



## Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 03:15 AM UTC

PDB ID : 6WLR / pdb\_00006wlr  
EMDB ID : EMD-21839  
Title : SAM-IV riboswitch with SAM models, 4.8 Angstrom resolution  
Authors : Kappel, K.; Zhang, K.; Su, Z.; Watkins, A.M.; Kladwang, W.; Li, S.; Pintilie, G.; Topkar, V.V.; Rangan, R.; Zheludev, I.N.; Yesselman, J.D.; Chiu, W.; Das, R.  
Deposited on : 2020-04-20  
Resolution : 4.80 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

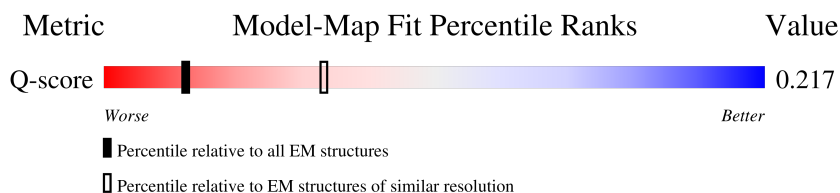
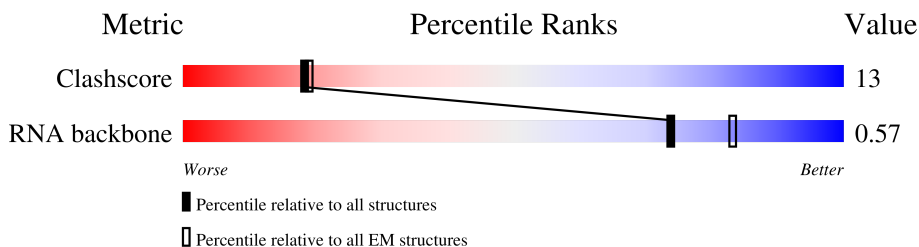
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

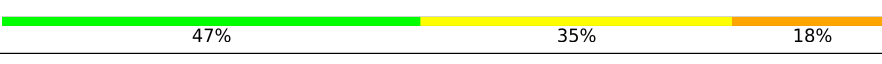
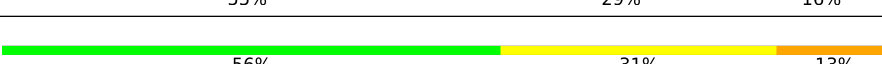
The reported resolution of this entry is 4.80 Å.

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.



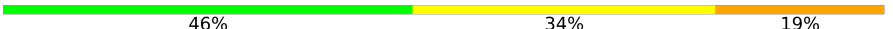
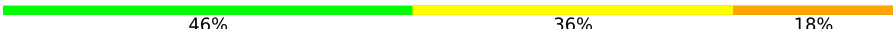
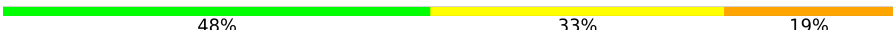
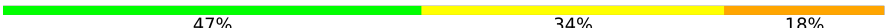
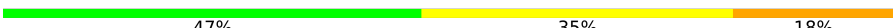
| Metric       | Whole archive<br>(#Entries) | EM structures<br>(#Entries) | Similar EM resolution<br>(#Entries, resolution range(Å)) |
|--------------|-----------------------------|-----------------------------|----------------------------------------------------------|
| Clashscore   | 229148                      | 23984                       | -                                                        |
| RNA backbone | 8273                        | 3508                        | -                                                        |
| Q-score      | -                           | 25397                       | 1575 ( 4.30 - 5.30 )                                     |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

| Mol | Chain | Length | Quality of chain                                                                     |
|-----|-------|--------|--------------------------------------------------------------------------------------|
| 1   | 1-A   | 119    |  |
| 1   | 10-A  | 119    |  |
| 1   | 11-A  | 119    |  |
| 1   | 12-A  | 119    |  |
| 1   | 13-A  | 119    |  |

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| Mol | Chain | Length | Quality of chain                                                                               |
|-----|-------|--------|------------------------------------------------------------------------------------------------|
| 1   | 14-A  | 119    |  52%31%17%   |
| 1   | 15-A  | 119    |  50%31%19%   |
| 1   | 16-A  | 119    |  46%34%19%   |
| 1   | 17-A  | 119    |  46%36%18%   |
| 1   | 18-A  | 119    |  48%33%19%   |
| 1   | 19-A  | 119    |  47%34%18%   |
| 1   | 2-A   | 119    |  53%32%15%   |
| 1   | 20-A  | 119    |  55%28%18%   |
| 1   | 3-A   | 119    |  52%31%17%   |
| 1   | 4-A   | 119    |  50%33%17%   |
| 1   | 5-A   | 119    |  47%35%18%   |
| 1   | 6-A   | 119    |  53%31%16%  |
| 1   | 7-A   | 119    |  52%33%15% |
| 1   | 8-A   | 119    |  51%31%18% |
| 1   | 9-A   | 119    |  54%32%14% |

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 76720 atoms, of which 25780 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called RNA (119-MER).

| Mol | Chain | Residues | Atoms         |           |           |          |          |          | AltConf | Trace |
|-----|-------|----------|---------------|-----------|-----------|----------|----------|----------|---------|-------|
| 1   | 1-A   | 119      | Total<br>3836 | C<br>1134 | H<br>1289 | N<br>465 | O<br>830 | P<br>118 | 0       | 0     |
| 1   | 2-A   | 119      | Total<br>3836 | C<br>1134 | H<br>1289 | N<br>465 | O<br>830 | P<br>118 | 0       | 0     |
| 1   | 3-A   | 119      | Total<br>3836 | C<br>1134 | H<br>1289 | N<br>465 | O<br>830 | P<br>118 | 0       | 0     |
| 1   | 4-A   | 119      | Total<br>3836 | C<br>1134 | H<br>1289 | N<br>465 | O<br>830 | P<br>118 | 0       | 0     |
| 1   | 5-A   | 119      | Total<br>3836 | C<br>1134 | H<br>1289 | N<br>465 | O<br>830 | P<br>118 | 0       | 0     |
| 1   | 6-A   | 119      | Total<br>3836 | C<br>1134 | H<br>1289 | N<br>465 | O<br>830 | P<br>118 | 0       | 0     |
| 1   | 7-A   | 119      | Total<br>3836 | C<br>1134 | H<br>1289 | N<br>465 | O<br>830 | P<br>118 | 0       | 0     |
| 1   | 8-A   | 119      | Total<br>3836 | C<br>1134 | H<br>1289 | N<br>465 | O<br>830 | P<br>118 | 0       | 0     |
| 1   | 9-A   | 119      | Total<br>3836 | C<br>1134 | H<br>1289 | N<br>465 | O<br>830 | P<br>118 | 0       | 0     |
| 1   | 10-A  | 119      | Total<br>3836 | C<br>1134 | H<br>1289 | N<br>465 | O<br>830 | P<br>118 | 0       | 0     |
| 1   | 11-A  | 119      | Total<br>3836 | C<br>1134 | H<br>1289 | N<br>465 | O<br>830 | P<br>118 | 0       | 0     |
| 1   | 12-A  | 119      | Total<br>3836 | C<br>1134 | H<br>1289 | N<br>465 | O<br>830 | P<br>118 | 0       | 0     |
| 1   | 13-A  | 119      | Total<br>3836 | C<br>1134 | H<br>1289 | N<br>465 | O<br>830 | P<br>118 | 0       | 0     |
| 1   | 14-A  | 119      | Total<br>3836 | C<br>1134 | H<br>1289 | N<br>465 | O<br>830 | P<br>118 | 0       | 0     |
| 1   | 15-A  | 119      | Total<br>3836 | C<br>1134 | H<br>1289 | N<br>465 | O<br>830 | P<br>118 | 0       | 0     |
| 1   | 16-A  | 119      | Total<br>3836 | C<br>1134 | H<br>1289 | N<br>465 | O<br>830 | P<br>118 | 0       | 0     |
| 1   | 17-A  | 119      | Total<br>3836 | C<br>1134 | H<br>1289 | N<br>465 | O<br>830 | P<br>118 | 0       | 0     |

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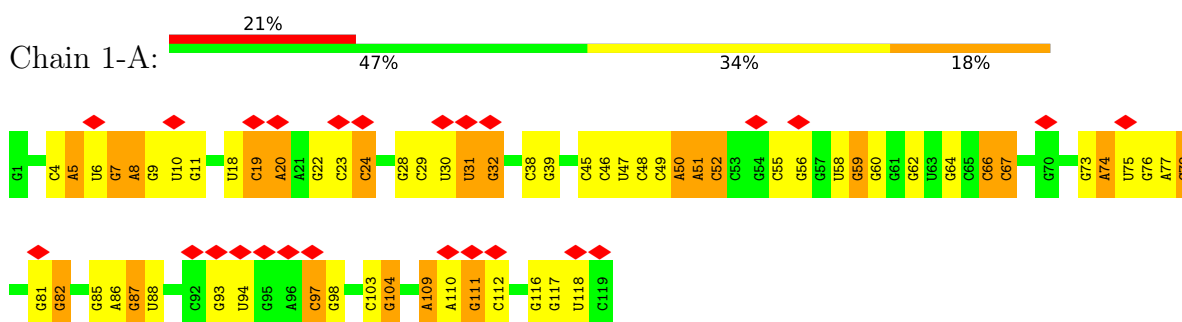
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| Mol | Chain | Residues | Atoms |      |      |     |     |     | AltConf | Trace |
|-----|-------|----------|-------|------|------|-----|-----|-----|---------|-------|
| 1   | 18-A  | 119      | Total | C    | H    | N   | O   | P   | 0       | 0     |
|     |       |          | 3836  | 1134 | 1289 | 465 | 830 | 118 |         |       |
| 1   | 19-A  | 119      | Total | C    | H    | N   | O   | P   | 0       | 0     |
|     |       |          | 3836  | 1134 | 1289 | 465 | 830 | 118 |         |       |
| 1   | 20-A  | 119      | Total | C    | H    | N   | O   | P   | 0       | 0     |
|     |       |          | 3836  | 1134 | 1289 | 465 | 830 | 118 |         |       |

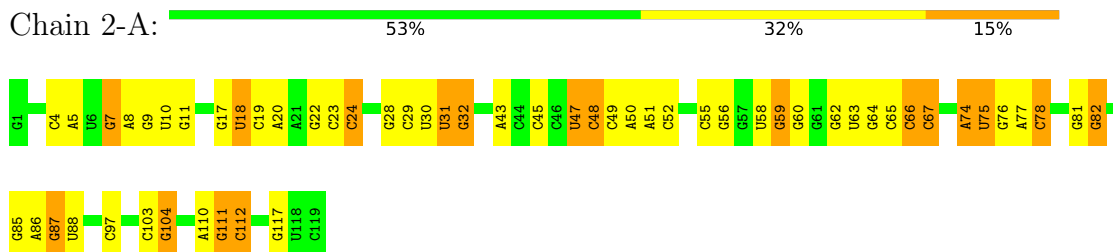
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-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. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

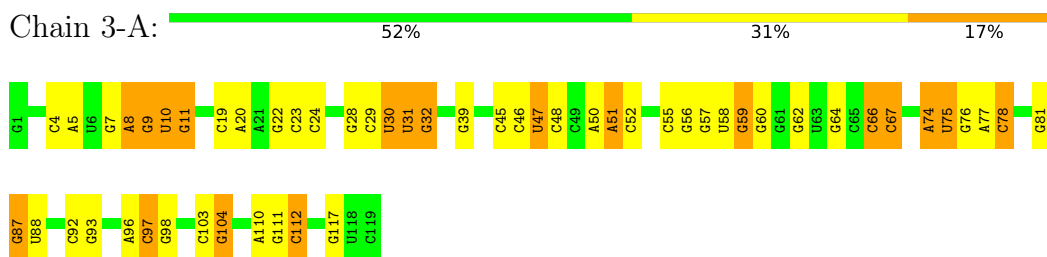
- Molecule 1: RNA (119-MER)



- Molecule 1: RNA (119-MER)

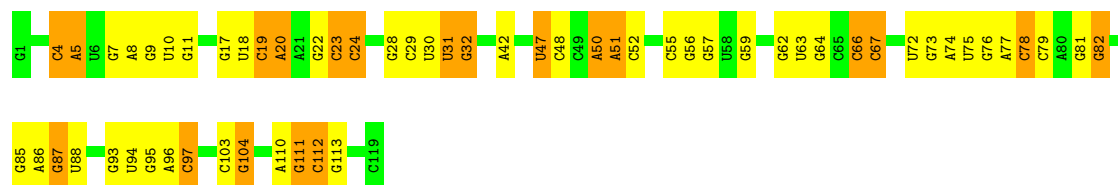


- Molecule 1: RNA (119-MER)



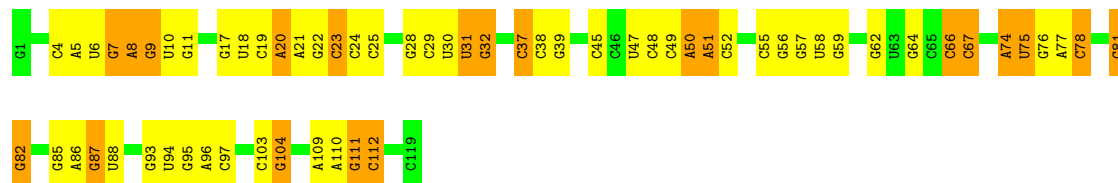
- Molecule 1: RNA (119-MER)





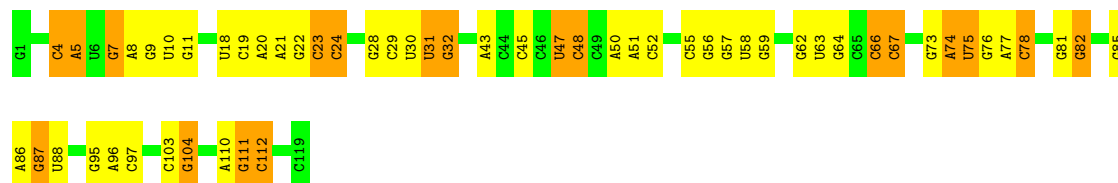
- Molecule 1: RNA (119-MER)

Chain 5-A: 47% 35% 18%



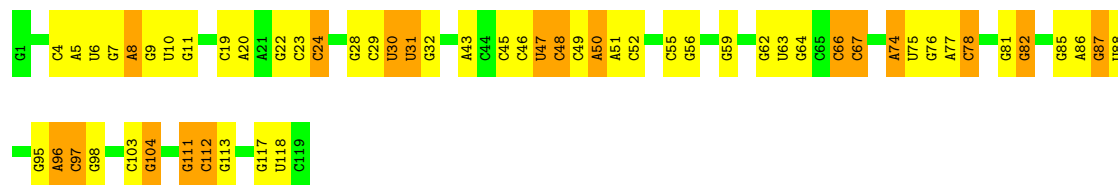
- Molecule 1: RNA (119-MER)

Chain 6-A: 53% 31% 16%



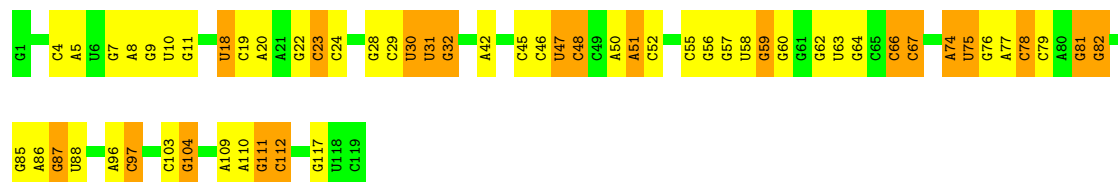
- Molecule 1: RNA (119-MER)

Chain 7-A: 52% 33% 15%



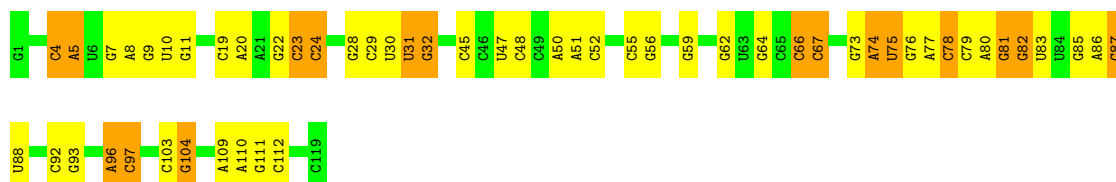
- Molecule 1: RNA (119-MER)

Chain 8-A: 51% 31% 18%

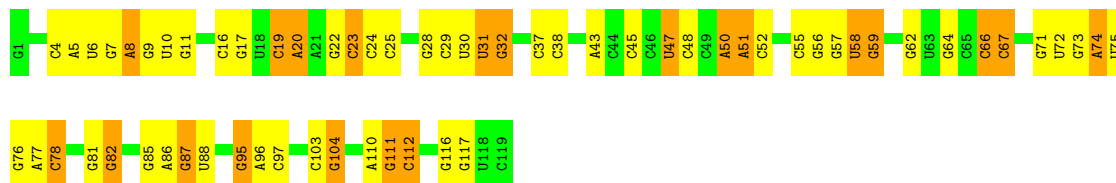


- Molecule 1: RNA (119-MER)

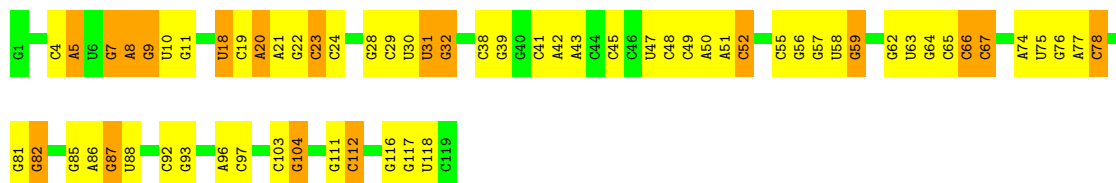
Chain 9-A: 54% 32% 14%



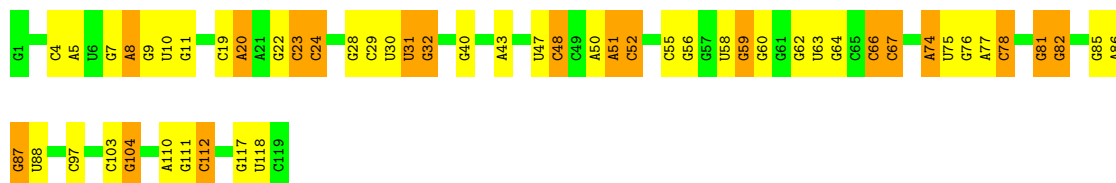
- Molecule 1: RNA (119-MER)



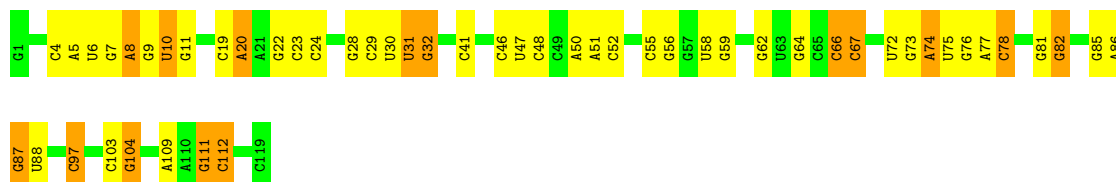
- Molecule 1: RNA (119-MER)



- Molecule 1: RNA (119-MER)

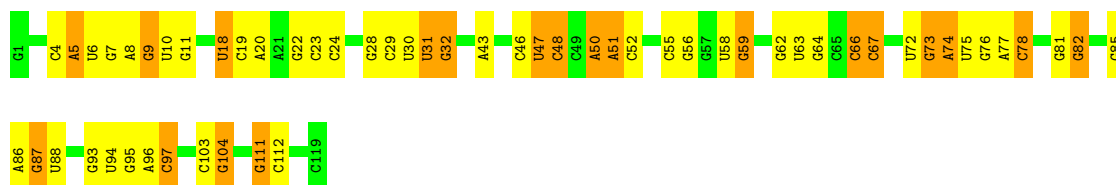


- Molecule 1: RNA (119-MER)



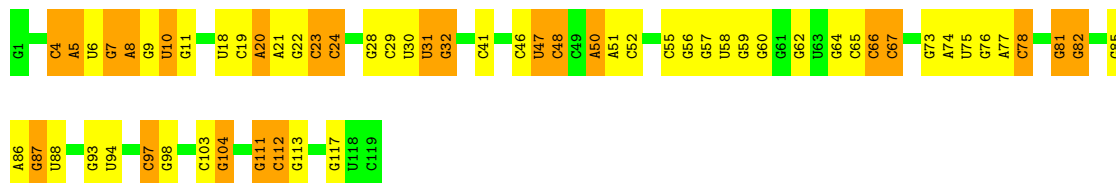
- Molecule 1: RNA (119-MER)





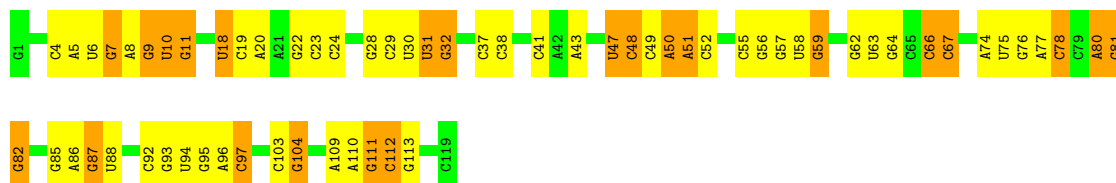
- Molecule 1: RNA (119-MER)

Chain 15-A: 50% 31% 19%



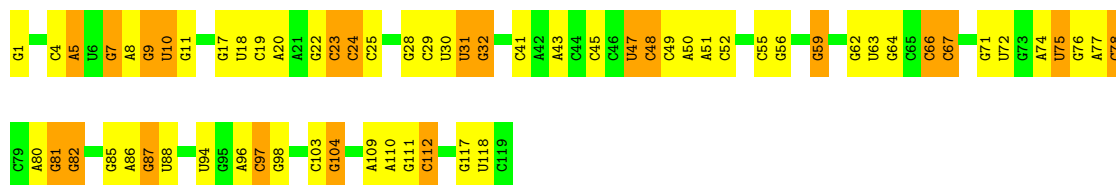
- Molecule 1: RNA (119-MER)

Chain 16-A: 46% 34% 19%



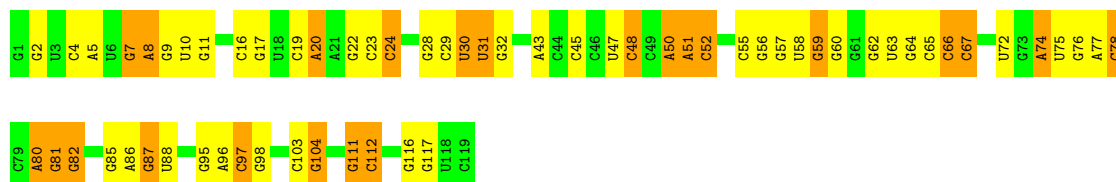
- Molecule 1: RNA (119-MER)

Chain 17-A: 46% 36% 18%



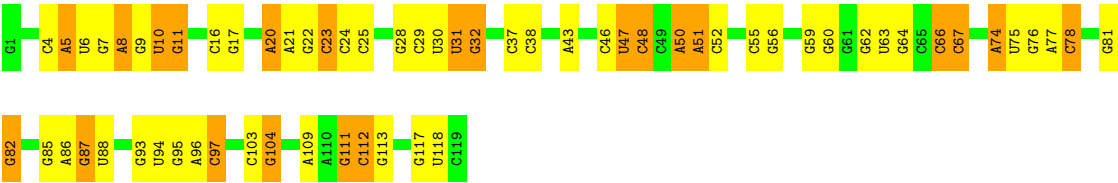
- Molecule 1: RNA (119-MER)

Chain 18-A: 48% 33% 19%

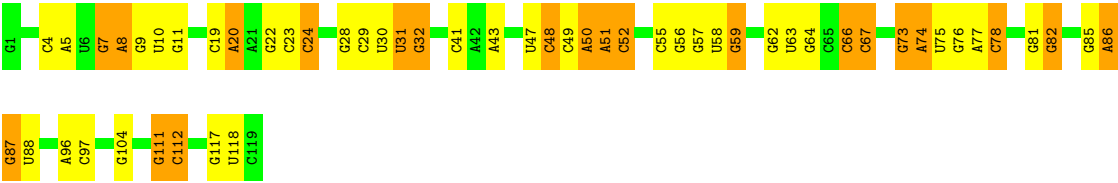


- Molecule 1: RNA (119-MER)

Chain 19-A: 47% 34% 18%



• Molecule 1: RNA (119-MER)



## 4 Experimental information

| Property                             | Value                           | Source    |
|--------------------------------------|---------------------------------|-----------|
| EM reconstruction method             | SINGLE PARTICLE                 | Depositor |
| Imposed symmetry                     | POINT, Not provided             |           |
| Number of particles used             | 225303                          | Depositor |
| Resolution determination method      | FSC 0.143 CUT-OFF               | Depositor |
| CTF correction method                | PHASE FLIPPING ONLY             | Depositor |
| Microscope                           | FEI TITAN KRIOS                 | Depositor |
| Voltage (kV)                         | 300                             | Depositor |
| Electron dose ( $e^-/\text{\AA}^2$ ) | 45.6                            | Depositor |
| Minimum defocus (nm)                 | Not provided                    |           |
| Maximum defocus (nm)                 | Not provided                    |           |
| Magnification                        | Not provided                    |           |
| Image detector                       | GATAN K2 SUMMIT (4k x 4k)       | Depositor |
| Maximum map value                    | 3.698                           | Depositor |
| Minimum map value                    | -2.322                          | Depositor |
| Average map value                    | 0.006                           | Depositor |
| Map value standard deviation         | 0.287                           | Depositor |
| Recommended contour level            | 1.2                             | Depositor |
| Map size ( $\text{\AA}$ )            | 178.07999, 178.07999, 178.07999 | wwPDB     |
| Map dimensions                       | 168, 168, 168                   | wwPDB     |
| Map angles ( $^\circ$ )              | 90.0, 90.0, 90.0                | wwPDB     |
| Pixel spacing ( $\text{\AA}$ )       | 1.06, 1.06, 1.06                | Depositor |

## 5 Model quality [i](#)

### 5.1 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 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   | 1-A   | 0.26         | 0/2847  | 0.32        | 0/4442  |
| 1   | 2-A   | 0.26         | 0/2847  | 0.32        | 0/4442  |
| 1   | 3-A   | 0.26         | 0/2847  | 0.32        | 0/4442  |
| 1   | 4-A   | 0.26         | 0/2847  | 0.32        | 0/4442  |
| 1   | 5-A   | 0.26         | 0/2847  | 0.32        | 0/4442  |
| 1   | 6-A   | 0.26         | 0/2847  | 0.32        | 0/4442  |
| 1   | 7-A   | 0.26         | 0/2847  | 0.32        | 0/4442  |
| 1   | 8-A   | 0.26         | 0/2847  | 0.32        | 0/4442  |
| 1   | 9-A   | 0.26         | 0/2847  | 0.32        | 0/4442  |
| 1   | 10-A  | 0.26         | 0/2847  | 0.32        | 0/4442  |
| 1   | 11-A  | 0.26         | 0/2847  | 0.32        | 0/4442  |
| 1   | 12-A  | 0.26         | 0/2847  | 0.32        | 0/4442  |
| 1   | 13-A  | 0.26         | 0/2847  | 0.32        | 0/4442  |
| 1   | 14-A  | 0.26         | 0/2847  | 0.32        | 0/4442  |
| 1   | 15-A  | 0.26         | 0/2847  | 0.32        | 0/4442  |
| 1   | 16-A  | 0.26         | 0/2847  | 0.32        | 0/4442  |
| 1   | 17-A  | 0.26         | 0/2847  | 0.32        | 0/4442  |
| 1   | 18-A  | 0.26         | 0/2847  | 0.32        | 0/4442  |
| 1   | 19-A  | 0.26         | 0/2847  | 0.32        | 0/4442  |
| 1   | 20-A  | 0.26         | 0/2847  | 0.32        | 0/4442  |
| All | All   | 0.26         | 0/56940 | 0.32        | 0/88840 |

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 outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 1   | 19-A  | 1                   | 0                   |

There are no bond length outliers.

There are no bond angle outliers.

All (1) chirality outliers are listed below:

| Mol | Chain | Res | Type | Atom |
|-----|-------|-----|------|------|
| 1   | 19-A  | 8   | A    | C3'  |

There are no planarity outliers.

## 5.2 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 the 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 within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1   | 1-A   | 2547  | 1289     | 1290     | 46      | 0            |
| 1   | 2-A   | 2547  | 1289     | 1290     | 54      | 0            |
| 1   | 3-A   | 2547  | 1289     | 1290     | 50      | 0            |
| 1   | 4-A   | 2547  | 1289     | 1290     | 43      | 0            |
| 1   | 5-A   | 2547  | 1289     | 1290     | 65      | 0            |
| 1   | 6-A   | 2547  | 1289     | 1290     | 48      | 0            |
| 1   | 7-A   | 2547  | 1289     | 1290     | 36      | 0            |
| 1   | 8-A   | 2547  | 1289     | 1290     | 57      | 0            |
| 1   | 9-A   | 2547  | 1289     | 1290     | 48      | 0            |
| 1   | 10-A  | 2547  | 1289     | 1290     | 61      | 0            |
| 1   | 11-A  | 2547  | 1289     | 1290     | 52      | 0            |
| 1   | 12-A  | 2547  | 1289     | 1290     | 47      | 0            |
| 1   | 13-A  | 2547  | 1289     | 1290     | 33      | 0            |
| 1   | 14-A  | 2547  | 1289     | 1290     | 52      | 0            |
| 1   | 15-A  | 2547  | 1289     | 1290     | 52      | 0            |
| 1   | 16-A  | 2547  | 1289     | 1290     | 54      | 0            |
| 1   | 17-A  | 2547  | 1289     | 1290     | 59      | 0            |
| 1   | 18-A  | 2547  | 1289     | 1290     | 44      | 0            |
| 1   | 19-A  | 2547  | 1289     | 1290     | 48      | 0            |
| 1   | 20-A  | 2547  | 1289     | 1290     | 51      | 0            |
| All | All   | 50940 | 25780    | 25800    | 1000    | 0            |

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 13.

All (1000) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1       | Atom-2       | Interatomic distance (Å) | Clash overlap (Å) |
|--------------|--------------|--------------------------|-------------------|
| 1:A:32:G:C8  | 1:A:32:G:OP2 | 1.77                     | 1.36              |
| 1:A:20:A:H8  | 1:A:20:A:OP2 | 1.09                     | 1.35              |
| 1:A:32:G:OP1 | 1:A:32:G:C8  | 1.84                     | 1.31              |
| 1:A:32:G:OP2 | 1:A:32:G:O4' | 1.53                     | 1.25              |
| 1:A:32:G:OP1 | 1:A:32:G:C8  | 1.90                     | 1.24              |
| 1:A:20:A:OP2 | 1:A:20:A:C8  | 1.90                     | 1.24              |
| 1:A:32:G:OP2 | 1:A:32:G:H8  | 1.05                     | 1.23              |
| 1:A:51:A:C8  | 1:A:51:A:OP2 | 1.95                     | 1.19              |
| 1:A:32:G:OP2 | 1:A:32:G:O4' | 1.61                     | 1.18              |
| 1:A:32:G:C8  | 1:A:32:G:OP2 | 1.97                     | 1.17              |
| 1:A:32:G:O4' | 1:A:32:G:OP1 | 1.63                     | 1.16              |
| 1:A:24:C:OP1 | 1:A:24:C:H3' | 1.51                     | 1.11              |
| 1:A:32:G:O4' | 1:A:32:G:OP1 | 1.68                     | 1.10              |
| 1:A:74:A:OP2 | 1:A:74:A:N9  | 1.85                     | 1.09              |
| 1:A:95:G:OP1 | 1:A:95:G:O4' | 1.69                     | 1.08              |
| 1:A:80:A:OP1 | 1:A:80:A:O4' | 1.72                     | 1.08              |
| 1:A:8:A:O4'  | 1:A:8:A:OP1  | 1.72                     | 1.06              |
| 1:A:32:G:H8  | 1:A:32:G:P   | 1.78                     | 1.05              |
| 1:A:32:G:C8  | 1:A:32:G:P   | 2.53                     | 1.02              |
| 1:A:32:G:C8  | 1:A:32:G:OP2 | 2.12                     | 1.02              |
| 1:A:8:A:C8   | 1:A:8:A:OP2  | 2.13                     | 1.02              |
| 1:A:20:A:O4' | 1:A:20:A:OP2 | 1.80                     | 1.00              |
| 1:A:74:A:OP2 | 1:A:74:A:O4' | 1.81                     | 0.99              |
| 1:A:32:G:OP2 | 1:A:32:G:H8  | 1.36                     | 0.97              |
| 1:A:32:G:OP2 | 1:A:32:G:C8  | 2.16                     | 0.97              |
| 1:A:32:G:OP2 | 1:A:32:G:C8  | 2.17                     | 0.97              |
| 1:A:74:A:OP2 | 1:A:74:A:C8  | 2.19                     | 0.96              |
| 1:A:96:A:OP2 | 1:A:96:A:H8  | 1.47                     | 0.95              |
| 1:A:74:A:C8  | 1:A:74:A:P   | 2.61                     | 0.94              |
| 1:A:75:U:O4' | 1:A:75:U:OP1 | 1.88                     | 0.92              |
| 1:A:19:C:O4' | 1:A:19:C:OP1 | 1.87                     | 0.92              |
| 1:A:32:G:H8  | 1:A:32:G:P   | 1.92                     | 0.92              |
| 1:A:32:G:H8  | 1:A:32:G:P   | 1.92                     | 0.92              |
| 1:A:82:G:H8  | 1:A:82:G:P   | 1.94                     | 0.91              |
| 1:A:8:A:OP2  | 1:A:8:A:O4'  | 1.88                     | 0.90              |
| 1:A:18:U:O2' | 1:A:19:C:P   | 2.29                     | 0.90              |
| 1:A:7:G:N3   | 1:A:7:G:H3'  | 1.86                     | 0.90              |
| 1:A:20:A:O2' | 1:A:21:A:OP2 | 1.89                     | 0.90              |
| 1:A:8:A:C4   | 1:A:8:A:OP2  | 2.25                     | 0.90              |
| 1:A:8:A:OP1  | 1:A:8:A:C4'  | 2.20                     | 0.88              |
| 1:A:82:G:OP1 | 1:A:82:G:C8  | 2.26                     | 0.88              |
| 1:A:46:C:O2' | 1:A:109:A:N6 | 2.07                     | 0.88              |

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| Atom-1        | Atom-2       | Interatomic distance (Å) | Clash overlap (Å) |
|---------------|--------------|--------------------------|-------------------|
| 1:A:32:G:H8   | 1:A:32:G:OP2 | 1.57                     | 0.88              |
| 1:A:7:G:O4'   | 1:A:7:G:OP2  | 1.92                     | 0.87              |
| 1:A:20:A:P    | 1:A:20:A:H8  | 1.97                     | 0.86              |
| 1:A:74:A:OP2  | 1:A:74:A:C1' | 2.24                     | 0.86              |
| 1:A:24:C:OP1  | 1:A:24:C:H3' | 1.76                     | 0.84              |
| 1:A:8:A:C8    | 1:A:8:A:OP2  | 2.29                     | 0.84              |
| 1:A:32:G:H8   | 1:A:32:G:P   | 2.01                     | 0.83              |
| 1:A:58:U:H4'  | 1:A:58:U:OP1 | 1.77                     | 0.82              |
| 1:A:32:G:OP1  | 1:A:32:G:C8  | 2.31                     | 0.82              |
| 1:A:96:A:H8   | 1:A:96:A:O5' | 1.61                     | 0.82              |
| 1:A:60:G:OP2  | 1:A:60:G:C8  | 2.32                     | 0.82              |
| 1:A:32:G:C8   | 1:A:32:G:P   | 2.73                     | 0.82              |
| 1:A:96:A:OP2  | 1:A:96:A:C8  | 2.32                     | 0.82              |
| 1:A:17:G:H4'  | 1:A:17:G:OP1 | 1.79                     | 0.81              |
| 1:A:32:G:P    | 1:A:32:G:H8  | 2.04                     | 0.81              |
| 1:A:32:G:H8   | 1:A:32:G:P   | 2.04                     | 0.81              |
| 1:A:32:G:C8   | 1:A:32:G:P   | 2.74                     | 0.81              |
| 1:A:96:A:O4'  | 1:A:96:A:OP1 | 1.99                     | 0.80              |
| 1:A:32:G:OP2  | 1:A:32:G:C1' | 2.28                     | 0.80              |
| 1:A:19:C:C6   | 1:A:19:C:OP1 | 2.33                     | 0.80              |
| 1:A:46:C:O2'  | 1:A:109:A:N6 | 2.14                     | 0.80              |
| 1:A:19:C:OP1  | 1:A:19:C:O4' | 2.00                     | 0.79              |
| 1:A:30:U:O2'  | 1:A:31:U:O5' | 2.01                     | 0.79              |
| 1:A:32:G:C8   | 1:A:32:G:P   | 2.76                     | 0.79              |
| 1:A:24:C:H6   | 1:A:24:C:P   | 2.06                     | 0.78              |
| 1:A:80:A:O2'  | 1:A:81:G:P   | 2.41                     | 0.78              |
| 1:A:95:G:OP1  | 1:A:95:G:C8  | 2.36                     | 0.78              |
| 1:A:82:G:P    | 1:A:82:G:C8  | 2.78                     | 0.77              |
| 1:A:82:G:OP1  | 1:A:82:G:C8  | 2.37                     | 0.77              |
| 1:A:32:G:H8   | 1:A:32:G:P   | 2.08                     | 0.77              |
| 1:A:23:C:OP2  | 1:A:23:C:C6  | 2.37                     | 0.77              |
| 1:A:60:G:OP2  | 1:A:60:G:H8  | 1.67                     | 0.77              |
| 1:A:24:C:H6   | 1:A:24:C:P   | 2.08                     | 0.76              |
| 1:A:10:U:O2'  | 1:A:11:G:O5' | 2.02                     | 0.76              |
| 1:A:30:U:O2'  | 1:A:32:G:OP1 | 2.03                     | 0.76              |
| 1:A:51:A:OP2  | 1:A:51:A:H8  | 1.67                     | 0.76              |
| 1:A:18:U:O2'  | 1:A:19:C:O5' | 2.03                     | 0.75              |
| 1:A:8:A:N6    | 1:A:65:C:O2' | 2.20                     | 0.75              |
| 1:A:8:A:H2'   | 1:A:8:A:OP1  | 1.85                     | 0.75              |
| 1:A:49:C:H5'' | 1:A:50:A:OP2 | 1.86                     | 0.75              |
| 1:A:8:A:H8    | 1:A:8:A:P    | 2.08                     | 0.75              |

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| Atom-1        | Atom-2       | Interatomic distance (Å) | Clash overlap (Å) |
|---------------|--------------|--------------------------|-------------------|
| 1:A:58:U:H4'  | 1:A:58:U:OP1 | 1.87                     | 0.75              |
| 1:A:74:A:C8   | 1:A:74:A:OP2 | 2.40                     | 0.74              |
| 1:A:8:A:C8    | 1:A:8:A:P    | 2.79                     | 0.74              |
| 1:A:73:G:O2'  | 1:A:74:A:O5' | 2.05                     | 0.74              |
| 1:A:51:A:C8   | 1:A:51:A:OP1 | 2.41                     | 0.74              |
| 1:A:30:U:O2'  | 1:A:31:U:O5' | 2.06                     | 0.74              |
| 1:A:19:C:O2'  | 1:A:20:A:OP2 | 2.06                     | 0.74              |
| 1:A:32:G:OP2  | 1:A:32:G:C1' | 2.35                     | 0.74              |
| 1:A:23:C:C2'  | 1:A:24:C:OP1 | 2.36                     | 0.74              |
| 1:A:37:C:O2'  | 1:A:38:C:P   | 2.46                     | 0.73              |
| 1:A:82:G:C8   | 1:A:82:G:OP1 | 2.40                     | 0.73              |
| 1:A:20:A:OP2  | 1:A:20:A:O4' | 2.05                     | 0.73              |
| 1:A:59:G:O2'  | 1:A:110:A:N1 | 2.21                     | 0.73              |
| 1:A:24:C:P    | 1:A:24:C:C6  | 2.81                     | 0.73              |
| 1:A:24:C:OP1  | 1:A:24:C:C6  | 2.41                     | 0.73              |
| 1:A:58:U:O4'  | 1:A:111:G:N2 | 2.22                     | 0.73              |
| 1:A:96:A:OP2  | 1:A:96:A:H8  | 1.72                     | 0.73              |
| 1:A:18:U:O2'  | 1:A:19:C:P   | 2.45                     | 0.73              |
| 1:A:5:A:O4'   | 1:A:73:G:O6  | 2.07                     | 0.73              |
| 1:A:31:U:O2'  | 1:A:32:G:OP2 | 2.06                     | 0.73              |
| 1:A:30:U:O2'  | 1:A:32:G:OP1 | 2.07                     | 0.73              |
| 1:A:32:G:OP1  | 1:A:32:G:C8  | 2.41                     | 0.73              |
| 1:A:51:A:O2'  | 1:A:52:C:OP2 | 2.05                     | 0.73              |
| 1:A:24:C:C6   | 1:A:24:C:OP2 | 2.42                     | 0.72              |
| 1:A:47:U:C4'  | 1:A:47:U:OP1 | 2.37                     | 0.72              |
| 1:A:4:C:O2'   | 1:A:5:A:OP1  | 2.06                     | 0.72              |
| 1:A:19:C:O4'  | 1:A:19:C:OP2 | 2.06                     | 0.72              |
| 1:A:19:C:O2'  | 1:A:20:A:P   | 2.47                     | 0.72              |
| 1:A:86:A:HO2' | 1:A:87:G:P   | 2.13                     | 0.72              |
| 1:A:30:U:O2'  | 1:A:32:G:OP1 | 2.07                     | 0.72              |
| 1:A:74:A:O2'  | 1:A:75:U:OP1 | 2.08                     | 0.72              |
| 1:A:32:G:H8   | 1:A:32:G:OP1 | 1.72                     | 0.72              |
| 1:A:8:A:OP2   | 1:A:8:A:N9   | 2.21                     | 0.72              |
| 1:A:32:G:H8   | 1:A:32:G:P   | 2.11                     | 0.72              |
| 1:A:32:G:C8   | 1:A:32:G:P   | 2.83                     | 0.71              |
| 1:A:20:A:OP2  | 1:A:20:A:H8  | 1.73                     | 0.71              |
| 1:A:30:U:H2'  | 1:A:31:U:H4' | 1.71                     | 0.71              |
| 1:A:59:G:H8   | 1:A:59:G:OP2 | 1.72                     | 0.71              |
| 1:A:24:C:P    | 1:A:24:C:C6  | 2.83                     | 0.71              |
| 1:A:51:A:H3'  | 1:A:51:A:OP1 | 1.90                     | 0.71              |
| 1:A:82:G:H8   | 1:A:82:G:P   | 2.13                     | 0.71              |

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| Atom-1        | Atom-2        | Interatomic distance (Å) | Clash overlap (Å) |
|---------------|---------------|--------------------------|-------------------|
| 1:A:46:C:O2'  | 1:A:109:A:N1  | 2.24                     | 0.71              |
| 1:A:32:G:O4'  | 1:A:32:G:P    | 2.49                     | 0.71              |
| 1:A:10:U:HO2' | 1:A:11:G:P    | 2.13                     | 0.71              |
| 1:A:51:A:H8   | 1:A:51:A:P    | 2.13                     | 0.71              |
| 1:A:32:G:H8   | 1:A:32:G:OP1  | 1.73                     | 0.71              |
| 1:A:23:C:O2'  | 1:A:24:C:OP1  | 2.09                     | 0.70              |
| 1:A:46:C:O2'  | 1:A:109:A:N6  | 2.23                     | 0.70              |
| 1:A:45:C:O2'  | 1:A:81:G:O2'  | 2.09                     | 0.70              |
| 1:A:32:G:OP1  | 1:A:32:G:C8   | 2.45                     | 0.69              |
| 1:A:82:G:OP1  | 1:A:82:G:H3'  | 1.92                     | 0.69              |
| 1:A:19:C:C6   | 1:A:19:C:OP1  | 2.45                     | 0.69              |
| 1:A:97:C:H6   | 1:A:97:C:OP2  | 1.75                     | 0.69              |
| 1:A:31:U:O2'  | 1:A:32:G:OP2  | 2.10                     | 0.69              |
| 1:A:48:C:O2'  | 1:A:111:G:N7  | 2.25                     | 0.69              |
| 1:A:42:A:N7   | 1:A:64:G:N2   | 2.40                     | 0.69              |
| 1:A:81:G:O2'  | 1:A:82:G:OP1  | 2.10                     | 0.69              |
| 1:A:82:G:OP1  | 1:A:82:G:H3'  | 1.93                     | 0.69              |
| 1:A:50:A:H3'  | 1:A:50:A:N3   | 2.08                     | 0.68              |
| 1:A:86:A:O2'  | 1:A:87:G:OP1  | 2.10                     | 0.68              |
| 1:A:32:G:O4'  | 1:A:32:G:P    | 2.51                     | 0.68              |
| 1:A:30:U:O2'  | 1:A:32:G:OP1  | 2.11                     | 0.68              |
| 1:A:32:G:OP2  | 1:A:32:G:C8   | 2.46                     | 0.68              |
| 1:A:8:A:C8    | 1:A:8:A:OP2   | 2.46                     | 0.68              |
| 1:A:19:C:P    | 1:A:19:C:H6   | 2.16                     | 0.68              |
| 1:A:6:U:OP1   | 1:A:6:U:C6    | 2.47                     | 0.68              |
| 1:A:6:U:OP1   | 1:A:6:U:H6    | 1.77                     | 0.68              |
| 1:A:19:C:OP1  | 1:A:19:C:H6   | 1.77                     | 0.68              |
| 1:A:50:A:O2'  | 1:A:51:A:OP1  | 2.11                     | 0.68              |
| 1:A:59:G:OP1  | 1:A:59:G:C8   | 2.46                     | 0.68              |
| 1:A:45:C:O2'  | 1:A:82:G:OP1  | 2.10                     | 0.68              |
| 1:A:96:A:O2'  | 1:A:97:C:OP1  | 2.10                     | 0.67              |
| 1:A:32:G:OP1  | 1:A:32:G:H3'  | 1.93                     | 0.67              |
| 1:A:30:U:O2'  | 1:A:32:G:OP1  | 2.12                     | 0.67              |
| 1:A:30:U:O2'  | 1:A:31:U:O5'  | 2.09                     | 0.67              |
| 1:A:110:A:OP2 | 1:A:110:A:O4' | 2.12                     | 0.67              |
| 1:A:47:U:OP1  | 1:A:47:U:H4'  | 1.94                     | 0.67              |
| 1:A:30:U:O2'  | 1:A:32:G:OP1  | 2.10                     | 0.67              |
| 1:A:96:A:OP2  | 1:A:96:A:C8   | 2.47                     | 0.67              |
| 1:A:96:A:O2'  | 1:A:97:C:OP1  | 2.11                     | 0.67              |
| 1:A:32:G:H8   | 1:A:32:G:P    | 2.16                     | 0.67              |
| 1:A:8:A:OP2   | 1:A:8:A:H8    | 1.78                     | 0.67              |

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| Atom-1       | Atom-2        | Interatomic distance (Å) | Clash overlap (Å) |
|--------------|---------------|--------------------------|-------------------|
| 1:A:9:G:OP1  | 1:A:9:G:C8    | 2.47                     | 0.67              |
| 1:A:8:A:H2'  | 1:A:8:A:P     | 2.35                     | 0.67              |
| 1:A:31:U:H2' | 1:A:32:G:C8   | 2.31                     | 0.66              |
| 1:A:8:A:O2'  | 1:A:9:G:OP1   | 2.11                     | 0.66              |
| 1:A:81:G:OP1 | 1:A:81:G:H2'  | 1.94                     | 0.66              |
| 1:A:31:U:H1' | 1:A:32:G:N7   | 2.10                     | 0.66              |
| 1:A:45:C:O2' | 1:A:82:G:OP2  | 2.12                     | 0.66              |
| 1:A:95:G:O2' | 1:A:96:A:OP1  | 2.12                     | 0.66              |
| 1:A:74:A:O2' | 1:A:76:G:O6   | 2.09                     | 0.66              |
| 1:A:19:C:O2' | 1:A:20:A:OP1  | 2.12                     | 0.66              |
| 1:A:24:C:OP1 | 1:A:24:C:H6   | 1.79                     | 0.66              |
| 1:A:73:G:O2' | 1:A:74:A:O5'  | 2.14                     | 0.66              |
| 1:A:74:A:C8  | 1:A:74:A:OP1  | 2.48                     | 0.65              |
| 1:A:32:G:C8  | 1:A:32:G:P    | 2.88                     | 0.65              |
| 1:A:47:U:N3  | 1:A:59:G:O6   | 2.29                     | 0.65              |
| 1:A:21:A:OP2 | 1:A:21:A:H8   | 1.79                     | 0.65              |
| 1:A:32:G:H8  | 1:A:32:G:P    | 2.19                     | 0.65              |
| 1:A:6:U:H6   | 1:A:6:U:OP2   | 1.80                     | 0.65              |
| 1:A:51:A:C8  | 1:A:51:A:P    | 2.89                     | 0.65              |
| 1:A:50:A:H3' | 1:A:50:A:N3   | 2.12                     | 0.65              |
| 1:A:7:G:OP1  | 1:A:65:C:O2'  | 2.15                     | 0.65              |
| 1:A:117:G:H8 | 1:A:117:G:OP2 | 1.79                     | 0.65              |
| 1:A:82:G:H8  | 1:A:82:G:OP2  | 1.80                     | 0.65              |
| 1:A:96:A:H8  | 1:A:96:A:O5'  | 1.79                     | 0.65              |
| 1:A:18:U:O2' | 1:A:19:C:OP2  | 2.15                     | 0.65              |
| 1:A:74:A:H3' | 1:A:74:A:N3   | 2.11                     | 0.64              |
| 1:A:7:G:O3'  | 1:A:8:A:O4'   | 2.14                     | 0.64              |
| 1:A:59:G:N2  | 1:A:110:A:O2' | 2.30                     | 0.64              |
| 1:A:97:C:OP2 | 1:A:97:C:C6   | 2.50                     | 0.64              |
| 1:A:24:C:OP2 | 1:A:24:C:C5   | 2.51                     | 0.64              |
| 1:A:37:C:O2' | 1:A:38:C:OP1  | 2.15                     | 0.64              |
| 1:A:73:G:C2' | 1:A:74:A:OP2  | 2.44                     | 0.64              |
| 1:A:81:G:O2' | 1:A:82:G:OP1  | 2.13                     | 0.64              |
| 1:A:8:A:H8   | 1:A:8:A:OP1   | 1.82                     | 0.63              |
| 1:A:73:G:O2' | 1:A:74:A:P    | 2.56                     | 0.63              |
| 1:A:24:C:OP1 | 1:A:24:C:C3'  | 2.40                     | 0.63              |
| 1:A:73:G:H2' | 1:A:74:A:OP2  | 1.99                     | 0.63              |
| 1:A:46:C:H3' | 1:A:47:U:H5'' | 1.79                     | 0.63              |
| 1:A:66:C:H4' | 1:A:67:C:OP1  | 1.97                     | 0.63              |
| 1:A:66:C:H4' | 1:A:67:C:OP1  | 1.97                     | 0.63              |
| 1:A:8:A:OP2  | 1:A:8:A:C8    | 2.51                     | 0.63              |

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| Atom-1        | Atom-2       | Interatomic distance (Å) | Clash overlap (Å) |
|---------------|--------------|--------------------------|-------------------|
| 1:A:66:C:H4'  | 1:A:67:C:OP1 | 1.97                     | 0.63              |
| 1:A:66:C:H4'  | 1:A:67:C:OP1 | 1.97                     | 0.63              |
| 1:A:66:C:H4'  | 1:A:67:C:OP1 | 1.97                     | 0.63              |
| 1:A:66:C:H4'  | 1:A:67:C:OP1 | 1.97                     | 0.63              |
| 1:A:66:C:H4'  | 1:A:67:C:OP1 | 1.97                     | 0.63              |
| 1:A:66:C:H4'  | 1:A:67:C:OP1 | 1.97                     | 0.63              |
| 1:A:66:C:H4'  | 1:A:67:C:OP1 | 1.97                     | 0.63              |
| 1:A:66:C:H4'  | 1:A:67:C:OP1 | 1.97                     | 0.63              |
| 1:A:66:C:H4'  | 1:A:67:C:OP1 | 1.97                     | 0.63              |
| 1:A:66:C:H4'  | 1:A:67:C:OP1 | 1.97                     | 0.63              |
| 1:A:66:C:H4'  | 1:A:67:C:OP1 | 1.98                     | 0.63              |
| 1:A:111:G:OP2 | 1:A:111:G:H8 | 1.82                     | 0.63              |
| 1:A:96:A:OP2  | 1:A:96:A:O4' | 2.16                     | 0.62              |
| 1:A:18:U:H4'  | 1:A:19:C:OP1 | 1.99                     | 0.62              |
| 1:A:66:C:H4'  | 1:A:67:C:OP1 | 1.98                     | 0.62              |
| 1:A:66:C:H4'  | 1:A:67:C:OP1 | 1.98                     | 0.62              |
| 1:A:20:A:P    | 1:A:20:A:C8  | 2.88                     | 0.62              |
| 1:A:20:A:H8   | 1:A:20:A:OP1 | 1.81                     | 0.62              |
| 1:A:66:C:H4'  | 1:A:67:C:OP1 | 1.97                     | 0.62              |
| 1:A:66:C:H4'  | 1:A:67:C:OP1 | 1.98                     | 0.62              |
| 1:A:66:C:H4'  | 1:A:67:C:OP1 | 1.98                     | 0.62              |
| 1:A:74:A:OP1  | 1:A:74:A:O4' | 2.17                     | 0.62              |
| 1:A:19:C:O4'  | 1:A:19:C:OP1 | 2.17                     | 0.62              |
| 1:A:6:U:OP1   | 1:A:6:U:H6   | 1.81                     | 0.62              |
| 1:A:32:G:OP1  | 1:A:32:G:C1' | 2.46                     | 0.62              |
| 1:A:66:C:H4'  | 1:A:67:C:OP1 | 1.98                     | 0.62              |
| 1:A:66:C:H4'  | 1:A:67:C:OP1 | 1.98                     | 0.62              |
| 1:A:30:U:O2'  | 1:A:32:G:OP1 | 2.07                     | 0.62              |
| 1:A:94:U:O2'  | 1:A:96:A:N7  | 2.32                     | 0.62              |
| 1:A:30:U:O2'  | 1:A:32:G:OP1 | 2.16                     | 0.62              |
| 1:A:95:G:C8   | 1:A:95:G:OP1 | 2.53                     | 0.62              |
| 1:A:4:C:O2'   | 1:A:6:U:OP2  | 2.17                     | 0.62              |
| 1:A:18:U:O2'  | 1:A:19:C:OP2 | 2.17                     | 0.62              |
| 1:A:30:U:O2'  | 1:A:32:G:OP1 | 2.13                     | 0.62              |
| 1:A:57:G:N3   | 1:A:112:C:N4 | 2.48                     | 0.62              |
| 1:A:47:U:C3'  | 1:A:48:C:H5' | 2.29                     | 0.62              |
| 1:A:94:U:O2'  | 1:A:96:A:N7  | 2.33                     | 0.62              |
| 1:A:19:C:H3'  | 1:A:19:C:OP1 | 1.99                     | 0.61              |
| 1:A:19:C:O2'  | 1:A:20:A:O5' | 2.17                     | 0.61              |
| 1:A:19:C:C6   | 1:A:19:C:OP1 | 2.53                     | 0.61              |
| 1:A:57:G:N3   | 1:A:112:C:N4 | 2.47                     | 0.61              |

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| Atom-1        | Atom-2        | Interatomic distance (Å) | Clash overlap (Å) |
|---------------|---------------|--------------------------|-------------------|
| 1:A:10:U:H2'  | 1:A:11:G:OP2  | 1.99                     | 0.61              |
| 1:A:5:A:C2'   | 1:A:6:U:OP2   | 2.49                     | 0.61              |
| 1:A:93:G:N2   | 1:A:97:C:N3   | 2.47                     | 0.61              |
| 1:A:73:G:HO2' | 1:A:74:A:P    | 2.24                     | 0.61              |
| 1:A:111:G:OP2 | 1:A:111:G:C8  | 2.53                     | 0.61              |
| 1:A:30:U:H4'  | 1:A:31:U:OP1  | 2.00                     | 0.61              |
| 1:A:32:G:H8   | 1:A:32:G:OP1  | 1.84                     | 0.61              |
| 1:A:5:A:O2'   | 1:A:23:C:N3   | 2.33                     | 0.61              |
| 1:A:74:A:O4'  | 1:A:76:G:O6   | 2.18                     | 0.61              |
| 1:A:32:G:P    | 1:A:32:G:C8   | 2.93                     | 0.61              |
| 1:A:58:U:O2'  | 1:A:111:G:N2  | 2.33                     | 0.61              |
| 1:A:95:G:OP1  | 1:A:95:G:H8   | 1.84                     | 0.61              |
| 1:A:19:C:O4'  | 1:A:19:C:OP1  | 2.19                     | 0.60              |
| 1:A:43:A:N6   | 1:A:63:U:O2   | 2.33                     | 0.60              |
| 1:A:97:C:O2'  | 1:A:98:G:OP1  | 2.15                     | 0.60              |
| 1:A:96:A:O5'  | 1:A:96:A:C8   | 2.49                     | 0.60              |
| 1:A:117:G:H8  | 1:A:117:G:OP2 | 1.83                     | 0.60              |
| 1:A:82:G:OP1  | 1:A:82:G:H8   | 1.84                     | 0.60              |
| 1:A:59:G:H8   | 1:A:59:G:O5'  | 1.84                     | 0.60              |
| 1:A:19:C:OP1  | 1:A:19:C:H6   | 1.84                     | 0.60              |
| 1:A:5:A:O2'   | 1:A:7:G:OP2   | 2.20                     | 0.60              |
| 1:A:74:A:O2'  | 1:A:76:G:O6   | 2.16                     | 0.60              |
| 1:A:45:C:O2'  | 1:A:82:G:OP2  | 2.19                     | 0.60              |
| 1:A:6:U:OP1   | 1:A:6:U:C6    | 2.55                     | 0.59              |
| 1:A:58:U:C2'  | 1:A:59:G:OP2  | 2.50                     | 0.59              |
| 1:A:45:C:O2'  | 1:A:82:G:OP2  | 2.19                     | 0.59              |
| 1:A:32:G:C8   | 1:A:32:G:P    | 2.94                     | 0.59              |
| 1:A:8:A:OP2   | 1:A:8:A:N9    | 2.36                     | 0.59              |
| 1:A:32:G:OP2  | 1:A:32:G:N9   | 2.35                     | 0.59              |
| 1:A:43:A:N6   | 1:A:63:U:O2   | 2.35                     | 0.59              |
| 1:A:45:C:O2'  | 1:A:82:G:OP2  | 2.19                     | 0.59              |
| 1:A:2:G:N7    | 1:A:74:A:N6   | 2.50                     | 0.59              |
| 1:A:18:U:O2'  | 1:A:19:C:OP2  | 2.15                     | 0.59              |
| 1:A:10:U:H4'  | 1:A:10:U:OP2  | 2.01                     | 0.59              |
| 1:A:74:A:OP2  | 1:A:74:A:C4   | 2.55                     | 0.59              |
| 1:A:93:G:N2   | 1:A:97:C:N3   | 2.48                     | 0.59              |
| 1:A:31:U:O2'  | 1:A:32:G:N7   | 2.34                     | 0.59              |
| 1:A:57:G:N3   | 1:A:112:C:N4  | 2.50                     | 0.58              |
| 1:A:74:A:H8   | 1:A:74:A:OP2  | 1.86                     | 0.58              |
| 1:A:30:U:O2'  | 1:A:31:U:O5'  | 2.21                     | 0.58              |
| 1:A:42:A:OP2  | 1:A:42:A:H8   | 1.85                     | 0.58              |

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| Atom-1        | Atom-2        | Interatomic distance (Å) | Clash overlap (Å) |
|---------------|---------------|--------------------------|-------------------|
| 1:A:80:A:HO2' | 1:A:81:G:P    | 2.20                     | 0.58              |
| 1:A:48:C:O2   | 1:A:112:C:N4  | 2.35                     | 0.58              |
| 1:A:31:U:H1'  | 1:A:32:G:C8   | 2.38                     | 0.58              |
| 1:A:30:U:O2'  | 1:A:31:U:H2'  | 2.04                     | 0.58              |
| 1:A:7:G:N7    | 1:A:41:C:O2'  | 2.36                     | 0.58              |
| 1:A:43:A:N6   | 1:A:63:U:O2   | 2.35                     | 0.58              |
| 1:A:109:A:O2' | 1:A:110:A:OP1 | 2.14                     | 0.58              |
| 1:A:19:C:HO2' | 1:A:20:A:P    | 2.25                     | 0.58              |
| 1:A:37:C:C2'  | 1:A:38:C:OP1  | 2.51                     | 0.58              |
| 1:A:51:A:H4'  | 1:A:52:C:OP2  | 2.02                     | 0.58              |
| 1:A:32:G:O4'  | 1:A:32:G:P    | 2.60                     | 0.58              |
| 1:A:30:U:C2'  | 1:A:31:U:H3'  | 2.34                     | 0.58              |
| 1:A:82:G:OP1  | 1:A:82:G:H8   | 1.87                     | 0.58              |
| 1:A:73:G:H3'  | 1:A:73:G:N3   | 2.18                     | 0.58              |
| 1:A:57:G:N3   | 1:A:112:C:N4  | 2.51                     | 0.58              |
| 1:A:51:A:OP1  | 1:A:51:A:H8   | 1.86                     | 0.57              |
| 1:A:63:U:O2'  | 1:A:79:C:OP1  | 2.22                     | 0.57              |
| 1:A:30:U:H2'  | 1:A:31:U:C5'  | 2.34                     | 0.57              |
| 1:A:47:U:H3'  | 1:A:48:C:H5'  | 1.86                     | 0.57              |
| 1:A:96:A:H8   | 1:A:96:A:O5'  | 1.87                     | 0.57              |
| 1:A:82:G:C8   | 1:A:82:G:P    | 2.94                     | 0.57              |
| 1:A:96:A:H8   | 1:A:96:A:O5'  | 1.88                     | 0.57              |
| 1:A:82:G:OP1  | 1:A:82:G:H8   | 1.86                     | 0.57              |
| 1:A:8:A:OP2   | 1:A:8:A:C5    | 2.57                     | 0.57              |
| 1:A:32:G:OP2  | 1:A:32:G:N9   | 2.38                     | 0.57              |
| 1:A:30:U:H4'  | 1:A:31:U:OP1  | 2.03                     | 0.57              |
| 1:A:49:C:C5'  | 1:A:50:A:OP2  | 2.53                     | 0.57              |
| 1:A:19:C:OP1  | 1:A:19:C:C6   | 2.57                     | 0.57              |
| 1:A:9:G:OP1   | 1:A:9:G:H8    | 1.88                     | 0.57              |
| 1:A:45:C:O2'  | 1:A:82:G:OP2  | 2.21                     | 0.57              |
| 1:A:31:U:H1'  | 1:A:32:G:C8   | 2.40                     | 0.57              |
| 1:A:19:C:P    | 1:A:19:C:C6   | 2.97                     | 0.57              |
| 1:A:51:A:O2'  | 1:A:52:C:OP1  | 2.20                     | 0.57              |
| 1:A:117:G:OP2 | 1:A:117:G:C8  | 2.57                     | 0.57              |
| 1:A:43:A:N6   | 1:A:63:U:O2   | 2.38                     | 0.57              |
| 1:A:30:U:H2'  | 1:A:31:U:H3'  | 1.87                     | 0.56              |
| 1:A:96:A:OP2  | 1:A:97:C:N4   | 2.36                     | 0.56              |
| 1:A:31:U:O2'  | 1:A:32:G:O5'  | 2.19                     | 0.56              |
| 1:A:43:A:N6   | 1:A:63:U:O2   | 2.38                     | 0.56              |
| 1:A:30:U:H2'  | 1:A:31:U:H3'  | 1.87                     | 0.56              |
| 1:A:47:U:O4'  | 1:A:110:A:N6  | 2.38                     | 0.56              |

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| Atom-1        | Atom-2        | Interatomic distance (Å) | Clash overlap (Å) |
|---------------|---------------|--------------------------|-------------------|
| 1:A:38:C:OP1  | 1:A:38:C:H4'  | 2.04                     | 0.56              |
| 1:A:59:G:N2   | 1:A:110:A:O2' | 2.38                     | 0.56              |
| 1:A:95:G:OP1  | 1:A:95:G:H8   | 1.87                     | 0.56              |
| 1:A:51:A:N6   | 1:A:117:G:O6  | 2.38                     | 0.56              |
| 1:A:18:U:O2'  | 1:A:19:C:OP1  | 2.21                     | 0.56              |
| 1:A:30:U:O2   | 1:A:32:G:O5'  | 2.24                     | 0.56              |
| 1:A:74:A:C8   | 1:A:74:A:OP2  | 2.57                     | 0.56              |
| 1:A:32:G:C8   | 1:A:32:G:OP2  | 2.49                     | 0.56              |
| 1:A:20:A:OP2  | 1:A:20:A:C8   | 2.59                     | 0.55              |
| 1:A:57:G:N3   | 1:A:112:C:N4  | 2.53                     | 0.55              |
| 1:A:97:C:H6   | 1:A:97:C:OP2  | 1.89                     | 0.55              |
| 1:A:45:C:O2'  | 1:A:82:G:OP2  | 2.24                     | 0.55              |
| 1:A:43:A:N6   | 1:A:63:U:O2   | 2.39                     | 0.55              |
| 1:A:48:C:H1'  | 1:A:111:G:C6  | 2.41                     | 0.55              |
| 1:A:82:G:C8   | 1:A:82:G:OP2  | 2.60                     | 0.55              |
| 1:A:5:A:N6    | 1:A:75:U:O4   | 2.38                     | 0.55              |
| 1:A:24:C:C6   | 1:A:24:C:OP1  | 2.60                     | 0.55              |
| 1:A:75:U:O2'  | 1:A:76:G:P    | 2.65                     | 0.55              |
| 1:A:109:A:OP1 | 1:A:109:A:H4' | 2.06                     | 0.55              |
| 1:A:110:A:H8  | 1:A:110:A:O5' | 1.89                     | 0.55              |
| 1:A:82:G:OP1  | 1:A:82:G:H8   | 1.90                     | 0.55              |
| 1:A:82:G:H8   | 1:A:82:G:P    | 2.30                     | 0.55              |
| 1:A:74:A:H4'  | 1:A:75:U:OP1  | 2.06                     | 0.55              |
| 1:A:23:C:H2'  | 1:A:24:C:OP1  | 2.05                     | 0.55              |
| 1:A:59:G:H2'  | 1:A:60:G:C8   | 2.42                     | 0.55              |
| 1:A:23:C:O4'  | 1:A:23:C:P    | 2.64                     | 0.55              |
| 1:A:30:U:H2'  | 1:A:32:G:OP2  | 2.07                     | 0.55              |
| 1:A:60:G:OP2  | 1:A:60:G:C8   | 2.59                     | 0.55              |
| 1:A:7:G:N3    | 1:A:7:G:C3'   | 2.64                     | 0.55              |
| 1:A:52:C:O4'  | 1:A:52:C:OP1  | 2.26                     | 0.55              |
| 1:A:10:U:C2'  | 1:A:11:G:OP2  | 2.55                     | 0.55              |
| 1:A:45:C:O2'  | 1:A:82:G:OP2  | 2.23                     | 0.54              |
| 1:A:47:U:H4'  | 1:A:47:U:OP1  | 2.07                     | 0.54              |
| 1:A:8:A:O4'   | 1:A:8:A:P     | 2.65                     | 0.54              |
| 1:A:23:C:O2'  | 1:A:25:C:OP2  | 2.26                     | 0.54              |
| 1:A:57:G:N2   | 1:A:111:G:N7  | 2.55                     | 0.54              |
| 1:A:63:U:O2'  | 1:A:79:C:OP1  | 2.26                     | 0.54              |
| 1:A:8:A:OP1   | 1:A:8:A:C2'   | 2.53                     | 0.54              |
| 1:A:18:U:O2'  | 1:A:19:C:O4'  | 2.19                     | 0.54              |
| 1:A:73:G:N3   | 1:A:73:G:C2'  | 2.70                     | 0.54              |
| 1:A:59:G:H8   | 1:A:59:G:O5'  | 1.91                     | 0.54              |

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| Atom-1        | Atom-2        | Interatomic distance (Å) | Clash overlap (Å) |
|---------------|---------------|--------------------------|-------------------|
| 1:A:95:G:O4'  | 1:A:95:G:P    | 2.65                     | 0.54              |
| 1:A:95:G:O2'  | 1:A:96:A:O4'  | 2.24                     | 0.54              |
| 1:A:48:C:O2   | 1:A:112:C:N4  | 2.40                     | 0.54              |
| 1:A:46:C:H3'  | 1:A:47:U:H5'' | 1.90                     | 0.54              |
| 1:A:24:C:OP1  | 1:A:24:C:C6   | 2.61                     | 0.54              |
| 1:A:50:A:H2'  | 1:A:51:A:H5'' | 1.90                     | 0.54              |
| 1:A:110:A:H8  | 1:A:110:A:O5' | 1.90                     | 0.54              |
| 1:A:82:G:OP1  | 1:A:82:G:H8   | 1.91                     | 0.54              |
| 1:A:32:G:O4'  | 1:A:32:G:P    | 2.64                     | 0.54              |
| 1:A:48:C:O2   | 1:A:112:C:N4  | 2.40                     | 0.53              |
| 1:A:51:A:N6   | 1:A:117:G:O6  | 2.41                     | 0.53              |
| 1:A:4:C:H2'   | 1:A:5:A:C4    | 2.44                     | 0.53              |
| 1:A:8:A:OP2   | 1:A:8:A:C1'   | 2.56                     | 0.53              |
| 1:A:24:C:H6   | 1:A:24:C:OP2  | 1.86                     | 0.53              |
| 1:A:60:G:OP2  | 1:A:60:G:H8   | 1.91                     | 0.53              |
| 1:A:64:G:H8   | 1:A:64:G:OP2  | 1.92                     | 0.53              |
| 1:A:32:G:OP2  | 1:A:32:G:H8   | 1.91                     | 0.53              |
| 1:A:97:C:OP2  | 1:A:97:C:C6   | 2.60                     | 0.53              |
| 1:A:51:A:OP2  | 1:A:51:A:N7   | 2.40                     | 0.53              |
| 1:A:43:A:N6   | 1:A:63:U:O2   | 2.39                     | 0.53              |
| 1:A:6:U:OP2   | 1:A:6:U:C6    | 2.59                     | 0.53              |
| 1:A:32:G:OP1  | 1:A:32:G:C1'  | 2.55                     | 0.53              |
| 1:A:49:C:O4'  | 1:A:111:G:O2' | 2.27                     | 0.53              |
| 1:A:32:G:H8   | 1:A:32:G:P    | 2.32                     | 0.53              |
| 1:A:30:U:O2'  | 1:A:31:U:H3'  | 2.09                     | 0.53              |
| 1:A:24:C:H3'  | 1:A:24:C:OP2  | 2.08                     | 0.53              |
| 1:A:58:U:O2'  | 1:A:59:G:OP1  | 2.26                     | 0.53              |
| 1:A:80:A:H4'  | 1:A:81:G:OP2  | 2.08                     | 0.53              |
| 1:A:50:A:O2'  | 1:A:51:A:O5'  | 2.25                     | 0.53              |
| 1:A:8:A:H2'   | 1:A:8:A:OP2   | 2.09                     | 0.52              |
| 1:A:10:U:H2'  | 1:A:11:G:OP2  | 2.08                     | 0.52              |
| 1:A:18:U:O2'  | 1:A:19:C:O4'  | 2.27                     | 0.52              |
| 1:A:30:U:O2'  | 1:A:31:U:H3'  | 2.09                     | 0.52              |
| 1:A:18:U:HO2' | 1:A:19:C:P    | 2.28                     | 0.52              |
| 1:A:93:G:N2   | 1:A:97:C:N3   | 2.54                     | 0.52              |
| 1:A:8:A:H8    | 1:A:8:A:O5'   | 1.92                     | 0.52              |
| 1:A:117:G:OP2 | 1:A:117:G:C8  | 2.62                     | 0.52              |
| 1:A:7:G:O4'   | 1:A:7:G:P     | 2.68                     | 0.52              |
| 1:A:7:G:O3'   | 1:A:41:C:O2'  | 2.27                     | 0.52              |
| 1:A:86:A:O2'  | 1:A:87:G:P    | 2.62                     | 0.52              |
| 1:A:30:U:O2   | 1:A:32:G:O5'  | 2.28                     | 0.52              |

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| Atom-1        | Atom-2        | Interatomic distance (Å) | Clash overlap (Å) |
|---------------|---------------|--------------------------|-------------------|
| 1:A:49:C:OP1  | 1:A:50:A:O4'  | 2.26                     | 0.52              |
| 1:A:58:U:O2'  | 1:A:111:G:N2  | 2.42                     | 0.52              |
| 1:A:19:C:OP1  | 1:A:19:C:C6   | 2.63                     | 0.52              |
| 1:A:17:G:N1   | 1:A:31:U:O2   | 2.42                     | 0.52              |
| 1:A:49:C:H4'  | 1:A:112:C:OP2 | 2.10                     | 0.52              |
| 1:A:37:C:HO2' | 1:A:38:C:P    | 2.28                     | 0.52              |
| 1:A:62:G:H1'  | 1:A:82:G:H4'  | 1.92                     | 0.52              |
| 1:A:32:G:OP1  | 1:A:32:G:H3'  | 2.10                     | 0.52              |
| 1:A:62:G:H1'  | 1:A:82:G:H4'  | 1.92                     | 0.52              |
| 1:A:62:G:H1'  | 1:A:82:G:H4'  | 1.92                     | 0.51              |
| 1:A:62:G:H1'  | 1:A:82:G:H4'  | 1.92                     | 0.51              |
| 1:A:62:G:H1'  | 1:A:82:G:H4'  | 1.92                     | 0.51              |
| 1:A:47:U:H4'  | 1:A:47:U:OP1  | 2.10                     | 0.51              |
| 1:A:62:G:H1'  | 1:A:82:G:H4'  | 1.92                     | 0.51              |
| 1:A:23:C:O2'  | 1:A:24:C:O5'  | 2.26                     | 0.51              |
| 1:A:62:G:H1'  | 1:A:82:G:H4'  | 1.92                     | 0.51              |
| 1:A:5:A:H2'   | 1:A:6:U:OP2   | 2.10                     | 0.51              |
| 1:A:62:G:H1'  | 1:A:82:G:H4'  | 1.92                     | 0.51              |
| 1:A:48:C:H1'  | 1:A:111:G:C6  | 2.46                     | 0.51              |
| 1:A:62:G:H1'  | 1:A:82:G:H4'  | 1.92                     | 0.51              |
| 1:A:30:U:O2   | 1:A:32:G:O5'  | 2.29                     | 0.51              |
| 1:A:62:G:H1'  | 1:A:82:G:H4'  | 1.93                     | 0.51              |
| 1:A:62:G:H1'  | 1:A:82:G:H4'  | 1.93                     | 0.51              |
| 1:A:48:C:H1'  | 1:A:111:G:C6  | 2.46                     | 0.51              |
| 1:A:62:G:H1'  | 1:A:82:G:H4'  | 1.92                     | 0.51              |
| 1:A:62:G:H1'  | 1:A:82:G:H4'  | 1.92                     | 0.51              |
| 1:A:50:A:H2'  | 1:A:51:A:H5'' | 1.90                     | 0.51              |
| 1:A:62:G:H1'  | 1:A:82:G:H4'  | 1.92                     | 0.51              |
| 1:A:62:G:H1'  | 1:A:82:G:H4'  | 1.92                     | 0.51              |
| 1:A:62:G:H1'  | 1:A:82:G:H4'  | 1.93                     | 0.51              |
| 1:A:62:G:H1'  | 1:A:82:G:H4'  | 1.93                     | 0.51              |
| 1:A:97:C:H6   | 1:A:97:C:O5'  | 1.92                     | 0.51              |
| 1:A:74:A:C2   | 1:A:74:A:OP1  | 2.64                     | 0.51              |
| 1:A:62:G:H1'  | 1:A:82:G:H4'  | 1.93                     | 0.51              |
| 1:A:62:G:H1'  | 1:A:82:G:H4'  | 1.93                     | 0.51              |
| 1:A:9:G:O2'   | 1:A:10:U:O3'  | 2.28                     | 0.51              |
| 1:A:62:G:H1'  | 1:A:82:G:H4'  | 1.93                     | 0.51              |
| 1:A:48:C:O2   | 1:A:112:C:N4  | 2.41                     | 0.51              |
| 1:A:23:C:H2'  | 1:A:23:C:O2   | 2.09                     | 0.51              |
| 1:A:10:U:O4   | 1:A:30:U:O2'  | 2.25                     | 0.51              |
| 1:A:7:G:OP2   | 1:A:7:G:H8    | 1.93                     | 0.51              |

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| Atom-1        | Atom-2        | Interatomic distance (Å) | Clash overlap (Å) |
|---------------|---------------|--------------------------|-------------------|
| 1:A:82:G:OP1  | 1:A:82:G:H8   | 1.94                     | 0.51              |
| 1:A:7:G:H1'   | 1:A:8:A:H2'   | 1.93                     | 0.51              |
| 1:A:57:G:N3   | 1:A:112:C:N4  | 2.54                     | 0.51              |
| 1:A:93:G:H3'  | 1:A:94:U:H5'' | 1.93                     | 0.50              |
| 1:A:17:G:N1   | 1:A:31:U:O2   | 2.44                     | 0.50              |
| 1:A:64:G:OP2  | 1:A:64:G:C8   | 2.64                     | 0.50              |
| 1:A:20:A:N6   | 1:A:31:U:O2'  | 2.44                     | 0.50              |
| 1:A:80:A:O2'  | 1:A:81:G:OP1  | 2.28                     | 0.50              |
| 1:A:47:U:O4   | 1:A:60:G:N1   | 2.45                     | 0.50              |
| 1:A:57:G:N3   | 1:A:112:C:N4  | 2.58                     | 0.50              |
| 1:A:30:U:O2   | 1:A:32:G:OP2  | 2.29                     | 0.50              |
| 1:A:5:A:O4'   | 1:A:73:G:O6   | 2.29                     | 0.50              |
| 1:A:59:G:H8   | 1:A:59:G:OP2  | 1.94                     | 0.50              |
| 1:A:32:G:OP2  | 1:A:32:G:C8   | 2.64                     | 0.50              |
| 1:A:8:A:OP1   | 1:A:8:A:H4'   | 2.10                     | 0.50              |
| 1:A:58:U:H2'  | 1:A:59:G:O4'  | 2.12                     | 0.50              |
| 1:A:59:G:OP1  | 1:A:59:G:H8   | 1.93                     | 0.50              |
| 1:A:75:U:H6   | 1:A:75:U:O5'  | 1.94                     | 0.50              |
| 1:A:9:G:OP2   | 1:A:39:G:N2   | 2.44                     | 0.50              |
| 1:A:31:U:HO2' | 1:A:32:G:P    | 2.35                     | 0.50              |
| 1:A:10:U:C2'  | 1:A:11:G:OP2  | 2.60                     | 0.50              |
| 1:A:96:A:H8   | 1:A:96:A:O5'  | 1.94                     | 0.50              |
| 1:A:47:U:H2'  | 1:A:48:C:H5'  | 1.93                     | 0.49              |
| 1:A:64:G:H4'  | 1:A:78:C:H4'  | 1.94                     | 0.49              |
| 1:A:64:G:H4'  | 1:A:78:C:H4'  | 1.94                     | 0.49              |
| 1:A:64:G:H4'  | 1:A:78:C:H4'  | 1.94                     | 0.49              |
| 1:A:30:U:O2   | 1:A:32:G:OP2  | 2.29                     | 0.49              |
| 1:A:109:A:C2' | 1:A:110:A:OP1 | 2.60                     | 0.49              |
| 1:A:64:G:H4'  | 1:A:78:C:H4'  | 1.94                     | 0.49              |
| 1:A:9:G:C4    | 1:A:39:G:N2   | 2.80                     | 0.49              |
| 1:A:57:G:N3   | 1:A:112:C:N4  | 2.57                     | 0.49              |
| 1:A:64:G:H4'  | 1:A:78:C:H4'  | 1.94                     | 0.49              |
| 1:A:64:G:H4'  | 1:A:78:C:H4'  | 1.94                     | 0.49              |
| 1:A:64:G:H4'  | 1:A:78:C:H4'  | 1.94                     | 0.49              |
| 1:A:64:G:H4'  | 1:A:78:C:H4'  | 1.94                     | 0.49              |
| 1:A:64:G:H4'  | 1:A:78:C:H4'  | 1.94                     | 0.49              |
| 1:A:64:G:H4'  | 1:A:78:C:H4'  | 1.94                     | 0.49              |
| 1:A:73:G:C2'  | 1:A:74:A:OP2  | 2.59                     | 0.49              |
| 1:A:73:G:N3   | 1:A:73:G:H2'  | 2.26                     | 0.49              |
| 1:A:64:G:H4'  | 1:A:78:C:H4'  | 1.94                     | 0.49              |
| 1:A:64:G:H4'  | 1:A:78:C:H4'  | 1.94                     | 0.49              |
| 1:A:64:G:H4'  | 1:A:78:C:H4'  | 1.94                     | 0.49              |

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| Atom-1        | Atom-2        | Interatomic distance (Å) | Clash overlap (Å) |
|---------------|---------------|--------------------------|-------------------|
| 1:A:64:G:H4'  | 1:A:78:C:H4'  | 1.94                     | 0.49              |
| 1:A:43:A:N6   | 1:A:63:U:O2   | 2.45                     | 0.49              |
| 1:A:64:G:H4'  | 1:A:78:C:H4'  | 1.94                     | 0.49              |
| 1:A:64:G:H4'  | 1:A:78:C:H4'  | 1.94                     | 0.49              |
| 1:A:64:G:H4'  | 1:A:78:C:H4'  | 1.94                     | 0.49              |
| 1:A:64:G:H4'  | 1:A:78:C:H4'  | 1.94                     | 0.49              |
| 1:A:64:G:H4'  | 1:A:78:C:H4'  | 1.94                     | 0.49              |
| 1:A:64:G:H4'  | 1:A:78:C:H4'  | 1.94                     | 0.49              |
| 1:A:18:U:HO2' | 1:A:19:C:P    | 2.35                     | 0.49              |
| 1:A:43:A:H8   | 1:A:43:A:O5'  | 1.95                     | 0.49              |
| 1:A:95:G:OP1  | 1:A:95:G:H8   | 1.95                     | 0.49              |
| 1:A:58:U:O2'  | 1:A:59:G:O4'  | 2.18                     | 0.49              |
| 1:A:64:G:H4'  | 1:A:78:C:H4'  | 1.94                     | 0.49              |
| 1:A:80:A:O2'  | 1:A:81:G:OP2  | 2.12                     | 0.49              |
| 1:A:30:U:H2'  | 1:A:31:U:O5'  | 2.12                     | 0.49              |
| 1:A:47:U:O4   | 1:A:60:G:C2   | 2.66                     | 0.49              |
| 1:A:37:C:H2'  | 1:A:38:C:OP1  | 2.13                     | 0.49              |
| 1:A:31:U:O3'  | 1:A:32:G:C8   | 2.66                     | 0.49              |
| 1:A:10:U:O2'  | 1:A:11:G:O5'  | 2.30                     | 0.49              |
| 1:A:80:A:OP1  | 1:A:80:A:C4'  | 2.59                     | 0.49              |
| 1:A:32:G:OP1  | 1:A:32:G:N9   | 2.38                     | 0.49              |
| 1:A:94:U:O2   | 1:A:97:C:N4   | 2.45                     | 0.49              |
| 1:A:112:C:H2' | 1:A:113:G:H5' | 1.95                     | 0.49              |
| 1:A:5:A:H5'   | 1:A:5:A:N3    | 2.27                     | 0.49              |
| 1:A:112:C:H6  | 1:A:112:C:O5' | 1.96                     | 0.49              |
| 1:A:94:U:O2   | 1:A:97:C:N4   | 2.46                     | 0.49              |
| 1:A:8:A:OP2   | 1:A:41:C:O2'  | 2.29                     | 0.49              |
| 1:A:30:U:H2'  | 1:A:31:U:C3'  | 2.43                     | 0.49              |
| 1:A:51:A:N6   | 1:A:118:U:O2' | 2.45                     | 0.48              |
| 1:A:31:U:H4'  | 1:A:32:G:O5'  | 2.13                     | 0.48              |
| 1:A:19:C:O2   | 1:A:32:G:O4'  | 2.30                     | 0.48              |
| 1:A:95:G:HO2' | 1:A:96:A:P    | 2.36                     | 0.48              |
| 1:A:6:U:OP1   | 1:A:6:U:H6    | 1.96                     | 0.48              |
| 1:A:43:A:N6   | 1:A:63:U:O2   | 2.45                     | 0.48              |
| 1:A:112:C:H6  | 1:A:112:C:O5' | 1.95                     | 0.48              |
| 1:A:74:A:OP2  | 1:A:74:A:H8   | 1.95                     | 0.48              |
| 1:A:31:U:H1'  | 1:A:32:G:C8   | 2.49                     | 0.48              |
| 1:A:85:G:H2'  | 1:A:86:A:C8   | 2.49                     | 0.48              |
| 1:A:82:G:H8   | 1:A:82:G:OP2  | 1.95                     | 0.48              |
| 1:A:32:G:P    | 1:A:32:G:C8   | 3.07                     | 0.48              |
| 1:A:85:G:H2'  | 1:A:86:A:C8   | 2.49                     | 0.48              |

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| <b>Atom-1</b> | <b>Atom-2</b> | <b>Interatomic distance (<math>\text{\AA}</math>)</b> | <b>Clash overlap (<math>\text{\AA}</math>)</b> |
|---------------|---------------|-------------------------------------------------------|------------------------------------------------|
| 1:A:18:U:H2'  | 1:A:18:U:O2   | 2.13                                                  | 0.48                                           |
| 1:A:47:U:C2'  | 1:A:48:C:H5'  | 2.44                                                  | 0.48                                           |
| 1:A:18:U:O2'  | 1:A:19:C:O5'  | 2.31                                                  | 0.48                                           |
| 1:A:94:U:O2'  | 1:A:96:A:N7   | 2.42                                                  | 0.48                                           |
| 1:A:51:A:OP1  | 1:A:51:A:C8   | 2.66                                                  | 0.48                                           |
| 1:A:10:U:OP2  | 1:A:66:C:O2'  | 2.25                                                  | 0.48                                           |
| 1:A:24:C:OP1  | 1:A:24:C:H6   | 1.96                                                  | 0.48                                           |
| 1:A:49:C:H5'  | 1:A:111:G:H1' | 1.96                                                  | 0.48                                           |
| 1:A:8:A:OP2   | 1:A:41:C:O2'  | 2.20                                                  | 0.48                                           |
| 1:A:18:U:N3   | 1:A:20:A:N7   | 2.62                                                  | 0.48                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:81:G:N2   | 1:A:83:U:O4   | 2.47                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:49:C:H3'  | 1:A:50:A:H5'  | 1.97                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:82:G:C8   | 1:A:82:G:P    | 3.06                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:28:G:C2   | 1:A:29:C:H1'  | 2.50                                                  | 0.47                                           |
| 1:A:32:G:H8   | 1:A:32:G:OP2  | 1.98                                                  | 0.47                                           |
| 1:A:74:A:O4'  | 1:A:75:U:OP1  | 2.32                                                  | 0.47                                           |
| 1:A:75:U:OP1  | 1:A:75:U:H6   | 1.97                                                  | 0.47                                           |
| 1:A:85:G:H2'  | 1:A:86:A:C8   | 2.49                                                  | 0.47                                           |
| 1:A:57:G:H1'  | 1:A:112:C:H42 | 1.79                                                  | 0.47                                           |
| 1:A:57:G:H1'  | 1:A:112:C:H42 | 1.79                                                  | 0.47                                           |
| 1:A:74:A:C4'  | 1:A:75:U:OP1  | 2.62                                                  | 0.47                                           |
| 1:A:31:U:O2'  | 1:A:32:G:P    | 2.73                                                  | 0.47                                           |



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| Atom-1        | Atom-2        | Interatomic distance (Å) | Clash overlap (Å) |
|---------------|---------------|--------------------------|-------------------|
| 1:A:97:C:H2'  | 1:A:98:G:O4'  | 2.15                     | 0.47              |
| 1:A:24:C:H3'  | 1:A:24:C:P    | 2.54                     | 0.47              |
| 1:A:59:G:H2'  | 1:A:60:G:C8   | 2.50                     | 0.47              |
| 1:A:18:U:C2'  | 1:A:19:C:OP1  | 2.62                     | 0.47              |
| 1:A:85:G:H2'  | 1:A:86:A:C8   | 2.50                     | 0.47              |
| 1:A:31:U:O3'  | 1:A:32:G:H8   | 1.97                     | 0.47              |
| 1:A:30:U:O2   | 1:A:32:G:OP2  | 2.33                     | 0.47              |
| 1:A:7:G:N1    | 1:A:41:C:O2'  | 2.48                     | 0.47              |
| 1:A:85:G:H2'  | 1:A:86:A:C8   | 2.50                     | 0.47              |
| 1:A:85:G:H2'  | 1:A:86:A:C8   | 2.50                     | 0.47              |
| 1:A:6:U:O2    | 1:A:8:A:N6    | 2.48                     | 0.47              |
| 1:A:19:C:O4'  | 1:A:19:C:P    | 2.73                     | 0.47              |
| 1:A:43:A:N6   | 1:A:63:U:O2   | 2.48                     | 0.47              |
| 1:A:60:G:C6   | 1:A:110:A:N6  | 2.82                     | 0.47              |
| 1:A:85:G:H2'  | 1:A:86:A:C8   | 2.50                     | 0.47              |
| 1:A:59:G:O2'  | 1:A:110:A:C2  | 2.68                     | 0.47              |
| 1:A:30:U:O2   | 1:A:32:G:OP2  | 2.32                     | 0.47              |
| 1:A:7:G:OP2   | 1:A:7:G:C8    | 2.68                     | 0.47              |
| 1:A:18:U:H2'  | 1:A:19:C:C6   | 2.50                     | 0.47              |
| 1:A:85:G:H2'  | 1:A:86:A:C8   | 2.49                     | 0.47              |
| 1:A:57:G:H1'  | 1:A:112:C:H42 | 1.79                     | 0.47              |
| 1:A:85:G:H2'  | 1:A:86:A:C8   | 2.50                     | 0.47              |
| 1:A:48:C:H1'  | 1:A:111:G:C5  | 2.51                     | 0.47              |
| 1:A:85:G:H2'  | 1:A:86:A:C8   | 2.50                     | 0.47              |
| 1:A:30:U:H2'  | 1:A:31:U:C4'  | 2.45                     | 0.46              |
| 1:A:76:G:OP2  | 1:A:76:G:H8   | 1.98                     | 0.46              |
| 1:A:47:U:C3'  | 1:A:48:C:C5'  | 2.93                     | 0.46              |
| 1:A:117:G:H2' | 1:A:118:U:O4' | 2.15                     | 0.46              |
| 1:A:18:U:O2'  | 1:A:19:C:O4'  | 2.29                     | 0.46              |
| 1:A:57:G:H1'  | 1:A:112:C:H42 | 1.80                     | 0.46              |
| 1:A:57:G:H1'  | 1:A:112:C:H42 | 1.80                     | 0.46              |
| 1:A:46:C:H2'  | 1:A:47:U:O4'  | 2.14                     | 0.46              |
| 1:A:96:A:H8   | 1:A:96:A:O5'  | 1.97                     | 0.46              |
| 1:A:57:G:H1'  | 1:A:112:C:H42 | 1.80                     | 0.46              |
| 1:A:58:U:O2   | 1:A:111:G:N1  | 2.44                     | 0.46              |
| 1:A:18:U:O2'  | 1:A:19:C:O4'  | 2.28                     | 0.46              |
| 1:A:85:G:H2'  | 1:A:86:A:C8   | 2.50                     | 0.46              |
| 1:A:85:G:H2'  | 1:A:86:A:C8   | 2.50                     | 0.46              |
| 1:A:32:G:C8   | 1:A:32:G:OP1  | 2.61                     | 0.46              |
| 1:A:57:G:H1'  | 1:A:112:C:H42 | 1.80                     | 0.46              |
| 1:A:30:U:O2'  | 1:A:31:U:H3'  | 2.14                     | 0.46              |

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| Atom-1        | Atom-2        | Interatomic distance (Å) | Clash overlap (Å) |
|---------------|---------------|--------------------------|-------------------|
| 1:A:51:A:N1   | 1:A:117:G:N2  | 2.60                     | 0.46              |
| 1:A:48:C:C6   | 1:A:48:C:OP2  | 2.69                     | 0.46              |
| 1:A:31:U:O2'  | 1:A:32:G:N7   | 2.44                     | 0.46              |
| 1:A:58:U:H2'  | 1:A:59:G:O4'  | 2.16                     | 0.46              |
| 1:A:30:U:H2'  | 1:A:31:U:H3'  | 1.98                     | 0.46              |
| 1:A:76:G:H2'  | 1:A:77:A:O4'  | 2.16                     | 0.46              |
| 1:A:112:C:H2' | 1:A:113:G:H5' | 1.98                     | 0.46              |
| 1:A:76:G:H2'  | 1:A:77:A:O4'  | 2.16                     | 0.46              |
| 1:A:76:G:H2'  | 1:A:77:A:O4'  | 2.16                     | 0.46              |
| 1:A:85:G:H2'  | 1:A:86:A:C8   | 2.51                     | 0.46              |
| 1:A:76:G:H2'  | 1:A:77:A:O4'  | 2.16                     | 0.46              |
| 1:A:76:G:H2'  | 1:A:77:A:O4'  | 2.16                     | 0.46              |
| 1:A:5:A:C2    | 1:A:23:C:C5   | 3.04                     | 0.46              |
| 1:A:76:G:H2'  | 1:A:77:A:O4'  | 2.16                     | 0.46              |
| 1:A:76:G:H2'  | 1:A:77:A:O4'  | 2.16                     | 0.46              |
| 1:A:19:C:H6   | 1:A:19:C:P    | 2.38                     | 0.46              |
| 1:A:85:G:H2'  | 1:A:86:A:C8   | 2.51                     | 0.46              |
| 1:A:76:G:H2'  | 1:A:77:A:O4'  | 2.16                     | 0.46              |
| 1:A:76:G:H2'  | 1:A:77:A:O4'  | 2.16                     | 0.46              |
| 1:A:76:G:H2'  | 1:A:77:A:O4'  | 2.16                     | 0.46              |
| 1:A:55:C:H2'  | 1:A:56:G:O4'  | 2.16                     | 0.46              |
| 1:A:55:C:H2'  | 1:A:56:G:O4'  | 2.16                     | 0.46              |
| 1:A:59:G:N3   | 1:A:111:G:N2  | 2.64                     | 0.46              |
| 1:A:76:G:H2'  | 1:A:77:A:O4'  | 2.16                     | 0.46              |
| 1:A:73:G:N3   | 1:A:73:G:C3'  | 2.79                     | 0.46              |
| 1:A:76:G:H2'  | 1:A:77:A:O4'  | 2.16                     | 0.46              |
| 1:A:55:C:H2'  | 1:A:56:G:O4'  | 2.16                     | 0.46              |
| 1:A:76:G:H2'  | 1:A:77:A:O4'  | 2.16                     | 0.46              |
| 1:A:55:C:H2'  | 1:A:56:G:O4'  | 2.16                     | 0.46              |
| 1:A:76:G:H2'  | 1:A:77:A:O4'  | 2.16                     | 0.46              |
| 1:A:76:G:H2'  | 1:A:77:A:O4'  | 2.16                     | 0.46              |
| 1:A:80:A:H4'  | 1:A:81:G:OP2  | 2.14                     | 0.46              |
| 1:A:76:G:H2'  | 1:A:77:A:O4'  | 2.16                     | 0.46              |
| 1:A:55:C:H2'  | 1:A:56:G:O4'  | 2.16                     | 0.46              |
| 1:A:7:G:N2    | 1:A:65:C:O2   | 2.48                     | 0.46              |
| 1:A:76:G:H2'  | 1:A:77:A:O4'  | 2.16                     | 0.46              |
| 1:A:5:A:OP2   | 1:A:5:A:C8    | 2.69                     | 0.46              |
| 1:A:55:C:H2'  | 1:A:56:G:O4'  | 2.16                     | 0.46              |
| 1:A:37:C:O2'  | 1:A:38:C:O5'  | 2.33                     | 0.46              |
| 1:A:55:C:H2'  | 1:A:56:G:O4'  | 2.16                     | 0.46              |
| 1:A:58:U:O2'  | 1:A:111:G:N2  | 2.49                     | 0.46              |

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| Atom-1        | Atom-2       | Interatomic distance (Å) | Clash overlap (Å) |
|---------------|--------------|--------------------------|-------------------|
| 1:A:76:G:OP2  | 1:A:76:G:C8  | 2.69                     | 0.46              |
| 1:A:55:C:H2'  | 1:A:56:G:O4' | 2.16                     | 0.46              |
| 1:A:55:C:H2'  | 1:A:56:G:O4' | 2.16                     | 0.46              |
| 1:A:59:G:OP2  | 1:A:59:G:C8  | 2.62                     | 0.46              |
| 1:A:76:G:H2'  | 1:A:77:A:O4' | 2.16                     | 0.46              |
| 1:A:55:C:H2'  | 1:A:56:G:O4' | 2.16                     | 0.46              |
| 1:A:55:C:H2'  | 1:A:56:G:O4' | 2.16                     | 0.46              |
| 1:A:76:G:H2'  | 1:A:77:A:O4' | 2.16                     | 0.46              |
| 1:A:55:C:H2'  | 1:A:56:G:O4' | 2.16                     | 0.46              |
| 1:A:20:A:O4'  | 1:A:20:A:P   | 2.73                     | 0.46              |
| 1:A:55:C:H2'  | 1:A:56:G:O4' | 2.16                     | 0.46              |
| 1:A:47:U:O2   | 1:A:47:U:H2' | 2.14                     | 0.46              |
| 1:A:55:C:H2'  | 1:A:56:G:O4' | 2.16                     | 0.46              |
| 1:A:55:C:H2'  | 1:A:56:G:O4' | 2.16                     | 0.46              |
| 1:A:76:G:H2'  | 1:A:77:A:O4' | 2.16                     | 0.46              |
| 1:A:103:C:H2' | 1:A:104:G:C8 | 2.51                     | 0.46              |
| 1:A:23:C:O2   | 1:A:25:C:C5  | 2.69                     | 0.46              |
| 1:A:55:C:H2'  | 1:A:56:G:O4' | 2.16                     | 0.46              |
| 1:A:55:C:H2'  | 1:A:56:G:O4' | 2.16                     | 0.46              |
| 1:A:55:C:H2'  | 1:A:56:G:O4' | 2.16                     | 0.46              |
| 1:A:55:C:H2'  | 1:A:56:G:O4' | 2.16                     | 0.46              |
| 1:A:49:C:H3'  | 1:A:50:A:H5' | 1.98                     | 0.46              |
| 1:A:49:C:OP1  | 1:A:50:A:O4' | 2.34                     | 0.45              |
| 1:A:95:G:H4'  | 1:A:96:A:C8  | 2.51                     | 0.45              |
| 1:A:75:U:OP1  | 1:A:75:U:C6  | 2.69                     | 0.45              |
| 1:A:55:C:H2'  | 1:A:56:G:O4' | 2.16                     | 0.45              |
| 1:A:48:C:OP2  | 1:A:48:C:H6  | 1.98                     | 0.45              |
| 1:A:75:U:O2'  | 1:A:76:G:OP2 | 2.31                     | 0.45              |
| 1:A:103:C:H2' | 1:A:104:G:C8 | 2.51                     | 0.45              |
| 1:A:19:C:OP2  | 1:A:19:C:C6  | 2.70                     | 0.45              |
| 1:A:50:A:HO2' | 1:A:51:A:C5' | 2.28                     | 0.45              |
| 1:A:20:A:OP1  | 1:A:20:A:C8  | 2.64                     | 0.45              |
| 1:A:30:U:H2'  | 1:A:31:U:C3' | 2.47                     | 0.45              |
| 1:A:24:C:H3'  | 1:A:24:C:P   | 2.56                     | 0.45              |
| 1:A:52:C:O4'  | 1:A:52:C:OP1 | 2.33                     | 0.45              |
| 1:A:86:A:H2'  | 1:A:87:G:O5' | 2.16                     | 0.45              |
| 1:A:103:C:H2' | 1:A:104:G:C8 | 2.52                     | 0.45              |
| 1:A:97:C:H6   | 1:A:97:C:O5' | 1.99                     | 0.45              |
| 1:A:48:C:H1'  | 1:A:111:G:C6 | 2.51                     | 0.45              |
| 1:A:58:U:O2'  | 1:A:111:G:N2 | 2.50                     | 0.45              |
| 1:A:59:G:H2'  | 1:A:60:G:C8  | 2.51                     | 0.45              |

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| Atom-1        | Atom-2        | Interatomic distance (Å) | Clash overlap (Å) |
|---------------|---------------|--------------------------|-------------------|
| 1:A:103:C:H2' | 1:A:104:G:C8  | 2.51                     | 0.45              |
| 1:A:103:C:H2' | 1:A:104:G:C8  | 2.51                     | 0.45              |
| 1:A:96:A:O5'  | 1:A:96:A:C8   | 2.69                     | 0.45              |
| 1:A:85:G:H2'  | 1:A:86:A:C8   | 2.52                     | 0.45              |
| 1:A:58:U:O2'  | 1:A:59:G:OP2  | 2.30                     | 0.45              |
| 1:A:30:U:H2'  | 1:A:31:U:H3'  | 1.98                     | 0.45              |
| 1:A:47:U:H4'  | 1:A:47:U:OP1  | 2.16                     | 0.45              |
| 1:A:94:U:O2   | 1:A:97:C:N4   | 2.49                     | 0.45              |
| 1:A:51:A:HO2' | 1:A:52:C:P    | 2.37                     | 0.45              |
| 1:A:51:A:H2'  | 1:A:52:C:O5'  | 2.15                     | 0.45              |
| 1:A:103:C:H2' | 1:A:104:G:C8  | 2.51                     | 0.45              |
| 1:A:50:A:C2'  | 1:A:51:A:OP2  | 2.63                     | 0.45              |
| 1:A:103:C:H2' | 1:A:104:G:C8  | 2.51                     | 0.45              |
| 1:A:80:A:H4'  | 1:A:81:G:O4'  | 2.16                     | 0.45              |
| 1:A:58:U:O4'  | 1:A:111:G:O6  | 2.35                     | 0.45              |
| 1:A:42:A:H8   | 1:A:42:A:O5'  | 2.00                     | 0.45              |
| 1:A:45:C:O2'  | 1:A:82:G:OP2  | 2.30                     | 0.45              |
| 1:A:30:U:H2'  | 1:A:31:U:H3'  | 1.99                     | 0.45              |
| 1:A:75:U:H3'  | 1:A:76:G:C8   | 2.52                     | 0.45              |
| 1:A:74:A:H8   | 1:A:74:A:P    | 2.40                     | 0.45              |
| 1:A:111:G:H2' | 1:A:112:C:C5  | 2.52                     | 0.45              |
| 1:A:113:G:H8  | 1:A:113:G:OP2 | 2.00                     | 0.45              |
| 1:A:19:C:OP2  | 1:A:19:C:C6   | 2.70                     | 0.45              |
| 1:A:103:C:H2' | 1:A:104:G:C8  | 2.51                     | 0.45              |
| 1:A:32:G:C8   | 1:A:32:G:OP1  | 2.63                     | 0.45              |
| 1:A:85:G:H2'  | 1:A:86:A:C8   | 2.52                     | 0.45              |
| 1:A:30:U:H2'  | 1:A:31:U:H3'  | 1.97                     | 0.45              |
| 1:A:31:U:O3'  | 1:A:32:G:H8   | 1.99                     | 0.45              |
| 1:A:17:G:H2'  | 1:A:18:U:C6   | 2.52                     | 0.45              |
| 1:A:49:C:H3'  | 1:A:50:A:C5'  | 2.47                     | 0.45              |
| 1:A:8:A:O5'   | 1:A:8:A:C8    | 2.70                     | 0.45              |
| 1:A:47:U:H2'  | 1:A:48:C:H5'' | 1.97                     | 0.45              |
| 1:A:48:C:H1'  | 1:A:111:G:N1  | 2.32                     | 0.45              |
| 1:A:57:G:H1'  | 1:A:112:C:H42 | 1.81                     | 0.45              |
| 1:A:81:G:H2'  | 1:A:81:G:N3   | 2.31                     | 0.45              |
| 1:A:103:C:H2' | 1:A:104:G:C8  | 2.52                     | 0.45              |
| 1:A:103:C:H2' | 1:A:104:G:C8  | 2.52                     | 0.44              |
| 1:A:74:A:N3   | 1:A:74:A:O5'  | 2.50                     | 0.44              |
| 1:A:20:A:H2'  | 1:A:21:A:O4'  | 2.16                     | 0.44              |
| 1:A:19:C:H3'  | 1:A:20:A:H5'  | 1.98                     | 0.44              |
| 1:A:93:G:N2   | 1:A:95:G:O6   | 2.50                     | 0.44              |

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| Atom-1        | Atom-2        | Interatomic distance (Å) | Clash overlap (Å) |
|---------------|---------------|--------------------------|-------------------|
| 1:A:85:G:H2'  | 1:A:86:A:C8   | 2.52                     | 0.44              |
| 1:A:31:U:O3'  | 1:A:32:G:H8   | 1.99                     | 0.44              |
| 1:A:20:A:H2'  | 1:A:21:A:O4'  | 2.17                     | 0.44              |
| 1:A:72:U:H2'  | 1:A:73:G:O4'  | 2.17                     | 0.44              |
| 1:A:9:G:H2'   | 1:A:10:U:H4'  | 2.00                     | 0.44              |
| 1:A:117:G:C6  | 1:A:118:U:C2  | 3.05                     | 0.44              |
| 1:A:32:G:OP2  | 1:A:32:G:N7   | 2.37                     | 0.44              |
| 1:A:10:U:O2'  | 1:A:11:G:P    | 2.66                     | 0.44              |
| 1:A:49:C:OP1  | 1:A:50:A:O4'  | 2.35                     | 0.44              |
| 1:A:85:G:H2'  | 1:A:86:A:C8   | 2.52                     | 0.44              |
| 1:A:73:G:H2'  | 1:A:74:A:O4'  | 2.17                     | 0.44              |
| 1:A:103:C:H2' | 1:A:104:G:C8  | 2.52                     | 0.44              |
| 1:A:51:A:OP1  | 1:A:51:A:H8   | 2.01                     | 0.44              |
| 1:A:4:C:H2'   | 1:A:5:A:H5''  | 1.99                     | 0.44              |
| 1:A:47:U:O4   | 1:A:60:G:N2   | 2.51                     | 0.44              |
| 1:A:95:G:H8   | 1:A:95:G:P    | 2.41                     | 0.44              |
| 1:A:30:U:H2'  | 1:A:31:U:OP2  | 2.17                     | 0.44              |
| 1:A:32:G:OP1  | 1:A:32:G:C3'  | 2.64                     | 0.44              |
| 1:A:95:G:O2'  | 1:A:96:A:P    | 2.75                     | 0.44              |
| 1:A:117:G:C2  | 1:A:118:U:C2  | 3.06                     | 0.44              |
| 1:A:72:U:H2'  | 1:A:73:G:O4'  | 2.18                     | 0.44              |
| 1:A:30:U:H2'  | 1:A:32:G:OP2  | 2.18                     | 0.44              |
| 1:A:57:G:H1'  | 1:A:112:C:H42 | 1.82                     | 0.44              |
| 1:A:17:G:N2   | 1:A:31:U:O2   | 2.51                     | 0.44              |
| 1:A:30:U:H3'  | 1:A:31:U:H5'' | 2.00                     | 0.44              |
| 1:A:103:C:H2' | 1:A:104:G:C8  | 2.52                     | 0.44              |
| 1:A:48:C:O2   | 1:A:111:G:O6  | 2.36                     | 0.44              |
| 1:A:18:U:O2'  | 1:A:19:C:OP2  | 2.35                     | 0.44              |
| 1:A:23:C:HO2' | 1:A:24:C:C5'  | 2.30                     | 0.44              |
| 1:A:31:U:O2'  | 1:A:32:G:N7   | 2.47                     | 0.44              |
| 1:A:103:C:H2' | 1:A:104:G:C8  | 2.53                     | 0.44              |
| 1:A:103:C:H2' | 1:A:104:G:C8  | 2.53                     | 0.44              |
| 1:A:37:C:H2'  | 1:A:38:C:O4'  | 2.18                     | 0.44              |
| 1:A:117:G:C2  | 1:A:118:U:H1' | 2.53                     | 0.44              |
| 1:A:4:C:H2'   | 1:A:5:A:H5''  | 1.99                     | 0.43              |
| 1:A:24:C:H3'  | 1:A:24:C:OP2  | 2.18                     | 0.43              |
| 1:A:48:C:H1'  | 1:A:111:G:C5  | 2.53                     | 0.43              |
| 1:A:43:A:H8   | 1:A:43:A:P    | 2.41                     | 0.43              |
| 1:A:8:A:C2    | 1:A:66:C:O4'  | 2.71                     | 0.43              |
| 1:A:37:C:H2'  | 1:A:38:C:O4'  | 2.18                     | 0.43              |
| 1:A:74:A:HO2' | 1:A:75:U:P    | 2.35                     | 0.43              |

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| Atom-1        | Atom-2        | Interatomic distance (Å) | Clash overlap (Å) |
|---------------|---------------|--------------------------|-------------------|
| 1:A:74:A:O4'  | 1:A:74:A:P    | 2.75                     | 0.43              |
| 1:A:8:A:N3    | 1:A:40:G:N2   | 2.65                     | 0.43              |
| 1:A:103:C:H2' | 1:A:104:G:C8  | 2.53                     | 0.43              |
| 1:A:31:U:O3'  | 1:A:32:G:H8   | 2.00                     | 0.43              |
| 1:A:31:U:O2'  | 1:A:32:G:C8   | 2.71                     | 0.43              |
| 1:A:19:C:O4'  | 1:A:19:C:P    | 2.75                     | 0.43              |
| 1:A:23:C:O2   | 1:A:25:C:C5   | 2.71                     | 0.43              |
| 1:A:30:U:H2'  | 1:A:31:U:OP2  | 2.18                     | 0.43              |
| 1:A:103:C:H2' | 1:A:104:G:C8  | 2.53                     | 0.43              |
| 1:A:19:C:HO2' | 1:A:20:A:P    | 2.40                     | 0.43              |
| 1:A:46:C:H2'  | 1:A:47:U:O4'  | 2.18                     | 0.43              |
| 1:A:30:U:C2'  | 1:A:31:U:H3'  | 2.49                     | 0.43              |
| 1:A:47:U:O2   | 1:A:59:G:N1   | 2.51                     | 0.43              |
| 1:A:30:U:C2'  | 1:A:32:G:OP1  | 2.66                     | 0.43              |
| 1:A:5:A:H8    | 1:A:5:A:O5'   | 2.01                     | 0.43              |
| 1:A:72:U:H6   | 1:A:72:U:O5'  | 2.01                     | 0.43              |
| 1:A:82:G:OP1  | 1:A:82:G:H8   | 2.01                     | 0.43              |
| 1:A:72:U:N3   | 1:A:73:G:N7   | 2.66                     | 0.43              |
| 1:A:95:G:OP1  | 1:A:95:G:C1'  | 2.63                     | 0.43              |
| 1:A:18:U:H3'  | 1:A:19:C:C5'  | 2.48                     | 0.43              |
| 1:A:5:A:OP2   | 1:A:74:A:N6   | 2.51                     | 0.43              |
| 1:A:46:C:H2'  | 1:A:47:U:C6   | 2.54                     | 0.43              |
| 1:A:8:A:N3    | 1:A:41:C:O2'  | 2.47                     | 0.43              |
| 1:A:6:U:H6    | 1:A:6:U:P     | 2.42                     | 0.43              |
| 1:A:109:A:C6  | 1:A:110:A:N6  | 2.87                     | 0.43              |
| 1:A:92:C:H2'  | 1:A:93:G:C8   | 2.54                     | 0.43              |
| 1:A:86:A:C2'  | 1:A:87:G:O5'  | 2.67                     | 0.43              |
| 1:A:85:G:H2'  | 1:A:86:A:C8   | 2.54                     | 0.43              |
| 1:A:94:U:H2'  | 1:A:95:G:O4'  | 2.19                     | 0.43              |
| 1:A:57:G:H1'  | 1:A:112:C:H42 | 1.84                     | 0.43              |
| 1:A:7:G:H2'   | 1:A:7:G:N3    | 2.33                     | 0.43              |
| 1:A:75:U:O5'  | 1:A:75:U:O2   | 2.36                     | 0.43              |
| 1:A:103:C:H2' | 1:A:104:G:C8  | 2.54                     | 0.43              |
| 1:A:19:C:OP1  | 1:A:19:C:H6   | 2.02                     | 0.43              |
| 1:A:23:C:O2'  | 1:A:24:C:C5   | 2.72                     | 0.43              |
| 1:A:31:U:O2'  | 1:A:32:G:P    | 2.77                     | 0.43              |
| 1:A:97:C:H2'  | 1:A:98:G:O4'  | 2.19                     | 0.42              |
| 1:A:30:U:HO2' | 1:A:31:U:P    | 2.38                     | 0.42              |
| 1:A:23:C:O2   | 1:A:25:C:C5   | 2.72                     | 0.42              |
| 1:A:74:A:O2'  | 1:A:75:U:P    | 2.77                     | 0.42              |
| 1:A:7:G:N2    | 1:A:64:G:N3   | 2.67                     | 0.42              |

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| Atom-1        | Atom-2         | Interatomic distance (Å) | Clash overlap (Å) |
|---------------|----------------|--------------------------|-------------------|
| 1:A:17:G:N2   | 1:A:31:U:O2    | 2.53                     | 0.42              |
| 1:A:30:U:H3'  | 1:A:31:U:H5''  | 2.00                     | 0.42              |
| 1:A:92:C:H2'  | 1:A:93:G:C8    | 2.54                     | 0.42              |
| 1:A:9:G:O2'   | 1:A:10:U:H4'   | 2.19                     | 0.42              |
| 1:A:97:C:H2'  | 1:A:98:G:H5'   | 2.02                     | 0.42              |
| 1:A:96:A:H8   | 1:A:96:A:O5'   | 2.02                     | 0.42              |
| 1:A:18:U:O2'  | 1:A:19:C:P     | 2.77                     | 0.42              |
| 1:A:93:G:H2'  | 1:A:94:U:O4'   | 2.20                     | 0.42              |
| 1:A:48:C:H1'  | 1:A:111:G:N1   | 2.35                     | 0.42              |
| 1:A:97:C:H2'  | 1:A:98:G:O4'   | 2.19                     | 0.42              |
| 1:A:47:U:H2'  | 1:A:48:C:C5'   | 2.49                     | 0.42              |
| 1:A:58:U:O2   | 1:A:111:G:N1   | 2.47                     | 0.42              |
| 1:A:74:A:H5'' | 1:A:76:G:O6    | 2.19                     | 0.42              |
| 1:A:85:G:H2'  | 1:A:86:A:C8    | 2.55                     | 0.42              |
| 1:A:93:G:H2'  | 1:A:94:U:O4'   | 2.19                     | 0.42              |
| 1:A:109:A:N3  | 1:A:110:A:N6   | 2.68                     | 0.42              |
| 1:A:45:C:O2'  | 1:A:82:G:OP1   | 2.38                     | 0.42              |
| 1:A:58:U:H4'  | 1:A:58:U:OP1   | 2.19                     | 0.42              |
| 1:A:59:G:H8   | 1:A:59:G:P     | 2.43                     | 0.42              |
| 1:A:71:G:C2   | 1:A:72:U:H1'   | 2.54                     | 0.42              |
| 1:A:111:G:OP2 | 1:A:111:G:H8   | 2.02                     | 0.42              |
| 1:A:43:A:N6   | 1:A:63:U:O2    | 2.50                     | 0.42              |
| 1:A:10:U:N3   | 1:A:32:G:OP2   | 2.52                     | 0.42              |
| 1:A:73:G:O2'  | 1:A:74:A:C8    | 2.73                     | 0.42              |
| 1:A:103:C:H2' | 1:A:104:G:C8   | 2.55                     | 0.42              |
| 1:A:117:G:H2' | 1:A:118:U:O4'  | 2.20                     | 0.42              |
| 1:A:19:C:H4'  | 1:A:20:A:OP2   | 2.18                     | 0.42              |
| 1:A:49:C:O2'  | 1:A:112:C:H5'' | 2.20                     | 0.42              |
| 1:A:30:U:O2'  | 1:A:31:U:H3'   | 2.19                     | 0.42              |
| 1:A:92:C:H2'  | 1:A:93:G:O4'   | 2.19                     | 0.42              |
| 1:A:59:G:H2'  | 1:A:60:G:H8    | 1.83                     | 0.42              |
| 1:A:103:C:H2' | 1:A:104:G:C8   | 2.55                     | 0.42              |
| 1:A:22:G:H5'' | 1:A:23:C:OP1   | 2.20                     | 0.42              |
| 1:A:30:U:HO2' | 1:A:31:U:P     | 2.43                     | 0.42              |
| 1:A:73:G:H2'  | 1:A:74:A:OP2   | 2.20                     | 0.42              |
| 1:A:96:A:O5'  | 1:A:96:A:C8    | 2.71                     | 0.42              |
| 1:A:47:U:H4'  | 1:A:110:A:C6   | 2.54                     | 0.42              |
| 1:A:116:G:H2' | 1:A:117:G:O4'  | 2.20                     | 0.42              |
| 1:A:51:A:O2'  | 1:A:52:C:P     | 2.77                     | 0.42              |
| 1:A:49:C:H4'  | 1:A:112:C:OP2  | 2.19                     | 0.42              |
| 1:A:60:G:N2   | 1:A:110:A:N7   | 2.61                     | 0.42              |

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| Atom-1        | Atom-2        | Interatomic distance (Å) | Clash overlap (Å) |
|---------------|---------------|--------------------------|-------------------|
| 1:A:7:G:O6    | 1:A:64:G:N2   | 2.53                     | 0.42              |
| 1:A:64:G:H4'  | 1:A:78:C:O3'  | 2.19                     | 0.42              |
| 1:A:31:U:O3'  | 1:A:32:G:C8   | 2.72                     | 0.42              |
| 1:A:109:A:H2' | 1:A:110:A:C8  | 2.55                     | 0.42              |
| 1:A:97:C:H6   | 1:A:97:C:O5'  | 2.03                     | 0.42              |
| 1:A:16:C:H2'  | 1:A:17:G:O4'  | 2.20                     | 0.42              |
| 1:A:64:G:H4'  | 1:A:78:C:O3'  | 2.19                     | 0.42              |
| 1:A:20:A:H8   | 1:A:20:A:OP2  | 2.03                     | 0.42              |
| 1:A:64:G:H4'  | 1:A:78:C:O3'  | 2.19                     | 0.42              |
| 1:A:64:G:H4'  | 1:A:78:C:O3'  | 2.19                     | 0.42              |
| 1:A:64:G:H4'  | 1:A:78:C:O3'  | 2.19                     | 0.41              |
| 1:A:64:G:H4'  | 1:A:78:C:O3'  | 2.19                     | 0.41              |
| 1:A:64:G:H4'  | 1:A:78:C:O3'  | 2.19                     | 0.41              |
| 1:A:64:G:H4'  | 1:A:78:C:O3'  | 2.19                     | 0.41              |
| 1:A:64:G:H4'  | 1:A:78:C:O3'  | 2.19                     | 0.41              |
| 1:A:64:G:H4'  | 1:A:78:C:O3'  | 2.19                     | 0.41              |
| 1:A:64:G:H4'  | 1:A:78:C:O3'  | 2.19                     | 0.41              |
| 1:A:81:G:O2'  | 1:A:82:G:P    | 2.78                     | 0.41              |
| 1:A:64:G:H4'  | 1:A:78:C:O3'  | 2.19                     | 0.41              |
| 1:A:64:G:H4'  | 1:A:78:C:O3'  | 2.19                     | 0.41              |
| 1:A:110:A:H8  | 1:A:110:A:O5' | 2.03                     | 0.41              |
| 1:A:64:G:H4'  | 1:A:78:C:O3'  | 2.19                     | 0.41              |
| 1:A:64:G:H4'  | 1:A:78:C:O3'  | 2.19                     | 0.41              |
| 1:A:64:G:H4'  | 1:A:78:C:O3'  | 2.19                     | 0.41              |
| 1:A:20:A:HO2' | 1:A:21:A:P    | 2.27                     | 0.41              |
| 1:A:64:G:H4'  | 1:A:78:C:O3'  | 2.19                     | 0.41              |
| 1:A:64:G:H4'  | 1:A:78:C:O3'  | 2.19                     | 0.41              |
| 1:A:117:G:H2' | 1:A:118:U:O4' | 2.20                     | 0.41              |
| 1:A:59:G:H2'  | 1:A:60:G:C8   | 2.55                     | 0.41              |
| 1:A:116:G:H2' | 1:A:117:G:O4' | 2.20                     | 0.41              |
| 1:A:64:G:H4'  | 1:A:78:C:O3'  | 2.19                     | 0.41              |
| 1:A:47:U:OP1  | 1:A:47:U:O4'  | 2.37                     | 0.41              |
| 1:A:31:U:O2   | 1:A:31:U:H2'  | 2.19                     | 0.41              |
| 1:A:38:C:H2'  | 1:A:39:G:O4'  | 2.20                     | 0.41              |
| 1:A:95:G:H2'  | 1:A:96:A:O4'  | 2.21                     | 0.41              |
| 1:A:50:A:O2'  | 1:A:51:A:OP2  | 2.33                     | 0.41              |
| 1:A:20:A:H2'  | 1:A:21:A:O4'  | 2.20                     | 0.41              |
| 1:A:30:U:O2'  | 1:A:31:U:C2'  | 2.69                     | 0.41              |
| 1:A:19:C:H2'  | 1:A:20:A:C8   | 2.56                     | 0.41              |
| 1:A:80:A:H5'' | 1:A:81:G:OP2  | 2.21                     | 0.41              |

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| Atom-1        | Atom-2        | Interatomic distance (Å) | Clash overlap (Å) |
|---------------|---------------|--------------------------|-------------------|
| 1:A:30:U:H4'  | 1:A:31:U:OP1  | 2.21                     | 0.41              |
| 1:A:117:G:H2' | 1:A:118:U:O4' | 2.20                     | 0.41              |
| 1:A:58:U:H2'  | 1:A:59:G:OP2  | 2.20                     | 0.41              |
| 1:A:116:G:H2' | 1:A:117:G:O4' | 2.20                     | 0.41              |
| 1:A:19:C:H1'  | 1:A:20:A:C8   | 2.56                     | 0.41              |
| 1:A:74:A:C2   | 1:A:76:G:C2   | 3.09                     | 0.41              |
| 1:A:92:C:H2'  | 1:A:93:G:C8   | 2.56                     | 0.41              |
| 1:A:50:A:O2'  | 1:A:51:A:O5'  | 2.33                     | 0.41              |
| 1:A:31:U:HO2' | 1:A:32:G:P    | 2.44                     | 0.41              |
| 1:A:80:A:O4'  | 1:A:80:A:P    | 2.72                     | 0.41              |
| 1:A:30:U:H2'  | 1:A:31:U:H5'' | 2.02                     | 0.41              |
| 1:A:1:G:O6    | 1:A:80:A:N6   | 2.52                     | 0.41              |
| 1:A:96:A:O5'  | 1:A:96:A:C8   | 2.66                     | 0.41              |
| 1:A:79:C:H2'  | 1:A:80:A:O5'  | 2.20                     | 0.41              |
| 1:A:19:C:OP2  | 1:A:19:C:H6   | 2.04                     | 0.41              |
| 1:A:18:U:H6   | 1:A:18:U:O5'  | 2.03                     | 0.41              |
| 1:A:17:G:C2   | 1:A:31:U:O2   | 2.74                     | 0.41              |
| 1:A:30:U:O2'  | 1:A:31:U:P    | 2.78                     | 0.41              |
| 1:A:30:U:H2'  | 1:A:31:U:C5'  | 2.51                     | 0.41              |
| 1:A:32:G:H8   | 1:A:32:G:P    | 2.43                     | 0.41              |
| 1:A:4:C:H4'   | 1:A:5:A:OP1   | 2.20                     | 0.41              |
| 1:A:19:C:H4'  | 1:A:20:A:O5'  | 2.21                     | 0.41              |
| 1:A:95:G:N3   | 1:A:95:G:C2'  | 2.84                     | 0.41              |
| 1:A:51:A:H2'  | 1:A:52:C:O5'  | 2.21                     | 0.41              |
| 1:A:38:C:H2'  | 1:A:39:G:O4'  | 2.21                     | 0.41              |
| 1:A:86:A:C2'  | 1:A:87:G:H5'  | 2.50                     | 0.41              |
| 1:A:87:G:C6   | 1:A:88:U:C4   | 3.09                     | 0.41              |
| 1:A:19:C:H4'  | 1:A:20:A:O5'  | 2.19                     | 0.41              |
| 1:A:87:G:C6   | 1:A:88:U:C4   | 3.09                     | 0.41              |
| 1:A:18:U:HO2' | 1:A:19:C:P    | 2.39                     | 0.41              |
| 1:A:87:G:C6   | 1:A:88:U:C4   | 3.09                     | 0.41              |
| 1:A:31:U:C1'  | 1:A:32:G:N7   | 2.81                     | 0.41              |
| 1:A:87:G:C6   | 1:A:88:U:C4   | 3.09                     | 0.41              |
| 1:A:111:G:C5  | 1:A:112:C:C4  | 3.09                     | 0.41              |
| 1:A:87:G:C6   | 1:A:88:U:C4   | 3.09                     | 0.41              |
| 1:A:71:G:C6   | 1:A:72:U:C2   | 3.09                     | 0.41              |
| 1:A:87:G:C6   | 1:A:88:U:C4   | 3.09                     | 0.41              |
| 1:A:87:G:C6   | 1:A:88:U:C4   | 3.10                     | 0.40              |
| 1:A:87:G:C6   | 1:A:88:U:C4   | 3.10                     | 0.40              |
| 1:A:87:G:C6   | 1:A:88:U:C4   | 3.09                     | 0.40              |
| 1:A:87:G:C6   | 1:A:88:U:C4   | 3.10                     | 0.40              |

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| Atom-1        | Atom-2        | Interatomic distance (Å) | Clash overlap (Å) |
|---------------|---------------|--------------------------|-------------------|
| 1:A:87:G:C6   | 1:A:88:U:C4   | 3.09                     | 0.40              |
| 1:A:87:G:C6   | 1:A:88:U:C4   | 3.10                     | 0.40              |
| 1:A:9:G:C4    | 1:A:39:G:N2   | 2.89                     | 0.40              |
| 1:A:87:G:C6   | 1:A:88:U:C4   | 3.10                     | 0.40              |
| 1:A:87:G:C6   | 1:A:88:U:C4   | 3.10                     | 0.40              |
| 1:A:31:U:HO2' | 1:A:32:G:P    | 2.43                     | 0.40              |
| 1:A:87:G:C6   | 1:A:88:U:C4   | 3.09                     | 0.40              |
| 1:A:87:G:C6   | 1:A:88:U:C4   | 3.10                     | 0.40              |
| 1:A:112:C:H2' | 1:A:113:G:H5' | 2.03                     | 0.40              |
| 1:A:112:C:H2' | 1:A:113:G:H5' | 2.03                     | 0.40              |
| 1:A:45:C:O2'  | 1:A:81:G:H2'  | 2.21                     | 0.40              |
| 1:A:49:C:H1'  | 1:A:112:C:C4  | 2.56                     | 0.40              |
| 1:A:87:G:C6   | 1:A:88:U:C4   | 3.09                     | 0.40              |
| 1:A:57:G:N2   | 1:A:112:C:N3  | 2.67                     | 0.40              |
| 1:A:87:G:C6   | 1:A:88:U:C4   | 3.10                     | 0.40              |
| 1:A:51:A:H2'  | 1:A:52:C:OP1  | 2.22                     | 0.40              |
| 1:A:87:G:C6   | 1:A:88:U:C4   | 3.09                     | 0.40              |
| 1:A:4:C:H2'   | 1:A:5:A:C5    | 2.56                     | 0.40              |
| 1:A:96:A:O2'  | 1:A:97:C:O4'  | 2.33                     | 0.40              |
| 1:A:109:A:C6  | 1:A:110:A:N1  | 2.89                     | 0.40              |
| 1:A:87:G:C6   | 1:A:88:U:C4   | 3.10                     | 0.40              |
| 1:A:80:A:H4'  | 1:A:81:G:C1'  | 2.51                     | 0.40              |
| 1:A:22:G:N2   | 1:A:67:C:N4   | 2.70                     | 0.40              |
| 1:A:22:G:N2   | 1:A:67:C:N4   | 2.70                     | 0.40              |
| 1:A:19:C:H6   | 1:A:19:C:O5'  | 2.05                     | 0.40              |
| 1:A:22:G:N2   | 1:A:67:C:N4   | 2.70                     | 0.40              |
| 1:A:30:U:H2'  | 1:A:31:U:OP2  | 2.21                     | 0.40              |
| 1:A:8:A:H8    | 1:A:8:A:P     | 2.45                     | 0.40              |
| 1:A:22:G:N2   | 1:A:67:C:N4   | 2.70                     | 0.40              |
| 1:A:116:G:H2' | 1:A:117:G:C8  | 2.56                     | 0.40              |
| 1:A:22:G:N2   | 1:A:67:C:N4   | 2.70                     | 0.40              |
| 1:A:96:A:O5'  | 1:A:96:A:H8   | 2.04                     | 0.40              |
| 1:A:16:C:H2'  | 1:A:17:G:O4'  | 2.21                     | 0.40              |
| 1:A:22:G:N2   | 1:A:67:C:N4   | 2.70                     | 0.40              |
| 1:A:47:U:H6   | 1:A:47:U:O5'  | 2.04                     | 0.40              |
| 1:A:22:G:N2   | 1:A:67:C:N4   | 2.70                     | 0.40              |
| 1:A:22:G:N2   | 1:A:67:C:N4   | 2.70                     | 0.40              |
| 1:A:16:C:H2'  | 1:A:17:G:C8   | 2.57                     | 0.40              |
| 1:A:22:G:N2   | 1:A:67:C:N4   | 2.70                     | 0.40              |
| 1:A:22:G:N2   | 1:A:67:C:N4   | 2.70                     | 0.40              |
| 1:A:22:G:N2   | 1:A:67:C:N4   | 2.70                     | 0.40              |

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| Atom-1       | Atom-2       | Interatomic distance (Å) | Clash overlap (Å) |
|--------------|--------------|--------------------------|-------------------|
| 1:A:5:A:O2'  | 1:A:6:U:P    | 2.78                     | 0.40              |
| 1:A:22:G:N2  | 1:A:67:C:N4  | 2.70                     | 0.40              |
| 1:A:22:G:N2  | 1:A:67:C:N4  | 2.70                     | 0.40              |
| 1:A:82:G:C2  | 1:A:109:A:C2 | 3.10                     | 0.40              |
| 1:A:22:G:N2  | 1:A:67:C:N4  | 2.70                     | 0.40              |
| 1:A:22:G:N2  | 1:A:67:C:N4  | 2.70                     | 0.40              |
| 1:A:22:G:N2  | 1:A:67:C:N4  | 2.70                     | 0.40              |
| 1:A:22:G:N2  | 1:A:67:C:N4  | 2.70                     | 0.40              |
| 1:A:95:G:H2' | 1:A:96:A:O4' | 2.22                     | 0.40              |
| 1:A:22:G:N2  | 1:A:67:C:N4  | 2.70                     | 0.40              |
| 1:A:22:G:N2  | 1:A:67:C:N4  | 2.70                     | 0.40              |
| 1:A:64:G:C6  | 1:A:65:C:N4  | 2.90                     | 0.40              |
| 1:A:22:G:N2  | 1:A:67:C:N4  | 2.70                     | 0.40              |
| 1:A:97:C:H2' | 1:A:98:G:C8  | 2.56                     | 0.40              |
| 1:A:8:A:P    | 1:A:8:A:C2'  | 3.06                     | 0.40              |

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

### 5.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

### 5.3.3 RNA [i](#)

| Mol | Chain | Analysed      | Backbone Outliers | Pucker Outliers |
|-----|-------|---------------|-------------------|-----------------|
| 1   | 1-A   | 118/119 (99%) | 29 (24%)          | 5 (4%)          |
| 1   | 10-A  | 118/119 (99%) | 29 (24%)          | 6 (5%)          |
| 1   | 11-A  | 118/119 (99%) | 29 (24%)          | 2 (1%)          |
| 1   | 12-A  | 118/119 (99%) | 29 (24%)          | 3 (2%)          |
| 1   | 13-A  | 118/119 (99%) | 29 (24%)          | 1 (0%)          |
| 1   | 14-A  | 118/119 (99%) | 29 (24%)          | 4 (3%)          |
| 1   | 15-A  | 118/119 (99%) | 29 (24%)          | 3 (2%)          |
| 1   | 16-A  | 118/119 (99%) | 29 (24%)          | 4 (3%)          |

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| Mol | Chain | Analysed        | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 1   | 17-A  | 118/119 (99%)   | 29 (24%)          | 1 (0%)          |
| 1   | 18-A  | 118/119 (99%)   | 29 (24%)          | 3 (2%)          |
| 1   | 19-A  | 118/119 (99%)   | 29 (24%)          | 3 (2%)          |
| 1   | 2-A   | 118/119 (99%)   | 29 (24%)          | 4 (3%)          |
| 1   | 20-A  | 118/119 (99%)   | 29 (24%)          | 3 (2%)          |
| 1   | 3-A   | 118/119 (99%)   | 29 (24%)          | 5 (4%)          |
| 1   | 4-A   | 118/119 (99%)   | 29 (24%)          | 2 (1%)          |
| 1   | 5-A   | 118/119 (99%)   | 29 (24%)          | 3 (2%)          |
| 1   | 6-A   | 118/119 (99%)   | 29 (24%)          | 1 (0%)          |
| 1   | 7-A   | 118/119 (99%)   | 29 (24%)          | 4 (3%)          |
| 1   | 8-A   | 118/119 (99%)   | 29 (24%)          | 4 (3%)          |
| 1   | 9-A   | 118/119 (99%)   | 29 (24%)          | 3 (2%)          |
| All | All   | 2360/2380 (99%) | 580 (24%)         | 64 (2%)         |

All (580) RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | 1-A   | 4   | C    |
| 1   | 1-A   | 5   | A    |
| 1   | 1-A   | 7   | G    |
| 1   | 1-A   | 8   | A    |
| 1   | 1-A   | 9   | G    |
| 1   | 1-A   | 10  | U    |
| 1   | 1-A   | 11  | G    |
| 1   | 1-A   | 20  | A    |
| 1   | 1-A   | 23  | C    |
| 1   | 1-A   | 24  | C    |
| 1   | 1-A   | 31  | U    |
| 1   | 1-A   | 32  | G    |
| 1   | 1-A   | 47  | U    |
| 1   | 1-A   | 48  | C    |
| 1   | 1-A   | 50  | A    |
| 1   | 1-A   | 51  | A    |
| 1   | 1-A   | 52  | C    |
| 1   | 1-A   | 59  | G    |
| 1   | 1-A   | 67  | C    |
| 1   | 1-A   | 74  | A    |
| 1   | 1-A   | 75  | U    |
| 1   | 1-A   | 78  | C    |
| 1   | 1-A   | 81  | G    |
| 1   | 1-A   | 82  | G    |
| 1   | 1-A   | 87  | G    |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | 1-A   | 97  | C    |
| 1   | 1-A   | 104 | G    |
| 1   | 1-A   | 111 | G    |
| 1   | 1-A   | 112 | C    |
| 1   | 2-A   | 4   | C    |
| 1   | 2-A   | 5   | A    |
| 1   | 2-A   | 7   | G    |
| 1   | 2-A   | 8   | A    |
| 1   | 2-A   | 9   | G    |
| 1   | 2-A   | 10  | U    |
| 1   | 2-A   | 11  | G    |
| 1   | 2-A   | 20  | A    |
| 1   | 2-A   | 23  | C    |
| 1   | 2-A   | 24  | C    |
| 1   | 2-A   | 31  | U    |
| 1   | 2-A   | 32  | G    |
| 1   | 2-A   | 47  | U    |
| 1   | 2-A   | 48  | C    |
| 1   | 2-A   | 50  | A    |
| 1   | 2-A   | 51  | A    |
| 1   | 2-A   | 52  | C    |
| 1   | 2-A   | 59  | G    |
| 1   | 2-A   | 67  | C    |
| 1   | 2-A   | 74  | A    |
| 1   | 2-A   | 75  | U    |
| 1   | 2-A   | 78  | C    |
| 1   | 2-A   | 81  | G    |
| 1   | 2-A   | 82  | G    |
| 1   | 2-A   | 87  | G    |
| 1   | 2-A   | 97  | C    |
| 1   | 2-A   | 104 | G    |
| 1   | 2-A   | 111 | G    |
| 1   | 2-A   | 112 | C    |
| 1   | 3-A   | 4   | C    |
| 1   | 3-A   | 5   | A    |
| 1   | 3-A   | 7   | G    |
| 1   | 3-A   | 8   | A    |
| 1   | 3-A   | 9   | G    |
| 1   | 3-A   | 10  | U    |
| 1   | 3-A   | 11  | G    |
| 1   | 3-A   | 20  | A    |
| 1   | 3-A   | 23  | C    |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | 3-A   | 24  | C    |
| 1   | 3-A   | 31  | U    |
| 1   | 3-A   | 32  | G    |
| 1   | 3-A   | 47  | U    |
| 1   | 3-A   | 48  | C    |
| 1   | 3-A   | 50  | A    |
| 1   | 3-A   | 51  | A    |
| 1   | 3-A   | 52  | C    |
| 1   | 3-A   | 59  | G    |
| 1   | 3-A   | 67  | C    |
| 1   | 3-A   | 74  | A    |
| 1   | 3-A   | 75  | U    |
| 1   | 3-A   | 78  | C    |
| 1   | 3-A   | 81  | G    |
| 1   | 3-A   | 82  | G    |
| 1   | 3-A   | 87  | G    |
| 1   | 3-A   | 97  | C    |
| 1   | 3-A   | 104 | G    |
| 1   | 3-A   | 111 | G    |
| 1   | 3-A   | 112 | C    |
| 1   | 4-A   | 4   | C    |
| 1   | 4-A   | 5   | A    |
| 1   | 4-A   | 7   | G    |
| 1   | 4-A   | 8   | A    |
| 1   | 4-A   | 9   | G    |
| 1   | 4-A   | 10  | U    |
| 1   | 4-A   | 11  | G    |
| 1   | 4-A   | 20  | A    |
| 1   | 4-A   | 23  | C    |
| 1   | 4-A   | 24  | C    |
| 1   | 4-A   | 31  | U    |
| 1   | 4-A   | 32  | G    |
| 1   | 4-A   | 47  | U    |
| 1   | 4-A   | 48  | C    |
| 1   | 4-A   | 50  | A    |
| 1   | 4-A   | 51  | A    |
| 1   | 4-A   | 52  | C    |
| 1   | 4-A   | 59  | G    |
| 1   | 4-A   | 67  | C    |
| 1   | 4-A   | 74  | A    |
| 1   | 4-A   | 75  | U    |
| 1   | 4-A   | 78  | C    |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | 4-A   | 81  | G    |
| 1   | 4-A   | 82  | G    |
| 1   | 4-A   | 87  | G    |
| 1   | 4-A   | 97  | C    |
| 1   | 4-A   | 104 | G    |
| 1   | 4-A   | 111 | G    |
| 1   | 4-A   | 112 | C    |
| 1   | 5-A   | 4   | C    |
| 1   | 5-A   | 5   | A    |
| 1   | 5-A   | 7   | G    |
| 1   | 5-A   | 8   | A    |
| 1   | 5-A   | 9   | G    |
| 1   | 5-A   | 10  | U    |
| 1   | 5-A   | 11  | G    |
| 1   | 5-A   | 20  | A    |
| 1   | 5-A   | 23  | C    |
| 1   | 5-A   | 24  | C    |
| 1   | 5-A   | 31  | U    |
| 1   | 5-A   | 32  | G    |
| 1   | 5-A   | 47  | U    |
| 1   | 5-A   | 48  | C    |
| 1   | 5-A   | 50  | A    |
| 1   | 5-A   | 51  | A    |
| 1   | 5-A   | 52  | C    |
| 1   | 5-A   | 59  | G    |
| 1   | 5-A   | 67  | C    |
| 1   | 5-A   | 74  | A    |
| 1   | 5-A   | 75  | U    |
| 1   | 5-A   | 78  | C    |
| 1   | 5-A   | 81  | G    |
| 1   | 5-A   | 82  | G    |
| 1   | 5-A   | 87  | G    |
| 1   | 5-A   | 97  | C    |
| 1   | 5-A   | 104 | G    |
| 1   | 5-A   | 111 | G    |
| 1   | 5-A   | 112 | C    |
| 1   | 6-A   | 4   | C    |
| 1   | 6-A   | 5   | A    |
| 1   | 6-A   | 7   | G    |
| 1   | 6-A   | 8   | A    |
| 1   | 6-A   | 9   | G    |
| 1   | 6-A   | 10  | U    |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | 6-A   | 11  | G    |
| 1   | 6-A   | 20  | A    |
| 1   | 6-A   | 23  | C    |
| 1   | 6-A   | 24  | C    |
| 1   | 6-A   | 31  | U    |
| 1   | 6-A   | 32  | G    |
| 1   | 6-A   | 47  | U    |
| 1   | 6-A   | 48  | C    |
| 1   | 6-A   | 50  | A    |
| 1   | 6-A   | 51  | A    |
| 1   | 6-A   | 52  | C    |
| 1   | 6-A   | 59  | G    |
| 1   | 6-A   | 67  | C    |
| 1   | 6-A   | 74  | A    |
| 1   | 6-A   | 75  | U    |
| 1   | 6-A   | 78  | C    |
| 1   | 6-A   | 81  | G    |
| 1   | 6-A   | 82  | G    |
| 1   | 6-A   | 87  | G    |
| 1   | 6-A   | 97  | C    |
| 1   | 6-A   | 104 | G    |
| 1   | 6-A   | 111 | G    |
| 1   | 6-A   | 112 | C    |
| 1   | 7-A   | 4   | C    |
| 1   | 7-A   | 5   | A    |
| 1   | 7-A   | 7   | G    |
| 1   | 7-A   | 8   | A    |
| 1   | 7-A   | 9   | G    |
| 1   | 7-A   | 10  | U    |
| 1   | 7-A   | 11  | G    |
| 1   | 7-A   | 20  | A    |
| 1   | 7-A   | 23  | C    |
| 1   | 7-A   | 24  | C    |
| 1   | 7-A   | 31  | U    |
| 1   | 7-A   | 32  | G    |
| 1   | 7-A   | 47  | U    |
| 1   | 7-A   | 48  | C    |
| 1   | 7-A   | 50  | A    |
| 1   | 7-A   | 51  | A    |
| 1   | 7-A   | 52  | C    |
| 1   | 7-A   | 59  | G    |
| 1   | 7-A   | 67  | C    |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | 7-A   | 74  | A    |
| 1   | 7-A   | 75  | U    |
| 1   | 7-A   | 78  | C    |
| 1   | 7-A   | 81  | G    |
| 1   | 7-A   | 82  | G    |
| 1   | 7-A   | 87  | G    |
| 1   | 7-A   | 97  | C    |
| 1   | 7-A   | 104 | G    |
| 1   | 7-A   | 111 | G    |
| 1   | 7-A   | 112 | C    |
| 1   | 8-A   | 4   | C    |
| 1   | 8-A   | 5   | A    |
| 1   | 8-A   | 7   | G    |
| 1   | 8-A   | 8   | A    |
| 1   | 8-A   | 9   | G    |
| 1   | 8-A   | 10  | U    |
| 1   | 8-A   | 11  | G    |
| 1   | 8-A   | 20  | A    |
| 1   | 8-A   | 23  | C    |
| 1   | 8-A   | 24  | C    |
| 1   | 8-A   | 31  | U    |
| 1   | 8-A   | 32  | G    |
| 1   | 8-A   | 47  | U    |
| 1   | 8-A   | 48  | C    |
| 1   | 8-A   | 50  | A    |
| 1   | 8-A   | 51  | A    |
| 1   | 8-A   | 52  | C    |
| 1   | 8-A   | 59  | G    |
| 1   | 8-A   | 67  | C    |
| 1   | 8-A   | 74  | A    |
| 1   | 8-A   | 75  | U    |
| 1   | 8-A   | 78  | C    |
| 1   | 8-A   | 81  | G    |
| 1   | 8-A   | 82  | G    |
| 1   | 8-A   | 87  | G    |
| 1   | 8-A   | 97  | C    |
| 1   | 8-A   | 104 | G    |
| 1   | 8-A   | 111 | G    |
| 1   | 8-A   | 112 | C    |
| 1   | 9-A   | 4   | C    |
| 1   | 9-A   | 5   | A    |
| 1   | 9-A   | 7   | G    |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | 9-A   | 8   | A    |
| 1   | 9-A   | 9   | G    |
| 1   | 9-A   | 10  | U    |
| 1   | 9-A   | 11  | G    |
| 1   | 9-A   | 20  | A    |
| 1   | 9-A   | 23  | C    |
| 1   | 9-A   | 24  | C    |
| 1   | 9-A   | 31  | U    |
| 1   | 9-A   | 32  | G    |
| 1   | 9-A   | 47  | U    |
| 1   | 9-A   | 48  | C    |
| 1   | 9-A   | 50  | A    |
| 1   | 9-A   | 51  | A    |
| 1   | 9-A   | 52  | C    |
| 1   | 9-A   | 59  | G    |
| 1   | 9-A   | 67  | C    |
| 1   | 9-A   | 74  | A    |
| 1   | 9-A   | 75  | U    |
| 1   | 9-A   | 78  | C    |
| 1   | 9-A   | 81  | G    |
| 1   | 9-A   | 82  | G    |
| 1   | 9-A   | 87  | G    |
| 1   | 9-A   | 97  | C    |
| 1   | 9-A   | 104 | G    |
| 1   | 9-A   | 111 | G    |
| 1   | 9-A   | 112 | C    |
| 1   | 10-A  | 4   | C    |
| 1   | 10-A  | 5   | A    |
| 1   | 10-A  | 7   | G    |
| 1   | 10-A  | 8   | A    |
| 1   | 10-A  | 9   | G    |
| 1   | 10-A  | 10  | U    |
| 1   | 10-A  | 11  | G    |
| 1   | 10-A  | 20  | A    |
| 1   | 10-A  | 23  | C    |
| 1   | 10-A  | 24  | C    |
| 1   | 10-A  | 31  | U    |
| 1   | 10-A  | 32  | G    |
| 1   | 10-A  | 47  | U    |
| 1   | 10-A  | 48  | C    |
| 1   | 10-A  | 50  | A    |
| 1   | 10-A  | 51  | A    |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | 10-A  | 52  | C    |
| 1   | 10-A  | 59  | G    |
| 1   | 10-A  | 67  | C    |
| 1   | 10-A  | 74  | A    |
| 1   | 10-A  | 75  | U    |
| 1   | 10-A  | 78  | C    |
| 1   | 10-A  | 81  | G    |
| 1   | 10-A  | 82  | G    |
| 1   | 10-A  | 87  | G    |
| 1   | 10-A  | 97  | C    |
| 1   | 10-A  | 104 | G    |
| 1   | 10-A  | 111 | G    |
| 1   | 10-A  | 112 | C    |
| 1   | 11-A  | 4   | C    |
| 1   | 11-A  | 5   | A    |
| 1   | 11-A  | 7   | G    |
| 1   | 11-A  | 8   | A    |
| 1   | 11-A  | 9   | G    |
| 1   | 11-A  | 10  | U    |
| 1   | 11-A  | 11  | G    |
| 1   | 11-A  | 20  | A    |
| 1   | 11-A  | 23  | C    |
| 1   | 11-A  | 24  | C    |
| 1   | 11-A  | 31  | U    |
| 1   | 11-A  | 32  | G    |
| 1   | 11-A  | 47  | U    |
| 1   | 11-A  | 48  | C    |
| 1   | 11-A  | 50  | A    |
| 1   | 11-A  | 51  | A    |
| 1   | 11-A  | 52  | C    |
| 1   | 11-A  | 59  | G    |
| 1   | 11-A  | 67  | C    |
| 1   | 11-A  | 74  | A    |
| 1   | 11-A  | 75  | U    |
| 1   | 11-A  | 78  | C    |
| 1   | 11-A  | 81  | G    |
| 1   | 11-A  | 82  | G    |
| 1   | 11-A  | 87  | G    |
| 1   | 11-A  | 97  | C    |
| 1   | 11-A  | 104 | G    |
| 1   | 11-A  | 111 | G    |
| 1   | 11-A  | 112 | C    |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | 12-A  | 4   | C    |
| 1   | 12-A  | 5   | A    |
| 1   | 12-A  | 7   | G    |
| 1   | 12-A  | 8   | A    |
| 1   | 12-A  | 9   | G    |
| 1   | 12-A  | 10  | U    |
| 1   | 12-A  | 11  | G    |
| 1   | 12-A  | 20  | A    |
| 1   | 12-A  | 23  | C    |
| 1   | 12-A  | 24  | C    |
| 1   | 12-A  | 31  | U    |
| 1   | 12-A  | 32  | G    |
| 1   | 12-A  | 47  | U    |
| 1   | 12-A  | 48  | C    |
| 1   | 12-A  | 50  | A    |
| 1   | 12-A  | 51  | A    |
| 1   | 12-A  | 52  | C    |
| 1   | 12-A  | 59  | G    |
| 1   | 12-A  | 67  | C    |
| 1   | 12-A  | 74  | A    |
| 1   | 12-A  | 75  | U    |
| 1   | 12-A  | 78  | C    |
| 1   | 12-A  | 81  | G    |
| 1   | 12-A  | 82  | G    |
| 1   | 12-A  | 87  | G    |
| 1   | 12-A  | 97  | C    |
| 1   | 12-A  | 104 | G    |
| 1   | 12-A  | 111 | G    |
| 1   | 12-A  | 112 | C    |
| 1   | 13-A  | 4   | C    |
| 1   | 13-A  | 5   | A    |
| 1   | 13-A  | 7   | G    |
| 1   | 13-A  | 8   | A    |
| 1   | 13-A  | 9   | G    |
| 1   | 13-A  | 10  | U    |
| 1   | 13-A  | 11  | G    |
| 1   | 13-A  | 20  | A    |
| 1   | 13-A  | 23  | C    |
| 1   | 13-A  | 24  | C    |
| 1   | 13-A  | 31  | U    |
| 1   | 13-A  | 32  | G    |
| 1   | 13-A  | 47  | U    |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | 13-A  | 48  | C    |
| 1   | 13-A  | 50  | A    |
| 1   | 13-A  | 51  | A    |
| 1   | 13-A  | 52  | C    |
| 1   | 13-A  | 59  | G    |
| 1   | 13-A  | 67  | C    |
| 1   | 13-A  | 74  | A    |
| 1   | 13-A  | 75  | U    |
| 1   | 13-A  | 78  | C    |
| 1   | 13-A  | 81  | G    |
| 1   | 13-A  | 82  | G    |
| 1   | 13-A  | 87  | G    |
| 1   | 13-A  | 97  | C    |
| 1   | 13-A  | 104 | G    |
| 1   | 13-A  | 111 | G    |
| 1   | 13-A  | 112 | C    |
| 1   | 14-A  | 4   | C    |
| 1   | 14-A  | 5   | A    |
| 1   | 14-A  | 7   | G    |
| 1   | 14-A  | 8   | A    |
| 1   | 14-A  | 9   | G    |
| 1   | 14-A  | 10  | U    |
| 1   | 14-A  | 11  | G    |
| 1   | 14-A  | 20  | A    |
| 1   | 14-A  | 23  | C    |
| 1   | 14-A  | 24  | C    |
| 1   | 14-A  | 31  | U    |
| 1   | 14-A  | 32  | G    |
| 1   | 14-A  | 47  | U    |
| 1   | 14-A  | 48  | C    |
| 1   | 14-A  | 50  | A    |
| 1   | 14-A  | 51  | A    |
| 1   | 14-A  | 52  | C    |
| 1   | 14-A  | 59  | G    |
| 1   | 14-A  | 67  | C    |
| 1   | 14-A  | 74  | A    |
| 1   | 14-A  | 75  | U    |
| 1   | 14-A  | 78  | C    |
| 1   | 14-A  | 81  | G    |
| 1   | 14-A  | 82  | G    |
| 1   | 14-A  | 87  | G    |
| 1   | 14-A  | 97  | C    |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | 14-A  | 104 | G    |
| 1   | 14-A  | 111 | G    |
| 1   | 14-A  | 112 | C    |
| 1   | 15-A  | 4   | C    |
| 1   | 15-A  | 5   | A    |
| 1   | 15-A  | 7   | G    |
| 1   | 15-A  | 8   | A    |
| 1   | 15-A  | 9   | G    |
| 1   | 15-A  | 10  | U    |
| 1   | 15-A  | 11  | G    |
| 1   | 15-A  | 20  | A    |
| 1   | 15-A  | 23  | C    |
| 1   | 15-A  | 24  | C    |
| 1   | 15-A  | 31  | U    |
| 1   | 15-A  | 32  | G    |
| 1   | 15-A  | 47  | U    |
| 1   | 15-A  | 48  | C    |
| 1   | 15-A  | 50  | A    |
| 1   | 15-A  | 51  | A    |
| 1   | 15-A  | 52  | C    |
| 1   | 15-A  | 59  | G    |
| 1   | 15-A  | 67  | C    |
| 1   | 15-A  | 74  | A    |
| 1   | 15-A  | 75  | U    |
| 1   | 15-A  | 78  | C    |
| 1   | 15-A  | 81  | G    |
| 1   | 15-A  | 82  | G    |
| 1   | 15-A  | 87  | G    |
| 1   | 15-A  | 97  | C    |
| 1   | 15-A  | 104 | G    |
| 1   | 15-A  | 111 | G    |
| 1   | 15-A  | 112 | C    |
| 1   | 16-A  | 4   | C    |
| 1   | 16-A  | 5   | A    |
| 1   | 16-A  | 7   | G    |
| 1   | 16-A  | 8   | A    |
| 1   | 16-A  | 9   | G    |
| 1   | 16-A  | 10  | U    |
| 1   | 16-A  | 11  | G    |
| 1   | 16-A  | 20  | A    |
| 1   | 16-A  | 23  | C    |
| 1   | 16-A  | 24  | C    |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | 16-A  | 31  | U    |
| 1   | 16-A  | 32  | G    |
| 1   | 16-A  | 47  | U    |
| 1   | 16-A  | 48  | C    |
| 1   | 16-A  | 50  | A    |
| 1   | 16-A  | 51  | A    |
| 1   | 16-A  | 52  | C    |
| 1   | 16-A  | 59  | G    |
| 1   | 16-A  | 67  | C    |
| 1   | 16-A  | 74  | A    |
| 1   | 16-A  | 75  | U    |
| 1   | 16-A  | 78  | C    |
| 1   | 16-A  | 81  | G    |
| 1   | 16-A  | 82  | G    |
| 1   | 16-A  | 87  | G    |
| 1   | 16-A  | 97  | C    |
| 1   | 16-A  | 104 | G    |
| 1   | 16-A  | 111 | G    |
| 1   | 16-A  | 112 | C    |
| 1   | 17-A  | 4   | C    |
| 1   | 17-A  | 5   | A    |
| 1   | 17-A  | 7   | G    |
| 1   | 17-A  | 8   | A    |
| 1   | 17-A  | 9   | G    |
| 1   | 17-A  | 10  | U    |
| 1   | 17-A  | 11  | G    |
| 1   | 17-A  | 20  | A    |
| 1   | 17-A  | 23  | C    |
| 1   | 17-A  | 24  | C    |
| 1   | 17-A  | 31  | U    |
| 1   | 17-A  | 32  | G    |
| 1   | 17-A  | 47  | U    |
| 1   | 17-A  | 48  | C    |
| 1   | 17-A  | 50  | A    |
| 1   | 17-A  | 51  | A    |
| 1   | 17-A  | 52  | C    |
| 1   | 17-A  | 59  | G    |
| 1   | 17-A  | 67  | C    |
| 1   | 17-A  | 74  | A    |
| 1   | 17-A  | 75  | U    |
| 1   | 17-A  | 78  | C    |
| 1   | 17-A  | 81  | G    |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | 17-A  | 82  | G    |
| 1   | 17-A  | 87  | G    |
| 1   | 17-A  | 97  | C    |
| 1   | 17-A  | 104 | G    |
| 1   | 17-A  | 111 | G    |
| 1   | 17-A  | 112 | C    |
| 1   | 18-A  | 4   | C    |
| 1   | 18-A  | 5   | A    |
| 1   | 18-A  | 7   | G    |
| 1   | 18-A  | 8   | A    |
| 1   | 18-A  | 9   | G    |
| 1   | 18-A  | 10  | U    |
| 1   | 18-A  | 11  | G    |
| 1   | 18-A  | 20  | A    |
| 1   | 18-A  | 23  | C    |
| 1   | 18-A  | 24  | C    |
| 1   | 18-A  | 31  | U    |
| 1   | 18-A  | 32  | G    |
| 1   | 18-A  | 47  | U    |
| 1   | 18-A  | 48  | C    |
| 1   | 18-A  | 50  | A    |
| 1   | 18-A  | 51  | A    |
| 1   | 18-A  | 52  | C    |
| 1   | 18-A  | 59  | G    |
| 1   | 18-A  | 67  | C    |
| 1   | 18-A  | 74  | A    |
| 1   | 18-A  | 75  | U    |
| 1   | 18-A  | 78  | C    |
| 1   | 18-A  | 81  | G    |
| 1   | 18-A  | 82  | G    |
| 1   | 18-A  | 87  | G    |
| 1   | 18-A  | 97  | C    |
| 1   | 18-A  | 104 | G    |
| 1   | 18-A  | 111 | G    |
| 1   | 18-A  | 112 | C    |
| 1   | 19-A  | 4   | C    |
| 1   | 19-A  | 5   | A    |
| 1   | 19-A  | 7   | G    |
| 1   | 19-A  | 8   | A    |
| 1   | 19-A  | 9   | G    |
| 1   | 19-A  | 10  | U    |
| 1   | 19-A  | 11  | G    |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | 19-A  | 20  | A    |
| 1   | 19-A  | 23  | C    |
| 1   | 19-A  | 24  | C    |
| 1   | 19-A  | 31  | U    |
| 1   | 19-A  | 32  | G    |
| 1   | 19-A  | 47  | U    |
| 1   | 19-A  | 48  | C    |
| 1   | 19-A  | 50  | A    |
| 1   | 19-A  | 51  | A    |
| 1   | 19-A  | 52  | C    |
| 1   | 19-A  | 59  | G    |
| 1   | 19-A  | 67  | C    |
| 1   | 19-A  | 74  | A    |
| 1   | 19-A  | 75  | U    |
| 1   | 19-A  | 78  | C    |
| 1   | 19-A  | 81  | G    |
| 1   | 19-A  | 82  | G    |
| 1   | 19-A  | 87  | G    |
| 1   | 19-A  | 97  | C    |
| 1   | 19-A  | 104 | G    |
| 1   | 19-A  | 111 | G    |
| 1   | 19-A  | 112 | C    |
| 1   | 20-A  | 4   | C    |
| 1   | 20-A  | 5   | A    |
| 1   | 20-A  | 7   | G    |
| 1   | 20-A  | 8   | A    |
| 1   | 20-A  | 9   | G    |
| 1   | 20-A  | 10  | U    |
| 1   | 20-A  | 11  | G    |
| 1   | 20-A  | 20  | A    |
| 1   | 20-A  | 23  | C    |
| 1   | 20-A  | 24  | C    |
| 1   | 20-A  | 31  | U    |
| 1   | 20-A  | 32  | G    |
| 1   | 20-A  | 47  | U    |
| 1   | 20-A  | 48  | C    |
| 1   | 20-A  | 50  | A    |
| 1   | 20-A  | 51  | A    |
| 1   | 20-A  | 52  | C    |
| 1   | 20-A  | 59  | G    |
| 1   | 20-A  | 67  | C    |
| 1   | 20-A  | 74  | A    |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | 20-A  | 75  | U    |
| 1   | 20-A  | 78  | C    |
| 1   | 20-A  | 81  | G    |
| 1   | 20-A  | 82  | G    |
| 1   | 20-A  | 87  | G    |
| 1   | 20-A  | 97  | C    |
| 1   | 20-A  | 104 | G    |
| 1   | 20-A  | 111 | G    |
| 1   | 20-A  | 112 | C    |

All (64) RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | 1-A   | 8   | A    |
| 1   | 1-A   | 19  | C    |
| 1   | 1-A   | 51  | A    |
| 1   | 1-A   | 66  | C    |
| 1   | 1-A   | 109 | A    |
| 1   | 2-A   | 5   | A    |
| 1   | 2-A   | 18  | U    |
| 1   | 2-A   | 50  | A    |
| 1   | 2-A   | 66  | C    |
| 1   | 3-A   | 10  | U    |
| 1   | 3-A   | 30  | U    |
| 1   | 3-A   | 66  | C    |
| 1   | 3-A   | 74  | A    |
| 1   | 3-A   | 75  | U    |
| 1   | 4-A   | 19  | C    |
| 1   | 4-A   | 66  | C    |
| 1   | 5-A   | 37  | C    |
| 1   | 5-A   | 66  | C    |
| 1   | 5-A   | 74  | A    |
| 1   | 6-A   | 66  | C    |
| 1   | 7-A   | 8   | A    |
| 1   | 7-A   | 30  | U    |
| 1   | 7-A   | 66  | C    |
| 1   | 7-A   | 96  | A    |
| 1   | 8-A   | 18  | U    |
| 1   | 8-A   | 30  | U    |
| 1   | 8-A   | 66  | C    |
| 1   | 8-A   | 74  | A    |
| 1   | 9-A   | 4   | C    |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | 9-A   | 66  | C    |
| 1   | 9-A   | 96  | A    |
| 1   | 10-A  | 19  | C    |
| 1   | 10-A  | 50  | A    |
| 1   | 10-A  | 58  | U    |
| 1   | 10-A  | 66  | C    |
| 1   | 10-A  | 74  | A    |
| 1   | 10-A  | 95  | G    |
| 1   | 11-A  | 18  | U    |
| 1   | 11-A  | 66  | C    |
| 1   | 12-A  | 23  | C    |
| 1   | 12-A  | 51  | A    |
| 1   | 12-A  | 66  | C    |
| 1   | 13-A  | 66  | C    |
| 1   | 14-A  | 5   | A    |
| 1   | 14-A  | 18  | U    |
| 1   | 14-A  | 66  | C    |
| 1   | 14-A  | 73  | G    |
| 1   | 15-A  | 20  | A    |
| 1   | 15-A  | 66  | C    |
| 1   | 15-A  | 97  | C    |
| 1   | 16-A  | 6   | U    |
| 1   | 16-A  | 18  | U    |
| 1   | 16-A  | 66  | C    |
| 1   | 16-A  | 80  | A    |
| 1   | 17-A  | 66  | C    |
| 1   | 18-A  | 30  | U    |
| 1   | 18-A  | 66  | C    |
| 1   | 18-A  | 80  | A    |
| 1   | 19-A  | 8   | A    |
| 1   | 19-A  | 10  | U    |
| 1   | 19-A  | 66  | C    |
| 1   | 20-A  | 66  | C    |
| 1   | 20-A  | 73  | G    |
| 1   | 20-A  | 86  | A    |

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

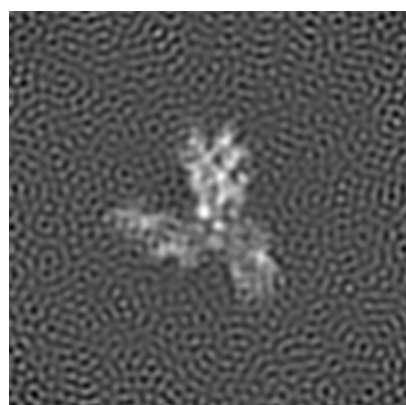
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21839. These allow visual inspection of the internal detail of the map and identification of artifacts.

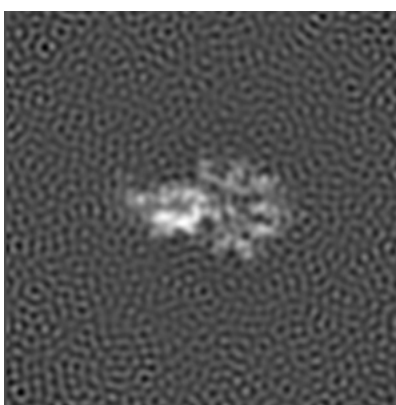
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

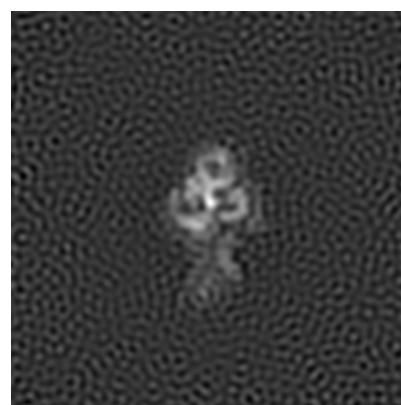
#### 6.1.1 Primary map



X



Y

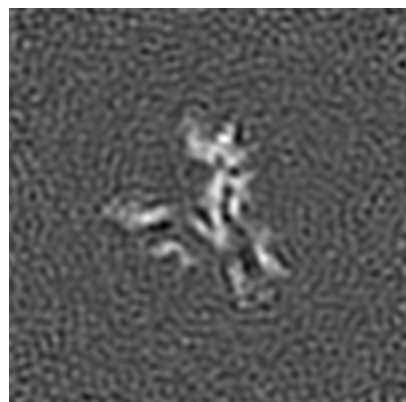


Z

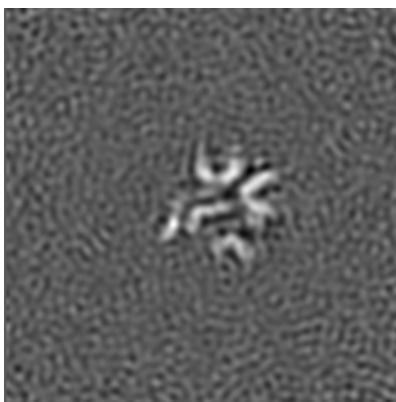
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

#### 6.2.1 Primary map



X Index: 84



Y Index: 84

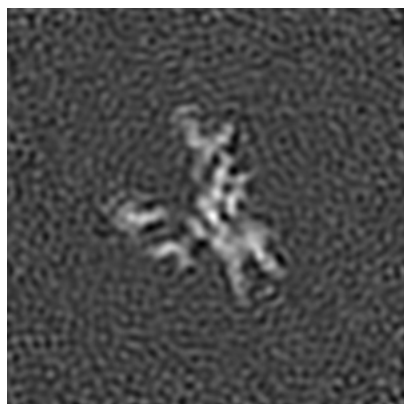


Z Index: 84

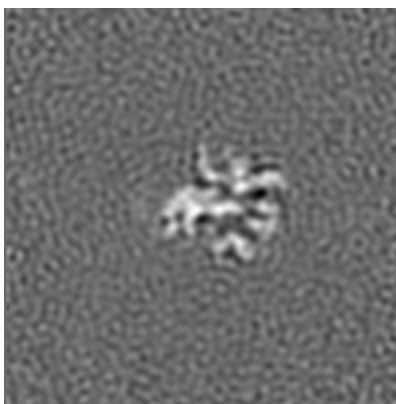
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

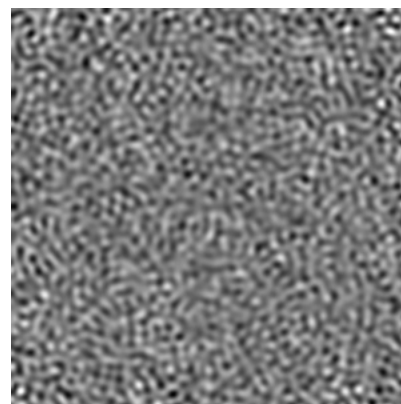
### 6.3.1 Primary map



X Index: 82



Y Index: 87

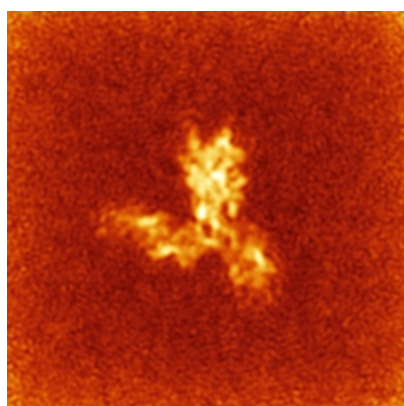


Z Index: 167

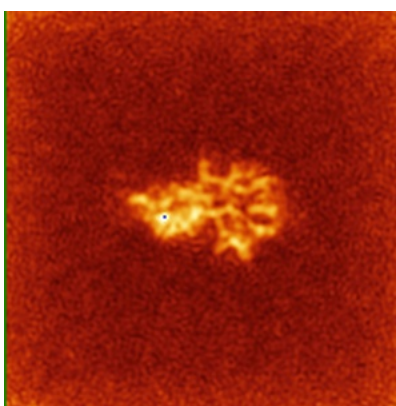
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

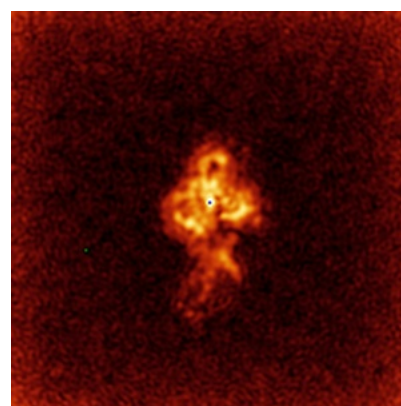
### 6.4.1 Primary map



X



Y

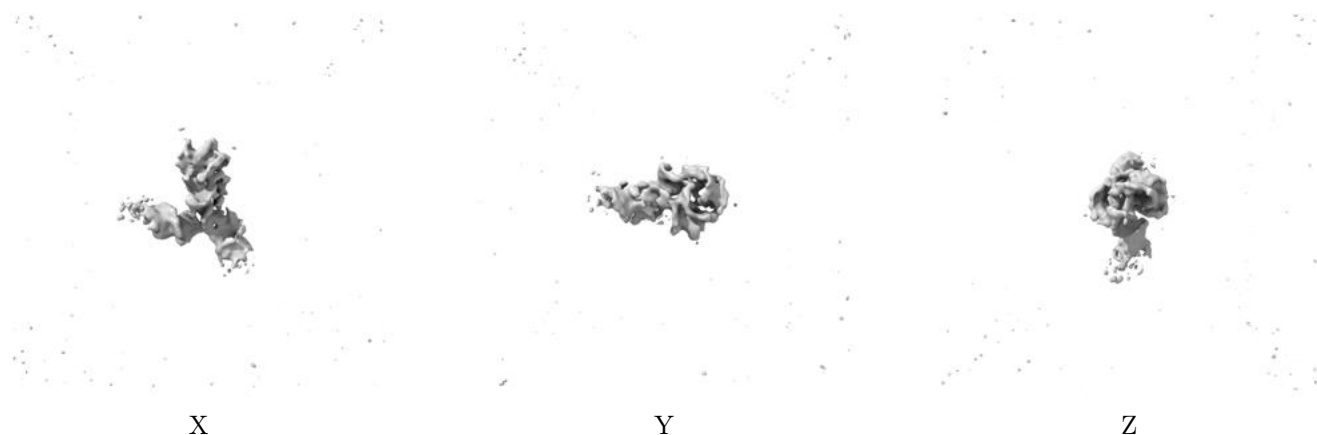


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.2. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

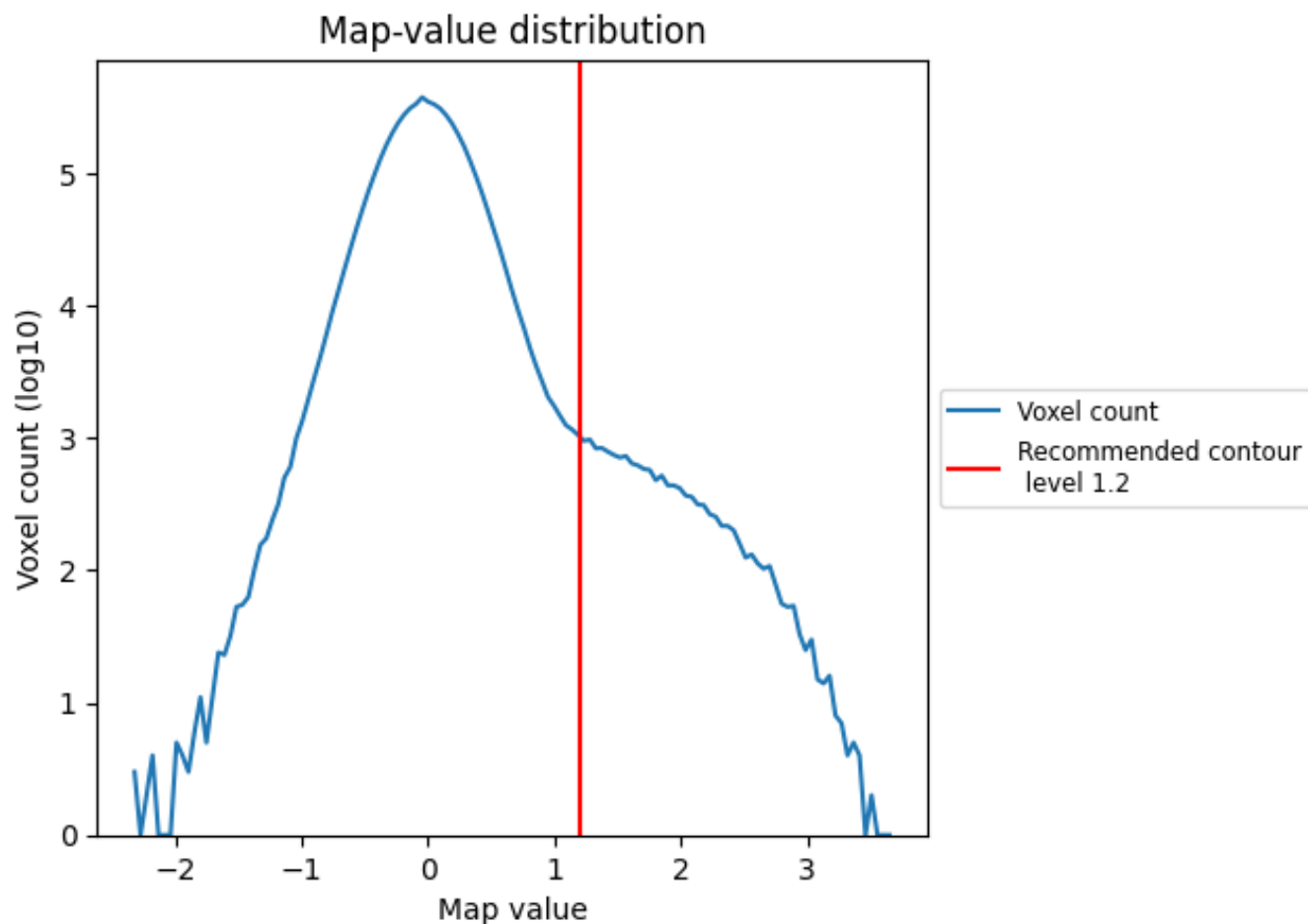
## 6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

## 7 Map analysis [i](#)

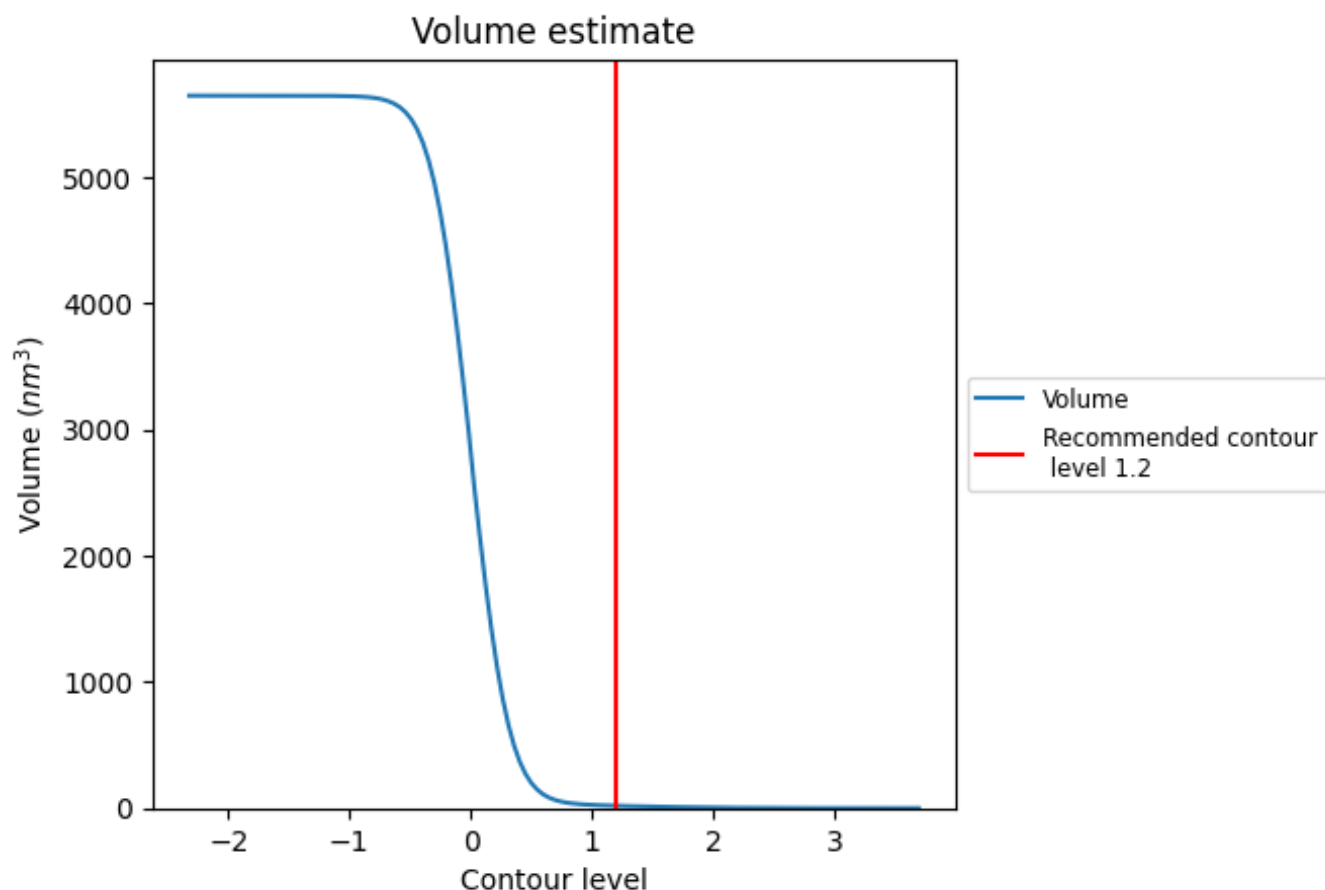
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

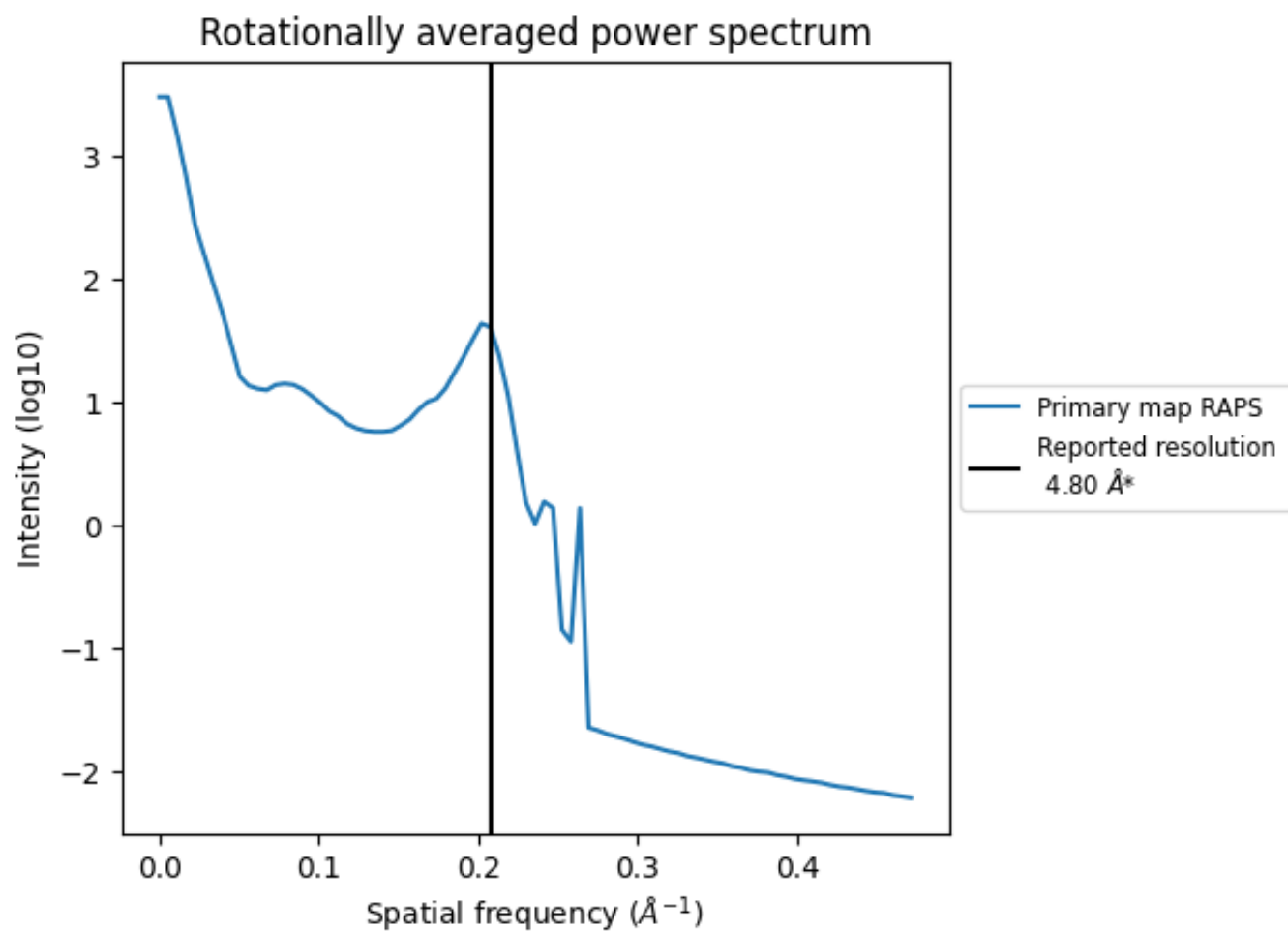
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 19 nm<sup>3</sup>; this corresponds to an approximate mass of 17 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum ⓘ



\*Reported resolution corresponds to spatial frequency of 0.208 Å<sup>-1</sup>

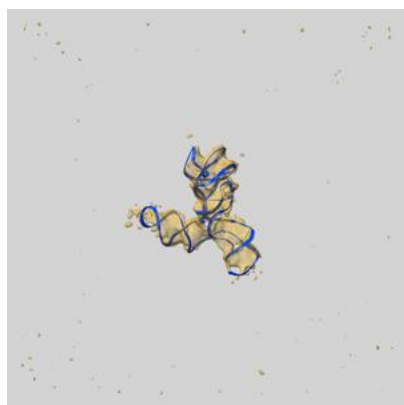
## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

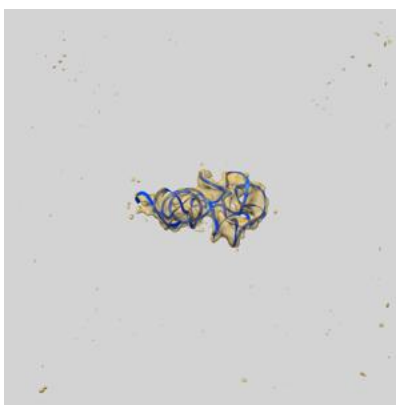
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21839 and PDB model 6WLR. Per-residue inclusion information can be found in section [3](#) on page [6](#).

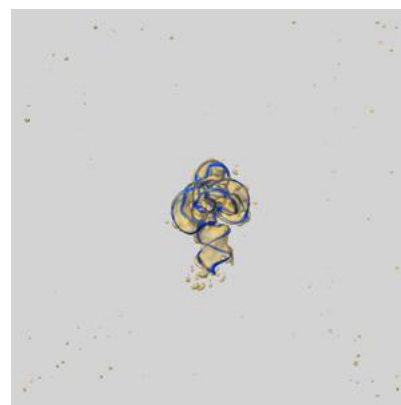
### 9.1 Map-model overlay [i](#)



X



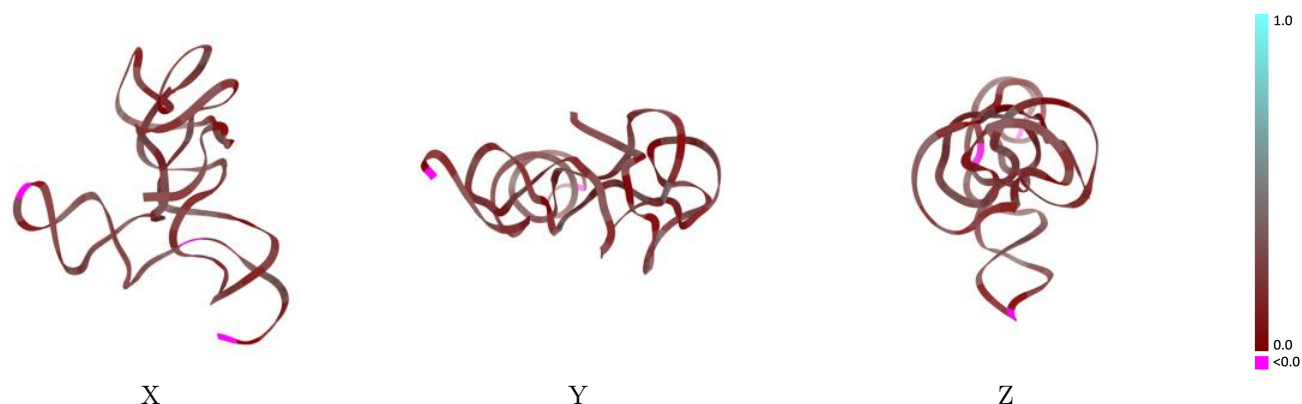
Y



Z

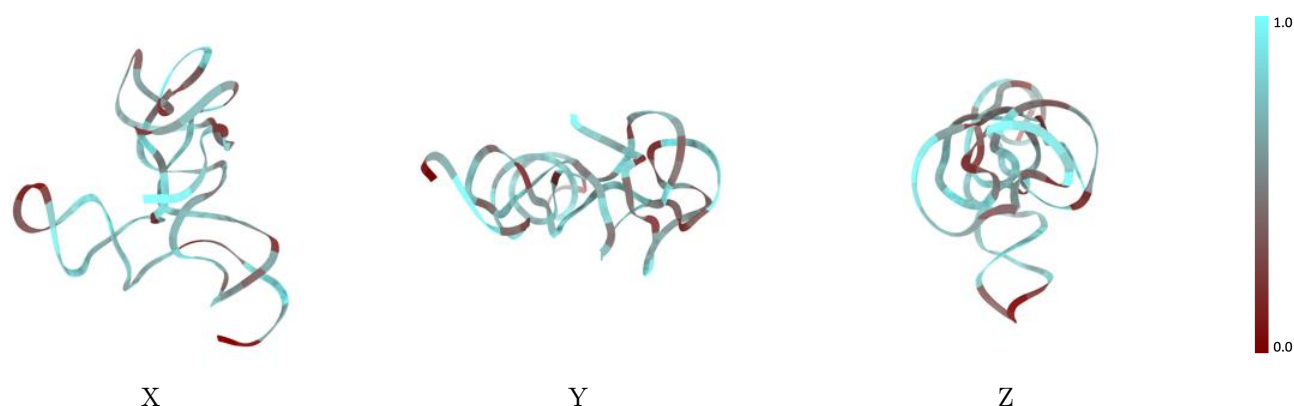
The images above show the 3D surface view of the map at the recommended contour level 1.2 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 9.2 Q-score mapped to coordinate model [i](#)



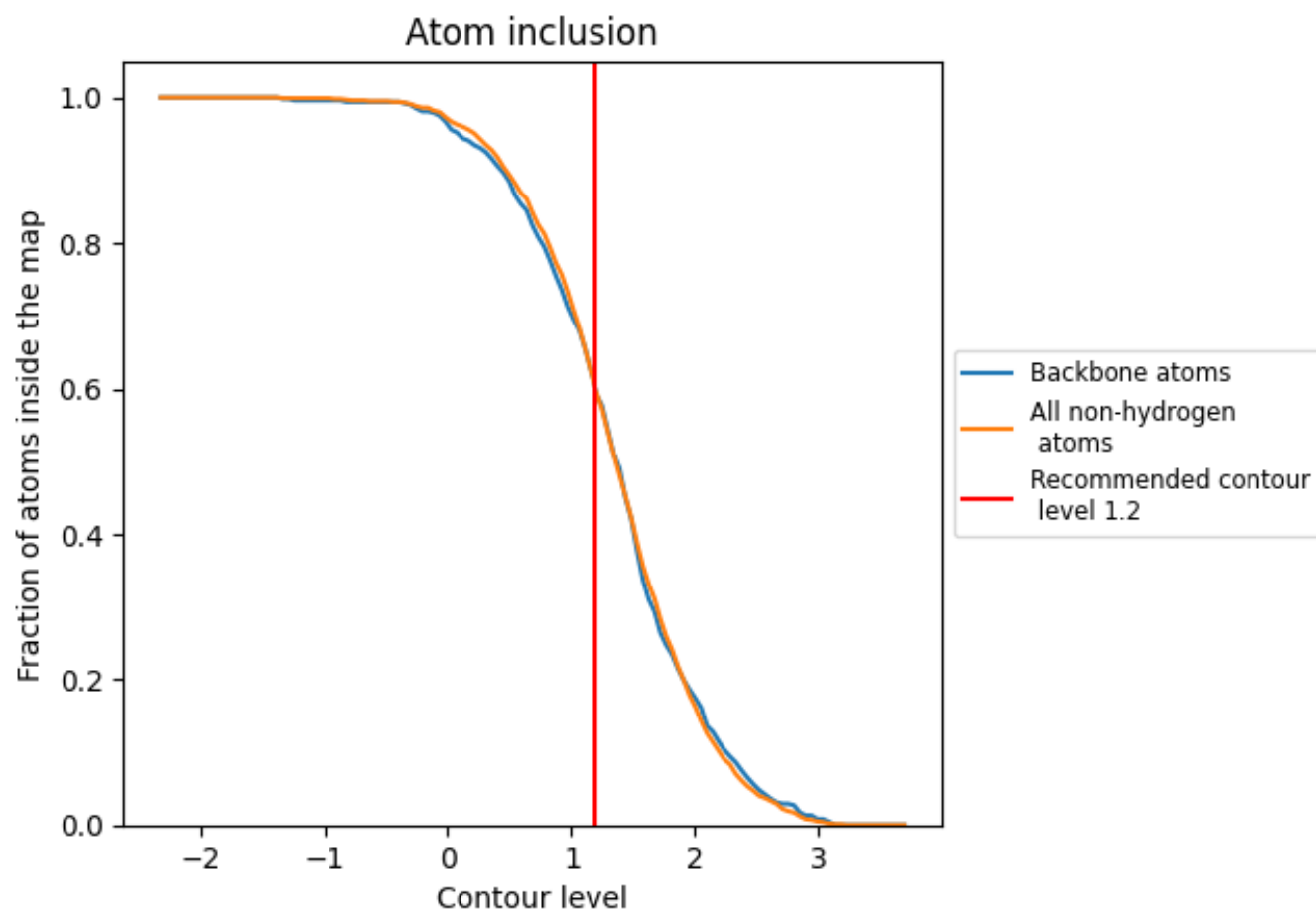
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1.2).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 60% of all backbone atoms, 60% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (1.2) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion     | Q-score            |
|-------|--------------------|--------------------|
| All   | <div></div> 0.5970 | <div></div> 0.2170 |
| A     | <div></div> 0.5990 | <div></div> 0.2170 |

