



wwPDB EM Validation Summary Report ⓘ

Nov 27, 2022 – 03:59 PM EST

PDB ID : 6WLN
EMDB ID : EMD-21835
Title : hc16 ligase product models, 10.0 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 : 10.00 Å(reported)

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

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

A user guide is available at

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

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

EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

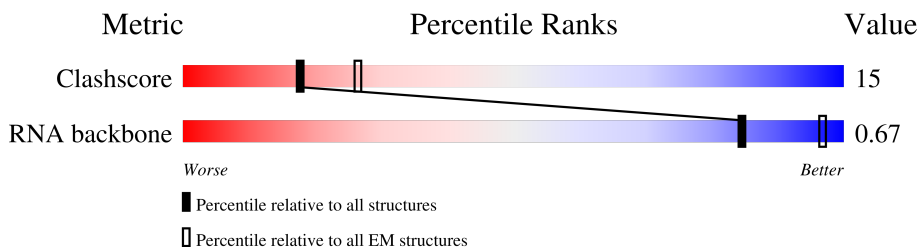
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 10.00 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.













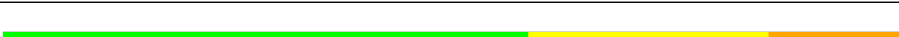


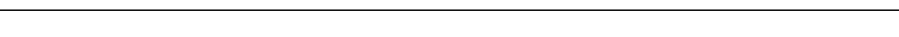
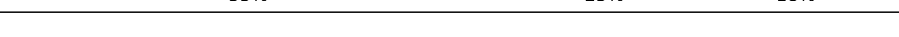
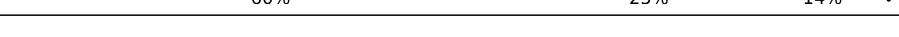



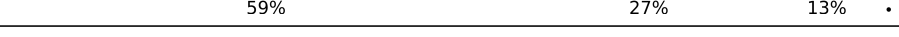





Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
RNA backbone	4643	859

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 ≥ 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	349	<div> <div>11%</div> <div>58%</div> <div>26%</div> <div>15%</div> <div>.</div> </div>
1	10-A	349	<div> <div>57%</div> <div>24%</div> <div>18%</div> <div>.</div> </div>
1	11-A	349	<div> <div>58%</div> <div>22%</div> <div>18%</div> <div>.</div> </div>
1	12-A	349	<div> <div>53%</div> <div>23%</div> <div>22%</div> <div>.</div> </div>
1	13-A	349	<div> <div>56%</div> <div>28%</div> <div>16%</div> </div>
1	14-A	349	<div> <div>56%</div> <div>26%</div> <div>17%</div> <div>.</div> </div>
1	15-A	349	<div> <div>55%</div> <div>24%</div> <div>19%</div> <div>.</div> </div>
1	16-A	349	<div> <div>58%</div> <div>23%</div> <div>19%</div> </div>
1	17-A	349	<div> <div>56%</div> <div>24%</div> <div>19%</div> </div>












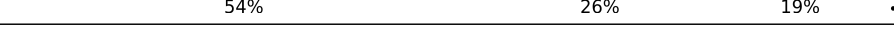







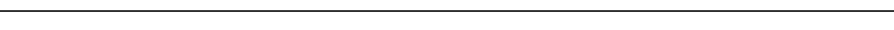

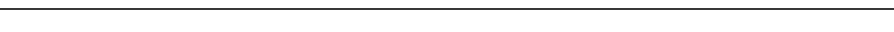
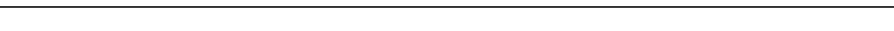


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Mol	Chain	Length	Quality of chain
1	18-A	349	
1	19-A	349	
1	2-A	349	
1	20-A	349	
1	21-A	349	
1	22-A	349	
1	23-A	349	
1	24-A	349	
1	25-A	349	
1	26-A	349	
1	27-A	349	
1	28-A	349	
1	29-A	349	
1	3-A	349	
1	30-A	349	
1	31-A	349	
1	32-A	349	
1	33-A	349	
1	34-A	349	
1	35-A	349	
1	36-A	349	
1	37-A	349	
1	38-A	349	
1	39-A	349	
1	4-A	349	









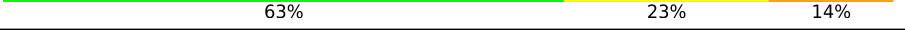
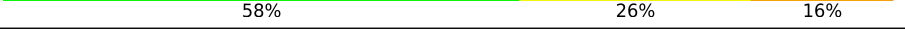
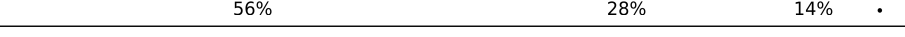

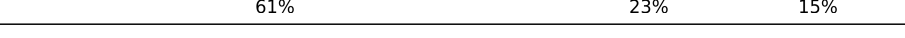
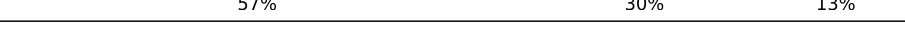
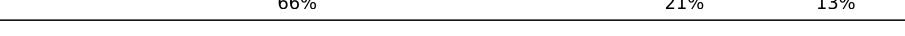


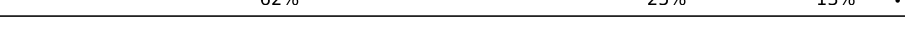
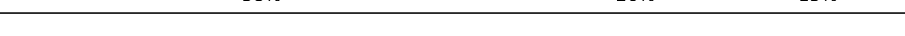


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Mol	Chain	Length	Quality of chain
1	40-A	349	 59% 24% 15% .
1	41-A	349	 52% 29% 19%
1	42-A	349	 58% 23% 18% .
1	43-A	349	 52% 29% 19% .
1	44-A	349	 55% 24% 19% .
1	45-A	349	 57% 25% 18%
1	46-A	349	 54% 25% 21% .
1	47-A	349	 55% 26% 19%
1	48-A	349	 52% 28% 19% .
1	49-A	349	 53% 27% 19% .
1	5-A	349	 56% 23% 20% .
1	50-A	349	 54% 26% 19% .
1	51-A	349	 56% 22% 21% .
1	52-A	349	 56% 27% 16% .
1	53-A	349	 52% 29% 17% .
1	54-A	349	 58% 25% 16% .
1	55-A	349	 52% 29% 19% .
1	56-A	349	 56% 23% 21%
1	57-A	349	 60% 24% 16% .
1	58-A	349	 55% 25% 19% .
1	59-A	349	 56% 25% 17% .
1	6-A	349	 56% 24% 19% .
1	60-A	349	 56% 28% 16%
1	61-A	349	 60% 27% 13%
1	62-A	349	 58% 27% 15% .

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Mol	Chain	Length	Quality of chain
1	63-A	349	 59% 25% 16% .
1	64-A	349	 63% 23% 13%
1	65-A	349	 59% 24% 16%
1	66-A	349	 62% 22% 15% .
1	67-A	349	 60% 24% 16%
1	68-A	349	 59% 26% 15% .
1	69-A	349	 62% 26% 12% .
1	7-A	349	 59% 29% 11% .
1	70-A	349	 63% 23% 14%
1	71-A	349	 58% 26% 16%
1	72-A	349	 56% 28% 14% .
1	73-A	349	 62% 24% 14% .
1	74-A	349	 61% 23% 15%
1	75-A	349	 57% 30% 13%
1	76-A	349	 66% 21% 13%
1	77-A	349	 60% 22% 18%
1	78-A	349	 60% 24% 16% .
1	79-A	349	 62% 25% 13% .
1	8-A	349	 58% 26% 15% .
1	80-A	349	 59% 25% 15% .
1	9-A	349	 55% 24% 19% .

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 898159 atoms, of which 301039 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 (349-MER).

Mol	Chain	Residues	Atoms						AltConf	Trace
1	1-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	2-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	3-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	4-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	5-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	6-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	7-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	8-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	9-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	10-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	11-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	12-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	13-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	14-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	15-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	16-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	17-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	18-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	19-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	20-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	21-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	22-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	23-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	24-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	25-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	26-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	27-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	28-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	29-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	30-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	31-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	32-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	33-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	34-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	35-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	36-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	37-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	38-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0

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Mol	Chain	Residues	Atoms						AltConf	Trace
1	39-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	40-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	41-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	42-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	43-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	44-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	45-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	46-A	349	Total 11226	C 3336	H 3762	N 1363	O 2417	P 348	0	0
1	47-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	48-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	49-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	50-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	51-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	52-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	53-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	54-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	55-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	56-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	57-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	58-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	59-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0

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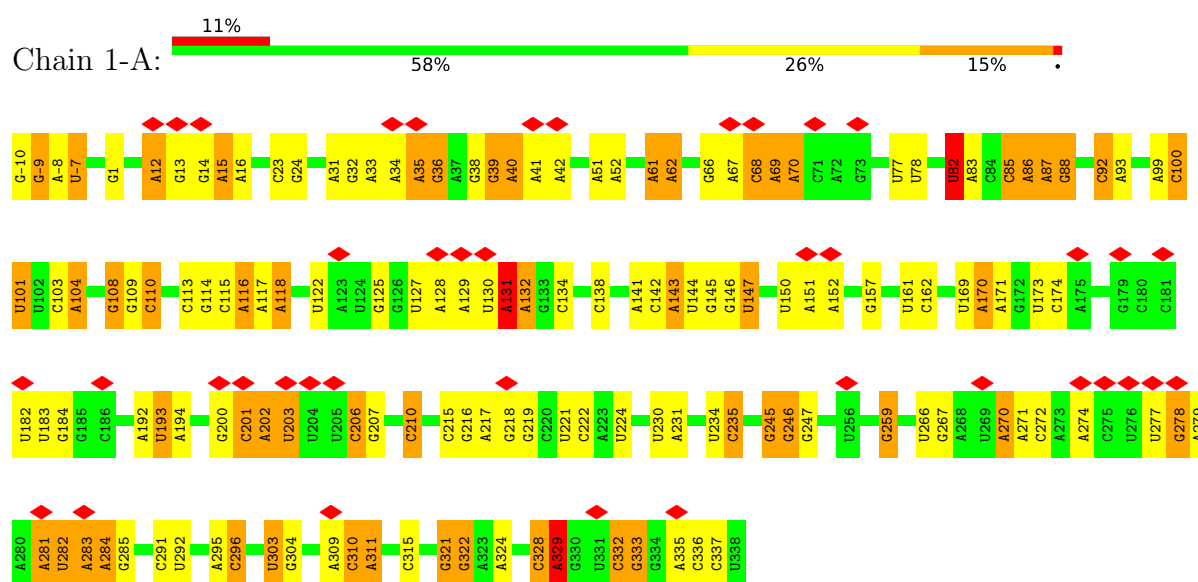
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Mol	Chain	Residues	Atoms						AltConf	Trace
1	60-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	61-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	62-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	63-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	64-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	65-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	66-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	67-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	68-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	69-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	70-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	71-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	72-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	73-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	74-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	75-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	76-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	77-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	78-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	79-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0
1	80-A	349	Total 11227	C 3336	H 3763	N 1363	O 2417	P 348	0	0

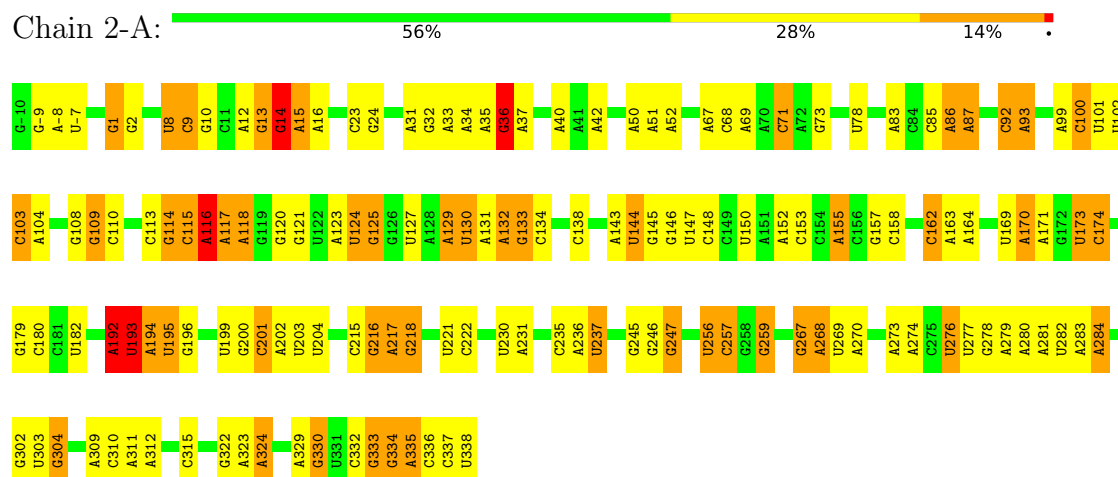
3 Residue-property plots

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.

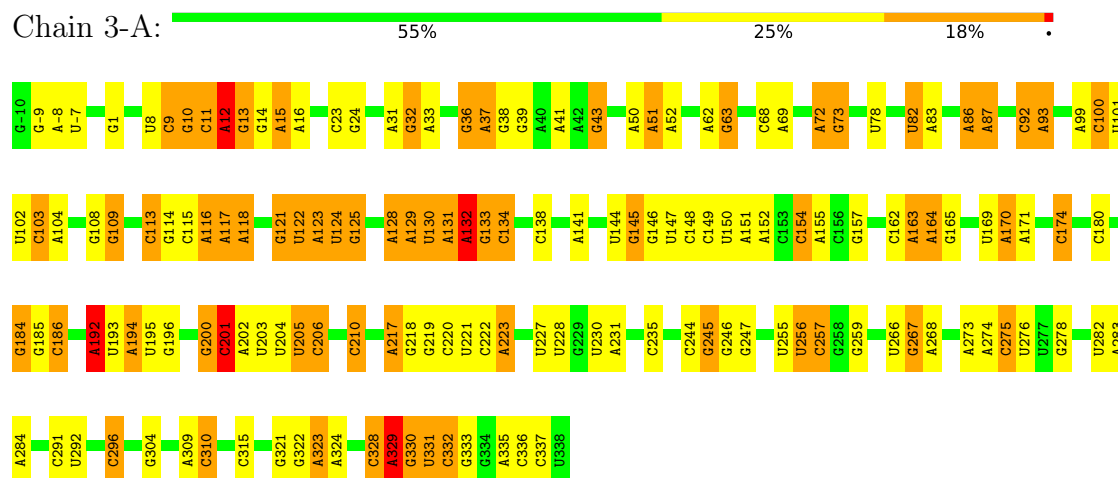
• Molecule 1: RNA (349-MER)



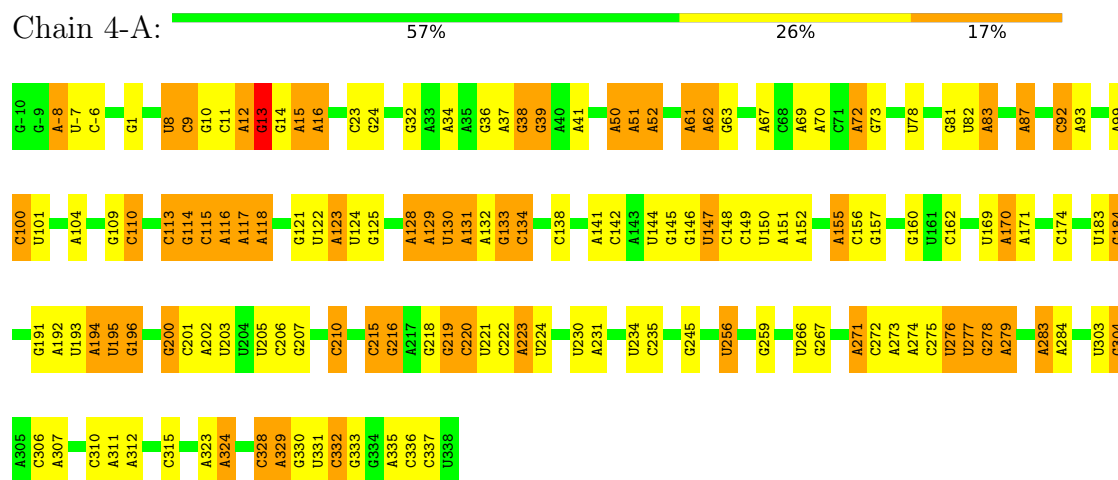
• Molecule 1: RNA (349-MER)



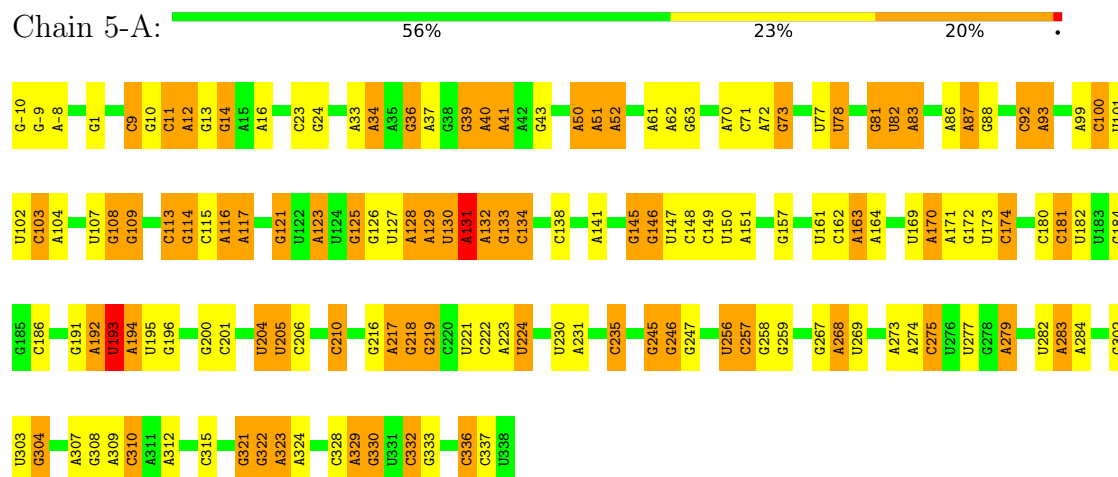
• Molecule 1: RNA (349-MER)



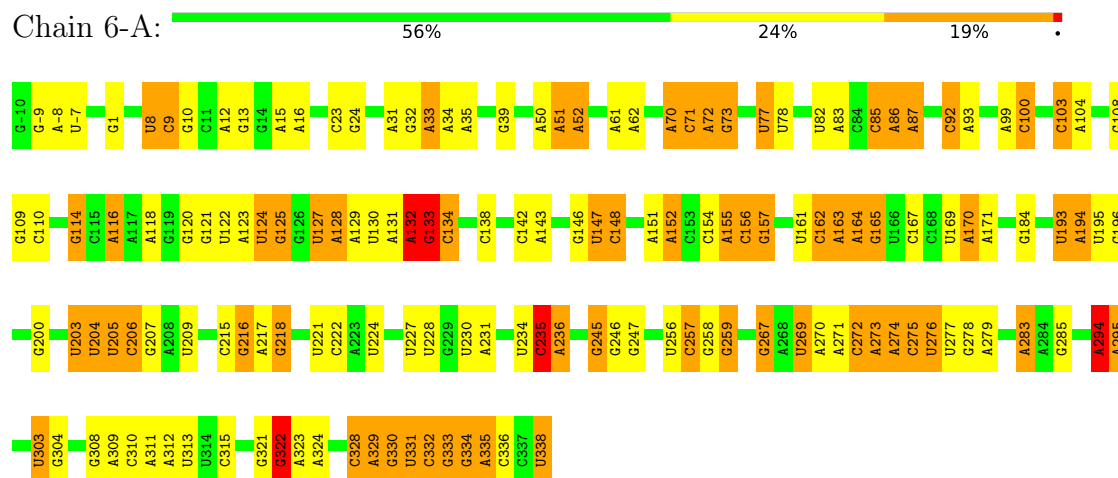
• Molecule 1: RNA (349-MER)



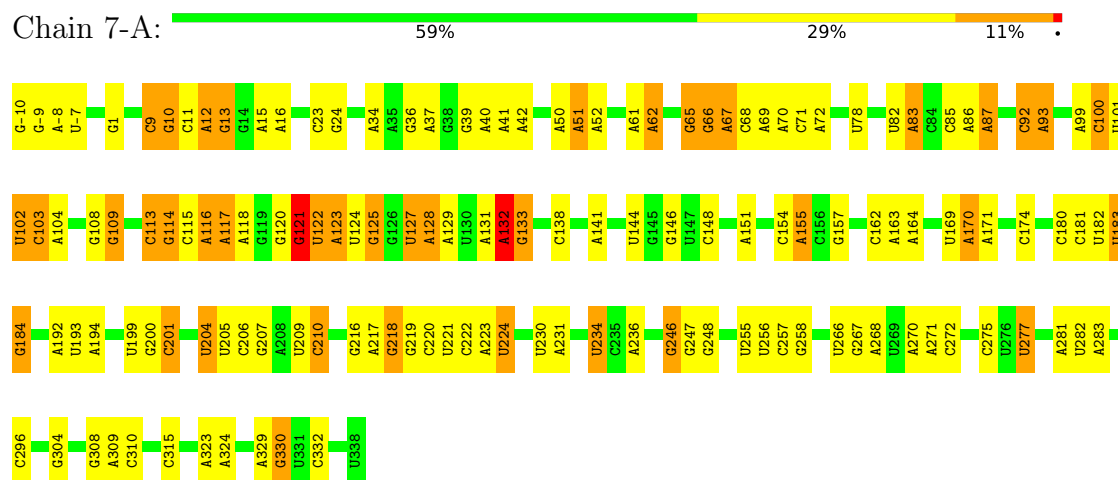
• Molecule 1: RNA (349-MER)



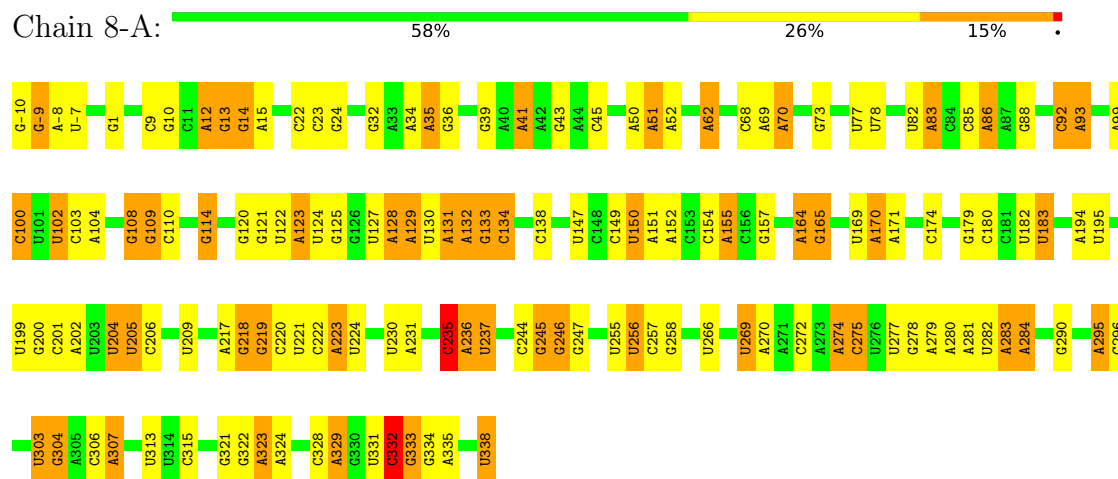
• Molecule 1: RNA (349-MER)



• Molecule 1: RNA (349-MER)

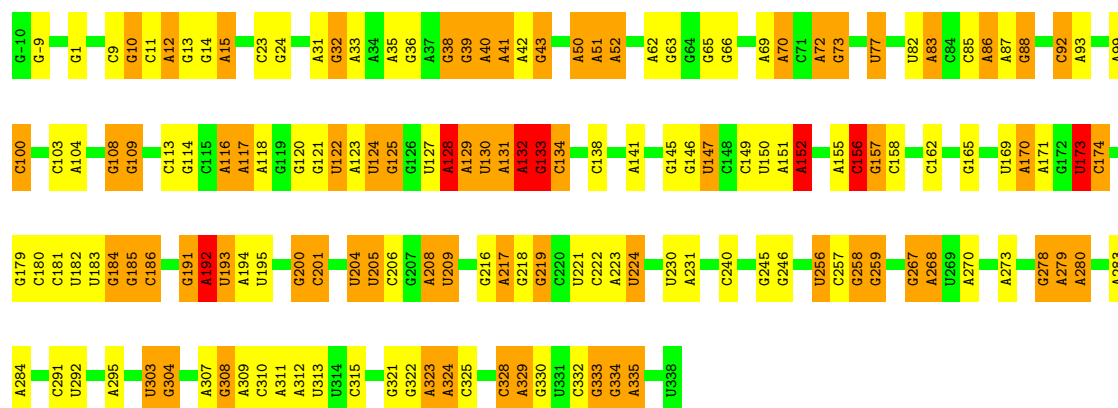


• Molecule 1: RNA (349-MER)



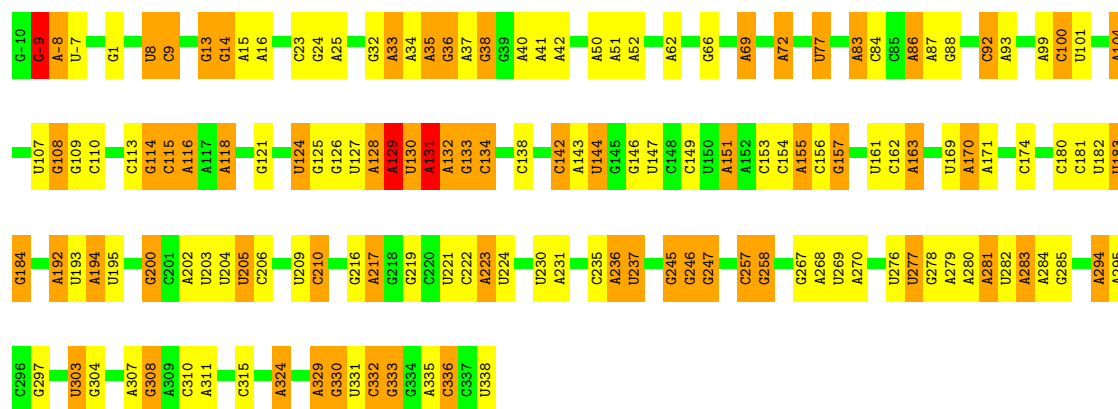
• Molecule 1: RNA (349-MER)

Chain 9-A:  55% 24% 19% .



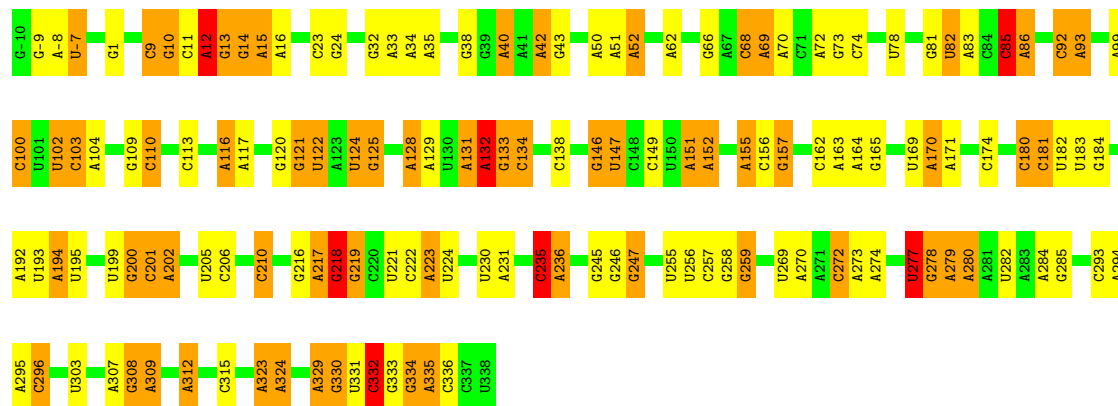
• Molecule 1: RNA (349-MER)

Chain 10-A:  57% 24% 18% .



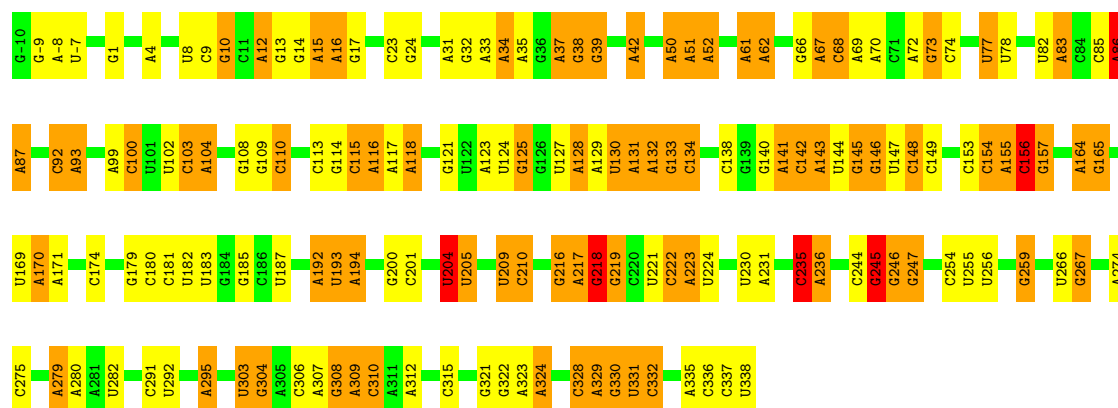
• Molecule 1: RNA (349-MER)

Chain 11-A:  58% 22% 18% .



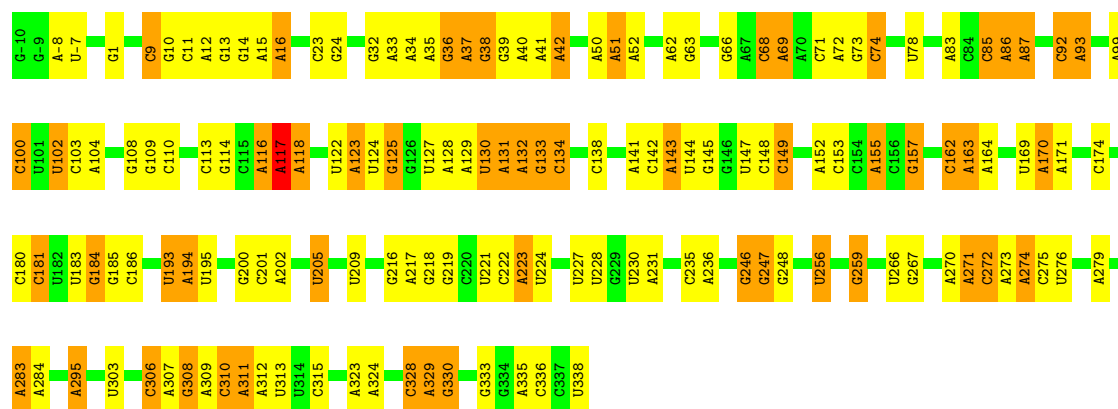
• Molecule 1: RNA (349-MER)

Chain 12-A: 



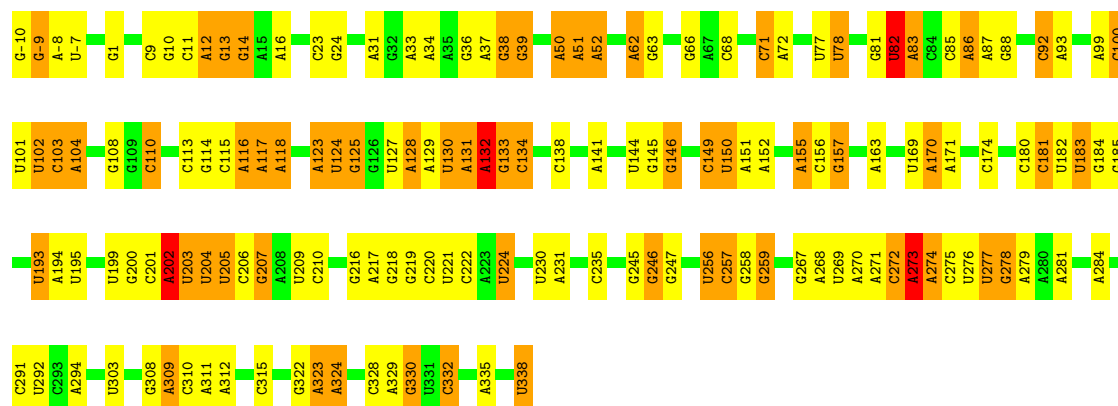
• Molecule 1: RNA (349-MER)

Chain 13-A: 



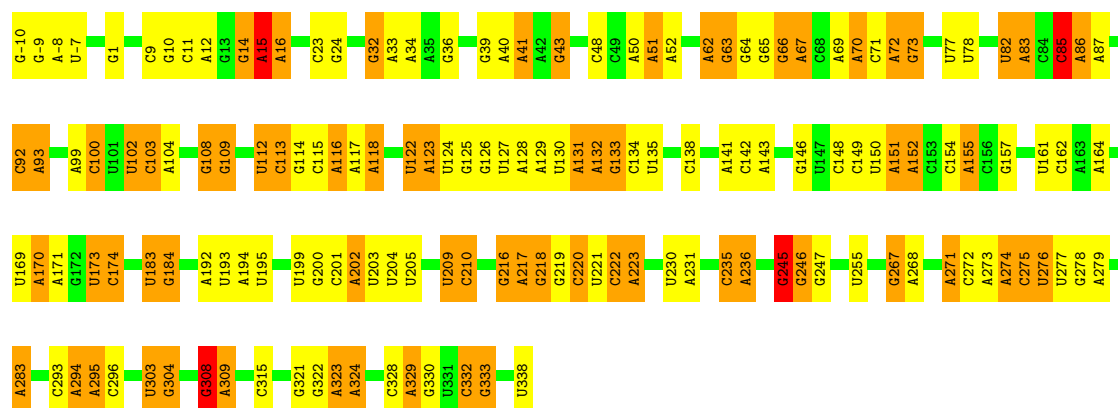
• Molecule 1: RNA (349-MER)

Chain 14-A: 



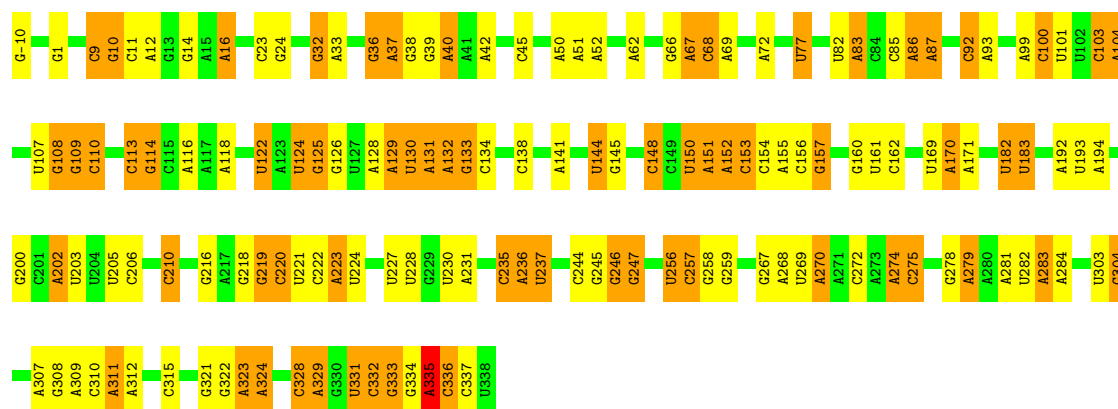
• Molecule 1: RNA (349-MER)

Chain 15-A: 



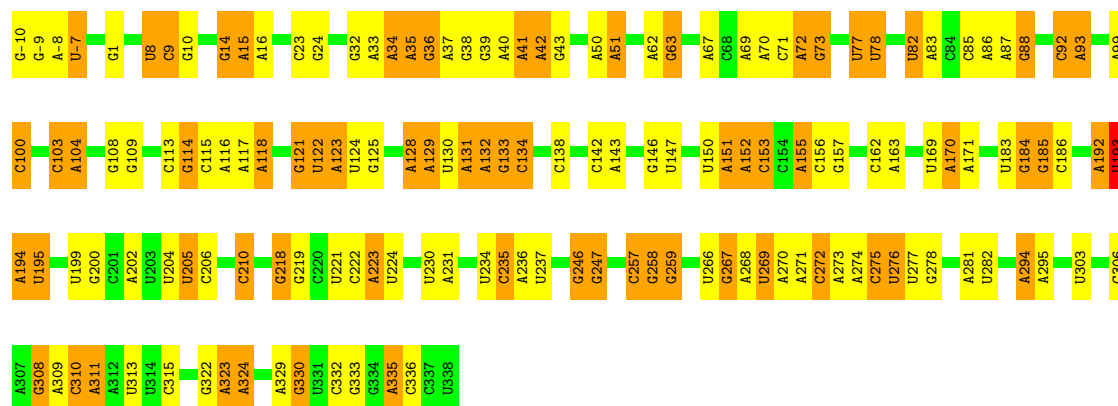
• Molecule 1: RNA (349-MER)

Chain 16-A: 



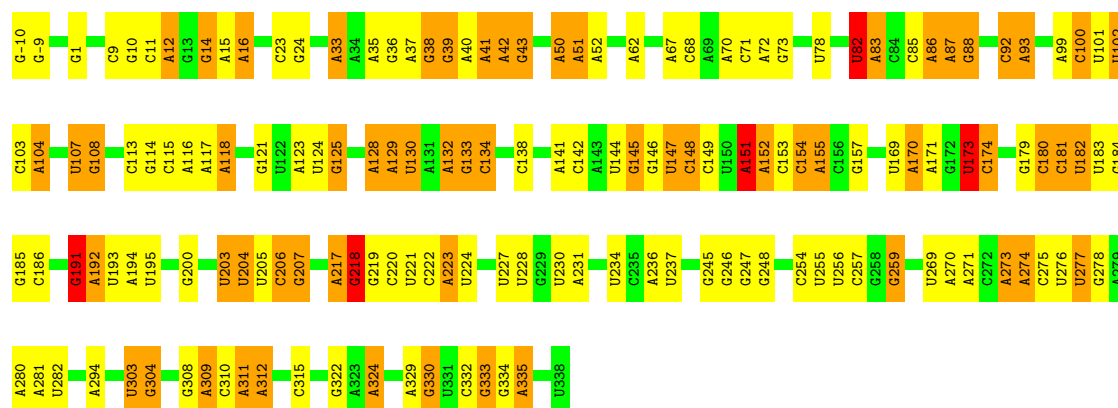
• Molecule 1: RNA (349-MER)

Chain 17-A: 



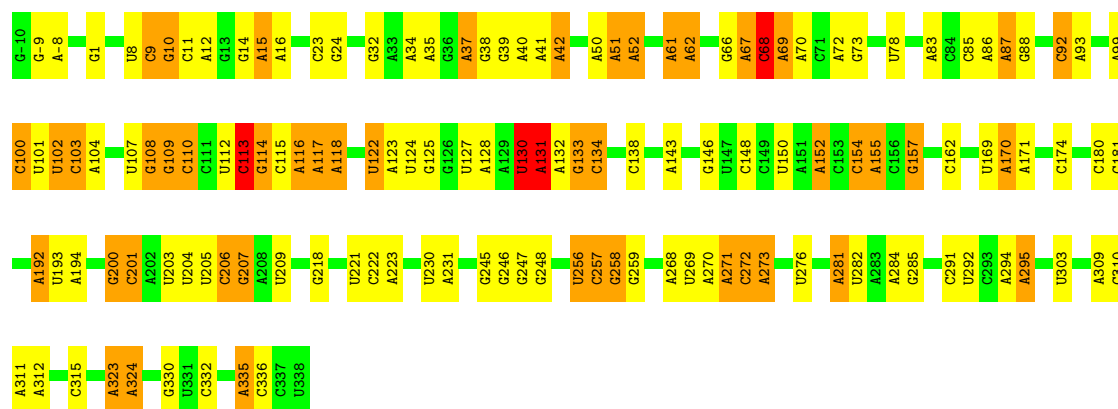
• Molecule 1: RNA (349-MER)

Chain 18-A:  55% 26% 17% .



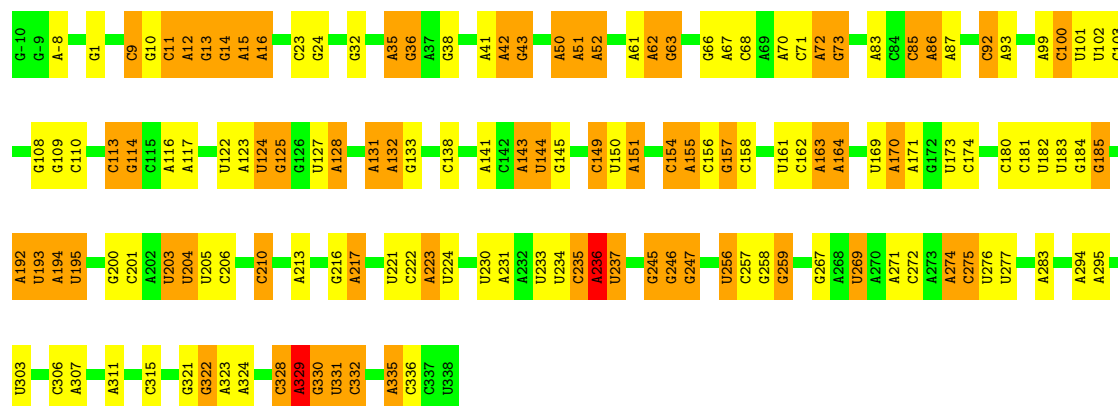
• Molecule 1: RNA (349-MER)

Chain 19-A:  60% 25% 13% .



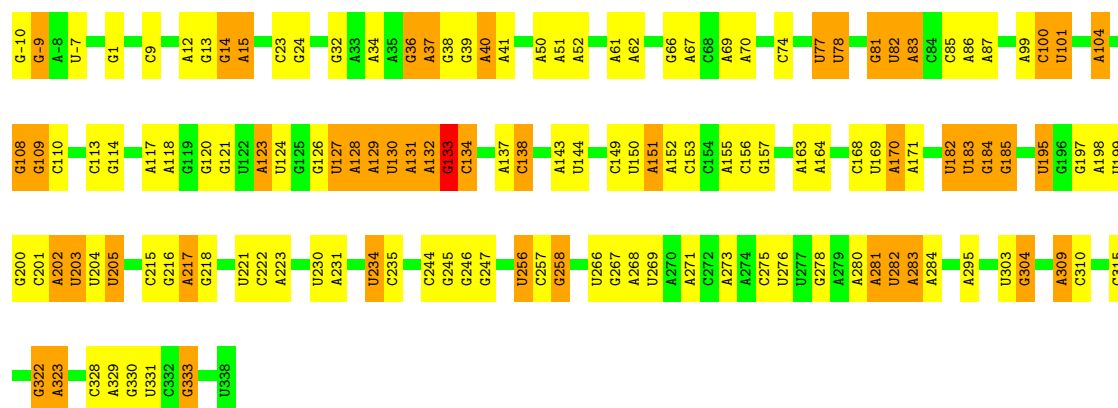
• Molecule 1: RNA (349-MER)

Chain 20-A:  58% 23% 19% .



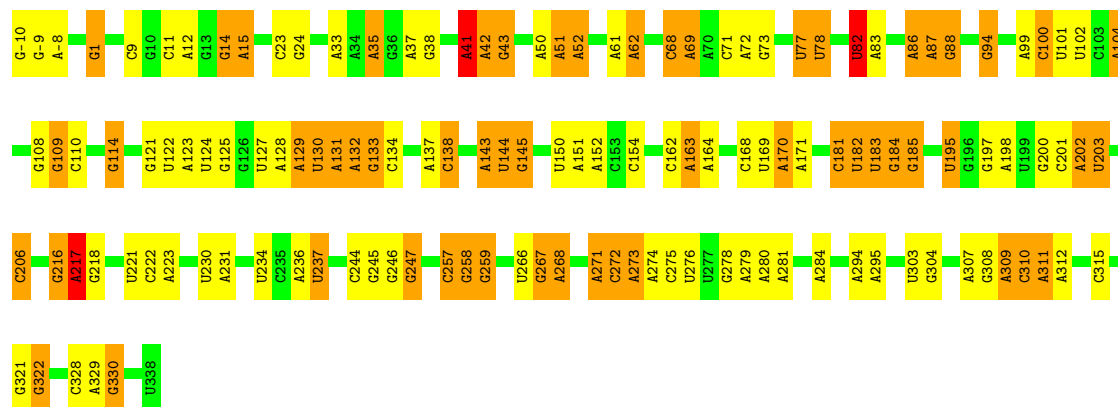
• Molecule 1: RNA (349-MER)

Chain 21-A: 



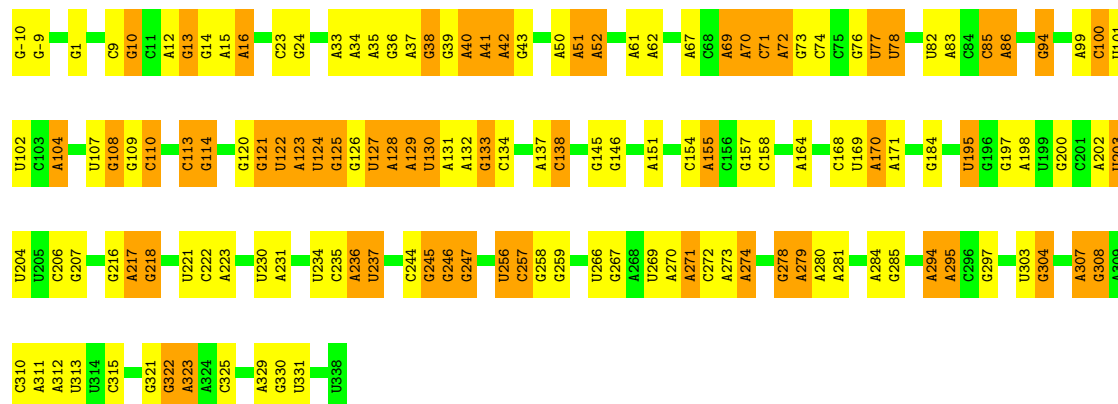
• Molecule 1: RNA (349-MER)

Chain 22-A: 

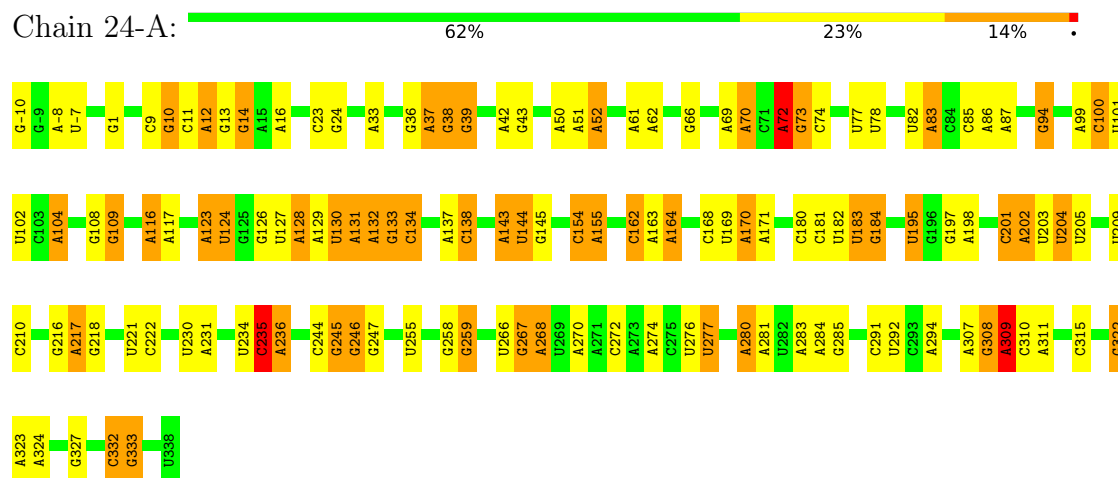


• Molecule 1: RNA (349-MER)

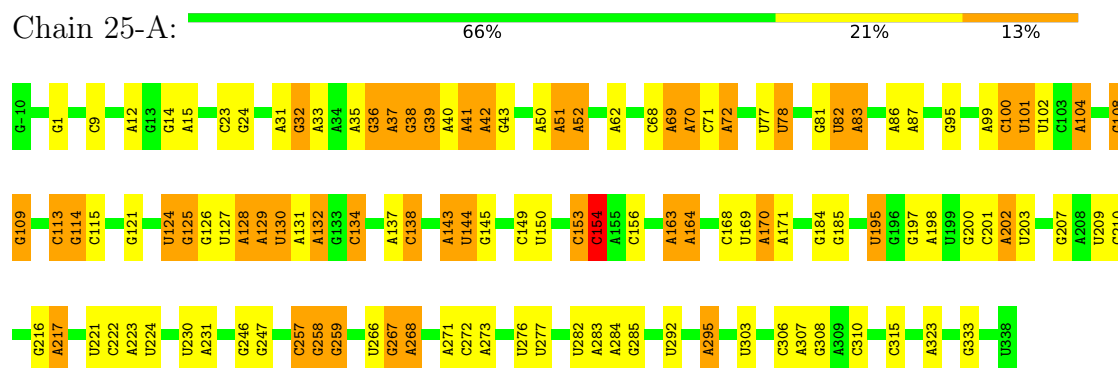
Chain 23-A: 



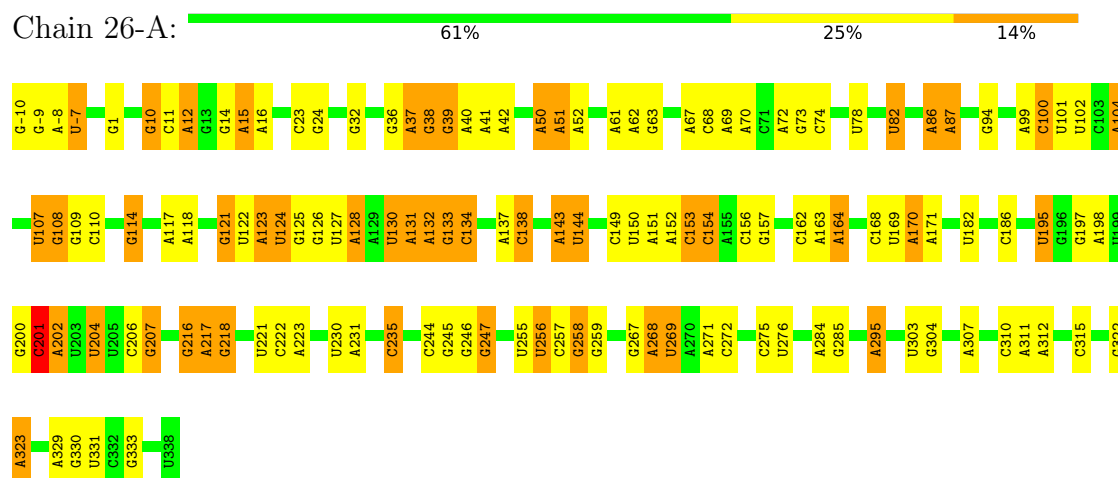
• Molecule 1: RNA (349-MER)



- Molecule 1: RNA (349-MER)

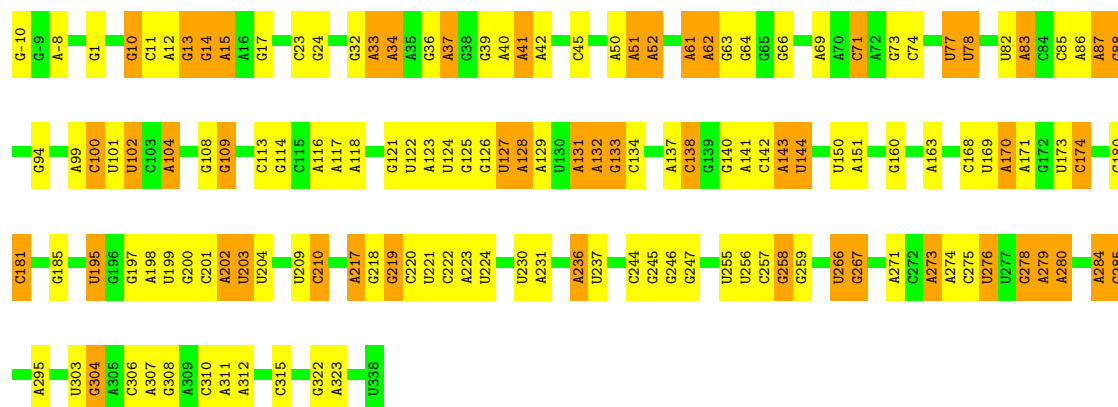


- Molecule 1: RNA (349-MER)



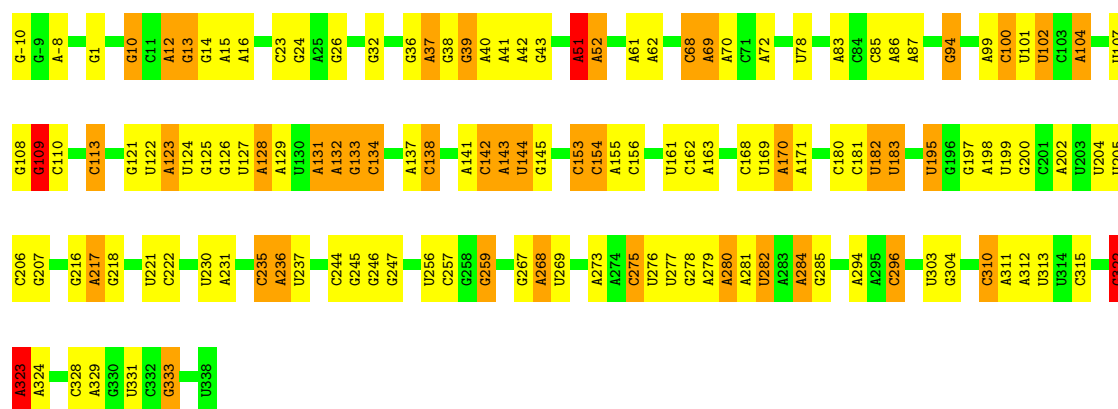
- Molecule 1: RNA (349-MER)





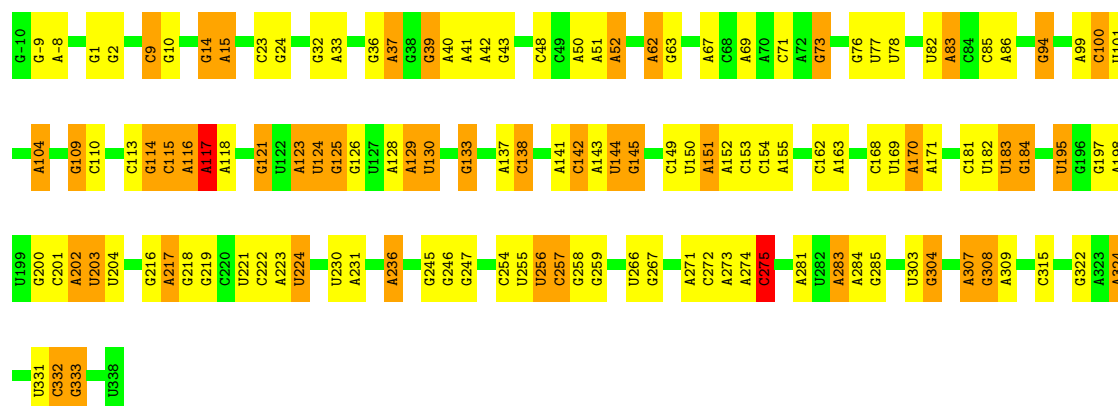
• Molecule 1: RNA (349-MER)

Chain 28-A: 61% 26% 12% .



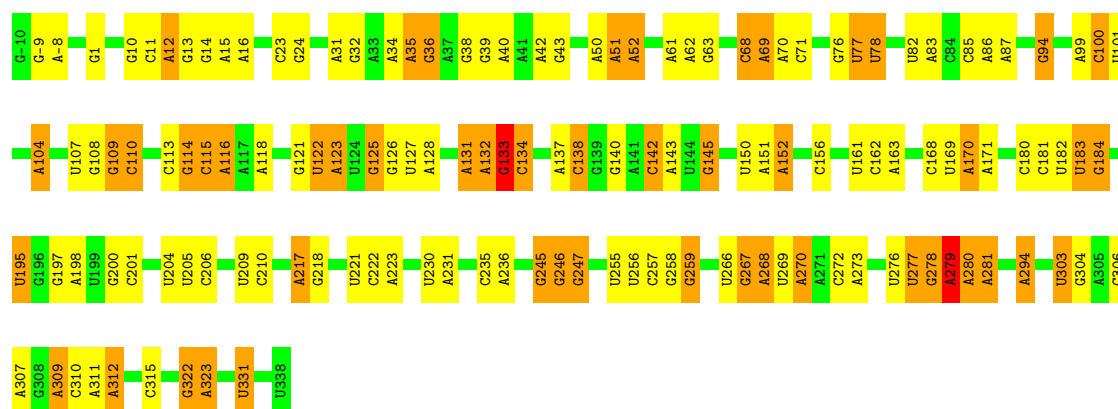
• Molecule 1: RNA (349-MER)

Chain 29-A: 62% 24% 13% .

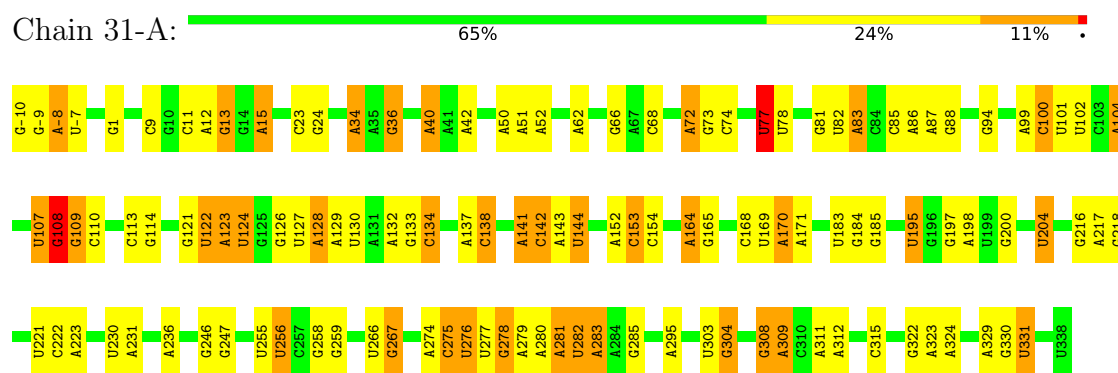


• Molecule 1: RNA (349-MER)

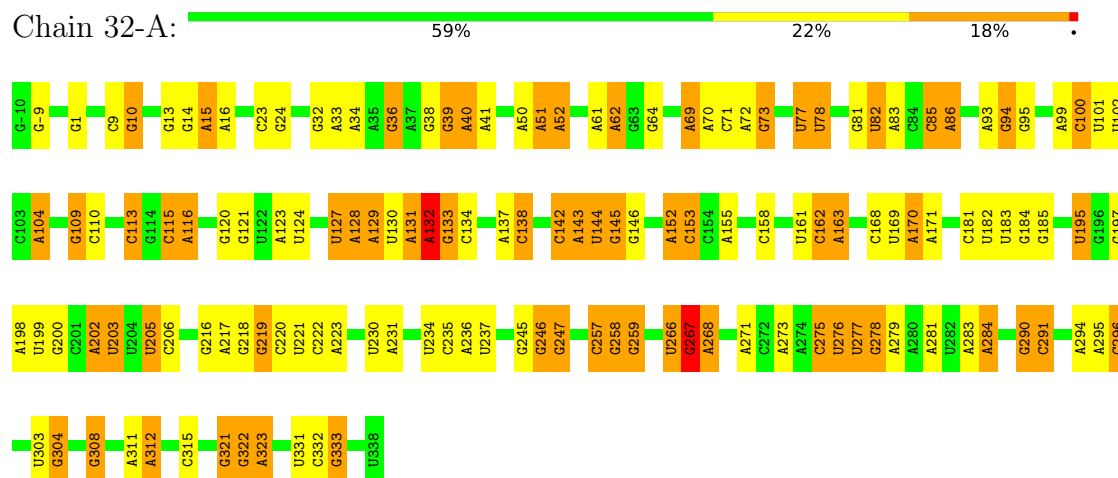
Chain 30-A: 60% 25% 14% .



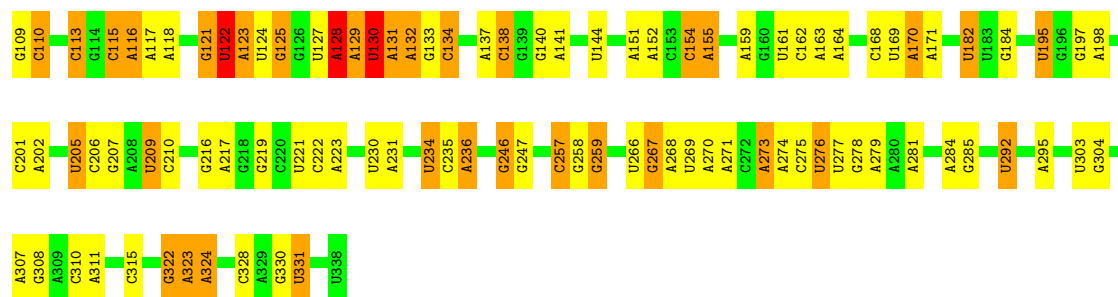
• Molecule 1: RNA (349-MER)



• Molecule 1: RNA (349-MER)

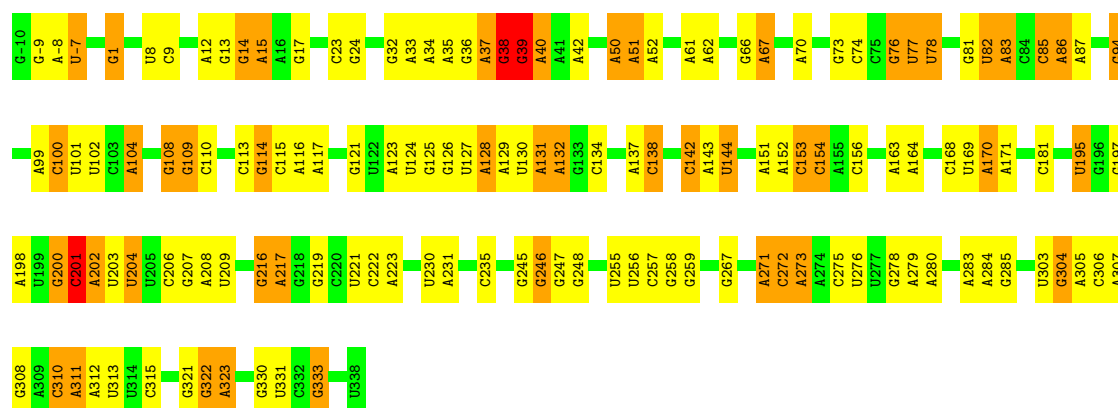


• Molecule 1: RNA (349-MER)



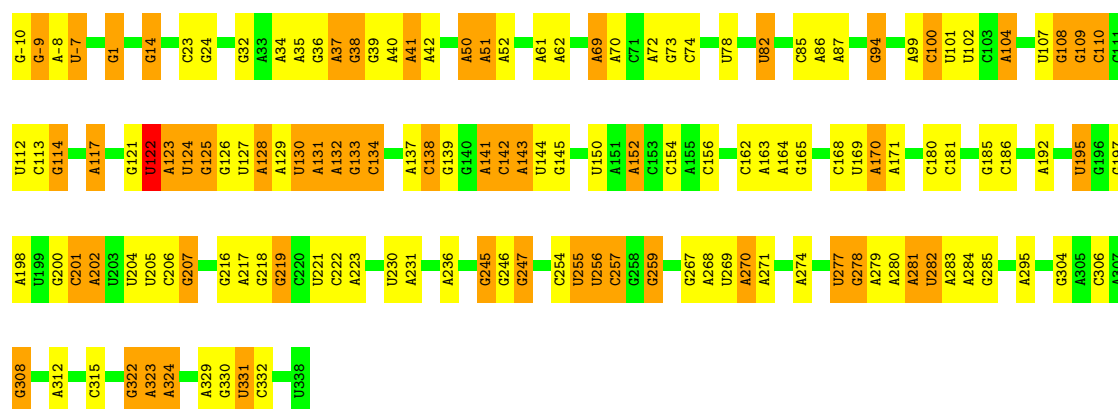
• Molecule 1: RNA (349-MER)

Chain 34-A: 59% 27% 13%



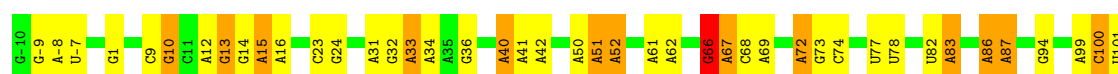
• Molecule 1: RNA (349-MER)

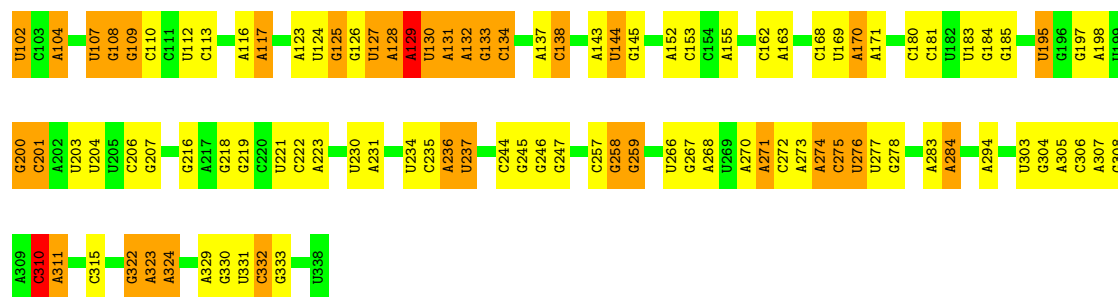
Chain 35-A: 59% 25% 16%



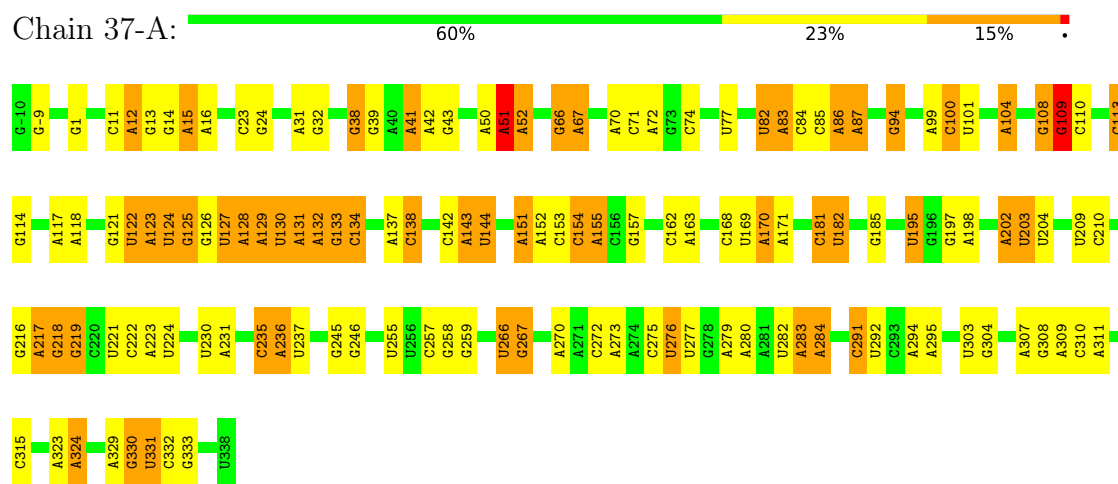
• Molecule 1: RNA (349-MER)

Chain 36-A: 59% 27% 13%

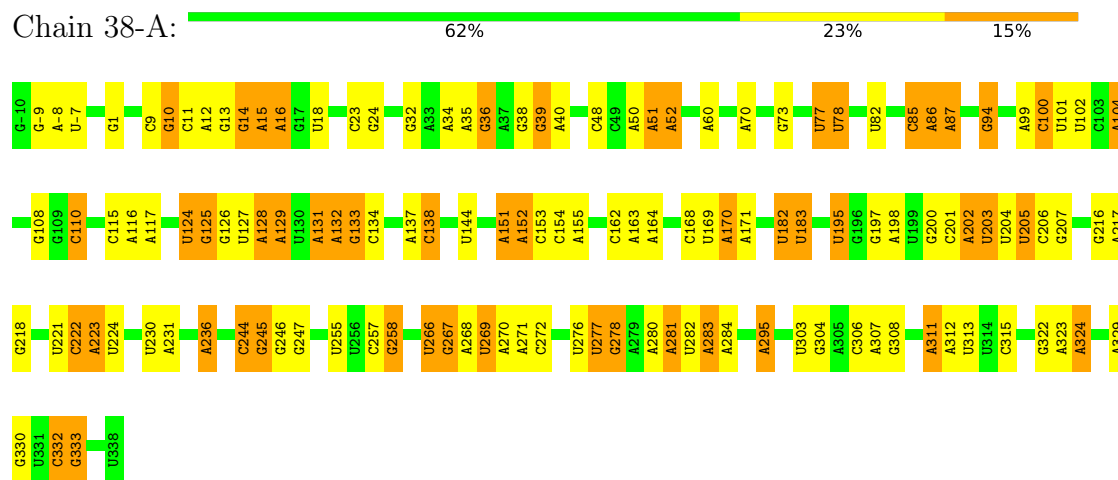




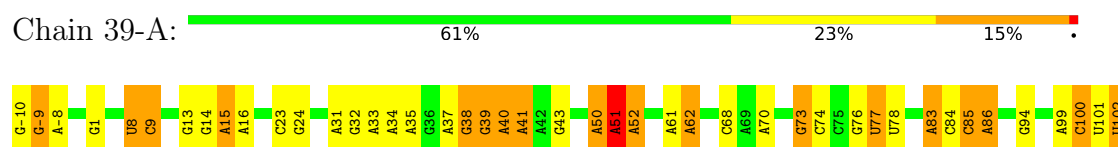
• Molecule 1: RNA (349-MER)

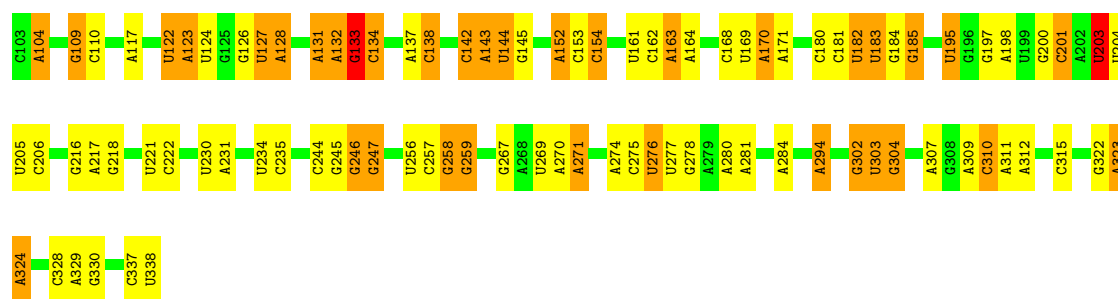


• Molecule 1: RNA (349-MER)



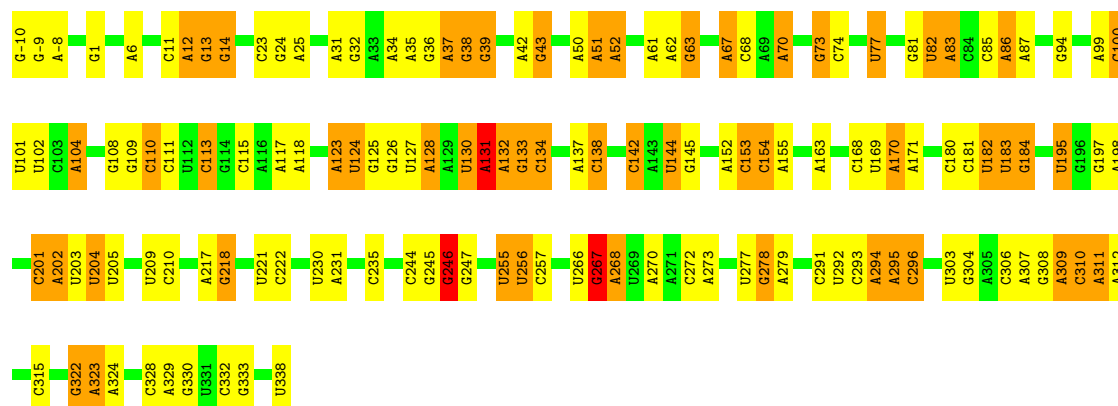
• Molecule 1: RNA (349-MER)





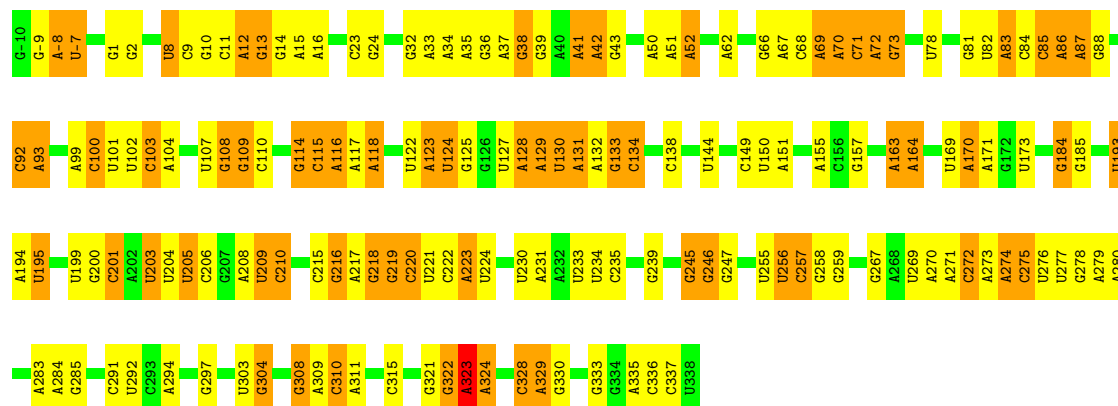
• Molecule 1: RNA (349-MER)

Chain 40-A: 59% 24% 15% .



• Molecule 1: RNA (349-MER)

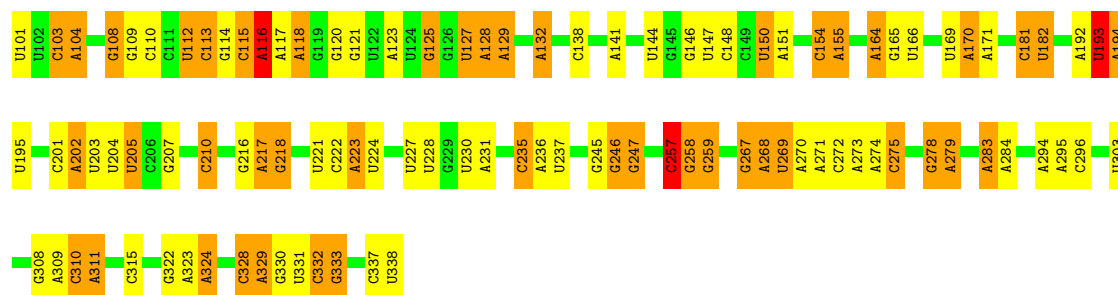
Chain 41-A: 52% 29% 19%



• Molecule 1: RNA (349-MER)

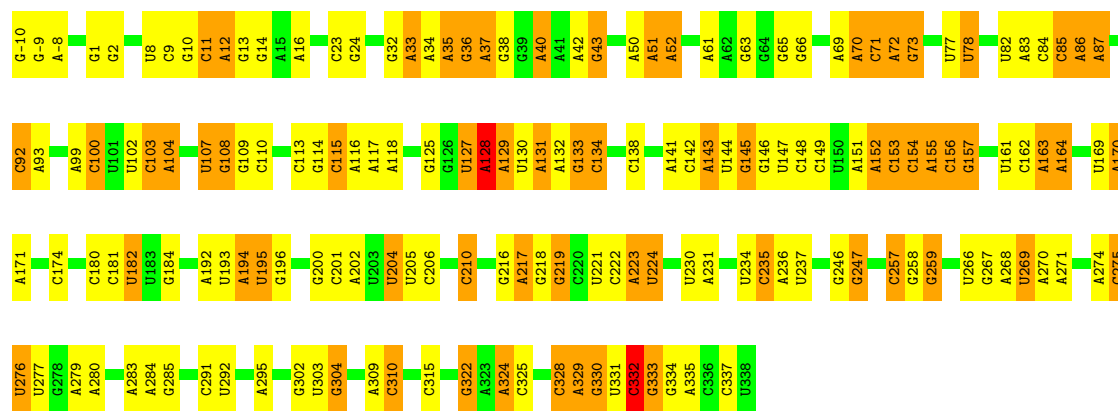
Chain 42-A: 58% 23% 18% .





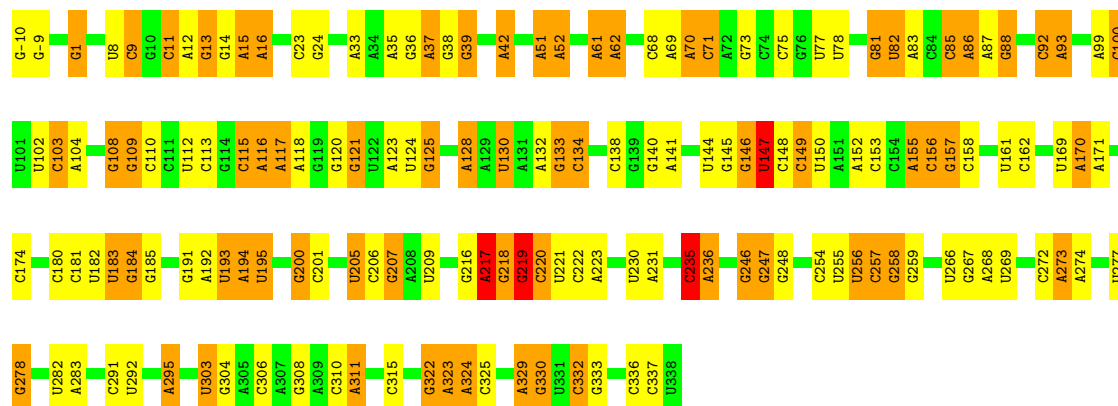
• Molecule 1: RNA (349-MER)

Chain 43-A: 52% 29% 19% .



• Molecule 1: RNA (349-MER)

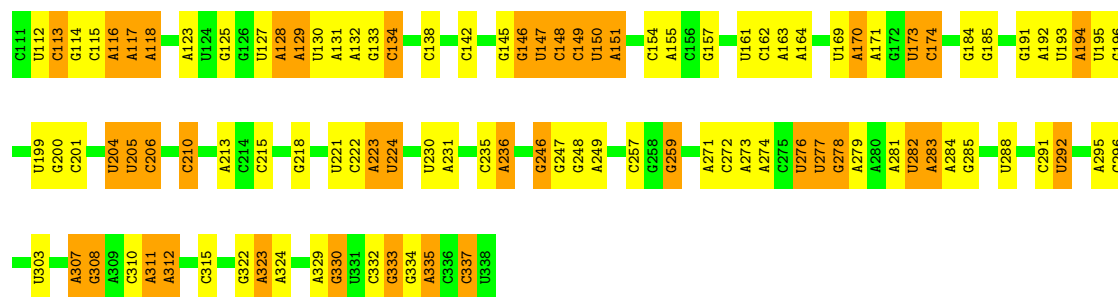
Chain 44-A: 55% 24% 19% .



• Molecule 1: RNA (349-MER)

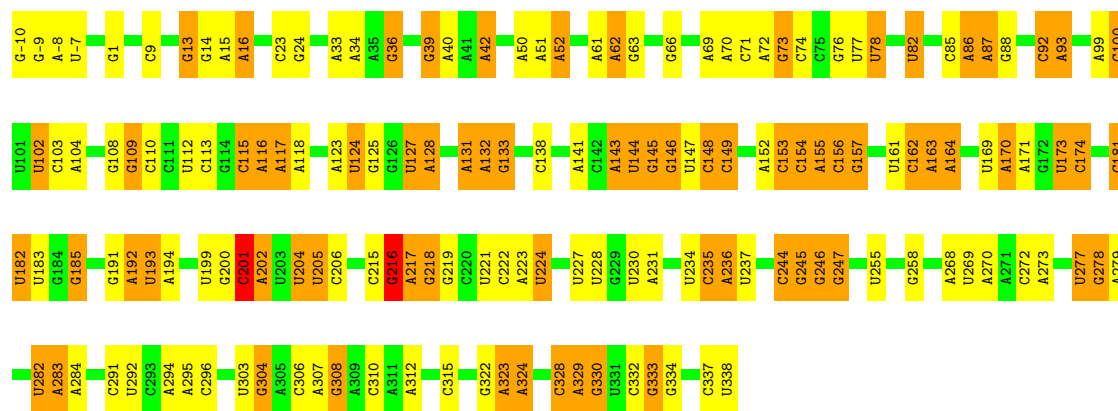
Chain 45-A: 57% 25% 18%





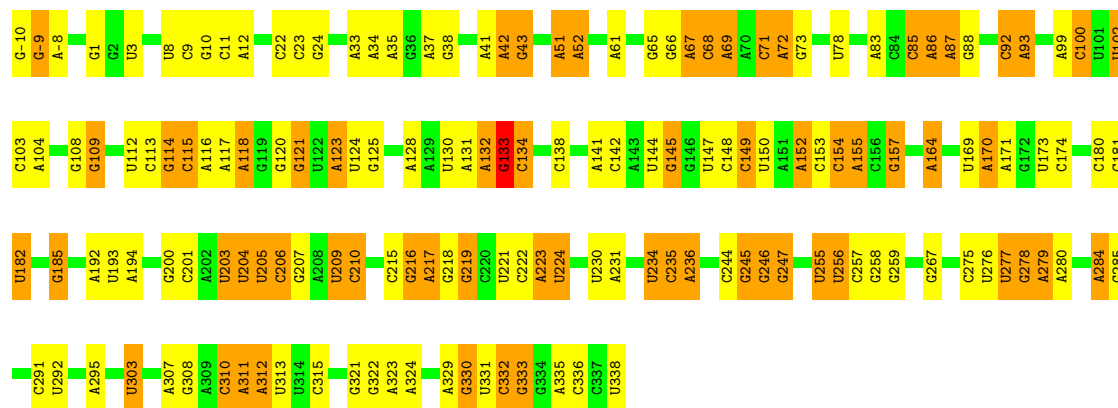
• Molecule 1: RNA (349-MER)

Chain 46-A: 54% 25% 21% .



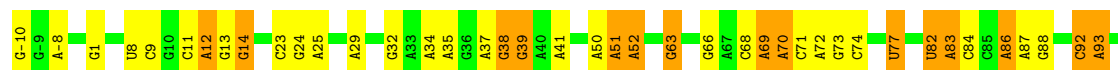
• Molecule 1: RNA (349-MER)

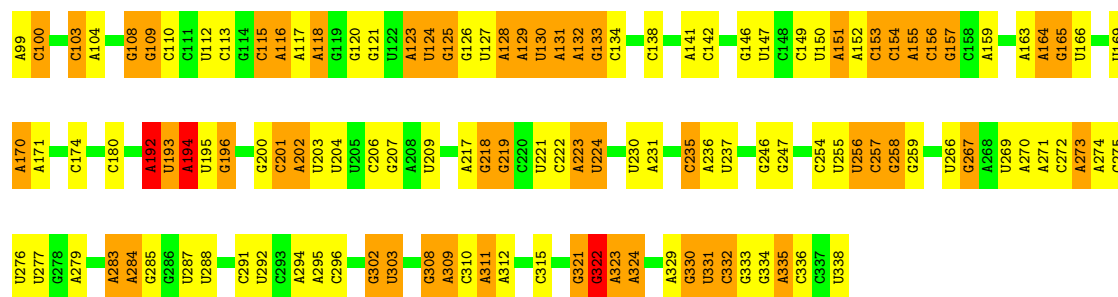
Chain 47-A: 55% 26% 19% .



• Molecule 1: RNA (349-MER)

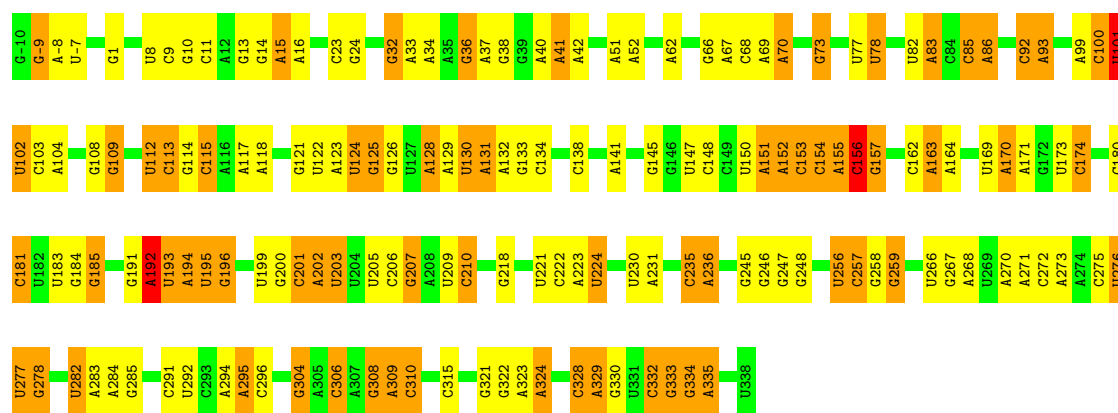
Chain 48-A: 52% 28% 19% .





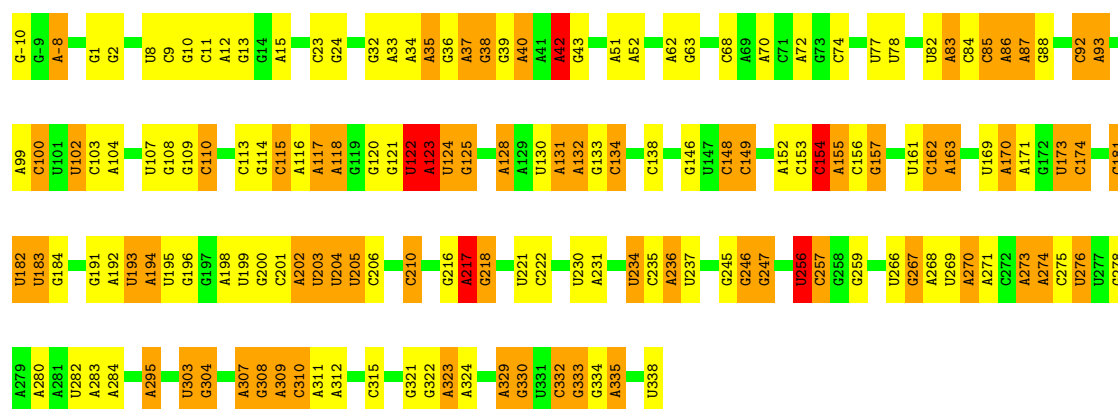
• Molecule 1: RNA (349-MER)

Chain 49-A: 53% 27% 19%



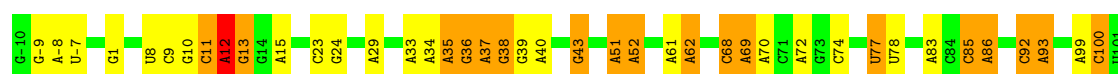
• Molecule 1: RNA (349-MER)

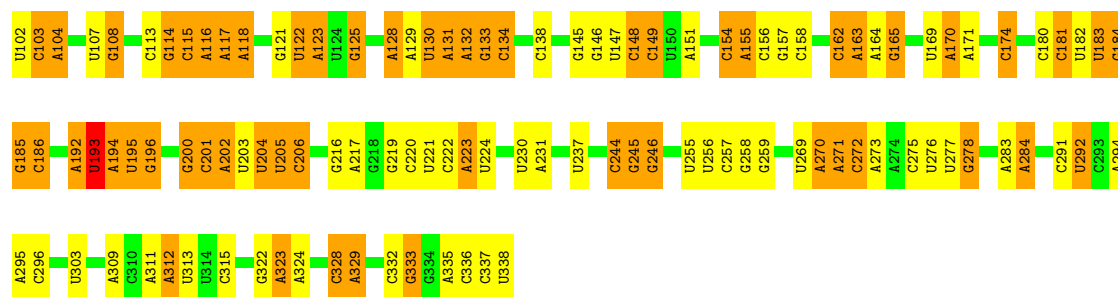
Chain 50-A: 54% 26% 19%



• Molecule 1: RNA (349-MER)

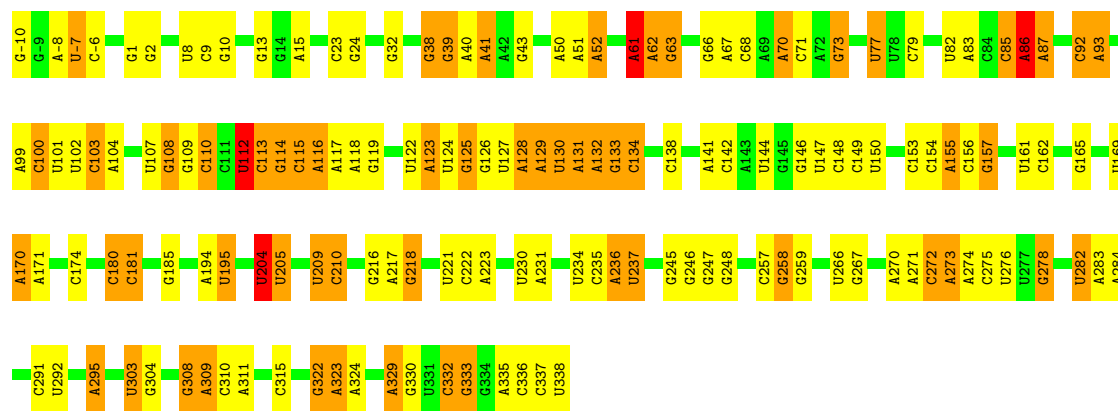
Chain 51-A: 56% 22% 21%





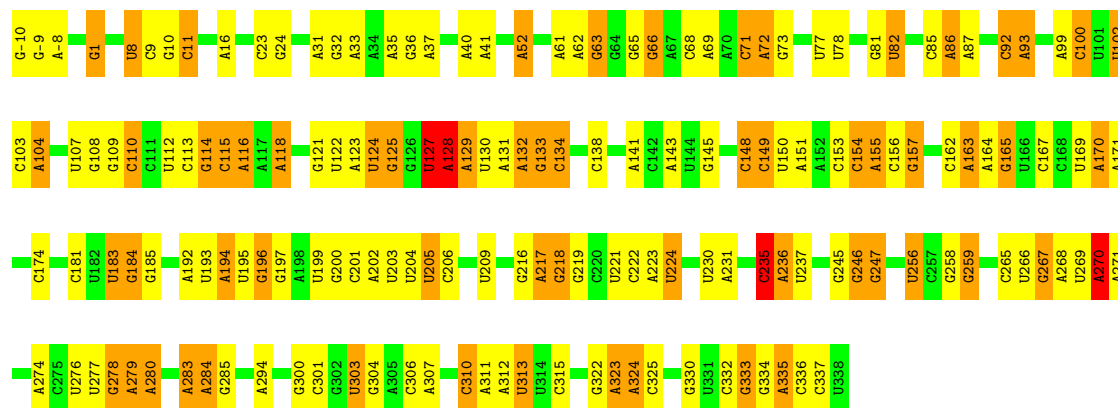
• Molecule 1: RNA (349-MER)

Chain 52-A: 56% 27% 16% .



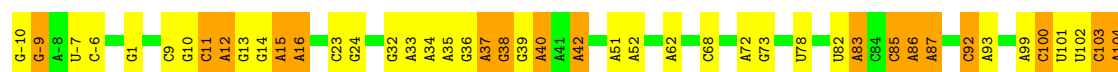
• Molecule 1: RNA (349-MER)

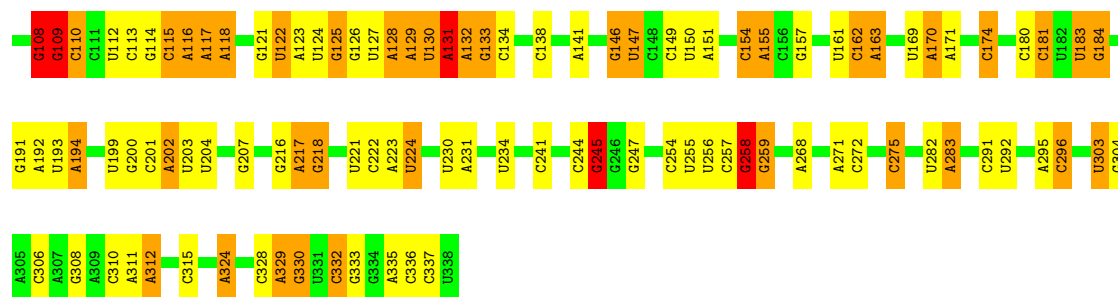
Chain 53-A: 52% 29% 17% .



• Molecule 1: RNA (349-MER)

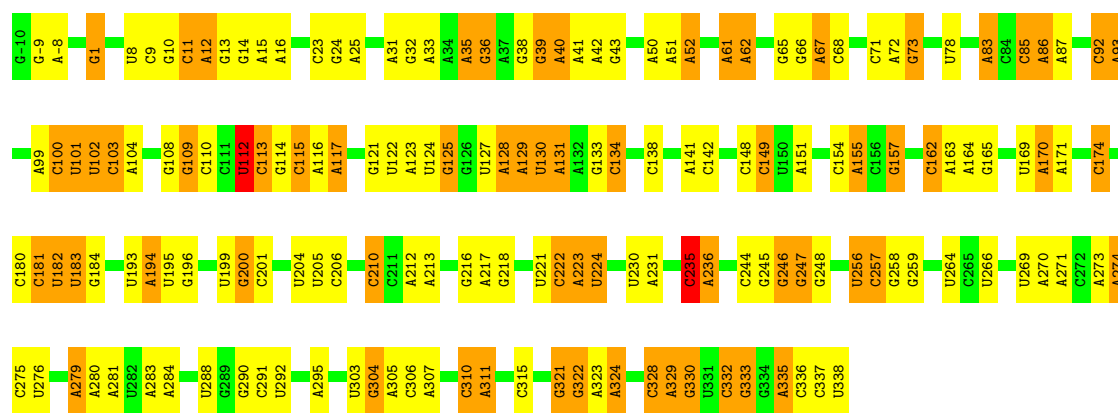
Chain 54-A: 58% 25% 16% .





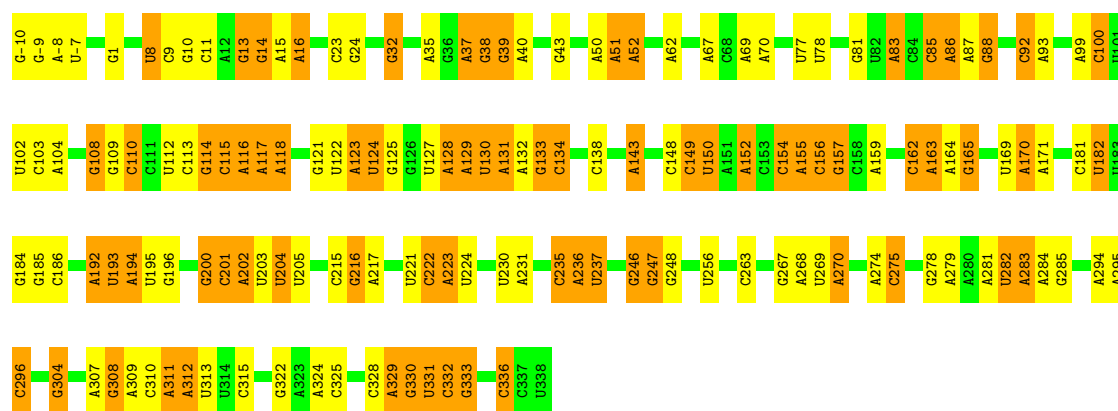
• Molecule 1: RNA (349-MER)

Chain 55-A: 52% 29% 19%



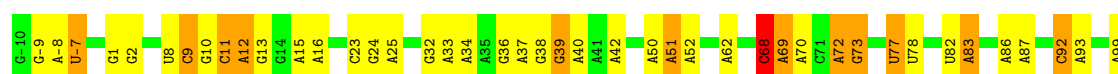
• Molecule 1: RNA (349-MER)

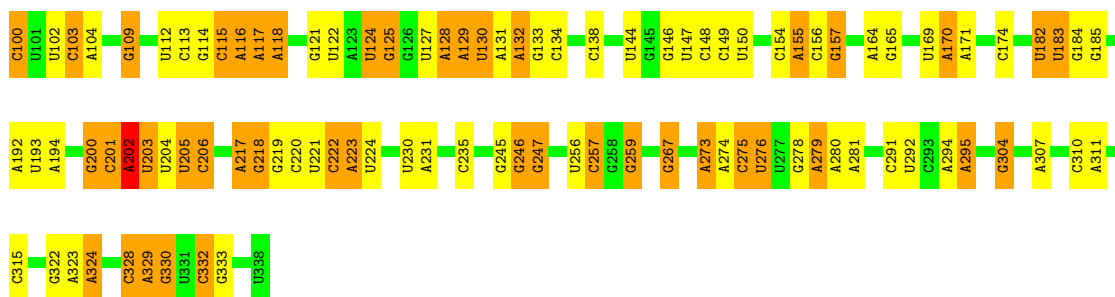
Chain 56-A: 56% 23% 21%



• Molecule 1: RNA (349-MER)

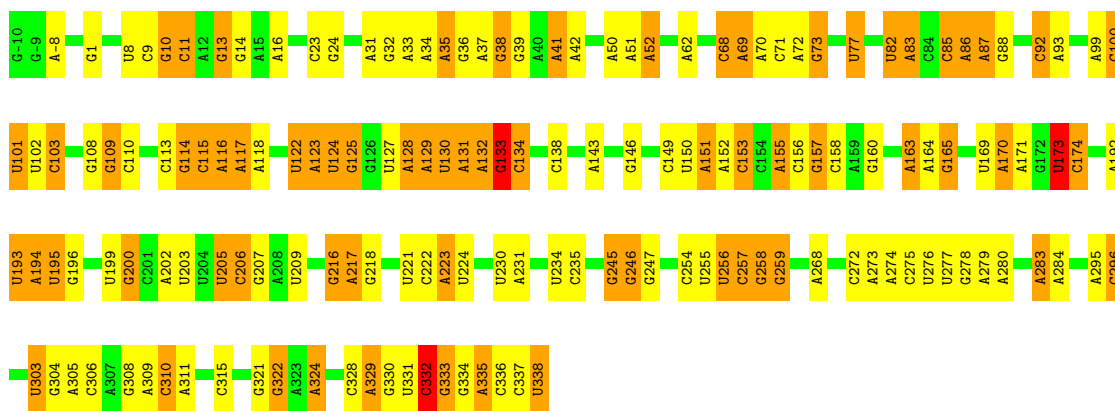
Chain 57-A: 60% 24% 16%





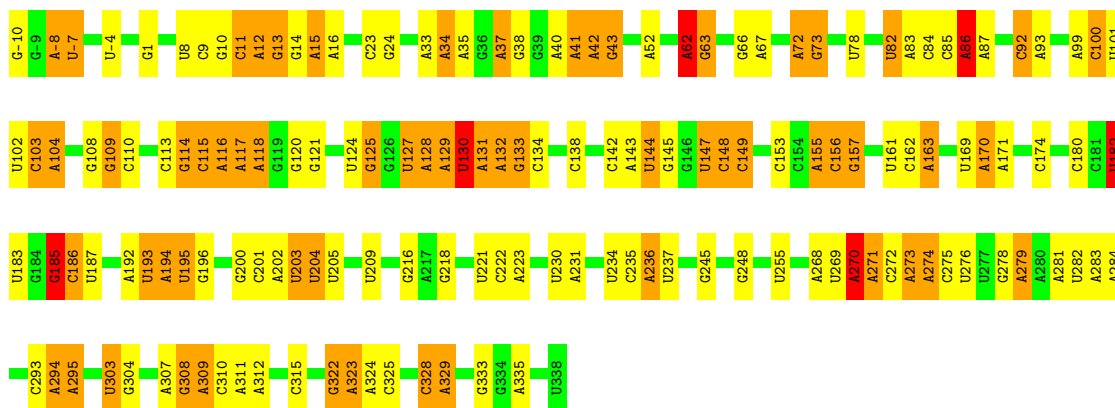
• Molecule 1: RNA (349-MER)

Chain 58-A: 55% 25% 19%



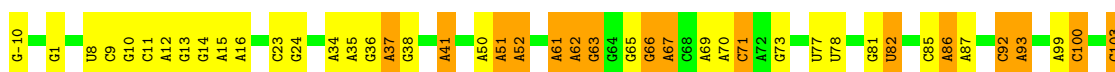
• Molecule 1: RNA (349-MER)

Chain 59-A: 56% 25% 17%



• Molecule 1: RNA (349-MER)

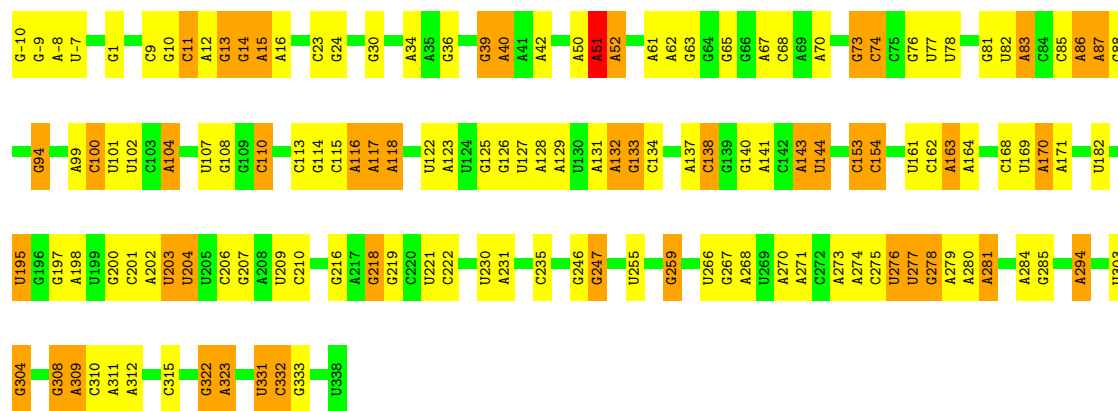
Chain 60-A: 56% 28% 16%





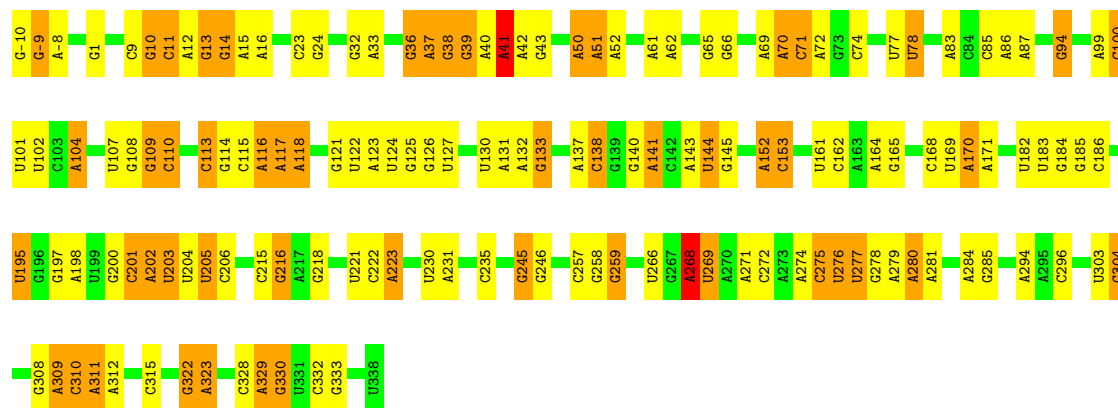
• Molecule 1: RNA (349-MER)

Chain 61-A: 60% 27% 13%



• Molecule 1: RNA (349-MER)

Chain 62-A: 58% 27% 15%



• Molecule 1: RNA (349-MER)

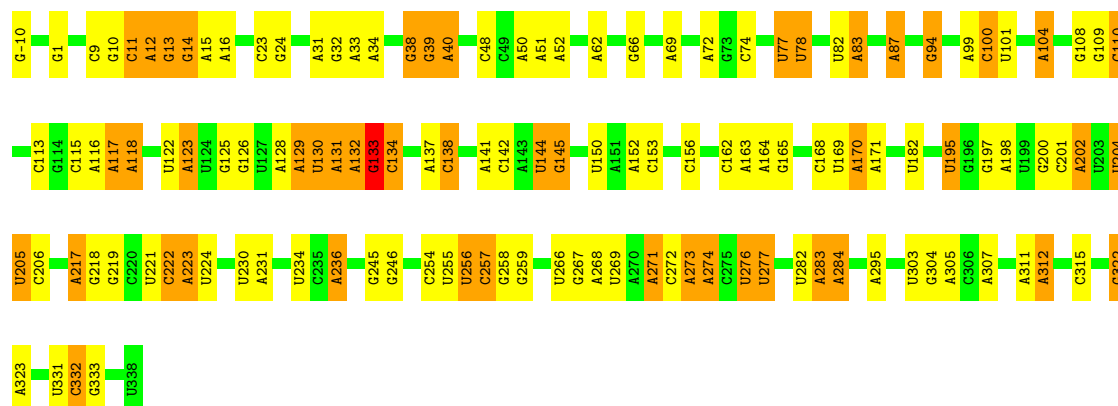
Chain 63-A: 59% 25% 16%





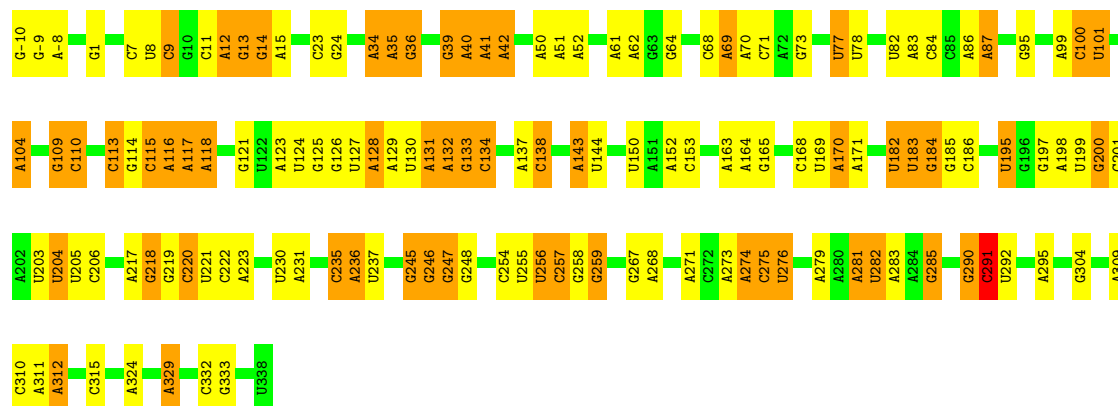
• Molecule 1: RNA (349-MER)

Chain 64-A: 63% 23% 13%



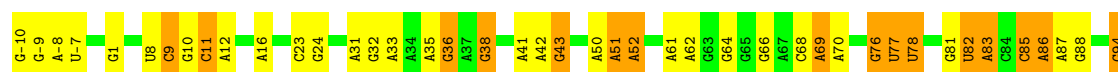
• Molecule 1: RNA (349-MER)

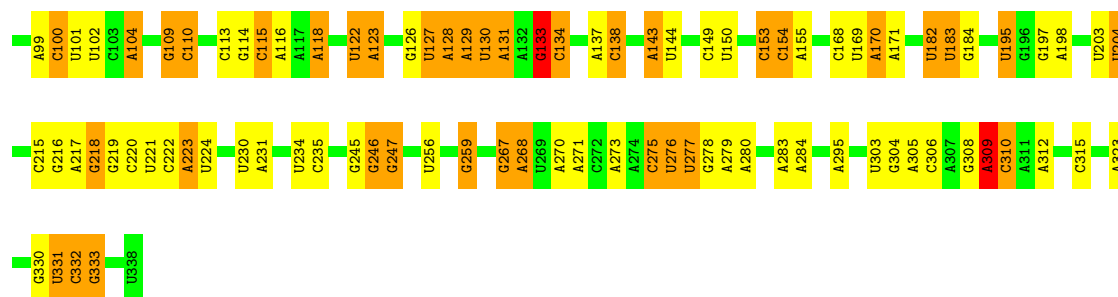
Chain 65-A: 59% 24% 16%



• Molecule 1: RNA (349-MER)

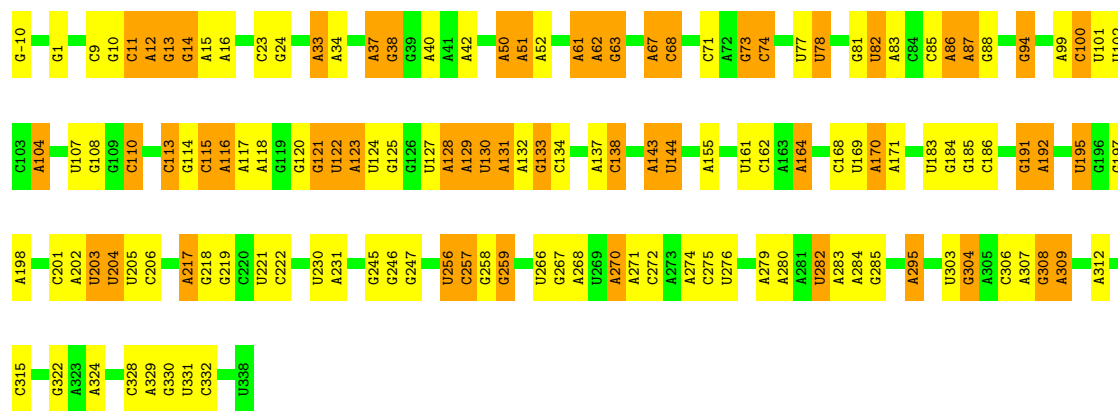
Chain 66-A: 62% 22% 15%





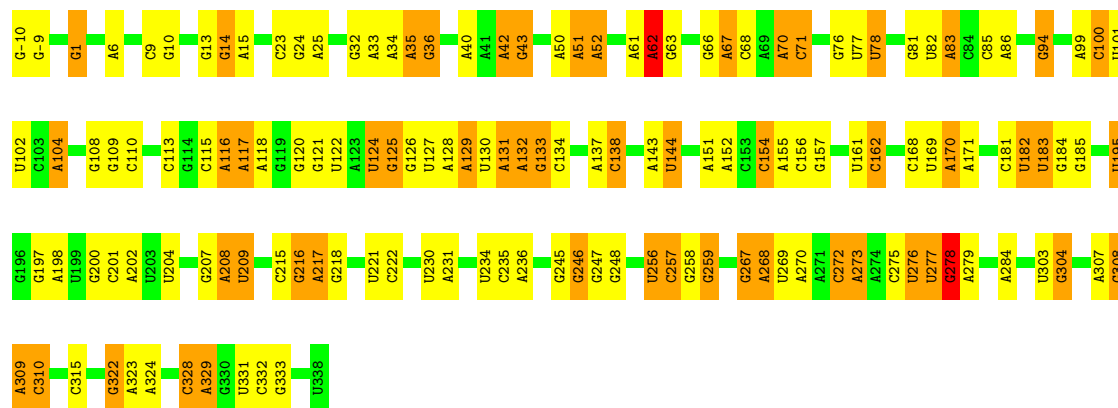
• Molecule 1: RNA (349-MER)

Chain 67-A: 60% 24% 16%



• Molecule 1: RNA (349-MER)

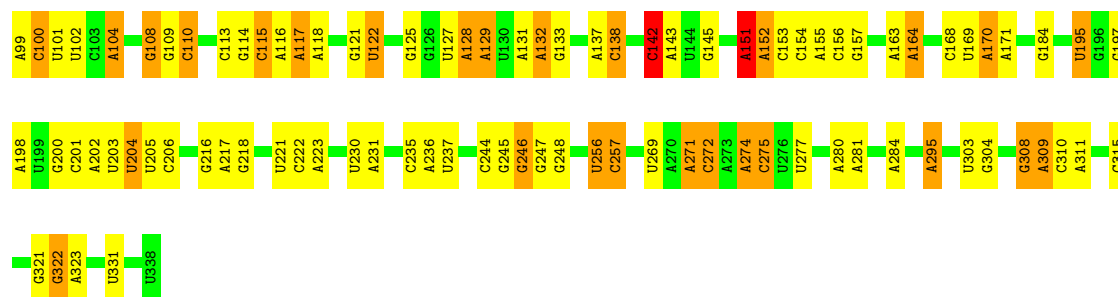
Chain 68-A: 59% 26% 15%



• Molecule 1: RNA (349-MER)

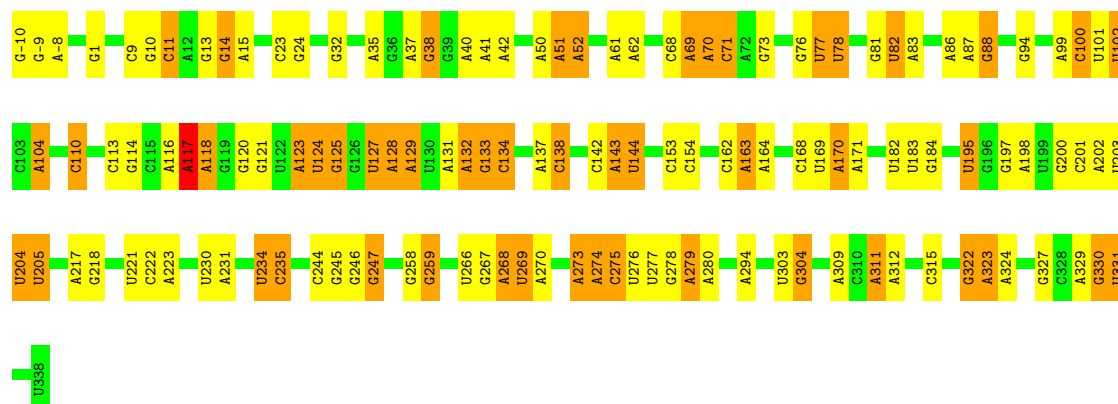
Chain 69-A: 62% 26% 12%





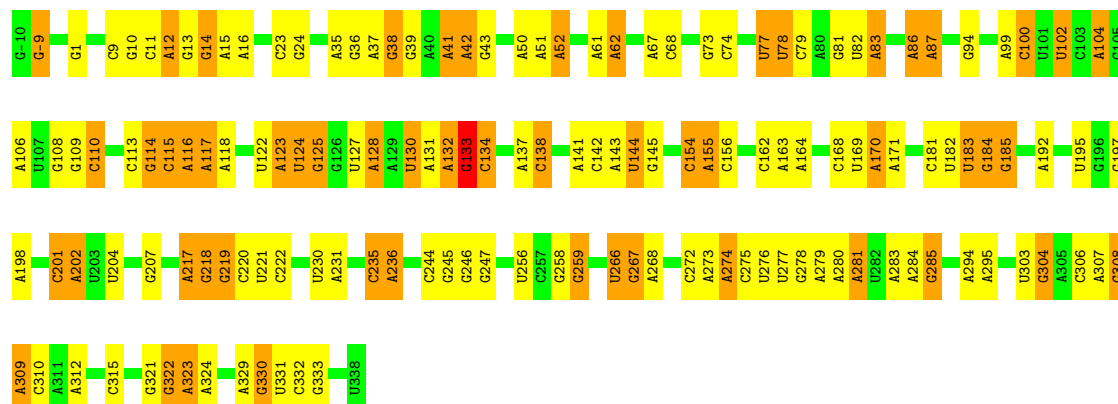
- Molecule 1: RNA (349-MER)

Chain 70-A: 63% 23% 14%



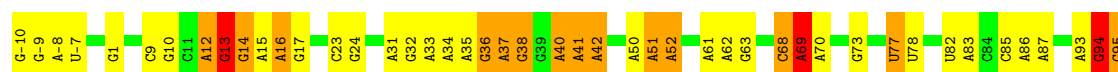
- Molecule 1: RNA (349-MER)

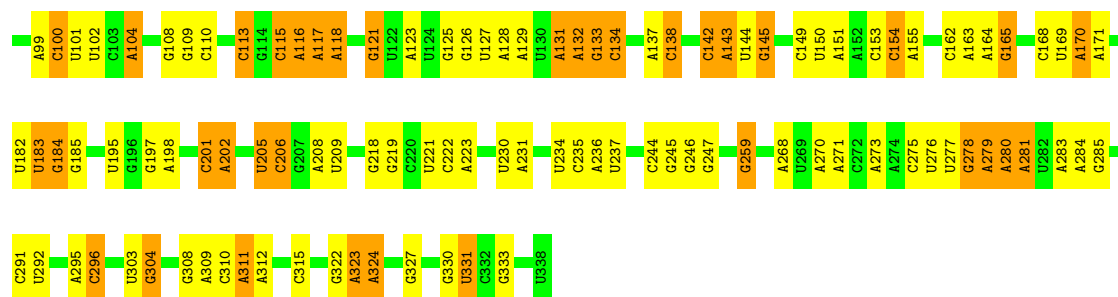
Chain 71-A: 58% 26% 16%



- Molecule 1: RNA (349-MER)

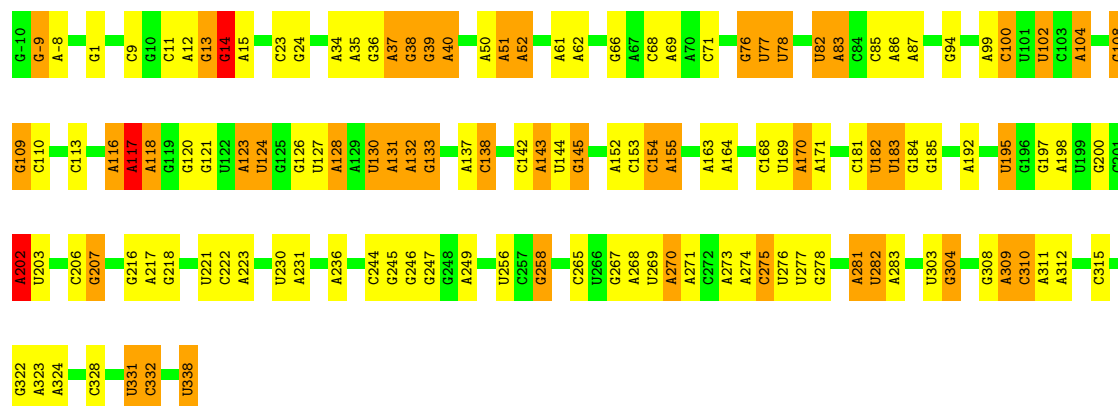
Chain 72-A: 56% 28% 14%





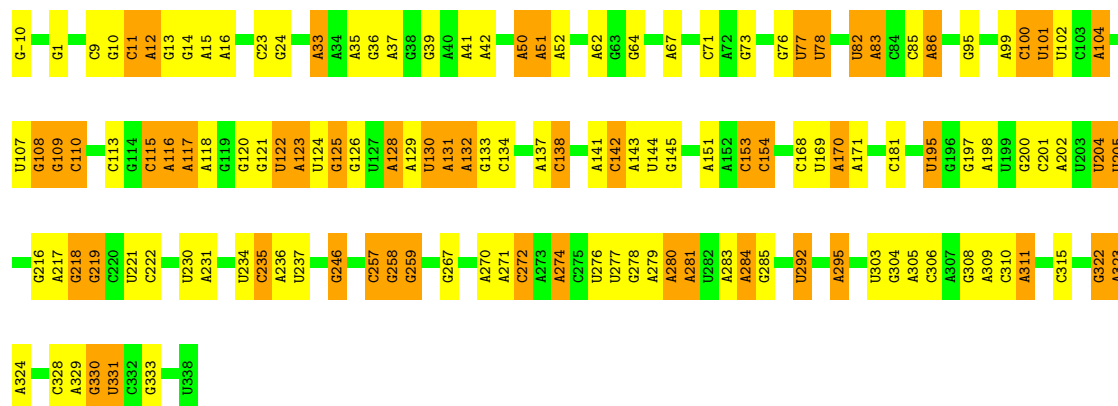
• Molecule 1: RNA (349-MER)

Chain 73-A: 62% 24% 14% .



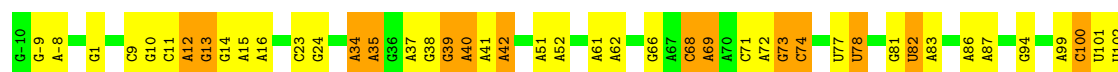
• Molecule 1: RNA (349-MER)

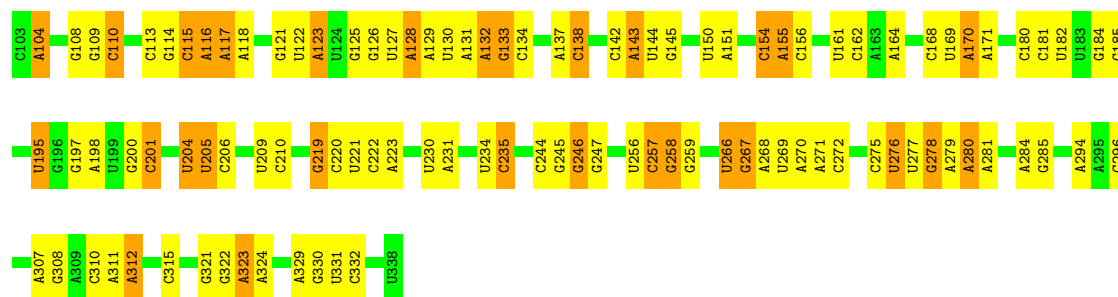
Chain 74-A: 61% 23% 15%



• Molecule 1: RNA (349-MER)

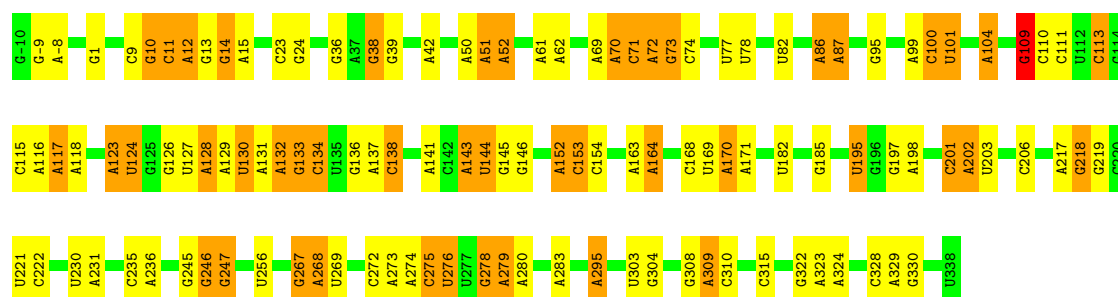
Chain 75-A: 57% 30% 13%





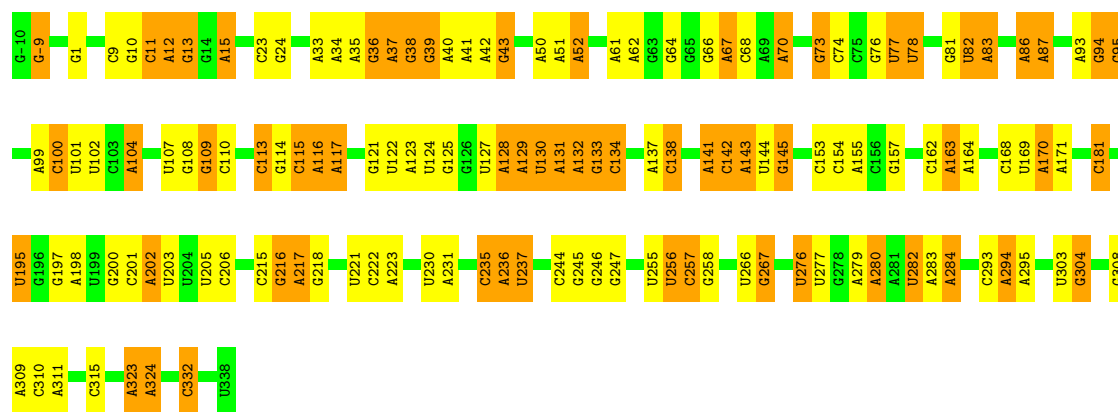
• Molecule 1: RNA (349-MER)

Chain 76-A: 66% 21% 13%



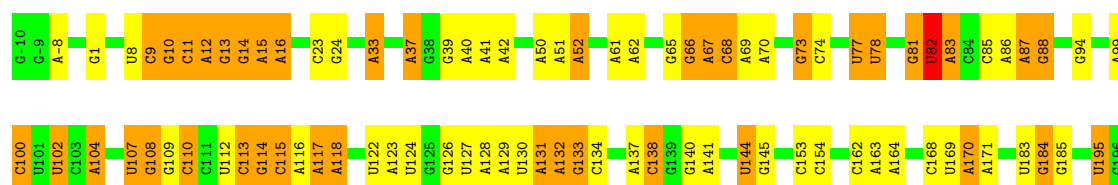
• Molecule 1: RNA (349-MER)

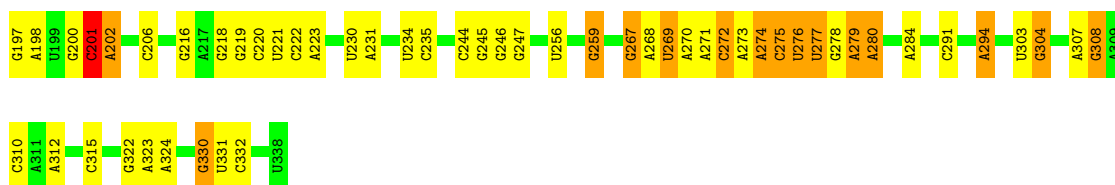
Chain 77-A: 60% 22% 18%



• Molecule 1: RNA (349-MER)

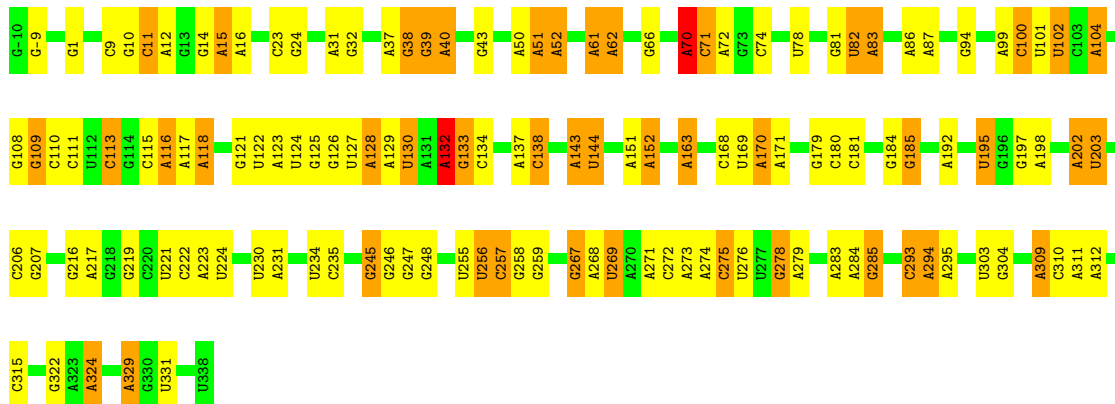
Chain 78-A: 60% 24% 16%





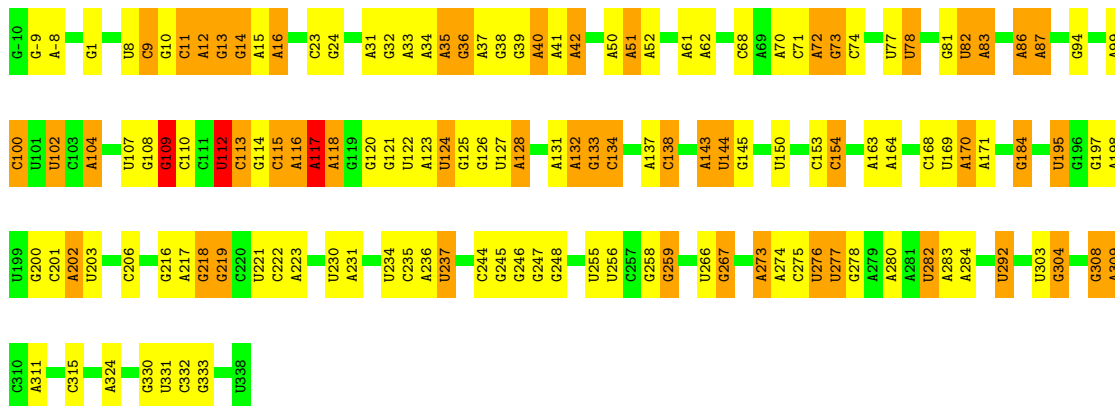
• Molecule 1: RNA (349-MER)

Chain 79-A: 62% 25% 13% .



• Molecule 1: RNA (349-MER)

Chain 80-A: 59% 25% 15% .



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	29191	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	34	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	0.163	Depositor
Minimum map value	-0.089	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.04	Depositor
Map size (\AA)	239.68001, 239.68001, 239.68001	wwPDB
Map dimensions	224, 224, 224	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.07, 1.07, 1.07	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.46	2/8356 (0.0%)	0.91	7/13028 (0.1%)
1	2-A	0.44	0/8356	0.93	11/13028 (0.1%)
1	3-A	0.45	3/8356 (0.0%)	0.93	14/13028 (0.1%)
1	4-A	0.44	0/8356	0.91	4/13028 (0.0%)
1	5-A	0.45	1/8356 (0.0%)	0.90	3/13028 (0.0%)
1	6-A	0.44	0/8356	0.92	7/13028 (0.1%)
1	7-A	0.44	0/8356	0.91	5/13028 (0.0%)
1	8-A	0.45	1/8356 (0.0%)	0.91	6/13028 (0.0%)
1	9-A	0.46	3/8356 (0.0%)	0.93	10/13028 (0.1%)
1	10-A	0.44	0/8356	0.91	8/13028 (0.1%)
1	11-A	0.47	3/8356 (0.0%)	0.91	8/13028 (0.1%)
1	12-A	0.45	3/8356 (0.0%)	0.91	5/13028 (0.0%)
1	13-A	0.44	0/8356	0.90	4/13028 (0.0%)
1	14-A	0.62	3/8356 (0.0%)	0.92	10/13028 (0.1%)
1	15-A	0.46	3/8356 (0.0%)	0.92	10/13028 (0.1%)
1	16-A	0.44	2/8355 (0.0%)	0.90	6/13024 (0.0%)
1	17-A	0.45	2/8356 (0.0%)	0.91	4/13028 (0.0%)
1	18-A	0.47	3/8356 (0.0%)	0.92	7/13028 (0.1%)
1	19-A	0.45	1/8356 (0.0%)	0.93	12/13028 (0.1%)
1	20-A	0.47	1/8356 (0.0%)	0.92	10/13028 (0.1%)
1	21-A	0.46	1/8356 (0.0%)	0.87	3/13028 (0.0%)
1	22-A	0.44	0/8356	0.86	3/13028 (0.0%)
1	23-A	0.45	1/8356 (0.0%)	0.85	0/13028
1	24-A	0.46	2/8356 (0.0%)	0.88	5/13028 (0.0%)
1	25-A	0.46	0/8356	0.87	2/13028 (0.0%)
1	26-A	0.45	1/8356 (0.0%)	0.86	1/13028 (0.0%)
1	27-A	0.44	0/8356	0.85	0/13028
1	28-A	0.46	1/8356 (0.0%)	0.89	8/13028 (0.1%)
1	29-A	0.45	1/8356 (0.0%)	0.87	4/13028 (0.0%)
1	30-A	0.46	1/8356 (0.0%)	0.87	3/13028 (0.0%)
1	31-A	0.46	1/8356 (0.0%)	0.86	3/13028 (0.0%)
1	32-A	0.45	0/8356	0.87	2/13028 (0.0%)
1	33-A	0.48	1/8356 (0.0%)	0.89	10/13028 (0.1%)
1	34-A	0.48	1/8356 (0.0%)	0.88	5/13028 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	35-A	0.45	1/8356 (0.0%)	0.86	2/13028 (0.0%)
1	36-A	0.46	2/8356 (0.0%)	0.89	9/13028 (0.1%)
1	37-A	0.46	1/8356 (0.0%)	0.86	3/13028 (0.0%)
1	38-A	0.45	0/8356	0.85	0/13028
1	39-A	0.45	1/8356 (0.0%)	0.88	7/13028 (0.1%)
1	40-A	0.45	0/8356	0.87	5/13028 (0.0%)
1	41-A	0.46	2/8355 (0.0%)	0.91	6/13024 (0.0%)
1	42-A	0.65	4/8356 (0.0%)	0.92	7/13028 (0.1%)
1	43-A	0.50	2/8355 (0.0%)	0.92	8/13024 (0.1%)
1	44-A	0.46	3/8355 (0.0%)	0.92	8/13024 (0.1%)
1	45-A	0.43	0/8355	0.90	2/13024 (0.0%)
1	46-A	0.44	1/8355 (0.0%)	0.90	4/13024 (0.0%)
1	47-A	0.45	3/8355 (0.0%)	0.91	6/13024 (0.0%)
1	48-A	0.48	1/8355 (0.0%)	0.92	11/13024 (0.1%)
1	49-A	0.72	3/8356 (0.0%)	0.92	11/13028 (0.1%)
1	50-A	0.50	4/8355 (0.0%)	0.94	11/13024 (0.1%)
1	51-A	0.45	1/8355 (0.0%)	0.91	5/13024 (0.0%)
1	52-A	0.46	3/8355 (0.0%)	0.91	7/13024 (0.1%)
1	53-A	0.48	2/8355 (0.0%)	0.91	8/13024 (0.1%)
1	54-A	0.45	3/8355 (0.0%)	0.90	8/13024 (0.1%)
1	55-A	0.46	2/8355 (0.0%)	0.89	3/13024 (0.0%)
1	56-A	0.51	1/8355 (0.0%)	0.91	6/13024 (0.0%)
1	57-A	0.44	1/8355 (0.0%)	0.91	7/13024 (0.1%)
1	58-A	0.47	3/8355 (0.0%)	0.90	4/13024 (0.0%)
1	59-A	0.47	2/8355 (0.0%)	0.92	11/13024 (0.1%)
1	60-A	0.49	2/8355 (0.0%)	0.90	4/13024 (0.0%)
1	61-A	0.45	0/8356	0.86	1/13028 (0.0%)
1	62-A	0.45	0/8356	0.86	3/13028 (0.0%)
1	63-A	0.46	1/8356 (0.0%)	0.85	1/13028 (0.0%)
1	64-A	0.45	0/8356	0.86	2/13028 (0.0%)
1	65-A	0.45	0/8356	0.87	2/13028 (0.0%)
1	66-A	0.45	0/8356	0.86	3/13028 (0.0%)
1	67-A	0.44	0/8356	0.86	1/13028 (0.0%)
1	68-A	0.46	1/8356 (0.0%)	0.87	2/13028 (0.0%)
1	69-A	0.46	0/8356	0.87	5/13028 (0.0%)
1	70-A	0.47	1/8356 (0.0%)	0.87	1/13028 (0.0%)
1	71-A	0.46	0/8356	0.88	5/13028 (0.0%)
1	72-A	0.47	2/8356 (0.0%)	0.87	4/13028 (0.0%)
1	73-A	0.47	2/8356 (0.0%)	0.87	2/13028 (0.0%)
1	74-A	0.46	0/8356	0.87	2/13028 (0.0%)
1	75-A	0.46	0/8356	0.86	0/13028
1	76-A	0.46	1/8356 (0.0%)	0.86	2/13028 (0.0%)
1	77-A	0.45	0/8356	0.86	1/13028 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	78-A	0.46	2/8356 (0.0%)	0.87	3/13028 (0.0%)
1	79-A	0.45	1/8356 (0.0%)	0.86	3/13028 (0.0%)
1	80-A	0.56	2/8356 (0.0%)	0.86	2/13028 (0.0%)
All	All	0.47	103/668461 (0.0%)	0.89	408/1042164 (0.0%)

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	2-A	1	0
1	3-A	1	0
1	6-A	1	0
1	10-A	1	0
1	19-A	1	0
1	20-A	1	0
1	46-A	1	0
1	48-A	1	0
1	68-A	1	0
All	All	9	0

The worst 5 of 103 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	49-A	112	U	O3'-P	44.23	2.14	1.61
1	14-A	82	U	O3'-P	39.70	2.08	1.61
1	42-A	112	U	O3'-P	34.31	2.02	1.61
1	80-A	112	U	O3'-P	30.94	1.98	1.61
1	42-A	8	U	O3'-P	27.31	1.94	1.61

The worst 5 of 408 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	7-A	93	A	OP1-P-O3'	-24.45	51.41	105.20
1	59-A	93	A	OP1-P-O3'	-24.45	51.42	105.20
1	42-A	93	A	OP1-P-O3'	-24.44	51.42	105.20
1	60-A	93	A	OP1-P-O3'	-24.44	51.42	105.20
1	58-A	93	A	OP1-P-O3'	-24.44	51.43	105.20

5 of 9 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	2-A	14	G	C3'
1	3-A	201	C	C3'
1	6-A	322	G	C3'
1	10-A	131	A	C3'
1	19-A	256	U	C3'

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in 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	7464	3763	3764	147	0
1	2-A	7464	3763	3764	162	0
1	3-A	7464	3763	3764	180	0
1	4-A	7464	3763	3764	161	0
1	5-A	7464	3763	3764	208	0
1	6-A	7464	3763	3764	181	0
1	7-A	7464	3763	3764	113	0
1	8-A	7464	3763	3764	148	0
1	9-A	7464	3763	3764	195	0
1	10-A	7464	3763	3764	185	0
1	11-A	7464	3763	3764	181	0
1	12-A	7464	3763	3763	208	0
1	13-A	7464	3763	3764	173	0
1	14-A	7464	3763	3764	174	0
1	15-A	7464	3763	3764	195	0
1	16-A	7464	3763	3765	192	0
1	17-A	7464	3763	3764	160	0
1	18-A	7464	3763	3763	162	0
1	19-A	7464	3763	3764	155	0
1	20-A	7464	3763	3763	203	0
1	21-A	7464	3763	3764	159	0
1	22-A	7464	3763	3764	161	0
1	23-A	7464	3763	3764	179	0
1	24-A	7464	3763	3764	127	0
1	25-A	7464	3763	3764	142	0
1	26-A	7464	3763	3764	156	0
1	27-A	7464	3763	3764	136	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	28-A	7464	3763	3764	168	0
1	29-A	7464	3763	3764	116	0
1	30-A	7464	3763	3764	174	0
1	31-A	7464	3763	3763	122	0
1	32-A	7464	3763	3764	147	0
1	33-A	7464	3763	3764	147	0
1	34-A	7464	3763	3763	148	0
1	35-A	7464	3763	3764	162	0
1	36-A	7464	3763	3764	161	0
1	37-A	7464	3763	3764	166	0
1	38-A	7464	3763	3764	170	0
1	39-A	7464	3763	3764	187	0
1	40-A	7464	3763	3764	178	0
1	41-A	7464	3763	3765	202	0
1	42-A	7464	3763	3764	168	0
1	43-A	7464	3763	3765	208	0
1	44-A	7464	3763	3765	191	0
1	45-A	7464	3763	3764	166	0
1	46-A	7464	3762	3764	179	0
1	47-A	7464	3763	3765	186	0
1	48-A	7464	3763	3765	177	0
1	49-A	7464	3763	3765	185	0
1	50-A	7464	3763	3765	208	0
1	51-A	7464	3763	3764	172	0
1	52-A	7464	3763	3765	216	0
1	53-A	7464	3763	3765	171	0
1	54-A	7464	3763	3765	180	0
1	55-A	7464	3763	3765	178	0
1	56-A	7464	3763	3764	192	0
1	57-A	7464	3763	3763	154	0
1	58-A	7464	3763	3765	177	0
1	59-A	7464	3763	3764	188	0
1	60-A	7464	3763	3765	168	0
1	61-A	7464	3763	3764	162	0
1	62-A	7464	3763	3764	149	0
1	63-A	7464	3763	3764	162	0
1	64-A	7464	3763	3764	128	0
1	65-A	7464	3763	3764	180	0
1	66-A	7464	3763	3764	165	0
1	67-A	7464	3763	3764	157	0
1	68-A	7464	3763	3764	155	0
1	69-A	7464	3763	3764	123	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	70-A	7464	3763	3764	158	0
1	71-A	7464	3763	3764	163	0
1	72-A	7464	3763	3764	149	0
1	73-A	7464	3763	3764	136	0
1	74-A	7464	3763	3764	146	0
1	75-A	7464	3763	3764	156	0
1	76-A	7464	3763	3764	145	0
1	77-A	7464	3763	3764	199	0
1	78-A	7464	3763	3764	145	0
1	79-A	7464	3763	3764	145	0
1	80-A	7464	3763	3764	176	0
All	All	597120	301039	301128	13354	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 15.

The worst 5 of 13354 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:322:G:C8	1:A:322:G:OP2	1.64	1.50
1:A:10:G:OP2	1:A:10:G:C8	1.66	1.47
1:A:104:A:OP2	1:A:104:A:C8	1.70	1.41
1:A:104:A:OP2	1:A:104:A:C8	1.70	1.40
1:A:104:A:OP2	1:A:104:A:C8	1.70	1.40

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	348/349 (99%)	80 (22%)	14 (4%)
1	10-A	348/349 (99%)	79 (22%)	12 (3%)
1	11-A	348/349 (99%)	83 (23%)	15 (4%)
1	12-A	348/349 (99%)	91 (26%)	21 (6%)
1	13-A	348/349 (99%)	91 (26%)	11 (3%)
1	14-A	348/349 (99%)	83 (23%)	9 (2%)
1	15-A	348/349 (99%)	81 (23%)	20 (5%)
1	16-A	347/349 (99%)	82 (23%)	15 (4%)
1	17-A	348/349 (99%)	87 (25%)	11 (3%)
1	18-A	348/349 (99%)	86 (24%)	15 (4%)
1	19-A	348/349 (99%)	81 (23%)	13 (3%)
1	2-A	348/349 (99%)	85 (24%)	11 (3%)
1	20-A	348/349 (99%)	84 (24%)	17 (4%)
1	21-A	348/349 (99%)	61 (17%)	13 (3%)
1	22-A	348/349 (99%)	73 (20%)	13 (3%)
1	23-A	348/349 (99%)	71 (20%)	13 (3%)
1	24-A	348/349 (99%)	69 (19%)	10 (2%)
1	25-A	348/349 (99%)	63 (18%)	10 (2%)
1	26-A	348/349 (99%)	61 (17%)	10 (2%)
1	27-A	348/349 (99%)	65 (18%)	10 (2%)
1	28-A	348/349 (99%)	59 (16%)	11 (3%)
1	29-A	348/349 (99%)	62 (17%)	8 (2%)
1	3-A	348/349 (99%)	88 (25%)	10 (2%)
1	30-A	348/349 (99%)	60 (17%)	10 (2%)
1	31-A	348/349 (99%)	60 (17%)	8 (2%)
1	32-A	348/349 (99%)	76 (21%)	20 (5%)
1	33-A	348/349 (99%)	60 (17%)	9 (2%)
1	34-A	348/349 (99%)	58 (16%)	10 (2%)
1	35-A	348/349 (99%)	71 (20%)	10 (2%)
1	36-A	348/349 (99%)	72 (20%)	13 (3%)
1	37-A	348/349 (99%)	59 (16%)	19 (5%)
1	38-A	348/349 (99%)	58 (16%)	12 (3%)
1	39-A	348/349 (99%)	68 (19%)	14 (4%)
1	4-A	348/349 (99%)	80 (22%)	14 (4%)
1	40-A	348/349 (99%)	62 (17%)	12 (3%)
1	41-A	347/349 (99%)	78 (22%)	14 (4%)
1	42-A	348/349 (99%)	75 (21%)	16 (4%)
1	43-A	347/349 (99%)	83 (23%)	13 (3%)
1	44-A	347/349 (99%)	81 (23%)	15 (4%)
1	45-A	347/349 (99%)	85 (24%)	12 (3%)
1	46-A	347/349 (99%)	82 (23%)	15 (4%)
1	47-A	347/349 (99%)	85 (24%)	13 (3%)
1	48-A	347/349 (99%)	93 (26%)	15 (4%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	49-A	348/349 (99%)	86 (24%)	11 (3%)
1	5-A	348/349 (99%)	89 (25%)	14 (4%)
1	50-A	347/349 (99%)	92 (26%)	16 (4%)
1	51-A	347/349 (99%)	85 (24%)	16 (4%)
1	52-A	347/349 (99%)	80 (23%)	11 (3%)
1	53-A	347/349 (99%)	84 (24%)	10 (2%)
1	54-A	347/349 (99%)	83 (23%)	15 (4%)
1	55-A	347/349 (99%)	80 (23%)	14 (4%)
1	56-A	347/349 (99%)	84 (24%)	19 (5%)
1	57-A	347/349 (99%)	74 (21%)	14 (4%)
1	58-A	347/349 (99%)	92 (26%)	17 (4%)
1	59-A	347/349 (99%)	92 (26%)	18 (5%)
1	6-A	348/349 (99%)	85 (24%)	22 (6%)
1	60-A	347/349 (99%)	82 (23%)	9 (2%)
1	61-A	348/349 (99%)	65 (18%)	11 (3%)
1	62-A	348/349 (99%)	74 (21%)	12 (3%)
1	63-A	348/349 (99%)	72 (20%)	16 (4%)
1	64-A	348/349 (99%)	63 (18%)	10 (2%)
1	65-A	348/349 (99%)	82 (23%)	9 (2%)
1	66-A	348/349 (99%)	61 (17%)	13 (3%)
1	67-A	348/349 (99%)	68 (19%)	11 (3%)
1	68-A	348/349 (99%)	68 (19%)	12 (3%)
1	69-A	348/349 (99%)	62 (17%)	8 (2%)
1	7-A	348/349 (99%)	81 (23%)	8 (2%)
1	70-A	348/349 (99%)	65 (18%)	12 (3%)
1	71-A	348/349 (99%)	76 (21%)	8 (2%)
1	72-A	348/349 (99%)	74 (21%)	14 (4%)
1	73-A	348/349 (99%)	71 (20%)	9 (2%)
1	74-A	348/349 (99%)	72 (20%)	12 (3%)
1	75-A	348/349 (99%)	67 (19%)	9 (2%)
1	76-A	348/349 (99%)	60 (17%)	11 (3%)
1	77-A	348/349 (99%)	73 (20%)	12 (3%)
1	78-A	348/349 (99%)	73 (20%)	12 (3%)
1	79-A	348/349 (99%)	68 (19%)	11 (3%)
1	8-A	348/349 (99%)	77 (22%)	10 (2%)
1	80-A	348/349 (99%)	66 (18%)	11 (3%)
1	9-A	348/349 (99%)	92 (26%)	16 (4%)
All	All	27821/27920 (99%)	6029 (21%)	1019 (3%)

5 of 6029 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1-A	-9	G

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Mol	Chain	Res	Type
1	1-A	-7	U
1	1-A	1	G
1	1-A	12	A
1	1-A	15	A

5 of 1019 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	37-A	128	A
1	68-A	272	C
1	45-A	51	A
1	67-A	308	G
1	74-A	130	U

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	49-A	3
1	56-A	2
1	43-A	2

Continued on next page...

Continued from previous page...

Mol	Chain	Number of breaks
1	53-A	2
1	59-A	2
1	60-A	2
1	50-A	2
1	48-A	2
1	42-A	2
1	16-A	1
1	41-A	1
1	58-A	1
1	47-A	1
1	44-A	1
1	54-A	1
1	45-A	1
1	51-A	1
1	55-A	1
1	52-A	1
1	57-A	1
1	46-A	1
1	14-A	1
1	80-A	1
1	20-A	1
1	33-A	1

The worst 5 of 35 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
16	A	154:C	O3'	155:A	P	4.63
41	A	112:U	O3'	113:C	P	2.86
58	A	8:U	O3'	9:C	P	2.72
47	A	112:U	O3'	113:C	P	2.67
44	A	112:U	O3'	113:C	P	2.63

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21835. 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: 112



Y Index: 112



Z Index: 112

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: 134



Y Index: 102

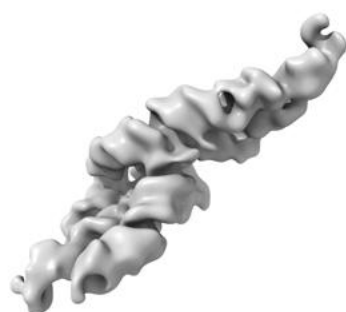


Z Index: 97

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

6.4 Orthogonal surface views [i](#)

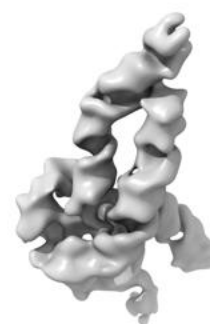
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

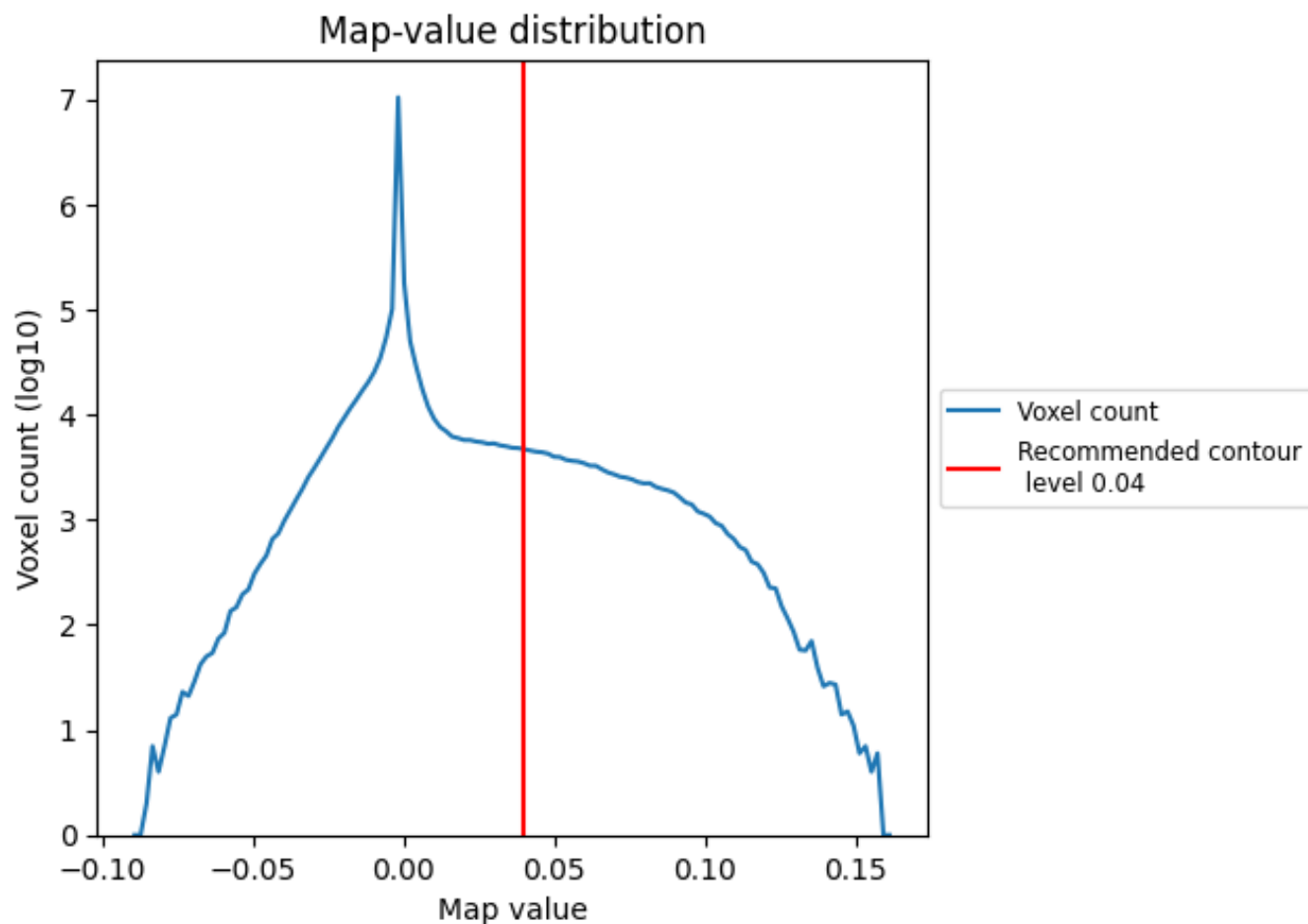
6.5 Mask visualisation

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

7 Map analysis [i](#)

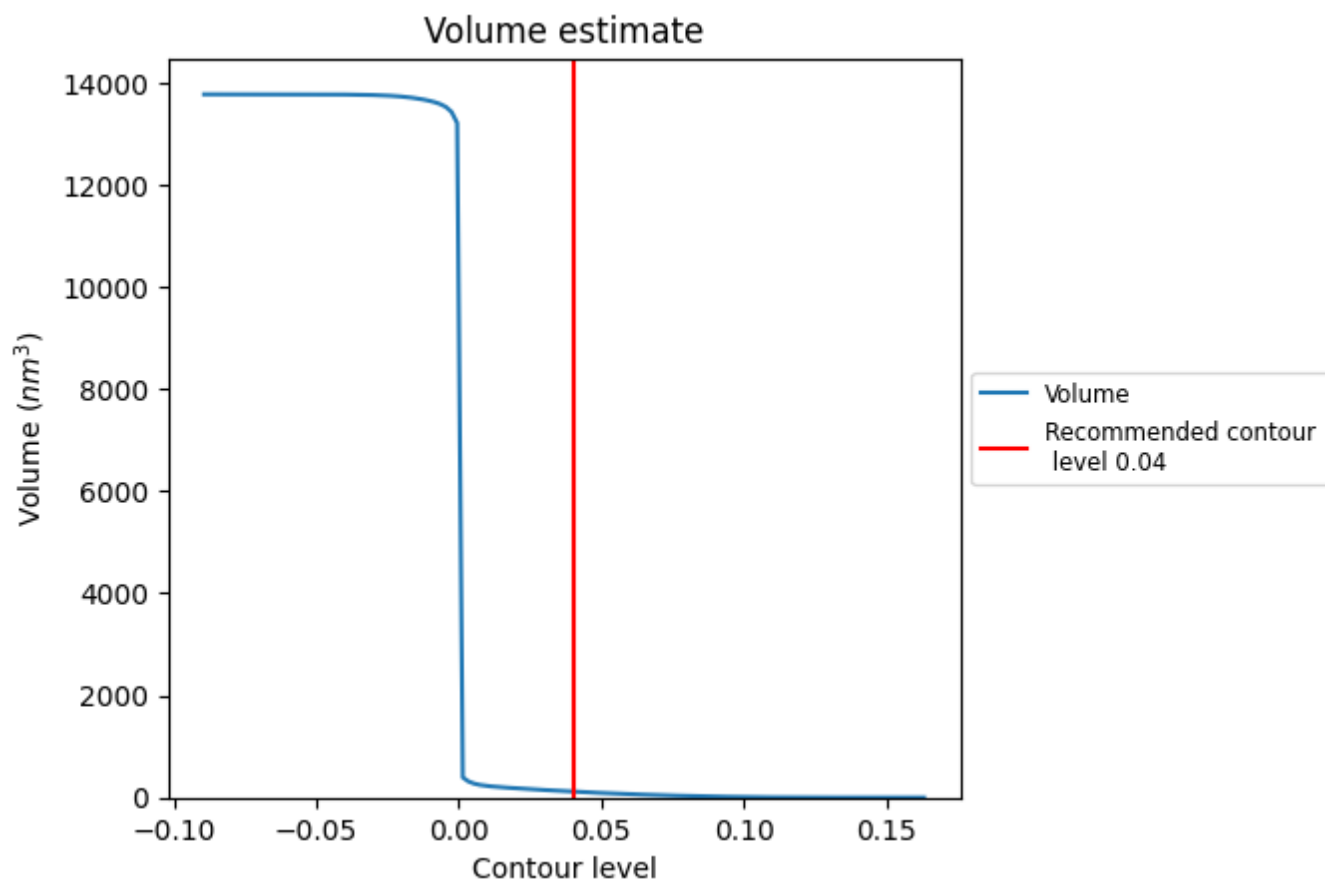
This section contains the results of statistical analysis of the map.

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.

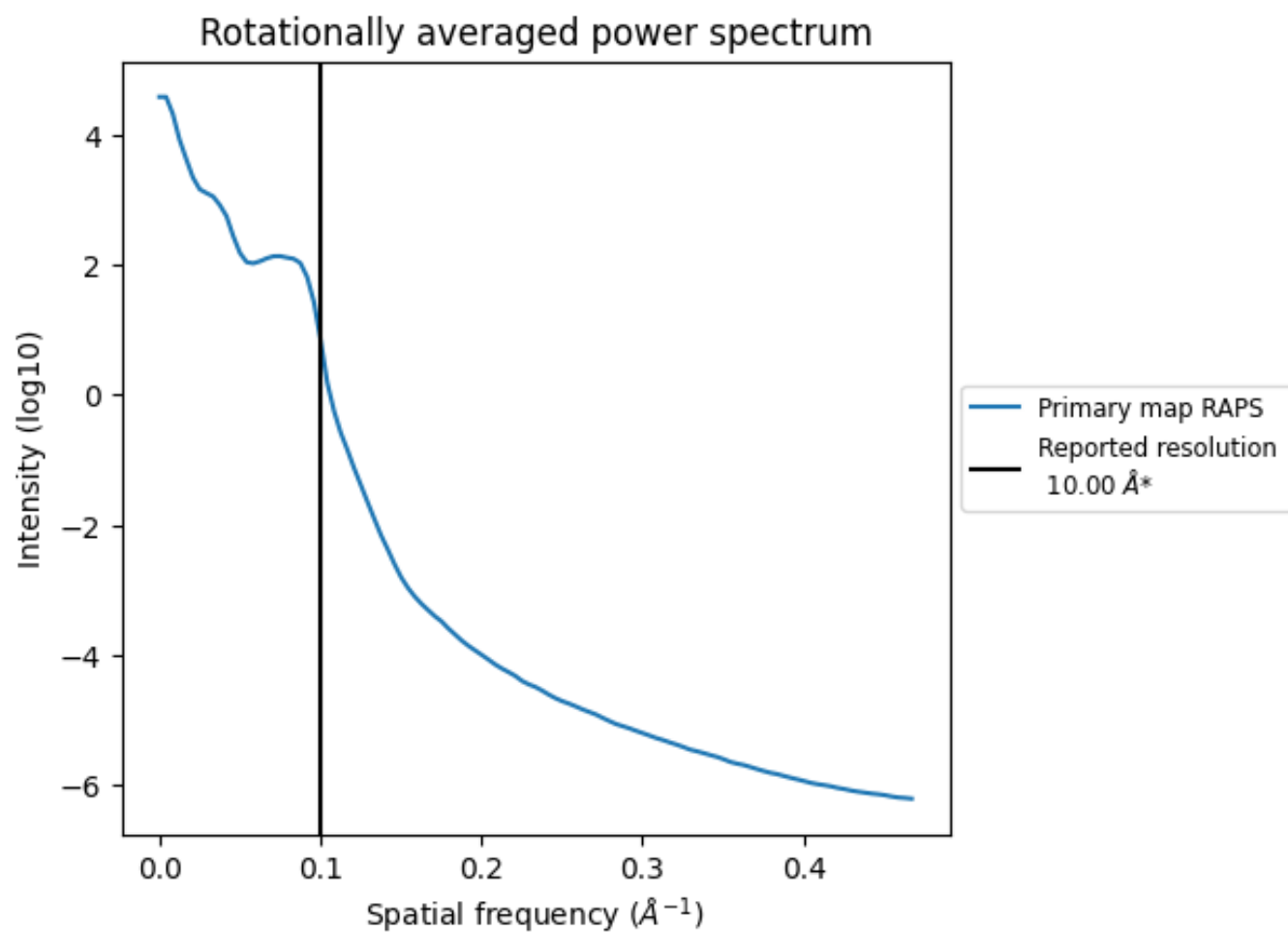
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 117 nm³; this corresponds to an approximate mass of 106 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 0.100 Å⁻¹

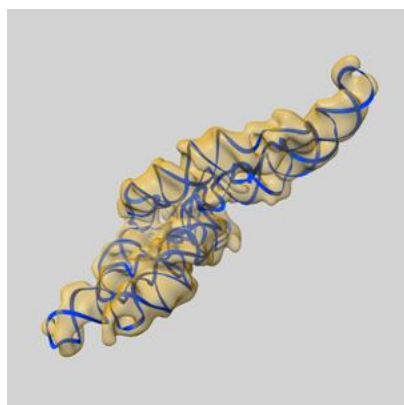
8 Fourier-Shell correlation ⓘ

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

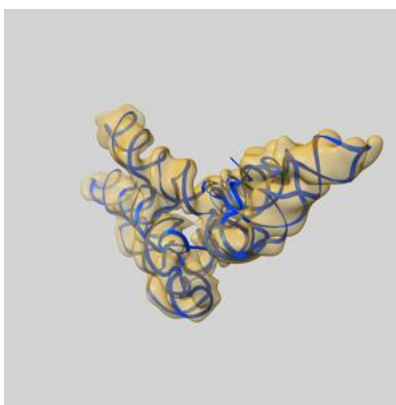
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21835 and PDB model 6WLN. Per-residue inclusion information can be found in section [3](#) on page [10](#).

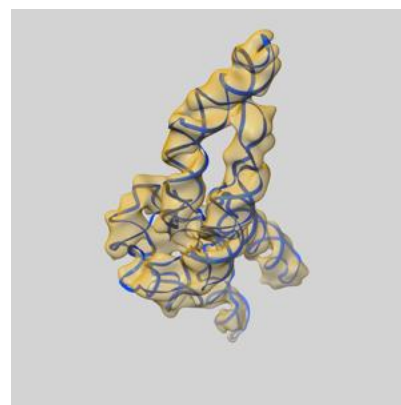
9.1 Map-model overlay [i](#)



X



Y



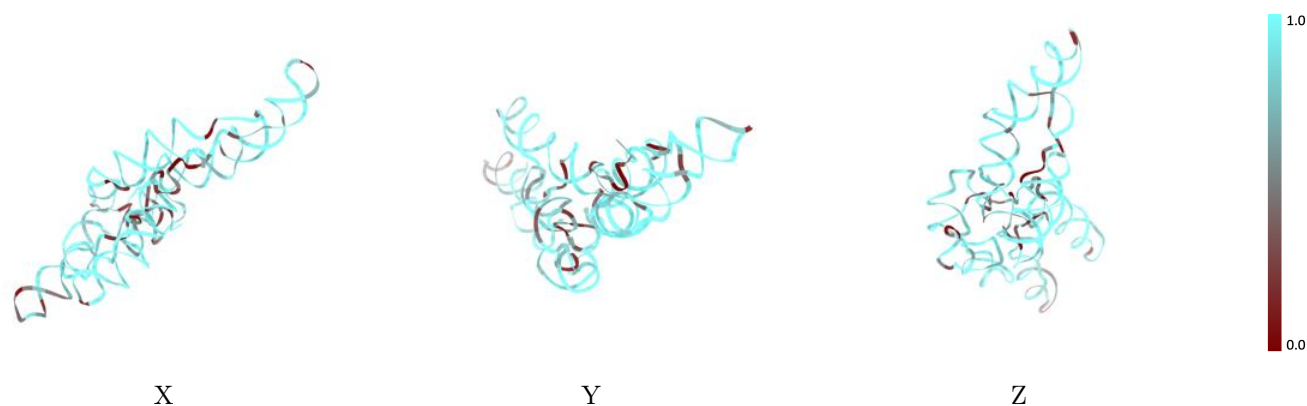
Z

The images above show the 3D surface view of the map at the recommended contour level 0.04 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](#)

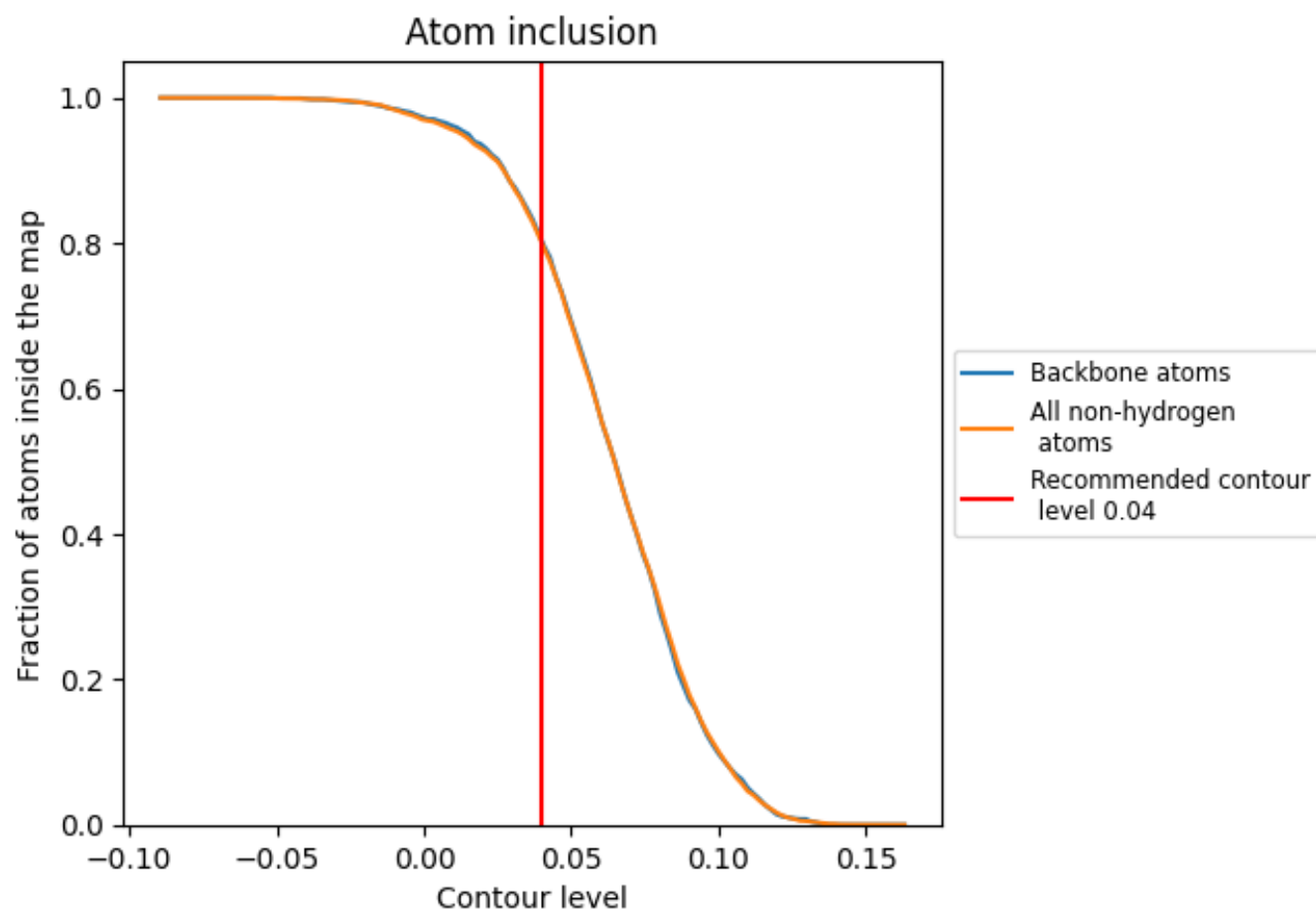
This section was not generated.

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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 80% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion
All	<div></div> 0.8012
A	<div></div> 0.7986

