



Full wwPDB NMR Structure Validation Report ⓘ

Jun 6, 2023 – 07:14 pm BST

PDB ID : 7ACT
BMRB ID : 34511
Title : The SARS-CoV-2 nucleocapsid phosphoprotein N-terminal domain in complex with 10mer ssRNA
Authors : Veverka, V.
Deposited on : 2020-09-11

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-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

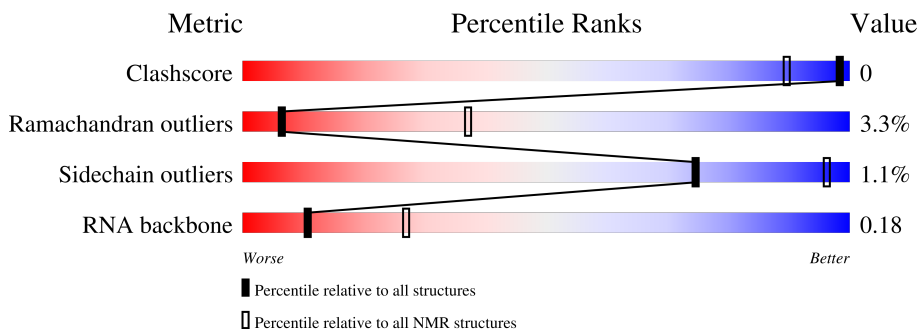
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 82%.

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
RNA backbone	4643	676

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

Mol	Chain	Length	Quality of chain
1	A	140	 74% 14% 10% .
2	B	10	 20% 50% 30%

2 Ensemble composition and analysis

This entry contains 10 models. Model 5 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:46-A:95, A:102-A:174 (123)	0.78	5

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 1 clusters and 5 single-model clusters were found.

Cluster number	Models
1	5, 6, 7, 8, 9
Single-model clusters	1; 2; 3; 4; 10

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2390 atoms, of which 1128 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Nucleoprotein.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	137	2072	661	1020	192	198	1	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	41	GLY	-	expression tag	UNP P0DTC9
A	42	ALA	-	expression tag	UNP P0DTC9
A	43	MET	-	expression tag	UNP P0DTC9

- Molecule 2 is a RNA chain called ssRNA.

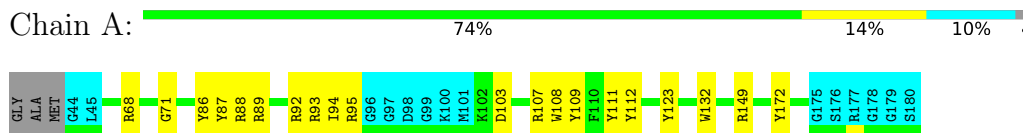
Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	P	
2	B	10	318	94	108	35	71	10	0

4 Residue-property plots [i](#)

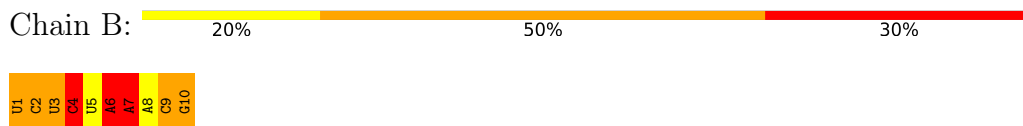
4.1 Average score per residue in the NMR ensemble

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: Nucleoprotein



- Molecule 2: ssRNA

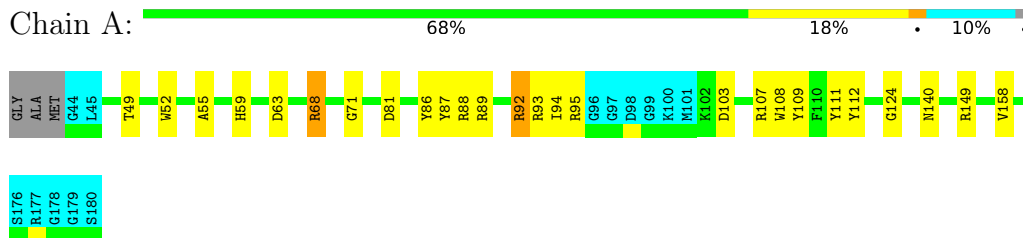


4.2 Scores per residue for each member of the ensemble

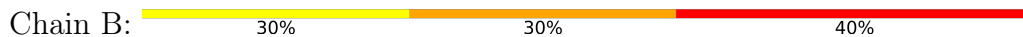
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Nucleoprotein



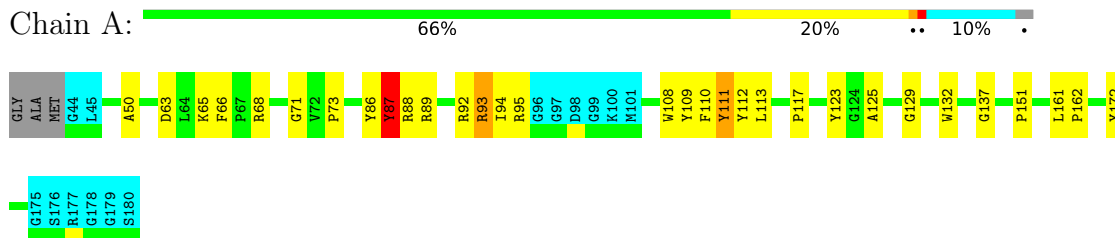
- Molecule 2: ssRNA



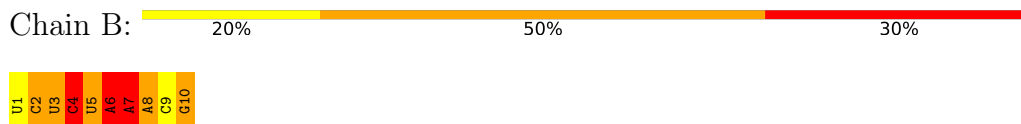


4.2.2 Score per residue for model 2

- Molecule 1: Nucleoprotein

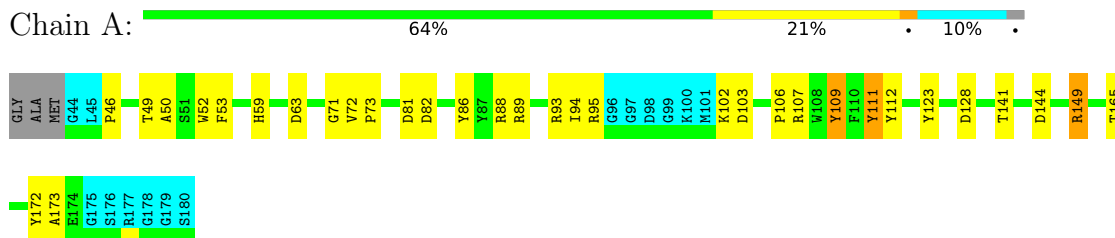


- Molecule 2: ssRNA

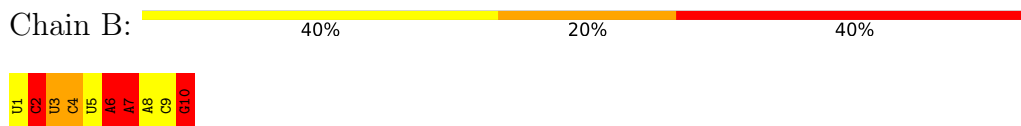


4.2.3 Score per residue for model 3

- Molecule 1: Nucleoprotein



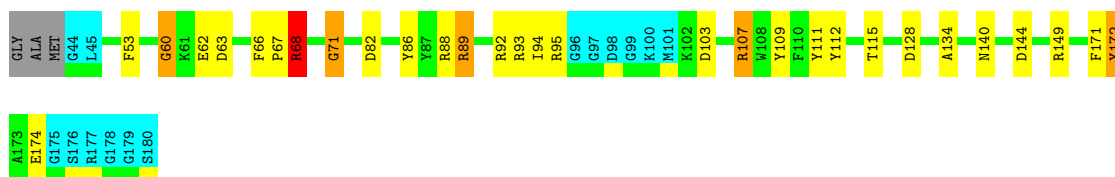
- Molecule 2: ssRNA



4.2.4 Score per residue for model 4

- Molecule 1: Nucleoprotein





- Molecule 2: ssRNA



4.2.5 Score per residue for model 5 (medoid)

- Molecule 1: Nucleoprotein

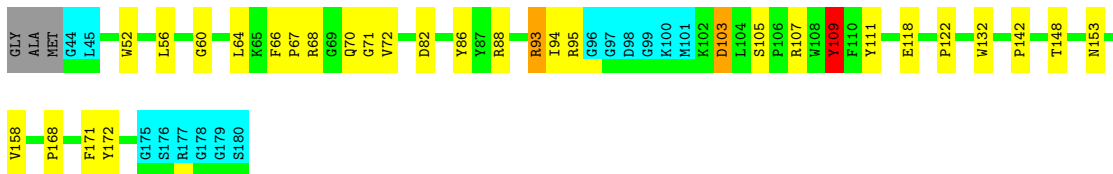


- Molecule 2: ssRNA



4.2.6 Score per residue for model 6

- Molecule 1: Nucleoprotein



- Molecule 2: ssRNA

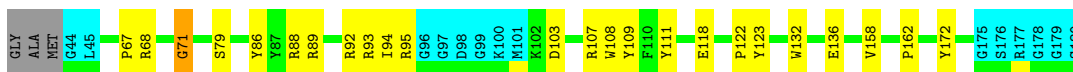




4.2.7 Score per residue for model 7

- Molecule 1: Nucleoprotein

Chain A: 71% 16% 10%



- Molecule 2: ssRNA

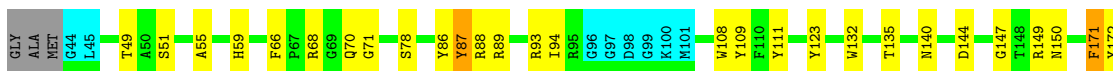
Chain B: 10% 50% 40%



4.2.8 Score per residue for model 8

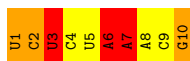
- Molecule 1: Nucleoprotein

Chain A: 66% 20% 10%



- Molecule 2: ssRNA

Chain B: 40% 30% 30%



4.2.9 Score per residue for model 9

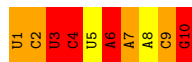
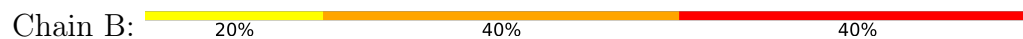
- Molecule 1: Nucleoprotein

Chain A: 64% 24% 10%



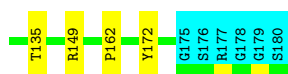


- Molecule 2: ssRNA



4.2.10 Score per residue for model 10

- Molecule 1: Nucleoprotein



- Molecule 2: ssRNA



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 10 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
YASARA	structure calculation	

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

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1665
Number of shifts mapped to atoms	1637
Number of unparsed shifts	0
Number of shifts with mapping errors	28
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	82%

6 Model quality i

6.1 Standard geometry i

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	1.59±0.03	6±2/997 (0.6± 0.2%)	1.99±0.07	30±5/1361 (2.2± 0.3%)
2	B	3.05±0.18	22±5/233 (9.4± 2.3%)	3.77±0.25	60±9/358 (16.7± 2.4%)
All	All	1.95	275/12300 (2.2%)	2.48	897/17190 (5.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	3.4±1.4
2	B	2.0±0.0	5.3±1.0
All	All	20	87

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
2	B	6	A	N9-C4	-14.96	1.28	1.37	4	4
2	B	1	U	OP3-P	-14.40	1.43	1.61	3	10
2	B	8	A	N7-C5	14.07	1.47	1.39	10	4
2	B	9	C	C4-N4	-11.15	1.24	1.33	10	4
2	B	9	C	N3-C4	-10.88	1.26	1.33	9	2
2	B	8	A	C6-N6	-10.32	1.25	1.33	5	3
2	B	10	G	N1-C2	-9.86	1.29	1.37	1	1
2	B	7	A	P-O5'	9.85	1.69	1.59	7	3
2	B	1	U	C5'-C4'	9.80	1.63	1.51	7	1
2	B	8	A	C6-N1	-9.79	1.28	1.35	1	4
2	B	2	C	N3-C4	-9.69	1.27	1.33	9	3
2	B	9	C	C5'-C4'	9.49	1.62	1.51	4	1
2	B	3	U	C2-N3	-9.46	1.31	1.37	4	1
2	B	1	U	O3'-P	-9.29	1.50	1.61	7	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
2	B	6	A	P-O5'	9.24	1.69	1.59	3	4
2	B	8	A	N9-C4	8.95	1.43	1.37	7	1
2	B	1	U	C4-C5	8.85	1.51	1.43	4	1
2	B	6	A	C5'-C4'	8.72	1.61	1.51	2	2
2	B	4	C	N3-C4	-8.72	1.27	1.33	2	3
2	B	9	C	C5-C6	8.37	1.41	1.34	10	3
2	B	6	A	C6-N1	-8.35	1.29	1.35	5	1
2	B	7	A	N7-C5	8.32	1.44	1.39	2	4
2	B	3	U	O3'-P	-8.18	1.51	1.61	1	1
2	B	5	U	C4-C5	8.16	1.50	1.43	4	3
2	B	7	A	N3-C4	8.14	1.39	1.34	1	1
2	B	6	A	C6-N6	-8.11	1.27	1.33	1	1
2	B	9	C	C4'-O4'	-8.05	1.35	1.45	5	2
2	B	8	A	N1-C2	-8.03	1.27	1.34	7	3
2	B	8	A	P-O5'	8.02	1.67	1.59	6	1
2	B	2	C	N1-C6	8.01	1.42	1.37	5	1
1	A	67	PRO	N-CD	-7.95	1.36	1.47	4	1
2	B	10	G	C2'-O2'	7.90	1.51	1.41	6	1
2	B	1	U	P-O5'	-7.79	1.51	1.59	3	2
2	B	5	U	P-O5'	-7.78	1.51	1.59	4	2
2	B	4	C	P-O5'	7.76	1.67	1.59	3	1
2	B	6	A	C4'-O4'	-7.62	1.35	1.45	1	1
2	B	9	C	O3'-P	-7.58	1.52	1.61	5	2
2	B	9	C	N1-C6	7.56	1.41	1.37	9	1
2	B	10	G	C2-N2	-7.55	1.26	1.34	7	2
1	A	88	ARG	CZ-NH1	-7.54	1.23	1.33	8	1
2	B	3	U	C3'-C2'	7.53	1.61	1.52	8	2
2	B	8	A	N3-C4	7.53	1.39	1.34	5	3
2	B	5	U	N1-C6	7.34	1.44	1.38	2	3
2	B	7	A	C2'-C1'	7.33	1.61	1.53	10	1
2	B	3	U	C5-C6	7.27	1.40	1.34	4	1
2	B	9	C	C2'-C1'	-7.25	1.45	1.53	6	1
2	B	8	A	N9-C8	7.23	1.43	1.37	3	6
2	B	2	C	C3'-O3'	-7.19	1.32	1.42	7	1
2	B	10	G	N9-C4	7.16	1.43	1.38	4	1
2	B	6	A	N9-C8	-7.16	1.32	1.37	3	4
2	B	6	A	N7-C5	7.16	1.43	1.39	10	2
1	A	93	ARG	CZ-NH1	-7.15	1.23	1.33	10	1
2	B	4	C	C4-C5	-7.14	1.37	1.43	5	2
2	B	3	U	C4-C5	7.11	1.50	1.43	5	2
2	B	7	A	C2'-O2'	7.06	1.50	1.41	9	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
2	B	5	U	N1-C2	7.04	1.44	1.38	3	2
2	B	5	U	C2-N3	7.03	1.42	1.37	2	1
2	B	6	A	C8-N7	-7.00	1.26	1.31	4	1
2	B	10	G	C5-C6	6.95	1.49	1.42	10	2
2	B	6	A	C2'-C1'	-6.93	1.45	1.53	5	2
2	B	6	A	O4'-C1'	6.86	1.50	1.41	6	1
2	B	9	C	P-O5'	-6.80	1.52	1.59	10	2
1	A	92	ARG	CZ-NH2	-6.77	1.24	1.33	10	1
1	A	112	TYR	CG-CD2	6.69	1.47	1.39	10	1
2	B	7	A	C6-N1	-6.68	1.30	1.35	7	3
1	A	124	GLY	CA-C	6.66	1.62	1.51	1	1
2	B	10	G	O4'-C1'	6.66	1.50	1.41	9	1
1	A	129	GLY	CA-C	6.66	1.62	1.51	2	1
2	B	7	A	N9-C4	6.64	1.41	1.37	7	2
2	B	4	C	C4-N4	-6.63	1.27	1.33	7	3
2	B	8	A	C4'-C3'	-6.60	1.45	1.53	1	2
2	B	5	U	C3'-C2'	-6.60	1.45	1.52	1	1
2	B	2	C	C4'-C3'	6.59	1.60	1.53	6	2
2	B	4	C	C5-C6	6.58	1.39	1.34	7	1
2	B	5	U	N3-C4	6.56	1.44	1.38	10	1
2	B	5	U	C5-C6	6.50	1.40	1.34	9	3
2	B	10	G	P-O5'	6.50	1.66	1.59	1	1
2	B	3	U	N1-C6	-6.47	1.32	1.38	6	1
2	B	7	A	N9-C8	6.45	1.43	1.37	6	1
2	B	6	A	N3-C4	6.43	1.38	1.34	7	1
1	A	59	HIS	CB-CG	6.43	1.61	1.50	3	2
2	B	10	G	C5-C4	-6.41	1.33	1.38	1	1
2	B	10	G	C6-O6	6.40	1.29	1.24	6	2
2	B	2	C	C3'-C2'	6.39	1.59	1.52	7	1
2	B	6	A	C5-C6	6.37	1.46	1.41	2	2
1	A	172	TYR	CE2-CZ	6.25	1.46	1.38	7	1
1	A	109	TYR	CD1-CE1	6.24	1.48	1.39	10	1
1	A	93	ARG	CZ-NH2	-6.21	1.25	1.33	10	3
1	A	68	ARG	CZ-NH2	-6.19	1.25	1.33	7	1
2	B	1	U	C2'-O2'	6.18	1.49	1.41	9	1
2	B	7	A	C5-C4	-6.17	1.34	1.38	9	2
1	A	93	ARG	NE-CZ	6.16	1.41	1.33	1	1
1	A	118	GLU	CD-OE1	-6.13	1.19	1.25	6	1
2	B	5	U	C5'-C4'	6.10	1.58	1.51	3	1
2	B	3	U	C4-O4	-6.08	1.18	1.23	10	1
1	A	107	ARG	CZ-NH2	-6.06	1.25	1.33	10	2

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	172	TYR	CE1-CZ	6.05	1.46	1.38	3	3
2	B	4	C	N1-C2	6.04	1.46	1.40	10	2
1	A	109	TYR	CE1-CZ	6.04	1.46	1.38	7	1
2	B	8	A	C2-N3	-6.03	1.28	1.33	3	1
2	B	2	C	C4-C5	-6.03	1.38	1.43	5	2
1	A	60	GLY	CA-C	6.01	1.61	1.51	5	1
2	B	3	U	C4'-C3'	-6.00	1.46	1.52	2	1
1	A	68	ARG	CZ-NH1	-5.99	1.25	1.33	8	1
2	B	2	C	C5'-C4'	5.94	1.58	1.51	5	2
1	A	95	ARG	CZ-NH2	-5.94	1.25	1.33	2	3
2	B	1	U	C2'-C1'	5.92	1.59	1.53	7	1
2	B	4	C	C5'-C4'	5.91	1.58	1.51	3	3
2	B	8	A	C3'-C2'	5.89	1.59	1.52	1	2
2	B	4	C	C2-O2	5.89	1.29	1.24	9	1
1	A	172	TYR	CG-CD1	5.87	1.46	1.39	8	1
2	B	2	C	C2'-C1'	-5.86	1.47	1.53	3	1
2	B	3	U	C2'-C1'	5.84	1.59	1.53	5	1
2	B	7	A	C5-C6	5.80	1.46	1.41	8	2
2	B	5	U	C2'-C1'	5.78	1.59	1.53	2	2
2	B	9	C	C2'-O2'	5.78	1.49	1.41	7	2
2	B	10	G	C6-N1	-5.77	1.35	1.39	2	2
2	B	10	G	N3-C4	5.77	1.39	1.35	1	1
2	B	2	C	P-O5'	5.76	1.65	1.59	1	1
2	B	1	U	N3-C4	-5.74	1.33	1.38	10	2
2	B	10	G	C2-N3	5.68	1.37	1.32	4	2
2	B	3	U	O4'-C1'	5.68	1.49	1.41	6	1
2	B	4	C	C3'-C2'	5.67	1.59	1.52	5	1
2	B	7	A	C6-N6	-5.63	1.29	1.33	10	2
1	A	149	ARG	CZ-NH1	-5.62	1.25	1.33	10	1
2	B	2	C	C5-C6	-5.62	1.29	1.34	10	1
2	B	10	G	N7-C5	5.57	1.42	1.39	10	3
2	B	8	A	C5'-C4'	5.56	1.58	1.51	9	1
2	B	2	C	C4-N4	-5.55	1.28	1.33	10	2
2	B	4	C	O3'-P	-5.52	1.54	1.61	7	1
2	B	2	C	C2-N3	5.51	1.40	1.35	9	2
2	B	5	U	C4'-C3'	-5.47	1.47	1.52	6	1
2	B	1	U	N1-C2	5.46	1.43	1.38	10	1
2	B	6	A	O3'-P	-5.44	1.54	1.61	1	1
1	A	71	GLY	CA-C	5.43	1.60	1.51	4	1
2	B	5	U	C4'-O4'	-5.42	1.38	1.45	9	1
1	A	123	TYR	CE2-CZ	5.42	1.45	1.38	8	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	109	TYR	CG-CD1	5.41	1.46	1.39	2	1
2	B	1	U	C5-C6	5.41	1.39	1.34	2	2
1	A	147	GLY	CA-C	5.41	1.60	1.51	8	1
1	A	123	TYR	CG-CD1	5.40	1.46	1.39	10	1
1	A	62	GLU	CD-OE2	-5.39	1.19	1.25	4	1
1	A	92	ARG	CZ-NH1	-5.38	1.26	1.33	5	1
1	A	73	PRO	N-CD	-5.37	1.40	1.47	2	1
1	A	62	GLU	CG-CD	5.37	1.60	1.51	4	1
1	A	137	GLY	CA-C	5.34	1.60	1.51	5	2
2	B	3	U	C2-O2	5.34	1.27	1.22	8	1
1	A	149	ARG	NE-CZ	5.33	1.40	1.33	1	1
1	A	92	ARG	NE-CZ	5.29	1.40	1.33	4	1
1	A	89	ARG	NE-CZ	5.29	1.40	1.33	2	1
1	A	171	PHE	CG-CD1	5.27	1.46	1.38	5	1
2	B	3	U	N1-C2	5.26	1.43	1.38	10	1
2	B	7	A	C4'-O4'	-5.25	1.38	1.45	8	1
2	B	6	A	C5-C4	-5.24	1.35	1.38	6	1
2	B	7	A	C4'-C3'	-5.24	1.47	1.52	4	1
1	A	78	SER	CB-OG	-5.21	1.35	1.42	8	1
1	A	170	GLY	CA-C	5.15	1.60	1.51	1	1
1	A	172	TYR	CG-CD2	5.14	1.45	1.39	2	2
1	A	112	TYR	CG-CD1	5.13	1.45	1.39	4	1
1	A	132	TRP	CD2-CE2	5.13	1.47	1.41	5	1
1	A	118	GLU	N-CA	5.12	1.56	1.46	7	1
1	A	51	SER	CB-OG	5.11	1.48	1.42	8	1
1	A	107	ARG	CZ-NH1	-5.06	1.26	1.33	6	1
1	A	86	TYR	CE2-CZ	5.05	1.45	1.38	9	1
1	A	109	TYR	CG-CD2	5.04	1.45	1.39	4	1
1	A	168	PRO	N-CD	-5.02	1.40	1.47	6	1
2	B	10	G	C5'-C4'	5.02	1.57	1.51	10	1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	B	2	C	N1-C2-O2	19.01	130.30	118.90	1	6
2	B	8	A	C8-N9-C4	-17.65	98.74	105.80	6	5
1	A	88	ARG	NE-CZ-NH1	17.04	128.82	120.30	5	4
2	B	4	C	C2-N3-C4	-16.79	111.51	119.90	2	4
2	B	3	U	O4'-C1'-N1	16.78	121.63	108.20	6	7
2	B	8	A	N9-C4-C5	16.29	112.32	105.80	6	6

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	B	8	A	C5-C6-N1	15.43	125.42	117.70	10	6
1	A	68	ARG	NE-CZ-NH1	15.34	127.97	120.30	5	6
2	B	7	A	N1-C6-N6	-14.99	109.61	118.60	9	6
2	B	10	G	C5-C6-O6	14.82	137.49	128.60	3	4
1	A	88	ARG	NE-CZ-NH2	-14.63	112.98	120.30	6	7
1	A	95	ARG	NE-CZ-NH2	-13.96	113.32	120.30	10	3
1	A	95	ARG	NE-CZ-NH1	13.91	127.26	120.30	10	8
1	A	123	TYR	CB-CG-CD1	-13.90	112.66	121.00	7	5
2	B	9	C	N3-C4-C5	13.89	127.46	121.90	9	6
2	B	4	C	N3-C4-C5	13.88	127.45	121.90	2	7
1	A	92	ARG	NE-CZ-NH1	13.80	127.20	120.30	7	4
2	B	4	C	N3-C2-O2	-13.54	112.42	121.90	7	5
2	B	8	A	N1-C6-N6	-13.53	110.48	118.60	9	7
2	B	6	A	N9-C4-C5	13.44	111.17	105.80	6	2
2	B	9	C	N3-C4-N4	-13.41	108.61	118.00	5	4
2	B	7	A	C5-C6-N1	13.35	124.38	117.70	7	5
2	B	2	C	C4-C5-C6	-13.29	110.76	117.40	5	5
1	A	107	ARG	NE-CZ-NH1	13.25	126.93	120.30	10	7
2	B	2	C	N3-C4-C5	13.06	127.12	121.90	5	4
1	A	172	TYR	CB-CG-CD1	-13.03	113.18	121.00	10	6
2	B	2	C	C1'-O4'-C4'	-13.00	99.50	109.90	2	4
2	B	6	A	N1-C6-N6	-12.96	110.83	118.60	8	8
2	B	5	U	O4'-C1'-N1	12.54	118.23	108.20	8	6
2	B	2	C	O4'-C1'-N1	12.41	118.13	108.20	6	7
2	B	10	G	O4'-C1'-N9	12.28	118.02	108.20	10	7
2	B	10	G	N1-C6-O6	-12.27	112.54	119.90	3	2
2	B	10	G	C8-N9-C4	-12.26	101.50	106.40	6	8
2	B	2	C	C5-C4-N4	12.25	128.78	120.20	10	3
2	B	4	C	N1-C2-N3	12.10	127.67	119.20	2	3
2	B	4	C	N3-C4-N4	-12.08	109.54	118.00	6	3
1	A	89	ARG	NE-CZ-NH1	12.05	126.32	120.30	3	8
2	B	8	A	C5-N7-C8	-11.78	98.01	103.90	4	2
2	B	3	U	C2-N3-C4	-11.77	119.94	127.00	3	5
1	A	172	TYR	CB-CG-CD2	11.71	128.02	121.00	10	3
1	A	111	TYR	CB-CG-CD1	-11.70	113.98	121.00	8	7
2	B	6	A	C5-C6-N1	11.70	123.55	117.70	10	6
2	B	8	A	N7-C8-N9	11.63	119.62	113.80	4	3
1	A	88	ARG	NH1-CZ-NH2	-11.61	106.63	119.40	10	3
2	B	5	U	N3-C2-O2	-11.55	114.11	122.20	7	4
2	B	4	C	C5-C4-N4	11.49	128.25	120.20	6	4
1	A	128	ASP	CB-CG-OD1	11.49	128.64	118.30	4	2

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	B	9	C	N3-C2-O2	-11.44	113.89	121.90	8	8
2	B	9	C	N1-C2-O2	11.26	125.66	118.90	4	6
1	A	93	ARG	NE-CZ-NH2	11.19	125.89	120.30	4	8
2	B	3	U	C5-C6-N1	-11.18	117.11	122.70	7	3
2	B	4	C	C6-N1-C2	-11.18	115.83	120.30	7	3
1	A	93	ARG	NE-CZ-NH1	11.14	125.87	120.30	5	6
2	B	10	G	N7-C8-N9	11.09	118.64	113.10	8	4
2	B	10	G	N3-C4-C5	-11.05	123.07	128.60	1	5
1	A	89	ARG	NE-CZ-NH2	-11.04	114.78	120.30	1	6
2	B	10	G	C2-N3-C4	10.91	117.36	111.90	9	2
1	A	149	ARG	NE-CZ-NH1	10.90	125.75	120.30	3	4
1	A	107	ARG	NE-CZ-NH2	-10.85	114.88	120.30	10	5
2	B	7	A	N9-C4-C5	10.83	110.13	105.80	9	3
2	B	2	C	N3-C4-N4	-10.75	110.48	118.00	10	4
2	B	3	U	N1-C2-N3	10.69	121.31	114.90	4	7
2	B	8	A	C5'-C4'-O4'	10.63	121.86	109.10	6	2
2	B	9	C	C3'-C2'-C1'	-10.61	93.02	101.50	5	4
2	B	1	U	N3-C2-O2	-10.59	114.78	122.20	2	6
2	B	4	C	N1-C2-O2	10.56	125.24	118.90	5	4
2	B	2	C	N3-C2-O2	-10.55	114.52	121.90	3	5
2	B	6	A	C6-C5-N7	10.52	139.67	132.30	7	4
2	B	4	C	C5-C6-N1	-10.50	115.75	121.00	4	4
2	B	4	C	O4'-C1'-N1	10.48	116.59	108.20	2	7
1	A	68	ARG	NE-CZ-NH2	10.46	125.53	120.30	10	5
2	B	2	C	C2-N3-C4	-10.37	114.72	119.90	10	4
2	B	10	G	N9-C4-C5	10.35	109.54	105.40	2	6
2	B	1	U	C5-C6-N1	-10.29	117.56	122.70	8	5
2	B	6	A	C4-C5-C6	-10.28	111.86	117.00	10	7
1	A	82	ASP	CB-CG-OD1	10.27	127.55	118.30	4	3
2	B	7	A	C8-N9-C4	-10.26	101.69	105.80	9	3
1	A	149	ARG	NE-CZ-NH2	-10.24	115.18	120.30	1	3
2	B	3	U	N3-C4-O4	-10.23	112.24	119.40	3	4
2	B	6	A	C8-N9-C4	10.13	109.85	105.80	4	4
2	B	2	C	O4'-C4'-C3'	10.13	114.20	106.10	2	2
2	B	3	U	N3-C2-O2	-10.07	115.15	122.20	2	8
2	B	3	U	C3'-C2'-C1'	-10.04	93.47	101.50	5	1
2	B	8	A	O4'-C1'-N9	10.03	116.23	108.20	8	5
2	B	1	U	O5'-P-OP1	-10.00	96.70	105.70	4	2
1	A	128	ASP	CB-CG-OD2	-9.91	109.38	118.30	4	2
2	B	10	G	N1-C2-N3	9.87	129.82	123.90	6	2
2	B	7	A	O4'-C1'-N9	9.86	116.09	108.20	7	4

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	B	2	C	C6-N1-C2	9.59	124.14	120.30	1	3
1	A	109	TYR	CB-CG-CD2	-9.53	115.28	121.00	10	3
1	A	111	TYR	CB-CG-CD2	9.40	126.64	121.00	4	5
2	B	3	U	C5-C4-O4	-9.26	120.35	125.90	8	5
2	B	4	C	C5'-C4'-O4'	9.25	120.20	109.10	7	3
2	B	7	A	C4'-C3'-C2'	-9.24	93.36	102.60	2	2
2	B	7	A	C6-N1-C2	-9.21	113.07	118.60	3	2
2	B	8	A	C3'-C2'-C1'	9.14	108.81	101.50	10	3
2	B	2	C	N1-C2-N3	-9.07	112.85	119.20	1	3
2	B	1	U	C1'-O4'-C4'	-9.05	102.66	109.90	2	3
2	B	9	C	O4'-C1'-C2'	9.02	115.72	107.60	8	1
1	A	72	VAL	CA-CB-CG1	9.01	124.41	110.90	10	2
1	A	89	ARG	NH1-CZ-NH2	-8.99	109.51	119.40	9	1
2	B	7	A	C4-C5-C6	-8.96	112.52	117.00	7	5
2	B	7	A	C5-N7-C8	-8.96	99.42	103.90	7	3
2	B	6	A	C5-C6-N6	8.88	130.80	123.70	6	4
2	B	8	A	C2-N3-C4	8.87	115.03	110.60	10	5
2	B	10	G	C5'-C4'-O4'	-8.75	98.59	109.10	9	2
2	B	5	U	C2-N3-C4	-8.75	121.75	127.00	1	4
2	B	5	U	C3'-C2'-C1'	8.69	108.45	101.50	8	1
2	B	3	U	C4-C5-C6	8.67	124.90	119.70	10	3
2	B	10	G	N3-C4-N9	8.61	131.16	126.00	7	1
1	A	109	TYR	CB-CG-CD1	-8.57	115.86	121.00	1	3
2	B	6	A	C3'-C2'-C1'	8.54	108.33	101.50	4	5
2	B	5	U	N1-C2-O2	-8.48	116.86	122.80	4	3
2	B	7	A	N3-C4-N9	-8.47	120.62	127.40	6	2
2	B	10	G	C5-N7-C8	-8.47	100.06	104.30	8	2
2	B	1	U	C5-C4-O4	8.46	130.98	125.90	5	3
2	B	8	A	C4-C5-N7	-8.43	106.49	110.70	6	3
1	A	174	GLU	OE1-CD-OE2	-8.38	113.24	123.30	8	2
2	B	4	C	C4-C5-C6	-8.32	113.24	117.40	7	3
1	A	93	ARG	NH1-CZ-NH2	-8.30	110.27	119.40	8	3
2	B	6	A	O4'-C1'-N9	8.27	114.81	108.20	4	4
2	B	1	U	N3-C4-O4	-8.25	113.62	119.40	5	1
2	B	9	C	P-O3'-C3'	8.25	129.60	119.70	1	2
2	B	7	A	C3'-C2'-C1'	8.22	108.08	101.50	2	2
1	A	92	ARG	NE-CZ-NH2	-8.21	116.19	120.30	7	4
1	A	108	TRP	NE1-CE2-CD2	-8.19	99.11	107.30	7	3
1	A	50	ALA	N-CA-CB	-8.15	98.68	110.10	5	3
1	A	171	PHE	CB-CG-CD2	-8.15	115.09	120.80	8	2
2	B	5	U	N1-C2-N3	8.09	119.75	114.90	4	3

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	B	6	A	C4-C5-N7	-8.07	106.67	110.70	6	2
2	B	9	C	C6-N1-C2	-8.01	117.09	120.30	8	4
2	B	10	G	N3-C2-N2	-8.01	114.30	119.90	4	4
2	B	9	C	C2-N3-C4	-7.99	115.91	119.90	1	3
2	B	5	U	C5-C6-N1	-7.97	118.71	122.70	5	3
2	B	9	C	C5-C4-N4	7.95	125.76	120.20	5	2
1	A	141	THR	CA-CB-CG2	-7.92	101.31	112.40	3	1
1	A	112	TYR	CB-CG-CD1	-7.92	116.25	121.00	1	2
2	B	7	A	C2-N3-C4	7.91	114.55	110.60	4	5
2	B	2	C	C5-C6-N1	7.87	124.94	121.00	5	1
2	B	7	A	C6-C5-N7	7.87	137.81	132.30	6	3
2	B	6	A	N7-C8-N9	7.85	117.72	113.80	3	2
1	A	132	TRP	CH2-CZ2-CE2	7.83	125.23	117.40	9	2
2	B	1	U	O4'-C1'-N1	7.78	114.42	108.20	1	5
2	B	6	A	C2-N3-C4	7.77	114.48	110.60	8	1
2	B	7	A	N1-C2-N3	-7.75	125.43	129.30	9	3
2	B	8	A	C6-C5-N7	7.72	137.70	132.30	10	1
2	B	9	C	O4'-C1'-N1	7.70	114.36	108.20	4	2
2	B	7	A	N7-C8-N9	7.70	117.65	113.80	7	1
1	A	111	TYR	CG-CD1-CE1	-7.69	115.14	121.30	5	3
1	A	110	PHE	CB-CG-CD1	-7.69	115.42	120.80	2	2
1	A	144	ASP	CB-CG-OD1	-7.67	111.40	118.30	8	1
2	B	10	G	C4-C5-C6	7.66	123.40	118.80	1	2
2	B	3	U	C6-N1-C2	-7.65	116.41	121.00	9	2
1	A	93	ARG	CD-NE-CZ	7.63	134.28	123.60	1	2
2	B	8	A	N3-C4-C5	-7.62	121.47	126.80	6	3
1	A	86	TYR	CB-CG-CD1	-7.61	116.43	121.00	1	2
2	B	1	U	C4-C5-C6	7.58	124.25	119.70	9	4
1	A	115	THR	CA-CB-CG2	7.57	122.99	112.40	4	1
2	B	3	U	O4'-C4'-C3'	7.52	112.11	106.10	10	5
2	B	9	C	C1'-O4'-C4'	-7.51	103.89	109.90	8	4
2	B	10	G	C1'-O4'-C4'	-7.50	103.90	109.90	9	2
1	A	108	TRP	CE2-CD2-CG	7.48	113.28	107.30	10	3
1	A	81	ASP	CB-CG-OD1	7.46	125.01	118.30	10	3
2	B	4	C	C5'-C4'-C3'	-7.41	104.14	116.00	9	4
2	B	1	U	C5'-C4'-C3'	-7.41	104.15	116.00	2	2
1	A	108	TRP	CD1-CG-CD2	-7.35	100.42	106.30	1	4
2	B	1	U	OP1-P-OP2	-7.33	108.61	119.60	6	5
2	B	5	U	C4'-C3'-C2'	-7.30	95.30	102.60	4	2
2	B	4	C	N1-C1'-C2'	-7.29	103.98	112.00	8	2
1	A	87	TYR	CB-CG-CD1	-7.23	116.66	121.00	5	4

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	B	10	G	C6-N1-C2	-7.23	120.76	125.10	6	3
2	B	3	U	N3-C4-C5	7.22	118.93	114.60	3	3
1	A	79	SER	N-CA-CB	-7.17	99.75	110.50	7	1
2	B	10	G	C5-C6-N1	7.15	115.07	111.50	4	3
2	B	5	U	N3-C4-C5	7.13	118.88	114.60	1	2
2	B	6	A	C5-N7-C8	-7.12	100.34	103.90	5	3
2	B	7	A	C1'-O4'-C4'	-7.07	104.25	109.90	10	3
1	A	132	TRP	CD1-NE1-CE2	7.06	115.36	109.00	8	2
2	B	1	U	N1-C2-O2	7.05	127.73	122.80	6	4
1	A	108	TRP	CD1-NE1-CE2	7.00	115.30	109.00	7	2
2	B	7	A	C5'-C4'-O4'	6.99	117.48	109.10	9	1
2	B	6	A	C5'-C4'-C3'	-6.98	104.83	116.00	3	1
1	A	172	TYR	CG-CD2-CE2	6.97	126.88	121.30	1	2
2	B	3	U	N1-C2-O2	6.97	127.68	122.80	2	1
2	B	5	U	C6-N1-C2	-6.96	116.83	121.00	4	2
1	A	63	ASP	CB-CG-OD2	6.95	124.56	118.30	9	5
2	B	7	A	C4-C5-N7	6.93	114.17	110.70	7	2
2	B	9	C	O4'-C4'-C3'	6.90	111.62	106.10	8	3
2	B	3	U	P-O3'-C3'	6.89	127.97	119.70	8	2
1	A	89	ARG	CD-NE-CZ	6.89	133.25	123.60	9	1
2	B	5	U	C5-C4-O4	-6.86	121.79	125.90	1	2
2	B	8	A	C4-C5-C6	-6.83	113.58	117.00	4	4
2	B	6	A	C4'-C3'-C2'	-6.82	95.78	102.60	4	1
2	B	8	A	C4'-C3'-C2'	-6.82	95.78	102.60	3	1
1	A	81	ASP	CB-CG-OD2	6.77	124.39	118.30	9	1
2	B	1	U	C4'-C3'-C2'	-6.76	95.84	102.60	2	1
1	A	109	TYR	CG-CD1-CE1	-6.72	115.92	121.30	1	1
2	B	4	C	P-O3'-C3'	6.70	127.73	119.70	3	2
2	B	10	G	O4'-C4'-C3'	6.70	111.46	106.10	7	3
1	A	144	ASP	CB-CG-OD2	6.69	124.32	118.30	8	1
1	A	132	TRP	NE1-CE2-CD2	-6.68	100.62	107.30	9	2
1	A	112	TYR	CB-CG-CD2	-6.65	117.01	121.00	2	2
1	A	172	TYR	CZ-CE2-CD2	6.63	125.77	119.80	10	1
1	A	112	TYR	CG-CD1-CE1	-6.62	116.00	121.30	1	1
1	A	66	PHE	CB-CG-CD2	6.62	125.44	120.80	6	2
1	A	123	TYR	CB-CG-CD2	6.60	124.96	121.00	3	1
2	B	1	U	N1-C2-N3	6.59	118.85	114.90	1	3
2	B	1	U	C6-N1-C2	6.59	124.95	121.00	8	1
2	B	1	U	O3'-P-O5'	6.58	116.51	104.00	10	1
2	B	10	G	C4-C5-N7	-6.56	108.17	110.80	3	2
2	B	1	U	N3-C4-C5	-6.56	110.66	114.60	6	2

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	86	TYR	CZ-CE2-CD2	-6.56	113.90	119.80	8	1
1	A	52	TRP	NE1-CE2-CD2	-6.55	100.75	107.30	3	2
1	A	88	ARG	CD-NE-CZ	6.52	132.73	123.60	8	1
2	B	6	A	O5'-P-OP2	6.50	118.50	110.70	4	1
2	B	6	A	O4'-C4'-C3'	6.50	111.30	106.10	1	2
2	B	8	A	C6-N1-C2	-6.43	114.74	118.60	8	4
1	A	52	TRP	CD2-CE3-CZ3	6.43	127.16	118.80	1	1
1	A	120	GLY	CA-C-O	-6.43	109.03	120.60	10	1
2	B	7	A	C5-C6-N6	6.40	128.82	123.70	6	5
2	B	1	U	C5'-C4'-O4'	6.37	116.75	109.10	1	1
2	B	6	A	C6-N1-C2	-6.37	114.78	118.60	6	1
2	B	8	A	C1'-O4'-C4'	-6.36	104.81	109.90	7	2
1	A	52	TRP	CD1-NE1-CE2	6.35	114.72	109.00	9	3
1	A	68	ARG	NH1-CZ-NH2	-6.33	112.44	119.40	9	2
1	A	161	LEU	CB-CG-CD1	6.32	121.75	111.00	2	1
2	B	2	C	C3'-C2'-C1'	6.31	106.55	101.50	3	1
2	B	5	U	P-O3'-C3'	6.31	127.27	119.70	4	1
2	B	3	U	C2'-C3'-O3'	6.30	123.79	113.70	6	1
1	A	108	TRP	NE1-CE2-CZ2	6.29	137.32	130.40	7	1
2	B	1	U	C2-N3-C4	-6.29	123.23	127.00	5	3
2	B	10	G	C6-C5-N7	-6.25	126.65	130.40	7	3
2	B	4	C	C1'-O4'-C4'	-6.24	104.91	109.90	5	1
2	B	10	G	N1-C2-N2	6.23	121.81	116.20	1	1
1	A	132	TRP	CZ3-CH2-CZ2	-6.22	114.14	121.60	9	1
2	B	6	A	O3'-P-O5'	6.22	115.81	104.00	7	1
2	B	9	C	C5'-C4'-O4'	-6.20	101.67	109.10	4	1
1	A	53	PHE	CB-CG-CD2	6.19	125.14	120.80	4	2
1	A	118	GLU	OE1-CD-OE2	-6.16	115.91	123.30	6	4
2	B	2	C	C5'-C4'-O4'	-6.15	101.72	109.10	9	1
2	B	10	G	N9-C1'-C2'	-6.10	105.29	112.00	9	2
2	B	6	A	N1-C2-N3	-6.09	126.26	129.30	8	2
1	A	72	VAL	CG1-CB-CG2	-6.09	101.16	110.90	3	2
2	B	10	G	O4'-C1'-C2'	6.08	113.07	107.60	4	1
1	A	90	ALA	CB-CA-C	6.07	119.20	110.10	9	1
1	A	123	TYR	CG-CD1-CE1	-6.02	116.49	121.30	7	2
2	B	8	A	C5'-C4'-C3'	-6.01	106.39	116.00	5	1
2	B	5	U	C5'-C4'-O4'	5.97	116.27	109.10	5	1
1	A	132	TRP	NE1-CE2-CZ2	5.95	136.94	130.40	9	2
1	A	104	LEU	CB-CG-CD2	5.92	121.06	111.00	10	2
1	A	62	GLU	OE1-CD-OE2	-5.90	116.22	123.30	10	1
2	B	1	U	C3'-C2'-C1'	5.89	106.22	101.50	5	2

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	B	6	A	N9-C1'-C2'	5.88	121.65	114.00	9	1
1	A	86	TYR	CB-CG-CD2	-5.86	117.48	121.00	4	1
2	B	7	A	N3-C4-C5	-5.86	122.70	126.80	4	1
1	A	103	ASP	CB-CG-OD2	5.83	123.55	118.30	9	3
1	A	86	TYR	CD1-CE1-CZ	5.83	125.05	119.80	7	1
1	A	67	PRO	N-CA-CB	5.81	110.27	103.30	6	1
1	A	82	ASP	CB-CG-OD2	-5.79	113.09	118.30	4	1
1	A	113	LEU	N-CA-CB	-5.79	98.83	110.40	2	1
1	A	162	PRO	N-CD-CG	5.78	111.86	103.20	10	1
2	B	9	C	C4-C5-C6	-5.77	114.51	117.40	10	2
1	A	111	TYR	CG-CD2-CE2	-5.76	116.69	121.30	1	2
1	A	148	THR	CA-CB-CG2	5.76	120.47	112.40	6	1
1	A	122	PRO	N-CA-CB	5.75	110.20	103.30	7	1
1	A	150	ASN	N-CA-CB	-5.75	100.25	110.60	8	1
1	A	106	PRO	N-CA-CB	5.75	110.20	103.30	3	1
1	A	92	ARG	NH1-CZ-NH2	-5.73	113.09	119.40	2	1
2	B	9	C	C2-N1-C1'	5.72	125.10	118.80	5	1
2	B	5	U	C4-C5-C6	5.71	123.13	119.70	6	3
1	A	110	PHE	CB-CG-CD2	5.70	124.79	120.80	2	1
1	A	111	TYR	CD1-CG-CD2	5.68	124.15	117.90	7	2
2	B	5	U	C1'-O4'-C4'	5.68	114.44	109.90	5	1
1	A	57	THR	CA-CB-CG2	5.67	120.33	112.40	10	1
1	A	173	ALA	N-CA-CB	-5.65	102.19	110.10	3	1
1	A	165	THR	CA-CB-CG2	5.64	120.30	112.40	3	1
2	B	4	C	O4'-C1'-C2'	5.61	112.65	107.60	5	1
1	A	134	ALA	N-CA-CB	-5.59	102.27	110.10	9	2
1	A	55	ALA	CB-CA-C	5.58	118.48	110.10	8	1
1	A	70	GLN	O-C-N	-5.57	113.72	123.20	6	1
1	A	92	ARG	CA-CB-CG	5.57	125.66	113.40	9	1
1	A	135	THR	CA-CB-CG2	5.57	120.20	112.40	10	1
1	A	154	ASN	CB-CG-OD1	-5.57	110.46	121.60	5	1
2	B	5	U	O4'-C4'-C3'	-5.57	98.43	104.00	5	2
2	B	7	A	C4-N9-C1'	-5.57	116.28	126.30	6	1
2	B	2	C	C6-N1-C1'	-5.55	114.14	120.80	2	1
1	A	108	TRP	CE2-CD2-CE3	-5.54	112.05	118.70	5	2
1	A	136	GLU	OE1-CD-OE2	-5.53	116.67	123.30	7	1
2	B	6	A	N3-C4-C5	-5.52	122.93	126.80	6	1
1	A	56	LEU	CB-CG-CD1	5.51	120.37	111.00	9	1
2	B	8	A	P-O3'-C3'	5.50	126.30	119.70	5	2
1	A	132	TRP	CD1-CG-CD2	-5.50	101.90	106.30	7	2
2	B	3	U	N1-C1'-C2'	-5.48	105.97	112.00	6	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	B	10	G	C3'-C2'-C1'	-5.43	97.16	101.50	9	1
1	A	144	ASP	N-CA-CB	-5.42	100.84	110.60	3	1
1	A	56	LEU	O-C-N	-5.42	114.03	122.70	6	1
1	A	46	PRO	N-CD-CG	5.41	111.32	103.20	3	1
1	A	133	VAL	CA-CB-CG2	5.40	118.99	110.90	9	1
1	A	138	ALA	CB-CA-C	5.39	118.19	110.10	9	1
1	A	65	LYS	CB-CG-CD	-5.39	97.59	111.60	2	1
1	A	108	TRP	CB-CG-CD2	5.37	133.58	126.60	8	1
2	B	8	A	N1-C2-N3	-5.37	126.62	129.30	4	1
1	A	173	ALA	O-C-N	-5.35	114.14	122.70	8	1
2	B	7	A	N9-C1'-C2'	5.34	120.94	114.00	1	1
2	B	2	C	C5'-C4'-C3'	-5.34	107.46	116.00	3	1
1	A	87	TYR	CB-CG-CD2	5.33	124.20	121.00	10	2
1	A	105	SER	N-CA-CB	5.33	118.49	110.50	6	1
2	B	8	A	OP2-P-O3'	5.32	116.90	105.20	1	1
2	B	3	U	C4'-C3'-C2'	-5.29	97.31	102.60	10	1
1	A	52	TRP	CB-CG-CD2	5.28	133.47	126.60	10	1
2	B	1	U	O4'-C4'-C3'	5.28	110.33	106.10	1	1
1	A	109	TYR	CD1-CG-CD2	5.28	123.70	117.90	8	1
1	A	119	ALA	N-CA-CB	-5.27	102.72	110.10	10	1
2	B	9	C	P-O5'-C5'	5.26	129.32	120.90	2	1
1	A	73	PRO	N-CA-CB	5.26	109.61	103.30	3	1
1	A	130	ILE	CA-CB-CG1	5.25	120.98	111.00	10	1
1	A	123	TYR	CD1-CE1-CZ	-5.24	115.08	119.80	3	1
1	A	104	LEU	CB-CG-CD1	-5.21	102.14	111.00	5	1
2	B	4	C	O5'-C5'-C4'	5.21	121.59	111.70	1	1
2	B	7	A	O4'-C4'-C3'	5.18	110.25	106.10	2	1
1	A	68	ARG	CD-NE-CZ	5.17	130.84	123.60	1	1
1	A	60	GLY	O-C-N	-5.17	114.43	122.70	4	1
2	B	5	U	N3-C4-O4	5.15	123.01	119.40	6	1
1	A	57	THR	OG1-CB-CG2	-5.15	98.16	110.00	9	1
1	A	107	ARG	NH1-CZ-NH2	-5.15	113.74	119.40	3	1
2	B	1	U	P-O3'-C3'	5.12	125.84	119.70	8	1
1	A	71	GLY	O-C-N	-5.11	114.52	122.70	7	1
1	A	52	TRP	NE1-CE2-CZ2	5.10	136.01	130.40	1	1
2	B	1	U	O5'-P-OP2	-5.10	101.11	105.70	5	1
2	B	4	C	P-O5'-C5'	5.08	129.03	120.90	7	1
1	A	55	ALA	N-CA-CB	-5.08	102.99	110.10	1	1
1	A	117	PRO	N-CD-CG	5.07	110.81	103.20	2	1
1	A	122	PRO	N-CD-CG	5.07	110.80	103.20	6	1
1	A	142	PRO	N-CD-CG	5.06	110.80	103.20	6	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	95	ARG	NH1-CZ-NH2	-5.06	113.83	119.40	3	1
2	B	9	C	N1-C1'-C2'	5.06	120.58	114.00	9	1
1	A	163	GLN	C-N-CA	5.04	132.88	122.30	9	1
2	B	9	C	OP1-P-OP2	-5.03	112.05	119.60	1	1
2	B	5	U	OP1-P-OP2	5.03	127.15	119.60	4	1
2	B	9	C	C5'-C4'-C3'	5.03	124.05	116.00	4	1
1	A	135	THR	N-CA-CB	5.03	119.85	110.30	8	1
1	A	112	TYR	CD1-CG-CD2	5.01	123.41	117.90	5	1
1	A	158	VAL	O-C-N	-5.00	114.69	122.70	1	1

All unique chiral outliers are listed below.

Mol	Chain	Res	Type	Atoms	Models (Total)
2	B	6	A	C3',C4'	10

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

Mol	Chain	Res	Type	Group	Models (Total)
2	B	4	C	Sidechain	8
2	B	6	A	Sidechain	8
2	B	7	A	Sidechain	7
2	B	2	C	Sidechain	7
2	B	1	U	Sidechain	6
2	B	3	U	Sidechain	5
2	B	5	U	Sidechain	4
1	A	87	TYR	Sidechain	3
1	A	86	TYR	Sidechain	3
1	A	93	ARG	Peptide,Sidechain	3
2	B	8	A	Sidechain	3
1	A	109	TYR	Sidechain	3
2	B	10	G	Sidechain	3
1	A	172	TYR	Sidechain	2
1	A	111	TYR	Sidechain	2
1	A	125	ALA	Mainchain,Peptide	2
1	A	171	PHE	Sidechain,Peptide	2
2	B	9	C	Sidechain	2
1	A	92	ARG	Sidechain	1
1	A	112	TYR	Sidechain	1
1	A	149	ARG	Peptide	1
1	A	68	ARG	Sidechain	1

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Mol	Chain	Res	Type	Group	Models (Total)
1	A	89	ARG	Sidechain	1
1	A	107	ARG	Sidechain	1
1	A	53	PHE	Sidechain	1
1	A	59	HIS	Sidechain	1
1	A	85	GLY	Mainchain	1
1	A	110	PHE	Mainchain	1
1	A	123	TYR	Sidechain	1
1	A	55	ALA	Peptide	1
1	A	88	ARG	Sidechain	1

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	967	939	938	0±0
2	B	210	108	100	0±0
All	All	11770	10470	10426	5

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 0.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:66:PHE:CE2	1:A:87:TYR:CE2	0.51	2.99	8	3
1:A:102:LYS:HE2	2:B:7:A:N3	0.42	2.29	3	1
1:A:110:PHE:CG	1:A:111:TYR:N	0.40	2.89	10	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	123/140 (88%)	105±3 (86±2%)	14±3 (11±2%)	4±1 (3±1%)	6	37
All	All	1230/1400 (88%)	1053 (86%)	136 (11%)	41 (3%)	6	37

All 13 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	71	GLY	10
1	A	94	ILE	10
1	A	49	THR	5
1	A	140	ASN	3
1	A	68	ARG	2
1	A	162	PRO	2
1	A	60	GLY	2
1	A	158	VAL	2
1	A	103	ASP	1
1	A	155	ALA	1
1	A	64	LEU	1
1	A	70	GLN	1
1	A	83	GLN	1

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	99/107 (93%)	98±1 (99±1%)	1±1 (1±1%)	74	96
All	All	990/1070 (93%)	979 (99%)	11 (1%)	74	96

All 8 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	103	ASP	3
1	A	53	PHE	2
1	A	151	PRO	1
1	A	144	ASP	1
1	A	174	GLU	1

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Mol	Chain	Res	Type	Models (Total)
1	A	109	TYR	1
1	A	153	ASN	1
1	A	67	PRO	1

6.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
2	B	9/10 (90%)	5±0 (56±5%)	2±1 (17±7%)	0.18±0.07
All	All	90/100 (90%)	50 (56%)	15 (17%)	0.18

The overall RNA backbone suiteness is 0.18.

All unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
2	B	3	U	10
2	B	6	A	10
2	B	7	A	10
2	B	10	G	10
2	B	4	C	8
2	B	9	C	2

All unique RNA pucker outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
2	B	6	A	10
2	B	9	C	3
2	B	2	C	1
2	B	8	A	1

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 82% for the well-defined parts and 82% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: starch_output

7.1.1 Bookkeeping i

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

Total number of shifts	1665
Number of shifts mapped to atoms	1637
Number of unparsed shifts	0
Number of shifts with mapping errors	28
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	24

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

- No matching atom found in the structure. All 28 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	41	GLY	C	179.457	0.003	.
1	A	41	GLY	CA	43.365	0.035	.
1	A	41	GLY	HA2	3.83	0.000	.
1	A	41	GLY	HA3	3.83	0.000	.
1	A	42	ALA	C	177.766	0.006	.
1	A	42	ALA	CA	52.621	0.023	.
1	A	42	ALA	CB	19.383	0.012	.
1	A	42	ALA	H	8.596	0.002	.
1	A	42	ALA	HA	4.345	0.000	.
1	A	42	ALA	N	123.828	0.003	.
1	A	42	ALA	HB1	1.375	0.000	.
1	A	42	ALA	HB2	1.375	0.000	.
1	A	42	ALA	HB3	1.375	0.000	.
1	A	43	MET	C	176.61	0.005	.

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List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	43	MET	CA	55.565	0.039	.
1	A	43	MET	CB	32.871	0.027	.
1	A	43	MET	CE	16.929	0.000	.
1	A	43	MET	CG	32.009	0.033	.
1	A	43	MET	H	8.503	0.001	.
1	A	43	MET	HA	4.459	0.000	.
1	A	43	MET	HB2	2.086	0.000	.
1	A	43	MET	HB3	2.013	0.000	.
1	A	43	MET	HG2	2.547	0.000	.
1	A	43	MET	HG3	2.614	0.000	.
1	A	43	MET	N	119.86	0.004	.
1	A	43	MET	HE1	2.082	0.000	.
1	A	43	MET	HE2	2.082	0.000	.
1	A	43	MET	HE3	2.082	0.000	.

7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	140	0.17 ± 0.11	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	119	0.03 ± 0.16	None needed (< 0.5 ppm)
$^{13}\text{C}'$	137	0.12 ± 0.10	None needed (< 0.5 ppm)
^{15}N	127	-0.54 ± 0.41	None needed (imprecise)

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 82%, i.e. 1501 atoms were assigned a chemical shift out of a possible 1839. 0 out of 12 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	600/606 (99%)	246/248 (99%)	243/246 (99%)	111/112 (99%)
Sidechain	797/894 (89%)	538/578 (93%)	239/272 (88%)	20/44 (45%)
Aromatic	104/154 (68%)	63/74 (85%)	38/74 (51%)	3/6 (50%)
Sugar	0/110 (0%)	0/60 (0%)	0/50 (0%)	0/0 (—%)
Base	0/75 (0%)	0/45 (0%)	0/19 (0%)	0/11 (0%)
Overall	1501/1839 (82%)	847/1005 (84%)	520/661 (79%)	134/173 (77%)

The following table shows the completeness of the chemical shift assignments for the full structure.

The overall completeness is 82%, i.e. 1632 atoms were assigned a chemical shift out of a possible 1980. 0 out of 13 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	677/683 (99%)	281/283 (99%)	271/274 (99%)	125/126 (99%)
Sidechain	851/958 (89%)	575/619 (93%)	255/291 (88%)	21/48 (44%)
Aromatic	104/154 (68%)	63/74 (85%)	38/74 (51%)	3/6 (50%)
Sugar	0/110 (0%)	0/60 (0%)	0/50 (0%)	0/0 (—%)
Base	0/75 (0%)	0/45 (0%)	0/19 (0%)	0/11 (0%)
Overall	1632/1980 (82%)	919/1081 (85%)	564/708 (80%)	149/191 (78%)

7.1.4 Statistically unusual chemical shifts [i](#)

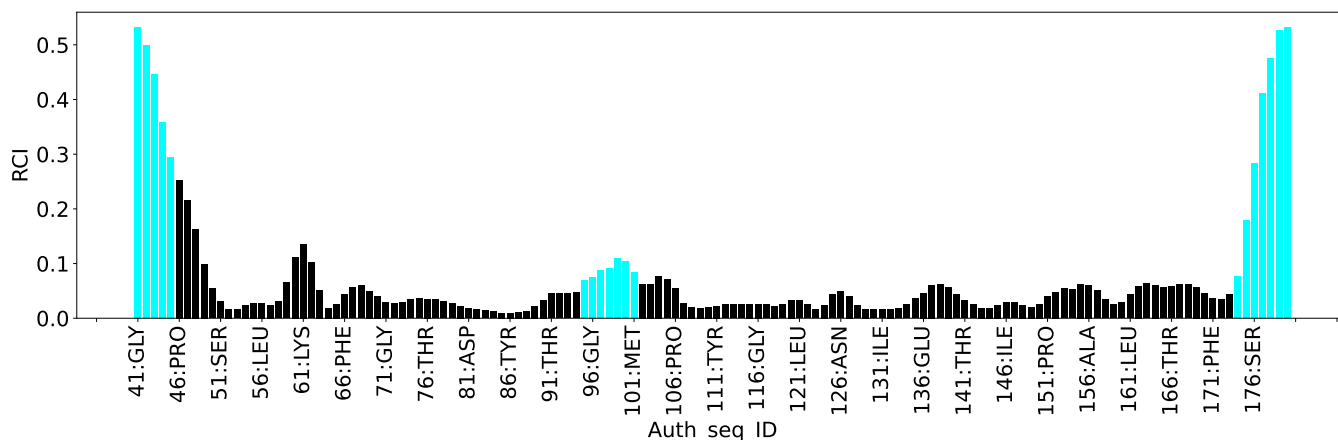
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	112	TYR	CE1	182.76	111.24 – 124.66	48.3
1	A	54	THR	HG1	6.34	0.08 – 2.19	24.6
1	A	165	THR	HG1	5.79	0.08 – 2.19	22.1
1	A	141	THR	HG1	5.78	0.08 – 2.19	22.0
1	A	87	TYR	CE1	129.73	111.24 – 124.66	8.8
1	A	149	ARG	HB3	-0.55	0.43 – 3.11	-8.6
1	A	89	ARG	HB3	-0.51	0.43 – 3.11	-8.5
1	A	87	TYR	HE1	5.00	5.59 – 7.82	-7.6
1	A	87	TYR	HE2	5.00	5.58 – 7.83	-7.5
1	A	64	LEU	HD11	-1.21	-0.61 – 2.12	-7.2
1	A	64	LEU	HD12	-1.21	-0.61 – 2.12	-7.2
1	A	64	LEU	HD13	-1.21	-0.61 – 2.12	-7.2
1	A	73	PRO	HD3	0.96	1.76 – 5.48	-7.1
1	A	64	LEU	HB3	-0.85	-0.26 – 3.31	-6.7
1	A	118	GLU	HB2	0.69	1.00 – 3.05	-6.5
1	A	73	PRO	HG3	-0.10	0.33 – 3.48	-6.3
1	A	71	GLY	HA2	1.75	2.15 – 5.77	-6.1
1	A	64	LEU	HB2	-0.33	-0.07 – 3.30	-5.8
1	A	123	TYR	HA	1.62	1.87 – 7.33	-5.5
1	A	87	TYR	HD1	5.43	5.49 – 8.39	-5.2
1	A	87	TYR	HD2	5.43	5.48 – 8.39	-5.2
1	A	64	LEU	HD21	-0.67	-0.65 – 2.13	-5.1
1	A	64	LEU	HD22	-0.67	-0.65 – 2.13	-5.1
1	A	64	LEU	HD23	-0.67	-0.65 – 2.13	-5.1

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:



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	7
Intra-residue ($ i-j =0$)	0
Sequential ($ i-j =1$)	0
Medium range ($ i-j >1$ and $ i-j <5$)	0
Long range ($ i-j \geq 5$)	0
Inter-chain	7
Hydrogen bond restraints	0
Disulfide bond restraints	0
Total dihedral-angle restraints	0
Number of unmapped restraints	0
Number of restraints per residue	0.0
Number of long range restraints per residue ¹	0.0

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

8.2 Residual restraint violations

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

8.2.1 Average number of distance violations per model

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

Bins (Å)	Average number of violations per model	Max (Å)
0.1-0.2 (Small)	0.3	0.17
0.2-0.5 (Medium)	0.4	0.34
>0.5 (Large)	2.2	2.34

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

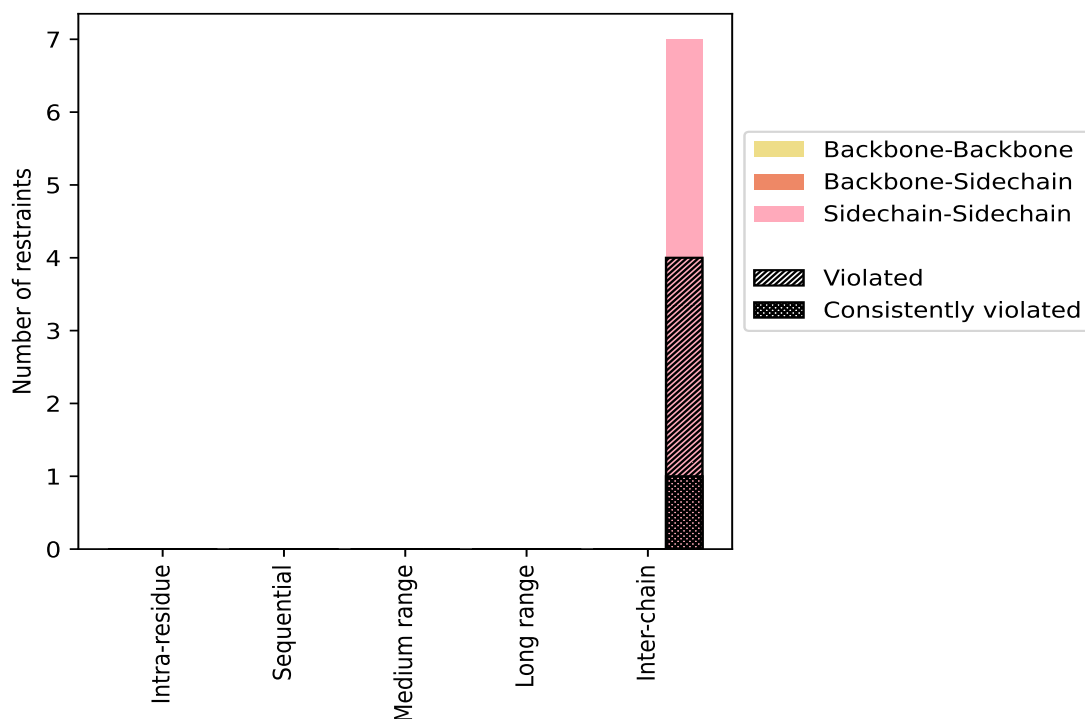
9.1 Summary of distance violations

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

Restrains type	Count	% ¹	Violated ³			Consistently Violated ⁴		
			Count	% ²	% ¹	Count	% ²	% ¹
Intra-residue (i-j =0)	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
Sequential (i-j =1)	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
Medium range (i-j >1 & i-j <5)	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
Long range (i-j ≥5)	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
Inter-chain	7	100.0	4	57.1	57.1	1	14.3	14.3
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	7	100.0	4	57.1	57.1	1	14.3	14.3
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	7	100.0	4	57.1	57.1	1	14.3	14.3
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	7	100.0	4	57.1	57.1	1	14.3	14.3

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 disulfid bonds are counted in their appropriate category on the x-axis

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

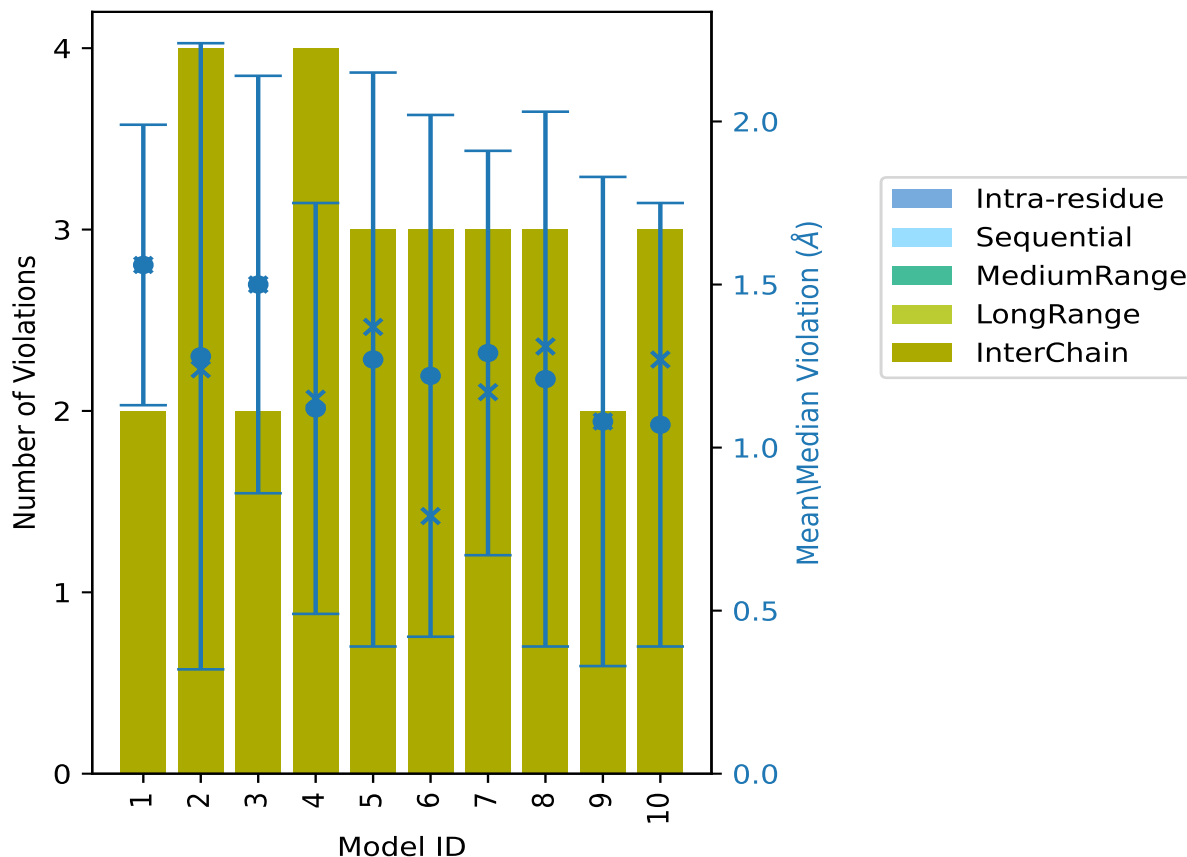
The following table provides the distance violation statistics for each model in the ensemble. Violations less than 0.1 Å are not included in the statistics.

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	0	0	0	0	2	2	1.56	1.99	0.43	1.56
2	0	0	0	0	4	4	1.28	2.34	0.96	1.24
3	0	0	0	0	2	2	1.5	2.14	0.64	1.5
4	0	0	0	0	4	4	1.12	1.92	0.63	1.15
5	0	0	0	0	3	3	1.27	2.3	0.88	1.37
6	0	0	0	0	3	3	1.22	2.34	0.8	0.79
7	0	0	0	0	3	3	1.29	2.11	0.62	1.17
8	0	0	0	0	3	3	1.21	2.16	0.82	1.31
9	0	0	0	0	2	2	1.08	1.82	0.75	1.08
10	0	0	0	0	3	3	1.07	1.79	0.68	1.27

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

⁵Inter-chain restraints, ⁶Standard deviation

9.2.1 Bar graph : Distance Violation statistics for each model [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, 3(IR:0, SQ:0, MR:0, LR:0, IC:3) 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	%
0	0	0	0	0	0	1	10.0
0	0	0	0	0	0	2	20.0
0	0	0	0	0	0	3	30.0
0	0	0	0	1	1	4	40.0

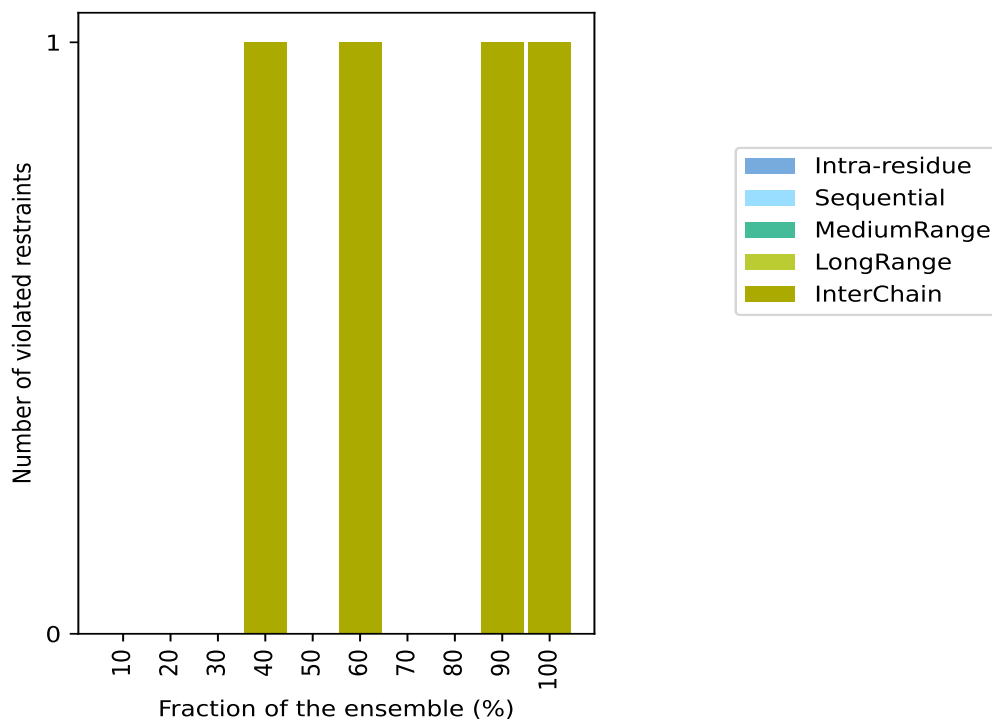
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Number of violated restraints						Fraction of the ensemble	
IR ¹	SQ ²	MR ³	LR ⁴	IC ⁵	Total	Count ⁶	%
0	0	0	0	0	0	5	50.0
0	0	0	0	1	1	6	60.0
0	0	0	0	0	0	7	70.0
0	0	0	0	0	0	8	80.0
0	0	0	0	1	1	9	90.0
0	0	0	0	1	1	10	100.0

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

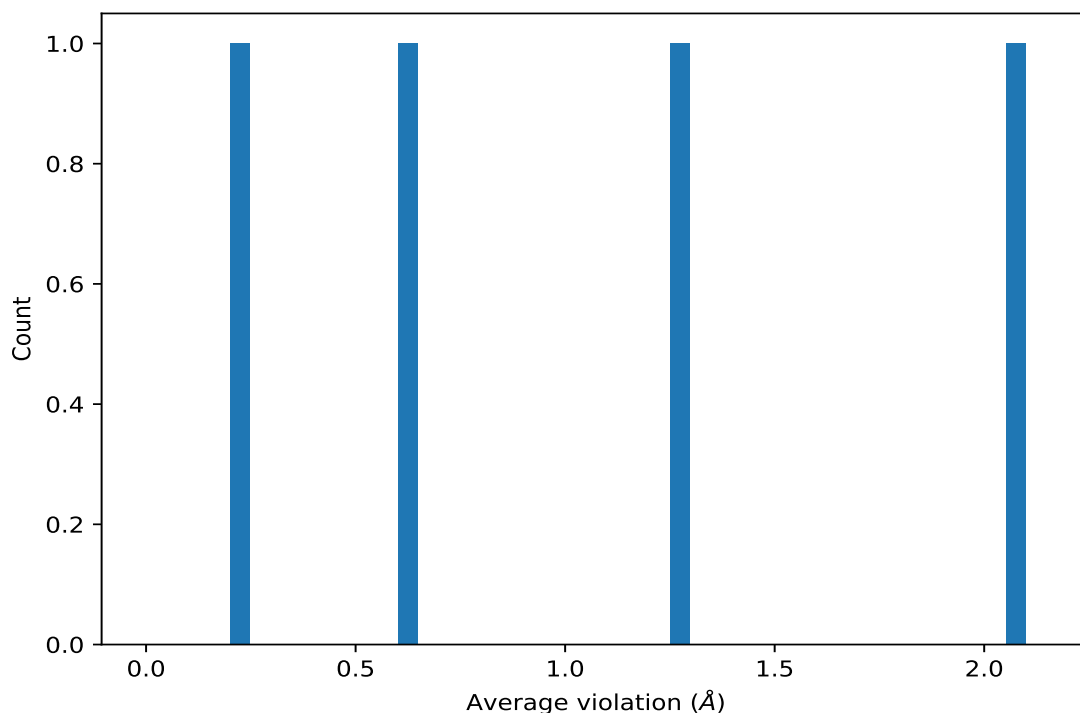
9.3.1 Bar graph : Distance violation statistics for the ensemble [i](#)



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

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

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



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

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

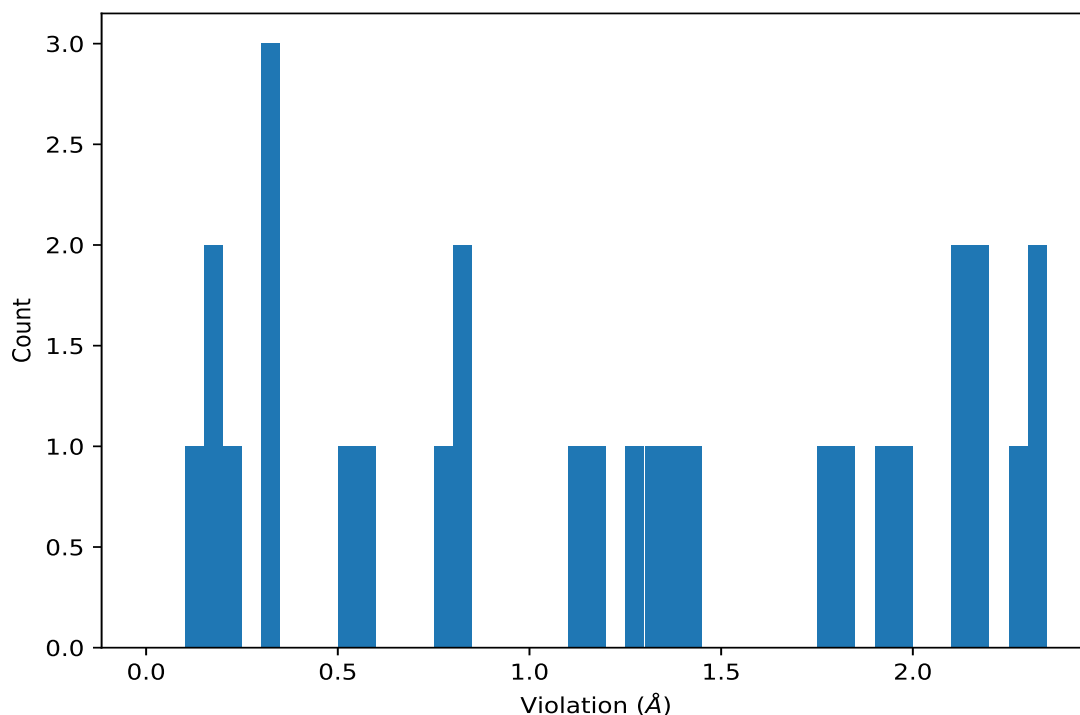
Key	Atom-1	Atom-2	Models ¹	Mean (Å)	SD ¹ (Å)	Median (Å)
(2,2)	1:A:88:ARG:NH2	2:B:6:A:P	10	2.07	0.18	2.12
(2,3)	1:A:61:LYS:NZ	2:B:3:U:P	9	1.27	0.47	1.27
(2,1)	1:A:177:ARG:HH21	2:B:10:G:P	6	0.22	0.07	0.2
(2,6)	1:A:107:ARG:NE	2:B:7:A:P	4	0.64	0.2	0.7

¹Number of violated models, ²Standard deviation

9.5 All violated distance restraints [i](#)

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

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



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

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

Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,3)	1:A:61:LYS:NZ	2:B:3:U:P	2	2.34
(2,2)	1:A:88:ARG:NH2	2:B:6:A:P	6	2.34
(2,2)	1:A:88:ARG:NH2	2:B:6:A:P	5	2.3
(2,2)	1:A:88:ARG:NH2	2:B:6:A:P	8	2.16
(2,2)	1:A:88:ARG:NH2	2:B:6:A:P	2	2.15
(2,2)	1:A:88:ARG:NH2	2:B:6:A:P	3	2.14
(2,2)	1:A:88:ARG:NH2	2:B:6:A:P	7	2.11
(2,2)	1:A:88:ARG:NH2	2:B:6:A:P	1	1.99
(2,2)	1:A:88:ARG:NH2	2:B:6:A:P	4	1.92
(2,2)	1:A:88:ARG:NH2	2:B:6:A:P	9	1.82
(2,2)	1:A:88:ARG:NH2	2:B:6:A:P	10	1.79
(2,3)	1:A:61:LYS:NZ	2:B:3:U:P	4	1.45
(2,3)	1:A:61:LYS:NZ	2:B:3:U:P	5	1.37
(2,3)	1:A:61:LYS:NZ	2:B:3:U:P	8	1.31
(2,3)	1:A:61:LYS:NZ	2:B:3:U:P	10	1.27
(2,3)	1:A:61:LYS:NZ	2:B:3:U:P	7	1.17

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Key	Atom-1	Atom-2	Model ID	Violation (Å)
(2,3)	1:A:61:LYS:NZ	2:B:3:U:P	1	1.14
(2,6)	1:A:107:ARG:NE	2:B:7:A:P	4	0.85
(2,3)	1:A:61:LYS:NZ	2:B:3:U:P	3	0.85
(2,6)	1:A:107:ARG:NE	2:B:7:A:P	6	0.79
(2,6)	1:A:107:ARG:NE	2:B:7:A:P	7	0.6
(2,3)	1:A:61:LYS:NZ	2:B:3:U:P	6	0.52
(2,6)	1:A:107:ARG:NE	2:B:7:A:P	2	0.34
(2,1)	1:A:177:ARG:HH21	2:B:10:G:P	9	0.33
(2,1)	1:A:177:ARG:HH21	2:B:10:G:P	2	0.31
(2,1)	1:A:177:ARG:HH21	2:B:10:G:P	4	0.24
(2,1)	1:A:177:ARG:HH21	2:B:10:G:P	8	0.17
(2,1)	1:A:177:ARG:HH21	2:B:10:G:P	10	0.16
(2,1)	1:A:177:ARG:HH21	2:B:10:G:P	5	0.14

10 Dihedral-angle violation analysis

No dihedral-angle restraints found