103:A:ARG:H	17	0.55
(1,927)	1:34:A:TYR:HE2	1:39:A:LYS:HE2	15	0.55
(1,927)	1:34:A:TYR:HE2	1:39:A:LYS:HE3	15	0.55
(1,680)	1:138:A:TYR:H	1:138:A:TYR:HE2	5	0.55
(1,2035)	1:135:A:ARG:HA	1:138:A:TYR:HD2	7	0.54
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD11	14	0.54
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD12	14	0.54
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD13	14	0.54
(1,1748)	1:135:A:ARG:HG2	1:138:A:TYR:HE2	5	0.54
(1,1748)	1:135:A:ARG:HG3	1:138:A:TYR:HE2	5	0.54
(1,1466)	1:85:A:TYR:HE2	1:118:A:VAL:HA	7	0.54
(1,1359)	1:25:A:PHE:HD2	1:103:A:ARG:HA	3	0.54
(1,624)	1:99:A:PHE:H	1:99:A:PHE:HE2	17	0.54
(1,3086)	1:99:A:PHE:HE2	1:100:A:PHE:HB3	7	0.53
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD11	15	0.53
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD12	15	0.53
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD13	15	0.53
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD21	15	0.53
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD22	15	0.53
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD23	15	0.53
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	4	0.53
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	4	0.53
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	4	0.53
(1,1466)	1:85:A:TYR:HE2	1:118:A:VAL:HA	13	0.52
(1,680)	1:138:A:TYR:H	1:138:A:TYR:HE2	7	0.52
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD11	9	0.51
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD12	9	0.51
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD13	9	0.51
(1,1466)	1:85:A:TYR:HE2	1:118:A:VAL:HA	16	0.51
(1,1343)	1:12:A:THR:HA	1:85:A:TYR:HE1	12	0.51
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	17	0.51
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	17	0.51
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	17	0.51
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD11	1	0.5
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD12	1	0.5
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD13	1	0.5

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1466)	1:85:A:TYR:HE2	1:118:A:VAL:HA	6	0.5
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	19	0.5
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	19	0.5
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	19	0.5
(1,2037)	1:34:A:TYR:HD2	1:37:A:LEU:H	13	0.49
(1,1788)	1:135:A:ARG:HG2	1:138:A:TYR:HD2	5	0.49
(1,1788)	1:135:A:ARG:HG3	1:138:A:TYR:HD2	5	0.49
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD11	15	0.49
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD12	15	0.49
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD13	15	0.49
(1,1343)	1:12:A:THR:HA	1:85:A:TYR:HE1	7	0.49
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD11	3	0.49
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD12	3	0.49
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD13	3	0.49
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD21	3	0.49
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD22	3	0.49
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD23	3	0.49
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD11	20	0.49
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD12	20	0.49
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD13	20	0.49
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD21	20	0.49
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD22	20	0.49
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD23	20	0.49
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD11	5	0.48
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD12	5	0.48
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD13	5	0.48
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	2	0.48
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	2	0.48
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	2	0.48
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	5	0.48
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	5	0.48
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	5	0.48
(1,685)	1:140:A:TYR:H	1:140:A:TYR:HE2	5	0.48
(1,1371)	1:34:A:TYR:HD2	1:39:A:LYS:HG2	14	0.47
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	9	0.47
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	9	0.47
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	9	0.47
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	11	0.47
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	11	0.47
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	11	0.47
(1,685)	1:140:A:TYR:H	1:140:A:TYR:HE2	1	0.47
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD11	13	0.46

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD12	13	0.46
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD13	13	0.46
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD11	13	0.46
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD12	13	0.46
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD13	13	0.46
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD21	13	0.46
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD22	13	0.46
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD23	13	0.46
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	12	0.46
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	12	0.46
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	12	0.46
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD21	1	0.45
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD22	1	0.45
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD23	1	0.45
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	6	0.45
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	6	0.45
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	6	0.45
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	8	0.45
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	8	0.45
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	8	0.45
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD21	18	0.44
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD22	18	0.44
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD23	18	0.44
(1,2128)	1:62:A:TYR:HE2	1:65:A:TYR:HB2	16	0.44
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD11	18	0.44
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD12	18	0.44
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD13	18	0.44
(1,1466)	1:85:A:TYR:HE2	1:118:A:VAL:HA	14	0.44
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB1	1	0.44
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB2	1	0.44
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB3	1	0.44
(1,624)	1:99:A:PHE:H	1:99:A:PHE:HE2	6	0.44
(1,685)	1:140:A:TYR:H	1:140:A:TYR:HE2	3	0.43
(1,1371)	1:34:A:TYR:HD2	1:39:A:LYS:HG2	11	0.42
(1,685)	1:140:A:TYR:H	1:140:A:TYR:HE2	4	0.42
(1,624)	1:99:A:PHE:H	1:99:A:PHE:HE2	4	0.42
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD11	3	0.41
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD12	3	0.41
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD13	3	0.41
(1,1371)	1:34:A:TYR:HD2	1:39:A:LYS:HG2	19	0.41
(1,685)	1:140:A:TYR:H	1:140:A:TYR:HE2	18	0.41
(1,1466)	1:85:A:TYR:HE2	1:118:A:VAL:HA	2	0.4

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,277)	1:99:A:PHE:H	1:99:A:PHE:HD2	7	0.4
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD11	4	0.39
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD12	4	0.39
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD13	4	0.39
(1,1082)	1:34:A:TYR:HD2	1:39:A:LYS:HG3	20	0.39
(1,685)	1:140:A:TYR:H	1:140:A:TYR:HE2	15	0.39
(1,2642)	1:140:A:TYR:HD2	1:141:A:LEU:H	19	0.38
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD11	10	0.38
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD12	10	0.38
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD13	10	0.38
(1,277)	1:99:A:PHE:H	1:99:A:PHE:HD2	17	0.38
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB1	5	0.37
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB2	5	0.37
(1,1006)	1:85:A:TYR:HD2	1:121:A:ALA:HB3	5	0.37
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	1	0.37
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	1	0.37
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	1	0.37
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	3	0.36
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	3	0.36
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	3	0.36
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	3	0.36
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	3	0.36
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	3	0.36
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	3	0.36
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	3	0.36
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	3	0.36
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	3	0.36
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	3	0.36
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	3	0.36
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	3	0.36
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	3	0.36
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	3	0.36
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	3	0.36
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	3	0.36
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	3	0.36
(1,1371)	1:34:A:TYR:HD2	1:39:A:LYS:HG2	13	0.36
(1,1343)	1:12:A:THR:HA	1:85:A:TYR:HE1	9	0.36
(1,1082)	1:34:A:TYR:HD2	1:39:A:LYS:HG3	9	0.36
(1,277)	1:99:A:PHE:H	1:99:A:PHE:HD2	2	0.35
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	10	0.34
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	10	0.34
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	10	0.34

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	10	0.34
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	10	0.34
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	10	0.34
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	10	0.34
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	10	0.34
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	10	0.34
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	10	0.34
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	10	0.34
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	10	0.34
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	10	0.34
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	10	0.34
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	10	0.34
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	10	0.34
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	10	0.34
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	10	0.34
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	15	0.34
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	15	0.34
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	15	0.34
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	15	0.34
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	15	0.34
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	15	0.34
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	15	0.34
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	15	0.34
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	15	0.34
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	15	0.34
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	15	0.34
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	15	0.34
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	15	0.34
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	15	0.34
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	15	0.34
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	15	0.34
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	15	0.34
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	15	0.34
(1,1371)	1:34:A:TYR:HD2	1:39:A:LYS:HG2	16	0.34
(1,685)	1:140:A:TYR:H	1:140:A:TYR:HE2	9	0.34
(1,277)	1:99:A:PHE:H	1:99:A:PHE:HD2	6	0.34
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	2	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	2	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	2	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	2	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	2	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	2	0.33

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	2	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	2	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	2	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	2	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	2	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	2	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	2	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	2	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	2	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	2	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	2	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	2	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	5	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	5	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	5	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	5	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	5	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	5	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	5	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	5	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	5	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	5	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	5	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	5	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	5	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	5	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	5	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	5	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	5	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	5	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	6	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	6	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	6	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	6	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	6	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	6	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	6	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	6	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	6	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	6	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	6	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	6	0.33

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	6	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	6	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	6	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	6	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	6	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	6	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	7	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	7	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	7	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	7	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	7	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	7	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	7	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	7	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	7	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	7	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	7	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	7	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	7	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	7	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	7	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	7	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	7	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	7	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	8	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	8	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	8	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	8	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	8	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	8	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	8	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	8	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	8	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	8	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	8	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	8	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	8	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	8	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	8	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	8	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	8	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	8	0.33

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	11	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	11	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	11	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	11	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	11	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	11	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	11	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	11	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	11	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	11	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	11	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	11	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	11	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	11	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	11	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	11	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	11	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	11	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	12	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	12	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	12	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	12	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	12	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	12	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	12	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	12	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	12	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	12	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	12	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	12	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	12	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	12	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	12	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	12	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	12	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	12	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	13	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	13	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	13	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	13	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	13	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	13	0.33

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	13	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	13	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	13	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	13	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	13	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	13	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	13	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	13	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	13	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	13	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	13	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	13	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	14	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	14	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	14	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	14	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	14	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	14	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	14	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	14	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	14	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	14	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	14	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	14	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	14	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	14	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	14	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	14	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	14	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	14	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	18	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	18	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	18	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	18	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	18	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	18	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	18	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	18	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	18	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	18	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	18	0.33
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	18	0.33

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	18	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	18	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	18	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	18	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	18	0.33
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	18	0.33
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD11	7	0.33
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD12	7	0.33
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD13	7	0.33
(1,1359)	1:25:A:PHE:HD2	1:103:A:ARG:HA	2	0.33
(1,1343)	1:12:A:THR:HA	1:85:A:TYR:HE1	13	0.33
(1,277)	1:99:A:PHE:H	1:99:A:PHE:HD2	4	0.33
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	16	0.32
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	16	0.32
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	16	0.32
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	16	0.32
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	16	0.32
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	16	0.32
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	16	0.32
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	16	0.32
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	16	0.32
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	16	0.32
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	16	0.32
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	16	0.32
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	16	0.32
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	16	0.32
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	16	0.32
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	16	0.32
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	16	0.32
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	16	0.32
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD11	16	0.32
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD12	16	0.32
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD13	16	0.32
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD21	16	0.32
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD22	16	0.32
(1,951)	1:62:A:TYR:HE1	1:136:A:LEU:HD23	16	0.32
(1,624)	1:99:A:PHE:H	1:99:A:PHE:HE2	15	0.32
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	4	0.31
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	4	0.31
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	4	0.31
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	4	0.31
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	4	0.31

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	4	0.31
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	4	0.31
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	4	0.31
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	4	0.31
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	4	0.31
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	4	0.31
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	4	0.31
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	4	0.31
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	4	0.31
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	4	0.31
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	4	0.31
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	4	0.31
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	4	0.31
(1,1343)	1:12:A:THR:HA	1:85:A:TYR:HE1	5	0.31
(1,685)	1:140:A:TYR:H	1:140:A:TYR:HE2	2	0.31
(1,685)	1:140:A:TYR:H	1:140:A:TYR:HE2	7	0.31
(1,685)	1:140:A:TYR:H	1:140:A:TYR:HE2	16	0.31
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD11	12	0.3
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD12	12	0.3
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD13	12	0.3
(1,1343)	1:12:A:THR:HA	1:85:A:TYR:HE1	1	0.3
(1,1343)	1:12:A:THR:HA	1:85:A:TYR:HE1	10	0.3
(1,277)	1:99:A:PHE:H	1:99:A:PHE:HD2	15	0.3
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	1	0.29
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	1	0.29
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	1	0.29
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	1	0.29
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	1	0.29
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	1	0.29
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	1	0.29
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	1	0.29
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	1	0.29
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	1	0.29
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	1	0.29
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	1	0.29
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	1	0.29
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	1	0.29
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	1	0.29
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	1	0.29
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	1	0.29
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	1	0.29
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	9	0.29

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	9	0.29
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	9	0.29
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	9	0.29
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	9	0.29
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	9	0.29
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	9	0.29
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	9	0.29
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	9	0.29
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	9	0.29
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	9	0.29
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	9	0.29
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	9	0.29
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	9	0.29
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	9	0.29
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	9	0.29
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	9	0.29
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	9	0.29
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	17	0.28
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	17	0.28
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	17	0.28
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	17	0.28
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	17	0.28
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	17	0.28
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	17	0.28
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	17	0.28
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	17	0.28
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	17	0.28
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	17	0.28
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	17	0.28
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	17	0.28
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	17	0.28
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	17	0.28
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	17	0.28
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	17	0.28
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	17	0.28
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	19	0.28
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	19	0.28
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	19	0.28
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	19	0.28
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	19	0.28
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	19	0.28
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	19	0.28

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	19	0.28
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	19	0.28
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	19	0.28
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	19	0.28
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	19	0.28
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	19	0.28
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	19	0.28
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	19	0.28
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	19	0.28
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	19	0.28
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	19	0.28
(1,624)	1:99:A:PHE:H	1:99:A:PHE:HE2	18	0.28
(1,685)	1:140:A:TYR:H	1:140:A:TYR:HE2	13	0.27
(1,277)	1:99:A:PHE:H	1:99:A:PHE:HD2	18	0.27
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	20	0.26
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	20	0.26
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	20	0.26
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4A	20	0.26
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4B	20	0.26
(1,3176)	1:23:A:ALA:HB1	2:201:A:PKA:H4C	20	0.26
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	20	0.26
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	20	0.26
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	20	0.26
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4A	20	0.26
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4B	20	0.26
(1,3176)	1:23:A:ALA:HB2	2:201:A:PKA:H4C	20	0.26
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	20	0.26
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	20	0.26
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	20	0.26
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4A	20	0.26
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4B	20	0.26
(1,3176)	1:23:A:ALA:HB3	2:201:A:PKA:H4C	20	0.26
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD11	17	0.26
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD12	17	0.26
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD13	17	0.26
(1,1759)	1:65:A:TYR:HE1	1:69:A:LYS:HG2	4	0.26
(1,1466)	1:85:A:TYR:HE2	1:118:A:VAL:HA	12	0.26
(1,1371)	1:34:A:TYR:HD2	1:39:A:LYS:HG2	15	0.26
(1,1343)	1:12:A:THR:HA	1:85:A:TYR:HE1	16	0.26
(1,685)	1:140:A:TYR:H	1:140:A:TYR:HE2	20	0.26
(1,1371)	1:34:A:TYR:HD2	1:39:A:LYS:HG2	12	0.25
(1,1371)	1:34:A:TYR:HD2	1:39:A:LYS:HG2	18	0.25

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1343)	1:12:A:THR:HA	1:85:A:TYR:HE1	20	0.25
(1,1082)	1:34:A:TYR:HD2	1:39:A:LYS:HG3	2	0.25
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	14	0.25
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	14	0.25
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	14	0.25
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	18	0.24
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	18	0.24
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	18	0.24
(1,685)	1:140:A:TYR:H	1:140:A:TYR:HE2	14	0.24
(1,277)	1:99:A:PHE:H	1:99:A:PHE:HD2	11	0.24
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	7	0.23
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	7	0.23
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	7	0.23
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	3	0.22
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	3	0.22
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	3	0.22
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	3	0.22
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	3	0.22
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	3	0.22
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	3	0.22
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	3	0.22
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	3	0.22
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	3	0.22
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	3	0.22
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	3	0.22
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	3	0.22
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	3	0.22
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	3	0.22
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	3	0.22
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	3	0.22
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	3	0.22
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	17	0.22
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	17	0.22
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	17	0.22
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	17	0.22
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	17	0.22
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	17	0.22
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	17	0.22
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	17	0.22
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	17	0.22
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	17	0.22
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	17	0.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	17	0.22
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	17	0.22
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	17	0.22
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	17	0.22
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	17	0.22
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	17	0.22
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	17	0.22
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD21	13	0.21
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD22	13	0.21
(1,2624)	1:140:A:TYR:HD2	1:141:A:LEU:HD23	13	0.21
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD11	6	0.21
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD12	6	0.21
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD13	6	0.21
(1,1371)	1:34:A:TYR:HD2	1:39:A:LYS:HG2	1	0.21
(1,1240)	1:20:A:PHE:HE2	1:51:A:PRO:HA	8	0.21
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	10	0.21
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	10	0.21
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	10	0.21
(1,624)	1:99:A:PHE:H	1:99:A:PHE:HE2	11	0.21
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	8	0.19
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	8	0.19
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	8	0.19
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	8	0.19
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	8	0.19
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	8	0.19
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	8	0.19
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	8	0.19
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	8	0.19
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	8	0.19
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	8	0.19
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	8	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	8	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	8	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	8	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	8	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	8	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	8	0.19
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	18	0.19
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	18	0.19
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	18	0.19
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	18	0.19
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	18	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	18	0.19
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	18	0.19
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	18	0.19
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	18	0.19
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	18	0.19
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	18	0.19
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	18	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	18	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	18	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	18	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	18	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	18	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	18	0.19
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	19	0.19
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	19	0.19
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	19	0.19
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	19	0.19
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	19	0.19
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	19	0.19
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	19	0.19
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	19	0.19
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	19	0.19
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	19	0.19
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	19	0.19
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	19	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	19	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	19	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	19	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	19	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	19	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	19	0.19
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	20	0.19
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	20	0.19
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	20	0.19
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	20	0.19
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	20	0.19
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	20	0.19
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	20	0.19
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	20	0.19
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	20	0.19
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	20	0.19
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	20	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	20	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	20	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	20	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	20	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	20	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	20	0.19
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	20	0.19
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD11	11	0.19
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD12	11	0.19
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD13	11	0.19
(1,1082)	1:34:A:TYR:HD2	1:39:A:LYS:HG3	5	0.19
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	13	0.18
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	13	0.18
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	13	0.18
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	13	0.18
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	13	0.18
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	13	0.18
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	13	0.18
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	13	0.18
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	13	0.18
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	13	0.18
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	13	0.18
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	13	0.18
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	13	0.18
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	13	0.18
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	13	0.18
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	13	0.18
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	13	0.18
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	13	0.18
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	15	0.18
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	15	0.18
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	15	0.18
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	15	0.18
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	15	0.18
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	15	0.18
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	15	0.18
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	15	0.18
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	15	0.18
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	15	0.18
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	15	0.18
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	15	0.18
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	15	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	15	0.18
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	15	0.18
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	15	0.18
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	15	0.18
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	15	0.18
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	11	0.17
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	11	0.17
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	11	0.17
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	11	0.17
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	11	0.17
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	11	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	11	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	11	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	11	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	11	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	11	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	11	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	11	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	11	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	11	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	11	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	11	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	11	0.17
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	14	0.17
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	14	0.17
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	14	0.17
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	14	0.17
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	14	0.17
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	14	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	14	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	14	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	14	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	14	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	14	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	14	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	14	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	14	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	14	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	14	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	14	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	14	0.17
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	16	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	16	0.17
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	16	0.17
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	16	0.17
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	16	0.17
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	16	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	16	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	16	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	16	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	16	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	16	0.17
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	16	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	16	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	16	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	16	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	16	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	16	0.17
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	16	0.17
(1,2642)	1:140:A:TYR:HD2	1:141:A:LEU:H	11	0.17
(1,1343)	1:12:A:THR:HA	1:85:A:TYR:HE1	8	0.17
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD11	16	0.17
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD12	16	0.17
(1,921)	1:62:A:TYR:HD1	1:136:A:LEU:HD13	16	0.17
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD11	8	0.16
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD12	8	0.16
(1,1760)	1:140:A:TYR:HD1	1:144:A:LEU:HD13	8	0.16
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	6	0.15
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	6	0.15
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	6	0.15
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	6	0.15
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	6	0.15
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	6	0.15
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	6	0.15
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	6	0.15
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	6	0.15
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	6	0.15
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	6	0.15
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	6	0.15
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	6	0.15
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	6	0.15
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	6	0.15
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	6	0.15
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	6	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	6	0.15
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	12	0.15
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	12	0.15
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	12	0.15
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	12	0.15
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	12	0.15
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	12	0.15
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	12	0.15
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	12	0.15
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	12	0.15
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	12	0.15
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	12	0.15
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	12	0.15
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	12	0.15
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	12	0.15
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	12	0.15
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	12	0.15
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	12	0.15
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	12	0.15
(1,1371)	1:34:A:TYR:HD2	1:39:A:LYS:HG2	3	0.15
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD21	15	0.15
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD22	15	0.15
(1,922)	1:62:A:TYR:HD1	1:136:A:LEU:HD23	15	0.15
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	5	0.14
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	5	0.14
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	5	0.14
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	5	0.14
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	5	0.14
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	5	0.14
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	5	0.14
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	5	0.14
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	5	0.14
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	5	0.14
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	5	0.14
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	5	0.14
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	5	0.14
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	5	0.14
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	5	0.14
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	5	0.14
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	5	0.14
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	5	0.14
(1,1955)	1:135:A:ARG:HG3	1:138:A:TYR:HD2	5	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,1954)	1:135:A:ARG:HG2	1:138:A:TYR:HD2	5	0.14
(1,1007)	1:34:A:TYR:HE2	1:39:A:LYS:HE2	18	0.14
(1,277)	1:99:A:PHE:H	1:99:A:PHE:HD2	5	0.14
(1,70)	1:166:A:ARG:HA	1:166:A:ARG:HD2	13	0.14
(1,70)	1:166:A:ARG:HA	1:166:A:ARG:HD3	13	0.14
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	4	0.13
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	4	0.13
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	4	0.13
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	4	0.13
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	4	0.13
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	4	0.13
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	4	0.13
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	4	0.13
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	4	0.13
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	4	0.13
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	4	0.13
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	4	0.13
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	4	0.13
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	4	0.13
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	4	0.13
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	4	0.13
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	4	0.13
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	4	0.13
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	7	0.13
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	7	0.13
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	7	0.13
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	7	0.13
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	7	0.13
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	7	0.13
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	7	0.13
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	7	0.13
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	7	0.13
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	7	0.13
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	7	0.13
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	7	0.13
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	7	0.13
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	7	0.13
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	7	0.13
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	7	0.13
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	7	0.13
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	7	0.13
(1,1008)	1:34:A:TYR:HE2	1:39:A:LYS:HE3	1	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,2642)	1:140:A:TYR:HD2	1:141:A:LEU:H	8	0.12
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	1	0.11
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	1	0.11
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	1	0.11
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	1	0.11
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	1	0.11
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	1	0.11
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	1	0.11
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	1	0.11
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	1	0.11
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	1	0.11
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	1	0.11
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	1	0.11
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	1	0.11
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	1	0.11
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	1	0.11
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	1	0.11
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	1	0.11
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	1	0.11
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	9	0.11
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	9	0.11
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	9	0.11
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	9	0.11
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	9	0.11
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	9	0.11
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	9	0.11
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	9	0.11
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	9	0.11
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	9	0.11
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	9	0.11
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	9	0.11
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	9	0.11
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	9	0.11
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	9	0.11
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	9	0.11
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	9	0.11
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	9	0.11
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	2	0.1
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	2	0.1
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	2	0.1
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6A	2	0.1
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6B	2	0.1

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,3181)	1:49:A:LEU:HD11	2:201:A:PKA:H6C	2	0.1
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	2	0.1
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	2	0.1
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	2	0.1
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6A	2	0.1
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6B	2	0.1
(1,3181)	1:49:A:LEU:HD12	2:201:A:PKA:H6C	2	0.1
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	2	0.1
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	2	0.1
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	2	0.1
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6A	2	0.1
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6B	2	0.1
(1,3181)	1:49:A:LEU:HD13	2:201:A:PKA:H6C	2	0.1

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

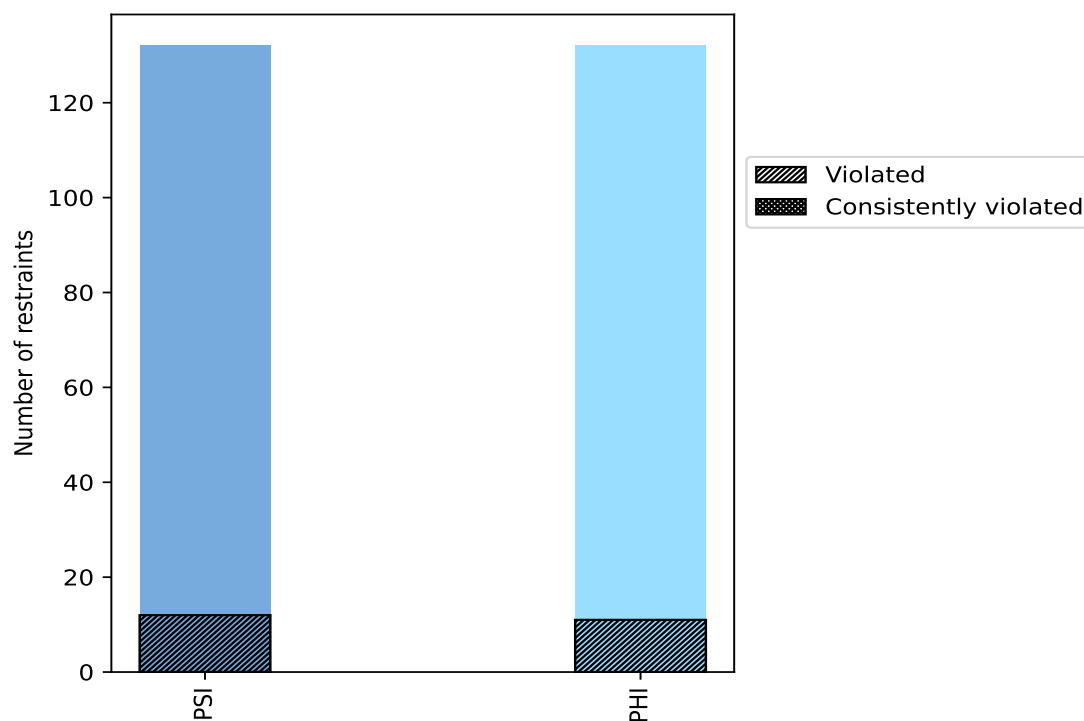
10.1 Summary of dihedral-angle violations [i](#)

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	132	50.0	12	9.1	4.5	0	0.0	0.0
PHI	132	50.0	11	8.3	4.2	0	0.0	0.0
Total	264	100.0	23	8.7	8.7	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](#)



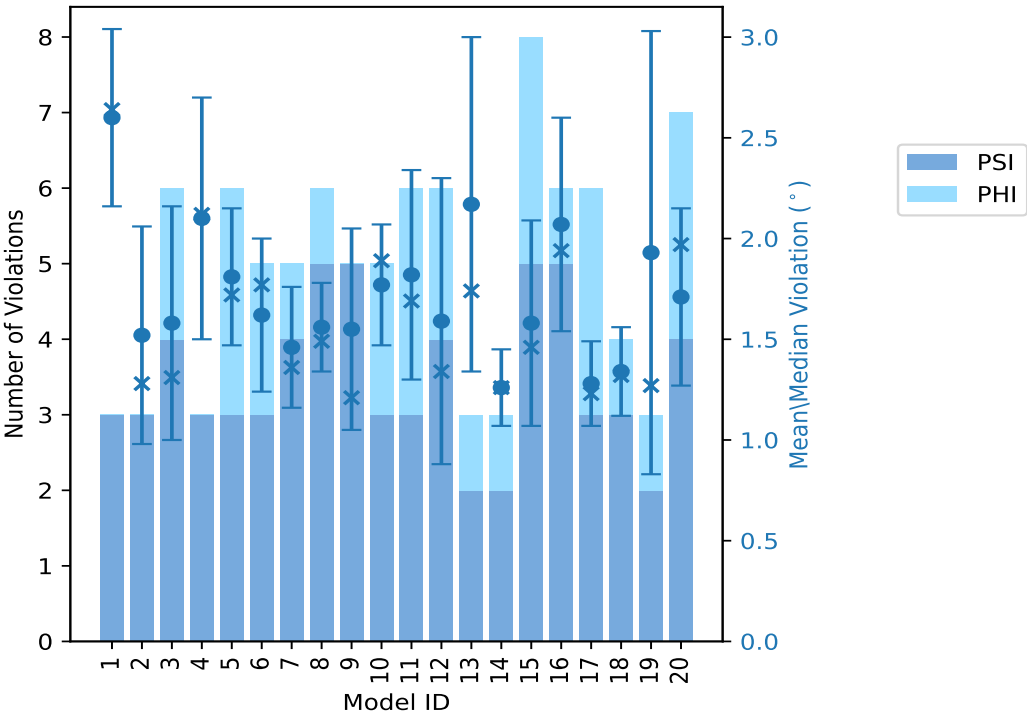
Violated and consistently violated restraints are shown using different hatch patterns in their respective categories

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	3	0	3	2.6	3.11	0.44	2.64
2	3	0	3	1.52	2.27	0.54	1.28
3	4	2	6	1.58	2.54	0.58	1.31
4	3	0	3	2.1	2.83	0.6	2.12
5	3	3	6	1.81	2.49	0.34	1.72
6	3	2	5	1.62	2.06	0.38	1.77
7	4	1	5	1.46	1.88	0.3	1.36
8	5	1	6	1.56	1.95	0.22	1.49
9	5	0	5	1.55	2.2	0.5	1.21
10	3	2	5	1.77	2.17	0.3	1.89
11	3	3	6	1.82	2.6	0.52	1.69
12	4	2	6	1.59	3.16	0.71	1.34
13	2	1	3	2.17	3.34	0.83	1.74
14	2	1	3	1.26	1.5	0.19	1.26
15	5	3	8	1.58	2.79	0.51	1.46
16	5	1	6	2.07	3.0	0.53	1.94
17	3	3	6	1.28	1.71	0.21	1.23
18	3	1	4	1.34	1.67	0.22	1.32
19	2	1	3	1.93	3.49	1.1	1.27
20	4	3	7	1.71	2.2	0.44	1.97

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	%
6	5	11	1	5.0
1	3	4	2	10.0
0	1	1	3	15.0
1	0	1	4	20.0
0	0	0	5	25.0
0	1	1	6	30.0
0	0	0	7	35.0
1	0	1	8	40.0
0	0	0	9	45.0
0	1	1	10	50.0
0	0	0	11	55.0

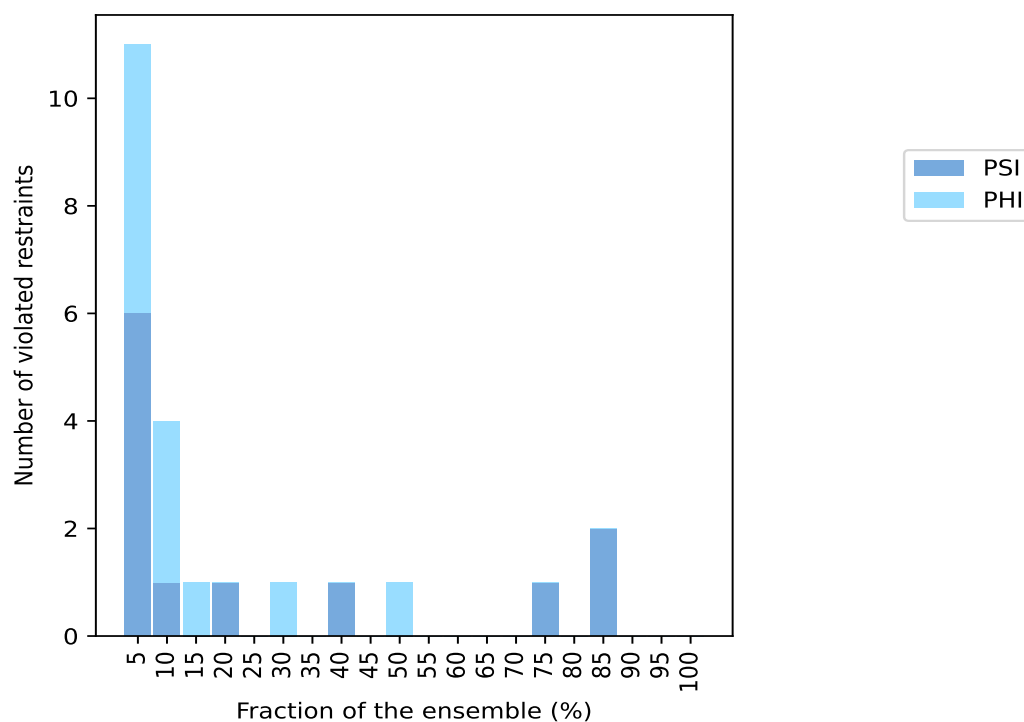
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Number of violated restraints			Fraction of the ensemble	
PSI	PHI	Total	Count ¹	%
0	0	0	12	60.0
0	0	0	13	65.0
0	0	0	14	70.0
1	0	1	15	75.0
0	0	0	16	80.0
2	0	2	17	85.0
0	0	0	18	90.0
0	0	0	19	95.0
0	0	0	20	100.0

¹ Number of models with violations

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

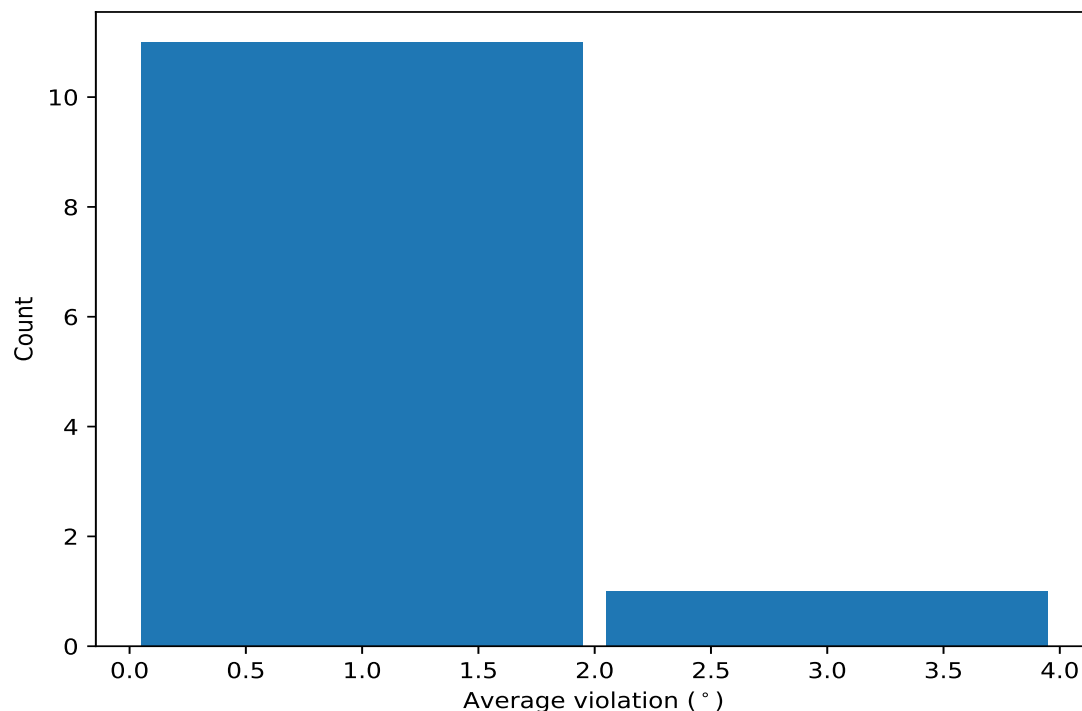


10.4 Most violated dihedral-angle restraints in the ensemble [i](#)

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.

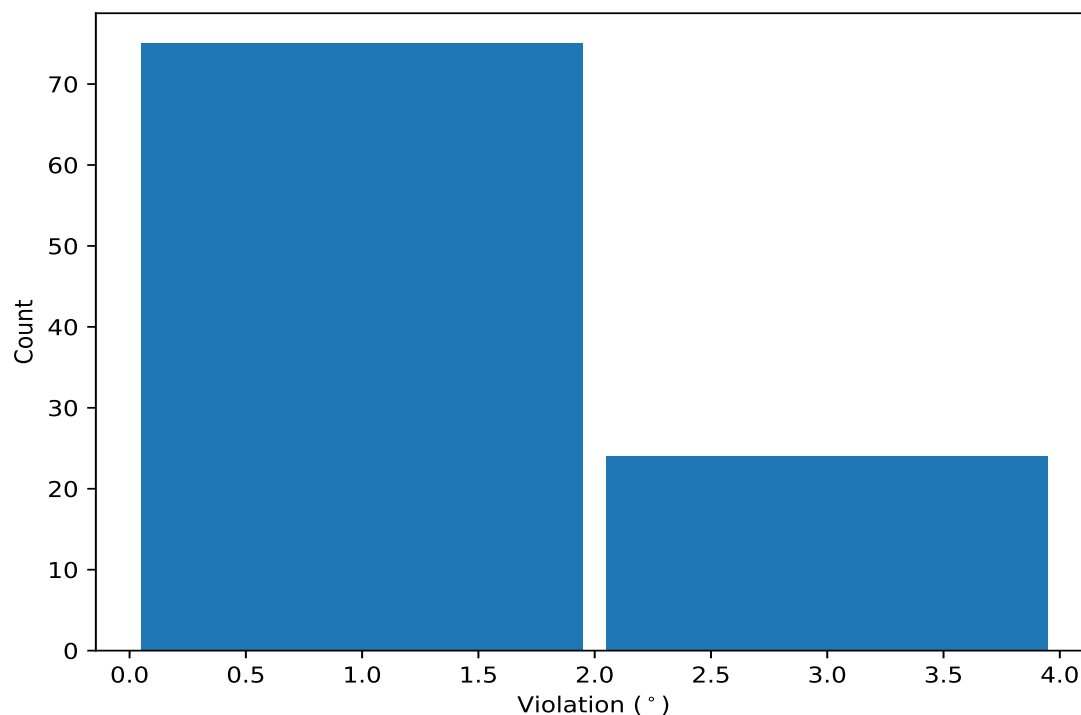
Key	Atom-1	Atom-2	Atom-3	Atom-4	Models ¹	Mean	SD ²	Median
(1,235)	1:125:A:ALA:N	1:125:A:ALA:CA	1:125:A:ALA:C	1:126:A:TRP:N	17	1.62	0.41	1.5
(1,159)	1:34:A:TYR:N	1:34:A:TYR:CA	1:34:A:TYR:C	1:35:A:ALA:N	17	1.35	0.28	1.3
(1,216)	1:105:A:MET:N	1:105:A:MET:CA	1:105:A:MET:C	1:106:A:GLY:N	15	2.44	0.63	2.49
(1,82)	1:100:A:PHE:C	1:101:A:GLY:N	1:101:A:GLY:CA	1:101:A:GLY:C	10	1.6	0.36	1.49
(1,190)	1:71:A:LEU:N	1:71:A:LEU:CA	1:71:A:LEU:C	1:72:A:GLY:N	8	1.66	0.61	1.49
(1,33)	1:41:A:SER:C	1:42:A:TRP:N	1:42:A:TRP:CA	1:42:A:TRP:C	6	1.93	0.57	1.77
(1,264)	1:158:A:ASN:N	1:158:A:ASN:CA	1:158:A:ASN:C	1:159:A:SER:N	4	1.51	0.37	1.35
(1,60)	1:74:A:PHE:C	1:75:A:THR:N	1:75:A:THR:CA	1:75:A:THR:C	3	1.49	0.62	1.05
(1,94)	1:115:A:VAL:C	1:116:A:SER:N	1:116:A:SER:CA	1:116:A:SER:C	2	1.94	0.05	1.94
(1,85)	1:106:A:GLY:C	1:107:A:TRP:N	1:107:A:TRP:CA	1:107:A:TRP:C	2	1.56	0.12	1.56
(1,211)	1:98:A:ILE:N	1:98:A:ILE:CA	1:98:A:ILE:C	1:99:A:PHE:N	2	1.48	0.05	1.48
(1,3)	1:5:A:TRP:C	1:6:A:VAL:N	1:6:A:VAL:CA	1:6:A:VAL:C	2	1.3	0.06	1.3

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 (°)
(1,216)	1:105:A:MET:N	1:105:A:MET:CA	1:105:A:MET:C	1:106:A:GLY:N	19	3.49
(1,216)	1:105:A:MET:N	1:105:A:MET:CA	1:105:A:MET:C	1:106:A:GLY:N	13	3.34
(1,216)	1:105:A:MET:N	1:105:A:MET:CA	1:105:A:MET:C	1:106:A:GLY:N	12	3.16
(1,190)	1:71:A:LEU:N	1:71:A:LEU:CA	1:71:A:LEU:C	1:72:A:GLY:N	1	3.11
(1,216)	1:105:A:MET:N	1:105:A:MET:CA	1:105:A:MET:C	1:106:A:GLY:N	16	3.0
(1,216)	1:105:A:MET:N	1:105:A:MET:CA	1:105:A:MET:C	1:106:A:GLY:N	4	2.83
(1,33)	1:41:A:SER:C	1:42:A:TRP:N	1:42:A:TRP:CA	1:42:A:TRP:C	15	2.79
(1,216)	1:105:A:MET:N	1:105:A:MET:CA	1:105:A:MET:C	1:106:A:GLY:N	1	2.64
(1,33)	1:41:A:SER:C	1:42:A:TRP:N	1:42:A:TRP:CA	1:42:A:TRP:C	11	2.6
(1,216)	1:105:A:MET:N	1:105:A:MET:CA	1:105:A:MET:C	1:106:A:GLY:N	3	2.54
(1,216)	1:105:A:MET:N	1:105:A:MET:CA	1:105:A:MET:C	1:106:A:GLY:N	5	2.49
(1,235)	1:125:A:ALA:N	1:125:A:ALA:CA	1:125:A:ALA:C	1:126:A:TRP:N	16	2.4
(1,60)	1:74:A:PHE:C	1:75:A:THR:N	1:75:A:THR:CA	1:75:A:THR:C	11	2.37
(1,216)	1:105:A:MET:N	1:105:A:MET:CA	1:105:A:MET:C	1:106:A:GLY:N	2	2.27

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Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,235)	1:125:A:ALA:N	1:125:A:ALA:CA	1:125:A:ALA:C	1:126:A:TRP:N	20	2.2
(1,216)	1:105:A:MET:N	1:105:A:MET:CA	1:105:A:MET:C	1:106:A:GLY:N	9	2.2
(1,104)	1:125:A:ALA:C	1:126:A:TRP:N	1:126:A:TRP:CA	1:126:A:TRP:C	3	2.2
(1,159)	1:34:A:TYR:N	1:34:A:TYR:CA	1:34:A:TYR:C	1:35:A:ALA:N	16	2.18
(1,82)	1:100:A:PHE:C	1:101:A:GLY:N	1:101:A:GLY:CA	1:101:A:GLY:C	20	2.18
(1,82)	1:100:A:PHE:C	1:101:A:GLY:N	1:101:A:GLY:CA	1:101:A:GLY:C	10	2.17
(1,264)	1:158:A:ASN:N	1:158:A:ASN:CA	1:158:A:ASN:C	1:159:A:SER:N	9	2.14
(1,235)	1:125:A:ALA:N	1:125:A:ALA:CA	1:125:A:ALA:C	1:126:A:TRP:N	4	2.12
(1,235)	1:125:A:ALA:N	1:125:A:ALA:CA	1:125:A:ALA:C	1:126:A:TRP:N	6	2.06
(1,235)	1:125:A:ALA:N	1:125:A:ALA:CA	1:125:A:ALA:C	1:126:A:TRP:N	1	2.04
(1,94)	1:115:A:VAL:C	1:116:A:SER:N	1:116:A:SER:CA	1:116:A:SER:C	20	1.99
(1,216)	1:105:A:MET:N	1:105:A:MET:CA	1:105:A:MET:C	1:106:A:GLY:N	20	1.97
(1,190)	1:71:A:LEU:N	1:71:A:LEU:CA	1:71:A:LEU:C	1:72:A:GLY:N	8	1.95
(1,164)	1:41:A:SER:N	1:41:A:SER:CA	1:41:A:SER:C	1:42:A:TRP:N	10	1.94
(1,216)	1:105:A:MET:N	1:105:A:MET:CA	1:105:A:MET:C	1:106:A:GLY:N	6	1.93
(1,94)	1:115:A:VAL:C	1:116:A:SER:N	1:116:A:SER:CA	1:116:A:SER:C	5	1.9
(1,32)	1:40:A:PRO:C	1:41:A:SER:N	1:41:A:SER:CA	1:41:A:SER:C	10	1.89
(1,82)	1:100:A:PHE:C	1:101:A:GLY:N	1:101:A:GLY:CA	1:101:A:GLY:C	7	1.88
(1,33)	1:41:A:SER:C	1:42:A:TRP:N	1:42:A:TRP:CA	1:42:A:TRP:C	5	1.83
(1,235)	1:125:A:ALA:N	1:125:A:ALA:CA	1:125:A:ALA:C	1:126:A:TRP:N	11	1.81
(1,235)	1:125:A:ALA:N	1:125:A:ALA:CA	1:125:A:ALA:C	1:126:A:TRP:N	15	1.81
(1,82)	1:100:A:PHE:C	1:101:A:GLY:N	1:101:A:GLY:CA	1:101:A:GLY:C	6	1.77
(1,216)	1:105:A:MET:N	1:105:A:MET:CA	1:105:A:MET:C	1:106:A:GLY:N	7	1.74
(1,159)	1:34:A:TYR:N	1:34:A:TYR:CA	1:34:A:TYR:C	1:35:A:ALA:N	13	1.74
(1,216)	1:105:A:MET:N	1:105:A:MET:CA	1:105:A:MET:C	1:106:A:GLY:N	8	1.73
(1,33)	1:41:A:SER:C	1:42:A:TRP:N	1:42:A:TRP:CA	1:42:A:TRP:C	17	1.71
(1,190)	1:71:A:LEU:N	1:71:A:LEU:CA	1:71:A:LEU:C	1:72:A:GLY:N	16	1.7
(1,85)	1:106:A:GLY:C	1:107:A:TRP:N	1:107:A:TRP:CA	1:107:A:TRP:C	16	1.68
(1,159)	1:34:A:TYR:N	1:34:A:TYR:CA	1:34:A:TYR:C	1:35:A:ALA:N	18	1.67
(1,217)	1:107:A:TRP:N	1:107:A:TRP:CA	1:107:A:TRP:C	1:108:A:ALA:N	15	1.65
(1,82)	1:100:A:PHE:C	1:101:A:GLY:N	1:101:A:GLY:CA	1:101:A:GLY:C	5	1.61
(1,235)	1:125:A:ALA:N	1:125:A:ALA:CA	1:125:A:ALA:C	1:126:A:TRP:N	5	1.6
(1,190)	1:71:A:LEU:N	1:71:A:LEU:CA	1:71:A:LEU:C	1:72:A:GLY:N	11	1.57
(1,211)	1:98:A:ILE:N	1:98:A:ILE:CA	1:98:A:ILE:C	1:99:A:PHE:N	8	1.53
(1,86)	1:107:A:TRP:C	1:108:A:ALA:N	1:108:A:ALA:CA	1:108:A:ALA:C	15	1.51
(1,235)	1:125:A:ALA:N	1:125:A:ALA:CA	1:125:A:ALA:C	1:126:A:TRP:N	14	1.5
(1,159)	1:34:A:TYR:N	1:34:A:TYR:CA	1:34:A:TYR:C	1:35:A:ALA:N	12	1.47
(1,235)	1:125:A:ALA:N	1:125:A:ALA:CA	1:125:A:ALA:C	1:126:A:TRP:N	10	1.46
(1,159)	1:34:A:TYR:N	1:34:A:TYR:CA	1:34:A:TYR:C	1:35:A:ALA:N	5	1.46
(1,235)	1:125:A:ALA:N	1:125:A:ALA:CA	1:125:A:ALA:C	1:126:A:TRP:N	8	1.45
(1,211)	1:98:A:ILE:N	1:98:A:ILE:CA	1:98:A:ILE:C	1:99:A:PHE:N	16	1.44
(1,85)	1:106:A:GLY:C	1:107:A:TRP:N	1:107:A:TRP:CA	1:107:A:TRP:C	13	1.44
(1,264)	1:158:A:ASN:N	1:158:A:ASN:CA	1:158:A:ASN:C	1:159:A:SER:N	8	1.42
(1,235)	1:125:A:ALA:N	1:125:A:ALA:CA	1:125:A:ALA:C	1:126:A:TRP:N	12	1.42
(1,190)	1:71:A:LEU:N	1:71:A:LEU:CA	1:71:A:LEU:C	1:72:A:GLY:N	15	1.41
(1,33)	1:41:A:SER:C	1:42:A:TRP:N	1:42:A:TRP:CA	1:42:A:TRP:C	3	1.41
(1,159)	1:34:A:TYR:N	1:34:A:TYR:CA	1:34:A:TYR:C	1:35:A:ALA:N	10	1.37
(1,82)	1:100:A:PHE:C	1:101:A:GLY:N	1:101:A:GLY:CA	1:101:A:GLY:C	11	1.37
(1,190)	1:71:A:LEU:N	1:71:A:LEU:CA	1:71:A:LEU:C	1:72:A:GLY:N	20	1.36
(1,159)	1:34:A:TYR:N	1:34:A:TYR:CA	1:34:A:TYR:C	1:35:A:ALA:N	7	1.36
(1,3)	1:5:A:TRP:C	1:6:A:VAL:N	1:6:A:VAL:CA	1:6:A:VAL:C	18	1.36

Continued on next page...

Continued from previous page...

Key	Atom-1	Atom-2	Atom-3	Atom-4	Model ID	Violation (°)
(1,159)	1:34:A:TYR:N	1:34:A:TYR:CA	1:34:A:TYR:C	1:35:A:ALA:N	4	1.35
(1,159)	1:34:A:TYR:N	1:34:A:TYR:CA	1:34:A:TYR:C	1:35:A:ALA:N	6	1.3
(1,82)	1:100:A:PHE:C	1:101:A:GLY:N	1:101:A:GLY:CA	1:101:A:GLY:C	8	1.3
(1,235)	1:125:A:ALA:N	1:125:A:ALA:CA	1:125:A:ALA:C	1:126:A:TRP:N	17	1.29
(1,264)	1:158:A:ASN:N	1:158:A:ASN:CA	1:158:A:ASN:C	1:159:A:SER:N	18	1.28
(1,159)	1:34:A:TYR:N	1:34:A:TYR:CA	1:34:A:TYR:C	1:35:A:ALA:N	2	1.28
(1,235)	1:125:A:ALA:N	1:125:A:ALA:CA	1:125:A:ALA:C	1:126:A:TRP:N	7	1.27
(1,33)	1:41:A:SER:C	1:42:A:TRP:N	1:42:A:TRP:CA	1:42:A:TRP:C	19	1.27
(1,82)	1:100:A:PHE:C	1:101:A:GLY:N	1:101:A:GLY:CA	1:101:A:GLY:C	14	1.26
(1,82)	1:100:A:PHE:C	1:101:A:GLY:N	1:101:A:GLY:CA	1:101:A:GLY:C	12	1.25
(1,3)	1:5:A:TRP:C	1:6:A:VAL:N	1:6:A:VAL:CA	1:6:A:VAL:C	17	1.24
(1,82)	1:100:A:PHE:C	1:101:A:GLY:N	1:101:A:GLY:CA	1:101:A:GLY:C	15	1.23
(1,264)	1:158:A:ASN:N	1:158:A:ASN:CA	1:158:A:ASN:C	1:159:A:SER:N	3	1.21
(1,224)	1:114:A:LEU:N	1:114:A:LEU:CA	1:114:A:LEU:C	1:115:A:VAL:N	9	1.21
(1,216)	1:105:A:MET:N	1:105:A:MET:CA	1:105:A:MET:C	1:106:A:GLY:N	17	1.21
(1,159)	1:34:A:TYR:N	1:34:A:TYR:CA	1:34:A:TYR:C	1:35:A:ALA:N	15	1.21
(1,103)	1:124:A:LEU:C	1:125:A:ALA:N	1:125:A:ALA:CA	1:125:A:ALA:C	20	1.18
(1,159)	1:34:A:TYR:N	1:34:A:TYR:CA	1:34:A:TYR:C	1:35:A:ALA:N	11	1.17
(1,159)	1:34:A:TYR:N	1:34:A:TYR:CA	1:34:A:TYR:C	1:35:A:ALA:N	17	1.16
(1,28)	1:34:A:TYR:C	1:35:A:ALA:N	1:35:A:ALA:CA	1:35:A:ALA:C	12	1.13
(1,159)	1:34:A:TYR:N	1:34:A:TYR:CA	1:34:A:TYR:C	1:35:A:ALA:N	9	1.12
(1,190)	1:71:A:LEU:N	1:71:A:LEU:CA	1:71:A:LEU:C	1:72:A:GLY:N	12	1.11
(1,235)	1:125:A:ALA:N	1:125:A:ALA:CA	1:125:A:ALA:C	1:126:A:TRP:N	9	1.1
(1,159)	1:34:A:TYR:N	1:34:A:TYR:CA	1:34:A:TYR:C	1:35:A:ALA:N	20	1.1
(1,235)	1:125:A:ALA:N	1:125:A:ALA:CA	1:125:A:ALA:C	1:126:A:TRP:N	3	1.07
(1,190)	1:71:A:LEU:N	1:71:A:LEU:CA	1:71:A:LEU:C	1:72:A:GLY:N	3	1.07
(1,225)	1:115:A:VAL:N	1:115:A:VAL:CA	1:115:A:VAL:C	1:116:A:SER:N	7	1.06
(1,191)	1:74:A:PHE:N	1:74:A:PHE:CA	1:74:A:PHE:C	1:75:A:THR:N	18	1.06
(1,214)	1:101:A:GLY:N	1:101:A:GLY:CA	1:101:A:GLY:C	1:102:A:ALA:N	15	1.05
(1,60)	1:74:A:PHE:C	1:75:A:THR:N	1:75:A:THR:CA	1:75:A:THR:C	6	1.05
(1,159)	1:34:A:TYR:N	1:34:A:TYR:CA	1:34:A:TYR:C	1:35:A:ALA:N	19	1.04
(1,60)	1:74:A:PHE:C	1:75:A:THR:N	1:75:A:THR:CA	1:75:A:THR:C	17	1.04
(1,159)	1:34:A:TYR:N	1:34:A:TYR:CA	1:34:A:TYR:C	1:35:A:ALA:N	14	1.03
(1,235)	1:125:A:ALA:N	1:125:A:ALA:CA	1:125:A:ALA:C	1:126:A:TRP:N	2	1.01