



Full wwPDB NMR Structure Validation Report ⓘ

Mar 25, 2026 – 09:27 PM UTC

PDB ID : 2K96 / pdb_00002k96
Title : Solution structure of the RDC-refined P2B-P3 pseudoknot from human telomerase RNA (delta U177)
Authors : Kim, N.-K.; Zhang, Q.; Zhou, J.; Theimer, C.A.; Peterson, R.D.; Feigon, J.
Deposited on : 2008-09-29

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

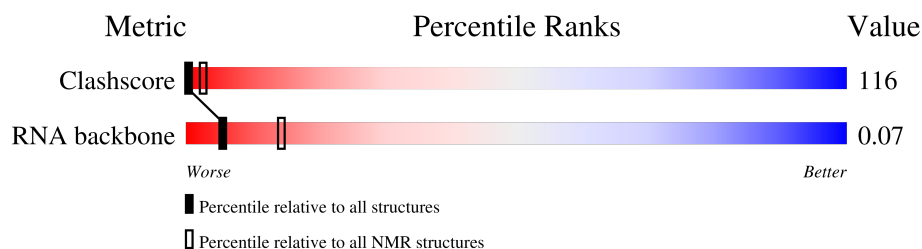
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	229148	14424
RNA backbone	8273	777

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	47	62% 38%

2 Ensemble composition and analysis ⓘ

This entry contains 20 models. This entry does not contain polypeptide chains, therefore identification of well-defined residues and clustering analysis are not possible. All residues are included in the validation scores.

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1495 atoms, of which 505 are hydrogens and 0 are deuteriums.

- Molecule 1 is a RNA chain called TELOMERASE RNA P2B-P3 PSEUDOKNOT.

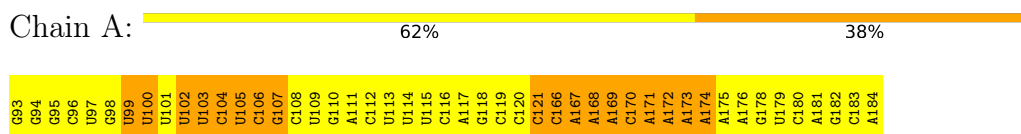
Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	P	
1	A	47	1495	445	505	173	326	46	0

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: TELOMERASE RNA P2B-P3 PSEUDOKNOT

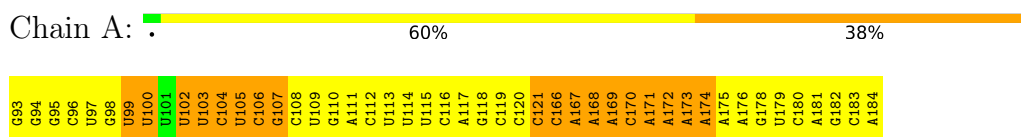


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

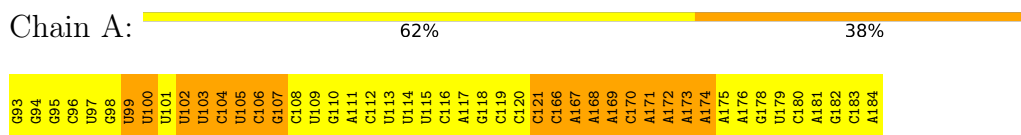
4.2.1 Score per residue for model 1

- Molecule 1: TELOMERASE RNA P2B-P3 PSEUDOKNOT



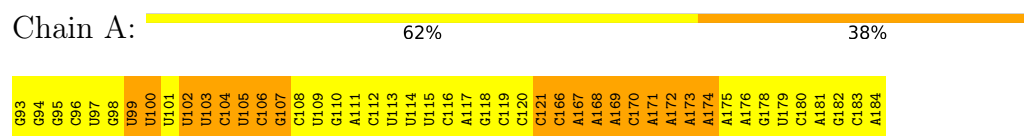
4.2.2 Score per residue for model 2

- Molecule 1: TELOMERASE RNA P2B-P3 PSEUDOKNOT



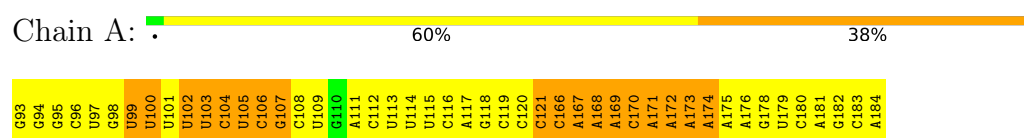
4.2.3 Score per residue for model 3

- Molecule 1: TELOMERASE RNA P2B-P3 PSEUDOKNOT



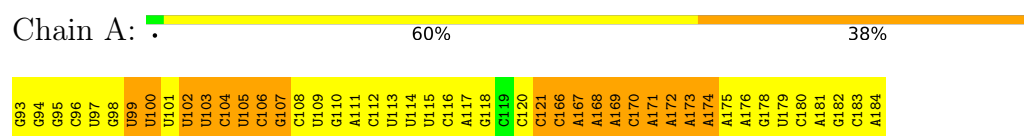
4.2.4 Score per residue for model 4

- Molecule 1: TELOMERASE RNA P2B-P3 PSEUDOKNOT



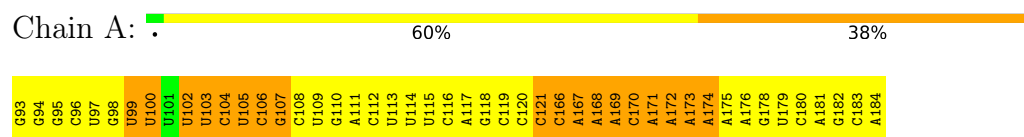
4.2.5 Score per residue for model 5

- Molecule 1: TELOMERASE RNA P2B-P3 PSEUDOKNOT



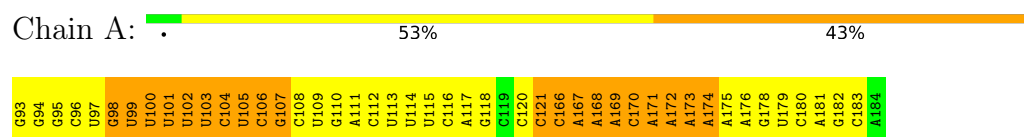
4.2.6 Score per residue for model 6

- Molecule 1: TELOMERASE RNA P2B-P3 PSEUDOKNOT



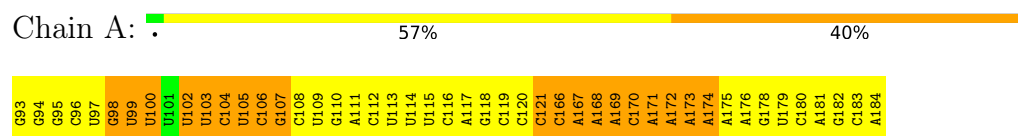
4.2.7 Score per residue for model 7

- Molecule 1: TELOMERASE RNA P2B-P3 PSEUDOKNOT



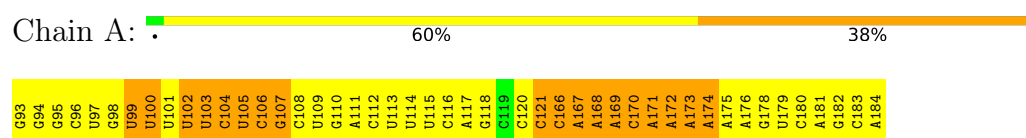
4.2.8 Score per residue for model 8

- Molecule 1: TELOMERASE RNA P2B-P3 PSEUDOKNOT



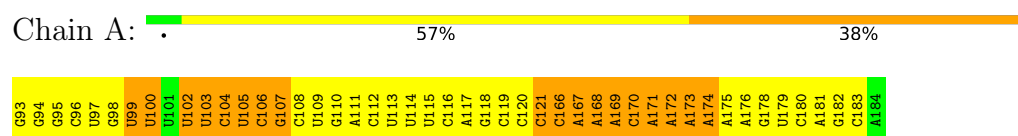
4.2.9 Score per residue for model 9

- Molecule 1: TELOMERASE RNA P2B-P3 PSEUDOKNOT



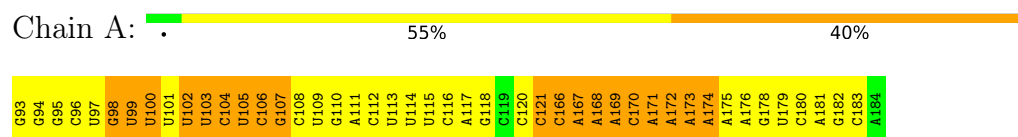
4.2.10 Score per residue for model 10

- Molecule 1: TELOMERASE RNA P2B-P3 PSEUDOKNOT



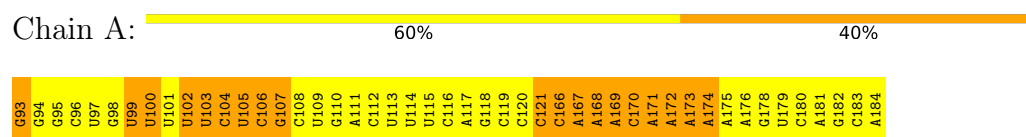
4.2.11 Score per residue for model 11

- Molecule 1: TELOMERASE RNA P2B-P3 PSEUDOKNOT



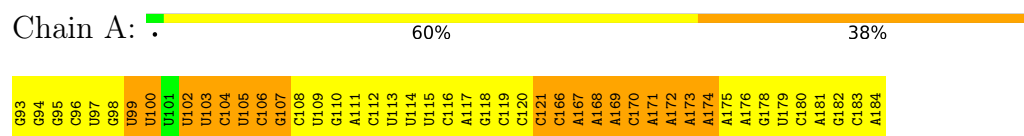
4.2.12 Score per residue for model 12

- Molecule 1: TELOMERASE RNA P2B-P3 PSEUDOKNOT



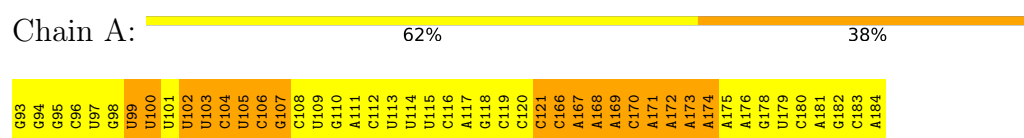
4.2.13 Score per residue for model 13

- Molecule 1: TELOMERASE RNA P2B-P3 PSEUDOKNOT



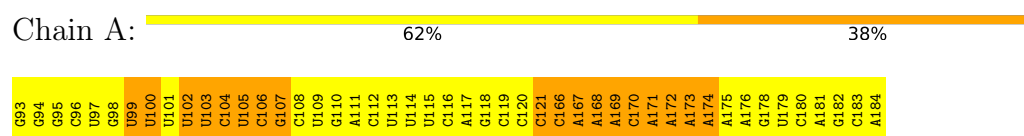
4.2.14 Score per residue for model 14

- Molecule 1: TELOMERASE RNA P2B-P3 PSEUDOKNOT



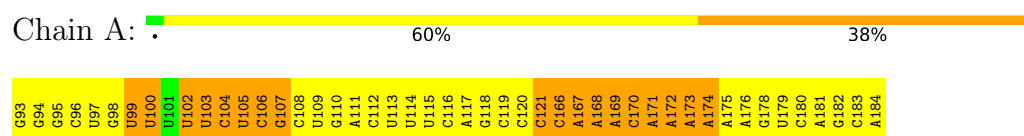
4.2.15 Score per residue for model 15

- Molecule 1: TELOMERASE RNA P2B-P3 PSEUDOKNOT



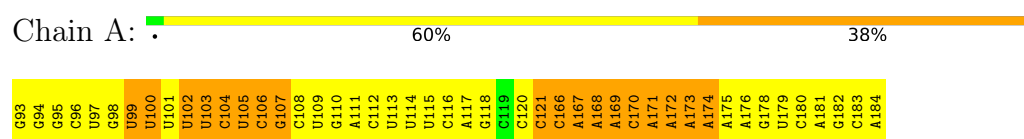
4.2.16 Score per residue for model 16

- Molecule 1: TELOMERASE RNA P2B-P3 PSEUDOKNOT



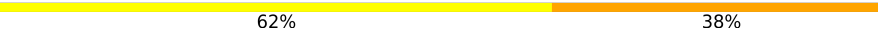
4.2.17 Score per residue for model 17

- Molecule 1: TELOMERASE RNA P2B-P3 PSEUDOKNOT



4.2.18 Score per residue for model 18

- Molecule 1: TELOMERASE RNA P2B-P3 PSEUDOKNOT

Chain A:  62% 38%

G93	G94	G95	C96	U97	G98	U99	U100	U101	U102	U103	C104	U105	C106	G107	C108	U109	G110	A111	C112	U113	U114	U115	C116	A117	G118	C119	C120	C121	C166	A167	A168	A169	C170	A171	A172	A173	A174	A175	A176	G178	U179	C180	A181	G182	C183	A184
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4.2.19 Score per residue for model 19

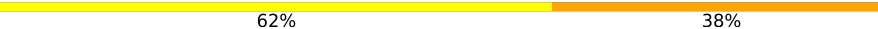
- Molecule 1: TELOMERASE RNA P2B-P3 PSEUDOKNOT

Chain A:  60% 40%

G93	G94	G95	C96	U97	G98	U99	U100	U101	U102	U103	C104	U105	C106	G107	C108	U109	G110	A111	C112	U113	U114	U115	C116	A117	G118	C119	C120	C121	C166	A167	A168	A169	C170	A171	A172	A173	A174	A175	A176	G178	U179	C180	A181	G182	C183	A184
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4.2.20 Score per residue for model 20

- Molecule 1: TELOMERASE RNA P2B-P3 PSEUDOKNOT

Chain A:  62% 38%

G93	G94	G95	C96	U97	G98	U99	U100	U101	U102	U103	C104	U105	C106	G107	C108	U109	G110	A111	C112	U113	U114	U115	C116	A117	G118	C119	C120	C121	C166	A167	A168	A169	C170	A171	A172	A173	A174	A175	A176	G178	U179	C180	A181	G182	C183	A184
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5 Refinement protocol and experimental data overview

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

Of the 200 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
X-PLOR NIH	structure solution	2.9.8
X-PLOR NIH	refinement	2.9.8

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

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	990	505	507	174±10
All	All	19800	10100	10140	3481

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 116.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:105:U:O3'	1:A:106:C:H3'	1.04	1.51	3	13
1:A:120:C:O2'	1:A:121:C:H5'	1.02	1.54	4	20
1:A:104:C:H4'	1:A:106:C:OP2	0.98	1.59	13	19
1:A:98:G:H5''	1:A:99:U:OP1	0.97	1.59	13	18
1:A:119:C:O2'	1:A:120:C:H5'	0.97	1.58	8	13
1:A:102:U:H5'	1:A:103:U:OP2	0.96	1.59	11	20
1:A:105:U:O2'	1:A:106:C:H2'	0.96	1.59	16	18
1:A:180:C:HO2'	1:A:181:A:H8	0.95	1.00	14	9
1:A:116:C:O2'	1:A:117:A:H5'	0.95	1.61	2	11
1:A:113:U:O2'	1:A:114:U:H5'	0.94	1.62	7	19
1:A:182:G:O2'	1:A:183:C:H5'	0.94	1.61	15	14
1:A:105:U:H5''	1:A:106:C:OP1	0.93	1.61	4	5
1:A:100:U:O2	1:A:173:A:H2'	0.93	1.62	14	14
1:A:96:C:O2'	1:A:97:U:H5'	0.92	1.64	15	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:104:C:O3'	1:A:105:U:H3'	0.91	1.64	3	20
1:A:99:U:HO2'	1:A:100:U:H6	0.90	1.01	16	19
1:A:97:U:H4'	1:A:170:C:OP2	0.89	1.66	2	4
1:A:96:C:H1'	1:A:168:A:O2'	0.89	1.67	14	17
1:A:167:A:O2'	1:A:168:A:H5''	0.89	1.67	14	1
1:A:183:C:O2'	1:A:184:A:H5'	0.88	1.69	12	12
1:A:172:A:O2'	1:A:173:A:H5''	0.88	1.69	15	8
1:A:103:U:H5'	1:A:108:C:OP2	0.87	1.70	2	4
1:A:104:C:OP1	1:A:106:C:H5''	0.86	1.70	7	6
1:A:115:U:H2'	1:A:116:C:O4'	0.86	1.70	13	19
1:A:168:A:H4'	1:A:169:A:OP2	0.85	1.69	5	2
1:A:171:A:HO2'	1:A:172:A:H8	0.85	0.88	20	3
1:A:97:U:H2'	1:A:98:G:O4'	0.84	1.72	6	17
1:A:104:C:H2'	1:A:109:U:O4	0.84	1.71	5	16
1:A:97:U:H5'	1:A:169:A:OP2	0.82	1.73	11	3
1:A:166:C:H6	1:A:166:C:O5'	0.81	1.58	18	15
1:A:106:C:O2'	1:A:107:G:P	0.81	2.39	2	1
1:A:99:U:O2'	1:A:100:U:C6	0.81	2.34	9	20
1:A:104:C:OP1	1:A:106:C:H4'	0.80	1.76	3	5
1:A:171:A:O2'	1:A:172:A:P	0.80	2.39	10	5
1:A:180:C:O2'	1:A:181:A:H8	0.80	1.59	16	7
1:A:169:A:H5''	1:A:170:C:OP2	0.80	1.75	4	3
1:A:100:U:O2	1:A:173:A:H3'	0.80	1.76	12	4
1:A:104:C:O5'	1:A:104:C:H6	0.79	1.60	12	12
1:A:171:A:O2'	1:A:172:A:H5'	0.79	1.75	4	8
1:A:117:A:HO2'	1:A:118:G:H8	0.79	1.21	15	1
1:A:178:G:H2'	1:A:179:U:O4'	0.78	1.79	16	19
1:A:99:U:C2	1:A:100:U:C5	0.78	2.71	5	20
1:A:106:C:H4'	1:A:107:G:OP2	0.78	1.79	7	8
1:A:167:A:H1'	1:A:168:A:OP1	0.78	1.79	16	1
1:A:104:C:O2'	1:A:105:U:OP1	0.77	2.03	4	7
1:A:111:A:C6	1:A:112:C:C4	0.77	2.73	18	20
1:A:104:C:C2	1:A:109:U:C5	0.77	2.72	9	12
1:A:104:C:H4'	1:A:105:U:OP2	0.77	1.79	15	9
1:A:178:G:C6	1:A:179:U:C4	0.77	2.72	19	20
1:A:97:U:H5'	1:A:169:A:OP1	0.77	1.80	16	2
1:A:109:U:HO2'	1:A:110:G:H8	0.76	1.23	16	11
1:A:167:A:O2'	1:A:168:A:P	0.76	2.42	16	1
1:A:184:A:H8	1:A:184:A:O5'	0.76	1.64	5	1
1:A:169:A:OP2	1:A:169:A:H8	0.76	1.63	6	2
1:A:173:A:O2'	1:A:174:A:P	0.76	2.44	18	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:105:U:P	1:A:180:C:C5	0.75	2.80	14	19
1:A:168:A:H5'	1:A:169:A:O5'	0.75	1.82	6	4
1:A:99:U:O2'	1:A:100:U:H6	0.74	1.66	14	20
1:A:106:C:OP1	1:A:106:C:H6	0.74	1.66	11	5
1:A:179:U:O2'	1:A:180:C:O4'	0.74	2.06	2	20
1:A:169:A:C6	1:A:170:C:N4	0.73	2.57	2	17
1:A:101:U:O2	1:A:174:A:H3'	0.73	1.83	12	1
1:A:110:G:H8	1:A:110:G:O5'	0.73	1.67	8	5
1:A:170:C:H2'	1:A:171:A:O4'	0.73	1.83	18	7
1:A:94:G:N3	1:A:95:G:C8	0.73	2.57	13	17
1:A:104:C:O2'	1:A:181:A:N6	0.73	2.21	20	15
1:A:98:G:O2'	1:A:99:U:C6	0.73	2.40	18	20
1:A:93:G:C6	1:A:94:G:C6	0.72	2.77	19	15
1:A:176:A:C6	1:A:178:G:C6	0.72	2.77	13	18
1:A:95:G:C2	1:A:120:C:C2	0.72	2.76	2	19
1:A:99:U:O2'	1:A:100:U:P	0.72	2.48	7	14
1:A:104:C:O2'	1:A:105:U:P	0.72	2.46	2	15
1:A:96:C:O2'	1:A:169:A:P	0.72	2.48	8	10
1:A:104:C:H5'	1:A:106:C:OP2	0.72	1.84	20	7
1:A:167:A:O2'	1:A:168:A:C8	0.71	2.43	17	17
1:A:99:U:C4	1:A:172:A:N1	0.71	2.59	11	18
1:A:121:C:O2'	1:A:166:C:P	0.71	2.48	17	8
1:A:106:C:H6	1:A:106:C:O5'	0.71	1.67	6	6
1:A:95:G:N2	1:A:120:C:C2	0.71	2.59	20	18
1:A:94:G:C2	1:A:95:G:C5	0.71	2.79	1	15
1:A:167:A:C6	1:A:168:A:N6	0.71	2.59	13	8
1:A:183:C:H6	1:A:183:C:O5'	0.70	1.69	11	10
1:A:169:A:O2'	1:A:170:C:P	0.70	2.49	20	2
1:A:171:A:O2'	1:A:172:A:H8	0.70	1.68	10	3
1:A:94:G:C4	1:A:95:G:C8	0.70	2.80	3	18
1:A:111:A:N6	1:A:112:C:N4	0.70	2.39	8	20
1:A:181:A:O2'	1:A:182:G:H5'	0.70	1.87	5	12
1:A:171:A:HO2'	1:A:172:A:C5'	0.70	1.99	16	3
1:A:173:A:N6	1:A:174:A:N6	0.69	2.40	2	8
1:A:182:G:HO2'	1:A:183:C:C5'	0.69	2.00	7	7
1:A:171:A:O2'	1:A:172:A:C8	0.69	2.45	19	6
1:A:105:U:O2'	1:A:106:C:C2'	0.69	2.40	13	17
1:A:97:U:O2'	1:A:98:G:H5'	0.69	1.87	6	5
1:A:111:A:C6	1:A:112:C:N4	0.69	2.61	8	20
1:A:93:G:C5	1:A:94:G:C5	0.69	2.81	20	15
1:A:116:C:C4	1:A:117:A:N7	0.69	2.61	1	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:98:G:O2'	1:A:172:A:N6	0.69	2.26	1	16
1:A:173:A:O2'	1:A:174:A:H8	0.69	1.70	2	10
1:A:93:G:O5'	1:A:93:G:C8	0.68	2.46	12	1
1:A:100:U:H6	1:A:100:U:OP1	0.68	1.71	6	5
1:A:101:U:O2	1:A:174:A:H2'	0.68	1.89	3	7
1:A:105:U:O2'	1:A:106:C:C3'	0.68	2.40	6	6
1:A:99:U:H1'	1:A:100:U:OP1	0.68	1.88	5	10
1:A:121:C:H5''	1:A:167:A:O4'	0.68	1.88	17	6
1:A:94:G:O2'	1:A:95:G:O5'	0.68	2.12	8	20
1:A:176:A:O2'	1:A:178:G:H5'	0.68	1.89	5	16
1:A:178:G:C5	1:A:179:U:C4	0.68	2.81	18	20
1:A:104:C:O3'	1:A:105:U:H6	0.68	1.72	14	16
1:A:173:A:O2'	1:A:174:A:C8	0.68	2.47	2	12
1:A:173:A:C6	1:A:174:A:C6	0.68	2.81	2	11
1:A:170:C:O2'	1:A:171:A:O5'	0.67	2.11	8	19
1:A:172:A:O2'	1:A:173:A:C5'	0.67	2.42	1	12
1:A:169:A:C2	1:A:170:C:C4	0.67	2.82	14	7
1:A:171:A:H1'	1:A:172:A:OP1	0.67	1.89	17	4
1:A:94:G:C2	1:A:95:G:C4	0.67	2.82	2	18
1:A:99:U:C5	1:A:172:A:N6	0.67	2.63	11	3
1:A:104:C:H5'	1:A:106:C:O5'	0.67	1.89	11	4
1:A:173:A:C4	1:A:174:A:C8	0.67	2.83	14	1
1:A:94:G:O2'	1:A:95:G:P	0.67	2.53	19	20
1:A:169:A:N1	1:A:170:C:N4	0.67	2.43	14	6
1:A:114:U:O2'	1:A:115:U:O4'	0.67	2.12	3	19
1:A:96:C:H4'	1:A:169:A:OP2	0.66	1.90	2	3
1:A:96:C:O2'	1:A:169:A:C5'	0.66	2.43	10	4
1:A:179:U:O2'	1:A:180:C:C6	0.66	2.46	4	9
1:A:93:G:N7	1:A:94:G:N7	0.66	2.43	18	12
1:A:121:C:H4'	1:A:166:C:OP2	0.66	1.89	16	7
1:A:171:A:O2'	1:A:172:A:C5'	0.66	2.43	8	10
1:A:104:C:HO2'	1:A:181:A:N6	0.66	1.88	19	4
1:A:173:A:C6	1:A:174:A:C5	0.66	2.84	14	1
1:A:104:C:C4'	1:A:106:C:OP2	0.66	2.43	17	14
1:A:100:U:H1'	1:A:173:A:OP2	0.66	1.91	5	4
1:A:118:G:O2'	1:A:169:A:N6	0.66	2.28	20	2
1:A:94:G:N2	1:A:95:G:C4	0.66	2.63	2	14
1:A:106:C:OP1	1:A:106:C:C6	0.66	2.49	1	6
1:A:166:C:O5'	1:A:166:C:C6	0.66	2.49	17	19
1:A:105:U:OP2	1:A:180:C:C5	0.65	2.49	5	17
1:A:103:U:OP2	1:A:104:C:N4	0.65	2.29	17	12

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:105:U:C5	1:A:182:G:O6	0.65	2.50	18	20
1:A:121:C:O4'	1:A:167:A:C2	0.65	2.49	17	20
1:A:104:C:O5'	1:A:106:C:P	0.65	2.54	1	2
1:A:182:G:O2'	1:A:183:C:C5'	0.65	2.45	5	13
1:A:168:A:OP1	1:A:168:A:H4'	0.65	1.92	19	10
1:A:176:A:N6	1:A:178:G:C6	0.65	2.64	9	10
1:A:105:U:OP1	1:A:180:C:C5	0.65	2.50	4	8
1:A:169:A:C6	1:A:170:C:C4	0.65	2.84	16	8
1:A:104:C:O5'	1:A:104:C:C6	0.65	2.50	14	5
1:A:169:A:H4'	1:A:170:C:OP1	0.65	1.91	20	2
1:A:105:U:O4	1:A:182:G:C5	0.65	2.49	3	15
1:A:170:C:O2'	1:A:171:A:C5'	0.65	2.44	18	9
1:A:169:A:OP2	1:A:169:A:C8	0.65	2.49	6	2
1:A:105:U:C5'	1:A:106:C:OP1	0.64	2.45	7	13
1:A:103:U:H3'	1:A:104:C:O4'	0.64	1.92	1	7
1:A:105:U:C2	1:A:107:G:O6	0.64	2.51	4	14
1:A:113:U:O2'	1:A:114:U:C5'	0.64	2.45	15	10
1:A:183:C:O2'	1:A:184:A:C5'	0.64	2.45	2	14
1:A:99:U:O2'	1:A:100:U:C5	0.64	2.51	6	11
1:A:117:A:O2'	1:A:118:G:C8	0.64	2.51	15	6
1:A:169:A:P	1:A:169:A:O4'	0.64	2.55	6	2
1:A:180:C:C2	1:A:181:A:N7	0.64	2.66	5	4
1:A:105:U:N3	1:A:107:G:O6	0.64	2.31	2	12
1:A:173:A:O2'	1:A:174:A:O5'	0.64	2.16	14	16
1:A:105:U:O2'	1:A:106:C:O2'	0.64	2.16	1	2
1:A:106:C:O2'	1:A:107:G:OP1	0.64	2.15	5	7
1:A:167:A:O2'	1:A:168:A:O5'	0.64	2.16	16	19
1:A:103:U:O5'	1:A:104:C:C5	0.64	2.51	18	12
1:A:99:U:C4	1:A:172:A:C6	0.64	2.86	11	9
1:A:103:U:O4	1:A:178:G:N7	0.63	2.31	15	19
1:A:104:C:N4	1:A:109:U:OP2	0.63	2.31	9	15
1:A:96:C:C1'	1:A:168:A:O2'	0.63	2.46	16	6
1:A:121:C:C4'	1:A:167:A:N3	0.63	2.61	19	18
1:A:93:G:O6	1:A:94:G:C6	0.63	2.52	2	15
1:A:166:C:O5'	1:A:166:C:H6	0.63	1.76	15	2
1:A:104:C:H1'	1:A:105:U:OP2	0.63	1.94	3	5
1:A:105:U:OP2	1:A:180:C:N4	0.63	2.32	9	8
1:A:105:U:H5''	1:A:180:C:OP2	0.63	1.94	3	6
1:A:105:U:OP2	1:A:180:C:C4	0.63	2.52	19	6
1:A:173:A:H1'	1:A:174:A:OP1	0.63	1.93	15	2
1:A:171:A:O2'	1:A:172:A:O5'	0.63	2.15	19	19

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:172:A:O2'	1:A:173:A:OP1	0.63	2.17	12	7
1:A:173:A:C6	1:A:174:A:N6	0.63	2.67	2	2
1:A:119:C:O2'	1:A:120:C:C5'	0.63	2.46	3	12
1:A:117:A:N6	1:A:118:G:O6	0.63	2.32	16	12
1:A:109:U:O4	1:A:182:G:C6	0.63	2.51	13	13
1:A:180:C:O2'	1:A:181:A:O5'	0.63	2.16	5	6
1:A:97:U:H5'	1:A:169:A:O5'	0.63	1.93	10	2
1:A:104:C:C2'	1:A:109:U:O4	0.63	2.47	11	17
1:A:166:C:O2'	1:A:167:A:P	0.63	2.57	13	3
1:A:93:G:O2'	1:A:94:G:O5'	0.62	2.17	6	5
1:A:180:C:O2'	1:A:181:A:C8	0.62	2.44	5	8
1:A:93:G:C6	1:A:94:G:C5	0.62	2.87	12	15
1:A:167:A:H2'	1:A:167:A:OP2	0.62	1.93	8	1
1:A:170:C:O2	1:A:171:A:H1'	0.62	1.94	16	5
1:A:173:A:O2'	1:A:174:A:OP1	0.62	2.15	18	2
1:A:105:U:OP1	1:A:180:C:C4	0.62	2.52	15	5
1:A:105:U:O4	1:A:183:C:N4	0.62	2.32	11	19
1:A:170:C:O2'	1:A:171:A:O4'	0.62	2.16	16	7
1:A:167:A:O2'	1:A:168:A:C5'	0.62	2.45	14	2
1:A:172:A:O2'	1:A:173:A:P	0.62	2.58	18	9
1:A:104:C:O3'	1:A:105:U:C6	0.62	2.53	14	20
1:A:100:U:C6	1:A:100:U:OP1	0.62	2.52	6	5
1:A:109:U:O2'	1:A:110:G:O5'	0.62	2.18	15	14
1:A:104:C:C5'	1:A:106:C:OP2	0.62	2.47	16	11
1:A:98:G:C5'	1:A:99:U:OP1	0.62	2.48	8	5
1:A:94:G:O2'	1:A:95:G:O4'	0.62	2.18	3	20
1:A:167:A:O2'	1:A:168:A:O4'	0.62	2.17	17	19
1:A:98:G:H4'	1:A:99:U:OP1	0.62	1.95	19	4
1:A:173:A:C1'	1:A:174:A:OP1	0.62	2.48	15	2
1:A:97:U:C2'	1:A:98:G:O4'	0.62	2.47	9	17
1:A:173:A:C2	1:A:174:A:C4	0.62	2.88	14	1
1:A:96:C:O2'	1:A:169:A:OP1	0.61	2.18	19	3
1:A:169:A:O2'	1:A:170:C:OP1	0.61	2.18	10	2
1:A:94:G:O2'	1:A:95:G:H8	0.61	1.78	17	8
1:A:105:U:O4	1:A:182:G:N7	0.61	2.33	5	15
1:A:101:U:H6	1:A:101:U:OP2	0.61	1.77	9	1
1:A:99:U:O2'	1:A:100:U:OP1	0.61	2.18	17	7
1:A:97:U:O2'	1:A:98:G:C5'	0.61	2.49	6	7
1:A:104:C:O2'	1:A:105:U:OP2	0.61	2.18	3	5
1:A:104:C:HO2'	1:A:105:U:P	0.61	2.19	3	8
1:A:93:G:O2'	1:A:94:G:O4'	0.61	2.19	8	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:97:U:O2'	1:A:98:G:O4'	0.61	2.18	11	6
1:A:166:C:O4'	1:A:167:A:C8	0.61	2.53	19	1
1:A:167:A:C1'	1:A:168:A:OP1	0.61	2.48	16	1
1:A:104:C:C5	1:A:109:U:OP2	0.61	2.53	7	4
1:A:169:A:N6	1:A:170:C:N4	0.61	2.49	16	7
1:A:106:C:C6	1:A:106:C:O5'	0.61	2.53	3	2
1:A:180:C:O2	1:A:181:A:C8	0.61	2.54	5	4
1:A:104:C:OP1	1:A:106:C:C4'	0.61	2.49	3	5
1:A:104:C:C4'	1:A:105:U:OP2	0.60	2.49	15	9
1:A:170:C:H4'	1:A:171:A:OP1	0.60	1.96	8	4
1:A:170:C:N4	1:A:171:A:C6	0.60	2.70	13	2
1:A:106:C:O5'	1:A:106:C:C6	0.60	2.53	8	5
1:A:104:C:O2	1:A:110:G:C6	0.60	2.55	13	4
1:A:171:A:O2'	1:A:172:A:OP1	0.60	2.19	10	5
1:A:99:U:O2'	1:A:100:U:O5'	0.60	2.19	14	6
1:A:93:G:C8	1:A:94:G:N7	0.60	2.69	20	11
1:A:172:A:O2'	1:A:173:A:O5'	0.60	2.20	4	11
1:A:104:C:O2'	1:A:109:U:O4	0.60	2.19	18	17
1:A:121:C:O3'	1:A:166:C:C6	0.60	2.55	16	2
1:A:167:A:O2'	1:A:168:A:H8	0.59	1.80	17	16
1:A:167:A:C2	1:A:168:A:C6	0.59	2.90	2	5
1:A:102:U:C5'	1:A:103:U:OP2	0.59	2.50	17	17
1:A:104:C:O5'	1:A:106:C:OP2	0.59	2.20	7	6
1:A:170:C:C2	1:A:171:A:C8	0.59	2.90	16	2
1:A:174:A:O2'	1:A:175:A:O4'	0.59	2.20	5	15
1:A:99:U:O2'	1:A:100:U:OP2	0.59	2.19	9	6
1:A:121:C:H4'	1:A:167:A:N3	0.59	2.11	19	6
1:A:174:A:O2'	1:A:175:A:O5'	0.59	2.21	2	16
1:A:183:C:O2	1:A:184:A:N7	0.59	2.35	6	1
1:A:104:C:N3	1:A:109:U:C6	0.59	2.69	13	9
1:A:178:G:N7	1:A:179:U:C5	0.59	2.71	1	19
1:A:117:A:C5	1:A:118:G:N7	0.59	2.71	6	9
1:A:166:C:O2'	1:A:167:A:O5'	0.59	2.21	16	2
1:A:93:G:H2'	1:A:94:G:O4'	0.59	1.96	12	6
1:A:121:C:O2'	1:A:166:C:OP2	0.59	2.21	2	1
1:A:180:C:O2	1:A:181:A:N7	0.59	2.35	5	4
1:A:105:U:OP1	1:A:181:A:N6	0.59	2.35	7	1
1:A:178:G:C5	1:A:179:U:C5	0.59	2.91	20	20
1:A:183:C:O2'	1:A:184:A:O5'	0.59	2.21	15	5
1:A:167:A:H3'	1:A:167:A:OP2	0.59	1.98	16	1
1:A:166:C:C5'	1:A:167:A:N7	0.59	2.65	16	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:104:C:C1'	1:A:105:U:OP2	0.58	2.50	3	9
1:A:93:G:O2'	1:A:94:G:C5'	0.58	2.50	8	4
1:A:96:C:H1'	1:A:168:A:HO2'	0.58	1.54	14	2
1:A:170:C:C4	1:A:171:A:C5	0.58	2.91	13	3
1:A:173:A:C4	1:A:174:A:N7	0.58	2.71	14	1
1:A:103:U:O4	1:A:179:U:O4	0.58	2.22	18	20
1:A:184:A:O5'	1:A:184:A:C8	0.58	2.53	5	1
1:A:98:G:C4'	1:A:99:U:OP1	0.58	2.51	11	4
1:A:121:C:O3'	1:A:166:C:C5	0.58	2.56	16	2
1:A:104:C:OP1	1:A:107:G:P	0.58	2.61	14	7
1:A:105:U:O2'	1:A:107:G:OP1	0.58	2.20	2	1
1:A:106:C:HO2'	1:A:107:G:P	0.58	2.17	2	1
1:A:111:A:C5	1:A:112:C:C4	0.58	2.92	18	19
1:A:96:C:O2'	1:A:169:A:OP2	0.58	2.21	19	5
1:A:170:C:O2'	1:A:171:A:C4'	0.58	2.52	12	5
1:A:170:C:O2	1:A:171:A:C1'	0.58	2.52	15	5
1:A:167:A:OP2	1:A:167:A:C3'	0.58	2.52	16	2
1:A:168:A:C4'	1:A:168:A:OP1	0.58	2.51	13	7
1:A:104:C:P	1:A:107:G:OP2	0.58	2.62	4	1
1:A:104:C:N4	1:A:109:U:O5'	0.58	2.37	13	4
1:A:95:G:C2	1:A:120:C:O2	0.58	2.57	1	6
1:A:104:C:O2	1:A:110:G:O6	0.58	2.22	13	19
1:A:105:U:H5''	1:A:106:C:OP2	0.58	1.98	17	4
1:A:99:U:O2	1:A:100:U:C5	0.57	2.57	8	8
1:A:105:U:C4	1:A:183:C:N4	0.57	2.71	7	16
1:A:169:A:C5	1:A:170:C:C4	0.57	2.92	2	5
1:A:169:A:C5'	1:A:170:C:OP2	0.57	2.51	6	1
1:A:171:A:C1'	1:A:172:A:OP1	0.57	2.52	17	4
1:A:111:A:C5	1:A:112:C:C5	0.57	2.93	20	20
1:A:99:U:C1'	1:A:100:U:OP1	0.57	2.52	7	8
1:A:167:A:OP2	1:A:167:A:C2'	0.57	2.52	8	2
1:A:170:C:O2'	1:A:171:A:P	0.57	2.62	16	3
1:A:183:C:HO2'	1:A:184:A:C5'	0.57	2.13	15	3
1:A:166:C:O4'	1:A:167:A:N7	0.57	2.38	2	1
1:A:121:C:C4'	1:A:166:C:OP2	0.57	2.52	16	7
1:A:170:C:HO2'	1:A:171:A:P	0.57	2.21	5	3
1:A:166:C:O2'	1:A:167:A:OP2	0.57	2.21	13	1
1:A:168:A:OP1	1:A:168:A:C4'	0.57	2.53	15	4
1:A:104:C:OP1	1:A:107:G:OP2	0.57	2.22	7	17
1:A:117:A:C6	1:A:118:G:C6	0.57	2.93	16	9
1:A:104:C:H5	1:A:109:U:OP2	0.56	1.83	6	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:105:U:H5	1:A:182:G:O6	0.56	1.83	14	6
1:A:115:U:O2'	1:A:116:C:H5'	0.56	2.00	17	4
1:A:172:A:C2	1:A:173:A:N7	0.56	2.72	6	5
1:A:104:C:C5'	1:A:106:C:P	0.56	2.93	11	4
1:A:105:U:O5'	1:A:106:C:OP2	0.56	2.23	13	1
1:A:169:A:C5	1:A:170:C:N4	0.56	2.74	20	5
1:A:107:G:H8	1:A:107:G:O5'	0.56	1.83	2	2
1:A:169:A:N1	1:A:170:C:C4	0.56	2.74	8	4
1:A:173:A:C5	1:A:174:A:N7	0.56	2.74	14	1
1:A:113:U:C4	1:A:114:U:C5	0.56	2.93	1	3
1:A:116:C:O2'	1:A:117:A:C5'	0.56	2.48	2	2
1:A:96:C:O2'	1:A:97:U:C5'	0.56	2.54	6	7
1:A:117:A:C6	1:A:118:G:C5	0.56	2.94	6	3
1:A:109:U:O4	1:A:182:G:N1	0.56	2.39	9	8
1:A:104:C:OP1	1:A:106:C:C5'	0.56	2.53	5	5
1:A:168:A:P	1:A:168:A:O4'	0.56	2.64	16	1
1:A:170:C:O2'	1:A:171:A:H5'	0.56	2.01	18	1
1:A:94:G:C2	1:A:95:G:C8	0.56	2.94	2	9
1:A:109:U:O2'	1:A:110:G:C8	0.55	2.57	16	5
1:A:118:G:H21	1:A:170:C:H41	0.55	1.44	1	4
1:A:96:C:HO2'	1:A:97:U:H5'	0.55	1.56	15	1
1:A:105:U:OP1	1:A:180:C:C6	0.55	2.58	5	2
1:A:169:A:OP2	1:A:169:A:O4'	0.55	2.23	5	2
1:A:117:A:O2'	1:A:118:G:H8	0.55	1.84	5	2
1:A:119:C:HO2'	1:A:120:C:C5'	0.55	2.14	20	1
1:A:93:G:C5	1:A:94:G:N7	0.55	2.75	12	11
1:A:106:C:O5'	1:A:106:C:H6	0.55	1.84	3	2
1:A:103:U:O4	1:A:178:G:O6	0.55	2.25	7	19
1:A:110:G:O5'	1:A:110:G:C8	0.54	2.57	8	2
1:A:175:A:O2'	1:A:176:A:H5'	0.54	2.02	12	1
1:A:109:U:O4	1:A:182:G:O6	0.54	2.26	3	9
1:A:174:A:O2'	1:A:175:A:C8	0.54	2.61	9	3
1:A:170:C:C2'	1:A:171:A:O5'	0.54	2.56	7	6
1:A:99:U:C6	1:A:172:A:N6	0.54	2.76	19	3
1:A:101:U:OP2	1:A:101:U:C6	0.54	2.59	9	1
1:A:104:C:C5'	1:A:106:C:O5'	0.54	2.54	11	2
1:A:98:G:C2	1:A:117:A:C2	0.54	2.94	20	7
1:A:110:G:C2	1:A:181:A:C6	0.54	2.96	1	2
1:A:96:C:O2'	1:A:97:U:O5'	0.54	2.25	6	2
1:A:104:C:C5	1:A:104:C:OP2	0.54	2.61	11	4
1:A:104:C:N4	1:A:109:U:P	0.54	2.81	10	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:101:U:H1'	1:A:174:A:O5'	0.54	2.02	12	1
1:A:96:C:HO2'	1:A:169:A:P	0.54	2.25	8	4
1:A:176:A:N6	1:A:178:G:O6	0.54	2.40	9	6
1:A:182:G:O2'	1:A:183:C:O5'	0.54	2.26	13	11
1:A:167:A:O2'	1:A:168:A:OP1	0.53	2.24	16	1
1:A:103:U:H5'	1:A:104:C:O5'	0.53	2.04	4	1
1:A:94:G:HO2'	1:A:95:G:H8	0.53	1.46	12	5
1:A:121:C:O4'	1:A:167:A:N3	0.53	2.41	17	3
1:A:104:C:OP1	1:A:107:G:O5'	0.53	2.26	17	7
1:A:119:C:O2'	1:A:120:C:O5'	0.53	2.27	10	2
1:A:95:G:N2	1:A:120:C:O2	0.53	2.41	16	3
1:A:105:U:O3'	1:A:106:C:C3'	0.53	2.57	1	3
1:A:118:G:H2'	1:A:119:C:O4'	0.53	2.04	2	2
1:A:98:G:HO2'	1:A:99:U:H6	0.53	1.41	11	2
1:A:178:G:O6	1:A:179:U:O4	0.53	2.26	5	20
1:A:180:C:H2'	1:A:181:A:N7	0.53	2.19	1	7
1:A:96:C:O3'	1:A:169:A:OP2	0.53	2.27	17	5
1:A:178:G:C6	1:A:179:U:O4	0.53	2.61	2	14
1:A:109:U:C4	1:A:182:G:N1	0.53	2.77	5	4
1:A:104:C:OP2	1:A:108:C:OP2	0.53	2.27	6	18
1:A:110:G:N1	1:A:181:A:C6	0.53	2.77	1	2
1:A:118:G:N2	1:A:170:C:H41	0.52	2.02	1	2
1:A:104:C:OP1	1:A:106:C:O3'	0.52	2.27	2	1
1:A:105:U:O5'	1:A:106:C:OP1	0.52	2.28	5	5
1:A:170:C:C2	1:A:171:A:N9	0.52	2.77	16	2
1:A:178:G:C2'	1:A:179:U:O4'	0.52	2.56	15	6
1:A:121:C:C4'	1:A:167:A:C2	0.52	2.93	14	11
1:A:104:C:C2'	1:A:105:U:OP2	0.52	2.57	6	5
1:A:172:A:HO2'	1:A:173:A:P	0.52	2.27	3	6
1:A:168:A:C5'	1:A:169:A:O5'	0.52	2.57	6	3
1:A:99:U:C2	1:A:172:A:C5	0.52	2.96	7	3
1:A:97:U:O4'	1:A:169:A:H5'	0.52	2.04	10	1
1:A:170:C:O2	1:A:171:A:O4'	0.52	2.27	19	2
1:A:104:C:OP1	1:A:106:C:O5'	0.52	2.28	1	1
1:A:106:C:C4'	1:A:107:G:OP2	0.52	2.57	4	7
1:A:113:U:H2'	1:A:114:U:O4'	0.52	2.05	3	1
1:A:179:U:H2'	1:A:180:C:C6	0.51	2.41	11	13
1:A:173:A:N3	1:A:174:A:C8	0.51	2.77	14	1
1:A:105:U:H3'	1:A:105:U:P	0.51	2.44	3	8
1:A:179:U:O2'	1:A:180:C:H6	0.51	1.87	4	7
1:A:96:C:O4'	1:A:168:A:H2'	0.51	2.05	6	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:168:A:C4'	1:A:169:A:OP2	0.51	2.51	5	2
1:A:166:C:H5'	1:A:167:A:N7	0.51	2.20	16	2
1:A:110:G:N1	1:A:181:A:N6	0.51	2.58	1	1
1:A:103:U:C5'	1:A:108:C:OP2	0.51	2.54	2	1
1:A:101:U:O2	1:A:175:A:OP2	0.51	2.29	12	3
1:A:104:C:O5'	1:A:105:U:O3'	0.51	2.28	7	1
1:A:170:C:C4'	1:A:170:C:OP1	0.51	2.58	11	1
1:A:168:A:H5''	1:A:169:A:O5'	0.51	2.06	16	1
1:A:118:G:H21	1:A:170:C:N4	0.51	2.04	1	1
1:A:104:C:P	1:A:108:C:OP2	0.51	2.68	19	3
1:A:104:C:OP1	1:A:106:C:OP2	0.51	2.28	4	1
1:A:117:A:N6	1:A:118:G:C6	0.51	2.79	16	2
1:A:170:C:C4'	1:A:171:A:OP1	0.51	2.58	8	2
1:A:121:C:C5'	1:A:167:A:N3	0.51	2.74	14	4
1:A:110:G:O5'	1:A:110:G:H8	0.51	1.89	9	5
1:A:170:C:N3	1:A:171:A:C4	0.51	2.79	13	2
1:A:166:C:C4'	1:A:167:A:C8	0.51	2.94	19	1
1:A:168:A:OP1	1:A:168:A:O4'	0.51	2.29	16	1
1:A:106:C:H5''	1:A:107:G:OP2	0.50	2.05	4	4
1:A:120:C:O2'	1:A:121:C:C5'	0.50	2.45	4	4
1:A:166:C:C5'	1:A:167:A:C5	0.50	2.93	8	2
1:A:109:U:H2'	1:A:110:G:C8	0.50	2.42	17	14
1:A:103:U:OP2	1:A:109:U:OP2	0.50	2.30	10	5
1:A:104:C:O5'	1:A:108:C:OP2	0.50	2.29	4	1
1:A:119:C:O4'	1:A:169:A:N6	0.50	2.44	1	1
1:A:172:A:O2'	1:A:173:A:O4'	0.50	2.29	12	1
1:A:173:A:HO2'	1:A:174:A:P	0.50	2.25	20	1
1:A:179:U:C2'	1:A:180:C:C6	0.50	2.95	1	9
1:A:103:U:O5'	1:A:108:C:OP1	0.50	2.30	7	1
1:A:104:C:O5'	1:A:106:C:O5'	0.50	2.30	1	1
1:A:167:A:N1	1:A:168:A:N6	0.50	2.60	2	1
1:A:174:A:O2'	1:A:175:A:H8	0.50	1.88	9	3
1:A:100:U:OP1	1:A:100:U:O4'	0.50	2.29	11	3
1:A:169:A:N6	1:A:170:C:H42	0.50	2.04	1	3
1:A:167:A:N1	1:A:168:A:C6	0.49	2.80	13	5
1:A:120:C:C4	1:A:121:C:N4	0.49	2.80	17	5
1:A:102:U:C5'	1:A:104:C:N4	0.49	2.76	1	2
1:A:98:G:O2'	1:A:99:U:O5'	0.49	2.30	19	1
1:A:96:C:C2	1:A:97:U:C5	0.49	3.00	6	2
1:A:96:C:O2'	1:A:169:A:H5''	0.49	2.07	1	4
1:A:172:A:H4'	1:A:173:A:OP1	0.49	2.07	2	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:101:U:O2'	1:A:175:A:OP2	0.49	2.31	17	7
1:A:105:U:C4'	1:A:106:C:OP1	0.49	2.60	20	12
1:A:171:A:C2'	1:A:172:A:OP1	0.49	2.60	20	5
1:A:167:A:C2'	1:A:168:A:OP1	0.49	2.61	16	1
1:A:103:U:O5'	1:A:104:C:OP2	0.48	2.31	10	5
1:A:179:U:HO2'	1:A:180:C:H6	0.48	1.51	16	2
1:A:121:C:HO2'	1:A:166:C:P	0.48	2.31	17	1
1:A:181:A:C6	1:A:182:G:N7	0.48	2.81	7	3
1:A:98:G:C2'	1:A:99:U:C6	0.48	2.96	1	14
1:A:103:U:O3'	1:A:106:C:OP2	0.48	2.32	4	1
1:A:105:U:OP2	1:A:180:C:H5	0.48	1.92	12	4
1:A:105:U:O3'	1:A:106:C:H2'	0.48	2.09	14	2
1:A:166:C:C5'	1:A:167:A:C8	0.48	2.97	16	2
1:A:106:C:H3'	1:A:106:C:P	0.48	2.49	13	4
1:A:104:C:P	1:A:106:C:OP2	0.48	2.72	4	1
1:A:96:C:O2'	1:A:169:A:O5'	0.47	2.32	20	2
1:A:98:G:N1	1:A:117:A:C6	0.47	2.82	1	1
1:A:167:A:C6	1:A:168:A:C6	0.47	3.02	16	3
1:A:99:U:C5	1:A:172:A:C6	0.47	3.02	11	3
1:A:173:A:HO2'	1:A:174:A:H8	0.47	1.48	7	1
1:A:119:C:HO2'	1:A:120:C:H5'	0.47	1.69	16	1
1:A:104:C:H41	1:A:109:U:P	0.47	2.32	10	2
1:A:115:U:C2'	1:A:116:C:O5'	0.47	2.62	17	1
1:A:173:A:C2'	1:A:174:A:O5'	0.47	2.62	20	1
1:A:180:C:H2'	1:A:181:A:C8	0.47	2.45	7	6
1:A:104:C:OP1	1:A:106:C:H3'	0.47	2.09	4	1
1:A:106:C:C5'	1:A:107:G:OP2	0.47	2.62	12	4
1:A:104:C:H5'	1:A:106:C:P	0.47	2.49	17	3
1:A:102:U:O2	1:A:176:A:OP2	0.47	2.33	3	3
1:A:166:C:H5''	1:A:167:A:C5	0.47	2.45	8	2
1:A:121:C:OP1	1:A:167:A:C4'	0.47	2.63	3	2
1:A:169:A:C4'	1:A:170:C:OP1	0.47	2.61	20	2
1:A:184:A:O5'	1:A:184:A:H8	0.46	1.92	15	1
1:A:118:G:O2'	1:A:119:C:H5'	0.46	2.09	3	1
1:A:180:C:C2'	1:A:181:A:C8	0.46	2.98	5	3
1:A:172:A:N3	1:A:173:A:N7	0.46	2.63	18	1
1:A:170:C:C2'	1:A:171:A:O4'	0.46	2.64	13	1
1:A:104:C:P	1:A:106:C:O5'	0.46	2.74	1	1
1:A:95:G:C2	1:A:120:C:N3	0.46	2.84	2	3
1:A:170:C:OP1	1:A:170:C:H4'	0.46	2.10	11	1
1:A:105:U:H5'	1:A:180:C:OP2	0.46	2.11	4	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:117:A:O2'	1:A:118:G:O5'	0.46	2.34	5	2
1:A:182:G:HO2'	1:A:183:C:H5'	0.46	1.60	7	1
1:A:169:A:O2'	1:A:170:C:O5'	0.46	2.33	20	1
1:A:104:C:C2	1:A:110:G:O6	0.46	2.69	6	2
1:A:108:C:H6	1:A:108:C:O5'	0.46	1.94	8	4
1:A:97:U:O2'	1:A:98:G:O5'	0.46	2.34	19	1
1:A:100:U:O2	1:A:173:A:C3'	0.46	2.63	20	1
1:A:104:C:C3'	1:A:105:U:H3'	0.46	2.41	18	11
1:A:94:G:O2'	1:A:95:G:C5'	0.46	2.64	15	4
1:A:109:U:N3	1:A:182:G:N1	0.46	2.64	5	1
1:A:173:A:N1	1:A:174:A:C5	0.45	2.84	14	1
1:A:113:U:O5'	1:A:113:U:H6	0.45	1.94	12	2
1:A:103:U:O2'	1:A:106:C:H5''	0.45	2.12	17	2
1:A:103:U:C4	1:A:178:G:N7	0.45	2.85	1	11
1:A:173:A:N1	1:A:174:A:C6	0.45	2.84	2	1
1:A:109:U:C2'	1:A:110:G:C8	0.45	2.99	16	4
1:A:109:U:C4	1:A:182:G:C6	0.45	3.05	5	1
1:A:170:C:C2	1:A:171:A:C1'	0.45	2.99	19	1
1:A:97:U:C5'	1:A:169:A:OP2	0.45	2.60	4	1
1:A:116:C:HO2'	1:A:117:A:H5'	0.45	1.71	1	1
1:A:104:C:HO2'	1:A:180:C:N4	0.45	2.10	5	1
1:A:174:A:O2'	1:A:175:A:C5'	0.45	2.65	14	1
1:A:105:U:H4'	1:A:106:C:OP1	0.44	2.12	20	2
1:A:173:A:N6	1:A:174:A:C6	0.44	2.85	14	1
1:A:98:G:C6	1:A:117:A:C6	0.44	3.05	1	1
1:A:114:U:H2'	1:A:115:U:C6	0.44	2.48	7	8
1:A:102:U:C4'	1:A:102:U:OP1	0.44	2.65	20	1
1:A:100:U:C1'	1:A:173:A:OP2	0.44	2.64	5	2
1:A:99:U:C2	1:A:100:U:C4	0.44	3.06	7	3
1:A:99:U:N3	1:A:172:A:C6	0.44	2.86	19	2
1:A:104:C:HO2'	1:A:181:A:H61	0.44	1.55	7	1
1:A:166:C:C3'	1:A:167:A:C8	0.44	3.01	16	2
1:A:109:U:HO2'	1:A:110:G:C5'	0.44	2.26	20	4
1:A:110:G:N2	1:A:181:A:C5	0.43	2.85	1	1
1:A:174:A:HO2'	1:A:175:A:P	0.43	2.35	19	1
1:A:104:C:N3	1:A:109:U:C5	0.43	2.87	15	5
1:A:102:U:H5''	1:A:104:C:N4	0.43	2.29	1	3
1:A:118:G:O2'	1:A:119:C:C5'	0.43	2.67	3	1
1:A:94:G:C2	1:A:95:G:N9	0.43	2.87	2	3
1:A:121:C:OP1	1:A:167:A:H4'	0.43	2.14	14	2
1:A:99:U:C2'	1:A:100:U:OP1	0.43	2.66	8	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:99:U:N3	1:A:172:A:N1	0.43	2.67	17	1
1:A:104:C:H4'	1:A:106:C:P	0.43	2.53	2	1
1:A:107:G:O5'	1:A:107:G:C8	0.42	2.70	2	1
1:A:120:C:N4	1:A:121:C:N4	0.42	2.66	14	1
1:A:170:C:HO2'	1:A:171:A:C4'	0.42	2.27	2	1
1:A:173:A:O2'	1:A:174:A:O4'	0.42	2.38	3	1
1:A:106:C:C2'	1:A:107:G:OP1	0.42	2.67	2	1
1:A:105:U:H6	1:A:105:U:O5'	0.42	1.97	7	1
1:A:166:C:H5''	1:A:167:A:C8	0.42	2.49	8	2
1:A:170:C:N4	1:A:171:A:C5	0.42	2.87	13	1
1:A:166:C:C6	1:A:166:C:P	0.42	3.13	16	1
1:A:94:G:O2'	1:A:95:G:C8	0.42	2.65	17	1
1:A:115:U:C4	1:A:116:C:C2	0.42	3.07	10	1
1:A:166:C:C2'	1:A:167:A:O5'	0.42	2.67	16	1
1:A:102:U:OP1	1:A:102:U:O4'	0.42	2.38	6	1
1:A:115:U:H2'	1:A:116:C:C5'	0.42	2.45	17	1
1:A:109:U:O2'	1:A:110:G:C5'	0.42	2.68	19	1
1:A:103:U:H5'	1:A:104:C:C6	0.42	2.49	19	1
1:A:182:G:H2'	1:A:183:C:C6	0.41	2.49	15	1
1:A:97:U:O2'	1:A:98:G:C4'	0.41	2.69	9	1
1:A:116:C:N4	1:A:117:A:N6	0.41	2.68	2	1
1:A:104:C:C4'	1:A:105:U:H3'	0.41	2.45	7	1
1:A:183:C:H2'	1:A:184:A:C8	0.41	2.51	15	1
1:A:93:G:C8	1:A:94:G:C8	0.41	3.08	20	1
1:A:105:U:O4	1:A:182:G:C6	0.41	2.74	2	2
1:A:99:U:N3	1:A:172:A:C2	0.41	2.89	12	3
1:A:94:G:N3	1:A:95:G:N9	0.41	2.68	19	1
1:A:115:U:C5	1:A:116:C:C2	0.41	3.08	10	1
1:A:104:C:H2'	1:A:109:U:C4	0.41	2.51	11	2
1:A:183:C:O5'	1:A:183:C:H6	0.41	1.99	13	1
1:A:93:G:HO2'	1:A:94:G:C5'	0.41	2.27	1	1
1:A:99:U:O2	1:A:100:U:C6	0.41	2.74	4	2
1:A:181:A:O2'	1:A:182:G:C5'	0.41	2.69	4	1
1:A:181:A:C2'	1:A:182:G:O5'	0.41	2.68	7	2
1:A:166:C:C6	1:A:166:C:OP2	0.41	2.74	9	1
1:A:166:C:HO2'	1:A:167:A:P	0.41	2.32	13	1
1:A:104:C:OP1	1:A:107:G:H3'	0.41	2.16	18	1
1:A:113:U:C2'	1:A:114:U:O5'	0.41	2.69	10	2
1:A:98:G:O2'	1:A:99:U:H6	0.41	1.95	11	1
1:A:94:G:N1	1:A:95:G:C5	0.40	2.89	2	1
1:A:105:U:HO2'	1:A:106:C:C2'	0.40	2.29	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:173:A:C1'	1:A:174:A:P	0.40	3.09	14	1
1:A:97:U:C4	1:A:98:G:N7	0.40	2.89	1	1
1:A:105:U:O2'	1:A:106:C:H3'	0.40	2.16	6	1
1:A:103:U:C4'	1:A:104:C:OP2	0.40	2.68	13	2
1:A:167:A:OP2	1:A:167:A:H2'	0.40	2.16	16	1
1:A:103:U:H5''	1:A:104:C:C6	0.40	2.51	1	1
1:A:105:U:N3	1:A:183:C:N4	0.40	2.69	7	1
1:A:173:A:C2	1:A:174:A:C5	0.40	3.10	14	1
1:A:121:C:H4'	1:A:167:A:C2	0.40	2.52	19	1

6.3 Torsion angles [i](#)

6.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

6.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

6.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers	Suiteness
1	A	46/47 (98%)	18±0 (39±0%)	9±1 (20±3%)	0.15±0.00
All	All	921/940 (98%)	360 (39%)	181 (20%)	0.15

The overall RNA backbone suiteness is 0.07.

All unique RNA backbone outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	A	99	U	20
1	A	100	U	20
1	A	102	U	20
1	A	103	U	20
1	A	104	C	20
1	A	105	U	20
1	A	106	C	20
1	A	107	G	20

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Mol	Chain	Res	Type	Models (Total)
1	A	121	C	20
1	A	166	C	20
1	A	167	A	20
1	A	168	A	20
1	A	169	A	20
1	A	170	C	20
1	A	171	A	20
1	A	172	A	20
1	A	173	A	20
1	A	174	A	20

All unique RNA pucker outliers are listed below:

Mol	Chain	Res	Type	Models (Total)
1	A	99	U	20
1	A	103	U	20
1	A	104	C	20
1	A	121	C	20
1	A	167	A	20
1	A	166	C	18
1	A	106	C	16
1	A	171	A	14
1	A	172	A	10
1	A	98	G	4
1	A	170	C	4
1	A	173	A	4
1	A	105	U	3
1	A	102	U	2
1	A	168	A	2
1	A	169	A	2
1	A	101	U	1
1	A	93	G	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 oligosaccharides in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

There are no such molecules in this entry.

6.8 Polymer linkage issues

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided