



# Full wwPDB NMR Structure Validation Report ⓘ

Apr 16, 2025 – 10:15 AM EDT

PDB ID : 8V4B / pdb\_00008v4b  
BMRB ID : 52188  
Title : NMR structure of a synthetic analogue of Ramoplanin A2  
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Deposited on : 2023-11-28

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 2022.3.0, CSD as543be (2022)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
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) : 2.42

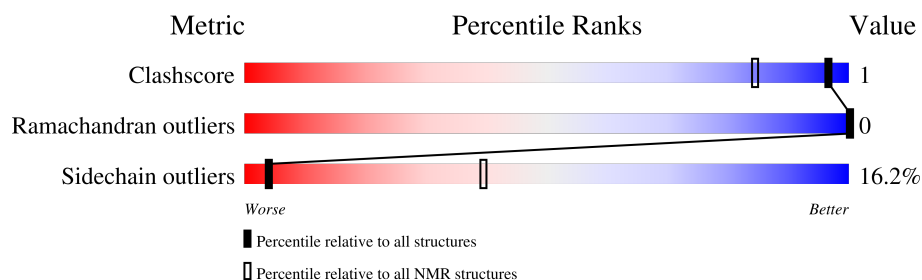
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 78%.

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



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	210492	14027
Ramachandran outliers	207382	12486
Sidechain outliers	206894	12463

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	17	<div> <div></div> <div>94%</div> <div></div> <div>6%</div> </div>

## 2 Ensemble composition and analysis ⓘ

This entry contains 20 models.

Cyrange was unable to find well-defined residues.

Error message: The number of core atoms ( 4) was below the domain threshold value ( 8).

NmrClust was unable to cluster the ensemble.

Error message: Wrapper check: not enough residues in core to run NmrClust

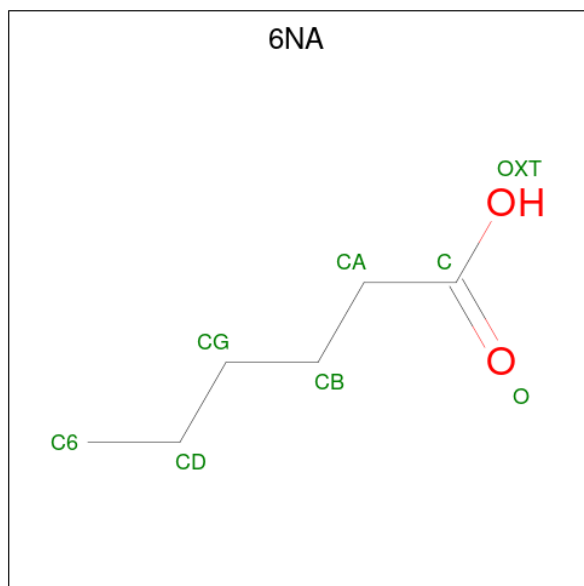
### 3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 283 atoms, of which 131 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Ramoplanin A2 synthetic analogue.

Mol	Chain	Residues	Atoms					Trace
1	A	17	Total	C	H	N	O	0
			265	97	120	21	27	

- Molecule 2 is HEXANOIC ACID (CCD ID: 6NA) (formula:  $C_6H_{12}O_2$ ).



Mol	Chain	Residues	Atoms			
2	A	1	Total	C	H	O
			18	6	11	1

## 4 Residue-property plots

### 4.1 Average score per residue in the NMR ensemble

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

- Molecule 1: Ramoplanin A2 synthetic analogue

Chain A: 



### 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: Ramoplanin A2 synthetic analogue

Chain A: 

There are no outlier residues in this chain.

#### 4.2.2 Score per residue for model 2

- Molecule 1: Ramoplanin A2 synthetic analogue

Chain A: 



#### 4.2.3 Score per residue for model 3

- Molecule 1: Ramoplanin A2 synthetic analogue

Chain A:  100%

There are no outlier residues in this chain.

#### 4.2.4 Score per residue for model 4

- Molecule 1: Ramoplanin A2 synthetic analogue

Chain A:  94% 6%



#### 4.2.5 Score per residue for model 5

- Molecule 1: Ramoplanin A2 synthetic analogue

Chain A:  94% 6%



#### 4.2.6 Score per residue for model 6

- Molecule 1: Ramoplanin A2 synthetic analogue

Chain A:  94% 6%



#### 4.2.7 Score per residue for model 7

- Molecule 1: Ramoplanin A2 synthetic analogue

Chain A:  94% 6%



#### 4.2.8 Score per residue for model 8

- Molecule 1: Ramoplanin A2 synthetic analogue

Chain A:  94% 6%



#### 4.2.9 Score per residue for model 9

- Molecule 1: Ramoplanin A2 synthetic analogue

Chain A:  94% 6%



#### 4.2.10 Score per residue for model 10

- Molecule 1: Ramoplanin A2 synthetic analogue

Chain A:  94% 6%



#### 4.2.11 Score per residue for model 11

- Molecule 1: Ramoplanin A2 synthetic analogue

Chain A:  94% 6%



#### 4.2.12 Score per residue for model 12


- Molecule 1: Ramoplanin A2 synthetic analogue

Chain A:  100%

There are no outlier residues in this chain.

#### 4.2.13 Score per residue for model 13

- Molecule 1: Ramoplanin A2 synthetic analogue

Chain A:  88% 12%



#### 4.2.14 Score per residue for model 14

- Molecule 1: Ramoplanin A2 synthetic analogue

Chain A:  94% 6%



#### 4.2.15 Score per residue for model 15

- Molecule 1: Ramoplanin A2 synthetic analogue

Chain A:  94% 6%



#### 4.2.16 Score per residue for model 16

- Molecule 1: Ramoplanin A2 synthetic analogue

Chain A:  94% 6%



#### 4.2.17 Score per residue for model 17

- Molecule 1: Ramoplanin A2 synthetic analogue

Chain A:  100%

There are no outlier residues in this chain.

#### 4.2.18 Score per residue for model 18

- Molecule 1: Ramoplanin A2 synthetic analogue




Chain A:  100%

There are no outlier residues in this chain.

#### 4.2.19 Score per residue for model 19

- Molecule 1: Ramoplanin A2 synthetic analogue

Chain A:  100%

There are no outlier residues in this chain.

#### 4.2.20 Score per residue for model 20

- Molecule 1: Ramoplanin A2 synthetic analogue

Chain A:  94% 6%



## 5 Refinement protocol and experimental data overview

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

Of the 200 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	refinement	3.97
CYANA	structure calculation	3.97

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	3
Total number of shifts	433
Number of shifts mapped to atoms	392
Number of unparsed shifts	0
Number of shifts with mapping errors	41
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	78%

## 6 Model quality

### 6.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 6NA, ORD, GHP, D4P, DTH, DPP, DAL

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

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 6.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	145	120	113	0±0
2	A	7	11	11	0±0
All	All	3040	2620	2498	4

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 1.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:17:DAL:HB3	2:A:101:6NA:H6C3	0.54	1.77	2	1
1:A:17:DAL:HB3	2:A:101:6NA:H6C2	0.52	1.82	13	1
2:A:101:6NA:H6C2	2:A:101:6NA:O	0.44	2.12	17	1
1:A:17:DAL:O	2:A:101:6NA:H6C3	0.41	2.16	7	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	4/17 (24%)	4±0 (100±0%)	0±0 (0±0%)	0±0 (0±0%)	100	100
All	All	80/340 (24%)	80 (100%)	0 (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	4/4 (100%)	3±0 (84±12%)	1±0 (16±12%)	4	39
All	All	80/80 (100%)	67 (84%)	13 (16%)	4	39

All 1 unique residues with a non-rotameric sidechain are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	2	ASN	13

### 6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

12 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types,

if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
1	D4P	A	7	1	10,11,12	1.06±0.00	0±0 (0±0%)
1	GHP	A	8	1	10,11,12	1.06±0.01	0±0 (0±0%)
1	ORD	A	5	1	6,7,8	0.48±0.01	0±0 (0±0%)
1	D4P	A	14	1	10,11,12	1.05±0.01	0±0 (0±0%)
1	D4P	A	12	1	10,11,12	1.06±0.01	0±0 (0±0%)
1	D4P	A	18	1	10,11,12	1.05±0.01	0±0 (0±0%)
1	GHP	A	4	1	10,11,12	1.06±0.01	0±0 (0±0%)
1	ORD	A	11	1	6,7,8	0.48±0.00	0±0 (0±0%)
1	DPP	A	3	1	4,5,6	0.66±0.01	0±0 (0±0%)

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

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
1	D4P	A	7	1	11,14,16	0.49±0.01	0±0 (0±0%)
1	GHP	A	8	1	11,14,16	0.49±0.01	0±0 (0±0%)
1	ORD	A	5	1	2,7,9	0.23±0.00	0±0 (0±0%)
1	D4P	A	14	1	11,14,16	0.49±0.01	0±0 (0±0%)
1	D4P	A	12	1	11,14,16	0.49±0.01	0±0 (0±0%)
1	D4P	A	18	1	11,14,16	0.49±0.01	0±0 (0±0%)
1	GHP	A	4	1	11,14,16	0.49±0.01	0±0 (0±0%)
1	ORD	A	11	1	2,7,9	0.23±0.00	0±0 (0±0%)
1	DPP	A	3	1	1,5,7	0.33±0.00	0±0 (0±0%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	ORD	A	11	1	-	0±0,5,6,8	-
1	D4P	A	18	1	-	0±0,4,6,8	0±0,1,1,1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	DPP	A	3	1	-	0±0,2,4,6	-
1	D4P	A	14	1	-	0±0,4,6,8	0±0,1,1,1
1	GHP	A	8	1	-	0±0,4,6,8	0±0,1,1,1
1	D4P	A	12	1	-	0±0,4,6,8	0±0,1,1,1
1	GHP	A	4	1	-	0±0,4,6,8	0±0,1,1,1
1	ORD	A	5	1	-	0±0,5,6,8	-
1	D4P	A	7	1	-	0±0,4,6,8	0±0,1,1,1

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 6.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 6.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	6NA	A	101	1	5,6,7	0.34±0.00	0±0 (0±0%)

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

the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	6NA	A	101	1	4,5,7	0.42±0.00	0±0 (0±0%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	6NA	A	101	1	-	0±0,4,4,5	-

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 6.7 Other polymers [i](#)

There are no such molecules in this entry.

## 6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 7 Chemical shift validation

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

### 7.1 Chemical shift list 1

File name: working\_cs.cif

Chemical shift list name: *assigned\_chemical\_shifts\_1*

#### 7.1.1 Bookkeeping

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

Total number of shifts	193
Number of shifts mapped to atoms	176
Number of unparsed shifts	0
Number of shifts with mapping errors	17
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- No matching atom found in the structure. All 17 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	1	6NA	H6C1	0.818	0.006	1
1	A	1	6NA	H6C2	0.818	0.006	1
1	A	1	6NA	H6C3	0.818	0.006	1
1	A	1	6NA	HAC1	2.102	0.006	1
1	A	1	6NA	HAC2	2.102	0.006	1
1	A	1	6NA	HBC1	1.452	0.008	1
1	A	1	6NA	HBC2	1.452	0.008	1
1	A	1	6NA	HDC1	1.206	0.007	1
1	A	1	6NA	HDC2	1.206	0.007	1
1	A	1	6NA	HGC1	1.161	0.004	1
1	A	1	6NA	HGC2	1.161	0.004	1
1	A	1	6NA	C6	15.769	0.000	1
1	A	1	6NA	CA	37.668	0.000	1
1	A	1	6NA	CB	27.084	0.000	1

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	1	6NA	CD	23.983	0.000	1
1	A	1	6NA	CG	32.842	0.000	1
1	A	2	ASN	H	7.972	0.003	1

### 7.1.2 Chemical shift referencing [i](#)

No chemical shift referencing corrections were calculated (not enough data).

### 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 77%, i.e. 50 atoms were assigned a chemical shift out of a possible 65. 0 out of 1 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	14/26 (54%)	11/11 (100%)	3/10 (30%)	0/5 (0%)
Sidechain	26/29 (90%)	18/19 (95%)	8/9 (89%)	0/1 (0%)
Aromatic	10/10 (100%)	5/5 (100%)	5/5 (100%)	0/0 (—%)
Overall	50/65 (77%)	34/35 (97%)	16/24 (67%)	0/6 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 77%, i.e. 50 atoms were assigned a chemical shift out of a possible 65. 0 out of 1 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	14/26 (54%)	11/11 (100%)	3/10 (30%)	0/5 (0%)
Sidechain	26/29 (90%)	18/19 (95%)	8/9 (89%)	0/1 (0%)
Aromatic	10/10 (100%)	5/5 (100%)	5/5 (100%)	0/0 (—%)
Overall	50/65 (77%)	34/35 (97%)	16/24 (67%)	0/6 (0%)

### 7.1.4 Statistically unusual chemical shifts [i](#)

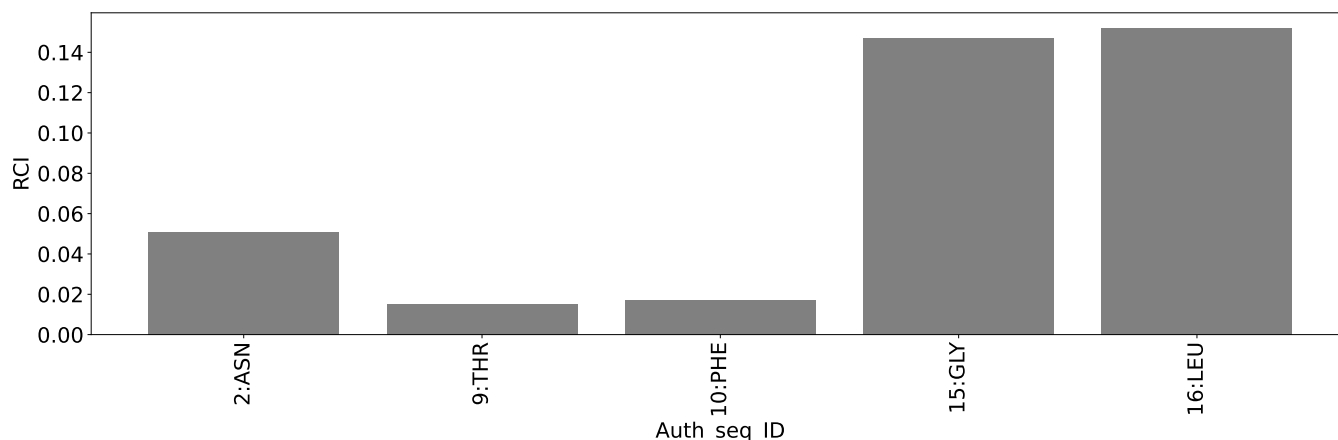
There are no statistically unusual chemical shifts.

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

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

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

Random coil index (RCI) for chain A:



## 7.2 Chemical shift list 2

File name: working\_cs.cif

Chemical shift list name: *assigned\_chemical\_shifts\_2*

### 7.2.1 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	119
Number of shifts mapped to atoms	107
Number of unparsed shifts	0
Number of shifts with mapping errors	12
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- No matching atom found in the structure. All 12 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
2	A	1	6NA	H6C1	0.812	0.006	1
2	A	1	6NA	H6C2	0.812	0.006	1
2	A	1	6NA	H6C3	0.812	0.006	1
2	A	1	6NA	HAC1	2.097	0.005	1
2	A	1	6NA	HAC2	2.097	0.005	1
2	A	1	6NA	HBC1	1.443	0.007	1
2	A	1	6NA	HBC2	1.443	0.007	1
2	A	1	6NA	HDC1	1.2	0.007	1
2	A	1	6NA	HDC2	1.2	0.007	1
2	A	1	6NA	HGC1	1.155	0.004	1
2	A	1	6NA	HGC2	1.155	0.004	1
2	A	2	ASN	H	8.08	0.000	1

### 7.2.2 Chemical shift referencing [i](#)

No chemical shift referencing corrections were calculated (not enough data).

### 7.2.3 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 52%, i.e. 34 atoms were assigned a chemical shift out of a possible 65. 0 out of 1 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	11/26 (42%)	11/11 (100%)	0/10 (0%)	0/5 (0%)
Sidechain	18/29 (62%)	18/19 (95%)	0/9 (0%)	0/1 (0%)
Aromatic	5/10 (50%)	5/5 (100%)	0/5 (0%)	0/0 (—%)
Overall	34/65 (52%)	34/35 (97%)	0/24 (0%)	0/6 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 52%, i.e. 34 atoms were assigned a chemical shift out of a possible 65. 0 out of 1 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	11/26 (42%)	11/11 (100%)	0/10 (0%)	0/5 (0%)
Sidechain	18/29 (62%)	18/19 (95%)	0/9 (0%)	0/1 (0%)
Aromatic	5/10 (50%)	5/5 (100%)	0/5 (0%)	0/0 (—%)
Overall	34/65 (52%)	34/35 (97%)	0/24 (0%)	0/6 (0%)

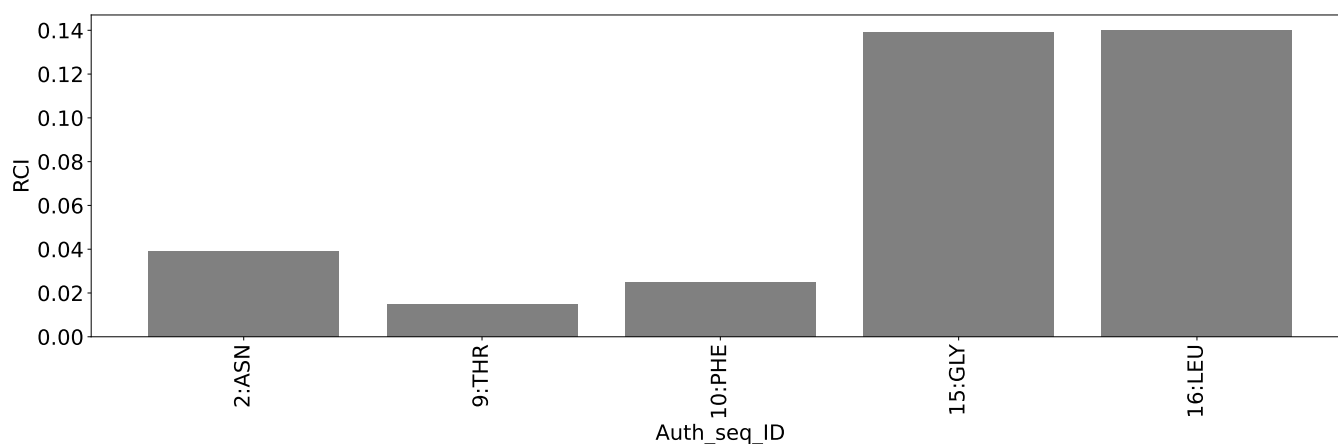
## 7.2.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

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

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

Random coil index (RCI) for chain A:



## 7.3 Chemical shift list 3

File name: working\_cs.cif

Chemical shift list name: *assigned\_chemical\_shifts\_3*

### 7.3.1 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	121
Number of shifts mapped to atoms	109
Number of unparsed shifts	0
Number of shifts with mapping errors	12
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- No matching atom found in the structure. All 12 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
3	A	1	6NA	H6C1	0.801	0.000	1
3	A	1	6NA	H6C2	0.801	0.000	1
3	A	1	6NA	H6C3	0.801	0.000	1
3	A	1	6NA	HAC1	2.107	0.000	1
3	A	1	6NA	HAC2	2.107	0.000	1
3	A	1	6NA	HBC1	1.446	0.000	1
3	A	1	6NA	HBC2	1.446	0.000	1
3	A	1	6NA	HDC1	1.184	0.000	1
3	A	1	6NA	HDC2	1.184	0.000	1
3	A	1	6NA	HGC1	1.154	0.000	1
3	A	1	6NA	HGC2	1.154	0.000	1
3	A	2	ASN	H	8.155	0.003	1

### 7.3.2 Chemical shift referencing ⓘ

No chemical shift referencing corrections were calculated (not enough data).

### 7.3.3 Completeness of resonance assignments ⓘ

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 54%, i.e. 35 atoms were assigned a chemical shift out of a possible 65. 0 out of 1 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	11/26 (42%)	11/11 (100%)	0/10 (0%)	0/5 (0%)
Sidechain	19/29 (66%)	19/19 (100%)	0/9 (0%)	0/1 (0%)
Aromatic	5/10 (50%)	5/5 (100%)	0/5 (0%)	0/0 (—%)
Overall	35/65 (54%)	35/35 (100%)	0/24 (0%)	0/6 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 54%, i.e. 35 atoms were assigned a chemical shift out of a possible 65. 0 out of 1 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	11/26 (42%)	11/11 (100%)	0/10 (0%)	0/5 (0%)
Sidechain	19/29 (66%)	19/19 (100%)	0/9 (0%)	0/1 (0%)

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	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Aromatic	5/10 (50%)	5/5 (100%)	0/5 (0%)	0/0 (—%)
Overall	35/65 (54%)	35/35 (100%)	0/24 (0%)	0/6 (0%)

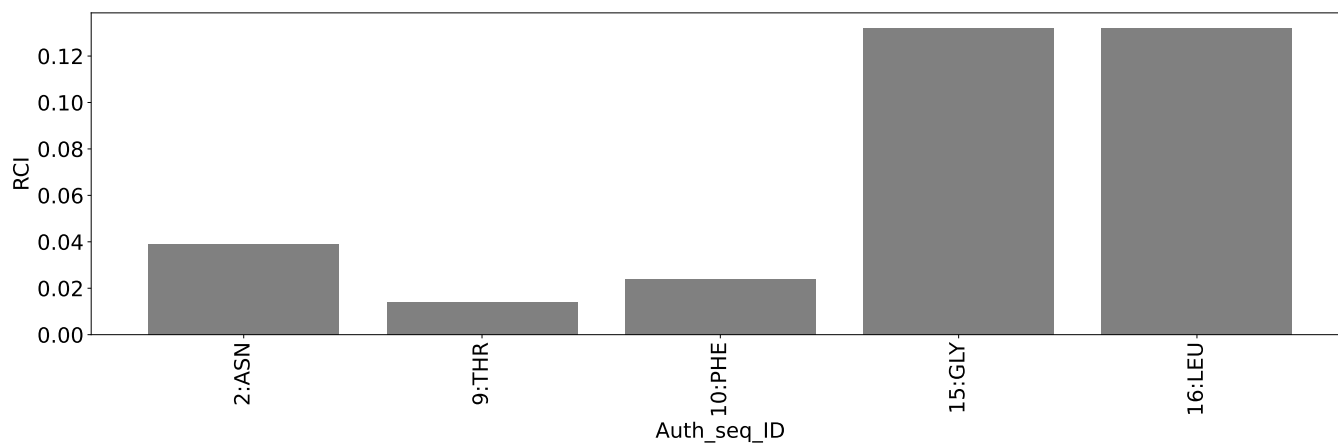
### 7.3.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

### 7.3.5 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:



## 8 NMR restraints analysis

### 8.1 Conformationally restricting restraints

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

Description	Value
Total distance restraints	338
Intra-residue ( $ i-j =0$ )	50
Sequential ( $ i-j =1$ )	120
Medium range ( $ i-j >1$ and $ i-j <5$ )	41
Long range ( $ i-j \geq 5$ )	119
Inter-chain	0
Hydrogen bond restraints	8
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	14
Number of restraints per residue	18.8
Number of long range restraints per residue <sup>1</sup>	6.9

<sup>1</sup>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

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

#### 8.2.1 Average number of distance violations per model

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

Bins (Å)	Average number of violations per model	Max (Å)
0.1-0.2 (Small)	3.5	0.2
0.2-0.5 (Medium)	3.6	0.5
>0.5 (Large)	28.6	3.46

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

Dihedral-angle violations less than  $1^\circ$  are not included in the calculation. There are no dihedral-angle violations



## 9 Distance violation analysis ⓘ

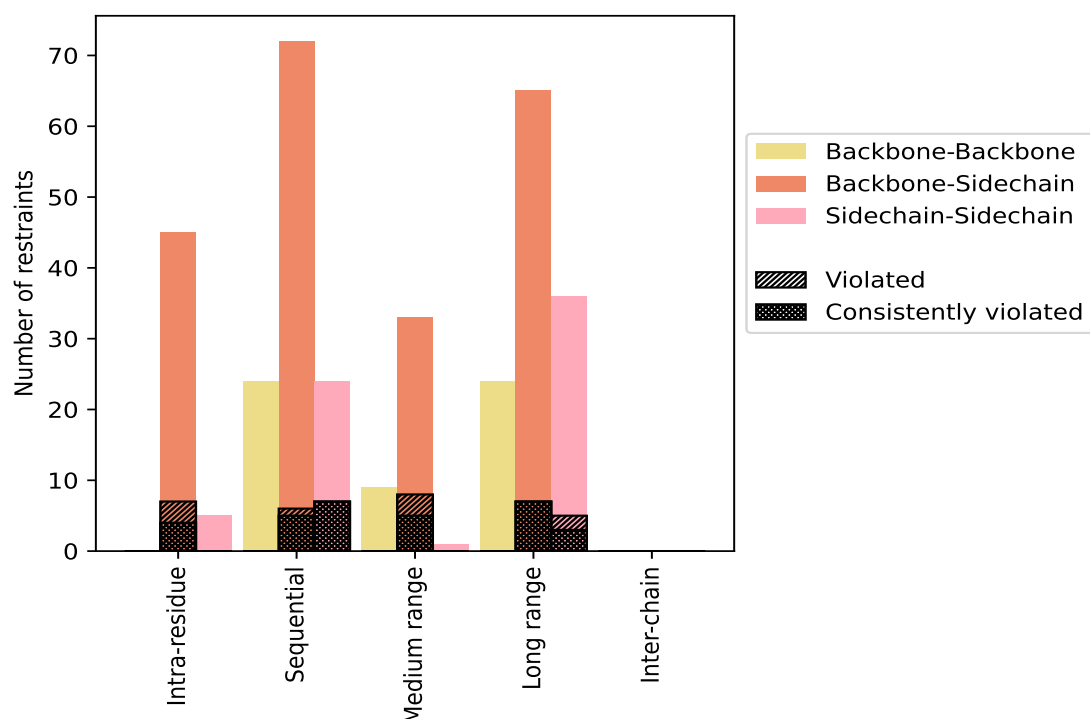
### 9.1 Summary of distance violations ⓘ

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

Restrains type	Count	% <sup>1</sup>	Violated <sup>3</sup>			Consistently Violated <sup>4</sup>		
			Count	% <sup>2</sup>	% <sup>1</sup>	Count	% <sup>2</sup>	% <sup>1</sup>
<b>Intra-residue (<math> i-j =0</math>)</b>	<b>50</b>	<b>14.8</b>	<b>7</b>	<b>14.0</b>	<b>2.1</b>	<b>4</b>	<b>8.0</b>	<b>1.2</b>
Backbone-Backbone	0	0.0	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	45	13.3	7	15.6	2.1	4	8.9	1.2
Sidechain-Sidechain	5	1.5	0	0.0	0.0	0	0.0	0.0
<b>Sequential (<math> i-j =1</math>)</b>	<b>120</b>	<b>35.5</b>	<b>13</b>	<b>10.8</b>	<b>3.8</b>	<b>12</b>	<b>10.0</b>	<b>3.6</b>
Backbone-Backbone	24	7.1	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	72	21.3	6	8.3	1.8	5	6.9	1.5
Sidechain-Sidechain	24	7.1	7	29.2	2.1	7	29.2	2.1
<b>Medium range (<math> i-j &gt;1</math> &amp; <math> i-j &lt;5</math>)</b>	<b>41</b>	<b>12.1</b>	<b>8</b>	<b>19.5</b>	<b>2.4</b>	<b>5</b>	<b>12.2</b>	<b>1.5</b>
Backbone-Backbone	9	2.7	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	31	9.2	8	25.8	2.4	5	16.1	1.5
Sidechain-Sidechain	1	0.3	0	0.0	0.0	0	0.0	0.0
<b>Long range (<math> i-j \geq 5</math>)</b>	<b>119</b>	<b>35.2</b>	<b>12</b>	<b>10.1</b>	<b>3.6</b>	<b>10</b>	<b>8.4</b>	<b>3.0</b>
Backbone-Backbone	24	7.1	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	61	18.0	7	11.5	2.1	7	11.5	2.1
Sidechain-Sidechain	34	10.1	5	14.7	1.5	3	8.8	0.9
<b>Inter-chain</b>	<b>0</b>	<b>0.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>
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
<b>Hydrogen bond</b>	<b>8</b>	<b>2.4</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>
<b>Disulfide bond</b>	<b>0</b>	<b>0.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>	<b>0</b>	<b>0.0</b>	<b>0.0</b>
<b>Total</b>	<b>338</b>	<b>100.0</b>	<b>40</b>	<b>11.8</b>	<b>11.8</b>	<b>31</b>	<b>9.2</b>	<b>9.2</b>
Backbone-Backbone	57	16.9	0	0.0	0.0	0	0.0	0.0
Backbone-Sidechain	215	63.6	28	13.0	8.3	21	9.8	6.2
Sidechain-Sidechain	66	19.5	12	18.2	3.6	10	15.2	3.0

<sup>1</sup> percentage calculated with respect to the total number of distance restraints, <sup>2</sup> percentage calculated with respect to the number of restraints in a particular restraint category, <sup>3</sup> violated in at least one model, <sup>4</sup> 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 <sup>6</sup> (Å)	Median (Å)
	IR <sup>1</sup>	SQ <sup>2</sup>	MR <sup>3</sup>	LR <sup>4</sup>	IC <sup>5</sup>	Total				
1	4	13	8	11	0	36	1.28	3.03	0.76	1.18
2	4	12	8	11	0	35	1.4	3.25	0.8	1.22
3	4	13	8	11	0	36	1.26	2.6	0.73	1.18
4	4	12	8	11	0	35	1.26	2.59	0.7	1.19
5	4	12	8	11	0	35	1.21	3.13	0.71	1.06
6	5	12	5	11	0	33	1.09	2.58	0.71	0.97
7	5	13	7	10	0	35	1.11	3.44	0.81	0.93
8	5	13	8	10	0	36	1.3	3.45	0.84	1.23
9	5	12	8	11	0	36	1.22	3.23	0.8	0.98
10	5	13	7	10	0	35	1.12	3.46	0.76	0.93

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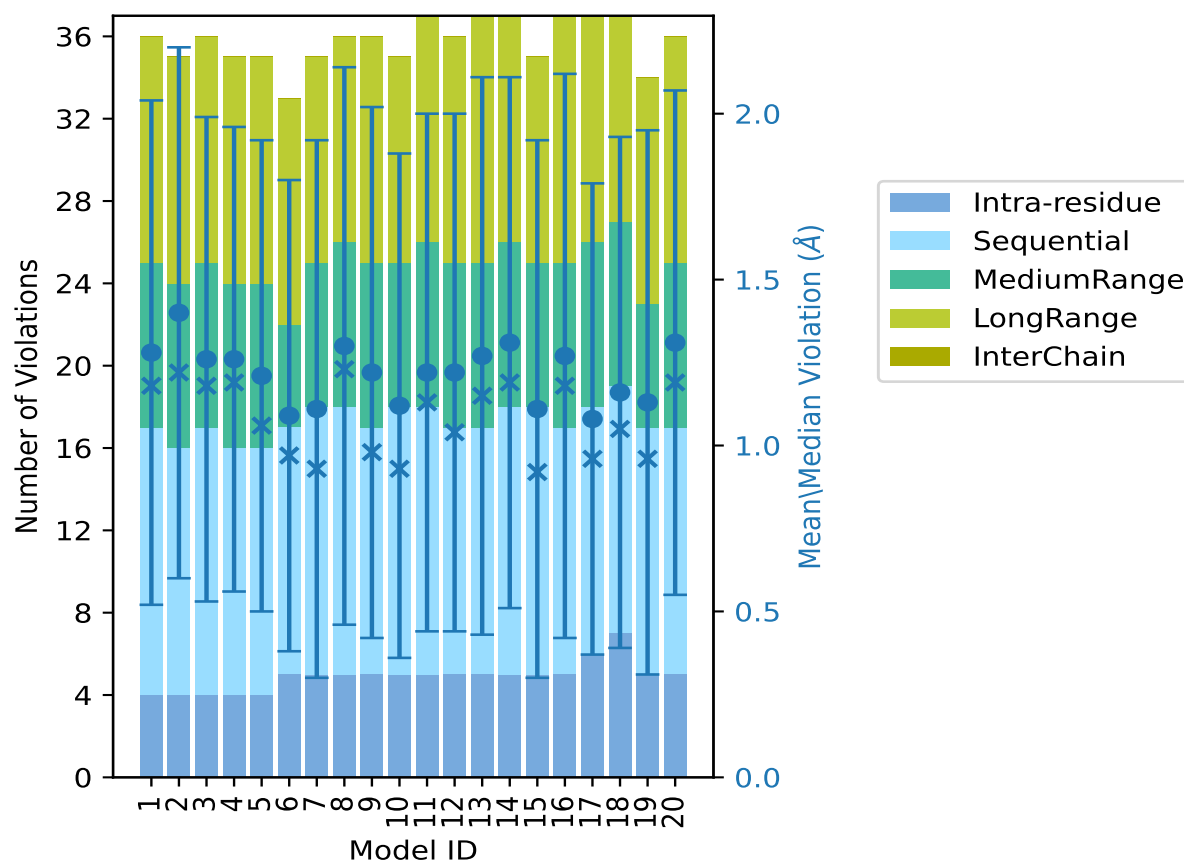
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Model ID	Number of violations						Mean (Å)	Max (Å)	SD <sup>6</sup> (Å)	Median (Å)
	IR <sup>1</sup>	SQ <sup>2</sup>	MR <sup>3</sup>	LR <sup>4</sup>	IC <sup>5</sup>	Total				
11	5	13	8	11	0	37	1.22	2.8	0.78	1.13
12	5	12	8	11	0	36	1.22	3.34	0.78	1.04
13	5	12	8	12	0	37	1.27	3.35	0.84	1.15
14	5	13	8	11	0	37	1.31	3.25	0.8	1.19
15	5	13	7	10	0	35	1.11	3.39	0.81	0.92
16	5	12	8	12	0	37	1.27	3.33	0.85	1.18
17	6	12	8	11	0	37	1.08	2.5	0.71	0.96
18	7	12	8	10	0	37	1.16	2.98	0.77	1.05
19	5	12	6	11	0	34	1.13	3.38	0.82	0.96
20	5	12	8	11	0	36	1.31	2.82	0.76	1.19

<sup>1</sup>Intra-residue restraints, <sup>2</sup>Sequential restraints, <sup>3</sup>Medium range restraints, <sup>4</sup>Long range restraints,

<sup>5</sup>Inter-chain restraints, <sup>6</sup>Standard deviation

### 9.2.1 Bar graph : Distance Violation statistics for each model ⓘ



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

### 9.3 Distance violation statistics for the ensemble

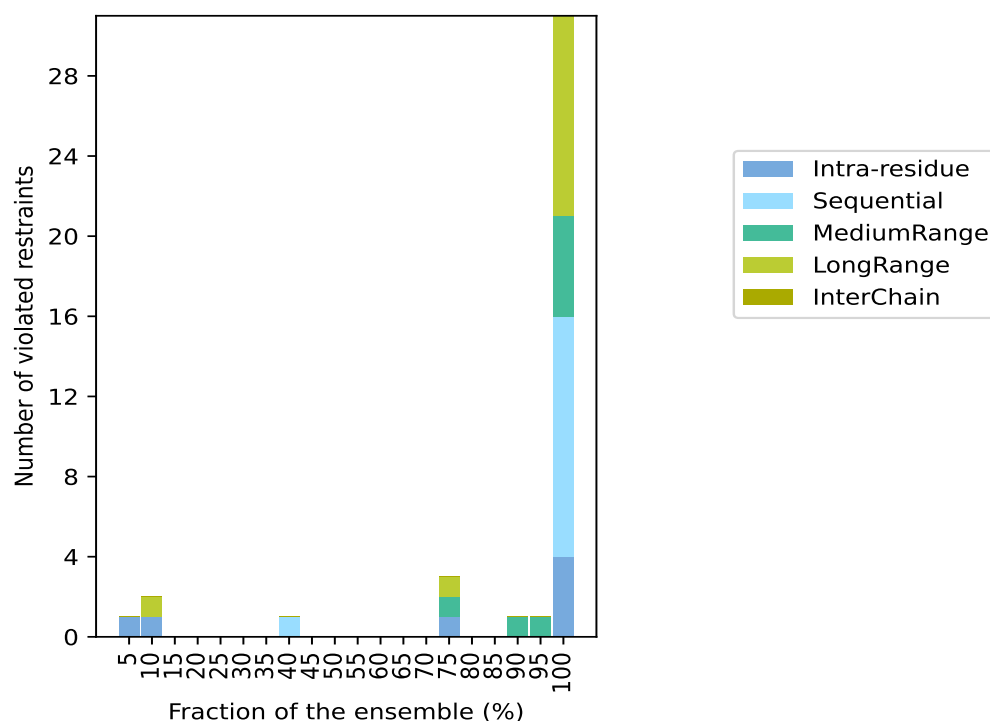
Violation analysis may find that some restraints are violated in few models and some are violated in most of models. The following table provides this information as number of violated restraints for a given fraction of the ensemble. In total, 290(IR:43, SQ:107, MR:33, LR:107, IC:0) restraints are not violated in the ensemble.

Number of violated restraints						Fraction of the ensemble	
IR <sup>1</sup>	SQ <sup>2</sup>	MR <sup>3</sup>	LR <sup>4</sup>	IC <sup>5</sup>	Total	Count <sup>6</sup>	%
1	0	0	0	0	1	1	5.0
1	0	0	1	0	2	2	10.0
0	0	0	0	0	0	3	15.0
0	0	0	0	0	0	4	20.0
0	0	0	0	0	0	5	25.0
0	0	0	0	0	0	6	30.0
0	0	0	0	0	0	7	35.0
0	1	0	0	0	1	8	40.0
0	0	0	0	0	0	9	45.0
0	0	0	0	0	0	10	50.0
0	0	0	0	0	0	11	55.0
0	0	0	0	0	0	12	60.0
0	0	0	0	0	0	13	65.0
0	0	0	0	0	0	14	70.0
1	0	1	1	0	3	15	75.0
0	0	0	0	0	0	16	80.0
0	0	0	0	0	0	17	85.0
0	0	1	0	0	1	18	90.0
0	0	1	0	0	1	19	95.0
4	12	5	10	0	31	20	100.0

<sup>1</sup>Intra-residue restraints, <sup>2</sup>Sequential restraints, <sup>3</sup>Medium range restraints, <sup>4</sup>Long range restraints,

<sup>5</sup>Inter-chain restraints, <sup>6</sup> Number of models with violations

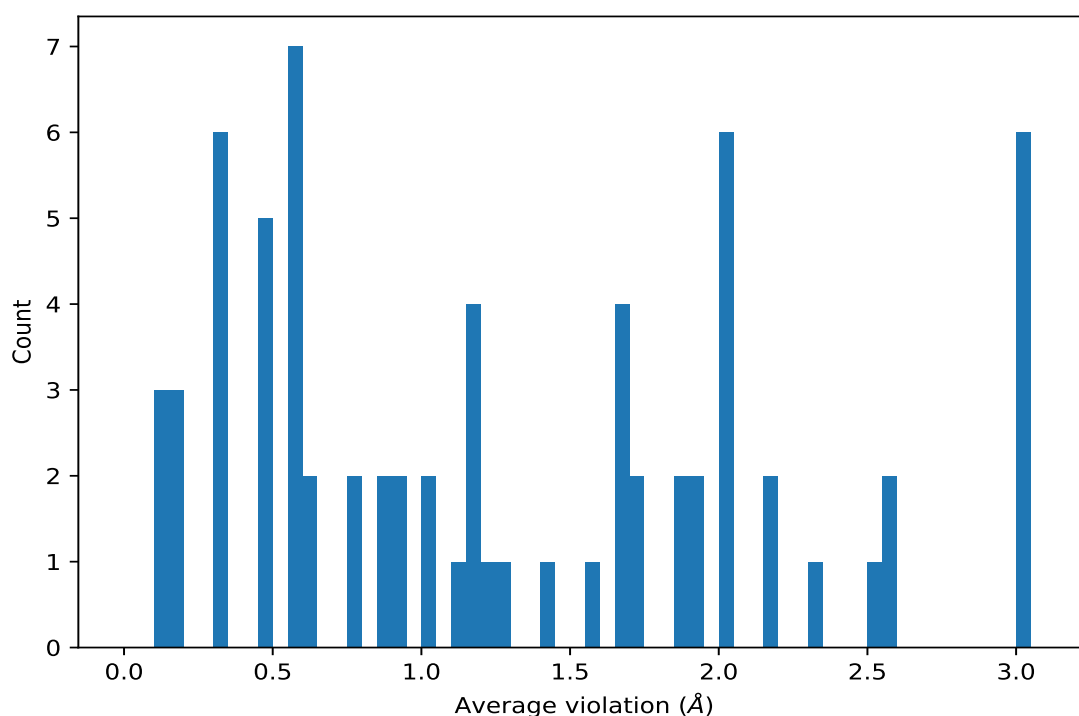
### 9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



## 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 <sup>1</sup>	Mean (Å)	SD <sup>1</sup> (Å)	Median (Å)
(1,164)	1:6:A:DTH:HG21	1:12:A:D4P:H4	20	3.04	0.41	3.24
(1,164)	1:6:A:DTH:HG22	1:12:A:D4P:H4	20	3.04	0.41	3.24
(1,164)	1:6:A:DTH:HG23	1:12:A:D4P:H4	20	3.04	0.41	3.24
(1,164)	1:6:A:DTH:HG22	1:12:A:D4P:H5	20	3.04	0.41	3.24
(1,164)	1:6:A:DTH:HG23	1:12:A:D4P:H5	20	3.04	0.41	3.24
(1,164)	1:6:A:DTH:HG21	1:12:A:D4P:H5	20	3.04	0.41	3.24
(1,189)	1:8:A:GHP:H	1:12:A:D4P:H4	20	2.56	0.14	2.58
(1,189)	1:8:A:GHP:H	1:12:A:D4P:H5	20	2.56	0.14	2.58
(1,155)	1:6:A:DTH:HA	1:7:A:D4P:H5	20	2.5	0.01	2.5
(1,291)	1:15:A:GLY:HA2	1:18:A:D4P:H4	20	2.31	0.57	2.46
(1,162)	1:6:A:DTH:HB	1:7:A:D4P:H5	20	2.18	0.29	2.25
(1,162)	1:6:A:DTH:HB	1:7:A:D4P:H4	20	2.18	0.29	2.25
(1,269)	1:13:A:DTH:HG23	1:14:A:D4P:H5	20	2.04	0.24	2.02
(1,269)	1:13:A:DTH:HG22	1:14:A:D4P:H5	20	2.04	0.24	2.02
(1,269)	1:13:A:DTH:HG23	1:14:A:D4P:H4	20	2.04	0.24	2.02
(1,269)	1:13:A:DTH:HG21	1:14:A:D4P:H5	20	2.04	0.24	2.02

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Key	Atom-1	Atom-2	Models <sup>1</sup>	Mean (Å)	SD <sup>1</sup> (Å)	Median (Å)
(1,269)	1:13:A:DTH:HG21	1:14:A:D4P:H4	20	2.04	0.24	2.02
(1,269)	1:13:A:DTH:HG22	1:14:A:D4P:H4	20	2.04	0.24	2.02
(1,176)	1:7:A:D4P:HA	1:12:A:D4P:H5	20	1.92	0.06	1.92
(1,176)	1:7:A:D4P:HA	1:12:A:D4P:H4	20	1.92	0.06	1.92
(1,157)	1:6:A:DTH:HB	1:12:A:D4P:H5	20	1.89	0.14	1.96
(1,157)	1:6:A:DTH:HB	1:12:A:D4P:H4	20	1.89	0.14	1.96
(1,252)	1:11:A:ORD:HG3	1:12:A:D4P:H5	20	1.74	0.39	1.86
(1,252)	1:11:A:ORD:HG2	1:12:A:D4P:H5	20	1.74	0.39	1.86
(1,288)	1:15:A:GLY:H	1:18:A:D4P:H4	20	1.7	0.51	1.84
(1,258)	1:12:A:D4P:H5	1:13:A:DTH:HG22	20	1.66	0.16	1.69
(1,258)	1:12:A:D4P:H5	1:13:A:DTH:HG21	20	1.66	0.16	1.69
(1,258)	1:12:A:D4P:H5	1:13:A:DTH:HG23	20	1.66	0.16	1.69
(1,281)	1:14:A:D4P:H5	1:15:A:GLY:HA3	20	1.55	0.04	1.56
(1,83)	1:4:A:GHP:HA	1:18:A:D4P:H4	20	1.43	0.45	1.54
(1,282)	1:14:A:D4P:H5	1:15:A:GLY:HA2	20	1.29	0.05	1.29
(1,297)	1:15:A:GLY:HA3	1:18:A:D4P:H4	20	1.22	0.56	1.34
(1,171)	1:7:A:D4P:H	1:7:A:D4P:H5	20	1.2	0.02	1.19
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H3	20	1.16	0.02	1.16
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H5	20	1.16	0.02	1.16
(1,43)	1:3:A:DPP:H	1:14:A:D4P:H5	20	1.0	0.1	1.02
(1,247)	1:11:A:ORD:HB2	1:12:A:D4P:H5	20	1.0	0.07	1.0
(1,271)	1:14:A:D4P:H	1:14:A:D4P:H5	20	0.93	0.01	0.93
(1,253)	1:12:A:D4P:H	1:12:A:D4P:H5	20	0.91	0.03	0.92
(1,24)	1:2:A:ASN:HA	1:14:A:D4P:H5	20	0.87	0.12	0.87
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H3	20	0.76	0.0	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H5	20	0.76	0.0	0.76
(1,99)	1:4:A:GHP:H3	1:13:A:DTH:H	20	0.62	0.01	0.62
(1,99)	1:4:A:GHP:H5	1:13:A:DTH:H	20	0.62	0.01	0.62
(1,280)	1:14:A:D4P:H5	1:15:A:GLY:HA2	20	0.6	0.05	0.6
(1,168)	1:6:A:DTH:HG21	1:7:A:D4P:H5	20	0.6	0.24	0.67
(1,168)	1:6:A:DTH:HG22	1:7:A:D4P:H5	20	0.6	0.24	0.67
(1,168)	1:6:A:DTH:HG23	1:7:A:D4P:H4	20	0.6	0.24	0.67
(1,168)	1:6:A:DTH:HG22	1:7:A:D4P:H4	20	0.6	0.24	0.67
(1,168)	1:6:A:DTH:HG23	1:7:A:D4P:H5	20	0.6	0.24	0.67
(1,168)	1:6:A:DTH:HG21	1:7:A:D4P:H4	20	0.6	0.24	0.67
(1,37)	1:2:A:ASN:HB3	1:14:A:D4P:H5	20	0.47	0.11	0.54
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG21	20	0.34	0.02	0.35
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG22	20	0.34	0.02	0.35
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG23	20	0.34	0.02	0.35
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG21	20	0.34	0.02	0.35
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG22	20	0.34	0.02	0.35
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG23	20	0.34	0.02	0.35

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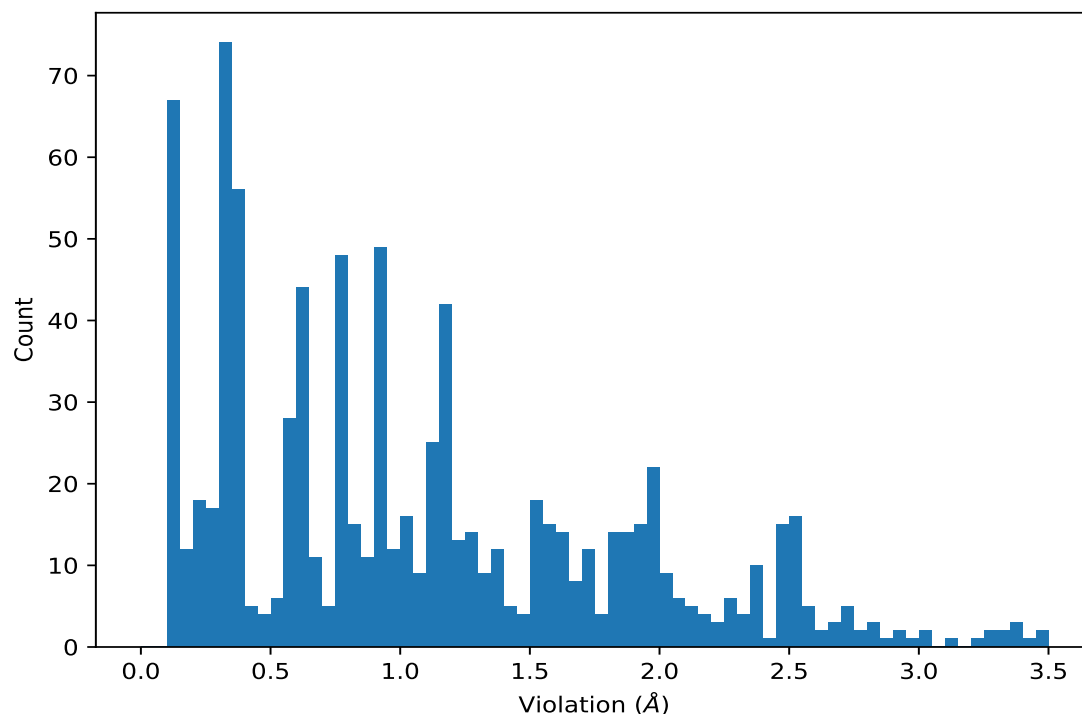
Key	Atom-1	Atom-2	Models <sup>1</sup>	Mean (Å)	SD <sup>1</sup> (Å)	Median (Å)
(1,100)	1:4:A:GHP:H3	1:6:A:DTH:H	20	0.18	0.04	0.18
(1,100)	1:4:A:GHP:H5	1:6:A:DTH:H	20	0.18	0.04	0.18
(1,325)	1:3:A:DPP:NG	1:18:A:D4P:CA	20	0.13	0.01	0.14
(1,329)	1:3:A:DPP:NG	1:18:A:D4P:CA	20	0.13	0.01	0.14
(1,277)	1:14:A:D4P:HA	1:18:A:D4P:H4	19	1.19	0.46	1.27
(1,274)	1:14:A:D4P:H	1:18:A:D4P:H4	18	1.12	0.44	1.23
(1,294)	1:15:A:GLY:HA3	1:18:A:D4P:H4	15	0.86	0.38	1.07
(1,142)	1:5:A:ORD:HG2	1:14:A:D4P:H5	15	0.49	0.14	0.55
(1,142)	1:5:A:ORD:HG3	1:14:A:D4P:H4	15	0.49	0.14	0.55
(1,142)	1:5:A:ORD:HG3	1:14:A:D4P:H5	15	0.49	0.14	0.55
(1,142)	1:5:A:ORD:HG2	1:14:A:D4P:H4	15	0.49	0.14	0.55
(1,320)	1:18:A:D4P:H	1:18:A:D4P:H5	15	0.16	0.06	0.13
(1,136)	1:5:A:ORD:HD2	1:14:A:D4P:H5	2	0.12	0.01	0.12

<sup>1</sup>Number of violated models, <sup>2</sup>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

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)
(1,164)	1:6:A:DTH:HG21	1:12:A:D4P:H5	10	3.46
(1,164)	1:6:A:DTH:HG23	1:12:A:D4P:H5	8	3.45
(1,164)	1:6:A:DTH:HG22	1:12:A:D4P:H5	7	3.44
(1,164)	1:6:A:DTH:HG22	1:12:A:D4P:H5	15	3.39
(1,164)	1:6:A:DTH:HG23	1:12:A:D4P:H4	19	3.38
(1,164)	1:6:A:DTH:HG21	1:12:A:D4P:H4	13	3.35
(1,164)	1:6:A:DTH:HG23	1:12:A:D4P:H5	12	3.34
(1,164)	1:6:A:DTH:HG21	1:12:A:D4P:H4	16	3.33
(1,164)	1:6:A:DTH:HG22	1:12:A:D4P:H4	2	3.25
(1,164)	1:6:A:DTH:HG23	1:12:A:D4P:H4	14	3.25
(1,164)	1:6:A:DTH:HG23	1:12:A:D4P:H4	9	3.23
(1,164)	1:6:A:DTH:HG22	1:12:A:D4P:H4	5	3.13
(1,164)	1:6:A:DTH:HG21	1:12:A:D4P:H4	1	3.03
(1,291)	1:15:A:GLY:HA2	1:18:A:D4P:H4	14	3.02
(1,164)	1:6:A:DTH:HG23	1:12:A:D4P:H4	18	2.98
(1,291)	1:15:A:GLY:HA2	1:18:A:D4P:H4	8	2.92
(1,291)	1:15:A:GLY:HA2	1:18:A:D4P:H4	16	2.91
(1,291)	1:15:A:GLY:HA2	1:18:A:D4P:H4	1	2.87
(1,291)	1:15:A:GLY:HA2	1:18:A:D4P:H4	2	2.84
(1,291)	1:15:A:GLY:HA2	1:18:A:D4P:H4	13	2.82
(1,291)	1:15:A:GLY:HA2	1:18:A:D4P:H4	20	2.82
(1,291)	1:15:A:GLY:HA2	1:18:A:D4P:H4	11	2.8
(1,164)	1:6:A:DTH:HG23	1:12:A:D4P:H4	20	2.76
(1,189)	1:8:A:GHP:H	1:12:A:D4P:H5	10	2.72
(1,189)	1:8:A:GHP:H	1:12:A:D4P:H5	8	2.71
(1,189)	1:8:A:GHP:H	1:12:A:D4P:H5	11	2.71
(1,189)	1:8:A:GHP:H	1:12:A:D4P:H5	15	2.71
(1,189)	1:8:A:GHP:H	1:12:A:D4P:H5	7	2.7
(1,189)	1:8:A:GHP:H	1:12:A:D4P:H5	13	2.69
(1,189)	1:8:A:GHP:H	1:12:A:D4P:H5	16	2.69
(1,291)	1:15:A:GLY:HA2	1:18:A:D4P:H4	9	2.67
(1,189)	1:8:A:GHP:H	1:12:A:D4P:H5	2	2.65
(1,189)	1:8:A:GHP:H	1:12:A:D4P:H5	3	2.6
(1,189)	1:8:A:GHP:H	1:12:A:D4P:H5	4	2.59
(1,189)	1:8:A:GHP:H	1:12:A:D4P:H5	6	2.58
(1,189)	1:8:A:GHP:H	1:12:A:D4P:H5	19	2.57
(1,189)	1:8:A:GHP:H	1:12:A:D4P:H4	9	2.56

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,164)	1:6:A:DTH:HG23	1:12:A:D4P:H4	3	2.56
(1,189)	1:8:A:GHP:H	1:12:A:D4P:H5	12	2.55
(1,164)	1:6:A:DTH:HG23	1:12:A:D4P:H4	11	2.54
(1,291)	1:15:A:GLY:HA2	1:18:A:D4P:H4	3	2.53
(1,155)	1:6:A:DTH:HA	1:7:A:D4P:H5	14	2.52
(1,155)	1:6:A:DTH:HA	1:7:A:D4P:H5	20	2.52
(1,155)	1:6:A:DTH:HA	1:7:A:D4P:H5	4	2.51
(1,155)	1:6:A:DTH:HA	1:7:A:D4P:H5	1	2.5
(1,155)	1:6:A:DTH:HA	1:7:A:D4P:H5	7	2.5
(1,155)	1:6:A:DTH:HA	1:7:A:D4P:H5	8	2.5
(1,155)	1:6:A:DTH:HA	1:7:A:D4P:H5	10	2.5
(1,155)	1:6:A:DTH:HA	1:7:A:D4P:H5	11	2.5
(1,155)	1:6:A:DTH:HA	1:7:A:D4P:H5	15	2.5
(1,155)	1:6:A:DTH:HA	1:7:A:D4P:H5	16	2.5
(1,155)	1:6:A:DTH:HA	1:7:A:D4P:H5	17	2.5
(1,155)	1:6:A:DTH:HA	1:7:A:D4P:H5	18	2.5
(1,155)	1:6:A:DTH:HA	1:7:A:D4P:H5	19	2.5
(1,162)	1:6:A:DTH:HB	1:7:A:D4P:H5	2	2.49
(1,162)	1:6:A:DTH:HB	1:7:A:D4P:H5	7	2.49
(1,162)	1:6:A:DTH:HB	1:7:A:D4P:H5	12	2.49
(1,155)	1:6:A:DTH:HA	1:7:A:D4P:H5	2	2.49
(1,155)	1:6:A:DTH:HA	1:7:A:D4P:H5	3	2.49
(1,155)	1:6:A:DTH:HA	1:7:A:D4P:H5	5	2.49
(1,155)	1:6:A:DTH:HA	1:7:A:D4P:H5	6	2.49
(1,155)	1:6:A:DTH:HA	1:7:A:D4P:H5	13	2.49
(1,189)	1:8:A:GHP:H	1:12:A:D4P:H4	14	2.48
(1,162)	1:6:A:DTH:HB	1:7:A:D4P:H5	1	2.48
(1,162)	1:6:A:DTH:HB	1:7:A:D4P:H5	4	2.48
(1,162)	1:6:A:DTH:HB	1:7:A:D4P:H5	15	2.48
(1,162)	1:6:A:DTH:HB	1:7:A:D4P:H5	18	2.48
(1,155)	1:6:A:DTH:HA	1:7:A:D4P:H5	9	2.48
(1,155)	1:6:A:DTH:HA	1:7:A:D4P:H5	12	2.48
(1,269)	1:13:A:DTH:HG22	1:14:A:D4P:H5	13	2.42
(1,252)	1:11:A:ORD:HG3	1:12:A:D4P:H5	19	2.4
(1,189)	1:8:A:GHP:H	1:12:A:D4P:H4	1	2.4
(1,291)	1:15:A:GLY:HA2	1:18:A:D4P:H4	4	2.38
(1,269)	1:13:A:DTH:HG21	1:14:A:D4P:H5	11	2.38
(1,189)	1:8:A:GHP:H	1:12:A:D4P:H4	5	2.38
(1,189)	1:8:A:GHP:H	1:12:A:D4P:H4	18	2.38
(1,162)	1:6:A:DTH:HB	1:7:A:D4P:H4	8	2.37
(1,269)	1:13:A:DTH:HG22	1:14:A:D4P:H5	16	2.35
(1,252)	1:11:A:ORD:HG3	1:12:A:D4P:H5	18	2.35

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,164)	1:6:A:DTH:HG21	1:12:A:D4P:H4	17	2.35
(1,189)	1:8:A:GHP:H	1:12:A:D4P:H4	17	2.34
(1,162)	1:6:A:DTH:HB	1:7:A:D4P:H4	17	2.34
(1,269)	1:13:A:DTH:HG22	1:14:A:D4P:H4	8	2.33
(1,269)	1:13:A:DTH:HG23	1:14:A:D4P:H5	9	2.32
(1,164)	1:6:A:DTH:HG22	1:12:A:D4P:H4	4	2.29
(1,189)	1:8:A:GHP:H	1:12:A:D4P:H4	20	2.26
(1,164)	1:6:A:DTH:HG22	1:12:A:D4P:H4	6	2.26
(1,288)	1:15:A:GLY:H	1:18:A:D4P:H4	20	2.25
(1,162)	1:6:A:DTH:HB	1:7:A:D4P:H4	9	2.25
(1,162)	1:6:A:DTH:HB	1:7:A:D4P:H4	14	2.25
(1,288)	1:15:A:GLY:H	1:18:A:D4P:H4	2	2.24
(1,288)	1:15:A:GLY:H	1:18:A:D4P:H4	16	2.24
(1,288)	1:15:A:GLY:H	1:18:A:D4P:H4	13	2.2
(1,291)	1:15:A:GLY:HA2	1:18:A:D4P:H4	18	2.16
(1,288)	1:15:A:GLY:H	1:18:A:D4P:H4	11	2.16
(1,269)	1:13:A:DTH:HG23	1:14:A:D4P:H5	1	2.16
(1,162)	1:6:A:DTH:HB	1:7:A:D4P:H4	16	2.16
(1,291)	1:15:A:GLY:HA2	1:18:A:D4P:H4	5	2.13
(1,288)	1:15:A:GLY:H	1:18:A:D4P:H4	14	2.12
(1,252)	1:11:A:ORD:HG2	1:12:A:D4P:H5	2	2.12
(1,269)	1:13:A:DTH:HG23	1:14:A:D4P:H5	2	2.1
(1,269)	1:13:A:DTH:HG22	1:14:A:D4P:H5	3	2.1
(1,288)	1:15:A:GLY:H	1:18:A:D4P:H4	8	2.09
(1,252)	1:11:A:ORD:HG2	1:12:A:D4P:H5	6	2.09
(1,252)	1:11:A:ORD:HG2	1:12:A:D4P:H5	9	2.08
(1,162)	1:6:A:DTH:HB	1:7:A:D4P:H4	20	2.08
(1,269)	1:13:A:DTH:HG21	1:14:A:D4P:H5	17	2.07
(1,252)	1:11:A:ORD:HG2	1:12:A:D4P:H5	3	2.06
(1,288)	1:15:A:GLY:H	1:18:A:D4P:H4	3	2.05
(1,291)	1:15:A:GLY:HA2	1:18:A:D4P:H4	12	2.03
(1,269)	1:13:A:DTH:HG21	1:14:A:D4P:H5	6	2.03
(1,269)	1:13:A:DTH:HG22	1:14:A:D4P:H5	14	2.02
(1,269)	1:13:A:DTH:HG23	1:14:A:D4P:H5	19	2.02
(1,269)	1:13:A:DTH:HG23	1:14:A:D4P:H5	20	2.01
(1,252)	1:11:A:ORD:HG3	1:12:A:D4P:H5	7	2.01
(1,269)	1:13:A:DTH:HG22	1:14:A:D4P:H5	5	2.0
(1,176)	1:7:A:D4P:HA	1:12:A:D4P:H5	10	2.0
(1,176)	1:7:A:D4P:HA	1:12:A:D4P:H5	8	1.99
(1,176)	1:7:A:D4P:HA	1:12:A:D4P:H5	11	1.99
(1,162)	1:6:A:DTH:HB	1:7:A:D4P:H4	19	1.99
(1,176)	1:7:A:D4P:HA	1:12:A:D4P:H5	15	1.98

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,162)	1:6:A:DTH:HB	1:7:A:D4P:H4	13	1.98
(1,157)	1:6:A:DTH:HB	1:12:A:D4P:H5	10	1.98
(1,157)	1:6:A:DTH:HB	1:12:A:D4P:H5	14	1.98
(1,157)	1:6:A:DTH:HB	1:12:A:D4P:H5	20	1.98
(1,269)	1:13:A:DTH:HG21	1:14:A:D4P:H5	12	1.97
(1,176)	1:7:A:D4P:HA	1:12:A:D4P:H5	7	1.97
(1,176)	1:7:A:D4P:HA	1:12:A:D4P:H5	13	1.97
(1,176)	1:7:A:D4P:HA	1:12:A:D4P:H5	16	1.97
(1,157)	1:6:A:DTH:HB	1:12:A:D4P:H5	2	1.97
(1,157)	1:6:A:DTH:HB	1:12:A:D4P:H5	7	1.97
(1,157)	1:6:A:DTH:HB	1:12:A:D4P:H5	13	1.97
(1,157)	1:6:A:DTH:HB	1:12:A:D4P:H5	16	1.97
(1,157)	1:6:A:DTH:HB	1:12:A:D4P:H5	19	1.97
(1,176)	1:7:A:D4P:HA	1:12:A:D4P:H5	9	1.96
(1,157)	1:6:A:DTH:HB	1:12:A:D4P:H5	1	1.96
(1,157)	1:6:A:DTH:HB	1:12:A:D4P:H5	5	1.96
(1,157)	1:6:A:DTH:HB	1:12:A:D4P:H5	8	1.96
(1,157)	1:6:A:DTH:HB	1:12:A:D4P:H5	9	1.96
(1,297)	1:15:A:GLY:HA3	1:18:A:D4P:H4	14	1.95
(1,288)	1:15:A:GLY:H	1:18:A:D4P:H4	1	1.95
(1,288)	1:15:A:GLY:H	1:18:A:D4P:H4	4	1.95
(1,176)	1:7:A:D4P:HA	1:12:A:D4P:H5	2	1.95
(1,157)	1:6:A:DTH:HB	1:12:A:D4P:H5	12	1.95
(1,157)	1:6:A:DTH:HB	1:12:A:D4P:H5	15	1.95
(1,83)	1:4:A:GHP:HA	1:18:A:D4P:H4	20	1.95
(1,157)	1:6:A:DTH:HB	1:12:A:D4P:H5	18	1.94
(1,176)	1:7:A:D4P:HA	1:12:A:D4P:H5	1	1.92
(1,252)	1:11:A:ORD:HG3	1:12:A:D4P:H5	12	1.91
(1,252)	1:11:A:ORD:HG3	1:12:A:D4P:H5	14	1.91
(1,176)	1:7:A:D4P:HA	1:12:A:D4P:H5	14	1.91
(1,162)	1:6:A:DTH:HB	1:7:A:D4P:H4	3	1.91
(1,157)	1:6:A:DTH:HB	1:12:A:D4P:H4	17	1.91
(1,83)	1:4:A:GHP:HA	1:18:A:D4P:H4	2	1.91
(1,269)	1:13:A:DTH:HG23	1:14:A:D4P:H4	15	1.9
(1,176)	1:7:A:D4P:HA	1:12:A:D4P:H5	3	1.9
(1,176)	1:7:A:D4P:HA	1:12:A:D4P:H5	4	1.9
(1,258)	1:12:A:D4P:H5	1:13:A:DTH:HG23	12	1.89
(1,176)	1:7:A:D4P:HA	1:12:A:D4P:H5	5	1.88
(1,176)	1:7:A:D4P:HA	1:12:A:D4P:H5	6	1.88
(1,176)	1:7:A:D4P:HA	1:12:A:D4P:H5	18	1.88
(1,176)	1:7:A:D4P:HA	1:12:A:D4P:H5	19	1.88
(1,252)	1:11:A:ORD:HG3	1:12:A:D4P:H5	20	1.87

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,176)	1:7:A:D4P:HA	1:12:A:D4P:H5	12	1.86
(1,83)	1:4:A:GHP:HA	1:18:A:D4P:H4	3	1.86
(1,258)	1:12:A:D4P:H5	1:13:A:DTH:HG22	20	1.85
(1,252)	1:11:A:ORD:HG3	1:12:A:D4P:H5	15	1.85
(1,176)	1:7:A:D4P:HA	1:12:A:D4P:H4	20	1.85
(1,297)	1:15:A:GLY:HA3	1:18:A:D4P:H4	8	1.84
(1,291)	1:15:A:GLY:HA2	1:18:A:D4P:H4	17	1.84
(1,258)	1:12:A:D4P:H5	1:13:A:DTH:HG22	4	1.84
(1,258)	1:12:A:D4P:H5	1:13:A:DTH:HG21	5	1.84
(1,258)	1:12:A:D4P:H5	1:13:A:DTH:HG23	6	1.83
(1,258)	1:12:A:D4P:H5	1:13:A:DTH:HG21	14	1.82
(1,83)	1:4:A:GHP:HA	1:18:A:D4P:H4	4	1.82
(1,83)	1:4:A:GHP:HA	1:18:A:D4P:H4	13	1.82
(1,83)	1:4:A:GHP:HA	1:18:A:D4P:H4	16	1.82
(1,297)	1:15:A:GLY:HA3	1:18:A:D4P:H4	1	1.81
(1,162)	1:6:A:DTH:HB	1:7:A:D4P:H4	11	1.81
(1,297)	1:15:A:GLY:HA3	1:18:A:D4P:H4	16	1.8
(1,258)	1:12:A:D4P:H5	1:13:A:DTH:HG23	17	1.8
(1,258)	1:12:A:D4P:H5	1:13:A:DTH:HG22	19	1.8
(1,176)	1:7:A:D4P:HA	1:12:A:D4P:H4	17	1.79
(1,83)	1:4:A:GHP:HA	1:18:A:D4P:H4	11	1.78
(1,291)	1:15:A:GLY:HA2	1:18:A:D4P:H4	10	1.77
(1,269)	1:13:A:DTH:HG23	1:14:A:D4P:H4	4	1.75
(1,297)	1:15:A:GLY:HA3	1:18:A:D4P:H4	2	1.73
(1,277)	1:14:A:D4P:HA	1:18:A:D4P:H4	20	1.73
(1,258)	1:12:A:D4P:H5	1:13:A:DTH:HG22	2	1.73
(1,288)	1:15:A:GLY:H	1:18:A:D4P:H4	5	1.72
(1,277)	1:14:A:D4P:HA	1:18:A:D4P:H4	2	1.72
(1,269)	1:13:A:DTH:HG21	1:14:A:D4P:H4	7	1.72
(1,162)	1:6:A:DTH:HB	1:7:A:D4P:H4	6	1.72
(1,157)	1:6:A:DTH:HB	1:12:A:D4P:H4	3	1.72
(1,297)	1:15:A:GLY:HA3	1:18:A:D4P:H4	13	1.71
(1,288)	1:15:A:GLY:H	1:18:A:D4P:H4	18	1.71
(1,258)	1:12:A:D4P:H5	1:13:A:DTH:HG21	3	1.71
(1,162)	1:6:A:DTH:HB	1:7:A:D4P:H4	5	1.71
(1,297)	1:15:A:GLY:HA3	1:18:A:D4P:H4	20	1.7
(1,252)	1:11:A:ORD:HG3	1:12:A:D4P:H5	4	1.7
(1,297)	1:15:A:GLY:HA3	1:18:A:D4P:H4	11	1.69
(1,274)	1:14:A:D4P:H	1:18:A:D4P:H4	16	1.68
(1,258)	1:12:A:D4P:H5	1:13:A:DTH:HG22	1	1.67
(1,83)	1:4:A:GHP:HA	1:18:A:D4P:H4	18	1.67
(1,277)	1:14:A:D4P:HA	1:18:A:D4P:H4	16	1.66

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,269)	1:13:A:DTH:HG22	1:14:A:D4P:H4	18	1.66
(1,157)	1:6:A:DTH:HB	1:12:A:D4P:H4	11	1.65
(1,83)	1:4:A:GHP:HA	1:18:A:D4P:H4	5	1.65
(1,297)	1:15:A:GLY:HA3	1:18:A:D4P:H4	9	1.64
(1,252)	1:11:A:ORD:HG3	1:12:A:D4P:H5	13	1.64
(1,162)	1:6:A:DTH:HB	1:7:A:D4P:H4	10	1.64
(1,288)	1:15:A:GLY:H	1:18:A:D4P:H4	9	1.63
(1,288)	1:15:A:GLY:H	1:18:A:D4P:H4	12	1.63
(1,281)	1:14:A:D4P:H5	1:15:A:GLY:HA3	14	1.63
(1,277)	1:14:A:D4P:HA	1:18:A:D4P:H4	13	1.62
(1,281)	1:14:A:D4P:H5	1:15:A:GLY:HA3	19	1.61
(1,281)	1:14:A:D4P:H5	1:15:A:GLY:HA3	2	1.6
(1,274)	1:14:A:D4P:H	1:18:A:D4P:H4	2	1.6
(1,274)	1:14:A:D4P:H	1:18:A:D4P:H4	11	1.6
(1,274)	1:14:A:D4P:H	1:18:A:D4P:H4	13	1.6
(1,281)	1:14:A:D4P:H5	1:15:A:GLY:HA3	1	1.59
(1,281)	1:14:A:D4P:H5	1:15:A:GLY:HA3	4	1.59
(1,281)	1:14:A:D4P:H5	1:15:A:GLY:HA3	20	1.59
(1,277)	1:14:A:D4P:HA	1:18:A:D4P:H4	11	1.59
(1,281)	1:14:A:D4P:H5	1:15:A:GLY:HA3	3	1.58
(1,281)	1:14:A:D4P:H5	1:15:A:GLY:HA3	5	1.58
(1,277)	1:14:A:D4P:HA	1:18:A:D4P:H4	3	1.58
(1,157)	1:6:A:DTH:HB	1:12:A:D4P:H4	4	1.58
(1,269)	1:13:A:DTH:HG22	1:14:A:D4P:H4	10	1.57
(1,291)	1:15:A:GLY:HA2	1:18:A:D4P:H4	6	1.56
(1,281)	1:14:A:D4P:H5	1:15:A:GLY:HA3	6	1.56
(1,281)	1:14:A:D4P:H5	1:15:A:GLY:HA3	12	1.56
(1,83)	1:4:A:GHP:HA	1:18:A:D4P:H4	12	1.56
(1,281)	1:14:A:D4P:H5	1:15:A:GLY:HA3	17	1.55
(1,274)	1:14:A:D4P:H	1:18:A:D4P:H4	20	1.55
(1,281)	1:14:A:D4P:H5	1:15:A:GLY:HA3	7	1.54
(1,258)	1:12:A:D4P:H5	1:13:A:DTH:HG21	10	1.54
(1,157)	1:6:A:DTH:HB	1:12:A:D4P:H4	6	1.54
(1,258)	1:12:A:D4P:H5	1:13:A:DTH:HG21	16	1.53
(1,281)	1:14:A:D4P:H5	1:15:A:GLY:HA3	11	1.52
(1,258)	1:12:A:D4P:H5	1:13:A:DTH:HG21	8	1.52
(1,258)	1:12:A:D4P:H5	1:13:A:DTH:HG22	9	1.52
(1,281)	1:14:A:D4P:H5	1:15:A:GLY:HA3	8	1.51
(1,281)	1:14:A:D4P:H5	1:15:A:GLY:HA3	9	1.51
(1,281)	1:14:A:D4P:H5	1:15:A:GLY:HA3	15	1.51
(1,281)	1:14:A:D4P:H5	1:15:A:GLY:HA3	16	1.51
(1,277)	1:14:A:D4P:HA	1:18:A:D4P:H4	4	1.51

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,258)	1:12:A:D4P:H5	1:13:A:DTH:HG23	7	1.51
(1,83)	1:4:A:GHP:HA	1:18:A:D4P:H4	14	1.51
(1,281)	1:14:A:D4P:H5	1:15:A:GLY:HA3	10	1.5
(1,281)	1:14:A:D4P:H5	1:15:A:GLY:HA3	13	1.5
(1,281)	1:14:A:D4P:H5	1:15:A:GLY:HA3	18	1.5
(1,258)	1:12:A:D4P:H5	1:13:A:DTH:HG21	13	1.5
(1,258)	1:12:A:D4P:H5	1:13:A:DTH:HG23	11	1.49
(1,274)	1:14:A:D4P:H	1:18:A:D4P:H4	8	1.48
(1,258)	1:12:A:D4P:H5	1:13:A:DTH:HG22	15	1.48
(1,83)	1:4:A:GHP:HA	1:18:A:D4P:H4	8	1.48
(1,274)	1:14:A:D4P:H	1:18:A:D4P:H4	14	1.44
(1,291)	1:15:A:GLY:HA2	1:18:A:D4P:H4	19	1.43
(1,297)	1:15:A:GLY:HA3	1:18:A:D4P:H4	3	1.41
(1,288)	1:15:A:GLY:H	1:18:A:D4P:H4	17	1.41
(1,277)	1:14:A:D4P:HA	1:18:A:D4P:H4	14	1.41
(1,258)	1:12:A:D4P:H5	1:13:A:DTH:HG21	18	1.4
(1,83)	1:4:A:GHP:HA	1:18:A:D4P:H4	17	1.39
(1,291)	1:15:A:GLY:HA2	1:18:A:D4P:H4	7	1.38
(1,282)	1:14:A:D4P:H5	1:15:A:GLY:HA2	14	1.38
(1,291)	1:15:A:GLY:HA2	1:18:A:D4P:H4	15	1.37
(1,277)	1:14:A:D4P:HA	1:18:A:D4P:H4	8	1.37
(1,83)	1:4:A:GHP:HA	1:18:A:D4P:H4	10	1.37
(1,252)	1:11:A:ORD:HG3	1:12:A:D4P:H5	8	1.36
(1,282)	1:14:A:D4P:H5	1:15:A:GLY:HA2	1	1.35
(1,282)	1:14:A:D4P:H5	1:15:A:GLY:HA2	2	1.35
(1,282)	1:14:A:D4P:H5	1:15:A:GLY:HA2	19	1.35
(1,274)	1:14:A:D4P:H	1:18:A:D4P:H4	3	1.35
(1,288)	1:15:A:GLY:H	1:18:A:D4P:H4	10	1.34
(1,282)	1:14:A:D4P:H5	1:15:A:GLY:HA2	4	1.34
(1,252)	1:11:A:ORD:HG3	1:12:A:D4P:H5	11	1.34
(1,294)	1:15:A:GLY:HA3	1:18:A:D4P:H4	14	1.33
(1,282)	1:14:A:D4P:H5	1:15:A:GLY:HA2	3	1.32
(1,282)	1:14:A:D4P:H5	1:15:A:GLY:HA2	5	1.32
(1,282)	1:14:A:D4P:H5	1:15:A:GLY:HA2	20	1.32
(1,282)	1:14:A:D4P:H5	1:15:A:GLY:HA2	12	1.3
(1,252)	1:11:A:ORD:HG3	1:12:A:D4P:H5	16	1.3
(1,282)	1:14:A:D4P:H5	1:15:A:GLY:HA2	6	1.29
(1,282)	1:14:A:D4P:H5	1:15:A:GLY:HA2	7	1.29
(1,282)	1:14:A:D4P:H5	1:15:A:GLY:HA2	17	1.28
(1,274)	1:14:A:D4P:H	1:18:A:D4P:H4	4	1.28
(1,277)	1:14:A:D4P:HA	1:18:A:D4P:H4	5	1.27
(1,252)	1:11:A:ORD:HG3	1:12:A:D4P:H5	1	1.27

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,297)	1:15:A:GLY:HA3	1:18:A:D4P:H4	4	1.26
(1,282)	1:14:A:D4P:H5	1:15:A:GLY:HA2	11	1.26
(1,282)	1:14:A:D4P:H5	1:15:A:GLY:HA2	8	1.25
(1,282)	1:14:A:D4P:H5	1:15:A:GLY:HA2	15	1.25
(1,282)	1:14:A:D4P:H5	1:15:A:GLY:HA2	16	1.25
(1,277)	1:14:A:D4P:HA	1:18:A:D4P:H4	18	1.25
(1,252)	1:11:A:ORD:HG3	1:12:A:D4P:H5	17	1.25
(1,83)	1:4:A:GHP:HA	1:18:A:D4P:H4	1	1.25
(1,282)	1:14:A:D4P:H5	1:15:A:GLY:HA2	9	1.24
(1,282)	1:14:A:D4P:H5	1:15:A:GLY:HA2	10	1.24
(1,282)	1:14:A:D4P:H5	1:15:A:GLY:HA2	13	1.24
(1,171)	1:7:A:D4P:H	1:7:A:D4P:H5	7	1.24
(1,171)	1:7:A:D4P:H	1:7:A:D4P:H5	8	1.24
(1,171)	1:7:A:D4P:H	1:7:A:D4P:H5	10	1.24
(1,171)	1:7:A:D4P:H	1:7:A:D4P:H5	11	1.23
(1,294)	1:15:A:GLY:HA3	1:18:A:D4P:H4	8	1.22
(1,171)	1:7:A:D4P:H	1:7:A:D4P:H5	2	1.22
(1,171)	1:7:A:D4P:H	1:7:A:D4P:H5	9	1.22
(1,171)	1:7:A:D4P:H	1:7:A:D4P:H5	15	1.22
(1,171)	1:7:A:D4P:H	1:7:A:D4P:H5	16	1.22
(1,171)	1:7:A:D4P:H	1:7:A:D4P:H5	13	1.21
(1,282)	1:14:A:D4P:H5	1:15:A:GLY:HA2	18	1.2
(1,171)	1:7:A:D4P:H	1:7:A:D4P:H5	1	1.2
(1,294)	1:15:A:GLY:HA3	1:18:A:D4P:H4	1	1.19
(1,274)	1:14:A:D4P:H	1:18:A:D4P:H4	1	1.19
(1,171)	1:7:A:D4P:H	1:7:A:D4P:H5	3	1.19
(1,171)	1:7:A:D4P:H	1:7:A:D4P:H5	4	1.19
(1,171)	1:7:A:D4P:H	1:7:A:D4P:H5	5	1.19
(1,171)	1:7:A:D4P:H	1:7:A:D4P:H5	6	1.19
(1,171)	1:7:A:D4P:H	1:7:A:D4P:H5	17	1.19
(1,171)	1:7:A:D4P:H	1:7:A:D4P:H5	19	1.19
(1,171)	1:7:A:D4P:H	1:7:A:D4P:H5	20	1.19
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H3	6	1.19
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H5	6	1.19
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H3	12	1.19
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H5	12	1.19
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H3	20	1.19
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H5	20	1.19
(1,43)	1:3:A:DPP:H	1:14:A:D4P:H5	14	1.19
(1,294)	1:15:A:GLY:HA3	1:18:A:D4P:H4	16	1.18
(1,252)	1:11:A:ORD:HG3	1:12:A:D4P:H5	5	1.18
(1,171)	1:7:A:D4P:H	1:7:A:D4P:H5	12	1.18

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,171)	1:7:A:D4P:H	1:7:A:D4P:H5	14	1.18
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H3	1	1.17
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H5	1	1.17
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H3	2	1.17
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H5	2	1.17
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H3	3	1.17
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H5	3	1.17
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H3	5	1.17
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H5	5	1.17
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H3	19	1.17
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H5	19	1.17
(1,43)	1:3:A:DPP:H	1:14:A:D4P:H5	20	1.17
(1,277)	1:14:A:D4P:HA	1:18:A:D4P:H4	1	1.16
(1,277)	1:14:A:D4P:HA	1:18:A:D4P:H4	12	1.16
(1,171)	1:7:A:D4P:H	1:7:A:D4P:H5	18	1.16
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H3	4	1.16
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H5	4	1.16
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H3	14	1.16
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H5	14	1.16
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H3	17	1.16
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H5	17	1.16
(1,252)	1:11:A:ORD:HG3	1:12:A:D4P:H5	10	1.15
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H3	9	1.15
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H5	9	1.15
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H3	10	1.15
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H5	10	1.15
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H3	13	1.15
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H5	13	1.15
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H3	8	1.14
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H5	8	1.14
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H3	15	1.14
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H5	15	1.14
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H3	16	1.14
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H5	16	1.14
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H3	11	1.13
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H5	11	1.13
(1,247)	1:11:A:ORD:HB2	1:12:A:D4P:H5	9	1.12
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H3	7	1.12
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H5	7	1.12
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H3	18	1.12
(1,55)	1:3:A:DPP:HA	1:4:A:GHP:H5	18	1.12
(1,43)	1:3:A:DPP:H	1:14:A:D4P:H5	12	1.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,43)	1:3:A:DPP:H	1:14:A:D4P:H5	19	1.12
(1,294)	1:15:A:GLY:HA3	1:18:A:D4P:H4	2	1.11
(1,43)	1:3:A:DPP:H	1:14:A:D4P:H5	18	1.11
(1,43)	1:3:A:DPP:H	1:14:A:D4P:H5	2	1.1
(1,294)	1:15:A:GLY:HA3	1:18:A:D4P:H4	13	1.09
(1,247)	1:11:A:ORD:HB2	1:12:A:D4P:H5	10	1.09
(1,294)	1:15:A:GLY:HA3	1:18:A:D4P:H4	20	1.08
(1,294)	1:15:A:GLY:HA3	1:18:A:D4P:H4	11	1.07
(1,247)	1:11:A:ORD:HB2	1:12:A:D4P:H5	16	1.07
(1,247)	1:11:A:ORD:HB2	1:12:A:D4P:H5	8	1.06
(1,247)	1:11:A:ORD:HB2	1:12:A:D4P:H5	11	1.06
(1,24)	1:2:A:ASN:HA	1:14:A:D4P:H5	5	1.06
(1,247)	1:11:A:ORD:HB2	1:12:A:D4P:H5	18	1.05
(1,297)	1:15:A:GLY:HA3	1:18:A:D4P:H4	18	1.04
(1,24)	1:2:A:ASN:HA	1:14:A:D4P:H5	6	1.04
(1,247)	1:11:A:ORD:HB2	1:12:A:D4P:H5	2	1.03
(1,43)	1:3:A:DPP:H	1:14:A:D4P:H5	6	1.03
(1,43)	1:3:A:DPP:H	1:14:A:D4P:H5	17	1.03
(1,297)	1:15:A:GLY:HA3	1:18:A:D4P:H4	5	1.02
(1,294)	1:15:A:GLY:HA3	1:18:A:D4P:H4	9	1.02
(1,247)	1:11:A:ORD:HB2	1:12:A:D4P:H5	3	1.02
(1,247)	1:11:A:ORD:HB2	1:12:A:D4P:H5	7	1.02
(1,43)	1:3:A:DPP:H	1:14:A:D4P:H5	1	1.02
(1,43)	1:3:A:DPP:H	1:14:A:D4P:H5	3	1.02
(1,43)	1:3:A:DPP:H	1:14:A:D4P:H5	4	1.02
(1,247)	1:11:A:ORD:HB2	1:12:A:D4P:H5	13	1.01
(1,24)	1:2:A:ASN:HA	1:14:A:D4P:H5	20	1.01
(1,247)	1:11:A:ORD:HB2	1:12:A:D4P:H5	15	1.0
(1,83)	1:4:A:GHP:HA	1:18:A:D4P:H4	7	1.0
(1,83)	1:4:A:GHP:HA	1:18:A:D4P:H4	15	0.99
(1,247)	1:11:A:ORD:HB2	1:12:A:D4P:H5	1	0.98
(1,247)	1:11:A:ORD:HB2	1:12:A:D4P:H5	19	0.98
(1,24)	1:2:A:ASN:HA	1:14:A:D4P:H5	3	0.98
(1,274)	1:14:A:D4P:H	1:18:A:D4P:H4	18	0.97
(1,253)	1:12:A:D4P:H	1:12:A:D4P:H5	20	0.97
(1,247)	1:11:A:ORD:HB2	1:12:A:D4P:H5	6	0.97
(1,24)	1:2:A:ASN:HA	1:14:A:D4P:H5	4	0.97
(1,24)	1:2:A:ASN:HA	1:14:A:D4P:H5	17	0.97
(1,24)	1:2:A:ASN:HA	1:14:A:D4P:H5	19	0.97
(1,247)	1:11:A:ORD:HB2	1:12:A:D4P:H5	17	0.96
(1,43)	1:3:A:DPP:H	1:14:A:D4P:H5	7	0.96
(1,274)	1:14:A:D4P:H	1:18:A:D4P:H4	5	0.95

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,271)	1:14:A:D4P:H	1:14:A:D4P:H5	3	0.95
(1,271)	1:14:A:D4P:H	1:14:A:D4P:H5	5	0.95
(1,271)	1:14:A:D4P:H	1:14:A:D4P:H5	6	0.95
(1,271)	1:14:A:D4P:H	1:14:A:D4P:H5	12	0.95
(1,253)	1:12:A:D4P:H	1:12:A:D4P:H5	12	0.95
(1,253)	1:12:A:D4P:H	1:12:A:D4P:H5	14	0.95
(1,247)	1:11:A:ORD:HB2	1:12:A:D4P:H5	5	0.95
(1,24)	1:2:A:ASN:HA	1:14:A:D4P:H5	14	0.95
(1,288)	1:15:A:GLY:H	1:18:A:D4P:H4	15	0.94
(1,277)	1:14:A:D4P:HA	1:18:A:D4P:H4	17	0.94
(1,271)	1:14:A:D4P:H	1:14:A:D4P:H5	1	0.94
(1,271)	1:14:A:D4P:H	1:14:A:D4P:H5	2	0.94
(1,271)	1:14:A:D4P:H	1:14:A:D4P:H5	17	0.94
(1,271)	1:14:A:D4P:H	1:14:A:D4P:H5	19	0.94
(1,253)	1:12:A:D4P:H	1:12:A:D4P:H5	5	0.94
(1,253)	1:12:A:D4P:H	1:12:A:D4P:H5	18	0.94
(1,297)	1:15:A:GLY:HA3	1:18:A:D4P:H4	12	0.93
(1,271)	1:14:A:D4P:H	1:14:A:D4P:H5	4	0.93
(1,271)	1:14:A:D4P:H	1:14:A:D4P:H5	7	0.93
(1,271)	1:14:A:D4P:H	1:14:A:D4P:H5	9	0.93
(1,271)	1:14:A:D4P:H	1:14:A:D4P:H5	10	0.93
(1,271)	1:14:A:D4P:H	1:14:A:D4P:H5	14	0.93
(1,271)	1:14:A:D4P:H	1:14:A:D4P:H5	16	0.93
(1,271)	1:14:A:D4P:H	1:14:A:D4P:H5	18	0.93
(1,271)	1:14:A:D4P:H	1:14:A:D4P:H5	20	0.93
(1,253)	1:12:A:D4P:H	1:12:A:D4P:H5	4	0.93
(1,253)	1:12:A:D4P:H	1:12:A:D4P:H5	17	0.93
(1,43)	1:3:A:DPP:H	1:14:A:D4P:H5	5	0.93
(1,24)	1:2:A:ASN:HA	1:14:A:D4P:H5	1	0.93
(1,288)	1:15:A:GLY:H	1:18:A:D4P:H4	7	0.92
(1,271)	1:14:A:D4P:H	1:14:A:D4P:H5	8	0.92
(1,271)	1:14:A:D4P:H	1:14:A:D4P:H5	11	0.92
(1,271)	1:14:A:D4P:H	1:14:A:D4P:H5	13	0.92
(1,271)	1:14:A:D4P:H	1:14:A:D4P:H5	15	0.92
(1,253)	1:12:A:D4P:H	1:12:A:D4P:H5	1	0.92
(1,253)	1:12:A:D4P:H	1:12:A:D4P:H5	3	0.92
(1,253)	1:12:A:D4P:H	1:12:A:D4P:H5	6	0.92
(1,253)	1:12:A:D4P:H	1:12:A:D4P:H5	19	0.92
(1,247)	1:11:A:ORD:HB2	1:12:A:D4P:H5	4	0.92
(1,43)	1:3:A:DPP:H	1:14:A:D4P:H5	13	0.92
(1,43)	1:3:A:DPP:H	1:14:A:D4P:H5	11	0.91
(1,43)	1:3:A:DPP:H	1:14:A:D4P:H5	15	0.91

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,277)	1:14:A:D4P:HA	1:18:A:D4P:H4	10	0.9
(1,253)	1:12:A:D4P:H	1:12:A:D4P:H5	2	0.9
(1,253)	1:12:A:D4P:H	1:12:A:D4P:H5	9	0.9
(1,247)	1:11:A:ORD:HB2	1:12:A:D4P:H5	14	0.9
(1,43)	1:3:A:DPP:H	1:14:A:D4P:H5	8	0.9
(1,24)	1:2:A:ASN:HA	1:14:A:D4P:H5	2	0.9
(1,253)	1:12:A:D4P:H	1:12:A:D4P:H5	7	0.89
(1,253)	1:12:A:D4P:H	1:12:A:D4P:H5	10	0.89
(1,43)	1:3:A:DPP:H	1:14:A:D4P:H5	16	0.89
(1,253)	1:12:A:D4P:H	1:12:A:D4P:H5	13	0.88
(1,253)	1:12:A:D4P:H	1:12:A:D4P:H5	16	0.87
(1,43)	1:3:A:DPP:H	1:14:A:D4P:H5	10	0.87
(1,253)	1:12:A:D4P:H	1:12:A:D4P:H5	8	0.86
(1,253)	1:12:A:D4P:H	1:12:A:D4P:H5	11	0.86
(1,253)	1:12:A:D4P:H	1:12:A:D4P:H5	15	0.86
(1,247)	1:11:A:ORD:HB2	1:12:A:D4P:H5	12	0.86
(1,168)	1:6:A:DTH:HG22	1:7:A:D4P:H5	4	0.86
(1,247)	1:11:A:ORD:HB2	1:12:A:D4P:H5	20	0.85
(1,168)	1:6:A:DTH:HG21	1:7:A:D4P:H5	1	0.85
(1,274)	1:14:A:D4P:H	1:18:A:D4P:H4	9	0.84
(1,168)	1:6:A:DTH:HG22	1:7:A:D4P:H5	2	0.84
(1,168)	1:6:A:DTH:HG23	1:7:A:D4P:H5	12	0.84
(1,43)	1:3:A:DPP:H	1:14:A:D4P:H5	9	0.84
(1,24)	1:2:A:ASN:HA	1:14:A:D4P:H5	9	0.84
(1,168)	1:6:A:DTH:HG23	1:7:A:D4P:H5	8	0.83
(1,168)	1:6:A:DTH:HG23	1:7:A:D4P:H5	14	0.83
(1,24)	1:2:A:ASN:HA	1:14:A:D4P:H5	10	0.83
(1,24)	1:2:A:ASN:HA	1:14:A:D4P:H5	12	0.83
(1,274)	1:14:A:D4P:H	1:18:A:D4P:H4	12	0.82
(1,168)	1:6:A:DTH:HG22	1:7:A:D4P:H5	15	0.82
(1,168)	1:6:A:DTH:HG22	1:7:A:D4P:H5	7	0.81
(1,83)	1:4:A:GHP:HA	1:18:A:D4P:H4	9	0.81
(1,294)	1:15:A:GLY:HA3	1:18:A:D4P:H4	3	0.79
(1,168)	1:6:A:DTH:HG23	1:7:A:D4P:H5	18	0.79
(1,24)	1:2:A:ASN:HA	1:14:A:D4P:H5	11	0.78
(1,24)	1:2:A:ASN:HA	1:14:A:D4P:H5	16	0.78
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H3	14	0.77
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H5	14	0.77
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H3	20	0.77
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H5	20	0.77
(1,24)	1:2:A:ASN:HA	1:14:A:D4P:H5	15	0.77
(1,288)	1:15:A:GLY:H	1:18:A:D4P:H4	19	0.76

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H3	1	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H5	1	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H3	2	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H5	2	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H3	3	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H5	3	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H3	4	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H5	4	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H3	5	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H5	5	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H3	6	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H5	6	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H3	7	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H5	7	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H3	8	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H5	8	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H3	9	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H5	9	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H3	10	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H5	10	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H3	11	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H5	11	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H3	12	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H5	12	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H3	13	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H5	13	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H3	15	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H5	15	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H3	16	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H5	16	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H3	17	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H5	17	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H3	18	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H5	18	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H3	19	0.76
(1,191)	1:8:A:GHP:H	1:8:A:GHP:H5	19	0.76
(1,24)	1:2:A:ASN:HA	1:14:A:D4P:H5	8	0.76
(1,24)	1:2:A:ASN:HA	1:14:A:D4P:H5	13	0.76
(1,297)	1:15:A:GLY:HA3	1:18:A:D4P:H4	17	0.73
(1,168)	1:6:A:DTH:HG21	1:7:A:D4P:H4	13	0.72
(1,288)	1:15:A:GLY:H	1:18:A:D4P:H4	6	0.71
(1,277)	1:14:A:D4P:HA	1:18:A:D4P:H4	9	0.71

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,24)	1:2:A:ASN:HA	1:14:A:D4P:H5	7	0.71
(1,274)	1:14:A:D4P:H	1:18:A:D4P:H4	10	0.7
(1,280)	1:14:A:D4P:H5	1:15:A:GLY:HA2	14	0.69
(1,297)	1:15:A:GLY:HA3	1:18:A:D4P:H4	10	0.66
(1,280)	1:14:A:D4P:H5	1:15:A:GLY:HA2	1	0.66
(1,280)	1:14:A:D4P:H5	1:15:A:GLY:HA2	2	0.66
(1,280)	1:14:A:D4P:H5	1:15:A:GLY:HA2	19	0.66
(1,280)	1:14:A:D4P:H5	1:15:A:GLY:HA2	4	0.65
(1,99)	1:4:A:GHP:H3	1:13:A:DTH:H	9	0.65
(1,99)	1:4:A:GHP:H5	1:13:A:DTH:H	9	0.65
(1,99)	1:4:A:GHP:H3	1:13:A:DTH:H	12	0.65
(1,99)	1:4:A:GHP:H5	1:13:A:DTH:H	12	0.65
(1,294)	1:15:A:GLY:HA3	1:18:A:D4P:H4	4	0.64
(1,99)	1:4:A:GHP:H3	1:13:A:DTH:H	7	0.64
(1,99)	1:4:A:GHP:H5	1:13:A:DTH:H	7	0.64
(1,99)	1:4:A:GHP:H3	1:13:A:DTH:H	13	0.64
(1,99)	1:4:A:GHP:H5	1:13:A:DTH:H	13	0.64
(1,99)	1:4:A:GHP:H3	1:13:A:DTH:H	16	0.64
(1,99)	1:4:A:GHP:H5	1:13:A:DTH:H	16	0.64
(1,280)	1:14:A:D4P:H5	1:15:A:GLY:HA2	3	0.63
(1,280)	1:14:A:D4P:H5	1:15:A:GLY:HA2	5	0.63
(1,280)	1:14:A:D4P:H5	1:15:A:GLY:HA2	20	0.63
(1,142)	1:5:A:ORD:HG2	1:14:A:D4P:H5	5	0.63
(1,99)	1:4:A:GHP:H3	1:13:A:DTH:H	2	0.63
(1,99)	1:4:A:GHP:H5	1:13:A:DTH:H	2	0.63
(1,99)	1:4:A:GHP:H3	1:13:A:DTH:H	5	0.63
(1,99)	1:4:A:GHP:H5	1:13:A:DTH:H	5	0.63
(1,99)	1:4:A:GHP:H3	1:13:A:DTH:H	8	0.63
(1,99)	1:4:A:GHP:H5	1:13:A:DTH:H	8	0.63
(1,99)	1:4:A:GHP:H3	1:13:A:DTH:H	15	0.63
(1,99)	1:4:A:GHP:H5	1:13:A:DTH:H	15	0.63
(1,24)	1:2:A:ASN:HA	1:14:A:D4P:H5	18	0.63
(1,168)	1:6:A:DTH:HG21	1:7:A:D4P:H4	17	0.62
(1,142)	1:5:A:ORD:HG2	1:14:A:D4P:H5	1	0.62
(1,142)	1:5:A:ORD:HG2	1:14:A:D4P:H5	3	0.62
(1,99)	1:4:A:GHP:H3	1:13:A:DTH:H	1	0.62
(1,99)	1:4:A:GHP:H5	1:13:A:DTH:H	1	0.62
(1,99)	1:4:A:GHP:H3	1:13:A:DTH:H	3	0.62
(1,99)	1:4:A:GHP:H5	1:13:A:DTH:H	3	0.62
(1,99)	1:4:A:GHP:H3	1:13:A:DTH:H	10	0.62
(1,99)	1:4:A:GHP:H5	1:13:A:DTH:H	10	0.62
(1,99)	1:4:A:GHP:H3	1:13:A:DTH:H	11	0.62

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,99)	1:4:A:GHP:H5	1:13:A:DTH:H	11	0.62
(1,99)	1:4:A:GHP:H3	1:13:A:DTH:H	18	0.62
(1,99)	1:4:A:GHP:H5	1:13:A:DTH:H	18	0.62
(1,99)	1:4:A:GHP:H3	1:13:A:DTH:H	19	0.62
(1,99)	1:4:A:GHP:H5	1:13:A:DTH:H	19	0.62
(1,280)	1:14:A:D4P:H5	1:15:A:GLY:HA2	12	0.61
(1,99)	1:4:A:GHP:H3	1:13:A:DTH:H	4	0.61
(1,99)	1:4:A:GHP:H5	1:13:A:DTH:H	4	0.61
(1,99)	1:4:A:GHP:H3	1:13:A:DTH:H	6	0.61
(1,99)	1:4:A:GHP:H5	1:13:A:DTH:H	6	0.61
(1,99)	1:4:A:GHP:H3	1:13:A:DTH:H	17	0.61
(1,99)	1:4:A:GHP:H5	1:13:A:DTH:H	17	0.61
(1,37)	1:2:A:ASN:HB3	1:14:A:D4P:H5	5	0.61
(1,37)	1:2:A:ASN:HB3	1:14:A:D4P:H5	6	0.61
(1,280)	1:14:A:D4P:H5	1:15:A:GLY:HA2	6	0.6
(1,280)	1:14:A:D4P:H5	1:15:A:GLY:HA2	7	0.6
(1,142)	1:5:A:ORD:HG3	1:14:A:D4P:H5	13	0.6
(1,99)	1:4:A:GHP:H3	1:13:A:DTH:H	14	0.6
(1,99)	1:4:A:GHP:H5	1:13:A:DTH:H	14	0.6
(1,99)	1:4:A:GHP:H3	1:13:A:DTH:H	20	0.6
(1,99)	1:4:A:GHP:H5	1:13:A:DTH:H	20	0.6
(1,280)	1:14:A:D4P:H5	1:15:A:GLY:HA2	17	0.59
(1,274)	1:14:A:D4P:H	1:18:A:D4P:H4	17	0.59
(1,142)	1:5:A:ORD:HG2	1:14:A:D4P:H5	6	0.59
(1,83)	1:4:A:GHP:HA	1:18:A:D4P:H4	19	0.59
(1,37)	1:2:A:ASN:HB3	1:14:A:D4P:H5	17	0.59
(1,142)	1:5:A:ORD:HG2	1:14:A:D4P:H5	2	0.58
(1,142)	1:5:A:ORD:HG2	1:14:A:D4P:H5	14	0.58
(1,37)	1:2:A:ASN:HB3	1:14:A:D4P:H5	3	0.58
(1,37)	1:2:A:ASN:HB3	1:14:A:D4P:H5	12	0.58
(1,280)	1:14:A:D4P:H5	1:15:A:GLY:HA2	11	0.57
(1,37)	1:2:A:ASN:HB3	1:14:A:D4P:H5	1	0.57
(1,37)	1:2:A:ASN:HB3	1:14:A:D4P:H5	20	0.57
(1,280)	1:14:A:D4P:H5	1:15:A:GLY:HA2	8	0.56
(1,280)	1:14:A:D4P:H5	1:15:A:GLY:HA2	15	0.56
(1,280)	1:14:A:D4P:H5	1:15:A:GLY:HA2	16	0.56
(1,37)	1:2:A:ASN:HB3	1:14:A:D4P:H5	4	0.56
(1,37)	1:2:A:ASN:HB3	1:14:A:D4P:H5	14	0.56
(1,280)	1:14:A:D4P:H5	1:15:A:GLY:HA2	9	0.55
(1,280)	1:14:A:D4P:H5	1:15:A:GLY:HA2	10	0.55
(1,280)	1:14:A:D4P:H5	1:15:A:GLY:HA2	13	0.55
(1,142)	1:5:A:ORD:HG2	1:14:A:D4P:H5	20	0.55

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,297)	1:15:A:GLY:HA3	1:18:A:D4P:H4	6	0.54
(1,37)	1:2:A:ASN:HB3	1:14:A:D4P:H5	19	0.54
(1,168)	1:6:A:DTH:HG23	1:7:A:D4P:H4	9	0.53
(1,37)	1:2:A:ASN:HB3	1:14:A:D4P:H5	2	0.53
(1,142)	1:5:A:ORD:HG3	1:14:A:D4P:H4	9	0.52
(1,280)	1:14:A:D4P:H5	1:15:A:GLY:HA2	18	0.51
(1,277)	1:14:A:D4P:HA	1:18:A:D4P:H4	15	0.49
(1,277)	1:14:A:D4P:HA	1:18:A:D4P:H4	7	0.48
(1,142)	1:5:A:ORD:HG2	1:14:A:D4P:H5	12	0.47
(1,168)	1:6:A:DTH:HG21	1:7:A:D4P:H4	16	0.46
(1,294)	1:15:A:GLY:HA3	1:18:A:D4P:H4	18	0.42
(1,168)	1:6:A:DTH:HG23	1:7:A:D4P:H4	20	0.42
(1,142)	1:5:A:ORD:HG2	1:14:A:D4P:H5	4	0.41
(1,294)	1:15:A:GLY:HA3	1:18:A:D4P:H4	5	0.4
(1,37)	1:2:A:ASN:HB3	1:14:A:D4P:H5	10	0.4
(1,297)	1:15:A:GLY:HA3	1:18:A:D4P:H4	19	0.39
(1,37)	1:2:A:ASN:HB3	1:14:A:D4P:H5	9	0.38
(1,37)	1:2:A:ASN:HB3	1:14:A:D4P:H5	15	0.38
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG21	2	0.37
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG22	2	0.37
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG23	2	0.37
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG21	2	0.37
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG22	2	0.37
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG23	2	0.37
(1,142)	1:5:A:ORD:HG3	1:14:A:D4P:H4	11	0.37
(1,142)	1:5:A:ORD:HG2	1:14:A:D4P:H5	19	0.37
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG21	7	0.36
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG22	7	0.36
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG23	7	0.36
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG21	7	0.36
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG22	7	0.36
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG23	7	0.36
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG21	8	0.36
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG22	8	0.36
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG23	8	0.36
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG21	8	0.36
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG22	8	0.36
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG23	8	0.36
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG21	9	0.36
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG22	9	0.36
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG23	9	0.36
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG21	9	0.36

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG22	9	0.36
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG23	9	0.36
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG21	10	0.36
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG22	10	0.36
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG23	10	0.36
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG21	10	0.36
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG22	10	0.36
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG23	10	0.36
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG21	12	0.36
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG22	12	0.36
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG23	12	0.36
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG21	12	0.36
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG22	12	0.36
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG23	12	0.36
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG21	16	0.36
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG22	16	0.36
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG23	16	0.36
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG21	16	0.36
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG22	16	0.36
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG23	16	0.36
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG21	20	0.36
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG22	20	0.36
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG23	20	0.36
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG21	20	0.36
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG22	20	0.36
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG23	20	0.36
(1,37)	1:2:A:ASN:HB3	1:14:A:D4P:H5	7	0.36
(1,37)	1:2:A:ASN:HB3	1:14:A:D4P:H5	8	0.36
(1,37)	1:2:A:ASN:HB3	1:14:A:D4P:H5	11	0.36
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG21	1	0.35
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG22	1	0.35
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG23	1	0.35
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG21	1	0.35
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG22	1	0.35
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG23	1	0.35
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG21	3	0.35
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG22	3	0.35
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG23	3	0.35
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG21	3	0.35
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG22	3	0.35
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG23	3	0.35
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG21	11	0.35

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG22	11	0.35
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG23	11	0.35
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG21	11	0.35
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG22	11	0.35
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG23	11	0.35
(1,168)	1:6:A:DTH:HG22	1:7:A:D4P:H4	5	0.35
(1,168)	1:6:A:DTH:HG21	1:7:A:D4P:H4	10	0.35
(1,320)	1:18:A:D4P:H	1:18:A:D4P:H5	20	0.34
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG21	4	0.34
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG22	4	0.34
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG23	4	0.34
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG21	4	0.34
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG22	4	0.34
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG23	4	0.34
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG21	6	0.33
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG22	6	0.33
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG23	6	0.33
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG21	6	0.33
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG22	6	0.33
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG23	6	0.33
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG21	14	0.33
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG22	14	0.33
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG23	14	0.33
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG21	14	0.33
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG22	14	0.33
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG23	14	0.33
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG21	15	0.33
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG22	15	0.33
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG23	15	0.33
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG21	15	0.33
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG22	15	0.33
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG23	15	0.33
(1,168)	1:6:A:DTH:HG23	1:7:A:D4P:H4	19	0.33
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG21	13	0.32
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG22	13	0.32
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG23	13	0.32
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG21	13	0.32
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG22	13	0.32
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG23	13	0.32
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG21	17	0.32
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG22	17	0.32
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG23	17	0.32

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG21	17	0.32
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG22	17	0.32
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG23	17	0.32
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG21	19	0.32
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG22	19	0.32
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG23	19	0.32
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG21	19	0.32
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG22	19	0.32
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG23	19	0.32
(1,83)	1:4:A:GHP:HA	1:18:A:D4P:H4	6	0.32
(1,37)	1:2:A:ASN:HB3	1:14:A:D4P:H5	16	0.32
(1,294)	1:15:A:GLY:HA3	1:18:A:D4P:H4	12	0.31
(1,274)	1:14:A:D4P:H	1:18:A:D4P:H4	7	0.31
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG21	5	0.31
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG22	5	0.31
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG23	5	0.31
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG21	5	0.31
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG22	5	0.31
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG23	5	0.31
(1,37)	1:2:A:ASN:HB3	1:14:A:D4P:H5	13	0.3
(1,297)	1:15:A:GLY:HA3	1:18:A:D4P:H4	7	0.29
(1,297)	1:15:A:GLY:HA3	1:18:A:D4P:H4	15	0.29
(1,274)	1:14:A:D4P:H	1:18:A:D4P:H4	15	0.29
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG21	18	0.29
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG22	18	0.29
(1,204)	1:8:A:GHP:H3	1:9:A:THR:HG23	18	0.29
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG21	18	0.29
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG22	18	0.29
(1,204)	1:8:A:GHP:H5	1:9:A:THR:HG23	18	0.29
(1,37)	1:2:A:ASN:HB3	1:14:A:D4P:H5	18	0.29
(1,142)	1:5:A:ORD:HG3	1:14:A:D4P:H4	16	0.28
(1,320)	1:18:A:D4P:H	1:18:A:D4P:H5	19	0.26
(1,168)	1:6:A:DTH:HG23	1:7:A:D4P:H4	3	0.26
(1,168)	1:6:A:DTH:HG23	1:7:A:D4P:H4	11	0.25
(1,100)	1:4:A:GHP:H3	1:6:A:DTH:H	12	0.25
(1,100)	1:4:A:GHP:H5	1:6:A:DTH:H	12	0.25
(1,100)	1:4:A:GHP:H3	1:6:A:DTH:H	2	0.24
(1,100)	1:4:A:GHP:H5	1:6:A:DTH:H	2	0.24
(1,100)	1:4:A:GHP:H3	1:6:A:DTH:H	6	0.24
(1,100)	1:4:A:GHP:H5	1:6:A:DTH:H	6	0.24
(1,100)	1:4:A:GHP:H3	1:6:A:DTH:H	20	0.24
(1,100)	1:4:A:GHP:H5	1:6:A:DTH:H	20	0.24

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,320)	1:18:A:D4P:H	1:18:A:D4P:H5	14	0.23
(1,100)	1:4:A:GHP:H3	1:6:A:DTH:H	5	0.23
(1,100)	1:4:A:GHP:H5	1:6:A:DTH:H	5	0.23
(1,100)	1:4:A:GHP:H3	1:6:A:DTH:H	3	0.22
(1,100)	1:4:A:GHP:H5	1:6:A:DTH:H	3	0.22
(1,168)	1:6:A:DTH:HG22	1:7:A:D4P:H4	6	0.21
(1,100)	1:4:A:GHP:H3	1:6:A:DTH:H	14	0.2
(1,100)	1:4:A:GHP:H5	1:6:A:DTH:H	14	0.2
(1,100)	1:4:A:GHP:H3	1:6:A:DTH:H	17	0.2
(1,100)	1:4:A:GHP:H5	1:6:A:DTH:H	17	0.2
(1,100)	1:4:A:GHP:H3	1:6:A:DTH:H	19	0.2
(1,100)	1:4:A:GHP:H5	1:6:A:DTH:H	19	0.2
(1,320)	1:18:A:D4P:H	1:18:A:D4P:H5	10	0.18
(1,100)	1:4:A:GHP:H3	1:6:A:DTH:H	1	0.18
(1,100)	1:4:A:GHP:H5	1:6:A:DTH:H	1	0.18
(1,320)	1:18:A:D4P:H	1:18:A:D4P:H5	16	0.17
(1,142)	1:5:A:ORD:HG2	1:14:A:D4P:H4	17	0.17
(1,100)	1:4:A:GHP:H3	1:6:A:DTH:H	4	0.17
(1,100)	1:4:A:GHP:H5	1:6:A:DTH:H	4	0.17
(1,320)	1:18:A:D4P:H	1:18:A:D4P:H5	18	0.16
(1,100)	1:4:A:GHP:H3	1:6:A:DTH:H	9	0.16
(1,100)	1:4:A:GHP:H5	1:6:A:DTH:H	9	0.16
(1,100)	1:4:A:GHP:H3	1:6:A:DTH:H	13	0.16
(1,100)	1:4:A:GHP:H5	1:6:A:DTH:H	13	0.16
(1,100)	1:4:A:GHP:H3	1:6:A:DTH:H	15	0.15
(1,100)	1:4:A:GHP:H5	1:6:A:DTH:H	15	0.15
(1,100)	1:4:A:GHP:H3	1:6:A:DTH:H	18	0.15
(1,100)	1:4:A:GHP:H5	1:6:A:DTH:H	18	0.15
(1,329)	1:3:A:DPP:NG	1:18:A:D4P:CA	1	0.14
(1,329)	1:3:A:DPP:NG	1:18:A:D4P:CA	2	0.14
(1,329)	1:3:A:DPP:NG	1:18:A:D4P:CA	3	0.14
(1,329)	1:3:A:DPP:NG	1:18:A:D4P:CA	4	0.14
(1,329)	1:3:A:DPP:NG	1:18:A:D4P:CA	5	0.14
(1,329)	1:3:A:DPP:NG	1:18:A:D4P:CA	6	0.14
(1,329)	1:3:A:DPP:NG	1:18:A:D4P:CA	7	0.14
(1,329)	1:3:A:DPP:NG	1:18:A:D4P:CA	8	0.14
(1,329)	1:3:A:DPP:NG	1:18:A:D4P:CA	9	0.14
(1,329)	1:3:A:DPP:NG	1:18:A:D4P:CA	12	0.14
(1,325)	1:3:A:DPP:NG	1:18:A:D4P:CA	1	0.14
(1,325)	1:3:A:DPP:NG	1:18:A:D4P:CA	2	0.14
(1,325)	1:3:A:DPP:NG	1:18:A:D4P:CA	3	0.14
(1,325)	1:3:A:DPP:NG	1:18:A:D4P:CA	4	0.14

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,325)	1:3:A:DPP:NG	1:18:A:D4P:CA	5	0.14
(1,325)	1:3:A:DPP:NG	1:18:A:D4P:CA	6	0.14
(1,325)	1:3:A:DPP:NG	1:18:A:D4P:CA	7	0.14
(1,325)	1:3:A:DPP:NG	1:18:A:D4P:CA	8	0.14
(1,325)	1:3:A:DPP:NG	1:18:A:D4P:CA	9	0.14
(1,325)	1:3:A:DPP:NG	1:18:A:D4P:CA	12	0.14
(1,100)	1:4:A:GHP:H3	1:6:A:DTH:H	7	0.14
(1,100)	1:4:A:GHP:H5	1:6:A:DTH:H	7	0.14
(1,100)	1:4:A:GHP:H3	1:6:A:DTH:H	10	0.14
(1,100)	1:4:A:GHP:H5	1:6:A:DTH:H	10	0.14
(1,329)	1:3:A:DPP:NG	1:18:A:D4P:CA	10	0.13
(1,329)	1:3:A:DPP:NG	1:18:A:D4P:CA	11	0.13
(1,329)	1:3:A:DPP:NG	1:18:A:D4P:CA	13	0.13
(1,329)	1:3:A:DPP:NG	1:18:A:D4P:CA	14	0.13
(1,329)	1:3:A:DPP:NG	1:18:A:D4P:CA	15	0.13
(1,329)	1:3:A:DPP:NG	1:18:A:D4P:CA	16	0.13
(1,329)	1:3:A:DPP:NG	1:18:A:D4P:CA	17	0.13
(1,329)	1:3:A:DPP:NG	1:18:A:D4P:CA	18	0.13
(1,329)	1:3:A:DPP:NG	1:18:A:D4P:CA	20	0.13
(1,325)	1:3:A:DPP:NG	1:18:A:D4P:CA	10	0.13
(1,325)	1:3:A:DPP:NG	1:18:A:D4P:CA	11	0.13
(1,325)	1:3:A:DPP:NG	1:18:A:D4P:CA	13	0.13
(1,325)	1:3:A:DPP:NG	1:18:A:D4P:CA	14	0.13
(1,325)	1:3:A:DPP:NG	1:18:A:D4P:CA	15	0.13
(1,325)	1:3:A:DPP:NG	1:18:A:D4P:CA	16	0.13
(1,325)	1:3:A:DPP:NG	1:18:A:D4P:CA	17	0.13
(1,325)	1:3:A:DPP:NG	1:18:A:D4P:CA	18	0.13
(1,325)	1:3:A:DPP:NG	1:18:A:D4P:CA	20	0.13
(1,320)	1:18:A:D4P:H	1:18:A:D4P:H5	9	0.13
(1,320)	1:18:A:D4P:H	1:18:A:D4P:H5	12	0.13
(1,320)	1:18:A:D4P:H	1:18:A:D4P:H5	13	0.13
(1,320)	1:18:A:D4P:H	1:18:A:D4P:H5	15	0.13
(1,136)	1:5:A:ORD:HD2	1:14:A:D4P:H5	16	0.13
(1,100)	1:4:A:GHP:H3	1:6:A:DTH:H	8	0.13
(1,100)	1:4:A:GHP:H5	1:6:A:DTH:H	8	0.13
(1,100)	1:4:A:GHP:H3	1:6:A:DTH:H	11	0.13
(1,100)	1:4:A:GHP:H5	1:6:A:DTH:H	11	0.13
(1,100)	1:4:A:GHP:H3	1:6:A:DTH:H	16	0.13
(1,100)	1:4:A:GHP:H5	1:6:A:DTH:H	16	0.13
(1,329)	1:3:A:DPP:NG	1:18:A:D4P:CA	19	0.12
(1,325)	1:3:A:DPP:NG	1:18:A:D4P:CA	19	0.12
(1,320)	1:18:A:D4P:H	1:18:A:D4P:H5	7	0.12

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(1,320)	1:18:A:D4P:H	1:18:A:D4P:H5	11	0.12
(1,320)	1:18:A:D4P:H	1:18:A:D4P:H5	17	0.12
(1,277)	1:14:A:D4P:HA	1:18:A:D4P:H4	19	0.12
(1,136)	1:5:A:ORD:HD2	1:14:A:D4P:H5	13	0.12
(1,320)	1:18:A:D4P:H	1:18:A:D4P:H5	8	0.11
(1,294)	1:15:A:GLY:HA3	1:18:A:D4P:H4	17	0.11
(1,320)	1:18:A:D4P:H	1:18:A:D4P:H5	6	0.1

## 10 Dihedral-angle violation analysis

No dihedral-angle restraints found