Full wwPDB NMR Structure Validation Report (i)

Jun 3, 2023 – 11:37 PM EDT

PDB ID	:	2KT0
BMRB ID	:	16680
Title	:	Solution structure of human stem cell transcription factor Nanog homeodomain fragment
Authors	:	Sahu, S.C.; Markley, J.L.; Center for Eukaryotic Structural Genomics (CESG)
Deposited on	:	2010-01-15

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 (i) 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 (1)) were used in the production of this report:

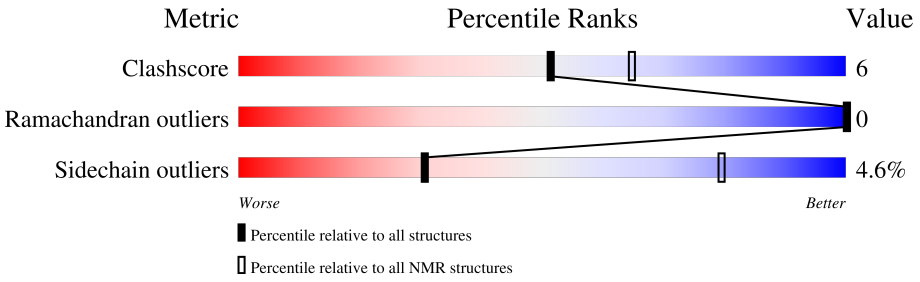
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.33

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
SOLUTION NMR

The overall completeness of chemical shifts assignment is 91%.

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	84	49% 7% 44%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 4 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:30-A:76 (47)	0.67	4

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

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

The models can be grouped into 3 clusters and 1 single-model cluster was found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1440 atoms, of which 734 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Homeobox protein NANOG.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	84	1440	440	734	133	130	3	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	-	expression tag	UNP Q6NSW7

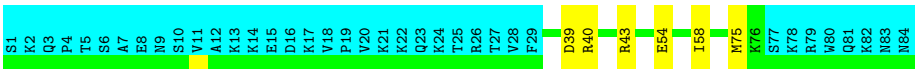
4 Residue-property plots (i)

4.1 Average score per residue in the NMR ensemble

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

• Molecule 1: Homeobox protein NANOG

Chain A: 49% 7% 44%



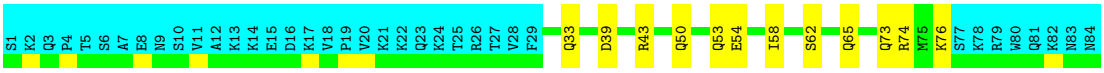
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: Homeobox protein NANOG

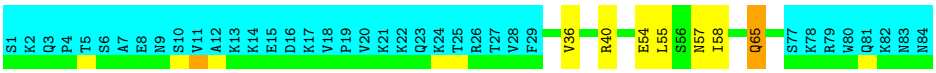
Chain A: 42% 14% 44%



4.2.2 Score per residue for model 2

• Molecule 1: Homeobox protein NANOG

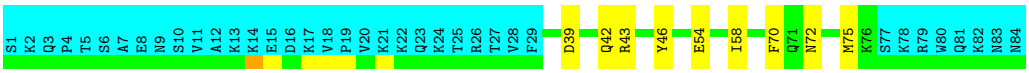
Chain A: 48% 7% • 44%



4.2.3 Score per residue for model 3

- Molecule 1: Homeobox protein NANOG

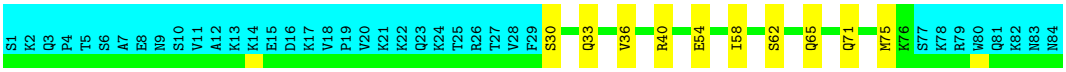
Chain A: 45% 11% 44%



4.2.4 Score per residue for model 4 (medoid)

- Molecule 1: Homeobox protein NANOG

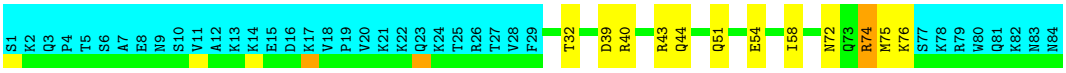
Chain A: 44% 12% 44%



4.2.5 Score per residue for model 5

- Molecule 1: Homeobox protein NANOG

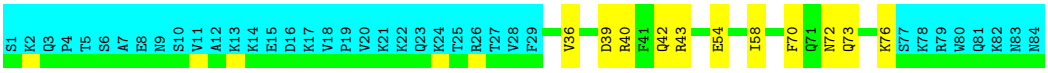
Chain A: 42% 13% • 44%



4.2.6 Score per residue for model 6

- Molecule 1: Homeobox protein NANOG

Chain A: 43% 13% 44%



4.2.7 Score per residue for model 7

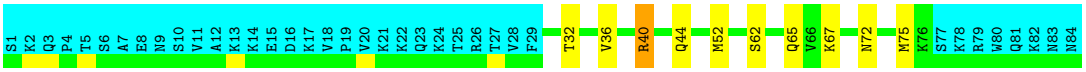
- Molecule 1: Homeobox protein NANOG

Chain A: 46% 10% 44%

4.2.8 Score per residue for model 8

- Molecule 1: Homeobox protein NANOG

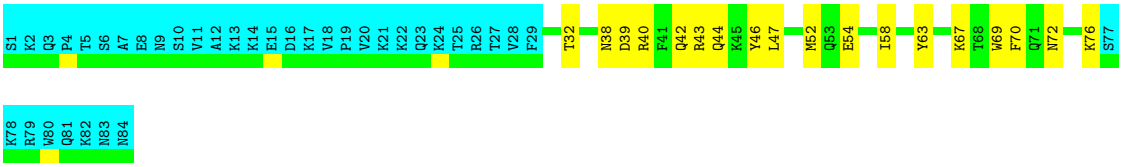
Chain A: 44% 11% • 44%



4.2.9 Score per residue for model 9

- Molecule 1: Homeobox protein NANOG

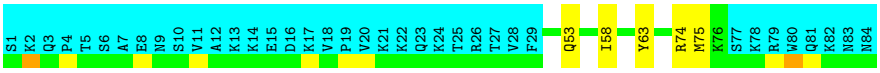
Chain A: 35% 21% 44%



4.2.10 Score per residue for model 10

- Molecule 1: Homeobox protein NANOG

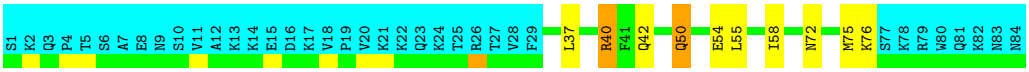
Chain A: 50% 6% 44%



4.2.11 Score per residue for model 11

- Molecule 1: Homeobox protein NANOG

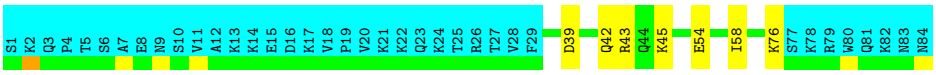
Chain A: 44% 10% • 44%



4.2.12 Score per residue for model 12

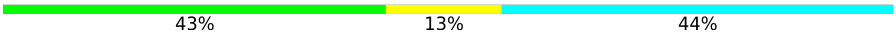
- Molecule 1: Homeobox protein NANOG

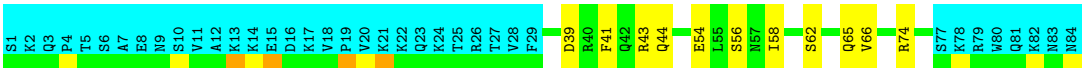
Chain A: 48% 8% 44%



4.2.13 Score per residue for model 13

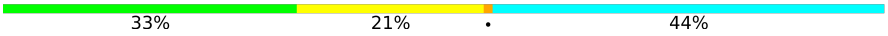
- Molecule 1: Homeobox protein NANOG

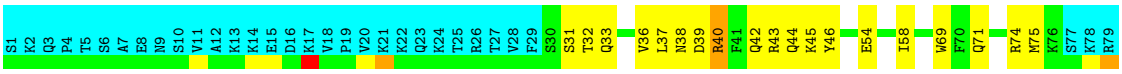
Chain A: 



4.2.14 Score per residue for model 14

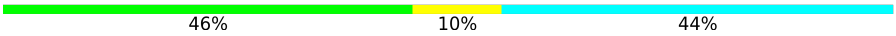
- Molecule 1: Homeobox protein NANOG

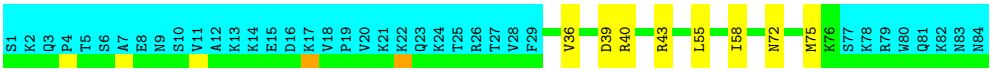
Chain A: 



4.2.15 Score per residue for model 15

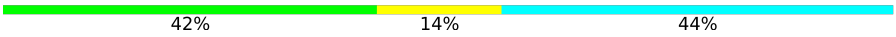
- Molecule 1: Homeobox protein NANOG

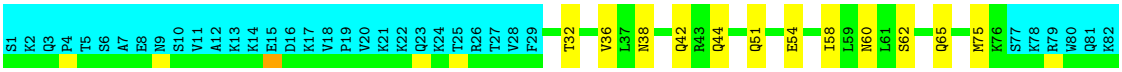
Chain A: 



4.2.16 Score per residue for model 16

- Molecule 1: Homeobox protein NANOG

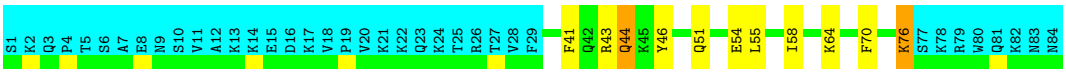
Chain A: 



4.2.17 Score per residue for model 17

- Molecule 1: Homeobox protein NANOG

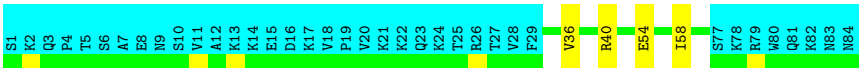
Chain A: 43% 11% • 44%



4.2.18 Score per residue for model 18

- Molecule 1: Homeobox protein NANOG

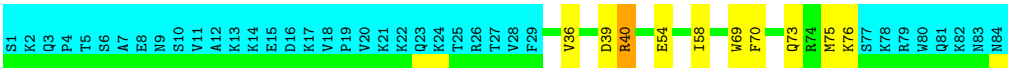
Chain A: 51% 5% 44%



4.2.19 Score per residue for model 19

- Molecule 1: Homeobox protein NANOG

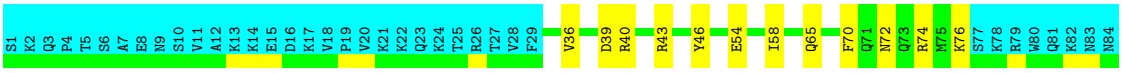
Chain A: 44% 11% • 44%



4.2.20 Score per residue for model 20

- Molecule 1: Homeobox protein NANOG

Chain A: 42% 14% 44%



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *MOLECULAR DYNAMICS IN EXPLICIT SOLVENT*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function*.

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

Software name	**Classification**	**Version**
CNS	refinement	1.21

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

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1128
Number of shifts mapped to atoms	1128
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	91%

6 Model quality (i)

6.1 Standard geometry (i)

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

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	403	411	411	5±2
All	All	8060	8220	8220	95

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 6.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:40:ARG:HH22	1:A:55:LEU:HG	0.72	1.44	11	1
1:A:46:TYR:HB3	1:A:70:PHE:HE1	0.69	1.47	9	3
1:A:72:ASN:HA	1:A:75:MET:HG2	0.65	1.69	15	5
1:A:62:SER:HB3	1:A:65:GLN:HG2	0.64	1.68	1	4
1:A:50:GLN:O	1:A:53:GLN:HG2	0.63	1.94	1	1
1:A:44:GLN:HA	1:A:44:GLN:HE21	0.62	1.53	17	1
1:A:65:GLN:HE21	1:A:65:GLN:HA	0.61	1.53	2	1
1:A:62:SER:HB3	1:A:65:GLN:HG3	0.60	1.73	4	1
1:A:39:ASP:O	1:A:43:ARG:HG2	0.58	1.97	20	10
1:A:76:LYS:HE2	1:A:76:LYS:HA	0.57	1.76	17	1
1:A:54:GLU:O	1:A:58:ILE:HG13	0.56	2.00	14	16
1:A:37:LEU:HA	1:A:40:ARG:HE	0.56	1.60	11	1
1:A:36:VAL:O	1:A:40:ARG:HG2	0.55	2.00	20	4
1:A:44:GLN:HG2	1:A:51:GLN:HE22	0.53	1.64	16	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:36:VAL:O	1:A:40:ARG:HD2	0.52	2.05	8	3
1:A:36:VAL:O	1:A:40:ARG:HD3	0.52	2.04	4	2
1:A:72:ASN:O	1:A:76:LYS:HG2	0.52	2.03	9	3
1:A:46:TYR:HB3	1:A:70:PHE:CE1	0.52	2.35	9	2
1:A:54:GLU:O	1:A:58:ILE:HG12	0.50	2.05	18	1
1:A:65:GLN:HA	1:A:65:GLN:OE1	0.50	2.07	20	1
1:A:50:GLN:O	1:A:54:GLU:HB2	0.49	2.07	11	1
1:A:74:ARG:NE	1:A:74:ARG:HA	0.49	2.22	20	1
1:A:30:SER:HB2	1:A:33:GLN:HG2	0.49	1.84	4	1
1:A:38:ASN:O	1:A:42:GLN:HG2	0.49	2.08	14	2
1:A:43:ARG:HA	1:A:43:ARG:NE	0.47	2.24	7	1
1:A:43:ARG:HA	1:A:43:ARG:HE	0.46	1.70	7	1
1:A:73:GLN:O	1:A:76:LYS:HG2	0.46	2.10	1	1
1:A:56:SER:HB3	1:A:66:VAL:HG21	0.46	1.87	13	1
1:A:46:TYR:HB3	1:A:70:PHE:HZ	0.46	1.69	3	1
1:A:41:PHE:HA	1:A:44:GLN:O	0.46	2.10	13	1
1:A:40:ARG:O	1:A:44:GLN:HB2	0.45	2.11	8	1
1:A:71:GLN:O	1:A:75:MET:HG2	0.45	2.10	14	1
1:A:45:LYS:HE2	1:A:46:TYR:CE2	0.45	2.47	14	1
1:A:56:SER:HB3	1:A:66:VAL:CG2	0.44	2.41	13	1
1:A:72:ASN:O	1:A:76:LYS:HG3	0.44	2.12	20	1
1:A:75:MET:HG3	1:A:76:LYS:N	0.44	2.27	5	1
1:A:62:SER:HB3	1:A:65:GLN:CG	0.43	2.43	8	1
1:A:70:PHE:O	1:A:73:GLN:HG3	0.42	2.14	6	1
1:A:52:MET:SD	1:A:67:LYS:HG2	0.42	2.55	8	2
1:A:73:GLN:OE1	1:A:76:LYS:HD3	0.42	2.15	19	1
1:A:47:LEU:HD13	1:A:52:MET:HB3	0.42	1.92	9	1
1:A:71:GLN:O	1:A:75:MET:HG3	0.42	2.15	4	1
1:A:32:THR:O	1:A:36:VAL:HG23	0.41	2.15	16	3
1:A:33:GLN:O	1:A:37:LEU:HG	0.41	2.16	14	1
1:A:63:TYR:O	1:A:67:LYS:HB2	0.41	2.15	9	1
1:A:53:GLN:HB3	1:A:63:TYR:CD1	0.41	2.50	10	1
1:A:62:SER:HB3	1:A:65:GLN:NE2	0.41	2.31	13	1
1:A:74:ARG:O	1:A:74:ARG:HD3	0.40	2.16	5	1
1:A:40:ARG:NH2	1:A:55:LEU:HG	0.40	2.24	11	1

6.3 Torsion angles (i)

6.3.1 Protein backbone (i)

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	47/84 (56%)	47±0 (100±0%)	0±0 (0±0%)	0±0 (0±0%)	100	100
All	All	940/1680 (56%)	939 (100%)	1 (0%)	0 (0%)	100	100

There are no Ramachandran outliers.

6.3.2 Protein sidechains (i)

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	47/82 (57%)	45±1 (95±3%)	2±1 (5±3%)	31	79
All	All	940/1640 (57%)	897 (95%)	43 (5%)	31	79

All 18 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	40	ARG	6
1	A	74	ARG	5
1	A	42	GLN	5
1	A	44	GLN	4
1	A	75	MET	4
1	A	55	LEU	3
1	A	69	TRP	3
1	A	50	GLN	2
1	A	60	ASN	2
1	A	33	GLN	1
1	A	57	ASN	1
1	A	65	GLN	1
1	A	32	THR	1

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Mol	Chain	Res	Type	Models (Total)
1	A	45	LYS	1
1	A	64	LYS	1
1	A	76	LYS	1
1	A	39	ASP	1
1	A	70	PHE	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 monosaccharides in this entry.

6.6 Ligand geometry (i)

There are no ligands in this entry.

6.7 Other polymers (i)

There are no such molecules in this entry.

6.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

7 Chemical shift validation (i)

The completeness of assignment taking into account all chemical shift lists is 91% for the well-defined parts and 91% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping (i)

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

Total number of shifts	1128
Number of shifts mapped to atoms	1128
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	3

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	84	-0.35 ± 0.16	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	84	0.13 ± 0.09	None needed (< 0.5 ppm)
$^{13}C'$	83	-0.32 ± 0.07	None needed (< 0.5 ppm)
^{15}N	81	-0.25 ± 0.21	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments (i)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 91%, i.e. 646 atoms were assigned a chemical shift out of a possible 709. 0 out of 9 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	235/235 (100%)	94/94 (100%)	94/94 (100%)	47/47 (100%)
Sidechain	364/424 (86%)	256/271 (94%)	108/127 (85%)	0/26 (0%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	47/50 (94%)	24/24 (100%)	23/25 (92%)	0/1 (0%)
Overall	646/709 (91%)	374/389 (96%)	225/246 (91%)	47/74 (64%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 91%, i.e. 1127 atoms were assigned a chemical shift out of a possible 1236. 0 out of 13 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	413/416 (99%)	165/166 (99%)	167/168 (99%)	81/82 (99%)
Sidechain	646/748 (86%)	450/475 (95%)	196/226 (87%)	0/47 (0%)
Aromatic	68/72 (94%)	35/35 (100%)	33/35 (94%)	0/2 (0%)
Overall	1127/1236 (91%)	650/676 (96%)	396/429 (92%)	81/131 (62%)

7.1.4 Statistically unusual chemical shifts (i)

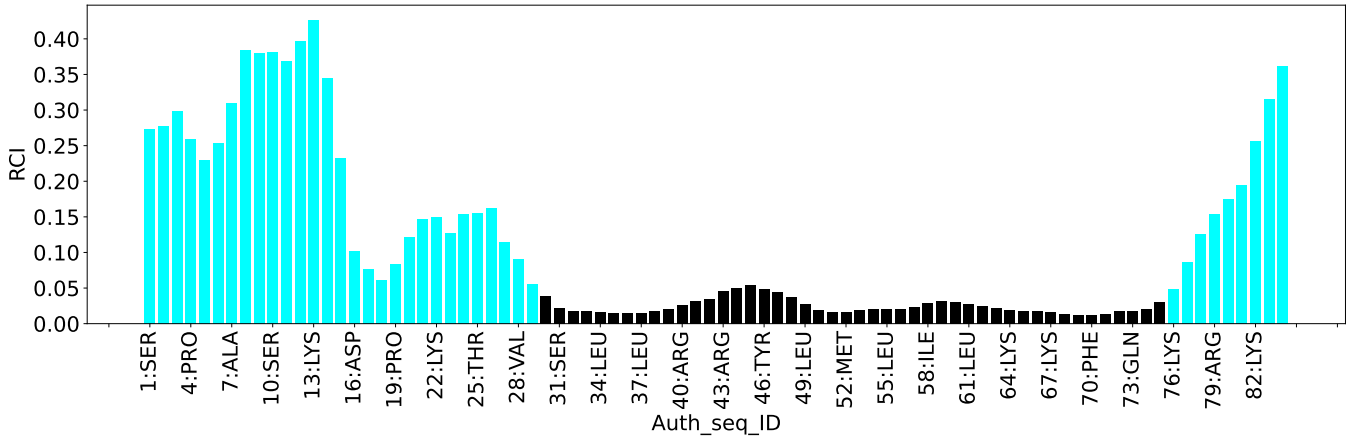
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	37	LEU	HB3	-0.75	-0.26 – 3.31	-6.4
1	A	73	GLN	HB3	0.42	0.71 – 3.33	-6.1
1	A	73	GLN	HB2	0.57	0.80 – 3.29	-5.9

7.1.5 Random Coil Index (RCI) plots (i)

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

Random coil index (RCI) for chain A:


RCI
0.00
0.05
0.10
0.15
0.20
0.25
0.30
0.35
0.40
1:SER
4:PRO
7:ALA
10:SER
13:LYS
16:ASP
19:PRO
22:LYS
25:THR
28:VAL
31:SER
34:LEU
37:LEU
40:ARG
43:ARG
46:TYR
49:LEU
52:MET
55:LEU
58:ILE
61:LEU
64:LYS
67:LYS
70:PHE
73:GLN
76:LYS
79:ARG
82:LYS
Auth_seq_ID

8 NMR restraints analysis (i)

8.1 Conformationally restricting restraints (i)

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	771
Intra-residue (|i-j|=0)	184
Sequential (|i-j|=1)	246
Medium range (|i-j|>1 and |i-j|<5)	163
Long range (|i-j|≥5)	136
Inter-chain	0
Hydrogen bond restraints	42
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	9.2
Number of long range restraints per residue[1]	1.6

[1]Long 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 (i)

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 (i)

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)	14.1	0.2
0.2-0.5 (Medium)	12.2	0.5
>0.5 (Large)	23.6	3.71

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

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

9 Distance violation analysis (i)

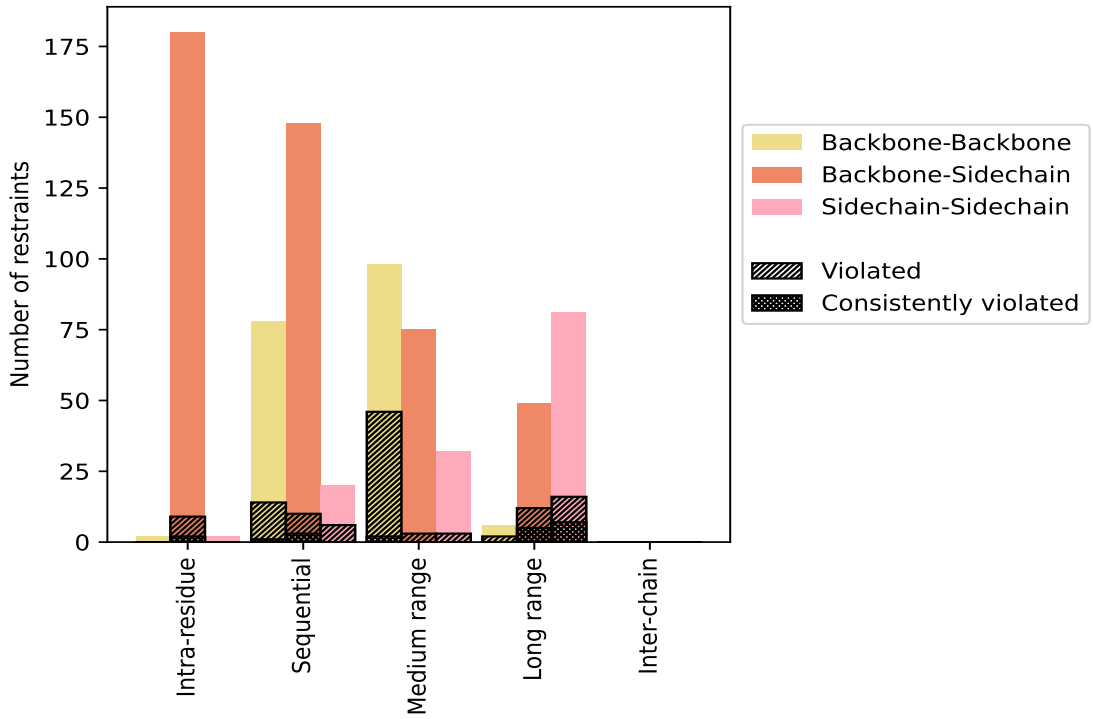
9.1 Summary of distance violations (i)

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

Restraints type	Count	%[1]	Violated[3]			Consistently Violated[4]		
			Count	%[2]	%[1]	Count	%[2]	%[1]
Intra-residue (|i-j|=0)	184	23.9	9	4.9	1.2	2	1.1	0.3
Backbone-Backbone	2	0.3	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	180	23.3	9	5.0	1.2	2	1.1	0.3
Sidechain-Sidechain	2	0.3	0	0.0	0.0	0	0.0	0.0
Sequential (|i-j|=1)	246	31.9	30	12.2	3.9	4	1.6	0.5
Backbone-Backbone	78	10.1	14	17.9	1.8	1	1.3	0.1
Backbone-Sidechain	148	19.2	10	6.8	1.3	3	2.0	0.4
Sidechain-Sidechain	20	2.6	6	30.0	0.8	0	0.0	0.0
Medium range (|i-j|>1 & |i-j|<5)	163	21.1	16	9.8	2.1	1	0.6	0.1
Backbone-Backbone	56	7.3	10	17.9	1.3	1	1.8	0.1
Backbone-Sidechain	75	9.7	3	4.0	0.4	0	0.0	0.0
Sidechain-Sidechain	32	4.2	3	9.4	0.4	0	0.0	0.0
Long range (|i-j|≥5)	136	17.6	30	22.1	3.9	12	8.8	1.6
Backbone-Backbone	6	0.8	2	33.3	0.3	0	0.0	0.0
Backbone-Sidechain	49	6.4	12	24.5	1.6	5	10.2	0.6
Sidechain-Sidechain	81	10.5	16	19.8	2.1	7	8.6	0.9
Inter-chain	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Hydrogen bond	42	5.4	36	85.7	4.7	1	2.4	0.1
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	771	100.0	121	15.7	15.7	20	2.6	2.6
Backbone-Backbone	184	23.9	62	33.7	8.0	3	1.6	0.4
Backbone-Sidechain	452	58.6	34	7.5	4.4	10	2.2	1.3
Sidechain-Sidechain	135	17.5	25	18.5	3.2	7	5.2	0.9

[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	4	11	13	19	0	47	0.88	2.86	0.89	0.45
2	3	6	11	19	0	39	1.01	2.89	0.89	0.77
3	6	8	15	20	0	49	0.95	3.45	0.96	0.59
4	5	10	18	18	0	51	0.92	3.33	0.99	0.47
5	4	11	16	22	0	53	0.88	3.13	0.96	0.37
6	7	6	15	15	0	43	1.03	3.37	1.05	0.5
7	4	11	21	21	0	57	0.79	2.84	0.84	0.37
8	6	10	13	20	0	49	0.88	2.99	0.86	0.45
9	4	7	16	19	0	46	1.01	3.43	1.03	0.6
10	5	9	15	16	0	45	0.79	2.72	0.78	0.33
11	4	11	16	20	0	51	0.92	3.37	0.97	0.37

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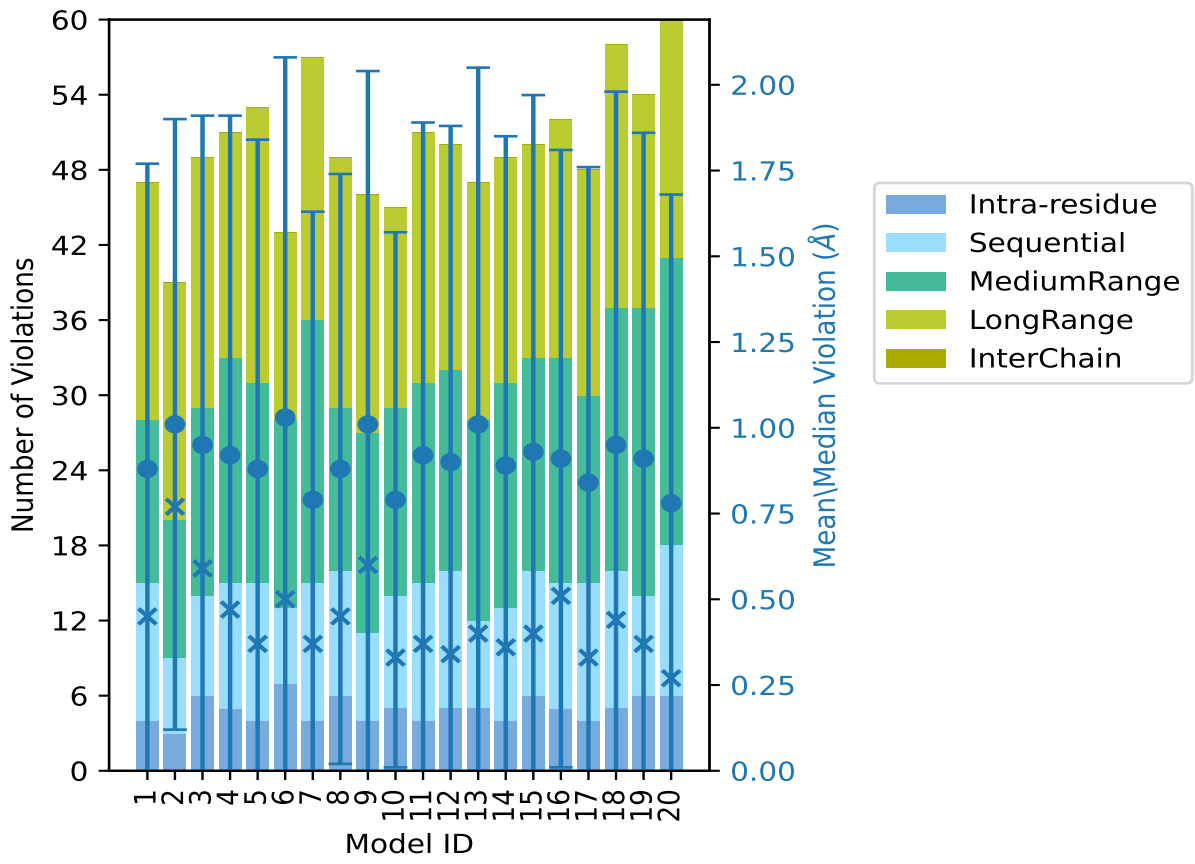
Model ID	Number of violations						Mean (Å)	Max (Å)	SD[6] (Å)	Median (Å)
	IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total				
12	5	11	16	18	0	50	0.9	3.24	0.98	0.34
13	5	7	16	19	0	47	1.01	3.35	1.04	0.4
14	4	9	18	18	0	49	0.89	3.2	0.96	0.36
15	6	10	17	17	0	50	0.93	3.58	1.04	0.4
16	5	10	18	19	0	52	0.91	2.92	0.9	0.51
17	4	11	15	18	0	48	0.84	3.1	0.92	0.33
18	5	11	21	21	0	58	0.95	3.71	1.03	0.44
19	6	8	23	17	0	54	0.91	3.38	0.95	0.37
20	6	12	23	19	0	60	0.78	3.3	0.9	0.27

[1]Intra-residue restraints, [2]Sequential restraints, [3]Medium range restraints, [4]Long range restraints, [5]Inter-chain restraints, [6]Standard deviation

9.2.1 Bar graph : Distance Violation statistics for each model (i)



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

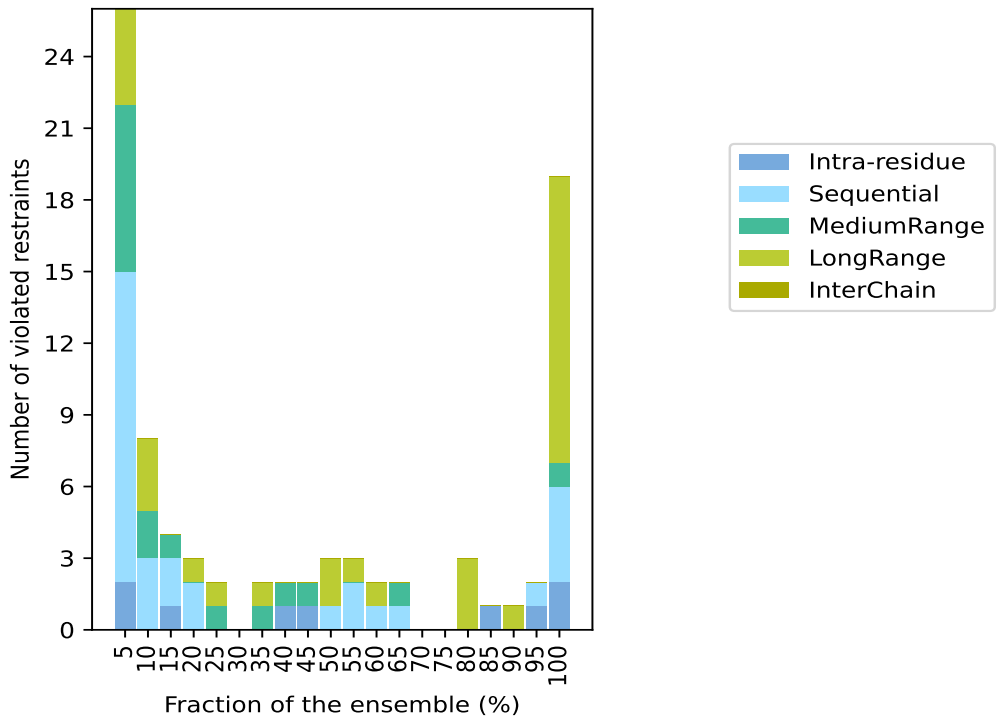
9.3 Distance violation statistics for the ensemble (i)

Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 644(IR:175, SQ:216, MR:147, LR:106, IC:0) restraints are not violated in the ensemble.

Number of violated restraints						Fraction of the ensemble	
IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total	Count[6]	%
2	13	7	4	0	26	1	5.0
0	3	2	3	0	8	2	10.0
1	2	1	0	0	4	3	15.0
0	2	0	1	0	3	4	20.0
0	0	1	1	0	2	5	25.0
0	0	0	0	0	0	6	30.0
0	0	1	1	0	2	7	35.0
1	0	1	0	0	2	8	40.0
1	0	1	0	0	2	9	45.0
0	1	0	2	0	3	10	50.0
0	2	0	1	0	3	11	55.0
0	1	0	1	0	2	12	60.0
0	1	1	0	0	2	13	65.0
0	0	0	0	0	0	14	70.0
0	0	0	0	0	0	15	75.0
0	0	0	3	0	3	16	80.0
1	0	0	0	0	1	17	85.0
0	0	0	1	0	1	18	90.0
1	1	0	0	0	2	19	95.0
2	4	1	12	0	19	20	100.0

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

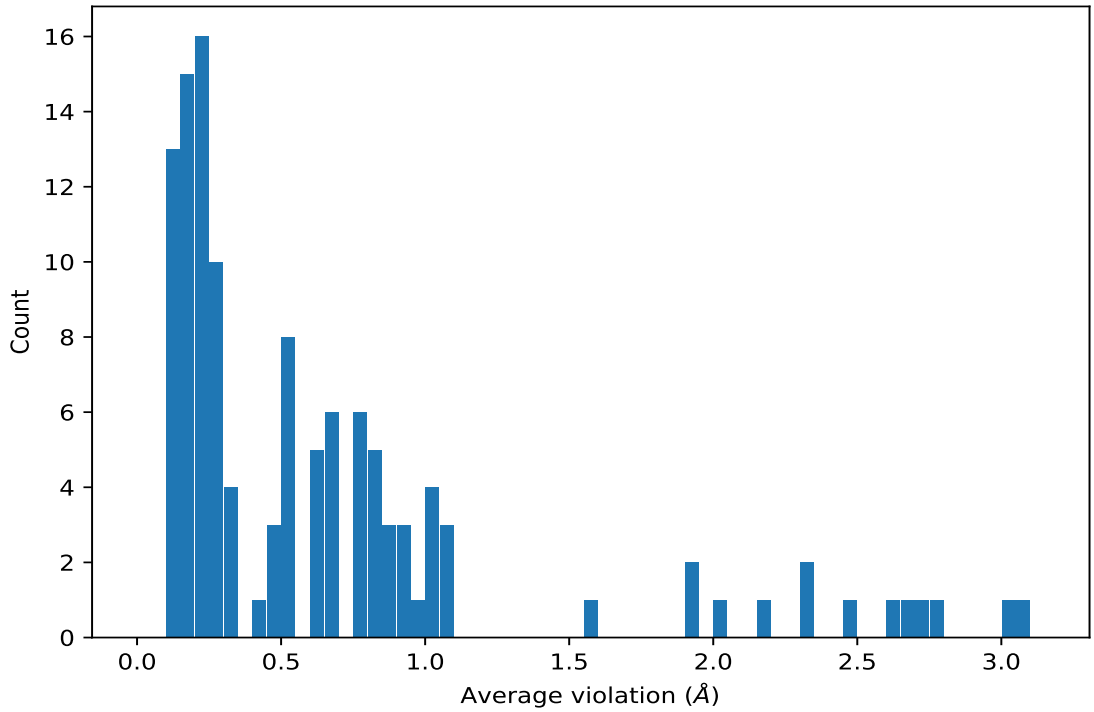
9.3.1 Bar graph : Distance violation statistics for the ensemble (i)



9.4 Most violated distance restraints in the ensemble (i)

9.4.1 Histogram : Distribution of mean distance violations (i)

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



9.4.2 Table: Most violated distance restraints (i)

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

Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(2,4)	1:A:52:MET:H	1:A:63:TYR:HE2	20	3.08	0.31	3.16
(1,214)	1:A:53:GLN:H	1:A:63:TYR:HE2	20	3.03	0.24	3.04
(1,349)	1:A:41:PHE:HE1	1:A:46:TYR:HD2	20	2.78	0.32	2.74
(1,361)	1:A:49:LEU:HA	1:A:63:TYR:HE2	20	2.72	0.48	2.79
(1,353)	1:A:53:GLN:HA	1:A:63:TYR:HD2	20	2.66	0.2	2.67
(1,356)	1:A:41:PHE:HD1	1:A:46:TYR:HD2	20	2.63	0.3	2.66
(1,207)	1:A:53:GLN:H	1:A:63:TYR:HD2	20	2.49	0.26	2.46
(1,460)	1:A:52:MET:HB2	1:A:63:TYR:HE2	20	2.31	0.28	2.27
(1,460)	1:A:52:MET:HB3	1:A:63:TYR:HE2	20	2.31	0.28	2.27
(1,362)	1:A:41:PHE:HE1	1:A:46:TYR:HE2	20	2.16	0.36	2.17
(1,461)	1:A:52:MET:HB2	1:A:63:TYR:HD2	20	1.93	0.22	1.94
(1,461)	1:A:52:MET:HB3	1:A:63:TYR:HD2	20	1.93	0.22	1.94
(2,60)	1:A:41:PHE:HD1	1:A:46:TYR:HE2	20	1.55	0.35	1.64
(2,6)	1:A:63:TYR:HE1	1:A:64:LYS:H	20	1.08	0.16	1.12
(1,465)	1:A:52:MET:HG2	1:A:63:TYR:HE2	20	1.04	0.26	1.08
(1,465)	1:A:52:MET:HG3	1:A:63:TYR:HE2	20	1.04	0.26	1.08

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Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(1,309)	1:A:63:TYR:HD1	1:A:64:LYS:HA	20	0.99	0.24	1.05
(1,352)	1:A:63:TYR:HA	1:A:63:TYR:HD2	20	0.87	0.08	0.88
(1,348)	1:A:46:TYR:H	1:A:46:TYR:HD1	20	0.69	0.17	0.74
(1,351)	1:A:63:TYR:HD1	1:A:64:LYS:H	20	0.68	0.1	0.7
(3,21)	1:A:53:GLN:O	1:A:57:ASN:H	20	0.31	0.07	0.33
(1,186)	1:A:72:ASN:H	1:A:75:MET:H	20	0.19	0.03	0.19
(1,42)	1:A:48:SER:H	1:A:49:LEU:H	20	0.16	0.03	0.16
(2,125)	1:A:45:LYS:HD2	1:A:46:TYR:HD1	19	0.77	0.34	0.71
(2,125)	1:A:45:LYS:HD3	1:A:46:TYR:HD1	19	0.77	0.34	0.71
(1,355)	1:A:41:PHE:HA	1:A:41:PHE:HE1	19	0.17	0.03	0.17
(1,466)	1:A:52:MET:HG2	1:A:63:TYR:HD2	18	0.52	0.19	0.5
(1,466)	1:A:52:MET:HG3	1:A:63:TYR:HD2	18	0.52	0.19	0.5
(3,22)	1:A:53:GLN:O	1:A:57:ASN:N	18	0.22	0.07	0.22
(1,350)	1:A:46:TYR:HA	1:A:46:TYR:HD2	17	0.21	0.07	0.19
(2,144)	1:A:49:LEU:HB2	1:A:63:TYR:HE2	16	1.05	0.46	1.08
(2,144)	1:A:49:LEU:HB3	1:A:63:TYR:HE2	16	1.05	0.46	1.08
(2,62)	1:A:1:SER:HB2	1:A:49:LEU:H	16	0.79	0.18	0.88
(2,62)	1:A:1:SER:HB3	1:A:49:LEU:H	16	0.79	0.18	0.88
(1,347)	1:A:61:LEU:HD21	1:A:66:VAL:HA	16	0.6	0.24	0.56
(1,347)	1:A:61:LEU:HD22	1:A:66:VAL:HA	16	0.6	0.24	0.56
(1,347)	1:A:61:LEU:HD23	1:A:66:VAL:HA	16	0.6	0.24	0.56
(3,1)	1:A:32:THR:O	1:A:36:VAL:H	15	0.25	0.1	0.31
(3,19)	1:A:52:MET:O	1:A:56:SER:H	14	0.22	0.06	0.19
(2,58)	1:A:29:PHE:HD1	1:A:33:GLN:H	13	2.04	0.67	2.06
(1,50)	1:A:55:LEU:HA	1:A:56:SER:H	13	0.12	0.01	0.12
(1,473)	1:A:53:GLN:HE21	1:A:63:TYR:HD2	12	0.81	0.41	0.75
(1,473)	1:A:53:GLN:HE22	1:A:63:TYR:HD2	12	0.81	0.41	0.75
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB2	12	0.67	0.28	0.77
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB3	12	0.67	0.28	0.77
(3,9)	1:A:36:VAL:O	1:A:40:ARG:H	12	0.23	0.08	0.2
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE21	11	0.85	0.1	0.9
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE22	11	0.85	0.1	0.9
(1,331)	1:A:37:LEU:HD11	1:A:66:VAL:HA	11	0.51	0.25	0.47
(1,331)	1:A:37:LEU:HD12	1:A:66:VAL:HA	11	0.51	0.25	0.47
(1,331)	1:A:37:LEU:HD13	1:A:66:VAL:HA	11	0.51	0.25	0.47
(1,14)	1:A:27:THR:HB	1:A:28:VAL:H	11	0.14	0.02	0.13
(2,63)	1:A:1:SER:HB2	1:A:53:GLN:H	10	0.77	0.26	0.9
(2,63)	1:A:1:SER:HB3	1:A:53:GLN:H	10	0.77	0.26	0.9
(1,363)	1:A:4:PRO:HG2	1:A:5:THR:HA	10	0.6	0.21	0.6
(1,363)	1:A:4:PRO:HG3	1:A:5:THR:HA	10	0.6	0.21	0.6
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE1	10	0.34	0.16	0.36
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE2	10	0.34	0.16	0.36

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Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE3	10	0.34	0.16	0.36
(3,11)	1:A:37:LEU:O	1:A:41:PHE:H	10	0.29	0.08	0.32
(3,41)	1:A:72:ASN:O	1:A:76:LYS:H	10	0.28	0.07	0.3
(3,2)	1:A:32:THR:O	1:A:36:VAL:N	10	0.24	0.06	0.26
(3,13)	1:A:38:ASN:O	1:A:42:GLN:H	10	0.23	0.05	0.25
(3,27)	1:A:65:GLN:O	1:A:69:TRP:H	10	0.21	0.07	0.22
(1,196)	1:A:29:PHE:H	1:A:29:PHE:HE2	9	0.42	0.17	0.39
(3,15)	1:A:50:GLN:O	1:A:54:GLU:H	9	0.25	0.06	0.26
(3,12)	1:A:37:LEU:O	1:A:41:PHE:N	9	0.24	0.06	0.25
(3,10)	1:A:36:VAL:O	1:A:40:ARG:N	9	0.19	0.08	0.15
(3,20)	1:A:52:MET:O	1:A:56:SER:N	9	0.17	0.05	0.18
(1,177)	1:A:63:TYR:H	1:A:66:VAL:H	9	0.14	0.02	0.13
(3,29)	1:A:66:VAL:O	1:A:70:PHE:H	8	0.26	0.08	0.3
(3,31)	1:A:67:LYS:O	1:A:71:GLN:H	8	0.25	0.08	0.26
(3,25)	1:A:64:LYS:O	1:A:68:THR:H	8	0.24	0.08	0.25
(1,83)	1:A:20:VAL:H	1:A:20:VAL:HB	8	0.16	0.02	0.16
(1,34)	1:A:38:ASN:HA	1:A:42:GLN:H	8	0.13	0.02	0.13
(2,80)	1:A:29:PHE:HD1	1:A:33:GLN:HG2	7	0.67	0.56	0.45
(2,80)	1:A:29:PHE:HD1	1:A:33:GLN:HG3	7	0.67	0.56	0.45
(3,37)	1:A:70:PHE:O	1:A:74:ARG:H	7	0.22	0.06	0.23
(1,215)	1:A:56:SER:H	1:A:66:VAL:HB	7	0.12	0.02	0.12
(3,30)	1:A:66:VAL:O	1:A:70:PHE:N	6	0.26	0.05	0.29
(3,3)	1:A:33:GLN:O	1:A:37:LEU:H	6	0.19	0.06	0.17
(3,32)	1:A:67:LYS:O	1:A:71:GLN:N	6	0.19	0.04	0.18
(3,33)	1:A:68:THR:O	1:A:72:ASN:H	5	0.2	0.05	0.21
(3,42)	1:A:72:ASN:O	1:A:76:LYS:N	5	0.19	0.04	0.2
(3,28)	1:A:65:GLN:O	1:A:69:TRP:N	5	0.18	0.05	0.16
(3,26)	1:A:64:LYS:O	1:A:68:THR:N	5	0.18	0.04	0.21
(3,38)	1:A:70:PHE:O	1:A:74:ARG:N	5	0.17	0.06	0.17
(1,293)	1:A:56:SER:HA	1:A:66:VAL:HA	5	0.13	0.02	0.13
(1,285)	1:A:56:SER:HA	1:A:58:ILE:H	5	0.13	0.02	0.12
(2,162)	1:A:53:GLN:HE21	1:A:63:TYR:HE2	4	1.01	0.28	1.02
(2,162)	1:A:53:GLN:HE22	1:A:63:TYR:HE2	4	1.01	0.28	1.02
(1,428)	1:A:45:LYS:HB2	1:A:46:TYR:HD1	4	0.28	0.13	0.24
(1,428)	1:A:45:LYS:HB3	1:A:46:TYR:HD1	4	0.28	0.13	0.24
(2,167)	1:A:55:LEU:HG	1:A:56:SER:HB2	4	0.2	0.1	0.17
(2,167)	1:A:55:LEU:HG	1:A:56:SER:HB3	4	0.2	0.1	0.17
(3,16)	1:A:50:GLN:O	1:A:54:GLU:N	4	0.16	0.02	0.16
(3,35)	1:A:69:TRP:O	1:A:73:GLN:H	3	0.25	0.06	0.25
(1,277)	1:A:11:VAL:HB	1:A:12:ALA:HA	3	0.22	0.1	0.15
(3,39)	1:A:71:GLN:O	1:A:75:MET:H	3	0.21	0.06	0.17
(3,36)	1:A:69:TRP:O	1:A:73:GLN:N	3	0.18	0.05	0.16

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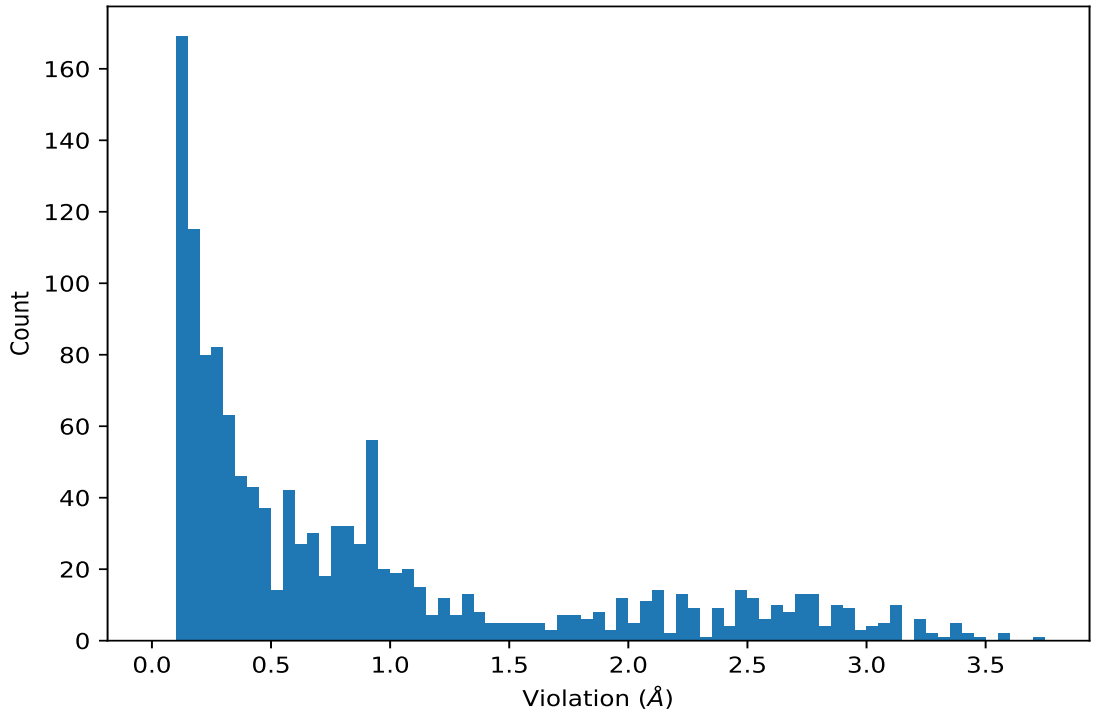
Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(3,4)	1:A:33:GLN:O	1:A:37:LEU:N	3	0.18	0.02	0.19
(1,81)	1:A:18:VAL:H	1:A:18:VAL:HB	3	0.14	0.01	0.13
(1,7)	1:A:17:LYS:HA	1:A:18:VAL:H	3	0.14	0.03	0.13
(1,55)	1:A:56:SER:HA	1:A:59:LEU:H	3	0.12	0.01	0.12
(1,339)	1:A:61:LEU:HD11	1:A:66:VAL:HA	2	0.92	0.04	0.92
(1,339)	1:A:61:LEU:HD12	1:A:66:VAL:HA	2	0.92	0.04	0.92
(1,339)	1:A:61:LEU:HD13	1:A:66:VAL:HA	2	0.92	0.04	0.92
(1,335)	1:A:47:LEU:HB3	1:A:52:MET:HE1	2	0.8	0.02	0.8
(1,335)	1:A:47:LEU:HB3	1:A:52:MET:HE2	2	0.8	0.02	0.8
(1,335)	1:A:47:LEU:HB3	1:A:52:MET:HE3	2	0.8	0.02	0.8
(1,340)	1:A:72:ASN:HA	1:A:75:MET:HE1	2	0.54	0.08	0.54
(1,340)	1:A:72:ASN:HA	1:A:75:MET:HE2	2	0.54	0.08	0.54
(1,340)	1:A:72:ASN:HA	1:A:75:MET:HE3	2	0.54	0.08	0.54
(1,237)	1:A:47:LEU:H	1:A:52:MET:HE1	2	0.46	0.02	0.46
(1,237)	1:A:47:LEU:H	1:A:52:MET:HE2	2	0.46	0.02	0.46
(1,237)	1:A:47:LEU:H	1:A:52:MET:HE3	2	0.46	0.02	0.46
(1,119)	1:A:22:LYS:H	1:A:23:GLN:H	2	0.2	0.02	0.2
(1,12)	1:A:5:THR:HA	1:A:6:SER:H	2	0.13	0.01	0.13
(1,143)	1:A:30:SER:H	1:A:34:LEU:H	2	0.12	0.0	0.12
(1,192)	1:A:47:LEU:HG	1:A:48:SER:H	2	0.12	0.0	0.12

[1]Number of violated models, [2]Standard 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)
(1,214)	1:A:53:GLN:H	1:A:63:TYR:HE2	18	3.71
(1,349)	1:A:41:PHE:HE1	1:A:46:TYR:HD2	15	3.58
(2,4)	1:A:52:MET:H	1:A:63:TYR:HE2	18	3.57
(2,58)	1:A:29:PHE:HD1	1:A:33:GLN:H	3	3.45
(2,4)	1:A:52:MET:H	1:A:63:TYR:HE2	9	3.43
(1,361)	1:A:49:LEU:HA	1:A:63:TYR:HE2	18	3.43
(1,214)	1:A:53:GLN:H	1:A:63:TYR:HE2	9	3.4
(2,4)	1:A:52:MET:H	1:A:63:TYR:HE2	19	3.38
(2,4)	1:A:52:MET:H	1:A:63:TYR:HE2	6	3.37
(1,361)	1:A:49:LEU:HA	1:A:63:TYR:HE2	11	3.37
(2,4)	1:A:52:MET:H	1:A:63:TYR:HE2	13	3.35
(2,4)	1:A:52:MET:H	1:A:63:TYR:HE2	4	3.33
(2,4)	1:A:52:MET:H	1:A:63:TYR:HE2	20	3.3
(1,361)	1:A:49:LEU:HA	1:A:63:TYR:HE2	4	3.25
(2,4)	1:A:52:MET:H	1:A:63:TYR:HE2	12	3.24
(1,214)	1:A:53:GLN:H	1:A:63:TYR:HE2	13	3.23

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,4)	1:A:52:MET:H	1:A:63:TYR:HE2	11	3.22
(1,214)	1:A:53:GLN:H	1:A:63:TYR:HE2	19	3.21
(2,4)	1:A:52:MET:H	1:A:63:TYR:HE2	15	3.2
(1,214)	1:A:53:GLN:H	1:A:63:TYR:HE2	14	3.2
(1,349)	1:A:41:PHE:HE1	1:A:46:TYR:HD2	3	3.15
(1,214)	1:A:53:GLN:H	1:A:63:TYR:HE2	6	3.15
(1,361)	1:A:49:LEU:HA	1:A:63:TYR:HE2	9	3.14
(1,349)	1:A:41:PHE:HE1	1:A:46:TYR:HD2	5	3.13
(2,4)	1:A:52:MET:H	1:A:63:TYR:HE2	14	3.12
(1,214)	1:A:53:GLN:H	1:A:63:TYR:HE2	12	3.12
(2,4)	1:A:52:MET:H	1:A:63:TYR:HE2	5	3.1
(1,356)	1:A:41:PHE:HD1	1:A:46:TYR:HD2	15	3.1
(1,349)	1:A:41:PHE:HE1	1:A:46:TYR:HD2	17	3.1
(1,214)	1:A:53:GLN:H	1:A:63:TYR:HE2	11	3.1
(1,361)	1:A:49:LEU:HA	1:A:63:TYR:HE2	19	3.09
(1,353)	1:A:53:GLN:HA	1:A:63:TYR:HD2	18	3.09
(1,361)	1:A:49:LEU:HA	1:A:63:TYR:HE2	12	3.08
(1,353)	1:A:53:GLN:HA	1:A:63:TYR:HD2	9	3.07
(1,214)	1:A:53:GLN:H	1:A:63:TYR:HE2	4	3.06
(1,361)	1:A:49:LEU:HA	1:A:63:TYR:HE2	20	3.04
(1,214)	1:A:53:GLN:H	1:A:63:TYR:HE2	5	3.04
(1,207)	1:A:53:GLN:H	1:A:63:TYR:HD2	18	3.04
(1,214)	1:A:53:GLN:H	1:A:63:TYR:HE2	15	3.03
(2,4)	1:A:52:MET:H	1:A:63:TYR:HE2	8	2.99
(1,361)	1:A:49:LEU:HA	1:A:63:TYR:HE2	13	2.99
(1,349)	1:A:41:PHE:HE1	1:A:46:TYR:HD2	9	2.96
(1,361)	1:A:49:LEU:HA	1:A:63:TYR:HE2	6	2.94
(1,349)	1:A:41:PHE:HE1	1:A:46:TYR:HD2	6	2.94
(1,349)	1:A:41:PHE:HE1	1:A:46:TYR:HD2	14	2.94
(1,356)	1:A:41:PHE:HD1	1:A:46:TYR:HD2	17	2.93
(1,356)	1:A:41:PHE:HD1	1:A:46:TYR:HD2	18	2.93
(1,349)	1:A:41:PHE:HE1	1:A:46:TYR:HD2	4	2.93
(1,349)	1:A:41:PHE:HE1	1:A:46:TYR:HD2	13	2.93
(1,356)	1:A:41:PHE:HD1	1:A:46:TYR:HD2	4	2.92
(1,214)	1:A:53:GLN:H	1:A:63:TYR:HE2	16	2.92
(2,4)	1:A:52:MET:H	1:A:63:TYR:HE2	16	2.9
(1,356)	1:A:41:PHE:HD1	1:A:46:TYR:HD2	13	2.9
(2,4)	1:A:52:MET:H	1:A:63:TYR:HE2	2	2.89
(1,214)	1:A:53:GLN:H	1:A:63:TYR:HE2	2	2.89
(1,214)	1:A:53:GLN:H	1:A:63:TYR:HE2	20	2.89
(1,362)	1:A:41:PHE:HE1	1:A:46:TYR:HE2	15	2.88
(1,356)	1:A:41:PHE:HD1	1:A:46:TYR:HD2	3	2.88

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,207)	1:A:53:GLN:H	1:A:63:TYR:HD2	9	2.88
(1,353)	1:A:53:GLN:HA	1:A:63:TYR:HD2	14	2.87
(1,214)	1:A:53:GLN:H	1:A:63:TYR:HE2	1	2.86
(2,58)	1:A:29:PHE:HD1	1:A:33:GLN:H	16	2.84
(2,4)	1:A:52:MET:H	1:A:63:TYR:HE2	7	2.84
(1,356)	1:A:41:PHE:HD1	1:A:46:TYR:HD2	9	2.84
(1,361)	1:A:49:LEU:HA	1:A:63:TYR:HE2	5	2.81
(1,460)	1:A:52:MET:HB2	1:A:63:TYR:HE2	13	2.8
(1,460)	1:A:52:MET:HB3	1:A:63:TYR:HE2	13	2.8
(1,356)	1:A:41:PHE:HD1	1:A:46:TYR:HD2	6	2.8
(1,353)	1:A:53:GLN:HA	1:A:63:TYR:HD2	17	2.8
(1,214)	1:A:53:GLN:H	1:A:63:TYR:HE2	17	2.8
(1,356)	1:A:41:PHE:HD1	1:A:46:TYR:HD2	5	2.79
(1,214)	1:A:53:GLN:H	1:A:63:TYR:HE2	8	2.79
(1,460)	1:A:52:MET:HB2	1:A:63:TYR:HE2	15	2.77
(1,460)	1:A:52:MET:HB3	1:A:63:TYR:HE2	15	2.77
(1,361)	1:A:49:LEU:HA	1:A:63:TYR:HE2	15	2.77
(1,349)	1:A:41:PHE:HE1	1:A:46:TYR:HD2	18	2.76
(1,214)	1:A:53:GLN:H	1:A:63:TYR:HE2	7	2.76
(1,207)	1:A:53:GLN:H	1:A:63:TYR:HD2	14	2.76
(1,353)	1:A:53:GLN:HA	1:A:63:TYR:HD2	15	2.74
(1,207)	1:A:53:GLN:H	1:A:63:TYR:HD2	19	2.74
(1,460)	1:A:52:MET:HB2	1:A:63:TYR:HE2	20	2.73
(1,460)	1:A:52:MET:HB3	1:A:63:TYR:HE2	20	2.73
(1,353)	1:A:53:GLN:HA	1:A:63:TYR:HD2	12	2.73
(1,207)	1:A:53:GLN:H	1:A:63:TYR:HD2	11	2.73
(1,214)	1:A:53:GLN:H	1:A:63:TYR:HE2	10	2.72
(1,207)	1:A:53:GLN:H	1:A:63:TYR:HD2	5	2.72
(1,353)	1:A:53:GLN:HA	1:A:63:TYR:HD2	1	2.71
(1,349)	1:A:41:PHE:HE1	1:A:46:TYR:HD2	11	2.71
(1,214)	1:A:53:GLN:H	1:A:63:TYR:HE2	3	2.71
(1,356)	1:A:41:PHE:HD1	1:A:46:TYR:HD2	20	2.7
(1,349)	1:A:41:PHE:HE1	1:A:46:TYR:HD2	7	2.7
(2,4)	1:A:52:MET:H	1:A:63:TYR:HE2	1	2.69
(1,353)	1:A:53:GLN:HA	1:A:63:TYR:HD2	6	2.69
(1,353)	1:A:53:GLN:HA	1:A:63:TYR:HD2	11	2.69
(1,353)	1:A:53:GLN:HA	1:A:63:TYR:HD2	13	2.68
(1,460)	1:A:52:MET:HB2	1:A:63:TYR:HE2	4	2.67
(1,460)	1:A:52:MET:HB3	1:A:63:TYR:HE2	4	2.67
(1,353)	1:A:53:GLN:HA	1:A:63:TYR:HD2	2	2.66
(1,349)	1:A:41:PHE:HE1	1:A:46:TYR:HD2	1	2.66
(1,353)	1:A:53:GLN:HA	1:A:63:TYR:HD2	3	2.65

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,353)	1:A:53:GLN:HA	1:A:63:TYR:HD2	19	2.65
(1,361)	1:A:49:LEU:HA	1:A:63:TYR:HE2	2	2.63
(1,356)	1:A:41:PHE:HD1	1:A:46:TYR:HD2	14	2.63
(2,4)	1:A:52:MET:H	1:A:63:TYR:HE2	10	2.61
(1,353)	1:A:53:GLN:HA	1:A:63:TYR:HD2	7	2.61
(1,349)	1:A:41:PHE:HE1	1:A:46:TYR:HD2	16	2.61
(1,361)	1:A:49:LEU:HA	1:A:63:TYR:HE2	16	2.6
(1,356)	1:A:41:PHE:HD1	1:A:46:TYR:HD2	12	2.6
(1,349)	1:A:41:PHE:HE1	1:A:46:TYR:HD2	20	2.6
(2,58)	1:A:29:PHE:HD1	1:A:33:GLN:H	18	2.58
(1,362)	1:A:41:PHE:HE1	1:A:46:TYR:HE2	5	2.58
(1,362)	1:A:41:PHE:HE1	1:A:46:TYR:HE2	17	2.58
(1,356)	1:A:41:PHE:HD1	1:A:46:TYR:HD2	19	2.57
(1,353)	1:A:53:GLN:HA	1:A:63:TYR:HD2	16	2.57
(1,356)	1:A:41:PHE:HD1	1:A:46:TYR:HD2	16	2.56
(1,207)	1:A:53:GLN:H	1:A:63:TYR:HD2	16	2.55
(2,4)	1:A:52:MET:H	1:A:63:TYR:HE2	3	2.54
(1,361)	1:A:49:LEU:HA	1:A:63:TYR:HE2	1	2.54
(1,353)	1:A:53:GLN:HA	1:A:63:TYR:HD2	8	2.54
(1,349)	1:A:41:PHE:HE1	1:A:46:TYR:HD2	12	2.54
(1,362)	1:A:41:PHE:HE1	1:A:46:TYR:HE2	13	2.53
(2,4)	1:A:52:MET:H	1:A:63:TYR:HE2	17	2.52
(1,460)	1:A:52:MET:HB2	1:A:63:TYR:HE2	6	2.52
(1,460)	1:A:52:MET:HB3	1:A:63:TYR:HE2	6	2.52
(1,361)	1:A:49:LEU:HA	1:A:63:TYR:HE2	7	2.51
(1,356)	1:A:41:PHE:HD1	1:A:46:TYR:HD2	7	2.51
(1,207)	1:A:53:GLN:H	1:A:63:TYR:HD2	7	2.5
(2,58)	1:A:29:PHE:HD1	1:A:33:GLN:H	6	2.49
(1,349)	1:A:41:PHE:HE1	1:A:46:TYR:HD2	19	2.49
(1,460)	1:A:52:MET:HB2	1:A:63:TYR:HE2	8	2.48
(1,460)	1:A:52:MET:HB3	1:A:63:TYR:HE2	8	2.48
(1,353)	1:A:53:GLN:HA	1:A:63:TYR:HD2	5	2.48
(1,207)	1:A:53:GLN:H	1:A:63:TYR:HD2	6	2.48
(1,207)	1:A:53:GLN:H	1:A:63:TYR:HD2	12	2.48
(1,460)	1:A:52:MET:HB2	1:A:63:TYR:HE2	12	2.47
(1,460)	1:A:52:MET:HB3	1:A:63:TYR:HE2	12	2.47
(1,361)	1:A:49:LEU:HA	1:A:63:TYR:HE2	14	2.47
(1,356)	1:A:41:PHE:HD1	1:A:46:TYR:HD2	11	2.46
(1,353)	1:A:53:GLN:HA	1:A:63:TYR:HD2	10	2.45
(1,349)	1:A:41:PHE:HE1	1:A:46:TYR:HD2	8	2.45
(1,207)	1:A:53:GLN:H	1:A:63:TYR:HD2	17	2.45
(1,207)	1:A:53:GLN:H	1:A:63:TYR:HD2	1	2.44

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,207)	1:A:53:GLN:H	1:A:63:TYR:HD2	13	2.44
(1,361)	1:A:49:LEU:HA	1:A:63:TYR:HE2	8	2.42
(1,349)	1:A:41:PHE:HE1	1:A:46:TYR:HD2	2	2.41
(1,362)	1:A:41:PHE:HE1	1:A:46:TYR:HE2	14	2.4
(1,207)	1:A:53:GLN:H	1:A:63:TYR:HD2	2	2.4
(1,207)	1:A:53:GLN:H	1:A:63:TYR:HD2	4	2.38
(1,362)	1:A:41:PHE:HE1	1:A:46:TYR:HE2	11	2.37
(1,460)	1:A:52:MET:HB2	1:A:63:TYR:HE2	19	2.36
(1,460)	1:A:52:MET:HB3	1:A:63:TYR:HE2	19	2.36
(1,460)	1:A:52:MET:HB2	1:A:63:TYR:HE2	18	2.35
(1,460)	1:A:52:MET:HB3	1:A:63:TYR:HE2	18	2.35
(1,207)	1:A:53:GLN:H	1:A:63:TYR:HD2	3	2.35
(1,353)	1:A:53:GLN:HA	1:A:63:TYR:HD2	4	2.31
(1,460)	1:A:52:MET:HB2	1:A:63:TYR:HE2	14	2.3
(1,460)	1:A:52:MET:HB3	1:A:63:TYR:HE2	14	2.3
(1,362)	1:A:41:PHE:HE1	1:A:46:TYR:HE2	4	2.29
(1,353)	1:A:53:GLN:HA	1:A:63:TYR:HD2	20	2.29
(1,362)	1:A:41:PHE:HE1	1:A:46:TYR:HE2	6	2.27
(2,58)	1:A:29:PHE:HD1	1:A:33:GLN:H	8	2.26
(1,461)	1:A:52:MET:HB2	1:A:63:TYR:HD2	13	2.26
(1,461)	1:A:52:MET:HB3	1:A:63:TYR:HD2	13	2.26
(1,362)	1:A:41:PHE:HE1	1:A:46:TYR:HE2	1	2.26
(1,461)	1:A:52:MET:HB2	1:A:63:TYR:HD2	20	2.24
(1,461)	1:A:52:MET:HB3	1:A:63:TYR:HD2	20	2.24
(1,460)	1:A:52:MET:HB2	1:A:63:TYR:HE2	1	2.24
(1,460)	1:A:52:MET:HB3	1:A:63:TYR:HE2	1	2.24
(1,461)	1:A:52:MET:HB2	1:A:63:TYR:HD2	4	2.23
(1,461)	1:A:52:MET:HB3	1:A:63:TYR:HD2	4	2.23
(1,207)	1:A:53:GLN:H	1:A:63:TYR:HD2	20	2.22
(1,461)	1:A:52:MET:HB2	1:A:63:TYR:HD2	15	2.2
(1,461)	1:A:52:MET:HB3	1:A:63:TYR:HD2	15	2.2
(1,460)	1:A:52:MET:HB2	1:A:63:TYR:HE2	5	2.2
(1,460)	1:A:52:MET:HB3	1:A:63:TYR:HE2	5	2.2
(1,362)	1:A:41:PHE:HE1	1:A:46:TYR:HE2	3	2.2
(1,356)	1:A:41:PHE:HD1	1:A:46:TYR:HD2	10	2.2
(1,207)	1:A:53:GLN:H	1:A:63:TYR:HD2	15	2.19
(1,362)	1:A:41:PHE:HE1	1:A:46:TYR:HE2	12	2.15
(1,460)	1:A:52:MET:HB2	1:A:63:TYR:HE2	2	2.14
(1,460)	1:A:52:MET:HB3	1:A:63:TYR:HE2	2	2.14
(1,207)	1:A:53:GLN:H	1:A:63:TYR:HD2	8	2.13
(1,356)	1:A:41:PHE:HD1	1:A:46:TYR:HD2	2	2.12
(1,460)	1:A:52:MET:HB2	1:A:63:TYR:HE2	11	2.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,460)	1:A:52:MET:HB3	1:A:63:TYR:HE2	11	2.11
(1,461)	1:A:52:MET:HB2	1:A:63:TYR:HD2	6	2.1
(1,461)	1:A:52:MET:HB3	1:A:63:TYR:HD2	6	2.1
(1,460)	1:A:52:MET:HB2	1:A:63:TYR:HE2	7	2.1
(1,460)	1:A:52:MET:HB3	1:A:63:TYR:HE2	7	2.1
(1,460)	1:A:52:MET:HB2	1:A:63:TYR:HE2	10	2.1
(1,460)	1:A:52:MET:HB3	1:A:63:TYR:HE2	10	2.1
(1,362)	1:A:41:PHE:HE1	1:A:46:TYR:HE2	9	2.1
(1,362)	1:A:41:PHE:HE1	1:A:46:TYR:HE2	19	2.1
(2,60)	1:A:41:PHE:HD1	1:A:46:TYR:HE2	13	2.09
(1,349)	1:A:41:PHE:HE1	1:A:46:TYR:HD2	10	2.09
(1,461)	1:A:52:MET:HB2	1:A:63:TYR:HD2	12	2.08
(1,461)	1:A:52:MET:HB3	1:A:63:TYR:HD2	12	2.08
(1,362)	1:A:41:PHE:HE1	1:A:46:TYR:HE2	7	2.08
(1,356)	1:A:41:PHE:HD1	1:A:46:TYR:HD2	1	2.08
(2,58)	1:A:29:PHE:HD1	1:A:33:GLN:H	19	2.07
(1,356)	1:A:41:PHE:HD1	1:A:46:TYR:HD2	8	2.07
(2,58)	1:A:29:PHE:HD1	1:A:33:GLN:H	13	2.06
(1,460)	1:A:52:MET:HB2	1:A:63:TYR:HE2	9	2.06
(1,460)	1:A:52:MET:HB3	1:A:63:TYR:HE2	9	2.06
(1,461)	1:A:52:MET:HB2	1:A:63:TYR:HD2	19	2.04
(1,461)	1:A:52:MET:HB3	1:A:63:TYR:HD2	19	2.04
(1,461)	1:A:52:MET:HB2	1:A:63:TYR:HD2	8	2.02
(1,461)	1:A:52:MET:HB3	1:A:63:TYR:HD2	8	2.02
(1,362)	1:A:41:PHE:HE1	1:A:46:TYR:HE2	16	2.01
(2,80)	1:A:29:PHE:HD1	1:A:33:GLN:HG2	3	1.99
(2,80)	1:A:29:PHE:HD1	1:A:33:GLN:HG3	3	1.99
(1,461)	1:A:52:MET:HB2	1:A:63:TYR:HD2	18	1.99
(1,461)	1:A:52:MET:HB3	1:A:63:TYR:HD2	18	1.99
(1,460)	1:A:52:MET:HB2	1:A:63:TYR:HE2	16	1.99
(1,460)	1:A:52:MET:HB3	1:A:63:TYR:HE2	16	1.99
(1,461)	1:A:52:MET:HB2	1:A:63:TYR:HD2	5	1.98
(1,461)	1:A:52:MET:HB3	1:A:63:TYR:HD2	5	1.98
(1,207)	1:A:53:GLN:H	1:A:63:TYR:HD2	10	1.98
(2,58)	1:A:29:PHE:HD1	1:A:33:GLN:H	12	1.97
(1,460)	1:A:52:MET:HB2	1:A:63:TYR:HE2	3	1.96
(1,460)	1:A:52:MET:HB3	1:A:63:TYR:HE2	3	1.96
(1,362)	1:A:41:PHE:HE1	1:A:46:TYR:HE2	2	1.92
(1,362)	1:A:41:PHE:HE1	1:A:46:TYR:HE2	18	1.92
(2,60)	1:A:41:PHE:HD1	1:A:46:TYR:HE2	15	1.91
(1,461)	1:A:52:MET:HB2	1:A:63:TYR:HD2	14	1.89
(1,461)	1:A:52:MET:HB3	1:A:63:TYR:HD2	14	1.89

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,60)	1:A:41:PHE:HD1	1:A:46:TYR:HE2	17	1.88
(2,144)	1:A:49:LEU:HB2	1:A:63:TYR:HE2	11	1.88
(2,144)	1:A:49:LEU:HB3	1:A:63:TYR:HE2	11	1.88
(1,461)	1:A:52:MET:HB2	1:A:63:TYR:HD2	11	1.86
(1,461)	1:A:52:MET:HB3	1:A:63:TYR:HD2	11	1.86
(2,60)	1:A:41:PHE:HD1	1:A:46:TYR:HE2	4	1.85
(1,461)	1:A:52:MET:HB2	1:A:63:TYR:HD2	2	1.84
(1,461)	1:A:52:MET:HB3	1:A:63:TYR:HD2	2	1.84
(1,361)	1:A:49:LEU:HA	1:A:63:TYR:HE2	3	1.84
(1,461)	1:A:52:MET:HB2	1:A:63:TYR:HD2	1	1.82
(1,461)	1:A:52:MET:HB3	1:A:63:TYR:HD2	1	1.82
(1,361)	1:A:49:LEU:HA	1:A:63:TYR:HE2	17	1.82
(1,461)	1:A:52:MET:HB2	1:A:63:TYR:HD2	7	1.79
(1,461)	1:A:52:MET:HB3	1:A:63:TYR:HD2	7	1.79
(1,460)	1:A:52:MET:HB2	1:A:63:TYR:HE2	17	1.79
(1,460)	1:A:52:MET:HB3	1:A:63:TYR:HE2	17	1.79
(2,144)	1:A:49:LEU:HB2	1:A:63:TYR:HE2	18	1.76
(2,144)	1:A:49:LEU:HB3	1:A:63:TYR:HE2	18	1.76
(1,362)	1:A:41:PHE:HE1	1:A:46:TYR:HE2	20	1.75
(2,60)	1:A:41:PHE:HD1	1:A:46:TYR:HE2	5	1.73
(2,60)	1:A:41:PHE:HD1	1:A:46:TYR:HE2	6	1.73
(1,461)	1:A:52:MET:HB2	1:A:63:TYR:HD2	16	1.73
(1,461)	1:A:52:MET:HB3	1:A:63:TYR:HD2	16	1.73
(1,361)	1:A:49:LEU:HA	1:A:63:TYR:HE2	10	1.73
(1,461)	1:A:52:MET:HB2	1:A:63:TYR:HD2	9	1.72
(1,461)	1:A:52:MET:HB3	1:A:63:TYR:HD2	9	1.72
(2,60)	1:A:41:PHE:HD1	1:A:46:TYR:HE2	14	1.7
(2,60)	1:A:41:PHE:HD1	1:A:46:TYR:HE2	9	1.69
(2,60)	1:A:41:PHE:HD1	1:A:46:TYR:HE2	12	1.68
(2,60)	1:A:41:PHE:HD1	1:A:46:TYR:HE2	3	1.65
(1,461)	1:A:52:MET:HB2	1:A:63:TYR:HD2	3	1.65
(1,461)	1:A:52:MET:HB3	1:A:63:TYR:HD2	3	1.65
(2,60)	1:A:41:PHE:HD1	1:A:46:TYR:HE2	18	1.64
(2,60)	1:A:41:PHE:HD1	1:A:46:TYR:HE2	19	1.63
(2,58)	1:A:29:PHE:HD1	1:A:33:GLN:H	4	1.59
(1,461)	1:A:52:MET:HB2	1:A:63:TYR:HD2	10	1.58
(1,461)	1:A:52:MET:HB3	1:A:63:TYR:HD2	10	1.58
(2,60)	1:A:41:PHE:HD1	1:A:46:TYR:HE2	7	1.57
(2,60)	1:A:41:PHE:HD1	1:A:46:TYR:HE2	11	1.57
(1,461)	1:A:52:MET:HB2	1:A:63:TYR:HD2	17	1.54
(1,461)	1:A:52:MET:HB3	1:A:63:TYR:HD2	17	1.54
(2,58)	1:A:29:PHE:HD1	1:A:33:GLN:H	20	1.52

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,60)	1:A:41:PHE:HD1	1:A:46:TYR:HE2	16	1.5
(1,362)	1:A:41:PHE:HE1	1:A:46:TYR:HE2	8	1.5
(1,473)	1:A:53:GLN:HE21	1:A:63:TYR:HD2	8	1.49
(1,473)	1:A:53:GLN:HE22	1:A:63:TYR:HD2	8	1.49
(1,473)	1:A:53:GLN:HE21	1:A:63:TYR:HD2	18	1.48
(1,473)	1:A:53:GLN:HE22	1:A:63:TYR:HD2	18	1.48
(2,60)	1:A:41:PHE:HD1	1:A:46:TYR:HE2	20	1.47
(2,58)	1:A:29:PHE:HD1	1:A:33:GLN:H	5	1.45
(1,465)	1:A:52:MET:HG2	1:A:63:TYR:HE2	18	1.43
(1,465)	1:A:52:MET:HG3	1:A:63:TYR:HE2	18	1.43
(2,144)	1:A:49:LEU:HB2	1:A:63:TYR:HE2	19	1.41
(2,144)	1:A:49:LEU:HB3	1:A:63:TYR:HE2	19	1.41
(2,162)	1:A:53:GLN:HE21	1:A:63:TYR:HE2	8	1.38
(2,162)	1:A:53:GLN:HE22	1:A:63:TYR:HE2	8	1.38
(1,309)	1:A:63:TYR:HD1	1:A:64:LYS:HA	1	1.38
(2,125)	1:A:45:LYS:HD2	1:A:46:TYR:HD1	1	1.36
(2,125)	1:A:45:LYS:HD3	1:A:46:TYR:HD1	1	1.36
(2,6)	1:A:63:TYR:HE1	1:A:64:LYS:H	1	1.35
(2,125)	1:A:45:LYS:HD2	1:A:46:TYR:HD1	3	1.35
(2,125)	1:A:45:LYS:HD3	1:A:46:TYR:HD1	3	1.35
(2,144)	1:A:49:LEU:HB2	1:A:63:TYR:HE2	9	1.34
(2,144)	1:A:49:LEU:HB3	1:A:63:TYR:HE2	9	1.34
(2,144)	1:A:49:LEU:HB2	1:A:63:TYR:HE2	4	1.32
(2,144)	1:A:49:LEU:HB3	1:A:63:TYR:HE2	4	1.32
(2,144)	1:A:49:LEU:HB2	1:A:63:TYR:HE2	12	1.31
(2,144)	1:A:49:LEU:HB3	1:A:63:TYR:HE2	12	1.31
(1,465)	1:A:52:MET:HG2	1:A:63:TYR:HE2	6	1.31
(1,465)	1:A:52:MET:HG3	1:A:63:TYR:HE2	6	1.31
(1,465)	1:A:52:MET:HG2	1:A:63:TYR:HE2	13	1.31
(1,465)	1:A:52:MET:HG3	1:A:63:TYR:HE2	13	1.31
(1,362)	1:A:41:PHE:HE1	1:A:46:TYR:HE2	10	1.31
(1,465)	1:A:52:MET:HG2	1:A:63:TYR:HE2	9	1.3
(1,465)	1:A:52:MET:HG3	1:A:63:TYR:HE2	9	1.3
(2,6)	1:A:63:TYR:HE1	1:A:64:LYS:H	7	1.28
(1,465)	1:A:52:MET:HG2	1:A:63:TYR:HE2	20	1.28
(1,465)	1:A:52:MET:HG3	1:A:63:TYR:HE2	20	1.28
(1,309)	1:A:63:TYR:HD1	1:A:64:LYS:HA	7	1.28
(1,309)	1:A:63:TYR:HD1	1:A:64:LYS:HA	17	1.28
(1,465)	1:A:52:MET:HG2	1:A:63:TYR:HE2	19	1.27
(1,465)	1:A:52:MET:HG3	1:A:63:TYR:HE2	19	1.27
(2,6)	1:A:63:TYR:HE1	1:A:64:LYS:H	16	1.24
(1,465)	1:A:52:MET:HG2	1:A:63:TYR:HE2	15	1.24

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,465)	1:A:52:MET:HG3	1:A:63:TYR:HE2	15	1.24
(2,6)	1:A:63:TYR:HE1	1:A:64:LYS:H	17	1.23
(1,309)	1:A:63:TYR:HD1	1:A:64:LYS:HA	16	1.23
(2,6)	1:A:63:TYR:HE1	1:A:64:LYS:H	11	1.22
(1,465)	1:A:52:MET:HG2	1:A:63:TYR:HE2	4	1.22
(1,465)	1:A:52:MET:HG3	1:A:63:TYR:HE2	4	1.22
(1,473)	1:A:53:GLN:HE21	1:A:63:TYR:HD2	9	1.21
(1,473)	1:A:53:GLN:HE22	1:A:63:TYR:HD2	9	1.21
(1,465)	1:A:52:MET:HG2	1:A:63:TYR:HE2	11	1.21
(1,465)	1:A:52:MET:HG3	1:A:63:TYR:HE2	11	1.21
(2,6)	1:A:63:TYR:HE1	1:A:64:LYS:H	12	1.18
(1,309)	1:A:63:TYR:HD1	1:A:64:LYS:HA	12	1.18
(2,58)	1:A:29:PHE:HD1	1:A:33:GLN:H	15	1.17
(2,6)	1:A:63:TYR:HE1	1:A:64:LYS:H	2	1.16
(2,6)	1:A:63:TYR:HE1	1:A:64:LYS:H	5	1.16
(2,144)	1:A:49:LEU:HB2	1:A:63:TYR:HE2	20	1.16
(2,144)	1:A:49:LEU:HB3	1:A:63:TYR:HE2	20	1.16
(2,162)	1:A:53:GLN:HE21	1:A:63:TYR:HE2	18	1.15
(2,162)	1:A:53:GLN:HE22	1:A:63:TYR:HE2	18	1.15
(2,125)	1:A:45:LYS:HD2	1:A:46:TYR:HD1	16	1.15
(2,125)	1:A:45:LYS:HD3	1:A:46:TYR:HD1	16	1.15
(1,309)	1:A:63:TYR:HD1	1:A:64:LYS:HA	11	1.15
(2,6)	1:A:63:TYR:HE1	1:A:64:LYS:H	3	1.14
(2,6)	1:A:63:TYR:HE1	1:A:64:LYS:H	19	1.14
(1,465)	1:A:52:MET:HG2	1:A:63:TYR:HE2	12	1.14
(1,465)	1:A:52:MET:HG3	1:A:63:TYR:HE2	12	1.14
(1,309)	1:A:63:TYR:HD1	1:A:64:LYS:HA	3	1.13
(2,60)	1:A:41:PHE:HD1	1:A:46:TYR:HE2	2	1.12
(1,309)	1:A:63:TYR:HD1	1:A:64:LYS:HA	2	1.12
(2,6)	1:A:63:TYR:HE1	1:A:64:LYS:H	9	1.11
(2,144)	1:A:49:LEU:HB2	1:A:63:TYR:HE2	5	1.11
(2,144)	1:A:49:LEU:HB3	1:A:63:TYR:HE2	5	1.11
(2,60)	1:A:41:PHE:HD1	1:A:46:TYR:HE2	1	1.08
(2,125)	1:A:45:LYS:HD2	1:A:46:TYR:HD1	20	1.08
(2,125)	1:A:45:LYS:HD3	1:A:46:TYR:HD1	20	1.08
(1,309)	1:A:63:TYR:HD1	1:A:64:LYS:HA	5	1.08
(2,125)	1:A:45:LYS:HD2	1:A:46:TYR:HD1	11	1.07
(2,125)	1:A:45:LYS:HD3	1:A:46:TYR:HD1	11	1.07
(1,309)	1:A:63:TYR:HD1	1:A:64:LYS:HA	19	1.07
(2,144)	1:A:49:LEU:HB2	1:A:63:TYR:HE2	2	1.06
(2,144)	1:A:49:LEU:HB3	1:A:63:TYR:HE2	2	1.06
(2,144)	1:A:49:LEU:HB2	1:A:63:TYR:HE2	6	1.06

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,144)	1:A:49:LEU:HB3	1:A:63:TYR:HE2	6	1.06
(1,347)	1:A:61:LEU:HD21	1:A:66:VAL:HA	4	1.06
(1,347)	1:A:61:LEU:HD22	1:A:66:VAL:HA	4	1.06
(1,347)	1:A:61:LEU:HD23	1:A:66:VAL:HA	4	1.06
(2,6)	1:A:63:TYR:HE1	1:A:64:LYS:H	20	1.05
(1,473)	1:A:53:GLN:HE21	1:A:63:TYR:HD2	2	1.05
(1,473)	1:A:53:GLN:HE22	1:A:63:TYR:HD2	2	1.05
(1,331)	1:A:37:LEU:HD11	1:A:66:VAL:HA	16	1.05
(1,331)	1:A:37:LEU:HD12	1:A:66:VAL:HA	16	1.05
(1,331)	1:A:37:LEU:HD13	1:A:66:VAL:HA	16	1.05
(2,6)	1:A:63:TYR:HE1	1:A:64:LYS:H	14	1.04
(2,6)	1:A:63:TYR:HE1	1:A:64:LYS:H	18	1.03
(2,58)	1:A:29:PHE:HD1	1:A:33:GLN:H	9	1.03
(1,465)	1:A:52:MET:HG2	1:A:63:TYR:HE2	8	1.03
(1,465)	1:A:52:MET:HG3	1:A:63:TYR:HE2	8	1.03
(1,309)	1:A:63:TYR:HD1	1:A:64:LYS:HA	9	1.03
(1,465)	1:A:52:MET:HG2	1:A:63:TYR:HE2	14	1.02
(1,465)	1:A:52:MET:HG3	1:A:63:TYR:HE2	14	1.02
(2,63)	1:A:1:SER:HB2	1:A:53:GLN:H	16	1.01
(2,63)	1:A:1:SER:HB3	1:A:53:GLN:H	16	1.01
(2,62)	1:A:1:SER:HB2	1:A:49:LEU:H	7	1.01
(2,62)	1:A:1:SER:HB3	1:A:49:LEU:H	7	1.01
(2,125)	1:A:45:LYS:HD2	1:A:46:TYR:HD1	2	1.01
(2,125)	1:A:45:LYS:HD3	1:A:46:TYR:HD1	2	1.01
(1,352)	1:A:63:TYR:HA	1:A:63:TYR:HD2	4	1.01
(2,125)	1:A:45:LYS:HD2	1:A:46:TYR:HD1	10	1.0
(2,125)	1:A:45:LYS:HD3	1:A:46:TYR:HD1	10	1.0
(1,465)	1:A:52:MET:HG2	1:A:63:TYR:HE2	5	1.0
(1,465)	1:A:52:MET:HG3	1:A:63:TYR:HE2	5	1.0
(2,6)	1:A:63:TYR:HE1	1:A:64:LYS:H	10	0.99
(2,125)	1:A:45:LYS:HD2	1:A:46:TYR:HD1	17	0.98
(2,125)	1:A:45:LYS:HD3	1:A:46:TYR:HD1	17	0.98
(2,62)	1:A:1:SER:HB2	1:A:49:LEU:H	13	0.97
(2,62)	1:A:1:SER:HB3	1:A:49:LEU:H	13	0.97
(2,62)	1:A:1:SER:HB2	1:A:49:LEU:H	14	0.97
(2,62)	1:A:1:SER:HB3	1:A:49:LEU:H	14	0.97
(2,144)	1:A:49:LEU:HB2	1:A:63:TYR:HE2	13	0.97
(2,144)	1:A:49:LEU:HB3	1:A:63:TYR:HE2	13	0.97
(1,352)	1:A:63:TYR:HA	1:A:63:TYR:HD2	6	0.97
(2,62)	1:A:1:SER:HB2	1:A:49:LEU:H	20	0.96
(2,62)	1:A:1:SER:HB3	1:A:49:LEU:H	20	0.96
(1,352)	1:A:63:TYR:HA	1:A:63:TYR:HD2	8	0.96

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,352)	1:A:63:TYR:HA	1:A:63:TYR:HD2	20	0.96
(1,347)	1:A:61:LEU:HD21	1:A:66:VAL:HA	10	0.96
(1,347)	1:A:61:LEU:HD22	1:A:66:VAL:HA	10	0.96
(1,347)	1:A:61:LEU:HD23	1:A:66:VAL:HA	10	0.96
(1,339)	1:A:61:LEU:HD11	1:A:66:VAL:HA	11	0.96
(1,339)	1:A:61:LEU:HD12	1:A:66:VAL:HA	11	0.96
(1,339)	1:A:61:LEU:HD13	1:A:66:VAL:HA	11	0.96
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB2	13	0.95
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB3	13	0.95
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB2	15	0.94
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB3	15	0.94
(1,348)	1:A:46:TYR:H	1:A:46:TYR:HD1	1	0.94
(1,309)	1:A:63:TYR:HD1	1:A:64:LYS:HA	18	0.94
(2,63)	1:A:1:SER:HB2	1:A:53:GLN:H	1	0.93
(2,63)	1:A:1:SER:HB3	1:A:53:GLN:H	1	0.93
(2,62)	1:A:1:SER:HB2	1:A:49:LEU:H	19	0.93
(2,62)	1:A:1:SER:HB3	1:A:49:LEU:H	19	0.93
(2,6)	1:A:63:TYR:HE1	1:A:64:LYS:H	8	0.93
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB2	11	0.93
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB3	11	0.93
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE21	19	0.93
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE22	19	0.93
(1,352)	1:A:63:TYR:HA	1:A:63:TYR:HD2	15	0.93
(1,352)	1:A:63:TYR:HA	1:A:63:TYR:HD2	14	0.92
(1,331)	1:A:37:LEU:HD11	1:A:66:VAL:HA	3	0.92
(1,331)	1:A:37:LEU:HD12	1:A:66:VAL:HA	3	0.92
(1,331)	1:A:37:LEU:HD13	1:A:66:VAL:HA	3	0.92
(1,309)	1:A:63:TYR:HD1	1:A:64:LYS:HA	14	0.92
(2,63)	1:A:1:SER:HB2	1:A:53:GLN:H	5	0.91
(2,63)	1:A:1:SER:HB3	1:A:53:GLN:H	5	0.91
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB2	1	0.91
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB3	1	0.91
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE21	10	0.91
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE22	10	0.91
(1,352)	1:A:63:TYR:HA	1:A:63:TYR:HD2	18	0.91
(1,348)	1:A:46:TYR:H	1:A:46:TYR:HD1	2	0.91
(1,347)	1:A:61:LEU:HD21	1:A:66:VAL:HA	18	0.91
(1,347)	1:A:61:LEU:HD22	1:A:66:VAL:HA	18	0.91
(1,347)	1:A:61:LEU:HD23	1:A:66:VAL:HA	18	0.91
(2,63)	1:A:1:SER:HB2	1:A:53:GLN:H	7	0.9
(2,63)	1:A:1:SER:HB3	1:A:53:GLN:H	7	0.9
(2,63)	1:A:1:SER:HB2	1:A:53:GLN:H	10	0.9

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,63)	1:A:1:SER:HB3	1:A:53:GLN:H	10	0.9
(2,63)	1:A:1:SER:HB2	1:A:53:GLN:H	18	0.9
(2,63)	1:A:1:SER:HB3	1:A:53:GLN:H	18	0.9
(2,62)	1:A:1:SER:HB2	1:A:49:LEU:H	4	0.9
(2,62)	1:A:1:SER:HB3	1:A:49:LEU:H	4	0.9
(2,62)	1:A:1:SER:HB2	1:A:49:LEU:H	12	0.9
(2,62)	1:A:1:SER:HB3	1:A:49:LEU:H	12	0.9
(2,62)	1:A:1:SER:HB2	1:A:49:LEU:H	16	0.9
(2,62)	1:A:1:SER:HB3	1:A:49:LEU:H	16	0.9
(2,60)	1:A:41:PHE:HD1	1:A:46:TYR:HE2	10	0.9
(2,162)	1:A:53:GLN:HE21	1:A:63:TYR:HE2	2	0.9
(2,162)	1:A:53:GLN:HE22	1:A:63:TYR:HE2	2	0.9
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE21	4	0.9
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE22	4	0.9
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE21	12	0.9
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE22	12	0.9
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE21	17	0.9
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE22	17	0.9
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE21	18	0.9
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE22	18	0.9
(1,352)	1:A:63:TYR:HA	1:A:63:TYR:HD2	11	0.9
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB2	16	0.89
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB3	16	0.89
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB2	20	0.89
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB3	20	0.89
(1,363)	1:A:4:PRO:HG2	1:A:5:THR:HA	16	0.89
(1,363)	1:A:4:PRO:HG3	1:A:5:THR:HA	16	0.89
(1,352)	1:A:63:TYR:HA	1:A:63:TYR:HD2	13	0.89
(1,352)	1:A:63:TYR:HA	1:A:63:TYR:HD2	19	0.89
(1,309)	1:A:63:TYR:HD1	1:A:64:LYS:HA	10	0.89
(2,63)	1:A:1:SER:HB2	1:A:53:GLN:H	17	0.88
(2,63)	1:A:1:SER:HB3	1:A:53:GLN:H	17	0.88
(2,6)	1:A:63:TYR:HE1	1:A:64:LYS:H	15	0.88
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE21	5	0.88
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE22	5	0.88
(1,363)	1:A:4:PRO:HG2	1:A:5:THR:HA	3	0.88
(1,363)	1:A:4:PRO:HG3	1:A:5:THR:HA	3	0.88
(1,339)	1:A:61:LEU:HD11	1:A:66:VAL:HA	7	0.88
(1,339)	1:A:61:LEU:HD12	1:A:66:VAL:HA	7	0.88
(1,339)	1:A:61:LEU:HD13	1:A:66:VAL:HA	7	0.88
(1,309)	1:A:63:TYR:HD1	1:A:64:LYS:HA	20	0.88
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE21	6	0.87

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE22	6	0.87
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE21	7	0.87
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE22	7	0.87
(1,352)	1:A:63:TYR:HA	1:A:63:TYR:HD2	5	0.87
(1,348)	1:A:46:TYR:H	1:A:46:TYR:HD1	8	0.86
(1,348)	1:A:46:TYR:H	1:A:46:TYR:HD1	10	0.86
(2,62)	1:A:1:SER:HB2	1:A:49:LEU:H	18	0.85
(2,62)	1:A:1:SER:HB3	1:A:49:LEU:H	18	0.85
(2,6)	1:A:63:TYR:HE1	1:A:64:LYS:H	13	0.85
(1,465)	1:A:52:MET:HG2	1:A:63:TYR:HE2	2	0.85
(1,465)	1:A:52:MET:HG3	1:A:63:TYR:HE2	2	0.85
(1,465)	1:A:52:MET:HG2	1:A:63:TYR:HE2	16	0.84
(1,465)	1:A:52:MET:HG3	1:A:63:TYR:HE2	16	0.84
(1,351)	1:A:63:TYR:HD1	1:A:64:LYS:H	1	0.84
(1,348)	1:A:46:TYR:H	1:A:46:TYR:HD1	11	0.84
(1,348)	1:A:46:TYR:H	1:A:46:TYR:HD1	17	0.84
(1,473)	1:A:53:GLN:HE21	1:A:63:TYR:HD2	14	0.83
(1,473)	1:A:53:GLN:HE22	1:A:63:TYR:HD2	14	0.83
(1,352)	1:A:63:TYR:HA	1:A:63:TYR:HD2	10	0.83
(1,347)	1:A:61:LEU:HD21	1:A:66:VAL:HA	5	0.83
(1,347)	1:A:61:LEU:HD22	1:A:66:VAL:HA	5	0.83
(1,347)	1:A:61:LEU:HD23	1:A:66:VAL:HA	5	0.83
(1,196)	1:A:29:PHE:H	1:A:29:PHE:HE2	3	0.83
(1,352)	1:A:63:TYR:HA	1:A:63:TYR:HD2	12	0.82
(1,335)	1:A:47:LEU:HB3	1:A:52:MET:HE1	7	0.82
(1,335)	1:A:47:LEU:HB3	1:A:52:MET:HE2	7	0.82
(1,335)	1:A:47:LEU:HB3	1:A:52:MET:HE3	7	0.82
(1,466)	1:A:52:MET:HG2	1:A:63:TYR:HD2	11	0.81
(1,466)	1:A:52:MET:HG3	1:A:63:TYR:HD2	11	0.81
(1,363)	1:A:4:PRO:HG2	1:A:5:THR:HA	11	0.81
(1,363)	1:A:4:PRO:HG3	1:A:5:THR:HA	11	0.81
(1,352)	1:A:63:TYR:HA	1:A:63:TYR:HD2	3	0.81
(1,352)	1:A:63:TYR:HA	1:A:63:TYR:HD2	7	0.81
(1,351)	1:A:63:TYR:HD1	1:A:64:LYS:H	17	0.81
(1,466)	1:A:52:MET:HG2	1:A:63:TYR:HD2	18	0.8
(1,466)	1:A:52:MET:HG3	1:A:63:TYR:HD2	18	0.8
(1,352)	1:A:63:TYR:HA	1:A:63:TYR:HD2	9	0.8
(1,352)	1:A:63:TYR:HA	1:A:63:TYR:HD2	16	0.8
(2,116)	1:A:40:ARG:HG2	1:A:41:PHE:HE1	15	0.79
(2,116)	1:A:40:ARG:HG3	1:A:41:PHE:HE1	15	0.79
(1,351)	1:A:63:TYR:HD1	1:A:64:LYS:H	7	0.79
(1,351)	1:A:63:TYR:HD1	1:A:64:LYS:H	16	0.79

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,348)	1:A:46:TYR:H	1:A:46:TYR:HD1	16	0.79
(2,6)	1:A:63:TYR:HE1	1:A:64:LYS:H	4	0.78
(1,473)	1:A:53:GLN:HE21	1:A:63:TYR:HD2	11	0.78
(1,473)	1:A:53:GLN:HE22	1:A:63:TYR:HD2	11	0.78
(1,465)	1:A:52:MET:HG2	1:A:63:TYR:HE2	7	0.78
(1,465)	1:A:52:MET:HG3	1:A:63:TYR:HE2	7	0.78
(1,352)	1:A:63:TYR:HA	1:A:63:TYR:HD2	1	0.78
(1,348)	1:A:46:TYR:H	1:A:46:TYR:HD1	12	0.78
(1,335)	1:A:47:LEU:HB3	1:A:52:MET:HE1	9	0.78
(1,335)	1:A:47:LEU:HB3	1:A:52:MET:HE2	9	0.78
(1,335)	1:A:47:LEU:HB3	1:A:52:MET:HE3	9	0.78
(1,352)	1:A:63:TYR:HA	1:A:63:TYR:HD2	2	0.77
(1,351)	1:A:63:TYR:HD1	1:A:64:LYS:H	2	0.77
(1,348)	1:A:46:TYR:H	1:A:46:TYR:HD1	3	0.77
(2,62)	1:A:1:SER:HB2	1:A:49:LEU:H	3	0.76
(2,62)	1:A:1:SER:HB3	1:A:49:LEU:H	3	0.76
(2,6)	1:A:63:TYR:HE1	1:A:64:LYS:H	6	0.76
(1,466)	1:A:52:MET:HG2	1:A:63:TYR:HD2	9	0.76
(1,466)	1:A:52:MET:HG3	1:A:63:TYR:HD2	9	0.76
(1,466)	1:A:52:MET:HG2	1:A:63:TYR:HD2	19	0.76
(1,466)	1:A:52:MET:HG3	1:A:63:TYR:HD2	19	0.76
(1,351)	1:A:63:TYR:HD1	1:A:64:LYS:H	9	0.76
(2,144)	1:A:49:LEU:HB2	1:A:63:TYR:HE2	1	0.75
(2,144)	1:A:49:LEU:HB3	1:A:63:TYR:HE2	1	0.75
(1,351)	1:A:63:TYR:HD1	1:A:64:LYS:H	12	0.75
(1,348)	1:A:46:TYR:H	1:A:46:TYR:HD1	7	0.75
(1,309)	1:A:63:TYR:HD1	1:A:64:LYS:HA	13	0.75
(1,309)	1:A:63:TYR:HD1	1:A:64:LYS:HA	15	0.75
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE21	8	0.74
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE22	8	0.74
(1,465)	1:A:52:MET:HG2	1:A:63:TYR:HE2	10	0.74
(1,465)	1:A:52:MET:HG3	1:A:63:TYR:HE2	10	0.74
(1,351)	1:A:63:TYR:HD1	1:A:64:LYS:H	3	0.73
(1,351)	1:A:63:TYR:HD1	1:A:64:LYS:H	11	0.73
(1,309)	1:A:63:TYR:HD1	1:A:64:LYS:HA	8	0.73
(2,125)	1:A:45:LYS:HD2	1:A:46:TYR:HD1	4	0.72
(2,125)	1:A:45:LYS:HD3	1:A:46:TYR:HD1	4	0.72
(1,473)	1:A:53:GLN:HE21	1:A:63:TYR:HD2	16	0.72
(1,473)	1:A:53:GLN:HE22	1:A:63:TYR:HD2	16	0.72
(1,351)	1:A:63:TYR:HD1	1:A:64:LYS:H	5	0.72
(1,348)	1:A:46:TYR:H	1:A:46:TYR:HD1	20	0.72
(1,347)	1:A:61:LEU:HD21	1:A:66:VAL:HA	15	0.72

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,347)	1:A:61:LEU:HD22	1:A:66:VAL:HA	15	0.72
(1,347)	1:A:61:LEU:HD23	1:A:66:VAL:HA	15	0.72
(2,125)	1:A:45:LYS:HD2	1:A:46:TYR:HD1	6	0.71
(2,125)	1:A:45:LYS:HD3	1:A:46:TYR:HD1	6	0.71
(2,63)	1:A:1:SER:HB2	1:A:53:GLN:H	13	0.69
(2,63)	1:A:1:SER:HB3	1:A:53:GLN:H	13	0.69
(1,363)	1:A:4:PRO:HG2	1:A:5:THR:HA	4	0.69
(1,363)	1:A:4:PRO:HG3	1:A:5:THR:HA	4	0.69
(1,352)	1:A:63:TYR:HA	1:A:63:TYR:HD2	17	0.69
(1,351)	1:A:63:TYR:HD1	1:A:64:LYS:H	19	0.69
(1,348)	1:A:46:TYR:H	1:A:46:TYR:HD1	19	0.69
(1,347)	1:A:61:LEU:HD21	1:A:66:VAL:HA	19	0.69
(1,347)	1:A:61:LEU:HD22	1:A:66:VAL:HA	19	0.69
(1,347)	1:A:61:LEU:HD23	1:A:66:VAL:HA	19	0.69
(2,62)	1:A:1:SER:HB2	1:A:49:LEU:H	5	0.68
(2,62)	1:A:1:SER:HB3	1:A:49:LEU:H	5	0.68
(2,62)	1:A:1:SER:HB2	1:A:49:LEU:H	10	0.68
(2,62)	1:A:1:SER:HB3	1:A:49:LEU:H	10	0.68
(1,351)	1:A:63:TYR:HD1	1:A:64:LYS:H	10	0.68
(1,465)	1:A:52:MET:HG2	1:A:63:TYR:HE2	1	0.67
(1,465)	1:A:52:MET:HG3	1:A:63:TYR:HE2	1	0.67
(1,351)	1:A:63:TYR:HD1	1:A:64:LYS:H	18	0.67
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE1	18	0.67
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE2	18	0.67
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE3	18	0.67
(1,348)	1:A:46:TYR:H	1:A:46:TYR:HD1	5	0.66
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB2	3	0.65
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB3	3	0.65
(2,125)	1:A:45:LYS:HD2	1:A:46:TYR:HD1	9	0.65
(2,125)	1:A:45:LYS:HD3	1:A:46:TYR:HD1	9	0.65
(1,473)	1:A:53:GLN:HE21	1:A:63:TYR:HD2	5	0.65
(1,473)	1:A:53:GLN:HE22	1:A:63:TYR:HD2	5	0.65
(1,473)	1:A:53:GLN:HE21	1:A:63:TYR:HD2	19	0.65
(1,473)	1:A:53:GLN:HE22	1:A:63:TYR:HD2	19	0.65
(2,80)	1:A:29:PHE:HD1	1:A:33:GLN:HG2	18	0.64
(2,80)	1:A:29:PHE:HD1	1:A:33:GLN:HG3	18	0.64
(2,125)	1:A:45:LYS:HD2	1:A:46:TYR:HD1	5	0.64
(2,125)	1:A:45:LYS:HD3	1:A:46:TYR:HD1	5	0.64
(1,466)	1:A:52:MET:HG2	1:A:63:TYR:HD2	6	0.64
(1,466)	1:A:52:MET:HG3	1:A:63:TYR:HD2	6	0.64
(1,351)	1:A:63:TYR:HD1	1:A:64:LYS:H	14	0.64
(1,347)	1:A:61:LEU:HD21	1:A:66:VAL:HA	2	0.64

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,347)	1:A:61:LEU:HD22	1:A:66:VAL:HA	2	0.64
(1,347)	1:A:61:LEU:HD23	1:A:66:VAL:HA	2	0.64
(1,363)	1:A:4:PRO:HG2	1:A:5:THR:HA	20	0.63
(1,363)	1:A:4:PRO:HG3	1:A:5:THR:HA	20	0.63
(1,351)	1:A:63:TYR:HD1	1:A:64:LYS:H	20	0.63
(2,60)	1:A:41:PHE:HD1	1:A:46:TYR:HE2	8	0.62
(2,162)	1:A:53:GLN:HE21	1:A:63:TYR:HE2	9	0.62
(2,162)	1:A:53:GLN:HE22	1:A:63:TYR:HE2	9	0.62
(1,466)	1:A:52:MET:HG2	1:A:63:TYR:HD2	5	0.62
(1,466)	1:A:52:MET:HG3	1:A:63:TYR:HD2	5	0.62
(1,340)	1:A:72:ASN:HA	1:A:75:MET:HE1	14	0.62
(1,340)	1:A:72:ASN:HA	1:A:75:MET:HE2	14	0.62
(1,340)	1:A:72:ASN:HA	1:A:75:MET:HE3	14	0.62
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB2	7	0.61
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB3	7	0.61
(2,144)	1:A:49:LEU:HB2	1:A:63:TYR:HE2	15	0.61
(2,144)	1:A:49:LEU:HB3	1:A:63:TYR:HE2	15	0.61
(2,125)	1:A:45:LYS:HD2	1:A:46:TYR:HD1	19	0.61
(2,125)	1:A:45:LYS:HD3	1:A:46:TYR:HD1	19	0.61
(1,466)	1:A:52:MET:HG2	1:A:63:TYR:HD2	20	0.6
(1,466)	1:A:52:MET:HG3	1:A:63:TYR:HD2	20	0.6
(2,80)	1:A:29:PHE:HD1	1:A:33:GLN:HG2	6	0.59
(2,80)	1:A:29:PHE:HD1	1:A:33:GLN:HG3	6	0.59
(2,62)	1:A:1:SER:HB2	1:A:49:LEU:H	9	0.59
(2,62)	1:A:1:SER:HB3	1:A:49:LEU:H	9	0.59
(1,465)	1:A:52:MET:HG2	1:A:63:TYR:HE2	3	0.59
(1,465)	1:A:52:MET:HG3	1:A:63:TYR:HE2	3	0.59
(1,351)	1:A:63:TYR:HD1	1:A:64:LYS:H	15	0.59
(1,348)	1:A:46:TYR:H	1:A:46:TYR:HD1	9	0.59
(2,144)	1:A:49:LEU:HB2	1:A:63:TYR:HE2	7	0.58
(2,144)	1:A:49:LEU:HB3	1:A:63:TYR:HE2	7	0.58
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE21	2	0.58
(1,522)	1:A:70:PHE:HZ	1:A:71:GLN:HE22	2	0.58
(1,363)	1:A:4:PRO:HG2	1:A:5:THR:HA	15	0.58
(1,363)	1:A:4:PRO:HG3	1:A:5:THR:HA	15	0.58
(2,84)	1:A:29:PHE:HE1	1:A:37:LEU:HD11	3	0.57
(2,84)	1:A:29:PHE:HE1	1:A:37:LEU:HD12	3	0.57
(2,84)	1:A:29:PHE:HE1	1:A:37:LEU:HD13	3	0.57
(2,84)	1:A:29:PHE:HE1	1:A:37:LEU:HD21	3	0.57
(2,84)	1:A:29:PHE:HE1	1:A:37:LEU:HD22	3	0.57
(2,84)	1:A:29:PHE:HE1	1:A:37:LEU:HD23	3	0.57
(2,42)	1:A:72:ASN:HB2	1:A:75:MET:HE1	14	0.57

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,42)	1:A:72:ASN:HB2	1:A:75:MET:HE2	14	0.57
(2,42)	1:A:72:ASN:HB2	1:A:75:MET:HE3	14	0.57
(1,466)	1:A:52:MET:HG2	1:A:63:TYR:HD2	4	0.57
(1,466)	1:A:52:MET:HG3	1:A:63:TYR:HD2	4	0.57
(1,351)	1:A:63:TYR:HD1	1:A:64:LYS:H	8	0.57
(1,351)	1:A:63:TYR:HD1	1:A:64:LYS:H	13	0.57
(1,465)	1:A:52:MET:HG2	1:A:63:TYR:HE2	17	0.56
(1,465)	1:A:52:MET:HG3	1:A:63:TYR:HE2	17	0.56
(1,363)	1:A:4:PRO:HG2	1:A:5:THR:HA	1	0.56
(1,363)	1:A:4:PRO:HG3	1:A:5:THR:HA	1	0.56
(1,347)	1:A:61:LEU:HD21	1:A:66:VAL:HA	1	0.56
(1,347)	1:A:61:LEU:HD22	1:A:66:VAL:HA	1	0.56
(1,347)	1:A:61:LEU:HD23	1:A:66:VAL:HA	1	0.56
(1,347)	1:A:61:LEU:HD21	1:A:66:VAL:HA	16	0.56
(1,347)	1:A:61:LEU:HD22	1:A:66:VAL:HA	16	0.56
(1,347)	1:A:61:LEU:HD23	1:A:66:VAL:HA	16	0.56
(2,62)	1:A:1:SER:HB2	1:A:49:LEU:H	8	0.55
(2,62)	1:A:1:SER:HB3	1:A:49:LEU:H	8	0.55
(1,348)	1:A:46:TYR:H	1:A:46:TYR:HD1	6	0.55
(1,348)	1:A:46:TYR:H	1:A:46:TYR:HD1	18	0.54
(1,331)	1:A:37:LEU:HD11	1:A:66:VAL:HA	17	0.53
(1,331)	1:A:37:LEU:HD12	1:A:66:VAL:HA	17	0.53
(1,331)	1:A:37:LEU:HD13	1:A:66:VAL:HA	17	0.53
(1,348)	1:A:46:TYR:H	1:A:46:TYR:HD1	14	0.52
(2,62)	1:A:1:SER:HB2	1:A:49:LEU:H	2	0.51
(2,62)	1:A:1:SER:HB3	1:A:49:LEU:H	2	0.51
(1,466)	1:A:52:MET:HG2	1:A:63:TYR:HD2	13	0.51
(1,466)	1:A:52:MET:HG3	1:A:63:TYR:HD2	13	0.51
(1,331)	1:A:37:LEU:HD11	1:A:66:VAL:HA	7	0.51
(1,331)	1:A:37:LEU:HD12	1:A:66:VAL:HA	7	0.51
(1,331)	1:A:37:LEU:HD13	1:A:66:VAL:HA	7	0.51
(1,196)	1:A:29:PHE:H	1:A:29:PHE:HE2	18	0.51
(1,309)	1:A:63:TYR:HD1	1:A:64:LYS:HA	6	0.5
(2,62)	1:A:1:SER:HB2	1:A:49:LEU:H	15	0.49
(2,62)	1:A:1:SER:HB3	1:A:49:LEU:H	15	0.49
(1,466)	1:A:52:MET:HG2	1:A:63:TYR:HD2	12	0.49
(1,466)	1:A:52:MET:HG3	1:A:63:TYR:HD2	12	0.49
(1,351)	1:A:63:TYR:HD1	1:A:64:LYS:H	4	0.49
(1,309)	1:A:63:TYR:HD1	1:A:64:LYS:HA	4	0.49
(1,428)	1:A:45:LYS:HB2	1:A:46:TYR:HD1	8	0.48
(1,428)	1:A:45:LYS:HB3	1:A:46:TYR:HD1	8	0.48
(1,351)	1:A:63:TYR:HD1	1:A:64:LYS:H	6	0.48

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,331)	1:A:37:LEU:HD11	1:A:66:VAL:HA	14	0.48
(1,331)	1:A:37:LEU:HD12	1:A:66:VAL:HA	14	0.48
(1,331)	1:A:37:LEU:HD13	1:A:66:VAL:HA	14	0.48
(1,237)	1:A:47:LEU:H	1:A:52:MET:HE1	7	0.48
(1,237)	1:A:47:LEU:H	1:A:52:MET:HE2	7	0.48
(1,237)	1:A:47:LEU:H	1:A:52:MET:HE3	7	0.48
(1,196)	1:A:29:PHE:H	1:A:29:PHE:HE2	4	0.48
(1,331)	1:A:37:LEU:HD11	1:A:66:VAL:HA	4	0.47
(1,331)	1:A:37:LEU:HD12	1:A:66:VAL:HA	4	0.47
(1,331)	1:A:37:LEU:HD13	1:A:66:VAL:HA	4	0.47
(1,466)	1:A:52:MET:HG2	1:A:63:TYR:HD2	16	0.46
(1,466)	1:A:52:MET:HG3	1:A:63:TYR:HD2	16	0.46
(1,347)	1:A:61:LEU:HD21	1:A:66:VAL:HA	20	0.46
(1,347)	1:A:61:LEU:HD22	1:A:66:VAL:HA	20	0.46
(1,347)	1:A:61:LEU:HD23	1:A:66:VAL:HA	20	0.46
(1,340)	1:A:72:ASN:HA	1:A:75:MET:HE1	8	0.46
(1,340)	1:A:72:ASN:HA	1:A:75:MET:HE2	8	0.46
(1,340)	1:A:72:ASN:HA	1:A:75:MET:HE3	8	0.46
(2,80)	1:A:29:PHE:HD1	1:A:33:GLN:HG2	8	0.45
(2,80)	1:A:29:PHE:HD1	1:A:33:GLN:HG3	8	0.45
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB2	8	0.45
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB3	8	0.45
(1,347)	1:A:61:LEU:HD21	1:A:66:VAL:HA	17	0.45
(1,347)	1:A:61:LEU:HD22	1:A:66:VAL:HA	17	0.45
(1,347)	1:A:61:LEU:HD23	1:A:66:VAL:HA	17	0.45
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE1	1	0.45
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE2	1	0.45
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE3	1	0.45
(2,125)	1:A:45:LYS:HD2	1:A:46:TYR:HD1	8	0.44
(2,125)	1:A:45:LYS:HD3	1:A:46:TYR:HD1	8	0.44
(1,466)	1:A:52:MET:HG2	1:A:63:TYR:HD2	14	0.44
(1,466)	1:A:52:MET:HG3	1:A:63:TYR:HD2	14	0.44
(1,348)	1:A:46:TYR:H	1:A:46:TYR:HD1	4	0.44
(1,347)	1:A:61:LEU:HD21	1:A:66:VAL:HA	3	0.44
(1,347)	1:A:61:LEU:HD22	1:A:66:VAL:HA	3	0.44
(1,347)	1:A:61:LEU:HD23	1:A:66:VAL:HA	3	0.44
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE1	8	0.44
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE2	8	0.44
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE3	8	0.44
(1,237)	1:A:47:LEU:H	1:A:52:MET:HE1	1	0.44
(1,237)	1:A:47:LEU:H	1:A:52:MET:HE2	1	0.44
(1,237)	1:A:47:LEU:H	1:A:52:MET:HE3	1	0.44

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,80)	1:A:29:PHE:HD1	1:A:33:GLN:HG2	19	0.43
(2,80)	1:A:29:PHE:HD1	1:A:33:GLN:HG3	19	0.43
(1,348)	1:A:46:TYR:H	1:A:46:TYR:HD1	15	0.43
(1,331)	1:A:37:LEU:HD11	1:A:66:VAL:HA	1	0.43
(1,331)	1:A:37:LEU:HD12	1:A:66:VAL:HA	1	0.43
(1,331)	1:A:37:LEU:HD13	1:A:66:VAL:HA	1	0.43
(1,466)	1:A:52:MET:HG2	1:A:63:TYR:HD2	15	0.42
(1,466)	1:A:52:MET:HG3	1:A:63:TYR:HD2	15	0.42
(1,451)	1:A:51:GLN:H	1:A:51:GLN:HG2	6	0.42
(1,451)	1:A:51:GLN:H	1:A:51:GLN:HG3	6	0.42
(1,347)	1:A:61:LEU:HD21	1:A:66:VAL:HA	12	0.42
(1,347)	1:A:61:LEU:HD22	1:A:66:VAL:HA	12	0.42
(1,347)	1:A:61:LEU:HD23	1:A:66:VAL:HA	12	0.42
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE1	13	0.42
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE2	13	0.42
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE3	13	0.42
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE1	6	0.41
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE2	6	0.41
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE3	6	0.41
(2,125)	1:A:45:LYS:HD2	1:A:46:TYR:HD1	7	0.4
(2,125)	1:A:45:LYS:HD3	1:A:46:TYR:HD1	7	0.4
(1,363)	1:A:4:PRO:HG2	1:A:5:THR:HA	14	0.4
(1,363)	1:A:4:PRO:HG3	1:A:5:THR:HA	14	0.4
(1,331)	1:A:37:LEU:HD11	1:A:66:VAL:HA	11	0.4
(1,331)	1:A:37:LEU:HD12	1:A:66:VAL:HA	11	0.4
(1,331)	1:A:37:LEU:HD13	1:A:66:VAL:HA	11	0.4
(1,331)	1:A:37:LEU:HD11	1:A:66:VAL:HA	13	0.4
(1,331)	1:A:37:LEU:HD12	1:A:66:VAL:HA	13	0.4
(1,331)	1:A:37:LEU:HD13	1:A:66:VAL:HA	13	0.4
(3,21)	1:A:53:GLN:O	1:A:57:ASN:H	19	0.39
(2,45)	1:A:72:ASN:HB3	1:A:75:MET:HE1	8	0.39
(2,45)	1:A:72:ASN:HB3	1:A:75:MET:HE2	8	0.39
(2,45)	1:A:72:ASN:HB3	1:A:75:MET:HE3	8	0.39
(1,347)	1:A:61:LEU:HD21	1:A:66:VAL:HA	13	0.39
(1,347)	1:A:61:LEU:HD22	1:A:66:VAL:HA	13	0.39
(1,347)	1:A:61:LEU:HD23	1:A:66:VAL:HA	13	0.39
(1,196)	1:A:29:PHE:H	1:A:29:PHE:HE2	6	0.39
(1,196)	1:A:29:PHE:H	1:A:29:PHE:HE2	8	0.39
(3,1)	1:A:32:THR:O	1:A:36:VAL:H	15	0.38
(3,1)	1:A:32:THR:O	1:A:36:VAL:H	18	0.38
(2,125)	1:A:45:LYS:HD2	1:A:46:TYR:HD1	15	0.38
(2,125)	1:A:45:LYS:HD3	1:A:46:TYR:HD1	15	0.38

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,466)	1:A:52:MET:HG2	1:A:63:TYR:HD2	7	0.38
(1,466)	1:A:52:MET:HG3	1:A:63:TYR:HD2	7	0.38
(3,9)	1:A:36:VAL:O	1:A:40:ARG:H	11	0.37
(3,21)	1:A:53:GLN:O	1:A:57:ASN:H	5	0.37
(3,21)	1:A:53:GLN:O	1:A:57:ASN:H	17	0.37
(3,11)	1:A:37:LEU:O	1:A:41:PHE:H	7	0.37
(2,80)	1:A:29:PHE:HD1	1:A:33:GLN:HG2	13	0.37
(2,80)	1:A:29:PHE:HD1	1:A:33:GLN:HG3	13	0.37
(2,125)	1:A:45:LYS:HD2	1:A:46:TYR:HD1	18	0.37
(2,125)	1:A:45:LYS:HD3	1:A:46:TYR:HD1	18	0.37
(1,466)	1:A:52:MET:HG2	1:A:63:TYR:HD2	8	0.37
(1,466)	1:A:52:MET:HG3	1:A:63:TYR:HD2	8	0.37
(1,196)	1:A:29:PHE:H	1:A:29:PHE:HE2	13	0.37
(3,41)	1:A:72:ASN:O	1:A:76:LYS:H	16	0.36
(3,29)	1:A:66:VAL:O	1:A:70:PHE:H	11	0.36
(3,21)	1:A:53:GLN:O	1:A:57:ASN:H	18	0.36
(3,11)	1:A:37:LEU:O	1:A:41:PHE:H	2	0.36
(3,11)	1:A:37:LEU:O	1:A:41:PHE:H	14	0.36
(2,82)	1:A:29:PHE:HD1	1:A:37:LEU:HD11	3	0.36
(2,82)	1:A:29:PHE:HD1	1:A:37:LEU:HD12	3	0.36
(2,82)	1:A:29:PHE:HD1	1:A:37:LEU:HD13	3	0.36
(2,82)	1:A:29:PHE:HD1	1:A:37:LEU:HD21	3	0.36
(2,82)	1:A:29:PHE:HD1	1:A:37:LEU:HD22	3	0.36
(2,82)	1:A:29:PHE:HD1	1:A:37:LEU:HD23	3	0.36
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB2	12	0.36
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB3	12	0.36
(2,167)	1:A:55:LEU:HG	1:A:56:SER:HB2	13	0.36
(2,167)	1:A:55:LEU:HG	1:A:56:SER:HB3	13	0.36
(2,125)	1:A:45:LYS:HD2	1:A:46:TYR:HD1	12	0.36
(2,125)	1:A:45:LYS:HD3	1:A:46:TYR:HD1	12	0.36
(1,473)	1:A:53:GLN:HE21	1:A:63:TYR:HD2	17	0.36
(1,473)	1:A:53:GLN:HE22	1:A:63:TYR:HD2	17	0.36
(1,277)	1:A:11:VAL:HB	1:A:12:ALA:HA	20	0.36
(3,9)	1:A:36:VAL:O	1:A:40:ARG:H	2	0.35
(3,21)	1:A:53:GLN:O	1:A:57:ASN:H	7	0.35
(3,21)	1:A:53:GLN:O	1:A:57:ASN:H	13	0.35
(3,10)	1:A:36:VAL:O	1:A:40:ARG:N	11	0.35
(1,363)	1:A:4:PRO:HG2	1:A:5:THR:HA	19	0.35
(1,363)	1:A:4:PRO:HG3	1:A:5:THR:HA	19	0.35
(1,350)	1:A:46:TYR:HA	1:A:46:TYR:HD2	13	0.35
(3,31)	1:A:67:LYS:O	1:A:71:GLN:H	15	0.34
(3,21)	1:A:53:GLN:O	1:A:57:ASN:H	3	0.34

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,21)	1:A:53:GLN:O	1:A:57:ASN:H	9	0.34
(3,11)	1:A:37:LEU:O	1:A:41:PHE:H	19	0.34
(3,1)	1:A:32:THR:O	1:A:36:VAL:H	3	0.34
(3,1)	1:A:32:THR:O	1:A:36:VAL:H	19	0.34
(1,473)	1:A:53:GLN:HE21	1:A:63:TYR:HD2	7	0.34
(1,473)	1:A:53:GLN:HE22	1:A:63:TYR:HD2	7	0.34
(1,196)	1:A:29:PHE:H	1:A:29:PHE:HE2	19	0.34
(3,37)	1:A:70:PHE:O	1:A:74:ARG:H	20	0.33
(3,31)	1:A:67:LYS:O	1:A:71:GLN:H	14	0.33
(3,22)	1:A:53:GLN:O	1:A:57:ASN:N	19	0.33
(3,21)	1:A:53:GLN:O	1:A:57:ASN:H	4	0.33
(3,21)	1:A:53:GLN:O	1:A:57:ASN:H	10	0.33
(3,21)	1:A:53:GLN:O	1:A:57:ASN:H	16	0.33
(3,11)	1:A:37:LEU:O	1:A:41:PHE:H	8	0.33
(3,1)	1:A:32:THR:O	1:A:36:VAL:H	9	0.33
(2,125)	1:A:45:LYS:HD2	1:A:46:TYR:HD1	14	0.33
(2,125)	1:A:45:LYS:HD3	1:A:46:TYR:HD1	14	0.33
(1,466)	1:A:52:MET:HG2	1:A:63:TYR:HD2	2	0.33
(1,466)	1:A:52:MET:HG3	1:A:63:TYR:HD2	2	0.33
(3,9)	1:A:36:VAL:O	1:A:40:ARG:H	9	0.32
(3,41)	1:A:72:ASN:O	1:A:76:LYS:H	9	0.32
(3,41)	1:A:72:ASN:O	1:A:76:LYS:H	11	0.32
(3,41)	1:A:72:ASN:O	1:A:76:LYS:H	13	0.32
(3,35)	1:A:69:TRP:O	1:A:73:GLN:H	14	0.32
(3,29)	1:A:66:VAL:O	1:A:70:PHE:H	14	0.32
(3,29)	1:A:66:VAL:O	1:A:70:PHE:H	19	0.32
(3,27)	1:A:65:GLN:O	1:A:69:TRP:H	6	0.32
(3,25)	1:A:64:LYS:O	1:A:68:THR:H	1	0.32
(3,25)	1:A:64:LYS:O	1:A:68:THR:H	12	0.32
(3,21)	1:A:53:GLN:O	1:A:57:ASN:H	6	0.32
(3,21)	1:A:53:GLN:O	1:A:57:ASN:H	8	0.32
(3,21)	1:A:53:GLN:O	1:A:57:ASN:H	20	0.32
(3,2)	1:A:32:THR:O	1:A:36:VAL:N	15	0.32
(3,19)	1:A:52:MET:O	1:A:56:SER:H	13	0.32
(3,19)	1:A:52:MET:O	1:A:56:SER:H	18	0.32
(3,1)	1:A:32:THR:O	1:A:36:VAL:H	7	0.32
(3,1)	1:A:32:THR:O	1:A:36:VAL:H	13	0.32
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE1	12	0.32
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE2	12	0.32
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE3	12	0.32
(3,41)	1:A:72:ASN:O	1:A:76:LYS:H	1	0.31
(3,29)	1:A:66:VAL:O	1:A:70:PHE:H	18	0.31

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,27)	1:A:65:GLN:O	1:A:69:TRP:H	10	0.31
(3,25)	1:A:64:LYS:O	1:A:68:THR:H	15	0.31
(3,21)	1:A:53:GLN:O	1:A:57:ASN:H	12	0.31
(3,2)	1:A:32:THR:O	1:A:36:VAL:N	18	0.31
(3,19)	1:A:52:MET:O	1:A:56:SER:H	16	0.31
(3,15)	1:A:50:GLN:O	1:A:54:GLU:H	16	0.31
(3,15)	1:A:50:GLN:O	1:A:54:GLU:H	19	0.31
(3,12)	1:A:37:LEU:O	1:A:41:PHE:N	14	0.31
(3,1)	1:A:32:THR:O	1:A:36:VAL:H	10	0.31
(2,63)	1:A:1:SER:HB2	1:A:53:GLN:H	8	0.31
(2,63)	1:A:1:SER:HB3	1:A:53:GLN:H	8	0.31
(1,350)	1:A:46:TYR:HA	1:A:46:TYR:HD2	15	0.31
(3,5)	1:A:34:LEU:O	1:A:38:ASN:H	17	0.3
(3,41)	1:A:72:ASN:O	1:A:76:LYS:H	14	0.3
(3,41)	1:A:72:ASN:O	1:A:76:LYS:H	15	0.3
(3,39)	1:A:71:GLN:O	1:A:75:MET:H	5	0.3
(3,31)	1:A:67:LYS:O	1:A:71:GLN:H	4	0.3
(3,31)	1:A:67:LYS:O	1:A:71:GLN:H	7	0.3
(3,30)	1:A:66:VAL:O	1:A:70:PHE:N	19	0.3
(3,22)	1:A:53:GLN:O	1:A:57:ASN:N	9	0.3
(3,22)	1:A:53:GLN:O	1:A:57:ASN:N	13	0.3
(3,12)	1:A:37:LEU:O	1:A:41:PHE:N	7	0.3
(3,11)	1:A:37:LEU:O	1:A:41:PHE:H	9	0.3
(1,428)	1:A:45:LYS:HB2	1:A:46:TYR:HD1	17	0.3
(1,428)	1:A:45:LYS:HB3	1:A:46:TYR:HD1	17	0.3
(1,348)	1:A:46:TYR:H	1:A:46:TYR:HD1	13	0.3
(3,30)	1:A:66:VAL:O	1:A:70:PHE:N	11	0.29
(3,30)	1:A:66:VAL:O	1:A:70:PHE:N	14	0.29
(3,29)	1:A:66:VAL:O	1:A:70:PHE:H	1	0.29
(3,25)	1:A:64:LYS:O	1:A:68:THR:H	20	0.29
(3,22)	1:A:53:GLN:O	1:A:57:ASN:N	7	0.29
(3,15)	1:A:50:GLN:O	1:A:54:GLU:H	18	0.29
(3,12)	1:A:37:LEU:O	1:A:41:PHE:N	2	0.29
(3,12)	1:A:37:LEU:O	1:A:41:PHE:N	19	0.29
(2,150)	1:A:49:LEU:HD11	1:A:63:TYR:HD2	8	0.29
(2,150)	1:A:49:LEU:HD12	1:A:63:TYR:HD2	8	0.29
(2,150)	1:A:49:LEU:HD13	1:A:63:TYR:HD2	8	0.29
(2,150)	1:A:49:LEU:HD21	1:A:63:TYR:HD2	8	0.29
(2,150)	1:A:49:LEU:HD22	1:A:63:TYR:HD2	8	0.29
(2,150)	1:A:49:LEU:HD23	1:A:63:TYR:HD2	8	0.29
(1,350)	1:A:46:TYR:HA	1:A:46:TYR:HD2	4	0.29
(3,41)	1:A:72:ASN:O	1:A:76:LYS:H	19	0.28

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,30)	1:A:66:VAL:O	1:A:70:PHE:N	18	0.28
(3,3)	1:A:33:GLN:O	1:A:37:LEU:H	7	0.28
(3,21)	1:A:53:GLN:O	1:A:57:ASN:H	14	0.28
(3,13)	1:A:38:ASN:O	1:A:42:GLN:H	17	0.28
(3,1)	1:A:32:THR:O	1:A:36:VAL:H	1	0.28
(1,350)	1:A:46:TYR:HA	1:A:46:TYR:HD2	18	0.28
(1,347)	1:A:61:LEU:HD21	1:A:66:VAL:HA	9	0.28
(1,347)	1:A:61:LEU:HD22	1:A:66:VAL:HA	9	0.28
(1,347)	1:A:61:LEU:HD23	1:A:66:VAL:HA	9	0.28
(3,9)	1:A:36:VAL:O	1:A:40:ARG:H	16	0.27
(3,33)	1:A:68:THR:O	1:A:72:ASN:H	5	0.27
(3,3)	1:A:33:GLN:O	1:A:37:LEU:H	4	0.27
(3,27)	1:A:65:GLN:O	1:A:69:TRP:H	19	0.27
(3,22)	1:A:53:GLN:O	1:A:57:ASN:N	5	0.27
(3,22)	1:A:53:GLN:O	1:A:57:ASN:N	20	0.27
(3,2)	1:A:32:THR:O	1:A:36:VAL:N	10	0.27
(3,2)	1:A:32:THR:O	1:A:36:VAL:N	13	0.27
(3,19)	1:A:52:MET:O	1:A:56:SER:H	4	0.27
(3,11)	1:A:37:LEU:O	1:A:41:PHE:H	20	0.27
(3,10)	1:A:36:VAL:O	1:A:40:ARG:N	9	0.27
(1,186)	1:A:72:ASN:H	1:A:75:MET:H	7	0.27
(3,37)	1:A:70:PHE:O	1:A:74:ARG:H	11	0.26
(3,32)	1:A:67:LYS:O	1:A:71:GLN:N	15	0.26
(3,22)	1:A:53:GLN:O	1:A:57:ASN:N	6	0.26
(3,2)	1:A:32:THR:O	1:A:36:VAL:N	3	0.26
(3,15)	1:A:50:GLN:O	1:A:54:GLU:H	4	0.26
(3,15)	1:A:50:GLN:O	1:A:54:GLU:H	7	0.26
(3,13)	1:A:38:ASN:O	1:A:42:GLN:H	3	0.26
(3,13)	1:A:38:ASN:O	1:A:42:GLN:H	15	0.26
(3,13)	1:A:38:ASN:O	1:A:42:GLN:H	18	0.26
(3,10)	1:A:36:VAL:O	1:A:40:ARG:N	2	0.26
(2,144)	1:A:49:LEU:HB2	1:A:63:TYR:HE2	14	0.26
(2,144)	1:A:49:LEU:HB3	1:A:63:TYR:HE2	14	0.26
(1,350)	1:A:46:TYR:HA	1:A:46:TYR:HD2	6	0.26
(1,350)	1:A:46:TYR:HA	1:A:46:TYR:HD2	14	0.26
(3,9)	1:A:36:VAL:O	1:A:40:ARG:H	17	0.25
(3,38)	1:A:70:PHE:O	1:A:74:ARG:N	20	0.25
(3,36)	1:A:69:TRP:O	1:A:73:GLN:N	14	0.25
(3,35)	1:A:69:TRP:O	1:A:73:GLN:H	20	0.25
(3,28)	1:A:65:GLN:O	1:A:69:TRP:N	6	0.25
(3,27)	1:A:65:GLN:O	1:A:69:TRP:H	5	0.25
(3,20)	1:A:52:MET:O	1:A:56:SER:N	16	0.25

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,2)	1:A:32:THR:O	1:A:36:VAL:N	19	0.25
(3,15)	1:A:50:GLN:O	1:A:54:GLU:H	9	0.25
(3,15)	1:A:50:GLN:O	1:A:54:GLU:H	10	0.25
(3,13)	1:A:38:ASN:O	1:A:42:GLN:H	5	0.25
(3,13)	1:A:38:ASN:O	1:A:42:GLN:H	11	0.25
(3,12)	1:A:37:LEU:O	1:A:41:PHE:N	8	0.25
(1,350)	1:A:46:TYR:HA	1:A:46:TYR:HD2	9	0.25
(1,347)	1:A:61:LEU:HD21	1:A:66:VAL:HA	8	0.25
(1,347)	1:A:61:LEU:HD22	1:A:66:VAL:HA	8	0.25
(1,347)	1:A:61:LEU:HD23	1:A:66:VAL:HA	8	0.25
(3,42)	1:A:72:ASN:O	1:A:76:LYS:N	14	0.24
(3,37)	1:A:70:PHE:O	1:A:74:ARG:H	14	0.24
(3,33)	1:A:68:THR:O	1:A:72:ASN:H	10	0.24
(3,30)	1:A:66:VAL:O	1:A:70:PHE:N	1	0.24
(3,28)	1:A:65:GLN:O	1:A:69:TRP:N	10	0.24
(3,27)	1:A:65:GLN:O	1:A:69:TRP:H	4	0.24
(3,22)	1:A:53:GLN:O	1:A:57:ASN:N	17	0.24
(3,21)	1:A:53:GLN:O	1:A:57:ASN:H	2	0.24
(3,19)	1:A:52:MET:O	1:A:56:SER:H	11	0.24
(3,13)	1:A:38:ASN:O	1:A:42:GLN:H	12	0.24
(2,63)	1:A:1:SER:HB2	1:A:53:GLN:H	11	0.24
(2,63)	1:A:1:SER:HB3	1:A:53:GLN:H	11	0.24
(1,363)	1:A:4:PRO:HG2	1:A:5:THR:HA	8	0.24
(1,363)	1:A:4:PRO:HG3	1:A:5:THR:HA	8	0.24
(1,355)	1:A:41:PHE:HA	1:A:41:PHE:HE1	13	0.24
(1,278)	1:A:11:VAL:HA	1:A:12:ALA:HA	20	0.24
(1,196)	1:A:29:PHE:H	1:A:29:PHE:HE2	16	0.24
(1,186)	1:A:72:ASN:H	1:A:75:MET:H	19	0.24
(3,41)	1:A:72:ASN:O	1:A:76:LYS:H	10	0.23
(3,37)	1:A:70:PHE:O	1:A:74:ARG:H	5	0.23
(3,32)	1:A:67:LYS:O	1:A:71:GLN:N	14	0.23
(3,22)	1:A:53:GLN:O	1:A:57:ASN:N	18	0.23
(3,13)	1:A:38:ASN:O	1:A:42:GLN:H	1	0.23
(3,11)	1:A:37:LEU:O	1:A:41:PHE:H	6	0.23
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB2	18	0.23
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB3	18	0.23
(1,186)	1:A:72:ASN:H	1:A:75:MET:H	18	0.23
(3,42)	1:A:72:ASN:O	1:A:76:LYS:N	16	0.22
(3,38)	1:A:70:PHE:O	1:A:74:ARG:N	14	0.22
(3,26)	1:A:64:LYS:O	1:A:68:THR:N	12	0.22
(3,20)	1:A:52:MET:O	1:A:56:SER:N	4	0.22
(3,20)	1:A:52:MET:O	1:A:56:SER:N	13	0.22

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,19)	1:A:52:MET:O	1:A:56:SER:H	19	0.22
(3,12)	1:A:37:LEU:O	1:A:41:PHE:N	20	0.22
(1,404)	1:A:39:ASP:HA	1:A:42:GLN:HG2	17	0.22
(1,404)	1:A:39:ASP:HA	1:A:42:GLN:HG3	17	0.22
(1,331)	1:A:37:LEU:HD11	1:A:66:VAL:HA	20	0.22
(1,331)	1:A:37:LEU:HD12	1:A:66:VAL:HA	20	0.22
(1,331)	1:A:37:LEU:HD13	1:A:66:VAL:HA	20	0.22
(1,186)	1:A:72:ASN:H	1:A:75:MET:H	5	0.22
(3,37)	1:A:70:PHE:O	1:A:74:ARG:H	8	0.21
(3,33)	1:A:68:THR:O	1:A:72:ASN:H	20	0.21
(3,31)	1:A:67:LYS:O	1:A:71:GLN:H	13	0.21
(3,29)	1:A:66:VAL:O	1:A:70:PHE:H	7	0.21
(3,26)	1:A:64:LYS:O	1:A:68:THR:N	1	0.21
(3,26)	1:A:64:LYS:O	1:A:68:THR:N	15	0.21
(3,25)	1:A:64:LYS:O	1:A:68:THR:H	18	0.21
(3,20)	1:A:52:MET:O	1:A:56:SER:N	18	0.21
(3,2)	1:A:32:THR:O	1:A:36:VAL:N	1	0.21
(3,2)	1:A:32:THR:O	1:A:36:VAL:N	9	0.21
(3,12)	1:A:37:LEU:O	1:A:41:PHE:N	9	0.21
(2,144)	1:A:49:LEU:HB2	1:A:63:TYR:HE2	16	0.21
(2,144)	1:A:49:LEU:HB3	1:A:63:TYR:HE2	16	0.21
(1,42)	1:A:48:SER:H	1:A:49:LEU:H	16	0.21
(1,355)	1:A:41:PHE:HA	1:A:41:PHE:HE1	7	0.21
(1,355)	1:A:41:PHE:HA	1:A:41:PHE:HE1	14	0.21
(1,331)	1:A:37:LEU:HD11	1:A:66:VAL:HA	5	0.21
(1,331)	1:A:37:LEU:HD12	1:A:66:VAL:HA	5	0.21
(1,331)	1:A:37:LEU:HD13	1:A:66:VAL:HA	5	0.21
(1,186)	1:A:72:ASN:H	1:A:75:MET:H	12	0.21
(1,186)	1:A:72:ASN:H	1:A:75:MET:H	20	0.21
(1,119)	1:A:22:LYS:H	1:A:23:GLN:H	17	0.21
(1,118)	1:A:20:VAL:H	1:A:21:LYS:H	4	0.21
(3,9)	1:A:36:VAL:O	1:A:40:ARG:H	6	0.2
(3,42)	1:A:72:ASN:O	1:A:76:LYS:N	13	0.2
(3,4)	1:A:33:GLN:O	1:A:37:LEU:N	4	0.2
(3,31)	1:A:67:LYS:O	1:A:71:GLN:H	20	0.2
(3,22)	1:A:53:GLN:O	1:A:57:ASN:N	12	0.2
(3,22)	1:A:53:GLN:O	1:A:57:ASN:N	16	0.2
(2,80)	1:A:29:PHE:HD1	1:A:33:GLN:HG2	12	0.2
(2,80)	1:A:29:PHE:HD1	1:A:33:GLN:HG3	12	0.2
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB2	5	0.2
(2,190)	1:A:70:PHE:HZ	1:A:71:GLN:HB3	5	0.2
(2,167)	1:A:55:LEU:HG	1:A:56:SER:HB2	16	0.2

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,167)	1:A:55:LEU:HG	1:A:56:SER:HB3	16	0.2
(1,42)	1:A:48:SER:H	1:A:49:LEU:H	11	0.2
(1,355)	1:A:41:PHE:HA	1:A:41:PHE:HE1	6	0.2
(1,186)	1:A:72:ASN:H	1:A:75:MET:H	2	0.2
(1,186)	1:A:72:ASN:H	1:A:75:MET:H	13	0.2
(1,186)	1:A:72:ASN:H	1:A:75:MET:H	15	0.2
(3,9)	1:A:36:VAL:O	1:A:40:ARG:H	18	0.19
(3,4)	1:A:33:GLN:O	1:A:37:LEU:N	7	0.19
(3,37)	1:A:70:PHE:O	1:A:74:ARG:H	15	0.19
(3,32)	1:A:67:LYS:O	1:A:71:GLN:N	7	0.19
(3,31)	1:A:67:LYS:O	1:A:71:GLN:H	16	0.19
(3,3)	1:A:33:GLN:O	1:A:37:LEU:H	20	0.19
(3,27)	1:A:65:GLN:O	1:A:69:TRP:H	18	0.19
(3,22)	1:A:53:GLN:O	1:A:57:ASN:N	4	0.19
(3,19)	1:A:52:MET:O	1:A:56:SER:H	5	0.19
(3,19)	1:A:52:MET:O	1:A:56:SER:H	12	0.19
(3,19)	1:A:52:MET:O	1:A:56:SER:H	17	0.19
(1,83)	1:A:20:VAL:H	1:A:20:VAL:HB	3	0.19
(1,466)	1:A:52:MET:HG2	1:A:63:TYR:HD2	3	0.19
(1,466)	1:A:52:MET:HG3	1:A:63:TYR:HD2	3	0.19
(1,428)	1:A:45:LYS:HB2	1:A:46:TYR:HD1	7	0.19
(1,428)	1:A:45:LYS:HB3	1:A:46:TYR:HD1	7	0.19
(1,42)	1:A:48:SER:H	1:A:49:LEU:H	4	0.19
(1,42)	1:A:48:SER:H	1:A:49:LEU:H	12	0.19
(1,355)	1:A:41:PHE:HA	1:A:41:PHE:HE1	4	0.19
(1,355)	1:A:41:PHE:HA	1:A:41:PHE:HE1	15	0.19
(1,355)	1:A:41:PHE:HA	1:A:41:PHE:HE1	18	0.19
(1,350)	1:A:46:TYR:HA	1:A:46:TYR:HD2	5	0.19
(1,350)	1:A:46:TYR:HA	1:A:46:TYR:HD2	7	0.19
(1,350)	1:A:46:TYR:HA	1:A:46:TYR:HD2	19	0.19
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE1	3	0.19
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE2	3	0.19
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE3	3	0.19
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE1	17	0.19
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE2	17	0.19
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE3	17	0.19
(1,196)	1:A:29:PHE:H	1:A:29:PHE:HE2	12	0.19
(1,186)	1:A:72:ASN:H	1:A:75:MET:H	8	0.19
(1,186)	1:A:72:ASN:H	1:A:75:MET:H	10	0.19
(3,9)	1:A:36:VAL:O	1:A:40:ARG:H	7	0.18
(3,32)	1:A:67:LYS:O	1:A:71:GLN:N	4	0.18
(3,27)	1:A:65:GLN:O	1:A:69:TRP:H	17	0.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,22)	1:A:53:GLN:O	1:A:57:ASN:N	3	0.18
(3,21)	1:A:53:GLN:O	1:A:57:ASN:H	1	0.18
(3,21)	1:A:53:GLN:O	1:A:57:ASN:H	11	0.18
(3,20)	1:A:52:MET:O	1:A:56:SER:N	11	0.18
(3,2)	1:A:32:THR:O	1:A:36:VAL:N	7	0.18
(3,19)	1:A:52:MET:O	1:A:56:SER:H	3	0.18
(3,16)	1:A:50:GLN:O	1:A:54:GLU:N	19	0.18
(3,12)	1:A:37:LEU:O	1:A:41:PHE:N	6	0.18
(1,7)	1:A:17:LYS:HA	1:A:18:VAL:H	13	0.18
(1,42)	1:A:48:SER:H	1:A:49:LEU:H	2	0.18
(1,355)	1:A:41:PHE:HA	1:A:41:PHE:HE1	2	0.18
(1,186)	1:A:72:ASN:H	1:A:75:MET:H	4	0.18
(1,186)	1:A:72:ASN:H	1:A:75:MET:H	11	0.18
(1,186)	1:A:72:ASN:H	1:A:75:MET:H	16	0.18
(1,186)	1:A:72:ASN:H	1:A:75:MET:H	17	0.18
(1,177)	1:A:63:TYR:H	1:A:66:VAL:H	10	0.18
(1,14)	1:A:27:THR:HB	1:A:28:VAL:H	9	0.18
(1,119)	1:A:22:LYS:H	1:A:23:GLN:H	15	0.18
(3,9)	1:A:36:VAL:O	1:A:40:ARG:H	4	0.17
(3,9)	1:A:36:VAL:O	1:A:40:ARG:H	5	0.17
(3,39)	1:A:71:GLN:O	1:A:75:MET:H	7	0.17
(3,39)	1:A:71:GLN:O	1:A:75:MET:H	18	0.17
(3,38)	1:A:70:PHE:O	1:A:74:ARG:N	11	0.17
(3,35)	1:A:69:TRP:O	1:A:73:GLN:H	19	0.17
(3,25)	1:A:64:LYS:O	1:A:68:THR:H	7	0.17
(3,22)	1:A:53:GLN:O	1:A:57:ASN:N	8	0.17
(3,19)	1:A:52:MET:O	1:A:56:SER:H	6	0.17
(3,16)	1:A:50:GLN:O	1:A:54:GLU:N	16	0.17
(3,15)	1:A:50:GLN:O	1:A:54:GLU:H	12	0.17
(3,10)	1:A:36:VAL:O	1:A:40:ARG:N	16	0.17
(3,1)	1:A:32:THR:O	1:A:36:VAL:H	2	0.17
(1,83)	1:A:20:VAL:H	1:A:20:VAL:HB	19	0.17
(1,466)	1:A:52:MET:HG2	1:A:63:TYR:HD2	17	0.17
(1,466)	1:A:52:MET:HG3	1:A:63:TYR:HD2	17	0.17
(1,42)	1:A:48:SER:H	1:A:49:LEU:H	3	0.17
(1,42)	1:A:48:SER:H	1:A:49:LEU:H	10	0.17
(1,42)	1:A:48:SER:H	1:A:49:LEU:H	19	0.17
(1,42)	1:A:48:SER:H	1:A:49:LEU:H	20	0.17
(1,402)	1:A:39:ASP:H	1:A:40:ARG:HB2	11	0.17
(1,402)	1:A:39:ASP:H	1:A:40:ARG:HB3	11	0.17
(1,355)	1:A:41:PHE:HA	1:A:41:PHE:HE1	8	0.17
(1,355)	1:A:41:PHE:HA	1:A:41:PHE:HE1	16	0.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,355)	1:A:41:PHE:HA	1:A:41:PHE:HE1	17	0.17
(1,355)	1:A:41:PHE:HA	1:A:41:PHE:HE1	19	0.17
(1,350)	1:A:46:TYR:HA	1:A:46:TYR:HD2	12	0.17
(1,350)	1:A:46:TYR:HA	1:A:46:TYR:HD2	20	0.17
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE1	5	0.17
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE2	5	0.17
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE3	5	0.17
(1,14)	1:A:27:THR:HB	1:A:28:VAL:H	18	0.17
(3,9)	1:A:36:VAL:O	1:A:40:ARG:H	3	0.16
(3,6)	1:A:34:LEU:O	1:A:38:ASN:N	17	0.16
(3,36)	1:A:69:TRP:O	1:A:73:GLN:N	20	0.16
(3,33)	1:A:68:THR:O	1:A:72:ASN:H	12	0.16
(3,30)	1:A:66:VAL:O	1:A:70:PHE:N	7	0.16
(3,28)	1:A:65:GLN:O	1:A:69:TRP:N	19	0.16
(3,26)	1:A:64:LYS:O	1:A:68:THR:N	20	0.16
(3,13)	1:A:38:ASN:O	1:A:42:GLN:H	13	0.16
(3,11)	1:A:37:LEU:O	1:A:41:PHE:H	16	0.16
(1,83)	1:A:20:VAL:H	1:A:20:VAL:HB	8	0.16
(1,83)	1:A:20:VAL:H	1:A:20:VAL:HB	15	0.16
(1,83)	1:A:20:VAL:H	1:A:20:VAL:HB	20	0.16
(1,81)	1:A:18:VAL:H	1:A:18:VAL:HB	15	0.16
(1,5)	1:A:11:VAL:HA	1:A:12:ALA:H	12	0.16
(1,42)	1:A:48:SER:H	1:A:49:LEU:H	1	0.16
(1,42)	1:A:48:SER:H	1:A:49:LEU:H	9	0.16
(1,42)	1:A:48:SER:H	1:A:49:LEU:H	14	0.16
(1,355)	1:A:41:PHE:HA	1:A:41:PHE:HE1	3	0.16
(1,355)	1:A:41:PHE:HA	1:A:41:PHE:HE1	9	0.16
(1,355)	1:A:41:PHE:HA	1:A:41:PHE:HE1	20	0.16
(1,34)	1:A:38:ASN:HA	1:A:42:GLN:H	20	0.16
(1,293)	1:A:56:SER:HA	1:A:66:VAL:HA	20	0.16
(1,285)	1:A:56:SER:HA	1:A:58:ILE:H	11	0.16
(1,216)	1:A:45:LYS:H	1:A:45:LYS:HG2	8	0.16
(1,215)	1:A:56:SER:H	1:A:66:VAL:HB	11	0.16
(1,186)	1:A:72:ASN:H	1:A:75:MET:H	6	0.16
(1,177)	1:A:63:TYR:H	1:A:66:VAL:H	4	0.16
(1,177)	1:A:63:TYR:H	1:A:66:VAL:H	9	0.16
(1,14)	1:A:27:THR:HB	1:A:28:VAL:H	15	0.16
(3,42)	1:A:72:ASN:O	1:A:76:LYS:N	15	0.15
(3,4)	1:A:33:GLN:O	1:A:37:LEU:N	20	0.15
(3,32)	1:A:67:LYS:O	1:A:71:GLN:N	13	0.15
(3,3)	1:A:33:GLN:O	1:A:37:LEU:H	2	0.15
(3,29)	1:A:66:VAL:O	1:A:70:PHE:H	20	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(3,28)	1:A:65:GLN:O	1:A:69:TRP:N	4	0.15
(3,19)	1:A:52:MET:O	1:A:56:SER:H	20	0.15
(3,16)	1:A:50:GLN:O	1:A:54:GLU:N	7	0.15
(3,10)	1:A:36:VAL:O	1:A:40:ARG:N	6	0.15
(3,10)	1:A:36:VAL:O	1:A:40:ARG:N	17	0.15
(1,83)	1:A:20:VAL:H	1:A:20:VAL:HB	10	0.15
(1,83)	1:A:20:VAL:H	1:A:20:VAL:HB	11	0.15
(1,42)	1:A:48:SER:H	1:A:49:LEU:H	6	0.15
(1,42)	1:A:48:SER:H	1:A:49:LEU:H	8	0.15
(1,34)	1:A:38:ASN:HA	1:A:42:GLN:H	15	0.15
(1,277)	1:A:11:VAL:HB	1:A:12:ALA:HA	7	0.15
(1,186)	1:A:72:ASN:H	1:A:75:MET:H	1	0.15
(1,186)	1:A:72:ASN:H	1:A:75:MET:H	9	0.15
(1,186)	1:A:72:ASN:H	1:A:75:MET:H	14	0.15
(1,182)	1:A:68:THR:H	1:A:71:GLN:H	14	0.15
(1,14)	1:A:27:THR:HB	1:A:28:VAL:H	17	0.15
(3,36)	1:A:69:TRP:O	1:A:73:GLN:N	19	0.14
(3,33)	1:A:68:THR:O	1:A:72:ASN:H	7	0.14
(3,3)	1:A:33:GLN:O	1:A:37:LEU:H	12	0.14
(3,25)	1:A:64:LYS:O	1:A:68:THR:H	13	0.14
(3,20)	1:A:52:MET:O	1:A:56:SER:N	17	0.14
(3,19)	1:A:52:MET:O	1:A:56:SER:H	2	0.14
(3,16)	1:A:50:GLN:O	1:A:54:GLU:N	10	0.14
(3,14)	1:A:38:ASN:O	1:A:42:GLN:N	17	0.14
(3,11)	1:A:37:LEU:O	1:A:41:PHE:H	4	0.14
(3,1)	1:A:32:THR:O	1:A:36:VAL:H	4	0.14
(3,1)	1:A:32:THR:O	1:A:36:VAL:H	5	0.14
(3,1)	1:A:32:THR:O	1:A:36:VAL:H	20	0.14
(2,167)	1:A:55:LEU:HG	1:A:56:SER:HB2	12	0.14
(2,167)	1:A:55:LEU:HG	1:A:56:SER:HB3	12	0.14
(1,55)	1:A:56:SER:HA	1:A:59:LEU:H	20	0.14
(1,50)	1:A:55:LEU:HA	1:A:56:SER:H	14	0.14
(1,473)	1:A:53:GLN:HE21	1:A:63:TYR:HD2	3	0.14
(1,473)	1:A:53:GLN:HE22	1:A:63:TYR:HD2	3	0.14
(1,428)	1:A:45:LYS:HB2	1:A:46:TYR:HD1	1	0.14
(1,428)	1:A:45:LYS:HB3	1:A:46:TYR:HD1	1	0.14
(1,42)	1:A:48:SER:H	1:A:49:LEU:H	15	0.14
(1,42)	1:A:48:SER:H	1:A:49:LEU:H	18	0.14
(1,350)	1:A:46:TYR:HA	1:A:46:TYR:HD2	17	0.14
(1,34)	1:A:38:ASN:HA	1:A:42:GLN:H	12	0.14
(1,293)	1:A:56:SER:HA	1:A:66:VAL:HA	4	0.14
(1,277)	1:A:11:VAL:HB	1:A:12:ALA:HA	4	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,177)	1:A:63:TYR:H	1:A:66:VAL:H	8	0.14
(1,154)	1:A:40:ARG:H	1:A:42:GLN:H	17	0.14
(1,12)	1:A:5:THR:HA	1:A:6:SER:H	18	0.14
(3,42)	1:A:72:ASN:O	1:A:76:LYS:N	19	0.13
(3,40)	1:A:71:GLN:O	1:A:75:MET:N	5	0.13
(3,32)	1:A:67:LYS:O	1:A:71:GLN:N	16	0.13
(3,3)	1:A:33:GLN:O	1:A:37:LEU:H	3	0.13
(3,29)	1:A:66:VAL:O	1:A:70:PHE:H	10	0.13
(3,27)	1:A:65:GLN:O	1:A:69:TRP:H	9	0.13
(3,27)	1:A:65:GLN:O	1:A:69:TRP:H	12	0.13
(3,22)	1:A:53:GLN:O	1:A:57:ASN:N	10	0.13
(3,22)	1:A:53:GLN:O	1:A:57:ASN:N	14	0.13
(3,21)	1:A:53:GLN:O	1:A:57:ASN:H	15	0.13
(3,2)	1:A:32:THR:O	1:A:36:VAL:N	2	0.13
(3,12)	1:A:37:LEU:O	1:A:41:PHE:N	16	0.13
(3,10)	1:A:36:VAL:O	1:A:40:ARG:N	3	0.13
(3,10)	1:A:36:VAL:O	1:A:40:ARG:N	5	0.13
(1,83)	1:A:20:VAL:H	1:A:20:VAL:HB	1	0.13
(1,81)	1:A:18:VAL:H	1:A:18:VAL:HB	6	0.13
(1,81)	1:A:18:VAL:H	1:A:18:VAL:HB	20	0.13
(1,7)	1:A:17:LYS:HA	1:A:18:VAL:H	12	0.13
(1,50)	1:A:55:LEU:HA	1:A:56:SER:H	4	0.13
(1,50)	1:A:55:LEU:HA	1:A:56:SER:H	10	0.13
(1,50)	1:A:55:LEU:HA	1:A:56:SER:H	17	0.13
(1,42)	1:A:48:SER:H	1:A:49:LEU:H	5	0.13
(1,42)	1:A:48:SER:H	1:A:49:LEU:H	13	0.13
(1,42)	1:A:48:SER:H	1:A:49:LEU:H	17	0.13
(1,355)	1:A:41:PHE:HA	1:A:41:PHE:HE1	5	0.13
(1,355)	1:A:41:PHE:HA	1:A:41:PHE:HE1	10	0.13
(1,350)	1:A:46:TYR:HA	1:A:46:TYR:HD2	11	0.13
(1,350)	1:A:46:TYR:HA	1:A:46:TYR:HD2	16	0.13
(1,34)	1:A:38:ASN:HA	1:A:42:GLN:H	1	0.13
(1,34)	1:A:38:ASN:HA	1:A:42:GLN:H	3	0.13
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE1	20	0.13
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE2	20	0.13
(1,336)	1:A:47:LEU:HG	1:A:52:MET:HE3	20	0.13
(1,293)	1:A:56:SER:HA	1:A:66:VAL:HA	11	0.13
(1,285)	1:A:56:SER:HA	1:A:58:ILE:H	20	0.13
(1,215)	1:A:56:SER:H	1:A:66:VAL:HB	15	0.13
(1,215)	1:A:56:SER:H	1:A:66:VAL:HB	18	0.13
(1,186)	1:A:72:ASN:H	1:A:75:MET:H	3	0.13
(1,177)	1:A:63:TYR:H	1:A:66:VAL:H	16	0.13

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,177)	1:A:63:TYR:H	1:A:66:VAL:H	17	0.13
(1,14)	1:A:27:THR:HB	1:A:28:VAL:H	10	0.13
(1,14)	1:A:27:THR:HB	1:A:28:VAL:H	19	0.13
(3,9)	1:A:36:VAL:O	1:A:40:ARG:H	15	0.12
(3,28)	1:A:65:GLN:O	1:A:69:TRP:N	5	0.12
(3,27)	1:A:65:GLN:O	1:A:69:TRP:H	11	0.12
(3,25)	1:A:64:LYS:O	1:A:68:THR:H	16	0.12
(3,22)	1:A:53:GLN:O	1:A:57:ASN:N	11	0.12
(3,20)	1:A:52:MET:O	1:A:56:SER:N	19	0.12
(3,19)	1:A:52:MET:O	1:A:56:SER:H	9	0.12
(3,13)	1:A:38:ASN:O	1:A:42:GLN:H	10	0.12
(3,1)	1:A:32:THR:O	1:A:36:VAL:H	12	0.12
(1,55)	1:A:56:SER:HA	1:A:59:LEU:H	18	0.12
(1,50)	1:A:55:LEU:HA	1:A:56:SER:H	3	0.12
(1,50)	1:A:55:LEU:HA	1:A:56:SER:H	7	0.12
(1,50)	1:A:55:LEU:HA	1:A:56:SER:H	8	0.12
(1,50)	1:A:55:LEU:HA	1:A:56:SER:H	11	0.12
(1,50)	1:A:55:LEU:HA	1:A:56:SER:H	16	0.12
(1,355)	1:A:41:PHE:HA	1:A:41:PHE:HE1	12	0.12
(1,350)	1:A:46:TYR:HA	1:A:46:TYR:HD2	3	0.12
(1,34)	1:A:38:ASN:HA	1:A:42:GLN:H	19	0.12
(1,285)	1:A:56:SER:HA	1:A:58:ILE:H	18	0.12
(1,215)	1:A:56:SER:H	1:A:66:VAL:HB	5	0.12
(1,192)	1:A:47:LEU:HG	1:A:48:SER:H	11	0.12
(1,177)	1:A:63:TYR:H	1:A:66:VAL:H	6	0.12
(1,143)	1:A:30:SER:H	1:A:34:LEU:H	9	0.12
(1,14)	1:A:27:THR:HB	1:A:28:VAL:H	11	0.12
(1,14)	1:A:27:THR:HB	1:A:28:VAL:H	12	0.12
(1,12)	1:A:5:THR:HA	1:A:6:SER:H	20	0.12
(3,41)	1:A:72:ASN:O	1:A:76:LYS:H	7	0.11
(3,38)	1:A:70:PHE:O	1:A:74:ARG:N	8	0.11
(3,38)	1:A:70:PHE:O	1:A:74:ARG:N	15	0.11
(3,37)	1:A:70:PHE:O	1:A:74:ARG:H	19	0.11
(3,31)	1:A:67:LYS:O	1:A:71:GLN:H	3	0.11
(3,26)	1:A:64:LYS:O	1:A:68:THR:N	18	0.11
(3,23)	1:A:63:TYR:O	1:A:67:LYS:H	1	0.11
(3,22)	1:A:53:GLN:O	1:A:57:ASN:N	2	0.11
(3,20)	1:A:52:MET:O	1:A:56:SER:N	3	0.11
(3,20)	1:A:52:MET:O	1:A:56:SER:N	5	0.11
(3,15)	1:A:50:GLN:O	1:A:54:GLU:H	1	0.11
(3,10)	1:A:36:VAL:O	1:A:40:ARG:N	4	0.11
(3,1)	1:A:32:THR:O	1:A:36:VAL:H	6	0.11

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,167)	1:A:55:LEU:HG	1:A:56:SER:HB2	18	0.11
(2,167)	1:A:55:LEU:HG	1:A:56:SER:HB3	18	0.11
(2,15)	1:A:52:MET:HA	1:A:63:TYR:HA	5	0.11
(1,7)	1:A:17:LYS:HA	1:A:18:VAL:H	5	0.11
(1,55)	1:A:56:SER:HA	1:A:59:LEU:H	11	0.11
(1,50)	1:A:55:LEU:HA	1:A:56:SER:H	1	0.11
(1,50)	1:A:55:LEU:HA	1:A:56:SER:H	5	0.11
(1,50)	1:A:55:LEU:HA	1:A:56:SER:H	9	0.11
(1,50)	1:A:55:LEU:HA	1:A:56:SER:H	20	0.11
(1,42)	1:A:48:SER:H	1:A:49:LEU:H	7	0.11
(1,4)	1:A:10:SER:HA	1:A:11:VAL:H	10	0.11
(1,359)	1:A:80:TRP:HD1	1:A:81:GLN:H	5	0.11
(1,355)	1:A:41:PHE:HA	1:A:41:PHE:HE1	1	0.11
(1,350)	1:A:46:TYR:HA	1:A:46:TYR:HD2	10	0.11
(1,34)	1:A:38:ASN:HA	1:A:42:GLN:H	7	0.11
(1,34)	1:A:38:ASN:HA	1:A:42:GLN:H	8	0.11
(1,3)	1:A:9:ASN:HA	1:A:10:SER:H	17	0.11
(1,293)	1:A:56:SER:HA	1:A:66:VAL:HA	10	0.11
(1,293)	1:A:56:SER:HA	1:A:66:VAL:HA	14	0.11
(1,285)	1:A:56:SER:HA	1:A:58:ILE:H	6	0.11
(1,285)	1:A:56:SER:HA	1:A:58:ILE:H	12	0.11
(1,279)	1:A:16:ASP:HA	1:A:17:LYS:HA	14	0.11
(1,276)	1:A:9:ASN:HA	1:A:10:SER:HA	14	0.11
(1,268)	1:A:61:LEU:HA	1:A:62:SER:HB3	18	0.11
(1,215)	1:A:56:SER:H	1:A:66:VAL:HB	1	0.11
(1,215)	1:A:56:SER:H	1:A:66:VAL:HB	2	0.11
(1,215)	1:A:56:SER:H	1:A:66:VAL:HB	12	0.11
(1,192)	1:A:47:LEU:HG	1:A:48:SER:H	1	0.11
(1,178)	1:A:64:LYS:H	1:A:66:VAL:H	15	0.11
(1,177)	1:A:63:TYR:H	1:A:66:VAL:H	13	0.11
(1,177)	1:A:63:TYR:H	1:A:66:VAL:H	18	0.11
(1,161)	1:A:48:SER:HA	1:A:50:GLN:H	20	0.11
(1,148)	1:A:38:ASN:H	1:A:39:ASP:HA	20	0.11
(1,143)	1:A:30:SER:H	1:A:34:LEU:H	10	0.11
(1,14)	1:A:27:THR:HB	1:A:28:VAL:H	1	0.11
(1,14)	1:A:27:THR:HB	1:A:28:VAL:H	7	0.11
(1,14)	1:A:27:THR:HB	1:A:28:VAL:H	16	0.11
(1,10)	1:A:20:VAL:HA	1:A:21:LYS:H	5	0.11

10 Dihedral-angle violation analysis (i)

Dihedral angle analysis failed due to data error in the dihedral angle restraints, possibly missing target value