Full wwPDB NMR Structure Validation Report (i)

Jun 3, 2023 – 06:09 AM EDT

PDB ID	:	5U3H
BMRB ID	:	30205
Title	:	Solution structure of apo PCP1 from yersiniabactin synthetase
Authors	:	Harden, B.J.; Frueh, D.P.
Deposited on	:	2016-12-02

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:

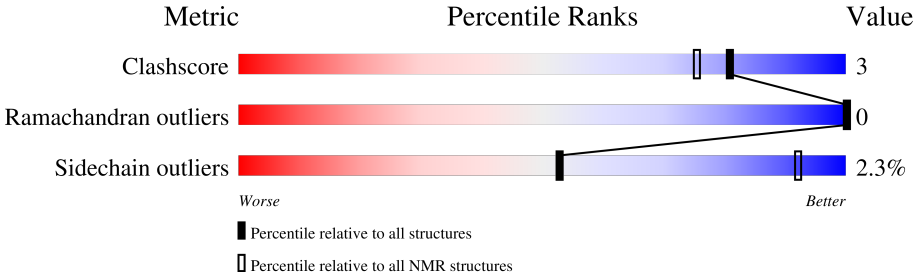
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
BMRB Restraints Analysis	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal 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 89%.

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	111	66% · 33%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 8 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *target function*.

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:24-A:97 (74)	0.53	8

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

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

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

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1710 atoms, of which 837 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called HMWP2 nonribosomal peptide synthetase.

Mol	Chain	Residues	Atoms					Trace
			Total	C	H	N	O	
1	A	111	1710	543	837	155	175	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP Q7CI41
A	2	THR	-	expression tag	UNP Q7CI41

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: HMWP2 nonribosomal peptide synthetase

Chain A: 66% • 33%

G1 T2 I3 D4 Y5 Q6 A7 L8 K9 R10 R11 H12 T13 P14 E15 A16 E17 N18 P19 A20 E21 A22 D23 V46 D98 V99 P100 V101 E102 Q103 P104 F105 V106 H107 S108 P109 E110 D111

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: HMWP2 nonribosomal peptide synthetase

Chain A: 64% • 33%

G1 T2 I3 D4 Y5 Q6 A7 L8 K9 R10 R11 H12 T13 P14 E15 A16 E17 N18 P19 A20 E21 A22 D23 Q38 V46 R86 D98 V99 P100 V101 E102 Q103 P104 F105 V106 H107 S108 P109 E110 D111

4.2.2 Score per residue for model 2

• Molecule 1: HMWP2 nonribosomal peptide synthetase

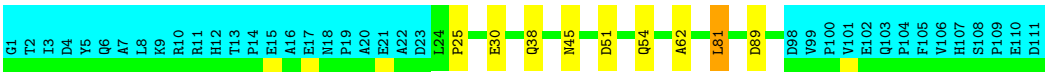
Chain A: 62% 5% 33%

G1 T2 I3 D4 Y5 Q6 A7 L8 K9 R10 R11 H12 T13 P14 E15 A16 E17 N18 P19 A20 E21 A22 D23 Q26 Q38 V46 T47 R48 A88 D98 V99 P100 V101 E102 Q103 P104 F105 V106 H107 S108 P109 E110 D111

4.2.3 Score per residue for model 3

- Molecule 1: HMWP2 nonribosomal peptide synthetase

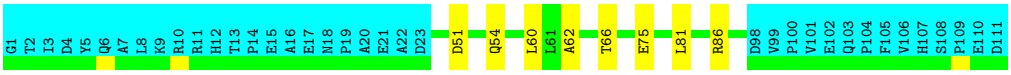
Chain A: 59% 7% • 33%



4.2.4 Score per residue for model 4

- Molecule 1: HMWP2 nonribosomal peptide synthetase

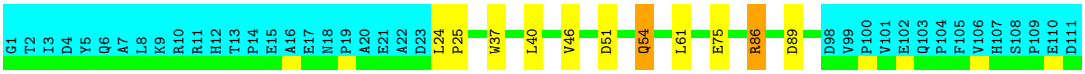
Chain A: 59% 7% 33%



4.2.5 Score per residue for model 5

- Molecule 1: HMWP2 nonribosomal peptide synthetase

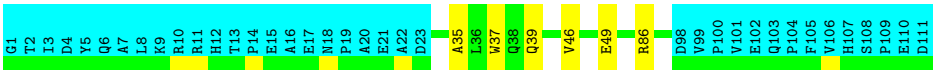
Chain A: 57% 8% • 33%



4.2.6 Score per residue for model 6

- Molecule 1: HMWP2 nonribosomal peptide synthetase

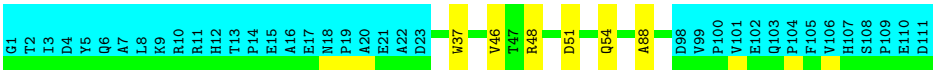
Chain A: 61% 5% 33%



4.2.7 Score per residue for model 7

- Molecule 1: HMWP2 nonribosomal peptide synthetase

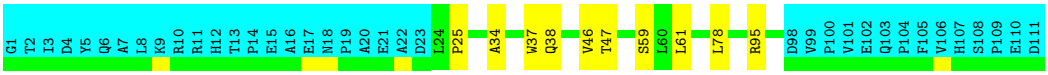
Chain A: 61% 5% 33%



4.2.8 Score per residue for model 8 (medoid)

- Molecule 1: HMWP2 nonribosomal peptide synthetase

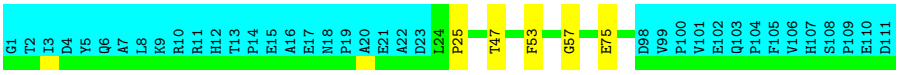
Chain A: 58% 9% 33%



4.2.9 Score per residue for model 9

- Molecule 1: HMWP2 nonribosomal peptide synthetase

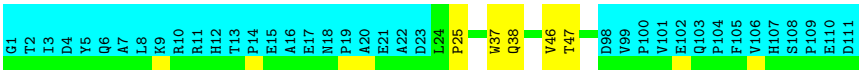
Chain A: 62% 5% 33%



4.2.10 Score per residue for model 10

- Molecule 1: HMWP2 nonribosomal peptide synthetase

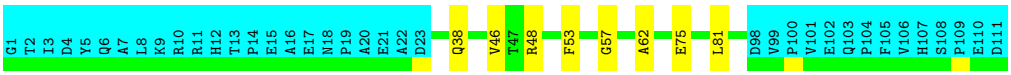
Chain A: 62% 5% 33%



4.2.11 Score per residue for model 11

- Molecule 1: HMWP2 nonribosomal peptide synthetase

Chain A: 59% 7% 33%



4.2.12 Score per residue for model 12

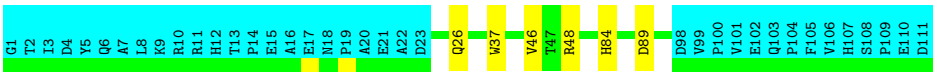
- Molecule 1: HMWP2 nonribosomal peptide synthetase

Chain A: 61% 5% 33%

4.2.13 Score per residue for model 13

- Molecule 1: HMWP2 nonribosomal peptide synthetase

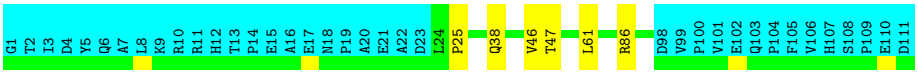
Chain A: 61% 5% 33%



4.2.14 Score per residue for model 14

- Molecule 1: HMWP2 nonribosomal peptide synthetase

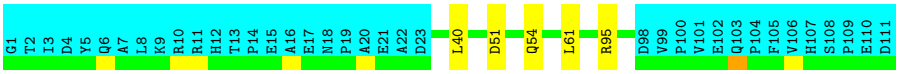
Chain A: 61% 5% 33%



4.2.15 Score per residue for model 15

- Molecule 1: HMWP2 nonribosomal peptide synthetase

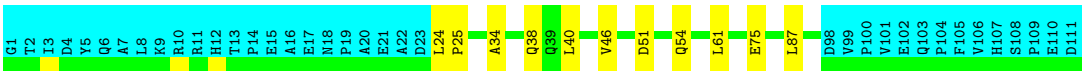
Chain A: 62% 5% 33%



4.2.16 Score per residue for model 16

- Molecule 1: HMWP2 nonribosomal peptide synthetase

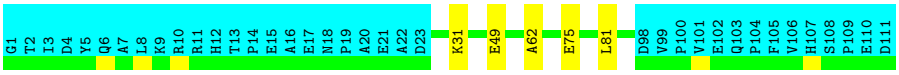
Chain A: 57% 10% 33%



4.2.17 Score per residue for model 17

- Molecule 1: HMWP2 nonribosomal peptide synthetase

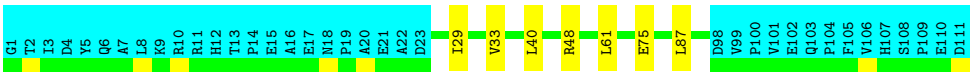
Chain A: 62% 5% 33%



4.2.18 Score per residue for model 18

- Molecule 1: HMWP2 nonribosomal peptide synthetase

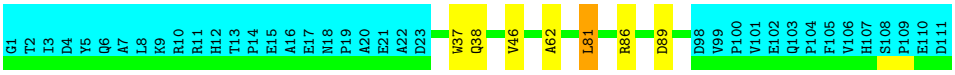
Chain A: 60% 6% 33%



4.2.19 Score per residue for model 19

- Molecule 1: HMWP2 nonribosomal peptide synthetase

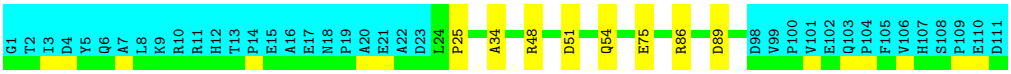
Chain A: 60% 5% • 33%



4.2.20 Score per residue for model 20

- Molecule 1: HMWP2 nonribosomal peptide synthetase

Chain A: 59% 7% 33%



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *molecular dynamics*.

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**
CYANA	structure calculation	
CNS	refinement	
CYANA	refinement	

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

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1304
Number of shifts mapped to atoms	1304
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	89%

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	579	568	566	3±1
All	All	11580	11360	11320	59

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:40:LEU:HB3	1:A:61:LEU:HD21	0.61	1.69	15	4
1:A:51:ASP:HB2	1:A:54:GLN:HB3	0.61	1.71	16	6
1:A:38:GLN:HG3	1:A:46:VAL:HG22	0.56	1.78	10	9
1:A:37:TRP:HB2	1:A:46:VAL:HG21	0.52	1.79	8	7
1:A:48:ARG:HG3	1:A:88:ALA:HB3	0.51	1.81	2	1
1:A:62:ALA:HB1	1:A:81:LEU:HD13	0.48	1.86	3	5
1:A:25:PRO:HD3	1:A:47:THR:HA	0.48	1.85	10	4
1:A:48:ARG:HA	1:A:87:LEU:HB3	0.47	1.85	18	2
1:A:25:PRO:HG2	1:A:34:ALA:HB2	0.46	1.87	20	2
1:A:26:GLN:HE22	1:A:48:ARG:HD3	0.45	1.71	2	1
1:A:59:SER:HB2	1:A:78:LEU:HD11	0.45	1.88	8	1
1:A:48:ARG:HB2	1:A:88:ALA:HB2	0.44	1.88	7	1
1:A:26:GLN:HB2	1:A:48:ARG:NH2	0.44	2.27	13	1
1:A:84:HIS:HB3	1:A:89:ASP:HB3	0.43	1.90	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:25:PRO:HB3	1:A:30:GLU:HB3	0.43	1.90	3	1
1:A:24:LEU:HD12	1:A:25:PRO:HD2	0.42	1.91	16	2
1:A:86:ARG:HB3	1:A:89:ASP:HB3	0.42	1.92	19	1
1:A:38:GLN:HE21	1:A:45:ASN:HA	0.42	1.74	3	1
1:A:51:ASP:HB2	1:A:54:GLN:HB2	0.42	1.92	4	1
1:A:34:ALA:HA	1:A:87:LEU:HD11	0.42	1.92	16	2
1:A:66:THR:HG23	1:A:81:LEU:HD12	0.41	1.92	4	1
1:A:53:PHE:HA	1:A:57:GLY:O	0.41	2.15	11	2
1:A:29:ILE:O	1:A:33:VAL:HG23	0.41	2.15	18	1
1:A:35:ALA:O	1:A:39:GLN:HG2	0.41	2.15	6	1
1:A:86:ARG:HB2	1:A:89:ASP:HB3	0.41	1.92	5	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	74/111 (67%)	72±1 (98±1%)	2±1 (2±1%)	0±0 (0±0%)	100	100
All	All	1480/2220 (67%)	1447 (98%)	33 (2%)	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	60/92 (65%)	59±1 (98±2%)	1±1 (2±2%)	53	92
All	All	1200/1840 (65%)	1172 (98%)	28 (2%)	53	92

All 11 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	75	GLU	9
1	A	86	ARG	6
1	A	81	LEU	2
1	A	89	ASP	2
1	A	61	LEU	2
1	A	95	ARG	2
1	A	60	LEU	1
1	A	54	GLN	1
1	A	31	LYS	1
1	A	49	GLU	1
1	A	48	ARG	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 89% for the well-defined parts and 88% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *PCP1_1383-1491_apo.str*

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	1304
Number of shifts mapped to atoms	1304
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	111	-0.11 ± 0.09	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	104	0.34 ± 0.09	None needed (< 0.5 ppm)
$^{13}C'$	108	-0.22 ± 0.12	None needed (< 0.5 ppm)
^{15}N	102	0.07 ± 0.26	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 89%, i.e. 897 atoms were assigned a chemical shift out of a possible 1006. 0 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	372/372 (100%)	152/152 (100%)	148/148 (100%)	72/72 (100%)
Sidechain	473/557 (85%)	323/361 (89%)	147/171 (86%)	3/25 (12%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	52/77 (68%)	31/38 (82%)	21/34 (62%)	0/5 (0%)
Overall	897/1006 (89%)	506/551 (92%)	316/353 (90%)	75/102 (74%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 88%, i.e. 1304 atoms were assigned a chemical shift out of a possible 1488. 0 out of 18 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	540/548 (99%)	219/222 (99%)	219/222 (99%)	102/104 (98%)
Sidechain	694/828 (84%)	472/534 (88%)	219/259 (85%)	3/35 (9%)
Aromatic	70/112 (62%)	42/55 (76%)	28/48 (58%)	0/9 (0%)
Overall	1304/1488 (88%)	733/811 (90%)	466/529 (88%)	105/148 (71%)

7.1.4 Statistically unusual chemical shifts (i)

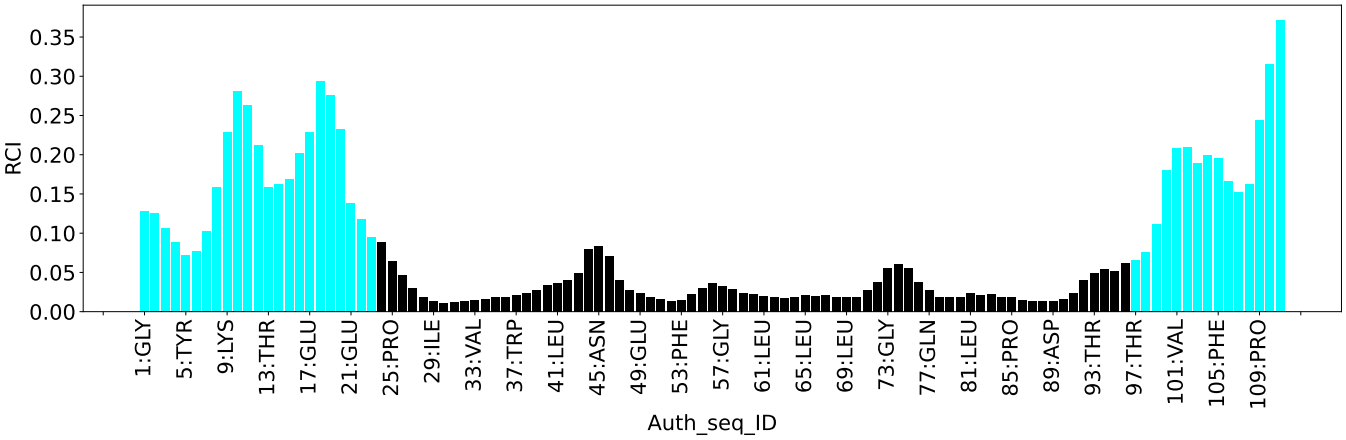
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	52	PHE	HD2	4.47	5.52 – 8.61	-8.4
1	A	52	PHE	HD1	4.47	5.51 – 8.60	-8.4

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
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
1:GLY
5:TYR
9:LYS
13:THR
17:GLU
21:GLU
25:PRO
29:ILE
33:VAL
37:TRP
41:LEU
45:ASN
49:GLU
53:PHE
57:GLY
61:LEU
65:LEU
69:LEU
73:GLY
77:GLN
81:LEU
85:PRO
89:ASP
93:THR
97:THR
101:VAL
105:PHE
109:PRO
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	1559
Intra-residue (|i-j|=0)	199
Sequential (|i-j|=1)	337
Medium range (|i-j|>1 and |i-j|<5)	408
Long range (|i-j|≥5)	615
Inter-chain	0
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	14.0
Number of long range restraints per residue[1]	5.5

[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)	3.9	0.2
0.2-0.5 (Medium)	12.6	0.5
>0.5 (Large)	6.7	1.0

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)

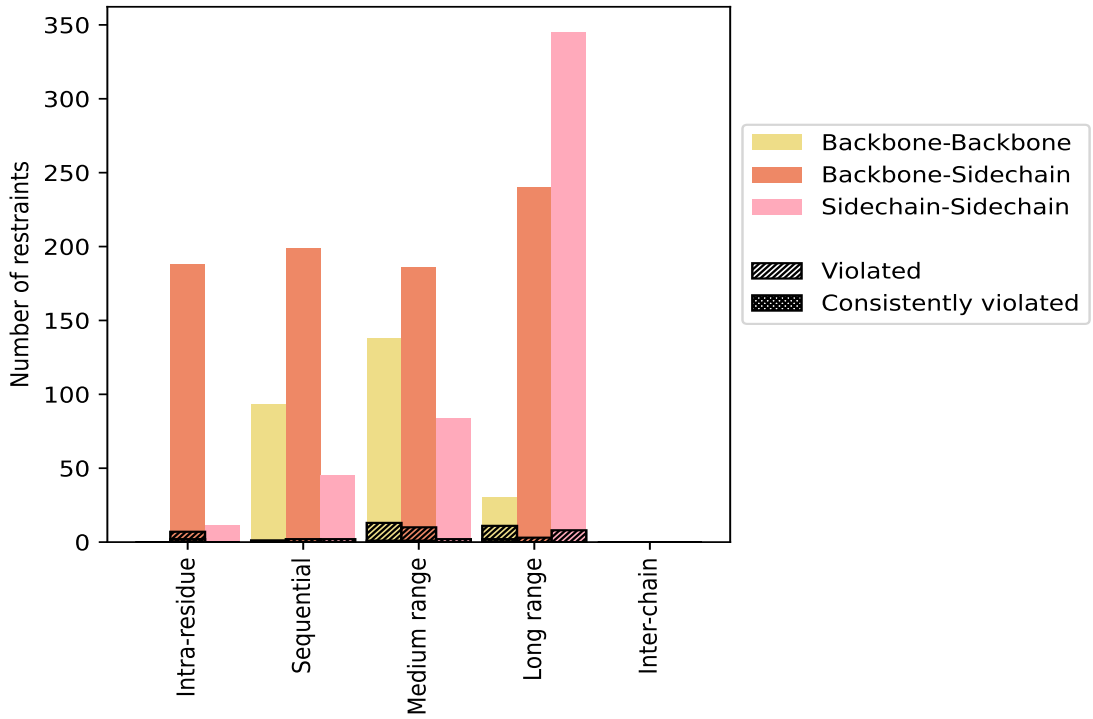
9.1 Summary of distance violations (i)

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)	199	12.8	7	3.5	0.4	2	1.0	0.1
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	188	12.1	7	3.7	0.4	2	1.1	0.1
Sidechain-Sidechain	11	0.7	0	0.0	0.0	0	0.0	0.0
Sequential (|i-j|=1)	337	21.6	5	1.5	0.3	1	0.3	0.1
Backbone-Backbone	93	6.0	1	1.1	0.1	1	1.1	0.1
Backbone-Sidechain	199	12.8	2	1.0	0.1	0	0.0	0.0
Sidechain-Sidechain	45	2.9	2	4.4	0.1	0	0.0	0.0
Medium range (|i-j|>1 & |i-j|<5)	408	26.2	25	6.1	1.6	2	0.5	0.1
Backbone-Backbone	138	8.9	13	9.4	0.8	1	0.7	0.1
Backbone-Sidechain	186	11.9	10	5.4	0.6	1	0.5	0.1
Sidechain-Sidechain	84	5.4	2	2.4	0.1	0	0.0	0.0
Long range (|i-j|≥5)	615	39.4	22	3.6	1.4	2	0.3	0.1
Backbone-Backbone	30	1.9	11	36.7	0.7	2	6.7	0.1
Backbone-Sidechain	240	15.4	3	1.2	0.2	0	0.0	0.0
Sidechain-Sidechain	345	22.1	8	2.3	0.5	0	0.0	0.0
Inter-chain	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Sidechain-Sidechain	0	0.0	0	0.0	0.0	0	0.0	0.0
Hydrogen bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Disulfide bond	0	0.0	0	0.0	0.0	0	0.0	0.0
Total	1559	100.0	59	3.8	3.8	7	0.4	0.4
Backbone-Backbone	261	16.7	25	9.6	1.6	4	1.5	0.3
Backbone-Sidechain	813	52.1	22	2.7	1.4	3	0.4	0.2
Sidechain-Sidechain	485	31.1	12	2.5	0.8	0	0.0	0.0

[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	2	11	7	0	24	0.4	1.0	0.25	0.34
2	4	2	7	7	0	20	0.36	0.9	0.19	0.3
3	5	2	14	7	0	28	0.39	0.84	0.19	0.36
4	4	3	13	6	0	26	0.42	0.81	0.18	0.4
5	5	4	10	5	0	24	0.4	0.87	0.19	0.38
6	3	3	8	5	0	19	0.38	0.88	0.2	0.32
7	3	2	10	7	0	22	0.44	0.98	0.24	0.36
8	4	3	11	5	0	23	0.43	0.89	0.21	0.45
9	4	4	9	7	0	24	0.4	0.95	0.22	0.37
10	4	3	8	6	0	21	0.42	0.88	0.2	0.36
11	3	2	11	8	0	24	0.37	0.86	0.21	0.29

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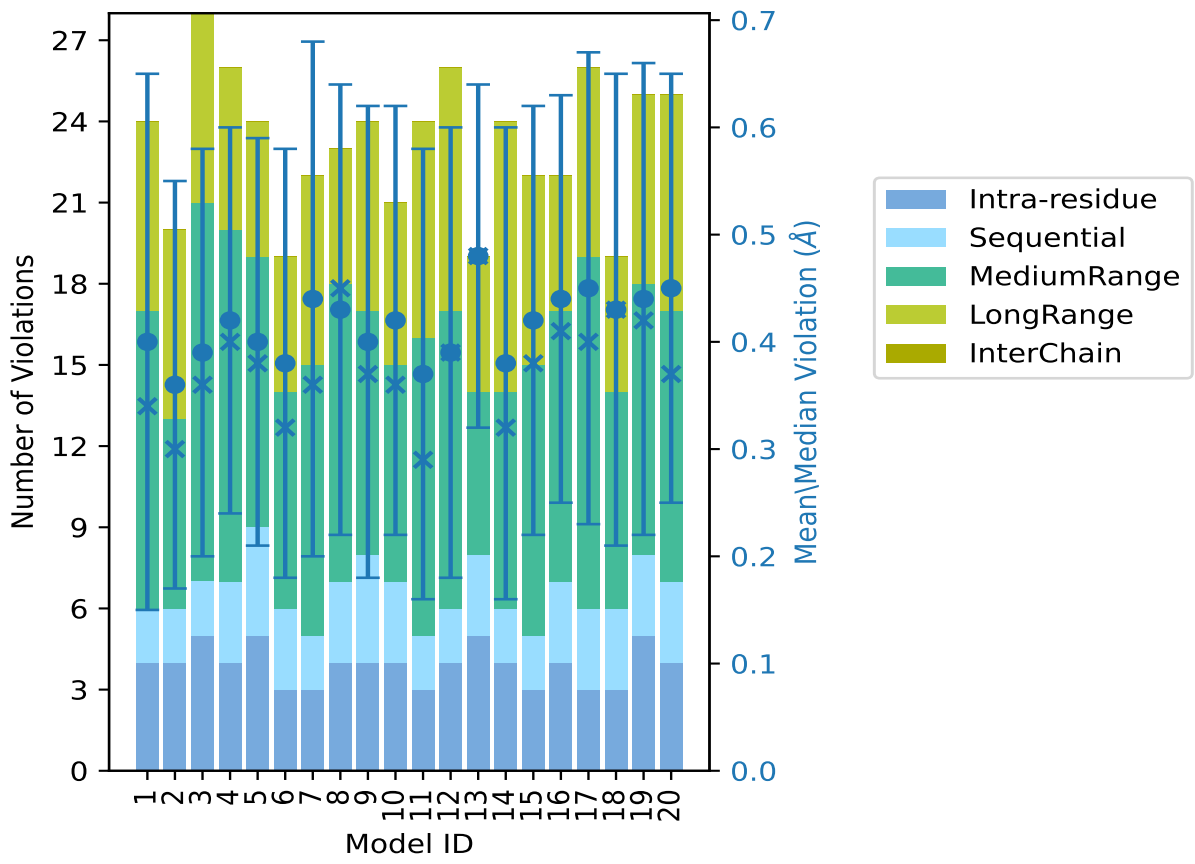
Model ID	Number of violations						Mean (Å)	Max (Å)	SD[6] (Å)	Median (Å)
	IR[1]	SQ[2]	MR[3]	LR[4]	IC[5]	Total				
12	4	2	11	9	0	26	0.39	0.92	0.21	0.39
13	5	3	6	5	0	19	0.48	0.82	0.16	0.48
14	4	2	8	10	0	24	0.38	0.91	0.22	0.32
15	3	2	10	7	0	22	0.42	0.92	0.2	0.38
16	4	3	10	5	0	22	0.44	0.89	0.19	0.41
17	3	3	13	7	0	26	0.45	0.92	0.22	0.4
18	3	3	8	5	0	19	0.43	0.91	0.22	0.43
19	5	3	10	7	0	25	0.44	0.93	0.22	0.42
20	4	3	10	8	0	25	0.45	0.89	0.2	0.37

[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

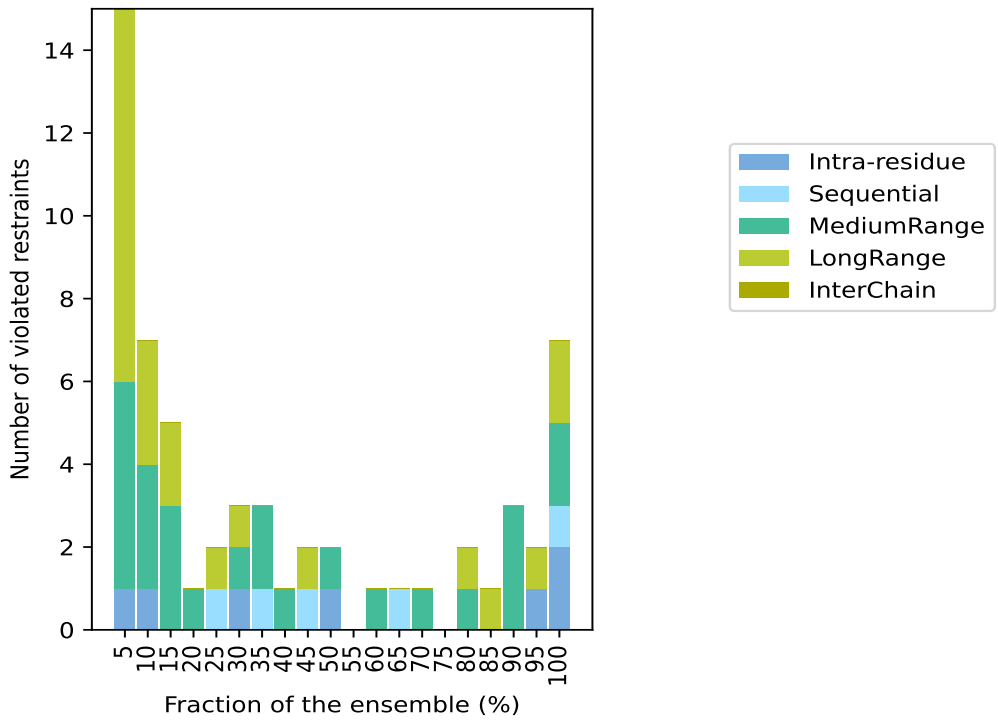
9.3 Distance violation statistics for the ensemble (i)

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, 1500(IR:192, SQ:332, MR:383, LR:593, 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]	%
1	0	5	9	0	15	1	5.0
1	0	3	3	0	7	2	10.0
0	0	3	2	0	5	3	15.0
0	0	1	0	0	1	4	20.0
0	1	0	1	0	2	5	25.0
1	0	1	1	0	3	6	30.0
0	1	2	0	0	3	7	35.0
0	0	1	0	0	1	8	40.0
0	1	0	1	0	2	9	45.0
1	0	1	0	0	2	10	50.0
0	0	0	0	0	0	11	55.0
0	0	1	0	0	1	12	60.0
0	1	0	0	0	1	13	65.0
0	0	1	0	0	1	14	70.0
0	0	0	0	0	0	15	75.0
0	0	1	1	0	2	16	80.0
0	0	0	1	0	1	17	85.0
0	0	3	0	0	3	18	90.0
1	0	0	1	0	2	19	95.0
2	1	2	2	0	7	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

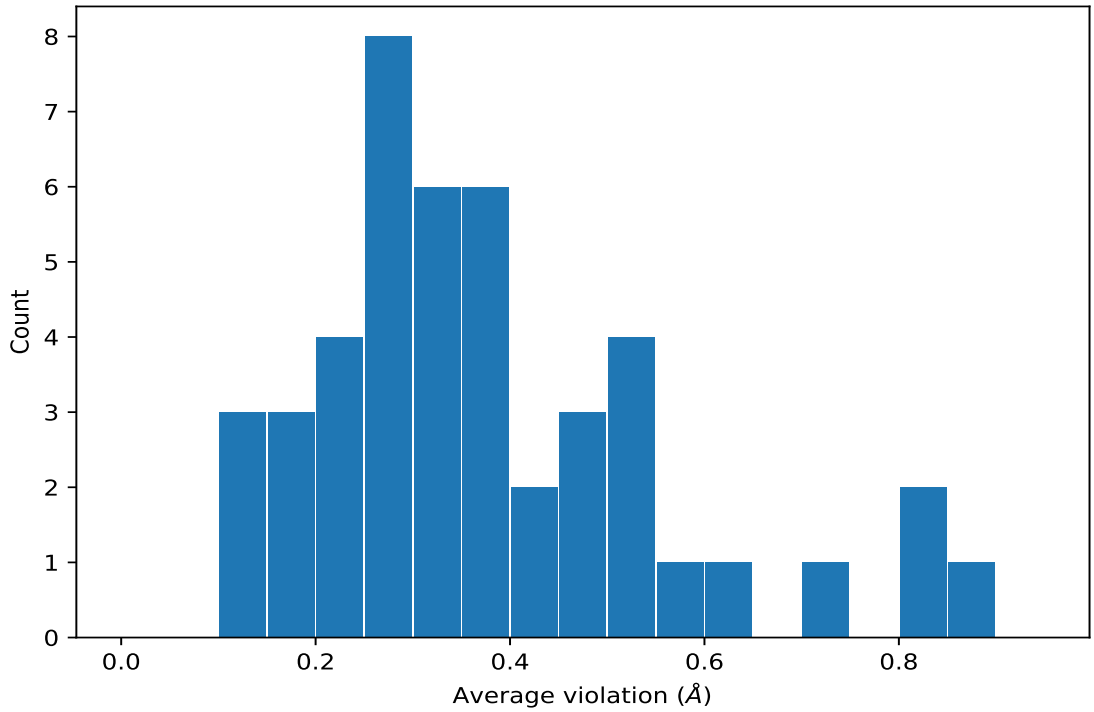
9.3.1 Bar graph : Distance violation statistics for the ensemble (i)



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)
(1,692)	1:A:67:GLY:H	1:A:76:ALA:HA	20	0.89	0.05	0.89
(2,325)	1:A:40:LEU:H	1:A:40:LEU:HG	20	0.51	0.03	0.51
(2,202)	1:A:60:LEU:H	1:A:63:THR:HB	20	0.5	0.13	0.52
(2,233)	1:A:71:GLN:H	1:A:72:ALA:HA	20	0.36	0.05	0.36
(1,694)	1:A:87:LEU:H	1:A:90:PHE:HA	20	0.35	0.11	0.34
(1,691)	1:A:66:THR:H	1:A:76:ALA:HA	20	0.35	0.1	0.34
(2,33)	1:A:65:LEU:HA	1:A:65:LEU:HG	20	0.31	0.02	0.3
(2,262)	1:A:78:LEU:HA	1:A:83:ASN:H	19	0.47	0.15	0.48
(2,336)	1:A:61:LEU:H	1:A:61:LEU:HG	19	0.33	0.09	0.32
(2,110)	1:A:26:GLN:H	1:A:30:GLU:H	18	0.54	0.12	0.57
(2,244)	1:A:74:TYR:HA	1:A:76:ALA:H	18	0.43	0.16	0.43
(2,181)	1:A:53:PHE:H	1:A:55:GLN:H	18	0.26	0.08	0.26
(2,267)	1:A:49:GLU:HA	1:A:86:ARG:H	17	0.59	0.2	0.6
(2,347)	1:A:37:TRP:HE3	1:A:87:LEU:H	16	0.39	0.11	0.38
(2,255)	1:A:78:LEU:HA	1:A:80:ASP:H	16	0.25	0.08	0.26
(2,225)	1:A:66:THR:HB	1:A:69:LEU:H	14	0.2	0.07	0.18

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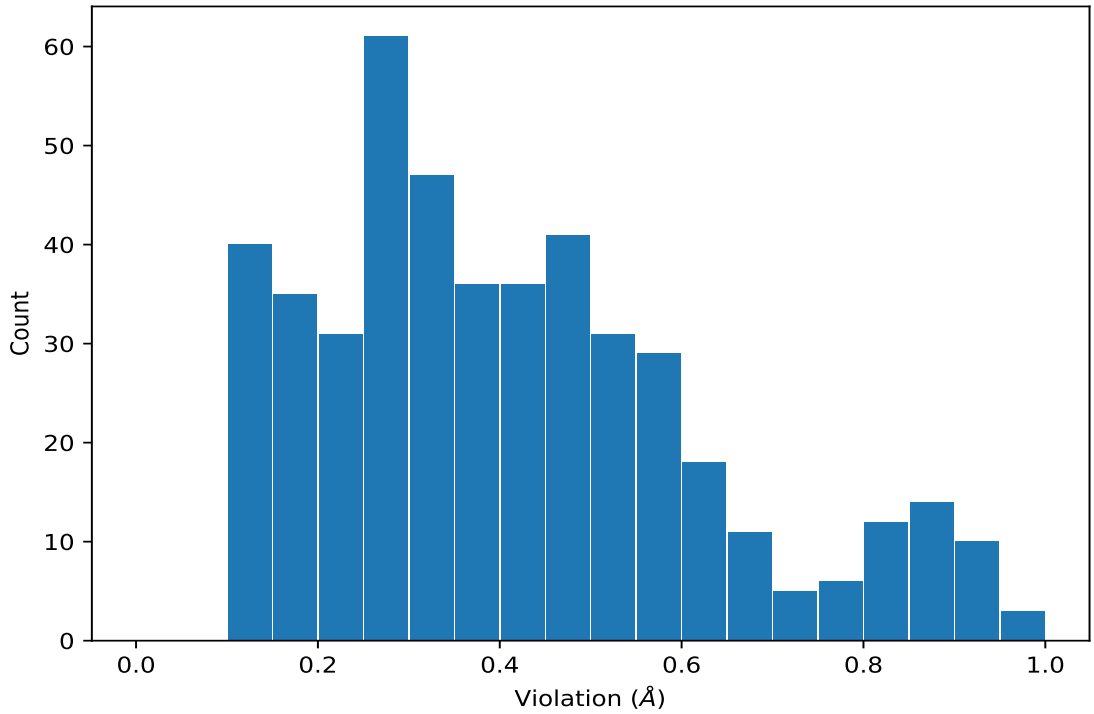
Key	Atom-1	Atom-2	Models[1]	Mean (Å)	SD[1] (Å)	Median (Å)
(1,485)	1:A:70:HIS:HD2	1:A:71:GLN:HG2	13	0.83	0.07	0.84
(2,231)	1:A:69:LEU:HA	1:A:71:GLN:H	12	0.29	0.1	0.29
(2,308)	1:A:97:THR:HB	1:A:99:VAL:H	10	0.49	0.17	0.58
(2,317)	1:A:24:LEU:H	1:A:24:LEU:HG	10	0.45	0.04	0.46
(1,129)	1:A:70:HIS:HD2	1:A:71:GLN:HG3	9	0.72	0.25	0.8
(1,473)	1:A:25:PRO:HB2	1:A:47:THR:HB	9	0.32	0.19	0.26
(1,681)	1:A:76:ALA:HA	1:A:79:SER:H	8	0.35	0.14	0.34
(1,574)	1:A:23:ASP:H	1:A:24:LEU:HG	7	0.33	0.05	0.33
(2,191)	1:A:54:GLN:HA	1:A:57:GLY:H	7	0.25	0.09	0.29
(2,278)	1:A:89:ASP:H	1:A:92:ALA:H	7	0.23	0.06	0.23
(2,344)	1:A:81:LEU:H	1:A:81:LEU:HG	6	0.41	0.14	0.44
(1,491)	1:A:49:GLU:HG2	1:A:86:ARG:HD3	6	0.35	0.27	0.26
(2,112)	1:A:28:ASP:H	1:A:30:GLU:H	6	0.27	0.12	0.28
(2,2)	1:A:25:PRO:HA	1:A:30:GLU:HA	5	0.27	0.11	0.3
(1,128)	1:A:70:HIS:HD2	1:A:71:GLN:HA	5	0.17	0.09	0.13
(1,690)	1:A:96:LYS:HB2	1:A:98:ASP:H	4	0.52	0.12	0.5
(1,190)	1:A:51:ASP:HB2	1:A:86:ARG:HD3	3	0.61	0.07	0.63
(2,94)	1:A:22:ALA:H	1:A:24:LEU:H	3	0.29	0.16	0.18
(2,333)	1:A:52:PHE:HZ	1:A:58:ASP:H	3	0.2	0.02	0.2
(2,193)	1:A:55:GLN:HA	1:A:57:GLY:H	3	0.17	0.04	0.19
(2,229)	1:A:66:THR:HB	1:A:70:HIS:H	3	0.14	0.02	0.14
(1,177)	1:A:80:ASP:HB2	1:A:84:HIS:HD2	2	0.84	0.05	0.84
(1,490)	1:A:51:ASP:HB2	1:A:86:ARG:HD2	2	0.31	0.14	0.31
(1,66)	1:A:51:ASP:HB3	1:A:86:ARG:HD2	2	0.3	0.16	0.3
(2,82)	1:A:105:PHE:HA	1:A:105:PHE:HZ	2	0.29	0.01	0.29
(2,275)	1:A:86:ARG:H	1:A:89:ASP:H	2	0.2	0.09	0.2
(2,272)	1:A:49:GLU:HA	1:A:88:ALA:H	2	0.18	0.06	0.18
(2,630)	1:A:86:ARG:HG2	1:A:88:ALA:H	2	0.14	0.02	0.14
(2,630)	1:A:86:ARG:HG3	1:A:88:ALA:H	2	0.14	0.02	0.14

[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)
(1,129)	1:A:70:HIS:HD2	1:A:71:GLN:HG3	1	1.0
(1,692)	1:A:67:GLY:H	1:A:76:ALA:HA	7	0.98
(1,692)	1:A:67:GLY:H	1:A:76:ALA:HA	1	0.97
(2,267)	1:A:49:GLU:HA	1:A:86:ARG:H	7	0.95
(1,692)	1:A:67:GLY:H	1:A:76:ALA:HA	9	0.95
(2,267)	1:A:49:GLU:HA	1:A:86:ARG:H	19	0.93
(1,692)	1:A:67:GLY:H	1:A:76:ALA:HA	12	0.92
(1,692)	1:A:67:GLY:H	1:A:76:ALA:HA	15	0.92
(1,692)	1:A:67:GLY:H	1:A:76:ALA:HA	17	0.92
(1,692)	1:A:67:GLY:H	1:A:76:ALA:HA	14	0.91
(1,485)	1:A:70:HIS:HD2	1:A:71:GLN:HG2	18	0.91
(1,485)	1:A:70:HIS:HD2	1:A:71:GLN:HG2	19	0.91
(1,692)	1:A:67:GLY:H	1:A:76:ALA:HA	2	0.9
(1,692)	1:A:67:GLY:H	1:A:76:ALA:HA	16	0.89
(1,692)	1:A:67:GLY:H	1:A:76:ALA:HA	18	0.89
(1,692)	1:A:67:GLY:H	1:A:76:ALA:HA	19	0.89

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,491)	1:A:49:GLU:HG2	1:A:86:ARG:HD3	20	0.89
(1,485)	1:A:70:HIS:HD2	1:A:71:GLN:HG2	8	0.89
(1,177)	1:A:80:ASP:HB2	1:A:84:HIS:HD2	17	0.89
(1,129)	1:A:70:HIS:HD2	1:A:71:GLN:HG3	12	0.89
(1,692)	1:A:67:GLY:H	1:A:76:ALA:HA	6	0.88
(1,692)	1:A:67:GLY:H	1:A:76:ALA:HA	10	0.88
(1,485)	1:A:70:HIS:HD2	1:A:71:GLN:HG2	17	0.88
(1,692)	1:A:67:GLY:H	1:A:76:ALA:HA	5	0.87
(1,485)	1:A:70:HIS:HD2	1:A:71:GLN:HG2	20	0.87
(1,692)	1:A:67:GLY:H	1:A:76:ALA:HA	11	0.86
(1,485)	1:A:70:HIS:HD2	1:A:71:GLN:HG2	11	0.86
(1,692)	1:A:67:GLY:H	1:A:76:ALA:HA	20	0.85
(1,692)	1:A:67:GLY:H	1:A:76:ALA:HA	3	0.84
(1,485)	1:A:70:HIS:HD2	1:A:71:GLN:HG2	3	0.84
(1,485)	1:A:70:HIS:HD2	1:A:71:GLN:HG2	5	0.84
(1,129)	1:A:70:HIS:HD2	1:A:71:GLN:HG3	10	0.84
(1,692)	1:A:67:GLY:H	1:A:76:ALA:HA	13	0.82
(2,267)	1:A:49:GLU:HA	1:A:86:ARG:H	1	0.81
(1,692)	1:A:67:GLY:H	1:A:76:ALA:HA	4	0.81
(1,485)	1:A:70:HIS:HD2	1:A:71:GLN:HG2	7	0.81
(1,129)	1:A:70:HIS:HD2	1:A:71:GLN:HG3	9	0.81
(1,692)	1:A:67:GLY:H	1:A:76:ALA:HA	8	0.8
(1,129)	1:A:70:HIS:HD2	1:A:71:GLN:HG3	4	0.8
(1,177)	1:A:80:ASP:HB2	1:A:84:HIS:HD2	11	0.79
(1,129)	1:A:70:HIS:HD2	1:A:71:GLN:HG3	16	0.79
(2,244)	1:A:74:TYR:HA	1:A:76:ALA:H	9	0.76
(1,485)	1:A:70:HIS:HD2	1:A:71:GLN:HG2	13	0.76
(1,129)	1:A:70:HIS:HD2	1:A:71:GLN:HG3	15	0.76
(1,160)	1:A:80:ASP:HA	1:A:84:HIS:HE1	13	0.75
(1,485)	1:A:70:HIS:HD2	1:A:71:GLN:HG2	6	0.74
(1,485)	1:A:70:HIS:HD2	1:A:71:GLN:HG2	2	0.73
(1,485)	1:A:70:HIS:HD2	1:A:71:GLN:HG2	14	0.73
(1,163)	1:A:80:ASP:HB3	1:A:84:HIS:HD2	17	0.73
(2,267)	1:A:49:GLU:HA	1:A:86:ARG:H	18	0.72
(2,267)	1:A:49:GLU:HA	1:A:86:ARG:H	4	0.7
(1,690)	1:A:96:LYS:HB2	1:A:98:ASP:H	8	0.69
(1,190)	1:A:51:ASP:HB2	1:A:86:ARG:HD3	14	0.69
(1,473)	1:A:25:PRO:HB2	1:A:47:THR:HB	16	0.68
(2,262)	1:A:78:LEU:HA	1:A:83:ASN:H	8	0.67
(2,262)	1:A:78:LEU:HA	1:A:83:ASN:H	14	0.66
(2,244)	1:A:74:TYR:HA	1:A:76:ALA:H	16	0.66
(2,202)	1:A:60:LEU:H	1:A:63:THR:HB	10	0.66

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,694)	1:A:87:LEU:H	1:A:90:PHE:HA	3	0.66
(2,267)	1:A:49:GLU:HA	1:A:86:ARG:H	9	0.65
(2,262)	1:A:78:LEU:HA	1:A:83:ASN:H	17	0.65
(2,262)	1:A:78:LEU:HA	1:A:83:ASN:H	15	0.64
(2,110)	1:A:26:GLN:H	1:A:30:GLU:H	3	0.64
(2,110)	1:A:26:GLN:H	1:A:30:GLU:H	5	0.64
(2,110)	1:A:26:GLN:H	1:A:30:GLU:H	20	0.64
(1,473)	1:A:25:PRO:HB2	1:A:47:THR:HB	17	0.64
(2,308)	1:A:97:THR:HB	1:A:99:VAL:H	20	0.63
(2,202)	1:A:60:LEU:H	1:A:63:THR:HB	6	0.63
(2,202)	1:A:60:LEU:H	1:A:63:THR:HB	7	0.63
(2,202)	1:A:60:LEU:H	1:A:63:THR:HB	20	0.63
(2,110)	1:A:26:GLN:H	1:A:30:GLU:H	10	0.63
(2,110)	1:A:26:GLN:H	1:A:30:GLU:H	14	0.63
(1,190)	1:A:51:ASP:HB2	1:A:86:ARG:HD3	15	0.63
(2,308)	1:A:97:THR:HB	1:A:99:VAL:H	16	0.62
(2,244)	1:A:74:TYR:HA	1:A:76:ALA:H	19	0.62
(2,110)	1:A:26:GLN:H	1:A:30:GLU:H	7	0.62
(2,308)	1:A:97:THR:HB	1:A:99:VAL:H	8	0.61
(2,308)	1:A:97:THR:HB	1:A:99:VAL:H	10	0.61
(2,267)	1:A:49:GLU:HA	1:A:86:ARG:H	14	0.61
(2,267)	1:A:49:GLU:HA	1:A:86:ARG:H	2	0.6
(2,267)	1:A:49:GLU:HA	1:A:86:ARG:H	12	0.6
(2,202)	1:A:60:LEU:H	1:A:63:THR:HB	4	0.6
(2,110)	1:A:26:GLN:H	1:A:30:GLU:H	8	0.6
(2,110)	1:A:26:GLN:H	1:A:30:GLU:H	12	0.6
(2,347)	1:A:37:TRP:HE3	1:A:87:LEU:H	7	0.59
(2,344)	1:A:81:LEU:H	1:A:81:LEU:HG	19	0.59
(2,267)	1:A:49:GLU:HA	1:A:86:ARG:H	17	0.59
(2,262)	1:A:78:LEU:HA	1:A:83:ASN:H	1	0.59
(2,37)	1:A:80:ASP:HA	1:A:84:HIS:HD2	17	0.58
(2,325)	1:A:40:LEU:H	1:A:40:LEU:HG	18	0.58
(2,308)	1:A:97:THR:HB	1:A:99:VAL:H	4	0.58
(2,308)	1:A:97:THR:HB	1:A:99:VAL:H	12	0.58
(2,267)	1:A:49:GLU:HA	1:A:86:ARG:H	20	0.58
(2,202)	1:A:60:LEU:H	1:A:63:THR:HB	15	0.58
(1,681)	1:A:76:ALA:HA	1:A:79:SER:H	19	0.58
(2,325)	1:A:40:LEU:H	1:A:40:LEU:HG	19	0.57
(2,262)	1:A:78:LEU:HA	1:A:83:ASN:H	9	0.57
(2,202)	1:A:60:LEU:H	1:A:63:THR:HB	5	0.57
(2,110)	1:A:26:GLN:H	1:A:30:GLU:H	1	0.57
(2,110)	1:A:26:GLN:H	1:A:30:GLU:H	16	0.57

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,474)	1:A:49:GLU:HG2	1:A:86:ARG:HD2	15	0.57
(2,262)	1:A:78:LEU:HA	1:A:83:ASN:H	13	0.56
(2,244)	1:A:74:TYR:HA	1:A:76:ALA:H	11	0.56
(2,202)	1:A:60:LEU:H	1:A:63:THR:HB	1	0.56
(2,110)	1:A:26:GLN:H	1:A:30:GLU:H	6	0.56
(2,110)	1:A:26:GLN:H	1:A:30:GLU:H	9	0.56
(2,110)	1:A:26:GLN:H	1:A:30:GLU:H	4	0.55
(1,690)	1:A:96:LYS:HB2	1:A:98:ASP:H	10	0.55
(2,347)	1:A:37:TRP:HE3	1:A:87:LEU:H	13	0.54
(2,325)	1:A:40:LEU:H	1:A:40:LEU:HG	3	0.54
(2,325)	1:A:40:LEU:H	1:A:40:LEU:HG	1	0.53
(2,202)	1:A:60:LEU:H	1:A:63:THR:HB	8	0.53
(2,202)	1:A:60:LEU:H	1:A:63:THR:HB	18	0.53
(2,347)	1:A:37:TRP:HE3	1:A:87:LEU:H	6	0.52
(2,344)	1:A:81:LEU:H	1:A:81:LEU:HG	3	0.52
(2,325)	1:A:40:LEU:H	1:A:40:LEU:HG	12	0.52
(2,325)	1:A:40:LEU:H	1:A:40:LEU:HG	17	0.52
(2,262)	1:A:78:LEU:HA	1:A:83:ASN:H	3	0.52
(2,202)	1:A:60:LEU:H	1:A:63:THR:HB	12	0.52
(2,202)	1:A:60:LEU:H	1:A:63:THR:HB	19	0.52
(2,110)	1:A:26:GLN:H	1:A:30:GLU:H	13	0.52
(1,691)	1:A:66:THR:H	1:A:76:ALA:HA	15	0.52
(1,691)	1:A:66:THR:H	1:A:76:ALA:HA	18	0.52
(2,94)	1:A:22:ALA:H	1:A:24:LEU:H	4	0.51
(2,325)	1:A:40:LEU:H	1:A:40:LEU:HG	4	0.51
(2,325)	1:A:40:LEU:H	1:A:40:LEU:HG	6	0.51
(2,325)	1:A:40:LEU:H	1:A:40:LEU:HG	7	0.51
(2,325)	1:A:40:LEU:H	1:A:40:LEU:HG	14	0.51
(2,325)	1:A:40:LEU:H	1:A:40:LEU:HG	16	0.51
(2,262)	1:A:78:LEU:HA	1:A:83:ASN:H	19	0.51
(2,202)	1:A:60:LEU:H	1:A:63:THR:HB	16	0.51
(1,681)	1:A:76:ALA:HA	1:A:79:SER:H	3	0.51
(1,190)	1:A:51:ASP:HB2	1:A:86:ARG:HD3	12	0.51
(2,347)	1:A:37:TRP:HE3	1:A:87:LEU:H	8	0.5
(2,325)	1:A:40:LEU:H	1:A:40:LEU:HG	5	0.5
(2,325)	1:A:40:LEU:H	1:A:40:LEU:HG	8	0.5
(2,325)	1:A:40:LEU:H	1:A:40:LEU:HG	10	0.5
(2,244)	1:A:74:TYR:HA	1:A:76:ALA:H	8	0.5
(2,202)	1:A:60:LEU:H	1:A:63:THR:HB	13	0.5
(2,325)	1:A:40:LEU:H	1:A:40:LEU:HG	13	0.49
(2,317)	1:A:24:LEU:H	1:A:24:LEU:HG	20	0.49
(2,267)	1:A:49:GLU:HA	1:A:86:ARG:H	13	0.49

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,244)	1:A:74:TYR:HA	1:A:76:ALA:H	14	0.49
(2,244)	1:A:74:TYR:HA	1:A:76:ALA:H	18	0.49
(1,126)	1:A:66:THR:HA	1:A:70:HIS:HE1	4	0.49
(2,347)	1:A:37:TRP:HE3	1:A:87:LEU:H	4	0.48
(2,325)	1:A:40:LEU:H	1:A:40:LEU:HG	9	0.48
(2,325)	1:A:40:LEU:H	1:A:40:LEU:HG	11	0.48
(2,317)	1:A:24:LEU:H	1:A:24:LEU:HG	19	0.48
(2,308)	1:A:97:THR:HB	1:A:99:VAL:H	3	0.48
(2,308)	1:A:97:THR:HB	1:A:99:VAL:H	13	0.48
(2,262)	1:A:78:LEU:HA	1:A:83:ASN:H	5	0.48
(2,244)	1:A:74:TYR:HA	1:A:76:ALA:H	5	0.48
(2,325)	1:A:40:LEU:H	1:A:40:LEU:HG	20	0.47
(2,317)	1:A:24:LEU:H	1:A:24:LEU:HG	9	0.47
(2,317)	1:A:24:LEU:H	1:A:24:LEU:HG	13	0.47
(2,317)	1:A:24:LEU:H	1:A:24:LEU:HG	16	0.47
(2,336)	1:A:61:LEU:H	1:A:61:LEU:HG	15	0.46
(2,325)	1:A:40:LEU:H	1:A:40:LEU:HG	15	0.46
(2,267)	1:A:49:GLU:HA	1:A:86:ARG:H	11	0.46
(2,262)	1:A:78:LEU:HA	1:A:83:ASN:H	18	0.46
(2,110)	1:A:26:GLN:H	1:A:30:GLU:H	18	0.46
(1,694)	1:A:87:LEU:H	1:A:90:PHE:HA	11	0.46
(1,694)	1:A:87:LEU:H	1:A:90:PHE:HA	15	0.46
(1,691)	1:A:66:THR:H	1:A:76:ALA:HA	8	0.46
(1,691)	1:A:66:THR:H	1:A:76:ALA:HA	13	0.46
(1,66)	1:A:51:ASP:HB3	1:A:86:ARG:HD2	7	0.46
(2,347)	1:A:37:TRP:HE3	1:A:87:LEU:H	19	0.45
(2,344)	1:A:81:LEU:H	1:A:81:LEU:HG	4	0.45
(2,336)	1:A:61:LEU:H	1:A:61:LEU:HG	10	0.45
(2,325)	1:A:40:LEU:H	1:A:40:LEU:HG	2	0.45
(2,317)	1:A:24:LEU:H	1:A:24:LEU:HG	5	0.45
(2,317)	1:A:24:LEU:H	1:A:24:LEU:HG	8	0.45
(2,262)	1:A:78:LEU:HA	1:A:83:ASN:H	20	0.45
(2,233)	1:A:71:GLN:H	1:A:72:ALA:HA	16	0.45
(2,202)	1:A:60:LEU:H	1:A:63:THR:HB	11	0.45
(1,694)	1:A:87:LEU:H	1:A:90:PHE:HA	17	0.45
(1,690)	1:A:96:LYS:HB2	1:A:98:ASP:H	3	0.45
(1,491)	1:A:49:GLU:HG2	1:A:86:ARG:HD3	9	0.45
(1,490)	1:A:51:ASP:HB2	1:A:86:ARG:HD2	7	0.45
(2,336)	1:A:61:LEU:H	1:A:61:LEU:HG	1	0.44
(2,317)	1:A:24:LEU:H	1:A:24:LEU:HG	1	0.44
(2,244)	1:A:74:TYR:HA	1:A:76:ALA:H	7	0.44
(2,202)	1:A:60:LEU:H	1:A:63:THR:HB	3	0.44

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,344)	1:A:81:LEU:H	1:A:81:LEU:HG	13	0.43
(2,336)	1:A:61:LEU:H	1:A:61:LEU:HG	18	0.43
(2,233)	1:A:71:GLN:H	1:A:72:ALA:HA	10	0.43
(2,233)	1:A:71:GLN:H	1:A:72:ALA:HA	12	0.43
(1,691)	1:A:66:THR:H	1:A:76:ALA:HA	20	0.43
(1,207)	1:A:80:ASP:HB2	1:A:93:THR:HB	2	0.43
(2,347)	1:A:37:TRP:HE3	1:A:87:LEU:H	9	0.42
(2,244)	1:A:74:TYR:HA	1:A:76:ALA:H	12	0.42
(2,233)	1:A:71:GLN:H	1:A:72:ALA:HA	9	0.42
(2,202)	1:A:60:LEU:H	1:A:63:THR:HB	2	0.42
(2,202)	1:A:60:LEU:H	1:A:63:THR:HB	17	0.42
(2,2)	1:A:25:PRO:HA	1:A:30:GLU:HA	19	0.42
(1,694)	1:A:87:LEU:H	1:A:90:PHE:HA	19	0.42
(1,691)	1:A:66:THR:H	1:A:76:ALA:HA	6	0.42
(1,691)	1:A:66:THR:H	1:A:76:ALA:HA	17	0.42
(2,336)	1:A:61:LEU:H	1:A:61:LEU:HG	5	0.41
(2,336)	1:A:61:LEU:H	1:A:61:LEU:HG	9	0.41
(2,267)	1:A:49:GLU:HA	1:A:86:ARG:H	10	0.41
(2,244)	1:A:74:TYR:HA	1:A:76:ALA:H	20	0.41
(2,231)	1:A:69:LEU:HA	1:A:71:GLN:H	4	0.41
(2,231)	1:A:69:LEU:HA	1:A:71:GLN:H	12	0.41
(2,231)	1:A:69:LEU:HA	1:A:71:GLN:H	16	0.41
(2,112)	1:A:28:ASP:H	1:A:30:GLU:H	13	0.41
(1,691)	1:A:66:THR:H	1:A:76:ALA:HA	4	0.41
(1,574)	1:A:23:ASP:H	1:A:24:LEU:HG	16	0.41
(2,336)	1:A:61:LEU:H	1:A:61:LEU:HG	16	0.4
(2,181)	1:A:53:PHE:H	1:A:55:GLN:H	4	0.4
(2,181)	1:A:53:PHE:H	1:A:55:GLN:H	19	0.4
(2,112)	1:A:28:ASP:H	1:A:30:GLU:H	17	0.4
(1,694)	1:A:87:LEU:H	1:A:90:PHE:HA	4	0.4
(1,694)	1:A:87:LEU:H	1:A:90:PHE:HA	5	0.4
(1,681)	1:A:76:ALA:HA	1:A:79:SER:H	5	0.4
(2,347)	1:A:37:TRP:HE3	1:A:87:LEU:H	12	0.39
(2,317)	1:A:24:LEU:H	1:A:24:LEU:HG	14	0.39
(2,262)	1:A:78:LEU:HA	1:A:83:ASN:H	12	0.39
(2,244)	1:A:74:TYR:HA	1:A:76:ALA:H	2	0.39
(2,233)	1:A:71:GLN:H	1:A:72:ALA:HA	18	0.39
(2,225)	1:A:66:THR:HB	1:A:69:LEU:H	5	0.39
(1,694)	1:A:87:LEU:H	1:A:90:PHE:HA	12	0.39
(1,129)	1:A:70:HIS:HD2	1:A:71:GLN:HG3	17	0.39
(2,347)	1:A:37:TRP:HE3	1:A:87:LEU:H	3	0.38
(2,262)	1:A:78:LEU:HA	1:A:83:ASN:H	6	0.38

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,262)	1:A:78:LEU:HA	1:A:83:ASN:H	16	0.38
(2,233)	1:A:71:GLN:H	1:A:72:ALA:HA	15	0.38
(2,231)	1:A:69:LEU:HA	1:A:71:GLN:H	15	0.38
(2,110)	1:A:26:GLN:H	1:A:30:GLU:H	19	0.38
(1,694)	1:A:87:LEU:H	1:A:90:PHE:HA	1	0.38
(1,690)	1:A:96:LYS:HB2	1:A:98:ASP:H	4	0.38
(2,7)	1:A:48:ARG:HA	1:A:87:LEU:HA	3	0.37
(2,255)	1:A:78:LEU:HA	1:A:80:ASP:H	17	0.37
(2,233)	1:A:71:GLN:H	1:A:72:ALA:HA	1	0.37
(2,233)	1:A:71:GLN:H	1:A:72:ALA:HA	11	0.37
(2,233)	1:A:71:GLN:H	1:A:72:ALA:HA	14	0.37
(2,233)	1:A:71:GLN:H	1:A:72:ALA:HA	17	0.37
(2,112)	1:A:28:ASP:H	1:A:30:GLU:H	18	0.37
(1,681)	1:A:76:ALA:HA	1:A:79:SER:H	20	0.37
(1,574)	1:A:23:ASP:H	1:A:24:LEU:HG	5	0.37
(2,347)	1:A:37:TRP:HE3	1:A:87:LEU:H	17	0.36
(2,267)	1:A:49:GLU:HA	1:A:86:ARG:H	3	0.36
(2,267)	1:A:49:GLU:HA	1:A:86:ARG:H	16	0.36
(2,233)	1:A:71:GLN:H	1:A:72:ALA:HA	7	0.36
(2,233)	1:A:71:GLN:H	1:A:72:ALA:HA	8	0.36
(2,2)	1:A:25:PRO:HA	1:A:30:GLU:HA	10	0.36
(2,191)	1:A:54:GLN:HA	1:A:57:GLY:H	15	0.36
(2,181)	1:A:53:PHE:H	1:A:55:GLN:H	5	0.36
(1,694)	1:A:87:LEU:H	1:A:90:PHE:HA	6	0.36
(1,691)	1:A:66:THR:H	1:A:76:ALA:HA	5	0.36
(1,574)	1:A:23:ASP:H	1:A:24:LEU:HG	20	0.36
(2,336)	1:A:61:LEU:H	1:A:61:LEU:HG	7	0.35
(2,317)	1:A:24:LEU:H	1:A:24:LEU:HG	10	0.35
(2,255)	1:A:78:LEU:HA	1:A:80:ASP:H	11	0.35
(2,233)	1:A:71:GLN:H	1:A:72:ALA:HA	3	0.35
(2,233)	1:A:71:GLN:H	1:A:72:ALA:HA	4	0.35
(2,233)	1:A:71:GLN:H	1:A:72:ALA:HA	5	0.35
(2,233)	1:A:71:GLN:H	1:A:72:ALA:HA	20	0.35
(2,191)	1:A:54:GLN:HA	1:A:57:GLY:H	4	0.35
(2,181)	1:A:53:PHE:H	1:A:55:GLN:H	14	0.35
(2,181)	1:A:53:PHE:H	1:A:55:GLN:H	20	0.35
(1,128)	1:A:70:HIS:HD2	1:A:71:GLN:HA	4	0.35
(2,255)	1:A:78:LEU:HA	1:A:80:ASP:H	1	0.34
(2,244)	1:A:74:TYR:HA	1:A:76:ALA:H	3	0.34
(2,233)	1:A:71:GLN:H	1:A:72:ALA:HA	2	0.34
(2,231)	1:A:69:LEU:HA	1:A:71:GLN:H	7	0.34
(1,691)	1:A:66:THR:H	1:A:76:ALA:HA	7	0.34

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,691)	1:A:66:THR:H	1:A:76:ALA:HA	19	0.34
(2,347)	1:A:37:TRP:HE3	1:A:87:LEU:H	20	0.33
(2,33)	1:A:65:LEU:HA	1:A:65:LEU:HG	1	0.33
(2,33)	1:A:65:LEU:HA	1:A:65:LEU:HG	2	0.33
(2,33)	1:A:65:LEU:HA	1:A:65:LEU:HG	3	0.33
(2,33)	1:A:65:LEU:HA	1:A:65:LEU:HG	14	0.33
(2,278)	1:A:89:ASP:H	1:A:92:ALA:H	20	0.33
(2,262)	1:A:78:LEU:HA	1:A:83:ASN:H	10	0.33
(2,233)	1:A:71:GLN:H	1:A:72:ALA:HA	19	0.33
(1,694)	1:A:87:LEU:H	1:A:90:PHE:HA	9	0.33
(1,694)	1:A:87:LEU:H	1:A:90:PHE:HA	20	0.33
(1,691)	1:A:66:THR:H	1:A:76:ALA:HA	3	0.33
(1,691)	1:A:66:THR:H	1:A:76:ALA:HA	12	0.33
(1,574)	1:A:23:ASP:H	1:A:24:LEU:HG	8	0.33
(2,336)	1:A:61:LEU:H	1:A:61:LEU:HG	3	0.32
(2,336)	1:A:61:LEU:H	1:A:61:LEU:HG	19	0.32
(2,33)	1:A:65:LEU:HA	1:A:65:LEU:HG	7	0.32
(2,233)	1:A:71:GLN:H	1:A:72:ALA:HA	6	0.32
(2,181)	1:A:53:PHE:H	1:A:55:GLN:H	9	0.32
(1,681)	1:A:76:ALA:HA	1:A:79:SER:H	17	0.32
(1,37)	1:A:37:TRP:HE3	1:A:86:ARG:HA	7	0.32
(2,336)	1:A:61:LEU:H	1:A:61:LEU:HG	17	0.31
(2,33)	1:A:65:LEU:HA	1:A:65:LEU:HG	6	0.31
(2,33)	1:A:65:LEU:HA	1:A:65:LEU:HG	8	0.31
(2,33)	1:A:65:LEU:HA	1:A:65:LEU:HG	11	0.31
(2,33)	1:A:65:LEU:HA	1:A:65:LEU:HG	12	0.31
(2,33)	1:A:65:LEU:HA	1:A:65:LEU:HG	18	0.31
(2,255)	1:A:78:LEU:HA	1:A:80:ASP:H	20	0.31
(2,244)	1:A:74:TYR:HA	1:A:76:ALA:H	15	0.31
(1,694)	1:A:87:LEU:H	1:A:90:PHE:HA	16	0.31
(1,574)	1:A:23:ASP:H	1:A:24:LEU:HG	9	0.31
(2,82)	1:A:105:PHE:HA	1:A:105:PHE:HZ	6	0.3
(2,347)	1:A:37:TRP:HE3	1:A:87:LEU:H	14	0.3
(2,344)	1:A:81:LEU:H	1:A:81:LEU:HG	5	0.3
(2,33)	1:A:65:LEU:HA	1:A:65:LEU:HG	9	0.3
(2,33)	1:A:65:LEU:HA	1:A:65:LEU:HG	10	0.3
(2,33)	1:A:65:LEU:HA	1:A:65:LEU:HG	15	0.3
(2,33)	1:A:65:LEU:HA	1:A:65:LEU:HG	16	0.3
(2,33)	1:A:65:LEU:HA	1:A:65:LEU:HG	17	0.3
(2,262)	1:A:78:LEU:HA	1:A:83:ASN:H	2	0.3
(2,231)	1:A:69:LEU:HA	1:A:71:GLN:H	14	0.3
(2,2)	1:A:25:PRO:HA	1:A:30:GLU:HA	20	0.3

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,181)	1:A:53:PHE:H	1:A:55:GLN:H	2	0.3
(1,691)	1:A:66:THR:H	1:A:76:ALA:HA	2	0.3
(1,681)	1:A:76:ALA:HA	1:A:79:SER:H	1	0.3
(2,347)	1:A:37:TRP:HE3	1:A:87:LEU:H	15	0.29
(2,336)	1:A:61:LEU:H	1:A:61:LEU:HG	13	0.29
(2,33)	1:A:65:LEU:HA	1:A:65:LEU:HG	4	0.29
(2,33)	1:A:65:LEU:HA	1:A:65:LEU:HG	13	0.29
(2,33)	1:A:65:LEU:HA	1:A:65:LEU:HG	20	0.29
(2,255)	1:A:78:LEU:HA	1:A:80:ASP:H	3	0.29
(2,225)	1:A:66:THR:HB	1:A:69:LEU:H	11	0.29
(2,191)	1:A:54:GLN:HA	1:A:57:GLY:H	8	0.29
(2,191)	1:A:54:GLN:HA	1:A:57:GLY:H	11	0.29
(1,694)	1:A:87:LEU:H	1:A:90:PHE:HA	2	0.29
(1,574)	1:A:23:ASP:H	1:A:24:LEU:HG	13	0.29
(1,473)	1:A:25:PRO:HB2	1:A:47:THR:HB	4	0.29
(2,82)	1:A:105:PHE:HA	1:A:105:PHE:HZ	3	0.28
(2,8)	1:A:51:ASP:HA	1:A:86:ARG:HA	14	0.28
(2,336)	1:A:61:LEU:H	1:A:61:LEU:HG	11	0.28
(2,336)	1:A:61:LEU:H	1:A:61:LEU:HG	12	0.28
(2,33)	1:A:65:LEU:HA	1:A:65:LEU:HG	5	0.28
(2,275)	1:A:86:ARG:H	1:A:89:ASP:H	7	0.28
(2,255)	1:A:78:LEU:HA	1:A:80:ASP:H	10	0.28
(2,255)	1:A:78:LEU:HA	1:A:80:ASP:H	12	0.28
(2,231)	1:A:69:LEU:HA	1:A:71:GLN:H	9	0.28
(2,181)	1:A:53:PHE:H	1:A:55:GLN:H	16	0.28
(1,694)	1:A:87:LEU:H	1:A:90:PHE:HA	13	0.28
(1,694)	1:A:87:LEU:H	1:A:90:PHE:HA	18	0.28
(1,691)	1:A:66:THR:H	1:A:76:ALA:HA	11	0.28
(1,491)	1:A:49:GLU:HG2	1:A:86:ARG:HD3	10	0.28
(2,33)	1:A:65:LEU:HA	1:A:65:LEU:HG	19	0.27
(2,278)	1:A:89:ASP:H	1:A:92:ALA:H	12	0.27
(2,255)	1:A:78:LEU:HA	1:A:80:ASP:H	6	0.27
(2,181)	1:A:53:PHE:H	1:A:55:GLN:H	12	0.27
(1,691)	1:A:66:THR:H	1:A:76:ALA:HA	1	0.27
(2,278)	1:A:89:ASP:H	1:A:92:ALA:H	17	0.26
(2,255)	1:A:78:LEU:HA	1:A:80:ASP:H	15	0.26
(2,110)	1:A:26:GLN:H	1:A:30:GLU:H	11	0.26
(1,691)	1:A:66:THR:H	1:A:76:ALA:HA	16	0.26
(1,574)	1:A:23:ASP:H	1:A:24:LEU:HG	19	0.26
(1,473)	1:A:25:PRO:HB2	1:A:47:THR:HB	2	0.26
(1,473)	1:A:25:PRO:HB2	1:A:47:THR:HB	9	0.26
(1,473)	1:A:25:PRO:HB2	1:A:47:THR:HB	11	0.26

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,347)	1:A:37:TRP:HE3	1:A:87:LEU:H	11	0.25
(2,336)	1:A:61:LEU:H	1:A:61:LEU:HG	8	0.25
(2,272)	1:A:49:GLU:HA	1:A:88:ALA:H	14	0.25
(2,231)	1:A:69:LEU:HA	1:A:71:GLN:H	10	0.25
(2,225)	1:A:66:THR:HB	1:A:69:LEU:H	3	0.25
(2,225)	1:A:66:THR:HB	1:A:69:LEU:H	19	0.25
(2,181)	1:A:53:PHE:H	1:A:55:GLN:H	10	0.25
(1,491)	1:A:49:GLU:HG2	1:A:86:ARG:HD3	6	0.25
(2,336)	1:A:61:LEU:H	1:A:61:LEU:HG	4	0.24
(2,255)	1:A:78:LEU:HA	1:A:80:ASP:H	19	0.24
(2,110)	1:A:26:GLN:H	1:A:30:GLU:H	2	0.24
(1,694)	1:A:87:LEU:H	1:A:90:PHE:HA	8	0.24
(1,694)	1:A:87:LEU:H	1:A:90:PHE:HA	10	0.24
(2,333)	1:A:52:PHE:HZ	1:A:58:ASP:H	18	0.23
(2,278)	1:A:89:ASP:H	1:A:92:ALA:H	7	0.23
(2,244)	1:A:74:TYR:HA	1:A:76:ALA:H	17	0.23
(2,225)	1:A:66:THR:HB	1:A:69:LEU:H	1	0.23
(2,191)	1:A:54:GLN:HA	1:A:57:GLY:H	12	0.23
(1,691)	1:A:66:THR:H	1:A:76:ALA:HA	14	0.23
(2,347)	1:A:37:TRP:HE3	1:A:87:LEU:H	1	0.22
(2,347)	1:A:37:TRP:HE3	1:A:87:LEU:H	5	0.22
(2,244)	1:A:74:TYR:HA	1:A:76:ALA:H	4	0.22
(2,181)	1:A:53:PHE:H	1:A:55:GLN:H	7	0.22
(1,694)	1:A:87:LEU:H	1:A:90:PHE:HA	14	0.22
(1,473)	1:A:25:PRO:HB2	1:A:47:THR:HB	20	0.22
(2,336)	1:A:61:LEU:H	1:A:61:LEU:HG	2	0.21
(2,278)	1:A:89:ASP:H	1:A:92:ALA:H	18	0.21
(2,255)	1:A:78:LEU:HA	1:A:80:ASP:H	2	0.21
(2,255)	1:A:78:LEU:HA	1:A:80:ASP:H	8	0.21
(2,244)	1:A:74:TYR:HA	1:A:76:ALA:H	6	0.21
(2,233)	1:A:71:GLN:H	1:A:72:ALA:HA	13	0.21
(2,193)	1:A:55:GLN:HA	1:A:57:GLY:H	5	0.21
(2,181)	1:A:53:PHE:H	1:A:55:GLN:H	3	0.21
(2,336)	1:A:61:LEU:H	1:A:61:LEU:HG	20	0.2
(2,333)	1:A:52:PHE:HZ	1:A:58:ASP:H	11	0.2
(2,278)	1:A:89:ASP:H	1:A:92:ALA:H	3	0.2
(2,262)	1:A:78:LEU:HA	1:A:83:ASN:H	11	0.2
(2,225)	1:A:66:THR:HB	1:A:69:LEU:H	8	0.2
(2,181)	1:A:53:PHE:H	1:A:55:GLN:H	6	0.2
(2,267)	1:A:49:GLU:HA	1:A:86:ARG:H	5	0.19
(2,231)	1:A:69:LEU:HA	1:A:71:GLN:H	1	0.19
(2,193)	1:A:55:GLN:HA	1:A:57:GLY:H	16	0.19

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,181)	1:A:53:PHE:H	1:A:55:GLN:H	15	0.19
(2,18)	1:A:76:ALA:HA	1:A:94:LEU:HA	1	0.19
(1,681)	1:A:76:ALA:HA	1:A:79:SER:H	4	0.19
(1,473)	1:A:25:PRO:HB2	1:A:47:THR:HB	15	0.19
(2,94)	1:A:22:ALA:H	1:A:24:LEU:H	3	0.18
(2,94)	1:A:22:ALA:H	1:A:24:LEU:H	6	0.18
(2,333)	1:A:52:PHE:HZ	1:A:58:ASP:H	17	0.18
(2,308)	1:A:97:THR:HB	1:A:99:VAL:H	15	0.18
(2,225)	1:A:66:THR:HB	1:A:69:LEU:H	17	0.18
(2,202)	1:A:60:LEU:H	1:A:63:THR:HB	9	0.18
(2,202)	1:A:60:LEU:H	1:A:63:THR:HB	14	0.18
(2,181)	1:A:53:PHE:H	1:A:55:GLN:H	1	0.18
(2,112)	1:A:28:ASP:H	1:A:30:GLU:H	11	0.18
(1,691)	1:A:66:THR:H	1:A:76:ALA:HA	10	0.18
(2,308)	1:A:97:THR:HB	1:A:99:VAL:H	14	0.17
(2,255)	1:A:78:LEU:HA	1:A:80:ASP:H	16	0.17
(2,231)	1:A:69:LEU:HA	1:A:71:GLN:H	5	0.17
(2,231)	1:A:69:LEU:HA	1:A:71:GLN:H	11	0.17
(2,229)	1:A:66:THR:HB	1:A:70:HIS:H	15	0.17
(2,225)	1:A:66:THR:HB	1:A:69:LEU:H	2	0.17
(2,181)	1:A:53:PHE:H	1:A:55:GLN:H	8	0.17
(2,181)	1:A:53:PHE:H	1:A:55:GLN:H	18	0.17
(2,102)	1:A:26:GLN:H	1:A:31:LYS:H	1	0.17
(1,490)	1:A:51:ASP:HB2	1:A:86:ARG:HD2	12	0.17
(2,79)	1:A:67:GLY:HA3	1:A:70:HIS:HB3	1	0.16
(2,344)	1:A:81:LEU:H	1:A:81:LEU:HG	2	0.16
(2,225)	1:A:66:THR:HB	1:A:69:LEU:H	14	0.16
(2,225)	1:A:66:THR:HB	1:A:69:LEU:H	20	0.16
(2,2)	1:A:25:PRO:HA	1:A:30:GLU:HA	3	0.16
(2,112)	1:A:28:ASP:H	1:A:30:GLU:H	1	0.16
(1,694)	1:A:87:LEU:H	1:A:90:PHE:HA	7	0.16
(1,129)	1:A:70:HIS:HD2	1:A:71:GLN:HG3	5	0.16
(2,630)	1:A:86:ARG:HG2	1:A:88:ALA:H	17	0.15
(2,630)	1:A:86:ARG:HG3	1:A:88:ALA:H	17	0.15
(2,470)	1:A:31:LYS:H	1:A:31:LYS:HD2	12	0.15
(2,470)	1:A:31:LYS:H	1:A:31:LYS:HD3	12	0.15
(2,262)	1:A:78:LEU:HA	1:A:83:ASN:H	4	0.15
(2,225)	1:A:66:THR:HB	1:A:69:LEU:H	16	0.15
(2,191)	1:A:54:GLN:HA	1:A:57:GLY:H	17	0.15
(2,181)	1:A:53:PHE:H	1:A:55:GLN:H	11	0.15
(1,673)	1:A:62:ALA:HA	1:A:67:GLY:H	14	0.15
(1,128)	1:A:70:HIS:HD2	1:A:71:GLN:HA	18	0.15

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,336)	1:A:61:LEU:H	1:A:61:LEU:HG	14	0.14
(2,278)	1:A:89:ASP:H	1:A:92:ALA:H	19	0.14
(2,255)	1:A:78:LEU:HA	1:A:80:ASP:H	7	0.14
(2,231)	1:A:69:LEU:HA	1:A:71:GLN:H	3	0.14
(2,229)	1:A:66:THR:HB	1:A:70:HIS:H	8	0.14
(2,225)	1:A:66:THR:HB	1:A:69:LEU:H	7	0.14
(2,225)	1:A:66:THR:HB	1:A:69:LEU:H	9	0.14
(1,691)	1:A:66:THR:H	1:A:76:ALA:HA	9	0.14
(1,681)	1:A:76:ALA:HA	1:A:79:SER:H	9	0.14
(2,2)	1:A:25:PRO:HA	1:A:30:GLU:HA	8	0.13
(2,112)	1:A:28:ASP:H	1:A:30:GLU:H	15	0.13
(1,66)	1:A:51:ASP:HB3	1:A:86:ARG:HD2	19	0.13
(1,128)	1:A:70:HIS:HD2	1:A:71:GLN:HA	6	0.13
(2,630)	1:A:86:ARG:HG2	1:A:88:ALA:H	6	0.12
(2,630)	1:A:86:ARG:HG3	1:A:88:ALA:H	6	0.12
(2,272)	1:A:49:GLU:HA	1:A:88:ALA:H	11	0.12
(2,255)	1:A:78:LEU:HA	1:A:80:ASP:H	4	0.12
(2,244)	1:A:74:TYR:HA	1:A:76:ALA:H	1	0.12
(2,229)	1:A:66:THR:HB	1:A:70:HIS:H	5	0.12
(2,193)	1:A:55:GLN:HA	1:A:57:GLY:H	9	0.12
(1,491)	1:A:49:GLU:HG2	1:A:86:ARG:HD3	12	0.12
(1,473)	1:A:25:PRO:HB2	1:A:47:THR:HB	12	0.12
(1,128)	1:A:70:HIS:HD2	1:A:71:GLN:HA	10	0.12
(2,275)	1:A:86:ARG:H	1:A:89:ASP:H	19	0.11
(2,255)	1:A:78:LEU:HA	1:A:80:ASP:H	18	0.11
(2,225)	1:A:66:THR:HB	1:A:69:LEU:H	12	0.11
(2,191)	1:A:54:GLN:HA	1:A:57:GLY:H	3	0.11
(1,491)	1:A:49:GLU:HG2	1:A:86:ARG:HD3	14	0.11
(1,468)	1:A:25:PRO:HB3	1:A:47:THR:HB	2	0.11
(1,128)	1:A:70:HIS:HD2	1:A:71:GLN:HA	9	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