Supporting Information for

Ensemble of Secondary Structures for Encapsidated Satellite Tobacco Mosaic Virus RNA Consistent with Chemical Probing and Crystallography Constraints

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Runhead: Schroeder et al.   STMV RNA Secondary Structures

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Materials and Methods

Virus Particle Purification

Infection of *Nicotiana tabacum cv.* Xanthi with STMV and Tobacco mild green mosaic virus (TMGMV) (ATCC #PV-586) and STMV particle purification followed the protocols of Valverde et. al.(*1*). Particles purified with PEG cuts only showed the same DMS pattern of modification as particles purified with PEG cuts followed by sucrose density gradient ultracentrifugation. An RT PCR assay using Invitrogen SuperScript III Reverse Transcription kit (catalogue number 1257-030) on RNA from proteinase K digested particles confirmed the absence of TMGMV RNA in the virus particle preparations.

Chemical probing

Chemical probing of STMV particles was done following the procedure of Rodriguez et al. for DMS probing of cucumber mosaic virus (*2*). The reaction conditions are 5 mM sodium borate pH 9.0 and 0.5 mM Na_2EDTA with either water, 0.5-2% v/v dimethyl sulfate (DMS), kethoxal, or 1-cyclohexyl 3-(2-morpholinoethyl)carbodiimide methyl p-toluene sulfonate (CMCT) on ice for 10 min. After quenching with stop buffer (167 mM Tris pH 7.5, 167 mM β-mercaptoethanol, 250 mM sodium acetate, and 17 mM Na_2EDTA, final concentrations after mixing), particles were treated with proteinase K in order to degrade the virus coat protein and then ethanol precipitated.

Conditions for chemical modification were also varied from 5, 10, 30, and 60 minutes; 0.5-2% v/v modification reagent; 4 and 25 ^oC; and different stocks of STMV particles. Conditions for quenching the modification reagent were tested for at least twice the exposure time at 25 ^oC with different buffers, including 3M sodium acetate pH 5, 1M potassium borate pH 6, and the final best stop buffer, 1 M Tris pH 7.5, 1 M β-mercaptoethanol, 1.5 M sodium acetate pH 5, and 100 mM Na_2EDTA (stock concentration). The best stop buffer gave the lowest background and the best signal to noise when reading reverse transcription reactions. Typically, 40 µL best stop buffer was added to 200 µL of STMV particles with buffer and chemical modification reagents. When the best stop buffer is added to reactions with kethoxal, the reaction immediately turns bright red and some precipitate forms. As a negative control, 2 or 8% v/v CMCT, 2 or 8% v/v kethoxal, 2% v/v DMS, or water was added to STMV particles in 5 mM sodium borate pH 9.0 and 0.5 mM Na_2EDTA and then immediately quenched with the best stop buffer. No stops above background were observed in reverse transcription reactions, indicating that the best stop buffer fully quenches the chemical modification reagents (Supporting Information Figure 1C). As a positive control, the proteinase digestion time was varied from 30 minutes to 2 hours at 37° C with 40-160 µg proteinase K. If other chemical modifications, other sources of RT stops, or degradation of the RNA occurred during RNA purification from viral particles, then changes in the number of RT stops would be observed in reverse transcription reactions as a function of proteinase K digestion time. No change in the modification patterns was observed, which confirms that the coat protein was completely digested, the RNA did not degrade significantly during protein digestion, and no modification reagents remained active during protein digestion. Thus, the observed chemical modification patterns report on the encapsidated RNA conformation.

Reverse transcription reactions were done with either AMV or SSRT III enzymes from Invitrogen following the protocols of Rodriguez et al. or Wilkinson et al., respectively (*2, 3*). Reverse transcription sequencing reactions on RNA from particles not exposed to chemical probing reagents show no stops due to hydrolysis of RNA in slightly basic buffers. A list of primer sequences used for reverse transcription reactions is included in Supporting Information

Table 2. Note that the region from nucleotides 802-920 was fully probed, but showed no strong DMS hits. In addition, the strong hits for kethoxal and CMCT occur primarily in the 5' and 3' regions of the STMV RNA. Nucleotides may be protected from chemical modification in many different ways. In addition to Watson-Crick pairing in an RNA helix, protein binding, RNA tertiary interactions, or slower diffusion of the modification agent towards the center of the virus particle may reduce accessibility or protect a nucleotide from chemical modification. Therefore, no constraints or interpretation is applied to nucleotides that do not show chemical modification.

Both traditional polyacrylamide gels with ^{32}P labeled primers and capillary gel electrophoresis with Cy5 fluorescent primers were used to analyze the DMS transcription reactions. The capillary gel electrophoresis results confirmed all prior PAGE results. An example of the DMS data and a sequencing reverse transcription reaction on particles in control reaction conditions are shown in Supporting Information Figure 1A, 1B, and 2A. DMS, CMCT, and kethoxal gave better signal to noise than SHAPE chemistry and protocols (*3*) on STMV particles (Supporting Information Figure 2). SHAPE protocols do not have a specific quenching step. SHAPE reagents are inactivated by reacting with water and slowly turn increasingly yellow during 30-60 minute reactions. Thus, SHAPE reagents could possibly continue to react during proteinase K digestion of the capsid protein.

The virus capsids swell slightly at basic pH and thus allow chemical modification reagents to enter the virion. The diameter of the icosahedrons increases from 17 to 18 nm (*4*). This change of 1 nm is small, less than half the diameter of an A-form helix (2.6 nm) (*5*). This small change allows small molecules access to the inside of the virion, but is too small for any large conformational changes. STMV is a very densely packed virion particle, and there is not sufficient room for conformational rearrangements with only a 1 nm change in diameter.

Capillary gel electrophoresis experiments were done on a Beckman CEQ8800 and were analyzed with Beckman Fragment Analysis software using default parameters for size standard 400 or fragment 600 parameters for size standard 600. Results from reverse transcription reactions with or without the chemical probing reagent or with 10% ddNTP for sequencing were aligned using internal Beckman size standard 400 or 600 and then overlaid. An example plot of capillary gel electrophoresis data is shown in Supporting Information Figures 1 and 2. Background signals from reactions with no chemical probing reagent were typical much less than signals from reactions in control conditions without the chemical probing reagent, so no subtraction of background traces was done. Sequencing reactions on control viral RNA not treated with DMS showed the correct sequence with no extraneous peaks, confirming that the DMS exposure and protein capsid digestion conditions do not cause RNA degradation and that the protein capsid has been completely digested. Traces were manually inspected and only the strongest peaks were selected as constraints for folding. This approach avoids errors associated with automated analysis (*6*). The approach to select only the strongest chemical probing hits as constraints allows for the possibility of the RNA existing in an ensemble of structures. For example, a weak hit may represent a weak hit in all structures of the ensemble or represent a strong hit in a minority of the structures. Nucleotides modified by DMS, kethoxal, or CMCT were prevented from forming a Watson-Crick pair flanked on both sides by Watson-Crick pairs (*7*). Modified nucleotides adjacent to helix ends and GU pairs were allowed to form Watson-Crick pairs. Because RNA tertiary interactions or protein interactions may also prevent chemical modification, no constraints were applied to unmodified nucleotides.

Supporting Information Table 1

Locations of Possible Helices of at Least Nine Watson-Crick or GU Pairs in STMV RNA

(30,956)-(38,948), 9

(31,442)-(40,433), 10

(37,570)-(46,561), 10

(51,709)-(59,701), 9

(54,858)-(62,850), 9

(56,350)-(64,342), 9

(60,929)-(68,921), 9

(64,720)-(74,710), 11*

(69,932)-(77,924), 9*

(70,932)-(81,921), 12*

(70,933)-(78,925), 9*

(85,1024)-(94,1015), 10

(134,492)-(144,482), 11

(134,702)-(143,693), 10

(135,1029)-(144,1020), 10

(139,454)-(148,445), 10*

(148,707)-(156,699), 9

(152,242)-(161,233), 10

(157,746)-(166,737), 10

(164,932)-(174,922), 11

(169,958)-(179,948), 11

(171,798)-(179,790), 9*

(171,864)-(180,855), 10

(171,919)-(179,911), 9*

(174,964)-(182,956), 9*

(188,836)-(198,826), 11*

(201,224)-(209,216), 9*

(227,962)-(235,954), 9

(265,631)-(273,623), 9

(268,742)-(279,731), 12

(268,835)-(277,826), 10

(271,963)-(280,954), 10

(275,862)-(283,854), 9*

(284,950)-(292,942), 9*

(285,494)-(293,486), 9*

(289,736)-(298,727), 10*

(333,475)-(341,467), 9

(363,1025)-(371,1017), 9

(368,446)-(376,438), 9*

(378,568)-(386,560), 9*

(435,539)-(443,531), 9*

(435,779)-(445,769), 11

(436,839)-(445,830), 10

(441,863)-(449,855), 9

(443,964)-(453,954), 11

(444,739)-(452,731), 9*

(448,862)-(458,852), 11*

(463,806)-(471,798), 9

(481,524)-(489,516), 9

(485,664)-(495,654), 11

(489,929)-(497,921), 9*

(516,1027)-(524,1019), 9

(521,838)-(529,830), 9

(532,955)-(540,947), 9*

(553,961)-(561,953), 9

(556,927)-(564,919), 9

(576,980)-(585,971), 10

(581,629)-(591,619), 11

(584,959)-(593,950), 10

(609,706)-(618,697), 10

(612,784)-(620,776), 9

(619,841)-(628,832), 10

(621,913)-(630,904), 10

(626,708)-(637,697), 12

(652,952)-(662,942), 11

(660,740)-(669,731), 10

(661,963)-(669,955), 9

(666,965)-(675,956), 10*

(697,960)-(705,952), 9

(701,899)-(710,890), 10

(724,928)-(732,920), 9*

(730,784)-(739,775), 10

(739,887)-(747,879), 9

(741,990)-(749,982), 9

(774,964)-(784,954), 11

(775,832)-(785,822), 11

(834,959)-(842,951), 9

(896,923)-(905,914), 10*

(907,955)-(916,946), 10

(916,984)-(924,976), 9

(949,1013)-(957,1005), 9

(950,1017)-(959,1008), 10

(951,1007)-(960,998), 10

Supporting Information Table 1: Helices are identified by the nucleotide numbers of the first pair, the last pair, and the length of the helix. Helices that are not consistent with the chemical modification constraints are marked with an asterisk.

Supporting Information Table 2: Primer Sequences for Reverse Transcription

Primer	Sequence
STMV 1000	5'CGAACAACGGTAGTCACACTAACGTATGC
STMV828	5'CAAGGCCGGTTACGCGCTAACCAGACTAACGGC
STMV599	5'TTACTTCTTACTTCGCATACATTGTCGGCT
STMV 480	5'CAGTAGAGTCACCAGTCTTGAACAATGGC
STMV 286	5'GGTATGGCTCTGACCCACGTTGGAGTCG
STMV 114 (^{32}P only)	5'GGCGACTGAAGGCCTCTTGTAGAAG

Supporting Information Table 3: *Crumple* Output for 14mer 5' GCUCUAAAAGAGAG

```
....(........)     .((.........))     ..(((.....))).     .((.(...)).)..
...((.......))     .(..(......).)     ..(((....).)).     .((......).)..
...((......).)     .(.((.....)).)     ..(((...)..)).     .(..(...)..)..
...((.....)..)     .(.((....).).)     ..((.......)).     .((.....)..)..
...((....)...)     .(.((...)..).)     ..(.(.....).).     .((....)...)..
...((...)....)     .(.(.......).)     ..(.(....)..).     .((...)....)..
...(.........)     .((.(....))..)     ..(((...))..).     .(.........)..
..(.(.......))     .((.(....).).)     ..((.....)..).     ....(.....)...
..(.(......).)     .(((...)).).)      ..(.(...)...).     ..(.(....))...
..(((.....)).)     .(((.....).).)     ..(.........).     ..(((...)))...
..(((....).).)     .(.(.(...)..).)    ....(......)..     ..((.....))...
..(((...)..).)     .((.........).)    ...((.....))..     ..(.(...).)...
..((.......).)     .(..(.....)..)     ...((....).)..     ..(.......)...
..(.(.....)..)     .((.(....))..)     ...((...)..)..     ....(....)....
..(.(....)...)     .(((...)))..)      ...(.......)..     ...((...))....
..(((...))...)     .(((.....))..)     ..(.(.....))..     ...(.....)....
..((.....)...)     .((.(...).).)      ..(.(....).)..     ..(.(...))....
..(.(...)....)     .((........)..)    ..(((...)))..      ..(......)....
..(..........)     .(..(....)...)     ..((.....))..      .(..(...))....
.(..(.......))     .(.((...))...)     ..(.(...).)..      .((.....))....
.((.(......)))     .(.(.....)...)     .(..(.....))..     .((....).)....
.((((.....))))     .((.(...))...)     .((.(....)))..     .((...)..)....
.((((....).)))     .((.......)...)    .((((...))))..     .(.......)....
.((((...)..)))     .(..(...)....)     .(((.....)))..     ....(...).....
.(((.......)))     .((.....)....)     .((.(...).))..     ..(.....).....
.((.(.....).))     .((....)....)      .((.......))..     ..(....)......
.((.(....)..))     .((...)......)     .(..(....).)..     ..(...).......
.((((...))..))     .(..........)      .(.((...))...      (...).........
.(((.....)..))     ....(.......).     .(.(.....).)..     ..............
.((.(...)...))     ..(.(......)).
```

Supporting Information Pseudocode

Crumple algorithm

Crumple is defined as a recursive function of two arguments: `I` and `S` (for intervals and structure).

`I` is a list of ranges `(i, j]`; each range is a segment of the sequence that has not yet been examined. Note that while the 5' end of each interval is exclusive, the 3' end is inclusive. This convention is merely for convenience later.

`S` is a (partial) secondary structure, represented as a set of pairs of bases: `(i, j)`.

To begin, `S` will be void of pairs: (*8*) (representing a totally single-stranded secondary structure), and `I` will contain one range: `(0, n]`, where n is the length of the sequence --- that is to say, no part of the sequence has been examined.

1. When crumple is called, it first examines I. If I contains zero ranges then it prints `S` and returns. Otherwise:

2. If `I` contains one or more ranges, it removes the next (the most recently added) range from `I`. Call this range `(i, j]`.

3. If `i` is equal to `j`, crumple immediately calls itself, with `S` and `I` (which is now one range shorter).

4. If `i` is not equal to `j`, then for EACH possible canonical pair `(k, j)` where `i < k < j`, crumple will call itself:

```
S' = S ∪ {(k, j)}
I' = (i, k-1).(k+1, j-1).I
crumple(I', S')
```

5. If `i` is not equal to `j` and all possible pairs `(k, j)` have been examined, crumple calls itself:

```
I' = (i, j-1).I
crumple(I', S)
```

Assembly algorithm

An 'assembly' is a scalar score and an associated set of helices.
Helices are scored using the equation
Helix score = 1 x # Watson-Crick pairs
                     + 2 x # GU pairs
                     + 3 x # terminal mismatches
                     + 4 x # internal mismatches
                     + 5 x asymmetry of internal loops
                     + 2 x # chemically modified nucleotides pairing adjacent to helix ends or GU

B is a m*n array of assemblies, where m is the length of the sequence, and n is the desired number of helices.
H is an array of helices indexed by length and by the index of the 3'-most base in the helix.

Ex:
......(((.((...)).))).....
12345678901234567890123456
                 ^

This helix would be identified as H[21][15], as it is 15 bases long and ends on base 21. If more than one helix has the same length and position, the helix with the best score is chosen and the others are discarded.

Pseudocode for *Assembly*:

assemble(H, B):

   B[0][:].score = inf
   B[0][:].assembly = {}
   B[:][0].score = inf
   B[:][0].assembly = {}

   for i from 1 to the number of helices desired:
     for j from 1 to the length of the sequence:
        B[i][j] = B[i][j-1]
         for all h in H[j][h]:
      let a be an assembly
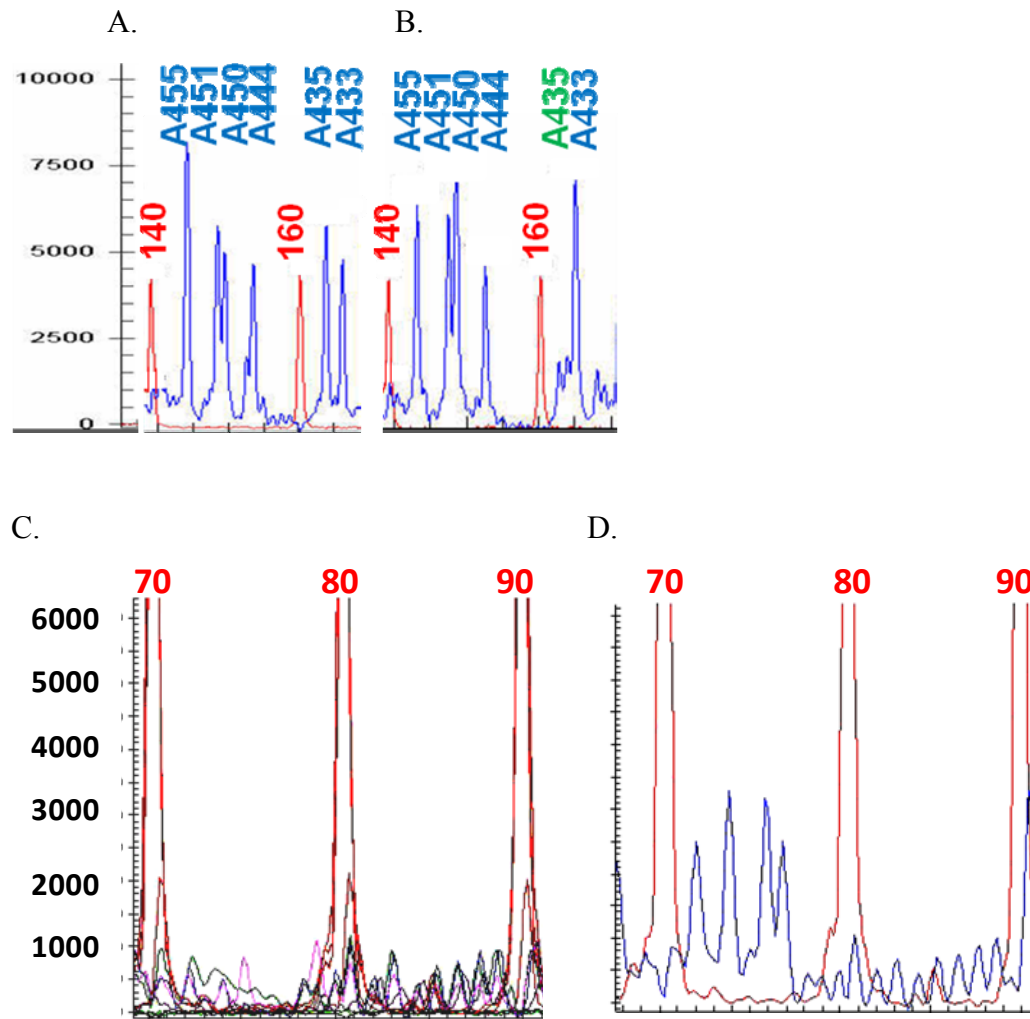   a.score = score(H[j][h]) + B[i-1][j-h].score) and
      a.helices = {H[j][h]} U B[i-1][j-h].helices

           if a.score < B[i][j], then
        B[i][j] = a

   return B[length of sequence][number of helices]

Supporting Information Figure 1

A.

B.

C.

D.

SI Figure 1: Sample data from capillary electrophoresis of reverse transcription primer extension reactions. The vertical scale is units of fluorescence intensity from Cy5 labelled primers. The horizontal scale is elution time. The red peaks are Beckman nucleotide size standards 400 (A and B) and 600 (C and D). SI Figure 1A is a reverse transcription reaction with dideoxy thymidine triphosphate (ddTTP) on STMV RNA extracted from particles treated with buffer only. SI Figure 1B shows the reverse transcription reaction on particles treated with 2% v/v DMS. The absence of a peak at A435 shows that this adenosine was not chemically modified by DMS. SI Figure 1C shows a negative control in which STMV particles were treated with 8% v/v CMCT (dark green), 2% v/v kethoxal (pink), 2% v/v DMS (purple), or water (dark blue) and then immediately quenched with best stop buffer. The control with 8% v/v kethoxal STMV RNA gave too little transcription for even the low level background to be observed. SI Figure 1D shows the control treated with 8% v/v CMCT STMV in a sequencing reaction with dideoxy adenosine triphosphate (ddATP) showing a positive signal in the reverse transcription that matches the STMV RNA sequence.

Supporting Information Figure 2

A. Capillary Electrophoresis Data for DMS Chemical Probing
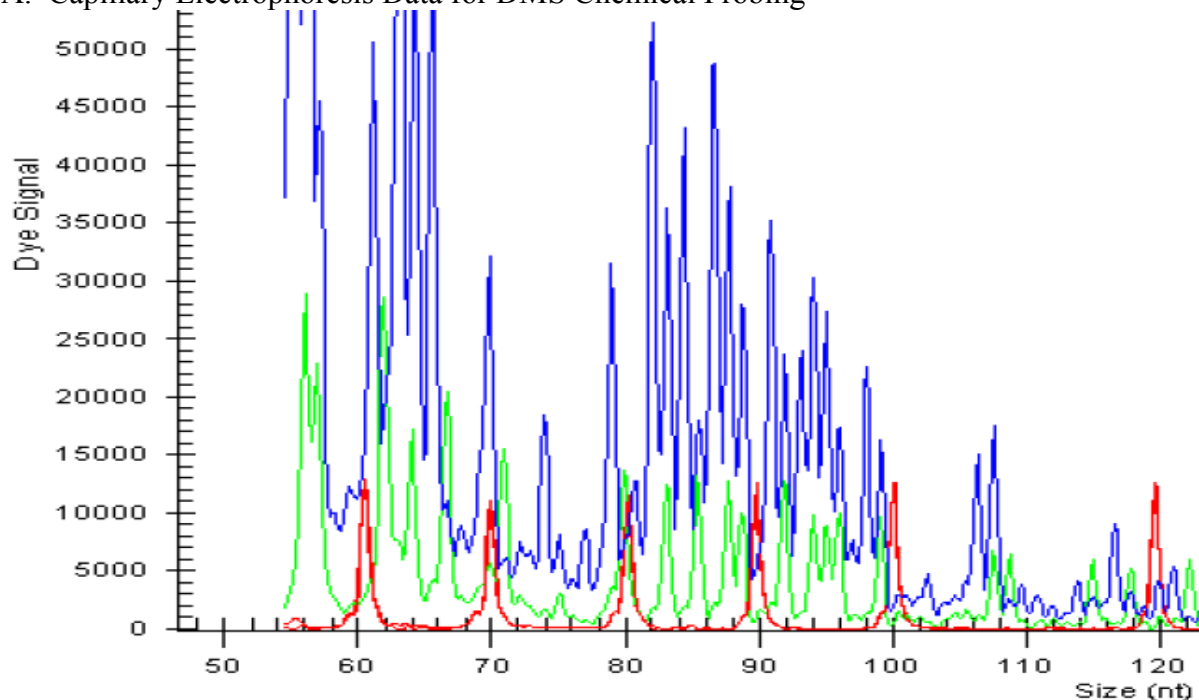
B. Capillary Electrophoresis Data for SHAPE Chemical Probing
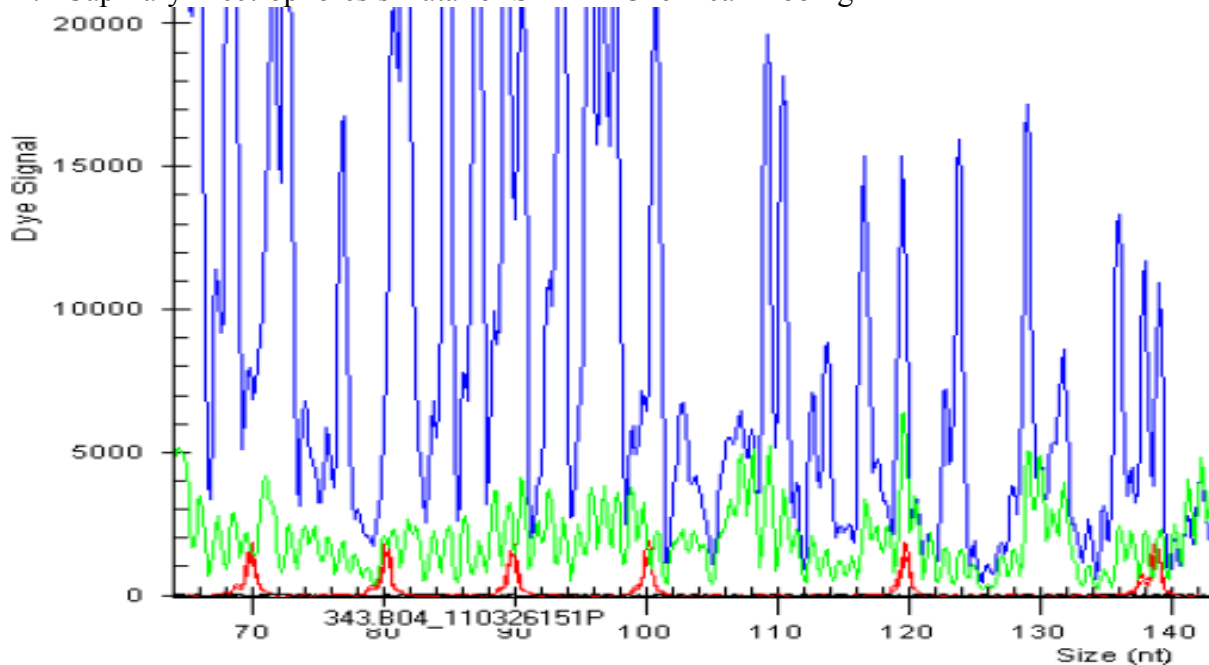
SI Figure 2: Data is processed with Beckman CEQ software. Blue peaks are from a ddT sequencing reaction on RNA from viral particles exposed only to buffer. Green peaks are from DMS (A) and SHAPE (B) reverse transcription reactions with primer STMV599. Red peaks are Beckman size standard 400. In assessing signal to noise, the absolute value of the peak intensity is not the important feature in capillary electrophoresis. The difference in height between modified and unmodified nucleotide peaks is larger for the DMS data.

Supporting Information Figure 3: 5'UTR HIV-1(*9, 10*)

5'GGACUCGGCUUGCUGAAGCGCGCACGGCAAGAGGCGAGGGGCGGCGACUGGUG
AGUACGCCAAAAAUUUUGACUAGCGGAGGCUAGAAGGAGAGAC
..M...........MM.....M................M....M........M....MMMMM............M......MM..M.M.M..

A. Secondary structure from chemical probing and mutagenesis experiments (*9, 10*)

...((((.((((((((.........)))))))...))))....(((((((....))).)))).............(((((....)))))..........

B. Secondary structure predicted by Sliding Windows and Assembly with chemical modification
and no asymmetry penalty:
...((((.((((((((.........))))..))).)))).....(((((((....))).)))).....(((((..(((((....))))))))))......

C. Secondary structure predicted by Sliding Windows and Assembly with chemical modification
........(((((((.........)))))))..................((((....)))).....(((((..(((((....)))))..))))....

D. Secondary Structure predicted by RNAStructure 4.6 with chemical modification (*7*)
...((((.((((((((.........)))))))...))))....(((((((....))).)))).....(((((..(((((....)))))..))))....

E. Centroid secondary structure predicted by Sfold with chemical modification (*11*)
....((((.(.(((((.........)))))...)...).))))........((((((.((.............))).))))…………………..

F. MFE secondary structure predicted by Sfold with chemical modification (*11*)
...((((.(((((((.........)))))..)).))))....(((..(((((.((.............))).)))))…..)))…………

G. Centroid secondary structure predicted by Sfold without chemical modification (*11*)
……………………………………((((((((....))).))))………..(((((....))))……….

H. MFE secondary structure predicted by Sfold without chemical modification (*11*)
....((((.(((((((.........)))))..)).)))).....(((((((....))).)))).....(((((..(((((....)))))..))))….

I. Centroid Secondary structure predicted by Vienna RNAFold with chemical modification (*12*)
...((((.((((((((.........))))))))...)))).....((..(((((.((.............)).)))))…..))............

J. MFE Secondary Structure predicted by Vienna RNAFold with chemical modification (*12*)
...((((.((((((((.........))))))))...))))....(((..(((((.((.............)).)))))…..)))...........

K. Centroid Secondary structure predicted by Vienna RNAFold without chemical
modification(*12*)
...((((.((((((((.........))))))))...))))....(((((((....))).))))...........(((((....)))))..........

L. MFE Secondary Structure predicted by Vienna RNAFold without chemical modification (*12*)
...((((.((((((((.........))))))))...))))....(((((((....))).)))).....(((((..(((((....)))))..))))....

Supporting Information Figure 3 (cont)
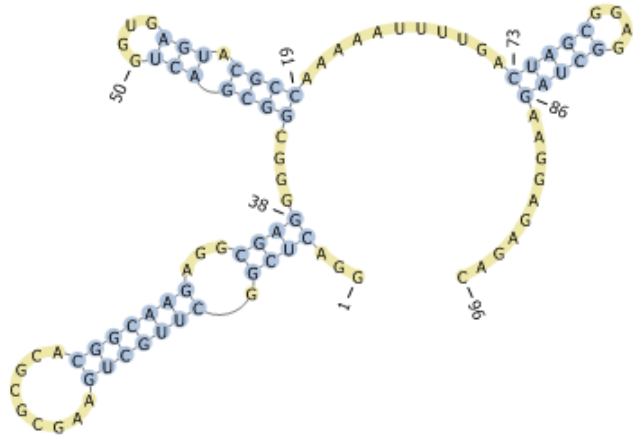
A. Chemical probing and mutagenesis experiments (*9, 10*)   B. Sliding Windows and Assembly (no asymmetry penalty)
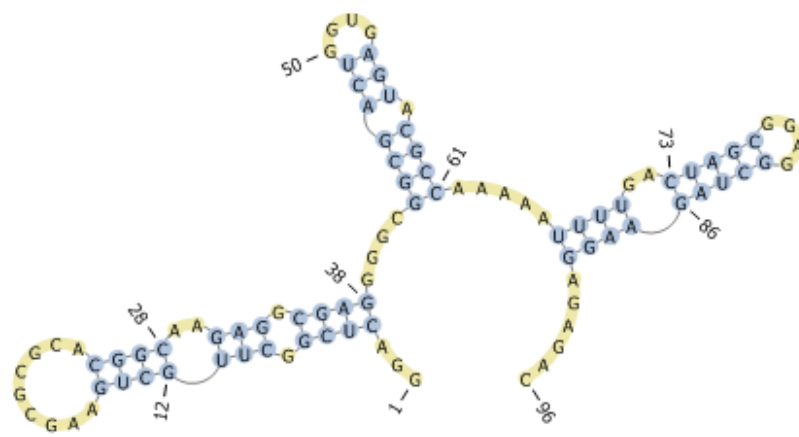
C. Sliding Windows and Assembly (with asymmetry penalty)   D. RNAStructure 4.6
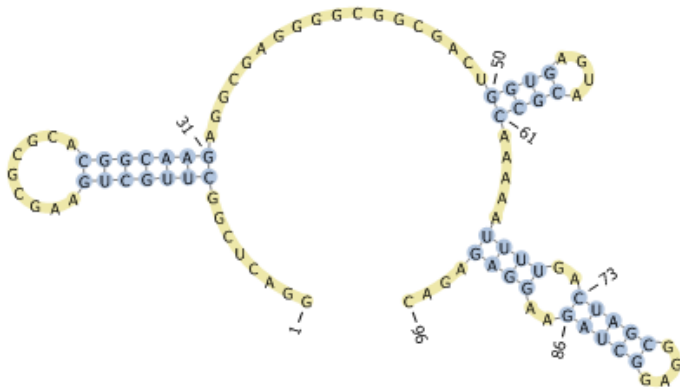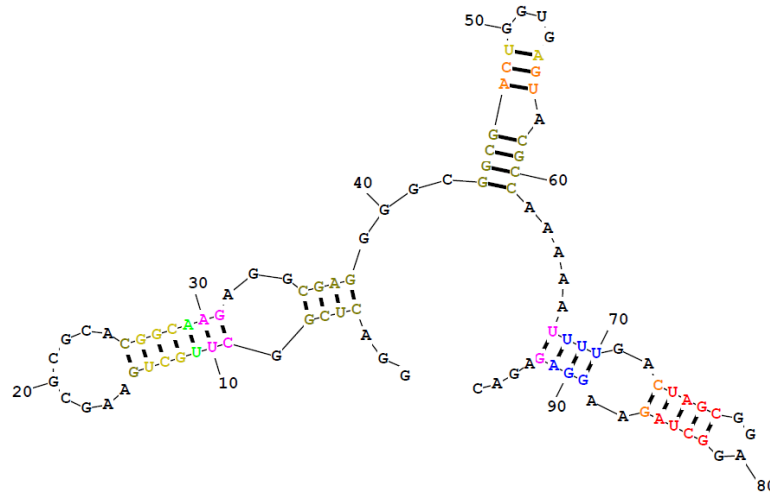
Supporting Information Figure 3 (cont.)
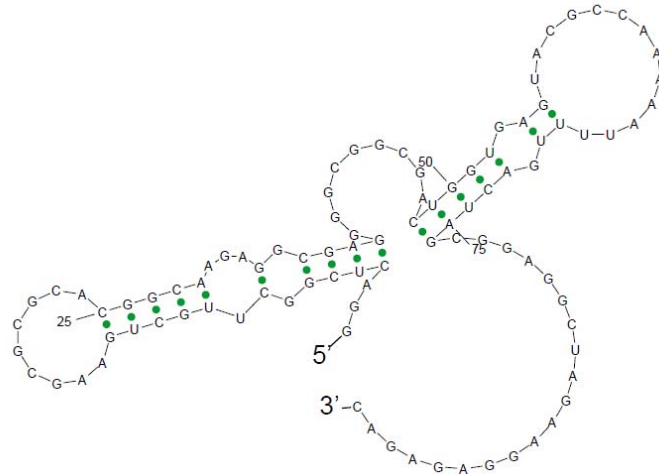
E. Sfold centroid with chemical modification   F. Sfold MFE with chemical modification
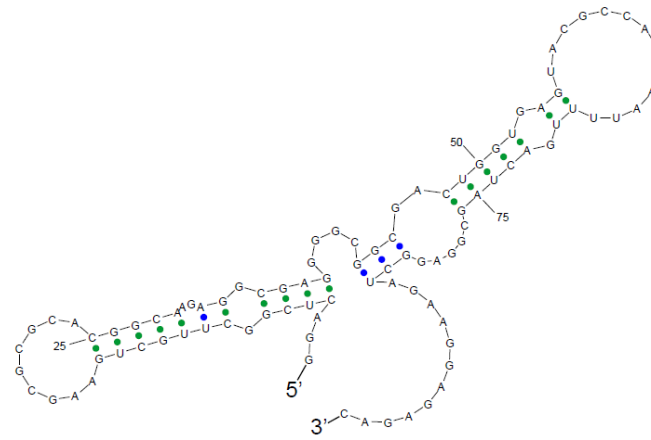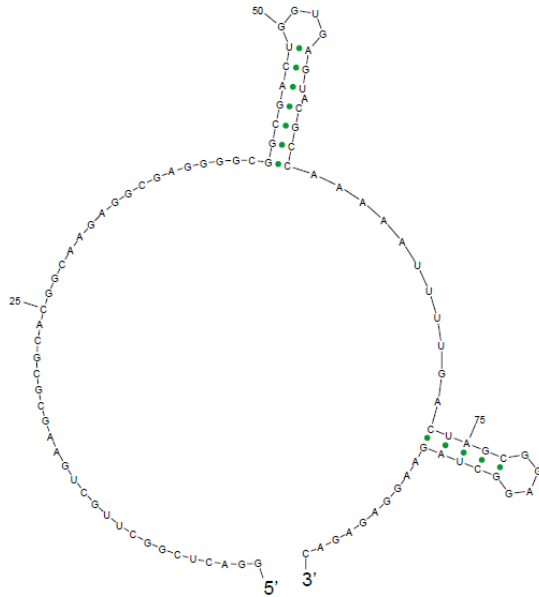
G. Sfold centroid without chemical modification   H. Sfold MFE without chemical modification
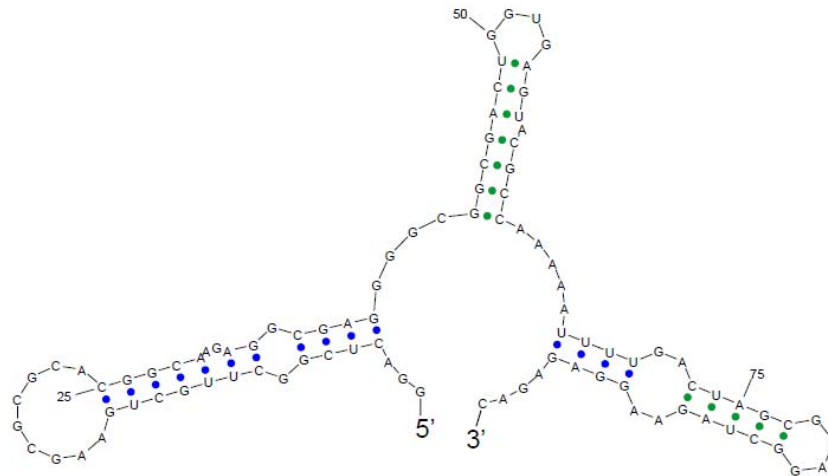
Supporting Information Figure 3 (cont.)
I. RNAfold centroid with chemical modification   J. RNAfold MFE with chemical modification
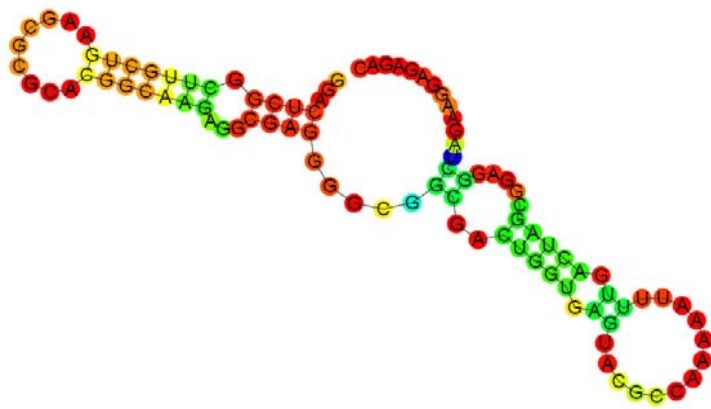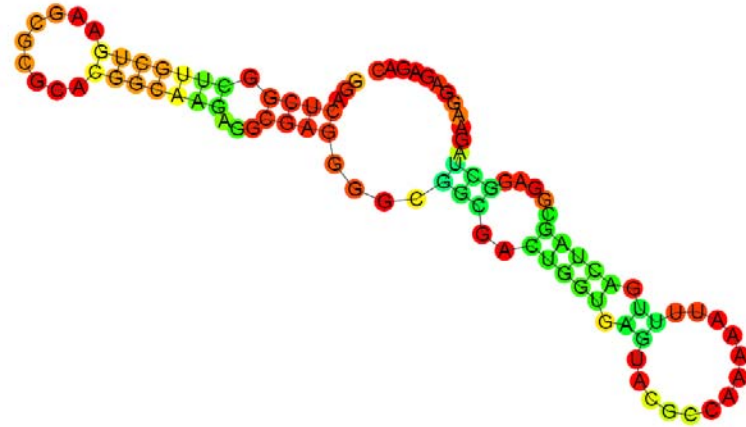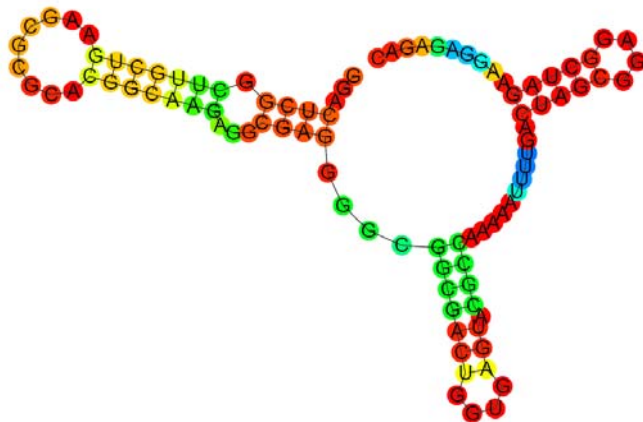
K. RNAfold centroid without chemical modification   L. RNAfold MFE without chemical modification
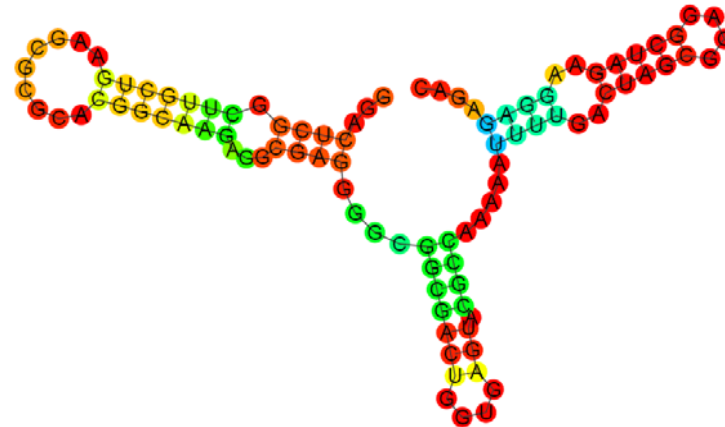
SI Figure 3: Secondary structure diagrams in figures A, B, and C are drawn using Pseudoviewer3D software (*13*). The nucleotide colors in RNAStructure 4.6 in figure D indicate base pairing probabilities ranging from red >99% to purple <50%. In figures E, F, G, and H from Sfold, the green, blue, and red dots between pairing nucleotides indicate base pairs that occur in both the ensemble centroid and minimum free energy structure, in the minimum free energy structure but not the centroid structure, or in the centroid structure but not in the minimum free energy structure, respectively. The nucleotide colors in figures I, J, K, ad L from Vienna RNAFold indicate base pairing probabilities ranging from red as 100% to purple as 0%.

Supporting Information Figure 4

A. Maximum pairing distance =50
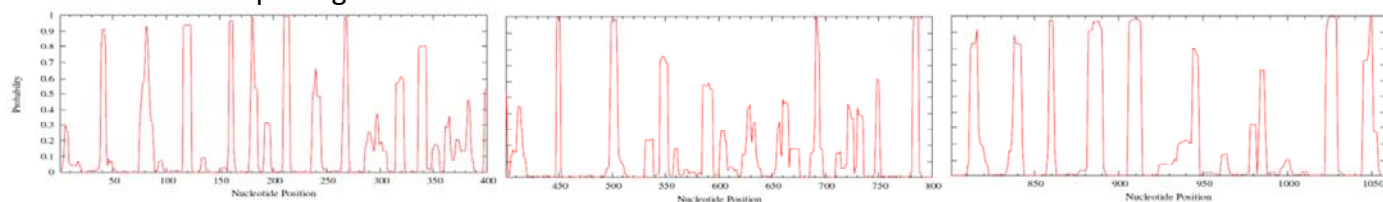
B. Maximum pairing distance =40
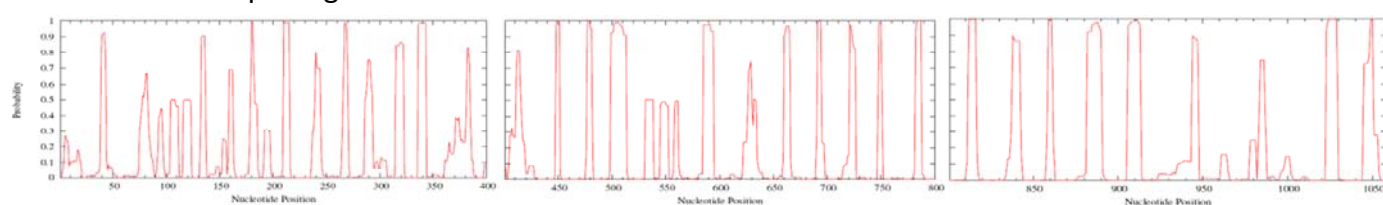
C. Maximum pairing distance =35
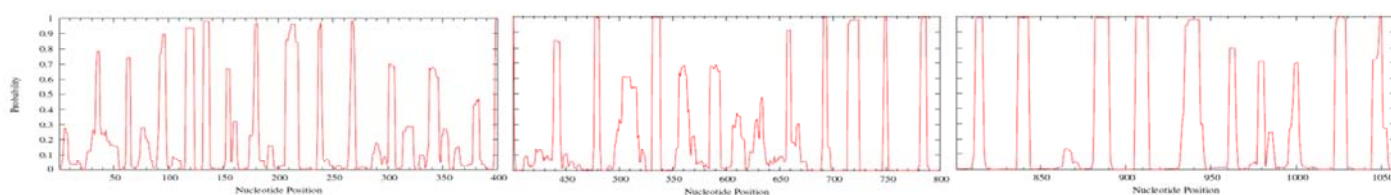
D. Maximum pairing distance =30
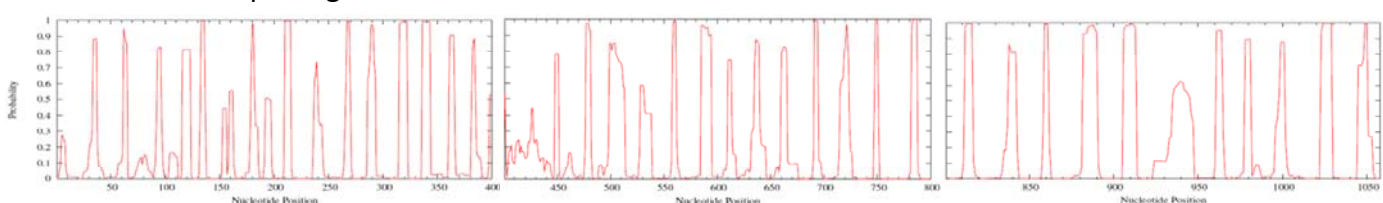
E. Maximum pairing distance =25
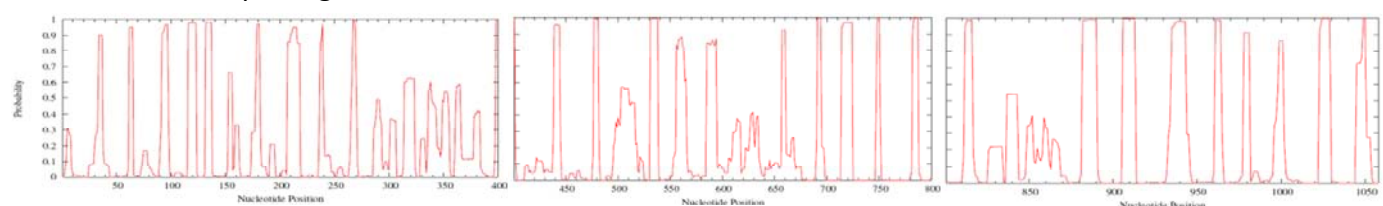
SI Figure 4: Plots of the probability of hairpin formation shown as normalize probability on the y-axis and nucleotide number on the x axis. The output is from the stochastic sampling and cluster analysis in the Sfold program (*14*). The plots are for nucleotides 1-400 (left), 401-800 (center),and 801-1058 (right). The maximum pairing restraint was 50 nucleotides (A.), 40 nucleotides (B), 35 nucleotides (C), 30 nucleotides (D), and 25 nucleotides (E). 134 chemically modified nucleotides were constrained as single stranded. The 5' end of the STMV RNA sequence shows more variation with changes in the maximum pairing restraint than the 3' end of the STMV RNA.

Supporting Information Figure 5

```
        |         |         |         |         |50        |
5'AGUAAACUUACCAAUCAAAAGACCUAACCAACAGGACUGUCGUGGUCAUUUAUGCUGUUGGGGGAC
  (((..(.(((...)).....))).)).(((((((......(((( ....))))))))))))....
  .............................((((((((.......(((((....))))))))))))....
  ..............................((((((((((((.....)))).......)))))))....
  ...................(((((....(.(((....))).).))))....(.((..........
  .(((....)))..........(((((......(((....)))...))))..((.(.(((((.(....))
  ..............................((((((((.(.................).)))))))....
  ..............((.(((......))).)). ......((.(((((.......)))).)).
  ..........................((.(((.......))).))

   |         |         |         |100       |         |
AUAGGGGGAAAACAUAUUGCCUUCUUCUACAAGAGGCCUUCAGUCGCCAUAAUUAC
(.((((.((.(....).)).)))).((((...)))).....................
..(((.((.(.....).)).)))).(((((...))))).................
.........................................(((.........)))..
...)).)..........((((...........)))).......(((((......
))).).)..)).......((((.(((....))))))).......(((((........
..........................(((((.((....))))))).........
..(((((((.((.....))))))))).............................
.......................((((((....))))))...........(((.(((...

   |         |         |150       |         |         |
UUGGCGCCCAAUUUUUGGGUUUCAGUUGCUGUUUCCAGCUAUGGGGAGAGGUAAGGUUAAACCAAA
((((.(((((....)))))).)))).((((.(((((((....)))))))..)))).(((...)))...
..((.(((((....))))))).))...((((.(((((((....)))))))..)))).(((...)))...
.(((.(((((....))))))).)))...(...(.((((...)))..).)..((.....)))...
.))))).((.....)).(.((....((((....)))..))).)........(((...)))...
)))))((((....)))).............((.(((((((....))))))).))...........
..((.(((((....)))))).))..((((.(((((((....)))))))..)))).............
.(((.(((((....)))))).)))....((.((((((....))))))).))................
..........))).)))...... ..((..(((....)))).)).......(((..(((...))).))

   |         |200       |         |         |         |250
CCGUAAAUCGACGGGUGACAAUUCGAAUGUUGUUACUAUGAUUAGAGCUGGAAGCUAUCCUAAGGUCAA
..............(((((((.........)))))))...(..(.(((....)))).)..).........
...............(((((((.......)))))))...(..(.(((...)))).)..)..
((((......)))))((((((((......))))))))...(((((.((.(((((....)))..)).)))))
.............(((((((.......))))))).......(((((..))))....((((..
.((.....))).(((((((.....))))))).(((((..(((...)))....))))).
...........(((((((.......)))))))..(..(.(((...))))..).....
..........(((((((.......)))))))..(((.(.((....)).)))).)
).......(((((((.......)))))))...((.((..........))..)).

   |         |         |         |         |300       |         |         |
UCCGACUCCAACGUGGGUCAGAGCCAUACCUUUCGAAGUGUCAGUUCAAUCUGGUAUUGCUUUUAAAGUACCGGU
((.(((((.....)))))).))((.(((((.(....).))))..)).......(((((((.....)))))))..
...((((((....))))))).(((.(((((....)))).)))))...((((((((.....))))))))((
)).(((.((...)))))).(((((.(((((....)))).)))))...(((((((.....))))))).((
((.(((.(((...))))))).)))))...........(((((((((.....)))))).))))....(.(((...
...((((((....))))))).(((((.(((((....)))).))))...((((((.....))))).((
....................(((((.(((((....))))).)))))...(((((((.....)))))))).
((.(((((.....))))))).))..........(((((((.....)))))))........(((((..((.
((.(((((.....))))))).)))........(((((((.....))))))))......((((..(((.
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```
         |              |350            |               |              |
CGGGUCACUAUUUUCGGCAAAUUUUCCGGACAGAUUCCUUUACAAGCGUCACAGUGAUGAGUGUCCGU
.((((((......))...)))).((((((..(((..((((.........))))).)))))))))...
((((...-...)))))).......((((((..(((.......................)))))))..
((((......))))))).......(((.....)))....((((...))))..........
..)))).....(((((.(...))))))............((......))....((((((..
((((....-..))))))).......(((.....)))..(((..(((((...)))))..)))..(..
..........(.(((((.(...))))))).).....(((..((((...))))).)))...
....))..))))))..(((..(((((.......))))..)).(((..(((((...)))))...))...
..))))..)))...((.(((.((.....)).))).)).......((((.((((.........))
```

```
   |400        |              |              |       |450       |          |
GCUUGGACCCAGUUAACACCGCCAGUAAAUGAGUACAGUUUUGUGAGGCUGAAGCCAUUGUUCAAGACUGGUGACUC
(((.((...(.((....))).)))))))....((((.((((((((.(((((....))).)))...)))))))...))))
.............................((((((((((((((....))).)))).)))))))..(((((
.............................(((((((...(((....))))....)))))))..(((((
..)))))).....................(((((......))))).................((...(((((
(((((....)))......))).(((......))).(((((...(((....)))..))))))...(((((
(((.((.......)))))......(((....))))).(((((...(((((
....((.((.((........)).)).))..(((((.......))))).................((((((
))..))).....................((((((....)))))....................((((((
```

```
       |              |         |500           |              |              |
UACUGAGGAGUUCGAAGGGCGUGCAUCAAACAUCAACACACGAGCUUCUGUAGGGUACAGGAUUCCAACUAAU
......((((((((...((.((.......)).)).....))))))))((((((((.....).)))))))...
(....))))))).....((((.((..........)).)))).((.(((...........)))..))..
(.....))))))).((((..((((.................))))..)))).((.(((..........)))..))..
(.....))))))).....))....((.....................)).....(((.((........)))...
(.....))))))).)).((..((((.............))))..))((((((...))))))..
(.....))))))).))...................................((.(((.....)))).))...
....))))))).....................................(((((.((.........)).))
....))))))))...(((.((.................)).))).....(((((.((........).).))
```

```
   |550        |              |       |              |       |600       |          |
UUGCGUCAGAAUACUGUGGCAGCCGACAAUGUAUGCGAAGUAAGAAGCAACUGUCGACAAGUCGCCUUGGUUAUUUCGUGU
((((((((.......))))).).).)))......((((((((((((.(((((.(((.......))).).))))..))))))))))
..((((((((.....))))).)).).(((..((.(((.........)))))))))...((((...))))...........((((
.(((..(((....))).).))).(((((..((.(((.........)))))))))))).(((((...))))).........
..(((((....)))..)).))...........((((..(.((........))..).)))).....(((.((
..((((((.(....).)))).)).(((((...((.((.........))))))))))..(((((...)))).........((((
..((((((....)))))).)).(((...((.((.........))))))))..............(((.((
)))......(((.(((....)).))).)))...........................(((((((.
)))......(((.(((....)).))).)))...................((.(((....))).))..((((.((...)
```

```
  |              |       |650           |              |              |       |700
UGUUUUAACUGAACCUCGACAUAAGCCUUUUGGAUCGAAGGUUAAACGAUCCGCUCCUCGCUUGAGCUUGAGGCGGCG
.((....))..((((((((..(((.....))).)))).)))))........(((((((((.......))))).)))))
((.......))))))).(((((.(((..)))))))..(((((((((.......))))).))))
..............((((((.......))))))....(((.((((((((...)))))).))))
((...))))))))...((.....((...)).))..(((((((((....)).)))).))))
((((((....)))).....))))).((((((....)))))))..(((((((((...)))).))))
((...))))))))....((((((.(((...))))))))))..((((((((....)))).)))))
...))))))))...(((...(((...))).)))...(((.(((......))).))))..........(
))...))))................(((((.(((...)).)))))..........((.(((((.....
```

```
    |           |           |           |         |750         |           |
UAUCUCUUAUGUCAACAGAGACACUUUGGUCUAUGGUUGUAUAAACAAUAGAUAGACUCCCGUUU
..(((((........))))).....(((((((.(((((...)))))..)))))))........
..(((((........))))).....(((((((.(((((...)))))..)))))))........
.)))))....((((......))))....(((((((.(((((...)))))..)))))))........
..(((((........))))).....(((((((.(((((...)))))..)))))))........
.......___(((.....))).....(((((((.(((((...)))))..)))))))........
..(((((........))))).....(((((((.(((((...)))))..)))))))........
(.(((((........)))))).)....(((((((..............)))))))........
....))))).))...............(((((((..............)))))))........


     |           |          |800         |           |           |           |
GCAAGAUUAGGGUUAACAGAUCUUGCCGUUAGUCUGGUUAGCGCGUAACCGGCCUUGAUUUAUGGAAUAGAUCCAU
(((((((((.........))))))))).(((((.(((((((.....))))))).).)))).((((((.....))))))
(((((((((........))))))))).(((((.(((((((.....))))))).).))))..((((((.....))))))
(((((((((.(.....).)))))))))....(.(.(((((.....))))))).).((((((.....))))))
(((((((((.(.....).)))))))))....(((((((.....))))))).....(((.
(((((((...(.....)..)))))))...(((.(((((((....))))))).-)))..(.(((((...-...))))
(((((((........))))))).....(.(((((((....))))))).).(((((((..)))))))..
(((((((........))))))).....((.(((((((....))))))).))...(((.((((
(((((((........))))))).......(((((....)))))............((.((((


   |850         |          |           |          |          |900         |          |
UGUCCAAUGGCUUUGCCAAUGGAACGCCGACGUGGCUGUAUAAUACGUCGUUGACAAGUACGAAAUCUUGUUAGUGUU
.(((((.((((...))))).))).))..((((((((.......))))))).((((((((......)))))))).....
.(((((.((((...)))).))).)).)..(((((((.......)))))))-(((((((......)))))))-....
.(((((.((((...)))).)))).)...(((((((.......)))))))((((((((.......)))))))).....
.(((....)))--.......)))...((((((((.......))))))))).(((((........)))))).....
.)((((.((((...)))).)))).)))..((((...)))).-((((.........((.........)))))).-....
..(((((.((((...)))).))))....(((((((.....)))))))..
(...)))))).)))-.............(((((.....-)))))).(((((((.....-..)))))))).-...
(...)))))).))-..............((((((...-...))))))...(((((...-...))))))-....


    |          |          |950         |          |          |
UUUCCCUCCACUUAAAUCGAAGGGUUUUGUUUUGGUCUUCCCGAACGCAUACGUUAGUGUGA
...((((((.(......).).))))...((((((.((....)).))))))..(((....)))...
...((((((.(.-....).).)))))..-((((((.((....)).))))))-.(((....)))...
...................(((((....))))))...................(.(((((...(((.(((.....
...((((..........))))...((((.(((...-...)))))))))((((.....)))))..
...((((((........).)))))...(((.(((...-...))))))..(((((....)))))).
..((((((.........))))).. .(((((.((....))).)))))..............
...........((((((......))))))).....................(((.(((((...)
..................(((((((.....-..)))))))............((((.(((((...)


   |          |1000        |          |          |          |          |1050
CUACCGUUGUUCGAAACAAGUAAAACAGGAAGGGGGUUCGAAUCCCUCCCUAACCGCGGGUAAGCGGCCCA3'
.(((.(((.....-.))).)).)))....(((.(((((.......))))).)))..((((......)))).....
.(((.(((......))).)))....(((.(((((........)))))).)))..((((......)))).....
))).))))))))...........(((.(((((.......))))).))).((((......)))).....
.....(((.....))).....((.(((((.(...).))))).)))..((((.-..))))...
(((...((.....)).)))..(((.(((((......))))).)))..((((..-..))))...
.(((.(((.....-.))).)))..(((.(((((......))))).)))
))).))).......................(((.(((((......))))).)))
))).))).....................(((.(((((......))))).)))
```

Supporting Information Figure 5 Legend

STMV sequence (Gen bank number NC_003796.1) is marked with vertical ticks every 10 nucleotides. Nucleotides in red showed a strong hit with dimethyl sulfate. Nucleotides in pink showed a strong hit with kethoxal or CMCT. Nucleotides in green are sites of natural point mutations in different STMV field isolates (*15-17*). Note that A444 is both DMS modified and a site of natural mutation, so it is in red and underlined. The secondary structures in black and blue were generated by RNAStructure 4.6(*7*) using 134 chemical modification constraints and a maximum pairing distance of 50 or 35 nucleotides, respectively, and then manually adjusting helices to form 30 helices of 9 pairs. The secondary structure in orange is the centroid structure generated with the SFOLD algorithm(*14*) using 134 chemical modification constraints and a maximum pairing distance of 35 nucleotides. The secondary structures in purple and green are examples of structures structure sampled from the first cluster generated by the SFOLD program using 134 chemical modification constraints and a maximum pairing distance of 30 nucleotides. The secondary structure in hot pink was generated by selecting the best 30 helices according to the following criteria: maximum number of Watson-Crick pairs, minimum number of asymmetric loops, minimal inclusion of chemically modified nucleotides as part of helix, a minimum of one nucleotide between helices, and similarity to the centroid structure. These criteria minimize deviations from A-form RNA helical conformations and thus maximize consistency with the crystallography data. The secondary structure in aqua was generated from sliding windows and assembly with constraints for pairing score, no asymmetry, 164 chemical modification, and priorities for less internal loops and less terminal mismatches, and no free energy considerations. The secondary structure in red was generated from sliding windows and assembly with constraints for pairing score, no asymmetry, 164 chemical modification with a chemical modification satisfaction score, and priorities for less internal loops and less terminal mismatches, at least 2 nucleotides between helices, and no free energy considerations. The secondary structure in red is also presented as the best representative structure in the ensemble in Figure 4 of the main text.

Supporting Information: Set of all possible hairpins consistent with experimental data

Entries are as follows:
final base number, length, structure, number of canonical pairs, number of GU pairs, asymmetry,
internal loops, terminal mismatches, chemical modification satisfaction score
Example: 242x24 lists the best helix that ends on base 242, and is 24 bases long (thus this helix
starts on base 218). Parentheses indicate Watson-Crick or GU base pairs.   Dots indicate
nucleotides in internal loops or hairpin loops. Slashes indicate noncanonical pairs at the ends of
helices.

All asymmetrical helices, all helices shorter than 9 base pairs, helices including more than 2
internal loop pairs, helices with more than four terminal mismatches, and helices that contradict
chemical modification data have been excluded. Only the highest scoring helix is shown.

```
1000x30:1000,30,((.((((///............///))).)),4,1,0,1,3,0
1003x22:1003,22,///(((.((....)).)))///,3,2,0,1,3,0
1020x27:1020,27,((.((((///.........///)))).)),2,3,0,1,3,0
1021x28:1021,28,((.((((///...........///)))).)),3,2,0,1,3,0
1033x21:1033,21,//((...((...))...))//,2,2,0,3,2,0
1036x22:1036,22,/((.((((/....//))).)))/,4,1,0,1,3,0
1036x22:1036,22,(((.((((/....//)))).))),5,1,0,1,2,0
1036x22:1036,22,(((.((///....///)).))),5,0,0,1,3,0
1037x22:1037,22,///(((((((....))))))))///,4,2,0,0,3,0
1037x23:1037,23,((.(((((/.....///)))).)),6,1,0,1,1,0
1037x23:1037,23,((.(((((//.....//)))).)),6,0,0,1,2,0
1037x23:1037,23,((.(((///.....///))).)),5,0,0,1,3,0
1038x24:1038,24,((..(((((((....)))))))..)),5,3,0,2,0,0
1038x24:1038,24,((..(((((......)))))..)),4,3,0,2,0,0
1038x24:1038,24,((..((((/....../))))..)),4,2,0,2,1,0
1038x24:1038,24,((..(((//......//))).)),3,2,0,2,2,0
1038x24:1038,24,((..((///......///))..)),2,2,0,2,3,0
1038x25:1038,25,(((.(((((.......))))).))),7,1,0,1,0,0
1038x25:1038,25,(((.(((((/.......///)))).))),7,0,0,1,1,0
1038x25:1038,25,(((.((((//.......//)))).))),6,0,0,1,2,0
1038x25:1038,25,(((.((///.......///))).))),5,0,0,1,3,0
1042x28:1042,28,((..(((((..........)))))..)),5,2,0,2,0,0
1042x28:1042,28,((..(((((/.........../)))))..)),5,1,0,2,1,0
1042x28:1042,28,((..((((//........../ /))))..)),4,1,0,2,2,0
1042x28:1042,28,((..((///..........///)).)),3,1,0,2,3,0
1054x21:1054,21,((.((.(((...))).)).)),6,1,0,2,0,0
1054x21:1054,21,((.((.((/.../)).)).)),5,1,0,2,1,0
1054x25:1054,25,((.((..((.......))..)).)),4,2,0,3,0,0
105x22:105,22,///(((((((....)))))))///,5,1,0,0,3,1
113x22:113,22,///((..((....))..))///,3,1,0,2,3,2
123x24:123,24,((...((//......//))...)),4,0,0,3,2,2
124x26:124,26,(((...((/......./))...))),4,1,0,3,1,2
129x28:129,28,((.((.((/.........../)).)).)),4,2,0,2,1,3
130x30:130,30,(((.((.((.............)).)).)))),5,2,0,2,0,3
130x30:130,30,(((.((///.............///)).)))),3,2,0,1,3,1
139x27:139,27,(((.((((//.........//)))).))),6,0,0,1,2,2
139x27:139,27,(((.((///.........///)).))),5,0,0,1,3,1
139x30:139,30,(((..(((//.............//)))..))),3,2,0,2,2,1
140x28:140,28,((..((///..........///)).)),4,0,0,2,3,2
141x21:141,21,((((((///...///)))))),2,4,0,0,3,3
141x30:141,30,(((..(((//.............//)))..))),4,1,0,2,2,3
144x21:144,21,/((..(((//...//)))..))/,2,2,0,2,3,0
146x24:146,24,((((.(((((....)))))).)))),6,3,0,1,0,6
146x24:146,24,((((.(((((......)))))))),5,3,0,1,0,5
146x24:146,24,((((.(((/....../)))).)))),4,3,0,1,1,5
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146x24:146,24,((((.(((//......//)).)))),3,3,0,1,2,4
146x25:146,25,((.((..((.......))..)).)),4,2,0,3,0,2
149x30:149,30,((.(((((.(((((....)))))).)))).)),7,4,0,2,0,7
149x30:149,30,((.(((((.(((......)))).)))).)),6,4,0,2,0,6
149x30:149,30,((.(((((.(((.......))).)))).)),5,4,0,2,0,6
149x30:149,30,((.(((((.((...........))).)))).)),4,4,0,2,0,5
149x30:149,30,((.(((((//............//))))).)),3,3,0,1,2,3
149x30:149,30,((.(((///............//))))).)),3,2,0,1,3,3
158x21:158,21,/((...((/.../))...))/,4,0,0,3,2,2
159x25:159,25,((.((((//......//)))).)),2,3,0,1,3,1
159x26:159,26,((..(((((/......./)))))..)),1,5,0,2,1,2
159x26:159,26,((..(((((/.......//))).)..)),1,4,0,2,2,1
159x26:159,26,((..(((//........///)).).)),1,3,0,2,3,0
160x21:160,21,/((..((//...//))..))/,2,2,0,2,3,1
161x23:161,23,((((..(((/...../))..)))),3,3,0,2,1,3
165x22:165,22,//((.((((....)))).))//,5,1,0,1,2,1
165x22:165,22,//((.((((.....))))))//,4,1,0,1,3,1
166x21:166,21,/(((..(((...))).))))/,2,4,0,2,1,0
166x21:166,21,/(((..((/.../))..))))/,1,4,0,2,2,0
166x24:166,24,((.((.((((....)))).)).)),6,2,0,2,0,1
166x24:166,24,((.((.(((.....))).)).)),5,2,0,2,0,1
166x24:166,24,((.((.((/....../)).)).)),4,2,0,2,1,1
167x22:167,22,/((..(((//....//)).))/,1,3,0,2,3,1
167x25:167,25,((...(((//......//))...)),2,2,0,3,2,1
167x26:167,26,((((.((.((((....)))).)).)))),6,3,0,2,0,1
167x26:167,26,((((.((.(((......))).)).)))),5,3,0,2,0,1
167x26:167,26,((((.((.((........))..)).)))),4,3,0,2,0,1
167x26:167,26,((((.((//........//)).)))),2,3,0,1,3,1
168x28:168,28,((((.((.((((....)))).)).))))),7,3,0,2,0,2
168x28:168,28,((((.((.(((......))).)).))))),6,3,0,2,0,2
168x28:168,28,((((.((.((........)).)).))))),5,3,0,2,0,2
168x28:168,28,((((.((//..........//)).))))),3,3,0,1,2,2
171x22:171,22,///(((((((....)))))))///,4,2,0,0,3,1
171x22:171,22,((.(((((((....)))))))).)),6,2,0,1,0,1
171x22:171,22,((.((((((/..../))))))))).)),5,2,0,1,1,1
171x22:171,22,((.(((((//..../))))))).)),4,2,0,1,2,1
171x22:171,22,((.((((///..../////))).)),3,2,0,1,3,1
172x23:172,23,((.((((((/...../))))))).)),4,3,0,1,1,2
172x23:172,23,((.(((((//...../))))))).)),3,3,0,1,2,2
172x23:172,23,((.((((///...../////))).)),2,3,0,1,3,2
172x26:172,26,((.((.(((........))).)).)),2,5,0,2,0,1
172x26:172,26,((.((.((/......../)).)).)),2,4,0,2,1,1
172x30:172,30,((..((.((((........)))).)).)),4,4,0,3,0,2
172x30:172,30,((..((.(((..........))).)).)),3,4,0,3,0,1
172x30:172,30,((..((.((.............)).)).)),3,3,0,3,0,1
172x30:172,30,((..(((//............//).)),2,2,0,2,3,1
173x25:173,25,(((.(((((.......))))).))),4,4,0,1,0,2
173x25:173,25,(((.(((((/....../))))).))),3,4,0,1,1,2
173x25:173,25,(((.((((//......//))).))),2,4,0,1,2,2
173x25:173,25,(((.((///.......///)).))),2,3,0,1,3,1
173x28:173,28,(((.((.(((........))).)).)))),2,6,0,2,0,1
173x28:173,28,(((.((.((..........))).)).)))),2,5,0,2,0,1
173x28:173,28,(((.((///..........///)).)))),2,3,0,1,3,1
174x22:174,22,//((...((....))...))//,2,2,0,3,2,0
174x24:174,24,((((((//......///))))))),3,3,0,0,3,0
176x27:176,27,((..((///.........///))..)),2,2,0,2,3,1
179x22:179,22,/(((.((//..../))).))))/,2,3,0,1,3,0
179x22:179,22,((((.((//..../))).))))),3,3,0,1,2,0
184x21:184,21,((...((//.../))...)),3,1,0,3,2,0
185x21:185,21,/((...(((...)))...))/,2,3,0,3,1,0
185x21:185,21,/((...((/.../))...))/,2,2,0,3,2,0
185x22:185,22,/((...((/..../))...))/,3,1,0,3,2,0
185x23:185,23,(((...((/...../))...))),4,1,0,3,1,1
190x21:190,21,//((..(((...)))..))//,5,0,0,2,2,1
```

```
190x21:190,21,//((..((/.../))..))//,4,0,0,2,3,1
190x21:190,21,/(((..(((...)))..))))/,6,0,0,2,1,1
190x21:190,21,/(((..((/.../))..))))/,5,0,0,2,2,1
193x22:193,22,/((.(((//....//))).)))/,5,0,0,1,3,3
196x28:196,28,((..((.(((........))).)).))..)),7,0,0,3,0,3
196x28:196,28,((..((.((..........)).)).)),6,0,0,3,0,2
196x28:196,28,((..((//.........///)).)),4,0,0,2,3,2
196x30:196,30,((...((//..........//))...)),2,2,0,3,2,2
210x25:210,25,((..((///.......///))..)),4,0,0,2,3,3
216x21:216,21,((...((//..//))...)),2,2,0,3,2,1
217x24:217,24,((...(((((....))))))...)),4,3,0,3,0,3
217x24:217,24,((...((((......))))...)),3,3,0,3,0,2
217x24:217,24,((...(((/....../)))...)),3,2,0,3,1,2
217x24:217,24,((...((//......//))...)),3,1,0,3,2,2
218x22:218,22,//((..(((....)))..))//,3,2,0,2,2,1
218x22:218,22,//((..((/..../))..))//,2,2,0,2,3,1
218x22:218,22,/(((..(((....)))..))))/,4,2,0,2,1,3
218x22:218,22,/(((..((/..../))..))))/,3,2,0,2,2,3
218x26:218,26,(((...((((((....)))))))...))),5,3,0,3,0,3
218x26:218,26,(((...((((......))))...))),4,3,0,3,0,2
218x26:218,26,(((...(((........)))...))),4,2,0,3,0,2
218x26:218,26,(((...((/........./))...))),4,1,0,3,1,2
223x22:223,22,((((((///....///))))))),5,1,0,0,3,1
224x24:224,24,(((((((//......//)))))))),5,2,0,0,2,1
224x24:224,24,((((((//......//)))))),4,2,0,0,3,0
226x25:226,25,(((..((((/.......//))))..))),3,3,0,2,1,3
226x25:226,25,(((..((//......//))..))),3,2,0,2,2,2
227x21:227,21,/((...(((...)))...))/,4,1,0,3,1,4
227x21:227,21,/((...((/.../))...))/,4,0,0,3,2,3
232x22:232,22,///((..((....))..))///,3,1,0,2,3,2
233x25:233,25,((.((.(((......))).).)).)),3,4,0,2,0,3
233x25:233,25,((.((.((/....../)).).)).)),2,4,0,2,1,2
234x26:234,26,((((.(((///........///)).)))),4,1,0,1,3,2
241x25:241,25,((.(((((//......//)))).)),2,3,0,1,3,0
242x24:242,24,(((.(((((//....../)))).)))),4,2,0,1,2,0
242x24:242,24,(((.((((//....../))).)))),3,2,0,1,3,0
245x21:245,21,(((.(((//...///)).)))),3,2,0,1,3,2
245x27:245,27,((..((((///.........///))..)),3,1,0,2,3,1
253x26:253,26,(((..(((//........//))..))),3,2,0,2,2,1
255x30:255,30,(((((..((............))..))))),5,2,0,2,0,2
274x23:274,23,(((.(((//..../))).)))),2,3,0,1,3,1
275x25:275,25,((((.(((//......//)).)))),3,3,0,1,2,1
278x26:278,26,((...(((//........//))...)),4,0,0,3,2,0
281x22:281,22,///((..((....))..))///,4,0,0,2,3,0
293x21:293,21,/((.((((//.../////)).))/,3,2,0,1,3,0
296x27:296,27,((..((.(((.......))).)).)),3,4,0,3,0,0
296x27:296,27,((..((.((.........)).)).)),3,3,0,3,0,0
296x27:296,27,((..((//........///)).)),2,2,0,2,3,0
297x29:297,29,(((..((.(((.......))).)).)))),3,5,0,3,0,0
297x29:297,29,(((..((.((.........)).)).)))),3,4,0,3,0,0
297x29:297,29,(((..((//........//))..)))),2,3,0,2,2,0
309x27:309,27,((..((///........///))..)),3,1,0,2,3,0
314x22:314,22,//((((((/..../))))))//,4,2,0,0,3,0
314x22:314,22,/((((((/..../)))))))/,4,3,0,0,2,0
314x22:314,22,/(((((((/....//)))))))/,3,3,0,0,3,0
314x22:314,22,((((((((/..../)))))))),5,3,0,0,1,0
314x22:314,22,(((((((//....//)))))))),4,3,0,0,2,0
314x22:314,22,((((((///....///)))))),3,3,0,0,3,0
318x21:318,21,/(((...((...))...))))/,3,2,0,3,1,0
319x29:319,29,((((((///...........///))))))),3,3,0,0,3,0
320x29:320,29,(((.((///...........///)).))),3,2,0,1,3,0
322x22:322,22,///((..((....))..))///,2,2,0,2,3,0
329x22:329,22,/(((((((//..../////)))))))/,5,1,0,0,3,1
329x22:329,22,((((((((//..../////)))))))),5,2,0,0,2,1
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329x22:329,22,(((((((///....///)))))),4,2,0,0,3,0
333x21:333,21,///((..((...))..))///,3,1,0,2,3,1
333x21:333,21,//(((..((...))..)))//,3,2,0,2,2,1
334x22:334,22,(((.(((//....///)).))),1,4,0,1,3,1
335x23:335,23,((...((//.....//))...)),0,4,0,3,2,0
335x30:335,30,(((((((//............//))))))),2,4,0,0,3,2
338x25:338,25,((.(((((//......//)))).))),2,3,0,1,3,0
343x21:343,21,/(((..(((...)))..))))/,3,3,0,2,1,0
343x21:343,21,/(((..((/...))..))))/,3,2,0,2,2,0
344x23:344,23,(((((..(((...)))..))))),5,3,0,2,0,3
344x23:344,23,(((((..((....))..))))),5,2,0,2,0,3
347x22:347,22,///((..((...))..))///,1,3,0,2,3,0
349x26:349,26,((...((//........//))...)),1,3,0,3,2,0
350x22:350,22,/(((((((//....//))))))),3,3,0,0,3,2
361x21:361,21,/(((..((/...))..))))/,1,4,0,2,2,0
361x22:361,22,//(((...((....))...))//,0,4,0,3,2,0
362x22:362,22,//(((.((/....))).))))//,2,3,0,1,3,0
363x25:363,25,((.(((..((.....))..))).)),3,4,0,3,0,1
363x25:363,25,((.(((//.......//)))).)),3,2,0,1,3,1
369x23:369,23,((.((.((/...../)).)).)),4,2,0,2,1,1
376x24:376,24,(((..(((/....../)))..))),3,3,0,2,1,3
376x24:376,24,(((..((//......//))..))),2,3,0,2,2,3
388x25:388,25,(((.(((//......../)))).))),4,1,0,1,3,4
391x24:391,24,(((.((//....../))..))),4,1,0,2,2,3
392x29:392,29,((((.(((//...........//)).)))),4,2,0,1,2,4
393x21:393,21,((..(((((...)))))..)),6,1,0,2,0,4
393x21:393,21,((..(((/.../)))).)),5,1,0,2,1,3
393x21:393,21,((..(((//...//))).)),4,1,0,2,2,2
393x21:393,21,((..((///...////))..)),3,1,0,2,3,1
394x23:394,23,(((..(((((...))))))..))),7,1,0,2,0,5
394x23:394,23,(((..((((....))))..))),6,1,0,2,0,4
394x23:394,23,(((..((/...../)))..))),5,1,0,2,1,3
394x23:394,23,(((..((//...../))..))),4,1,0,2,2,2
398x27:398,27,((..(((((/........./))))..)),3,3,0,2,1,1
398x27:398,27,((..(((//.........//))..)),3,2,0,2,2,1
398x27:398,27,((..(((//.........///))..)),3,1,0,2,3,1
39x21:39,21,/((.(((//...//))).))/,5,0,0,1,3,0
401x22:401,22,//((..(((....)))..))//,4,1,0,2,2,3
401x22:401,22,//((..((/..../))..))//,4,0,0,2,3,2
402x21:402,21,///((..((...))..))///,2,2,0,2,3,1
402x21:402,21,//(((..((...))..)))//,3,2,0,2,2,1
402x21:402,21,/((((..((...))..))))/,4,2,0,2,1,2
403x22:403,22,/((..(((/..../)))..))/,3,2,0,2,2,2
403x22:403,22,/((..((//....//))..))/,2,2,0,2,3,2
405x27:405,27,((..(((((/........./))))..)),4,2,0,2,1,1
405x27:405,27,((..(((//.........//))..)),4,1,0,2,2,1
405x27:405,27,((..(((//.........///))..)),4,0,0,2,3,1
406x22:406,22,///(((((....)))))///,2,4,0,0,3,2
406x29:406,29,(((..((((............))))..))),5,2,0,2,0,1
406x29:406,29,(((..(((/............/)))..))),5,1,0,2,1,1
406x29:406,29,(((..((//............//))..))),5,0,0,2,2,1
415x23:415,23,((..((///...../////)..)),2,2,0,2,3,1
419x24:419,24,((...(((/.....))))...)),4,2,0,3,0,3
419x24:419,24,((...(((/...../)))...)),4,1,0,3,1,3
419x24:419,24,((...((//....../))...)),4,0,0,3,2,2
429x21:429,21,/(((.((//.../))).))))/,4,1,0,1,3,4
432x28:432,28,((.(((.(((/........../)).)).)).)),6,0,0,2,1,3
434x25:434,25,((...(((//......//)))...)),4,0,0,3,2,2
437x24:437,24,((...(((//....../))))...)),3,1,0,3,2,1
441x30:441,30,(((.((///.............///)).))),4,1,0,1,3,4
442x29:442,29,(((..(((//...........//))..))),4,1,0,2,2,2
443x23:443,23,((..((///...../////))..)),4,0,0,2,3,3
443x26:443,26,(((.((///......../////)).))),3,2,0,1,3,1
449x21:449,21,//((...((...))...))//,1,3,0,3,2,0
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449x21:449,21,/(((...((...))...)))/,2,3,0,3,1,0
451x22:451,22,//((...((....))...))//,2,2,0,3,2,2
452x22:452,22,///((((((....)))))))///,4,2,0,0,3,1
455x22:455,22,//(((((/..../))))))//,3,3,0,0,3,4
459x24:459,24,((..((///......///))..)),2,2,0,2,3,1
463x21:463,21,//((.(((/.../))).))//,2,3,0,1,3,1
464x26:464,26,((..((///........///))..)),2,2,0,2,3,2
465x27:465,27,((.(((((//........//)))))).)),4,2,0,1,2,3
465x27:465,27,((.(((((//........//)))).)),4,1,0,1,3,2
474x24:474,24,((.(((((/....../)))))).)),4,3,0,1,1,2
474x24:474,24,((.(((((//...../)))))).)),4,2,0,1,2,2
474x24:474,24,((.(((///...../)))))).)),4,1,0,1,3,2
477x30:477,30,((.((.(((((.......))))).)).)),5,4,0,2,0,2
477x30:477,30,((.((.((((...........)))).)).)),5,3,0,2,0,2
477x30:477,30,((.((.(((.............))).)).)),5,2,0,2,0,2
477x30:477,30,((.((.(((/.............../))).)).)),5,1,0,2,1,2
481x21:481,21,//((...((...))...))//,3,1,0,3,2,1
483x25:483,25,((..((///......///))..)),2,2,0,2,3,1
488x21:488,21,((...((//.../))...)),2,2,0,3,2,0
489x23:489,23,(((...((/...../))...))),2,3,0,3,1,0
493x28:493,28,((..((((//.........//))))..)),3,2,0,2,2,0
493x28:493,28,((..((///.........///))..)),2,2,0,2,3,0
494x21:494,21,/((..(((((...))))..))/,3,3,0,2,1,2
494x21:494,21,/((..(((/.../)))..))/,3,2,0,2,2,1
494x21:494,21,/((..((//.../))..))/,2,2,0,2,3,0
494x21:494,21,(((..(((((...))))..))),3,4,0,2,0,2
494x21:494,21,(((..(((/.../)))..))),3,3,0,2,1,1
494x21:494,21,((..((//.../))..))),2,3,0,2,2,0
495x27:495,27,((...((//........//))...)),3,1,0,3,2,1
497x29:497,29,(((.(((//.........../)))).)))),2,3,0,1,3,0
502x21:502,21,((.((.(((.../))).)).)),4,2,0,2,1,0
514x21:514,21,//((..((/.../))..))//,4,0,0,2,3,3
51x22:51,22,((..((///....///))..)),3,1,0,2,3,0
51x26:51,26,((...((//........//))...)),4,0,0,3,2,2
521x29:521,29,(((.(((//.........../)))).))),3,2,0,1,3,1
529x22:529,22,((.((((//....//)))).)),4,1,0,1,3,3
530x30:530,30,((..((((//............//))))..)),4,1,0,2,2,2
530x30:530,30,((..((///............///))..)),3,1,0,2,3,1
539x23:539,23,((.(((.(((...))).))).)),4,4,0,2,0,2
539x23:539,23,((.(((.((.....)).))).)),4,3,0,2,0,2
539x23:539,23,((.((((//....//))).)),3,2,0,1,3,1
53x22:53,22,///((..((....))..))///,1,3,0,2,3,1
53x22:53,22,//(((..((....))..)))//,1,4,0,2,2,1
540x24:540,24,(((.(((//....../))).))),2,3,0,1,3,0
545x22:545,22,/((.(((((//....//)))).)))/,4,1,0,1,3,1
546x23:546,23,((...((//....../)))...)),3,1,0,3,2,0
54x23:54,23,((.((.(((...../)).)).)),5,1,0,2,1,3
54x26:54,26,((..((///........///))..)),3,1,0,2,3,1
550x22:550,22,((...((//..../)))...)),2,2,0,3,2,1
551x26:551,26,((((.(((//......../))).))))),3,3,0,1,2,1
553x30:553,30,((((((.((.............)).))))))),4,4,0,1,0,1
553x30:553,30,((((((//............//))))))),2,4,0,0,3,0
554x23:554,23,((..((///....////))..)),3,1,0,2,3,2
559x22:559,22,/((..((//..../))..))/,4,0,0,2,3,1
559x22:559,22,(((..((//..../))..))),5,0,0,2,2,1
560x24:560,24,((((..((/....../))..)))),6,0,0,2,1,1
563x21:563,21,//((.((((...))))))//,5,1,0,1,2,3
563x21:563,21,//((.(((/.../)))))//,4,1,0,1,3,2
563x30:563,30,((.(((((..((.........))..))))).)),8,0,0,3,0,2
563x30:563,30,((.(((((//............//))))).)),6,0,0,1,2,1
563x30:563,30,((.(((///.............///))).)),5,0,0,1,3,1
566x22:566,22,((...((//..../))...)),2,2,0,3,2,1
56x23:56,23,((..((///.....////))..)),2,2,0,2,3,1
570x22:570,22,//((..((/..../))..))//,4,0,0,2,3,1
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570x22:570,22,/(((..((/..../))..)))/,5,0,0,2,2,1
570x23:570,23,((..(((//.....//))))..)),2,3,0,2,2,0
570x23:570,23,((..((///.....///))..)),2,2,0,2,3,0
57x21:57,21,//((...((...))...))//,1,3,0,3,2,1
57x29:57,29,((.((.((.((.......)).)).))),7,1,0,3,0,3
57x29:57,29,((.((.(((...........//)).)).)),5,1,0,2,1,2
580x22:580,22,/((.(((//..../))))..)))/,4,1,0,1,3,1
580x22:580,22,(((.(((//..../))))..)))),5,1,0,1,2,1
580x22:580,22,(((.((///..../////))..)))),4,1,0,1,3,1
581x22:581,22,/((..(((//..../))..))/,4,0,0,2,3,1
586x22:586,22,///((..((...))..))///,3,1,0,2,3,0
586x22:586,22,//(((..((...))..))))//,4,1,0,2,2,0
589x29:589,29,(((.(((//..........///)).))),4,1,0,1,3,1
58x22:58,22,/((.(((((....)))))).))/,2,5,0,1,1,3
58x22:58,22,/((.(((((/..../)))))).))/,2,4,0,1,2,3
58x22:58,22,/((.((((//..../////)).))/,2,3,0,1,3,2
592x22:592,22,///((..((...))..))///,3,1,0,2,3,0
59x21:59,21,//((..((/.../))..))//,2,2,0,2,3,1
59x22:59,22,/((.(((((//..../////)).))/,1,4,0,1,3,2
59x25:59,25,(((.(((//......///)).)))),3,2,0,1,3,3
601x24:601,24,((..(((//......//)))..)),3,2,0,2,2,0
601x24:601,24,((..((///......///))..)),2,2,0,2,3,0
602x26:602,26,(((..((((/......../)))..)))),4,2,0,2,1,0
602x26:602,26,(((..((//........//))..)))),3,2,0,2,2,0
607x30:607,30,(((..((((/............./))..)))),4,2,0,2,1,0
607x30:607,30,(((..((//.............//))..)))),4,1,0,2,2,0
60x23:60,23,((.((..((.....))..)).)),2,4,0,3,0,1
616x25:616,25,((.((.(((.......))).)).)),6,1,0,2,0,0
616x25:616,25,((.((.(((......./)).)).)),5,1,0,2,1,0
616x30:616,30,((...((//............//))...)),3,1,0,3,2,0
61x25:61,25,(((.((..((.....))..)).)))),3,4,0,3,0,1
61x25:61,25,(((.((///.......///)).)))),2,3,0,1,3,0
620x28:620,28,((.((((///.........///))).)),5,0,0,1,3,0
622x21:622,21,//(((.((/.../)).))))//,3,2,0,1,3,0
623x30:623,30,((.(((((/............./)))))).)),4,3,0,1,1,0
623x30:623,30,((.(((((//............//)))))).)),4,2,0,1,2,0
623x30:623,30,((.((((//.............//))))).)),4,1,0,1,3,0
624x21:624,21,((..(((((...)))))..)),3,4,0,2,0,0
624x21:624,21,((..((((/.../)))))..)),3,3,0,2,1,0
624x21:624,21,((..(((//.../)))))..)),2,3,0,2,2,0
624x21:624,21,((..(((//.../////)..)),2,2,0,2,3,0
626x22:626,22,///(((.((....))).)))///,3,2,0,1,3,0
626x22:626,22,//(((((.((....)).)))))//,4,2,0,1,2,0
627x27:627,27,((.(((..((((((...))))))..)).)),3,6,0,3,0,0
627x27:627,27,((.(((..((((.....)))))..)).)),3,5,0,3,0,0
627x27:627,27,((.(((..((.......)))..)).)),2,5,0,3,0,0
627x27:627,27,((.(((..((.........)).)).)),2,4,0,3,0,0
631x26:631,26,(((..(((//........//))..)))),5,0,0,2,2,0
632x28:632,28,(((((..((/........./))..))))),6,0,0,2,1,0
633x26:633,26,(((.((((//........//)))).)))),2,3,0,1,3,0
633x30:633,30,(((((..((.............))..))))),6,1,0,2,0,0
635x21:635,21,//(((.((/.../)).)))))//,1,4,0,1,3,0
635x29:635,29,(((.((((//..........///)).)))),3,2,0,1,3,0
638x21:638,21,//((...((...))...))//,3,1,0,3,2,0
638x21:638,21,((((...((...))...)))),5,1,0,3,0,0
639x23:639,23,(((((...((...))...))))),5,2,0,3,0,0
63x24:63,24,((.(((((//......//)))).)),1,5,0,1,2,3
63x24:63,24,((.(((///......///))).)),1,4,0,1,3,3
640x25:640,25,((((((...((...))...)))))),5,3,0,3,0,0
640x25:640,25,((((((///.......///)))))),4,2,0,0,3,0
641x23:641,23,(((.((///.....///)).))),4,1,0,1,3,1
641x27:641,27,(((((((...((...))...))))))),6,3,0,3,0,1
641x27:641,27,(((((((//.........//))))))),5,2,0,0,2,1
641x27:641,27,(((((((///.........///))))))),4,2,0,0,3,1
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642x21:642,21,(((.(((///...///)).))).)))),4,1,0,1,3,2
642x22:642,22,/((...((/..../))...)))/,2,2,0,3,2,1
646x30:646,30,((...(((/............//)))...)),2,2,0,3,2,1
647x21:647,21,((..((((/...//)))).)),4,2,0,2,1,2
647x21:647,21,((..((((/...//)))).)),4,1,0,2,2,1
647x21:647,21,((..(((//...//))).)),3,1,0,2,3,0
64x21:64,21,//((...((...))...)))//,2,2,0,3,2,2
64x28:64,28,((.((((//..........//)))).)),2,3,0,1,3,1
652x23:652,23,(((.(((//....//)).))),3,2,0,1,3,3
653x25:653,25,((((.(((//......//))).)))),4,2,0,1,2,5
659x21:659,21,/((..(((//...//))..)))/,3,1,0,2,3,2
65x21:65,21,/((.((.((...)).)).)).))/,2,4,0,2,1,2
665x26:665,26,((.((..((........))..)).)),5,1,0,3,0,2
666x21:666,21,/((..((((...)))).))/,4,2,0,2,1,5
666x21:666,21,/((..(((/...//)))..))/,4,1,0,2,2,4
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666x21:666,21,(((..(((/...//)))..)))),5,1,0,2,1,4
666x21:666,21,(((..(((//...//))..)))),4,1,0,2,2,2
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667x23:667,23,((((..(((.....)))..)))),6,1,0,2,0,5
667x23:667,23,((((..((/...../))..)))),5,1,0,2,1,3
66x22:66,22,/((.(((((/..../))))).))/,3,3,0,1,2,3
66x22:66,22,/((.((((//..../////)))).))/,2,3,0,1,3,2
677x21:677,21,//((.(((...)))).))//,4,2,0,1,2,4
677x21:677,21,//((.(((/...//)))).))//,3,2,0,1,3,4
67x22:67,22,///(((.((...)).))))///,0,5,0,1,3,4
67x25:67,25,((.((.((.((...)).)).)).)),4,4,0,3,0,3
67x25:67,25,((.((.(((/......./)).)).)),3,3,0,2,1,2
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683x30:683,30,((...((//...........//)))...)),3,1,0,3,2,1
689x25:689,25,(((.(((//......//))).))),4,1,0,1,3,1
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68x27:68,27,(((.((.((........)).)).))),3,4,0,2,0,3
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693x22:693,22,(((.(((//....//))).))),4,1,0,1,3,3
694x24:694,24,((((.(((/....../))).)))),6,1,0,1,1,4
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697x29:697,29,((((.(((//..........//)))))),4,2,0,1,2,2
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697x30:697,30,((.(((((//...........//))))).)),5,1,0,1,2,4
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706x22:706,22,/((..((((.....)))))..))/,3,3,0,2,1,0
706x22:706,22,/((..(((/....//))).))/,3,2,0,2,2,0
706x22:706,22,/((..(((/....//))..))/,3,1,0,2,3,0
706x25:706,25,(((.(((//......//))).))),3,2,0,1,3,0
707x27:707,27,((((.(((//......//))).)))),4,2,0,1,2,0
711x22:711,22,//((.(((/..../))).))//,3,2,0,1,3,0
718x21:718,21,((.((.((/../)).)).)),1,5,0,2,1,0
71x21:71,21,//((...((...))...)))//,1,3,0,3,2,2
731x25:731,25,((.((((((/....../)))))).)),7,0,0,1,1,3
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731x25:731,25,((.((((//....../////))).)),5,0,0,1,3,2
732x29:732,29,((.((.((((.((.....)).)))).)).)),8,1,0,3,0,5
732x29:732,29,((.((.((............)))).)).)),6,1,0,2,0,3
732x29:732,29,((.((.(((/............/)).)).)),5,1,0,2,1,2
73x25:73,25,(((.((((///......./////))).)))),1,4,0,1,3,5
740x22:740,22,///((.(((.....))).)))///,3,2,0,1,3,2
741x24:741,24,((..((.(((.....))).))..)),4,3,0,3,0,2
741x24:741,24,((..((.((......)).))..)),4,2,0,3,0,2
741x24:741,24,((..(((//...../////))..)),3,1,0,2,3,2
752x22:752,22,/((..((((//....////))..)))/,2,2,0,2,3,1
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756x22:756,22,/((...((/..../))...))/,2,2,0,3,2,1
758x22:758,22,///((.(((....))).))///,5,0,0,1,3,1
758x22:758,22,//((((.(((....))).))))//,6,0,0,1,2,2
758x22:758,22,//((((.((/..../))).))))//,5,0,0,1,3,1
75x30:75,30,((.((((//...........///))).)),2,3,0,1,3,4
763x22:763,22,//(((((.((....)).)))))//,4,2,0,1,2,2
763x28:763,28,(((((((//.........///)))))))),6,0,0,0,3,0
764x30:764,30,((((((((//............///)))))))),6,1,0,0,2,0
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768x28:768,28,(((..(((//.........//)))..))),4,1,0,2,2,0
770x21:770,21,/((...((/.../))...))/,4,0,0,3,2,1
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783x21:783,21,/((..(((((...)))))..))/,3,3,0,2,1,0
783x21:783,21,/((..(((/.../)))..))/,2,3,0,2,2,0
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783x21:783,21,(((..(((((...))))..))),4,3,0,2,0,0
783x21:783,21,(((..(((/.../)))..))),3,3,0,2,1,0
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784x23:784,23,((((..((((...))))..)))),5,3,0,2,0,0
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786x28:786,28,(((.(((//.........///)).))),3,2,0,1,3,0
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798x22:798,22,///((((((....))))))///,3,3,0,0,3,0
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816x21:816,21,//(((((((...)))))))//,4,3,0,0,2,2
816x21:816,21,//(((((/.../)))))))//,4,2,0,0,3,2
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829x22:829,22,///((..((....))..))///,4,0,0,2,3,0
82x30:82,30,((...((//............//)))...)),3,1,0,3,2,3
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843x21:843,21,//((...((...))...))//,2,2,0,3,2,1
844x22:844,22,///(((.((....)).)))///,2,3,0,1,3,3
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857x28:857,28,((..((//...........///))..)),2,2,0,2,3,0
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864x22:864,22,//((..(((...))).))//,4,1,0,2,2,0
864x22:864,22,//((..((/..../))..))//,3,1,0,2,3,0
870x28:870,28,((((((//.........////)))))),6,0,0,0,3,2
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87x27:87,27,((.((.(((/........./)).)).)),5,1,0,2,1,2
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887x27:887,27,(((...((/........./))...))),2,3,0,3,1,3
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89x22:89,22,/(((.((//..../))).)))/,3,2,0,1,3,3
89x26:89,26,((..(((//........//))..)),2,3,0,2,2,2
89x26:89,26,((..(((//........///))..)),2,2,0,2,3,1
89x28:89,28,(((.((//...........//)).)))),3,2,0,1,3,3
89x29:89,29,((((..((/.........../))..)))),4,2,0,2,1,6
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900x21:900,21,((((.(((//...//)).)))))),1,5,0,1,2,1
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905x23:905,23,((...(((//...../)))...)),4,1,0,3,1,4
905x23:905,23,((...((//...../)))...)),3,1,0,3,2,2
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906x25:906,25,(((...(((.......)))...))),4,2,0,3,0,4
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907x28:907,28,((..((///.........///))..)),3,1,0,2,3,2
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908x21:908,21,//((..((/...../))..))//,3,1,0,2,3,1
90x21:90,21,//(((.((/.../)).))))//,4,1,0,1,3,5
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911x21:911,21,///((..((...))..)).)))//,4,0,0,2,3,1
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91x22:91,22,/((((..((....))..)))))/,4,2,0,2,1,6
91x30:91,30,((((..(((.............)))..)))),3,4,0,2,0,5
91x30:91,30,((((..((/............./))..)))),3,3,0,2,1,4
921x24:921,24,(((((((//....../)))))))),6,2,0,0,1,6
921x24:921,24,(((((((//....../)))))))),5,2,0,0,2,6
921x24:921,24,((((((//....../)))))))),4,2,0,0,3,6
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922x26:922,26,((((((((/......./))))))))),5,3,0,0,1,7
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922x26:922,26,((((((///......///))))))),3,3,0,0,3,7
923x22:923,22,((...((((....))))...)),5,1,0,3,0,4
923x22:923,22,((...(((/..../)))...)),4,1,0,3,1,3
923x22:923,22,((...((//..../))...)),4,0,0,3,2,3
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928x22:928,22,//((((..((....))..))))/,4,1,0,2,2,5
928x26:928,26,(((.(((//........//))).))),4,2,0,1,2,5
928x26:928,26,(((.((///........///)).))),4,1,0,1,3,3
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929x30:929,30,((.((((//............//)))).)),4,2,0,1,2,6
929x30:929,30,((.(((///............///))).)),4,1,0,1,3,4
92x24:92,24,(((((((..((....))..))))))),5,3,0,2,0,7
92x24:92,24,(((((((///......///))))))),3,3,0,0,3,6
932x29:932,29,((...(((/............./)))...)),4,1,0,3,1,3
932x29:932,29,((...(((//...........//))...)),3,1,0,3,2,1
93x24:93,24,(((((((///......///))))))),3,3,0,0,3,7
93x30:93,30,((...(((/............./)))...)),5,0,0,3,1,2
93x30:93,30,((...(((//............//)))...)),4,0,0,3,2,1
94x23:94,23,((((.(((//...../))).))))),4,2,0,1,2,4
94x24:94,24,((((.(((//......//)).))))),3,3,0,1,2,6
94x25:94,25,(((((((///......///))))))),3,3,0,0,3,8
94x26:94,26,((((((((//......../)))))))),4,3,0,0,2,8
94x26:94,26,(((((((//........///))))))),3,3,0,0,3,7
951x21:951,21,//((..((/.../)).)))//,3,1,0,2,3,1
955x21:955,21,((..((.((...)).))..)),5,1,0,3,0,3
955x21:955,21,((..(((//.../))).)),4,0,0,2,3,3
958x21:958,21,///((.(((...))).))///,3,2,0,1,3,3
958x22:958,22,//((...((....))...))//,3,1,0,3,2,3
959x21:959,21,/((...(((...)))...))/,4,1,0,3,1,3
959x21:959,21,/((...((/.../))...))/,4,0,0,3,2,3
959x22:959,22,//((.((((...)))).))//,5,1,0,1,2,4
959x22:959,22,//((.(((/..../))).))//,4,1,0,1,3,3
961x21:961,21,/(((((((//...//))))))/,3,3,0,0,3,2
961x21:961,21,(((((((//...//))))))),4,3,0,0,2,3
961x21:961,21,((((((//...///)))))),4,2,0,0,3,3
961x27:961,27,(((.(((///........///))).))),4,1,0,1,3,3
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965x21:965,21,/((((((((//.../))))))))/,2,4,0,0,3,0
966x21:966,21,//((..(((...)))..))//,0,5,0,2,2,0
966x21:966,21,//((..((/.../))..))//,0,4,0,2,3,0
966x21:966,21,/(((..(((...)))..)))/,1,5,0,2,1,0
966x21:966,21,/(((..((/.../))..)))/,1,4,0,2,2,0
966x22:966,22,//(((.((/..../)).)))//,1,4,0,1,3,0
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968x26:968,26,((..(((//........//))).)).)),3,2,0,2,2,0
968x26:968,26,((..(((//........//))).)),2,2,0,2,3,0
969x28:969,28,(((..(((.((......)).))).))).))),4,4,0,3,0,0
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973x22:973,22,//(((((.((....)).)))))//,5,1,0,1,2,0
973x22:973,22,/(((((.((....)).))))))/,5,2,0,1,1,0
976x21:976,21,//((...((...))...))//,3,1,0,3,2,0
982x28:982,28,((...(((//........../))...)),3,1,0,3,2,0
983x22:983,22,/((..(((//..../))..)))/,3,1,0,2,3,0
986x22:986,22,//((...((....))...))//,2,2,0,3,2,0
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995x21:995,21,//(((.(((/.../))).)))//,5,0,0,1,3,0
995x21:995,21,/(((.(((((...))))).))))/,7,0,0,1,1,0
995x21:995,21,/(((.(((/.../))).))))/,6,0,0,1,2,0
995x21:995,21,//(((.((//.../)).)))//,5,0,0,1,3,0
996x24:996,24,((...(((//......//)))...)),4,0,0,3,2,0
997x26:997,26,(((...(((/........./))...))),4,1,0,3,1,0
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