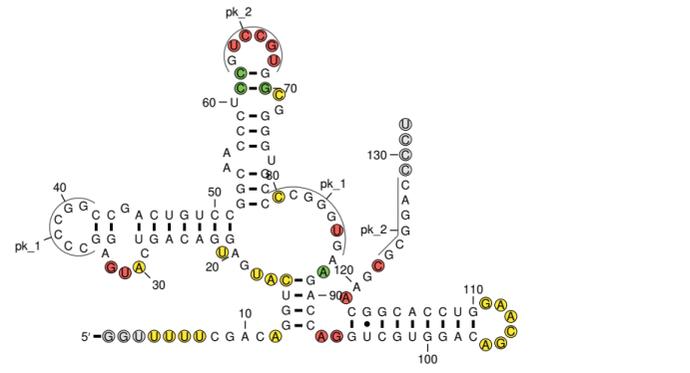
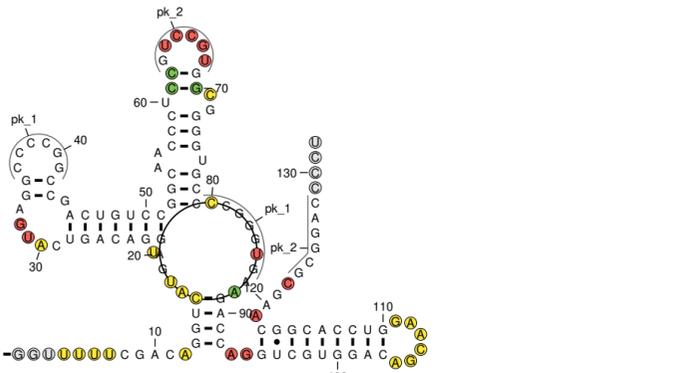


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SAM-IV NC_003888.3/2308784-2308334 multistem=original
 Shrinking nucs & bonds using
 nucShrinkWithCircleNuc and pairBondScaleWithOneSeq
 because circle_nuc or #=GR ... CLEAVAGE was used
 To disable this warning message:
 #=GF R2R SetDrawingParam nucShrinkWithCircleNuc 1 drawingParams.pairBondScaleWithCircleNuc 1
 See note1 in manual for more information.



SAM-IV NC_003888.3/2308784-2308334 multistem=solver internalloop=solver2
 Shrinking nucs & bonds using
 nucShrinkWithCircleNuc and pairBondScaleWithOneSeq
 because circle_nuc or #=GR ... CLEAVAGE was used
 To disable this warning message:
 #=GF R2R SetDrawingParam nucShrinkWithCircleNuc 1 drawingParams.pairBondScaleWithCircleNuc 1
 See note1 in manual for more information.



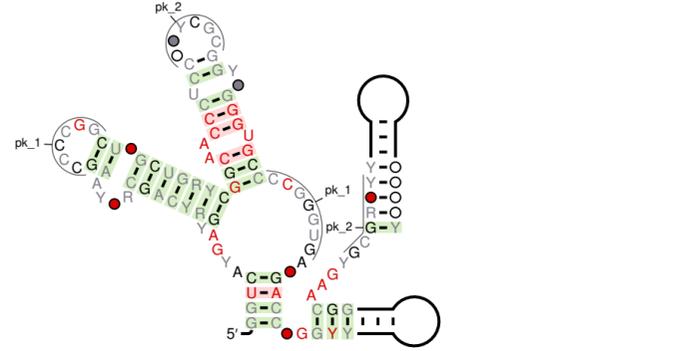
SAM-IV NC_003888.3/2308784-2308334 pseudoknot=1
 Shrinking nucs & bonds using
 nucShrinkWithCircleNuc and pairBondScaleWithOneSeq
 because circle_nuc or #=GR ... CLEAVAGE was used
 To disable this warning message:
 #=GF R2R SetDrawingParam nucShrinkWithCircleNuc 1 drawingParams.pairBondScaleWithCircleNuc 1
 See note1 in manual for more information.



SAM-IV NC_003888.3/2308784-2308334 pseudoknot=2
 Shrinking nucs & bonds using
 nucShrinkWithCircleNuc and pairBondScaleWithOneSeq
 because circle_nuc or #=GR ... CLEAVAGE was used
 To disable this warning message:
 #=GF R2R SetDrawingParam nucShrinkWithCircleNuc 1 drawingParams.pairBondScaleWithCircleNuc 1
 See note1 in manual for more information.

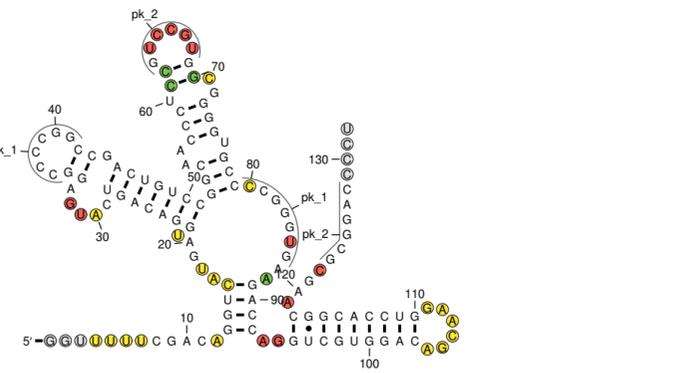


SAM-IV.cons

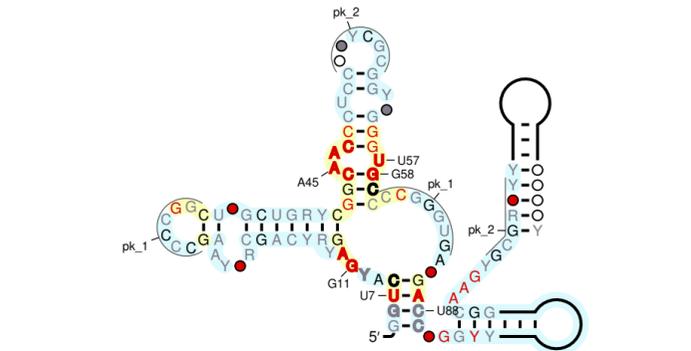


SAM-IV.cons NC_003888.3/2308784-2308334

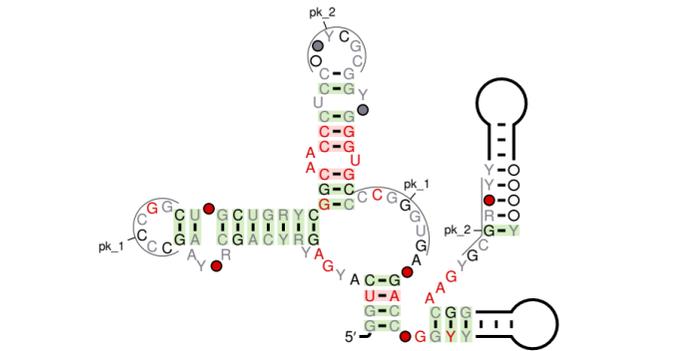
Shrinking nucs & bonds using
 nucShrinkWithCircleNuc and pairBondScaleWithOneSeq
 because circle_nuc or #=GR ... CLEAVAGE was used
 To disable this warning message:
 #=GF R2R SetDrawingParam nucShrinkWithCircleNuc 1 drawingParams.pairBondScaleWithCircleNuc 1
 See note1 in manual for more information.



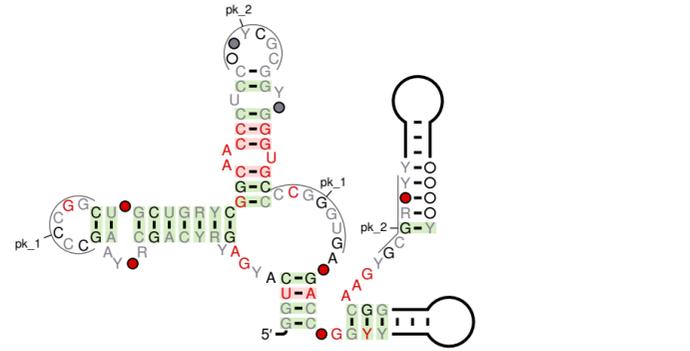
SAM-IV.cons Weinberg2008-Fig1=1 multistem=original



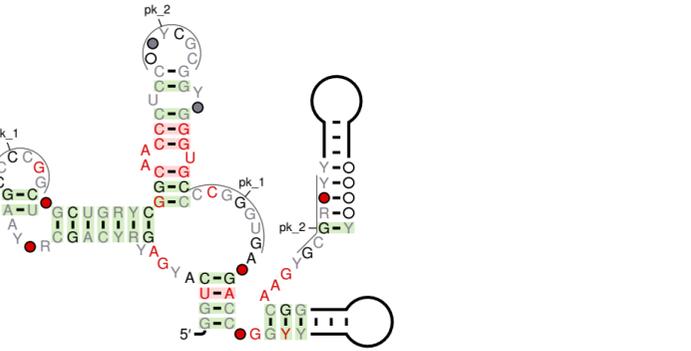
SAM-IV.cons multistem=bulge



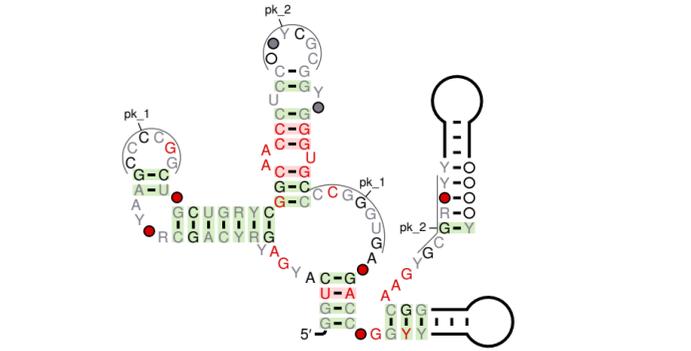
SAM-IV.cons multistem=original



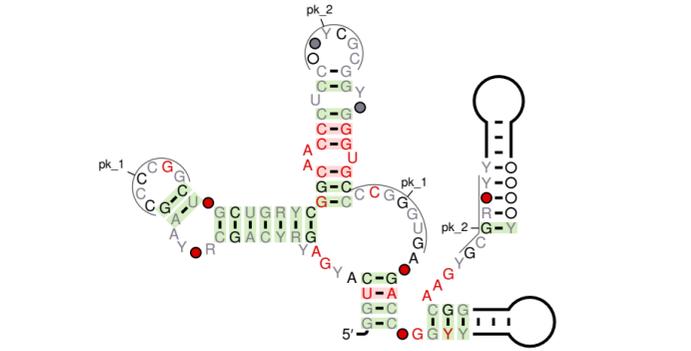
SAM-IV.cons multistem=original internalloop=solver



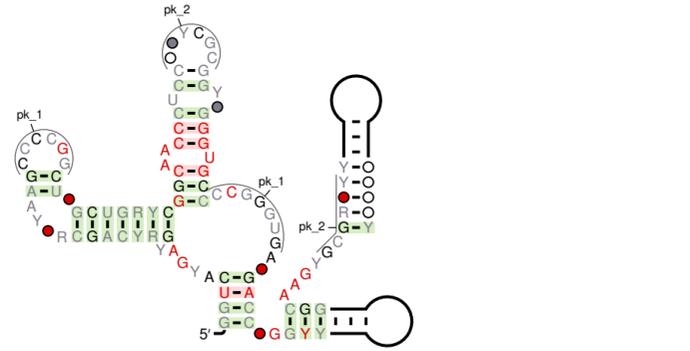
SAM-IV.cons multistem=original internalloop=solver2



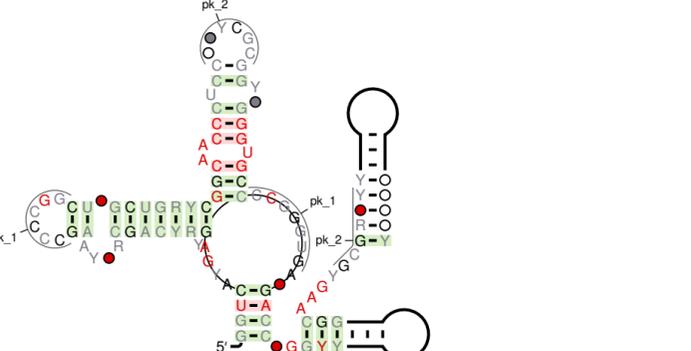
SAM-IV.cons multistem=original internalloop=solver3



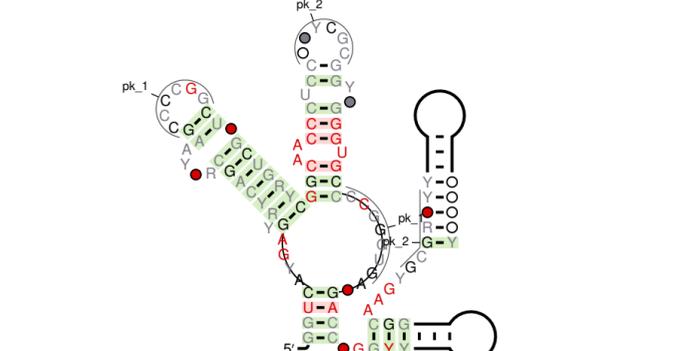
SAM-IV.cons multistem=original internalloop=turn



SAM-IV.cons multistem=solver



SAM-IV.cons multistem=solver2



SAM-IV.cons pseudoknot=1



SAM-IV.cons pseudoknot=2



SAM-IV.cons skeleton-with-bp



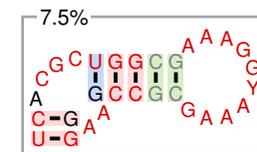
WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg and Breaker, 2011 wrote:

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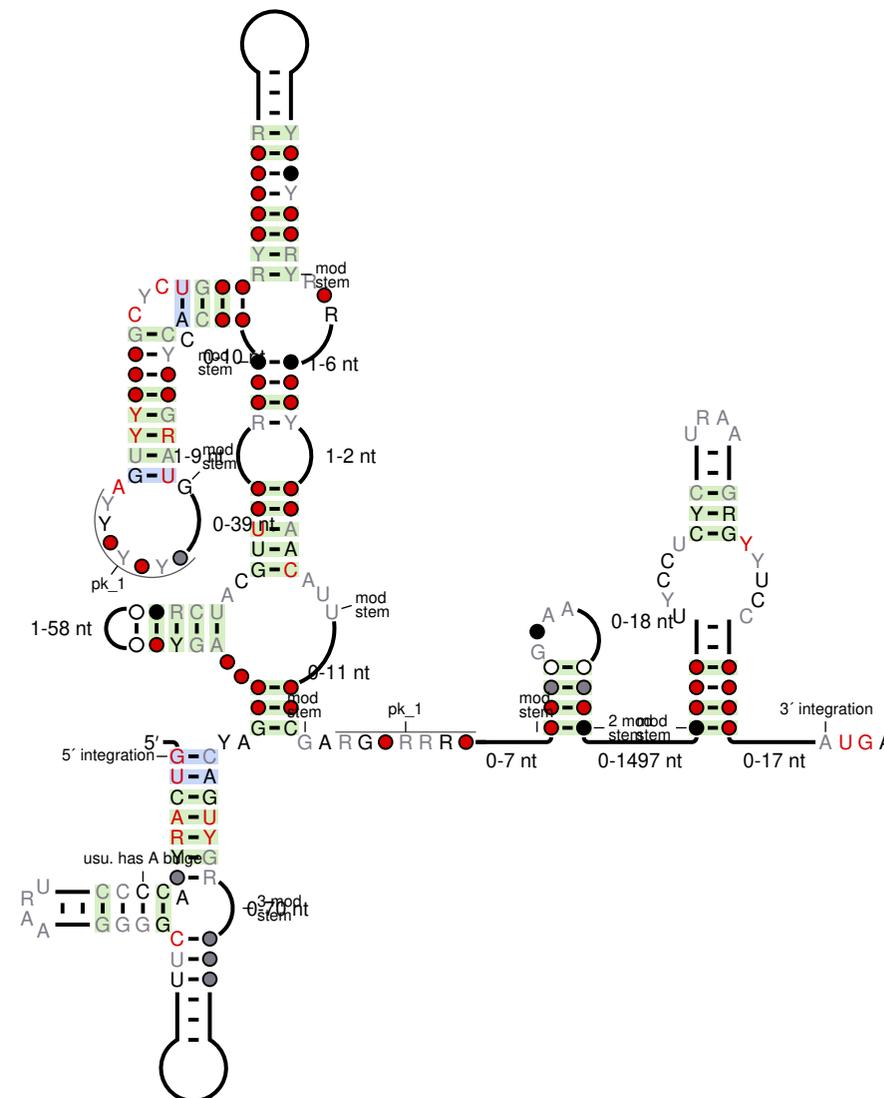
To disable this warning, run r2r with --disable-usage-warning

HEARO-RYGCAA.cons

subfam_weight=0.0745961

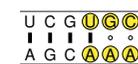


HEARO.cons

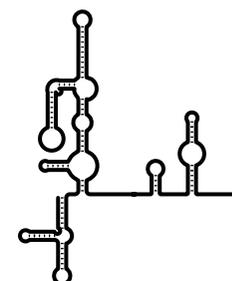


HEARO.cons NZ_ABYK0100021.1/61949-61536 pknot=1

Shrinking nucs & bonds using
nucShrinkWithCircleNuc and pairBondScaleWithOneSeq
because circle_nuc or #=GR ... CLEAVAGE was used
To disable this warning message:
#=GF R2R SetDrawingParam nucShrinkWithCircleNuc 1 drawingParams.pairBondScaleWithCircleNuc 1
See note1 in manual for more information.

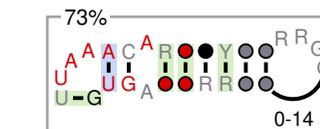


HEARO.cons skeleton-with-bp



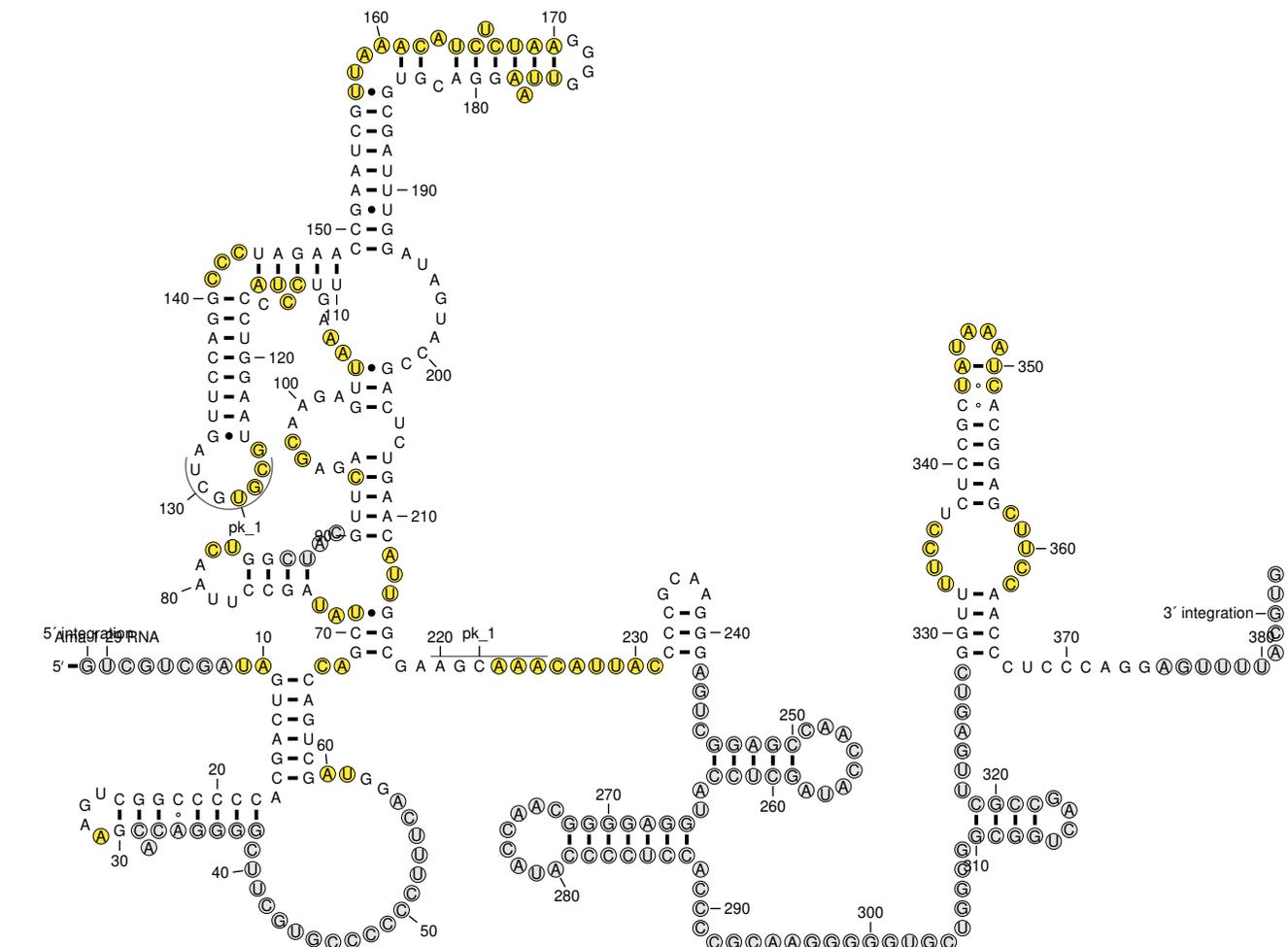
HEARO-UAA.cons

subfam_weight=0.732286



HEARO.cons NZ_ABYK0100021.1/61949-61536

Shrinking nucs & bonds using
nucShrinkWithCircleNuc and pairBondScaleWithOneSeq
because circle_nuc or #=GR ... CLEAVAGE was used
To disable this warning message:
#=GF R2R SetDrawingParam nucShrinkWithCircleNuc 1 drawingParams.pairBondScaleWithCircleNuc 1
See note1 in manual for more information.

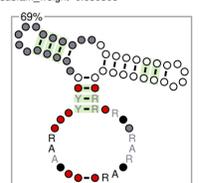


HEARO.cons pknot=1

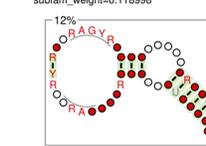


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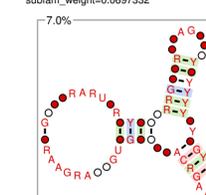
GOLLD-3vnottruncated.cons



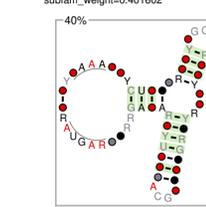
GOLLD-3vp1.cons



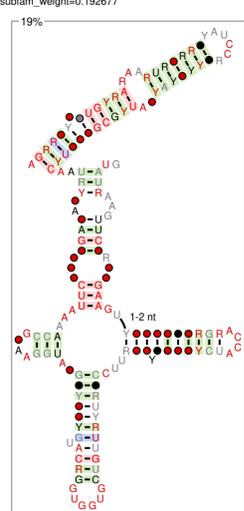
GOLLD-3vp12.cons



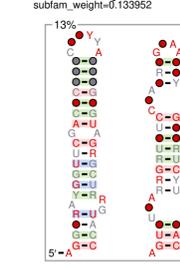
GOLLD-3vp23.cons



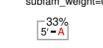
GOLLD-d3classic.cons



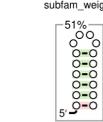
GOLLD-d3justone.cons



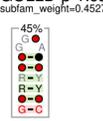
GOLLD-d3valid.cons



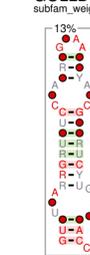
GOLLD-p-1-surround.cons



GOLLD-p-1.cons



GOLLD-p-2.cons



GOLLD-pknot1.cons



GOLLD-pknot2.cons



GOLLD-pknot3.cons



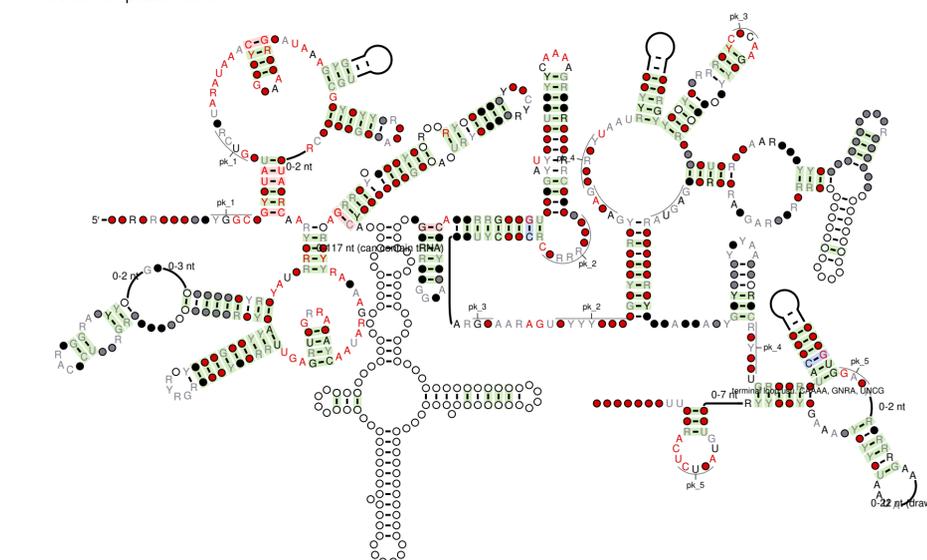
GOLLD-pknot4.cons



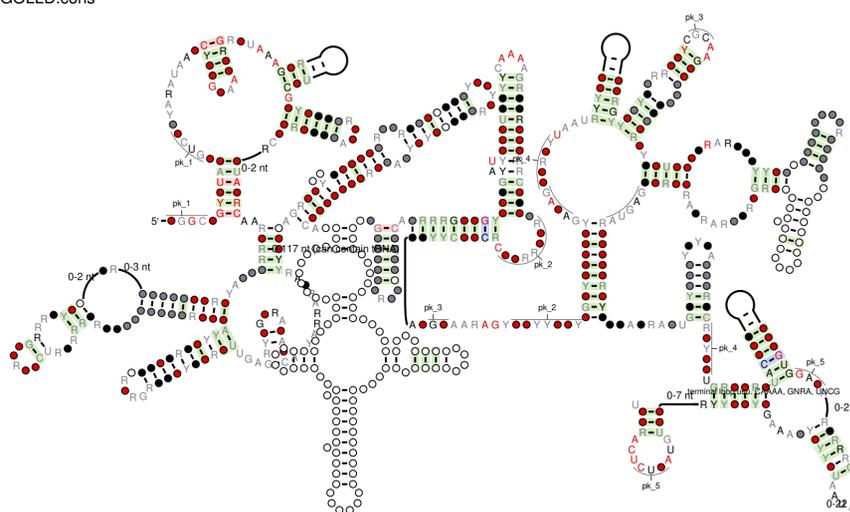
GOLLD-pknot5.cons



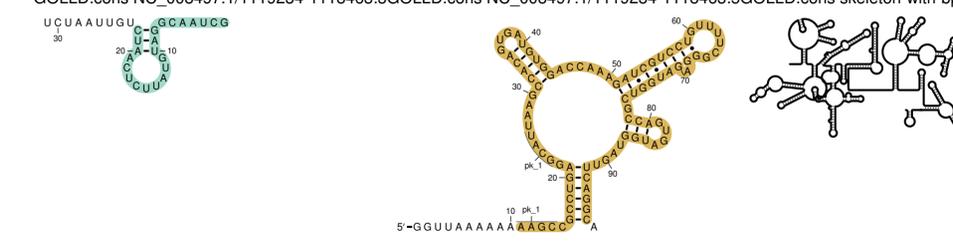
GOLLD-skipbadd2.cons



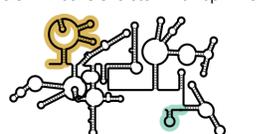
GOLLD.cons



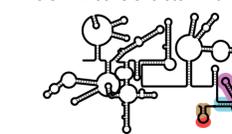
GOLLD.cons NC_008497.1/1119234-1118463:3GOLLD.cons NC_008497.1/1119234-1118463:5GOLLD.cons skeleton-with-bp



GOLLD.cons skeleton-with-bp RACE-skeleton=1



GOLLD.cons skeleton-with-bp align-skeleton=1



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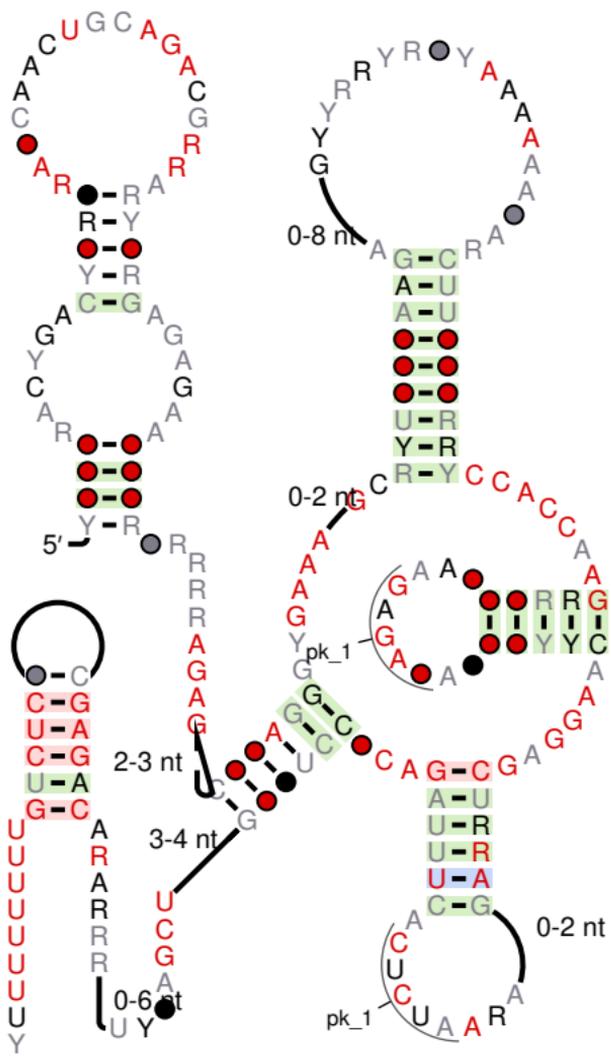
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation can result from an incorrect alignment of sequences, or from alignments of sequences that do not function as structured RNAs. Unfortunately, there is no accepted method to assign confidence that entirely eliminates the need to analyze the full alignment."

To disable this warning, run r2r with
 --disable-usage-warning

IMES-1-pknot.cons
 subfam_weight=1

- G-C
- A-U
- G-C
- A-U
- A

IMES-1.cons

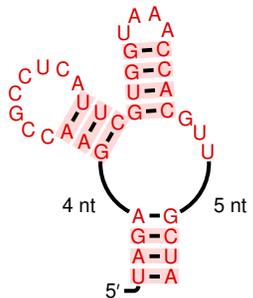


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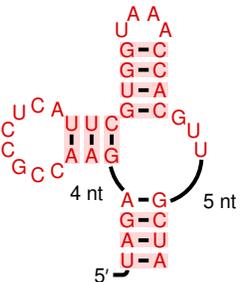
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation can result from an incorrect alignment of sequences, or from alignments of sequences that do not function as structured RNAs. Unfortunately, there is no accepted method to assign confidence that entirely eliminates the need to analyze the full alignment."

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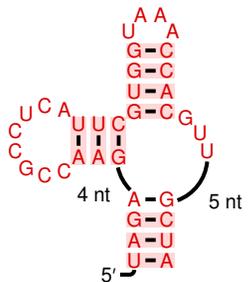
demo-multistem-HEARO2.cons



demo-multistem-HEARO2.cons solver=1

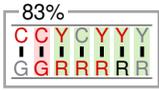


demo-multistem-HEARO2.cons solver=2

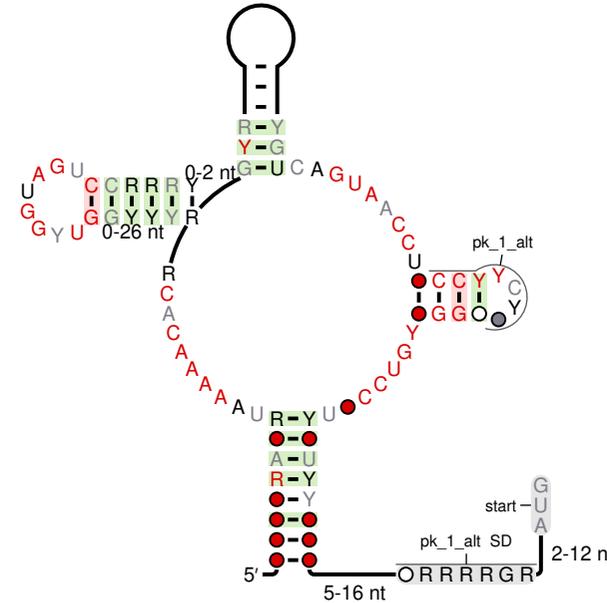


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yjdF-AUG.cons
subfam_weight=0.832593



yjdF.cons

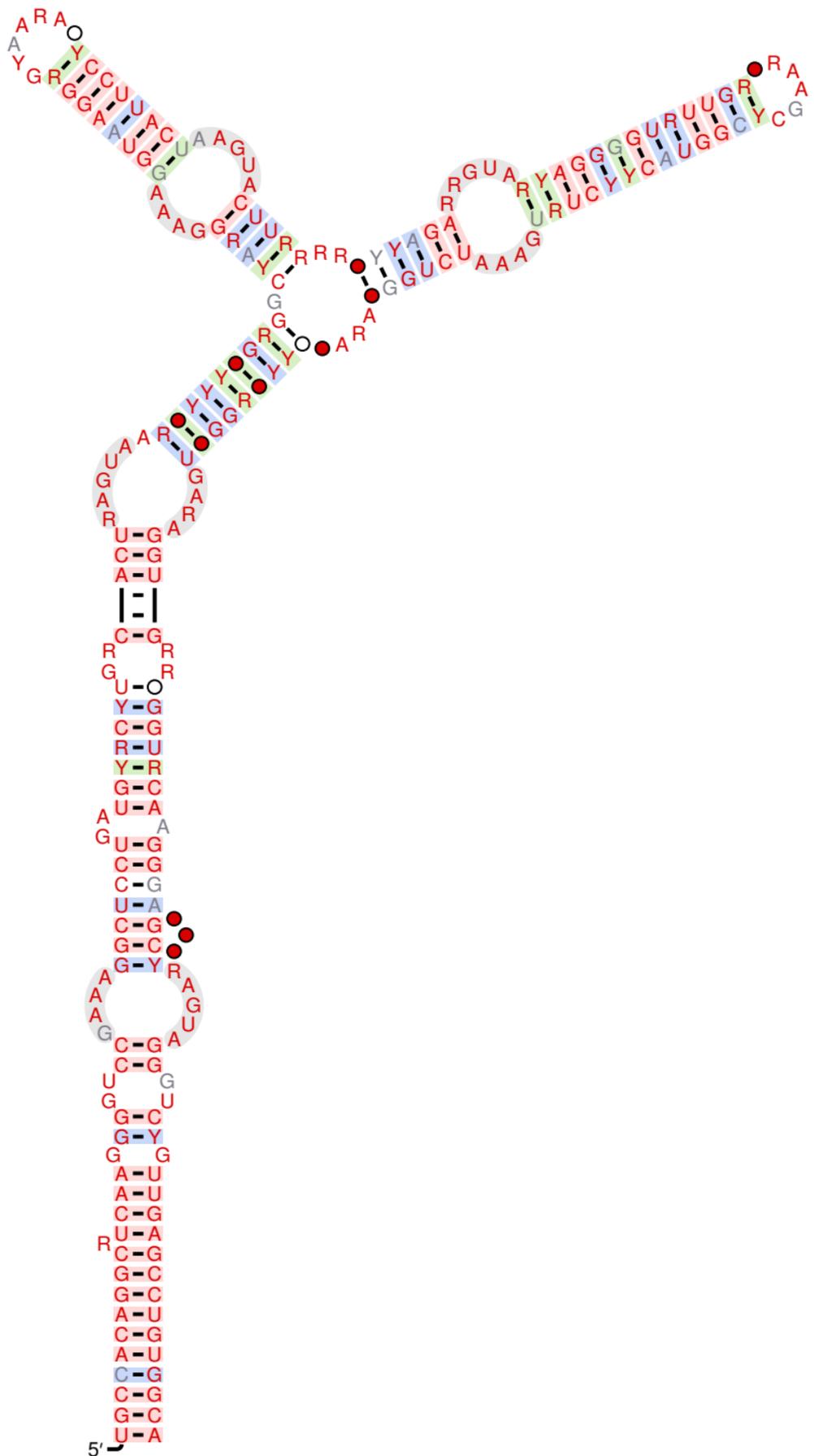


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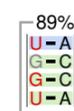
To disable this warning, run r2r with
--disable-usage-warning

Dictyoglomi-1.cons



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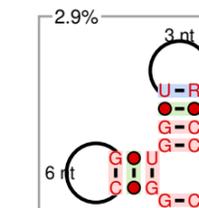
manA-pknot1.cons
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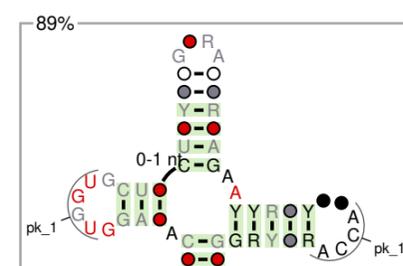
manA-pknot2.cons
 subfam_weight=1



manA-var1.cons
 subfam_weight=0.028518



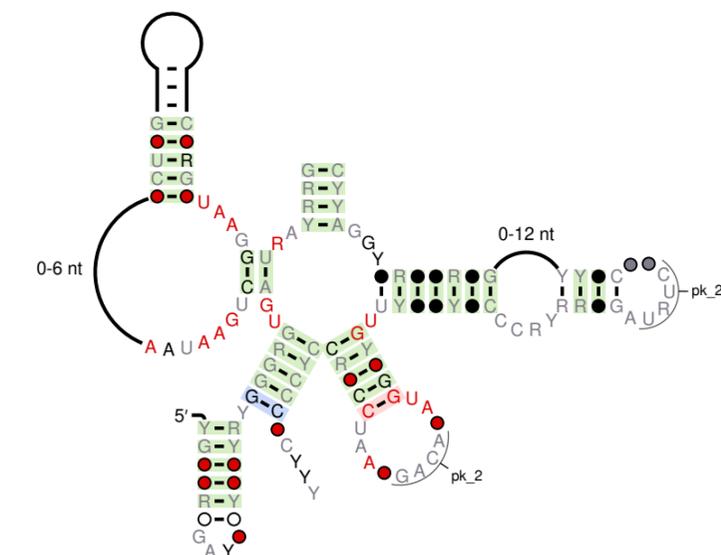
manA-var2.cons
 subfam_weight=0.891987



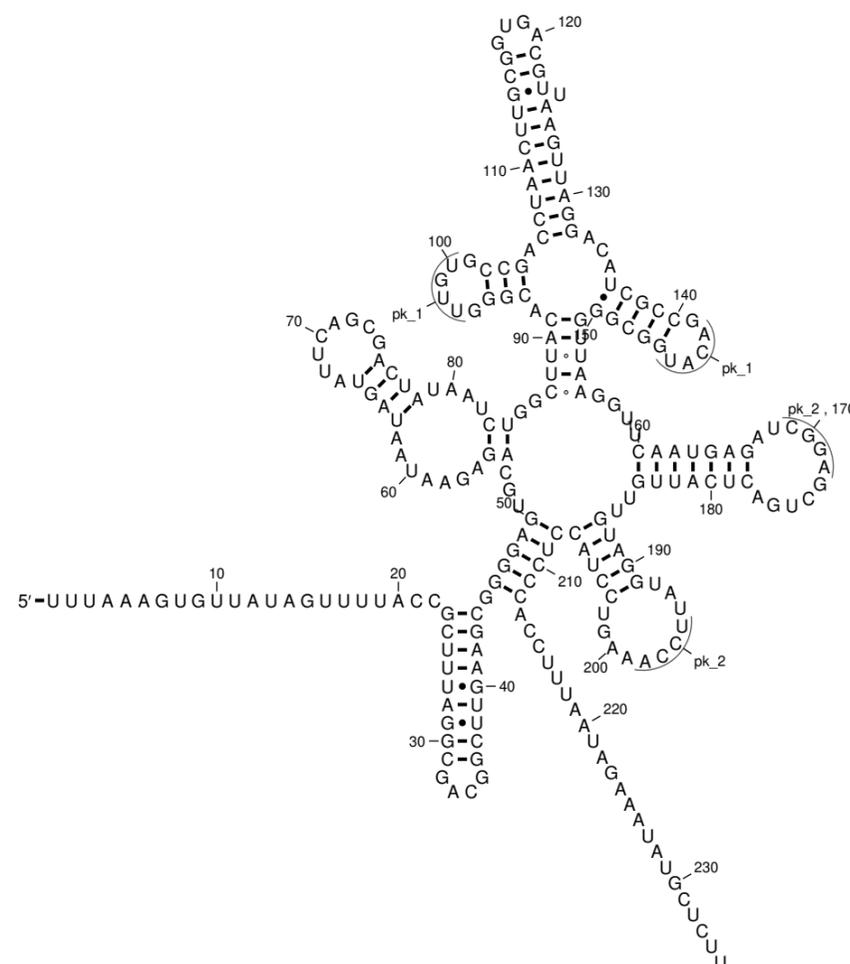
manA-var3.cons
 subfam_weight=0.0794949



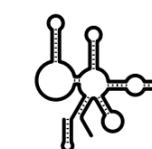
manA.cons



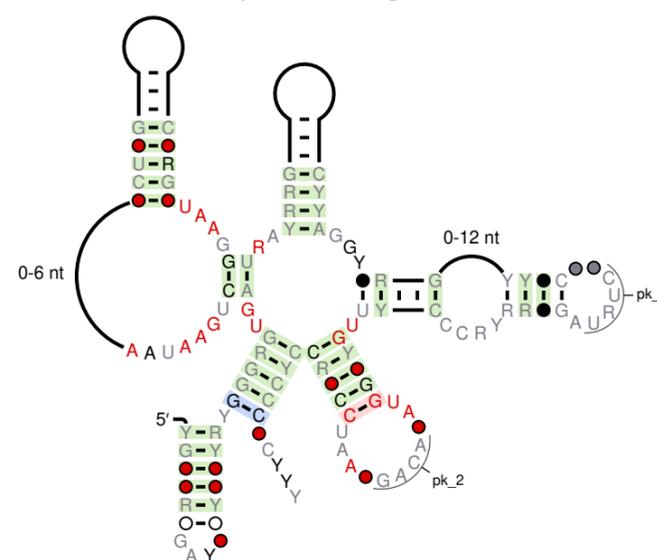
manA.cons NZ_AAOJ01000001.1/468755-469351



manA.cons skeleton varhairpin=1 var-right-stem=1 manA.cons skeleton-with-bp varhairpin=1 var-right-stem=1



manA.cons varhairpin=1 var-right-stem=1

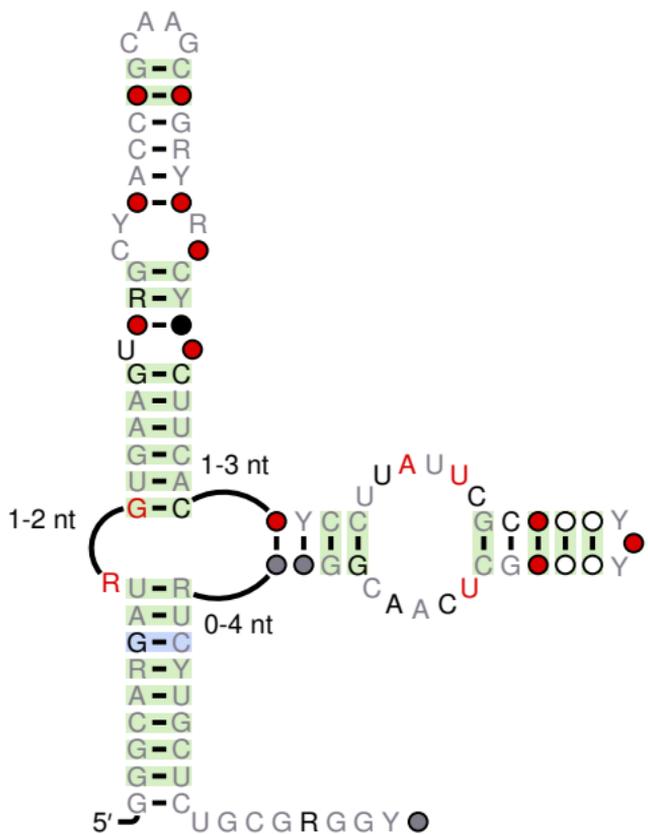


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To disable this warning, run r2r with
 --disable-usage-warning

traJ-II.cons



WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg and Breaker, 2011 wrote:

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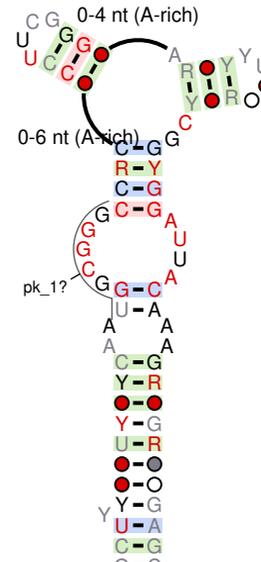
To disable this warning, run r2r with --disable-usage-warning

Bacteroidales-1-pknot.cons

subfam_weight=1



Bacteroidales-1.cons



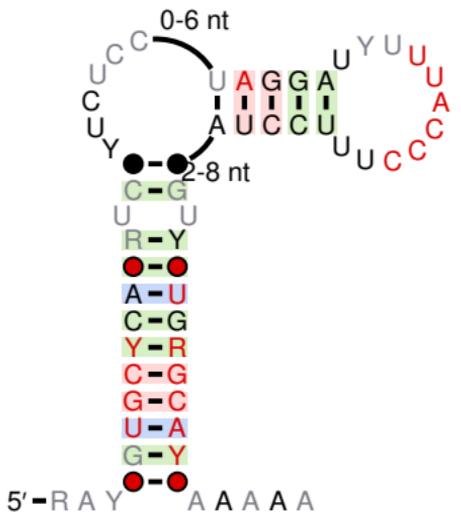
5'-AGCCGYAYY●RYURGAUYGGARACUCAUCA—CGGAGAOAA—●CUCAAAUUCYUGUY●Y●CGGAGUUU●RYCRYAUC●●YRGUGCGGCU

11-17 nt

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To disable this warning, run r2r with `--disable-usage-warning`

potC.cons

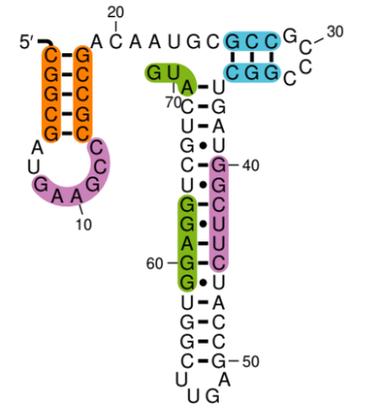


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg and Breaker, 2011 wrote:

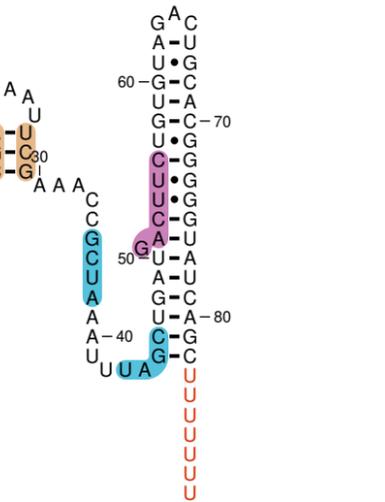
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation can result from an incorrect alignment of sequences, or from alignments of sequences that do not function as structured RNAs. Unfortunately, there is no accepted method to assign confidence that entirely eliminates the need to analyze the full alignment."

To disable this warning, run r2r with --disable-usage-warning

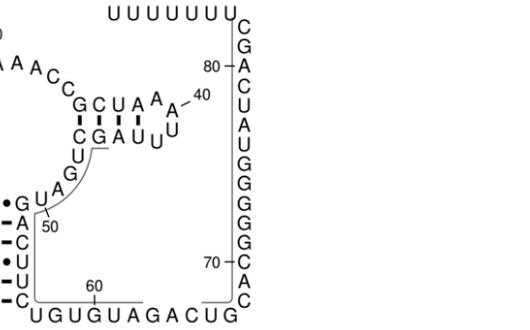
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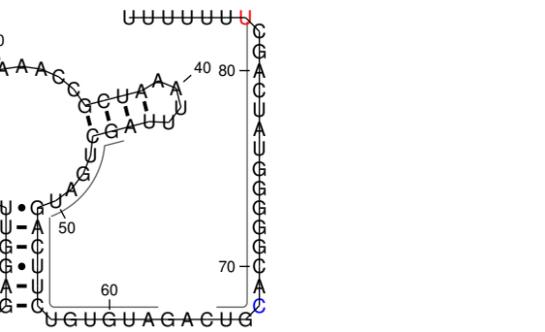
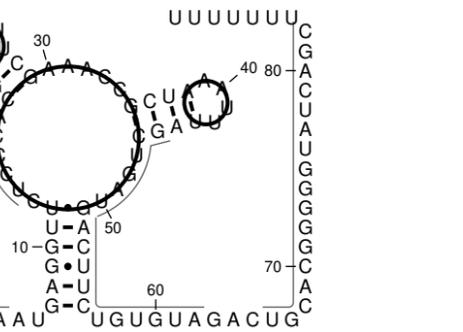
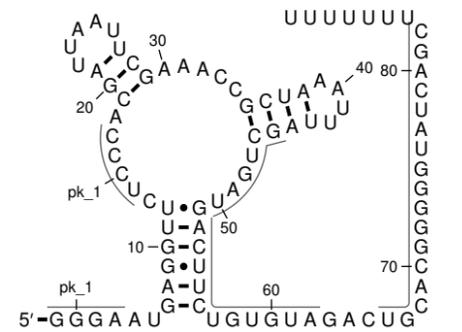
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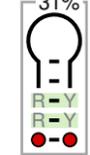


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crcB-P2.cons

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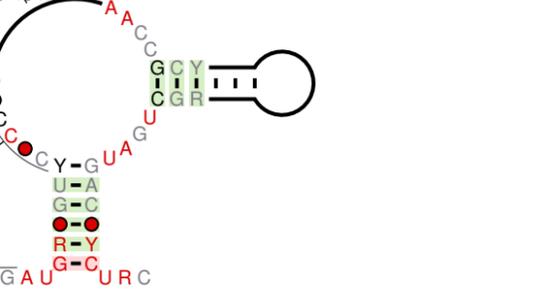
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subfam_weight=1

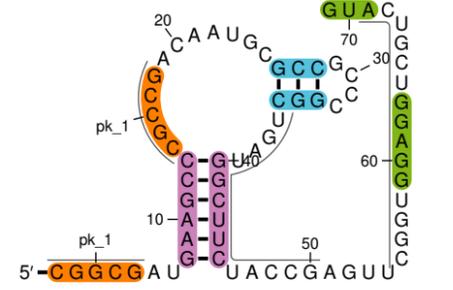


crcB.cons

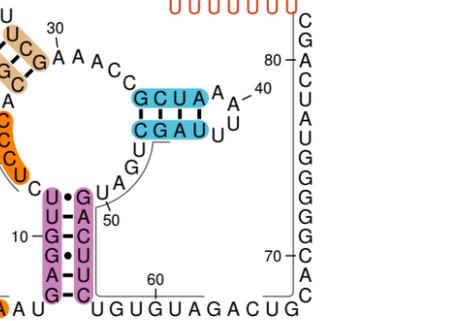
present when backbone range more than 12 nt



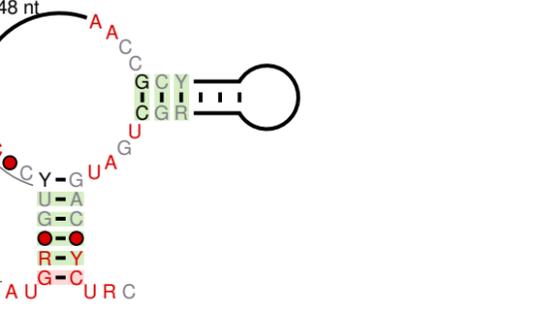
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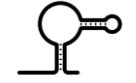
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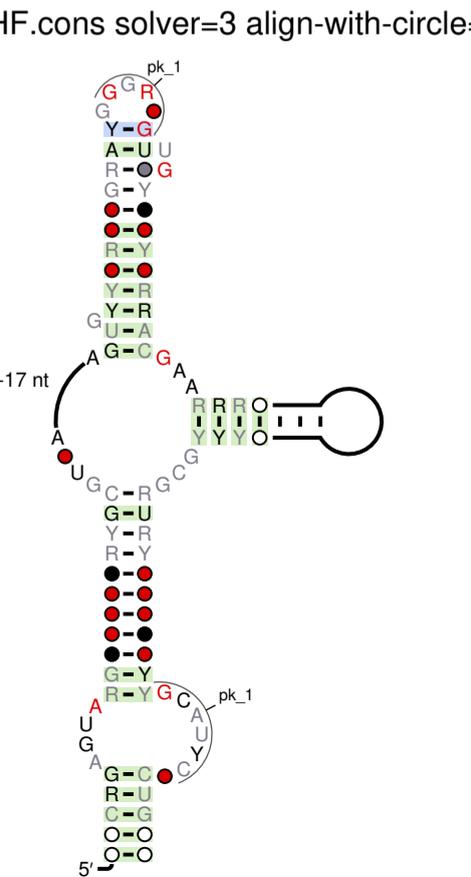
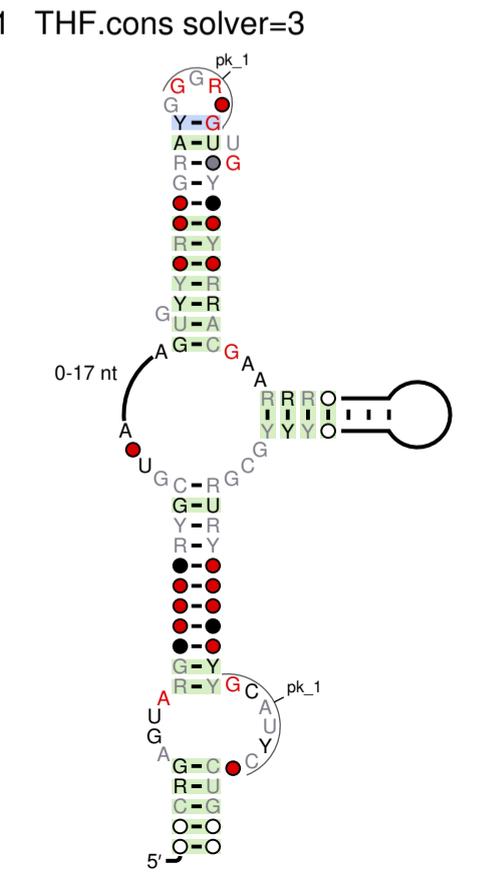
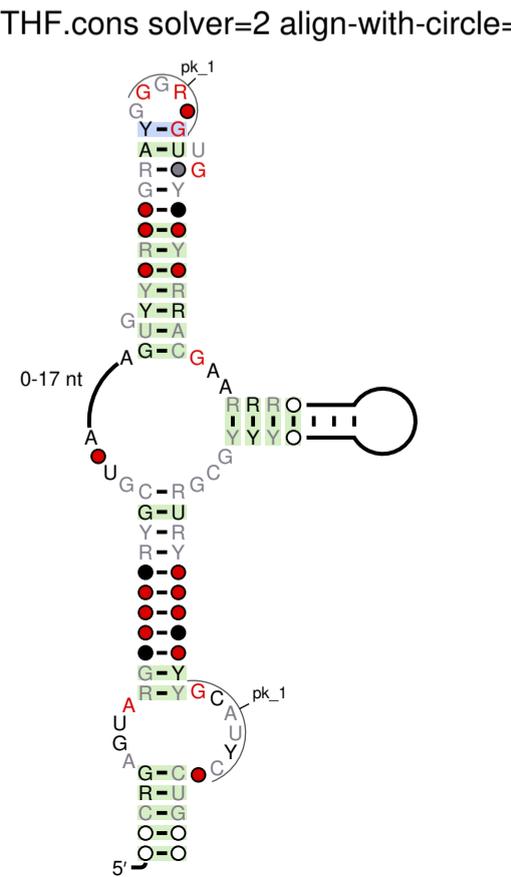
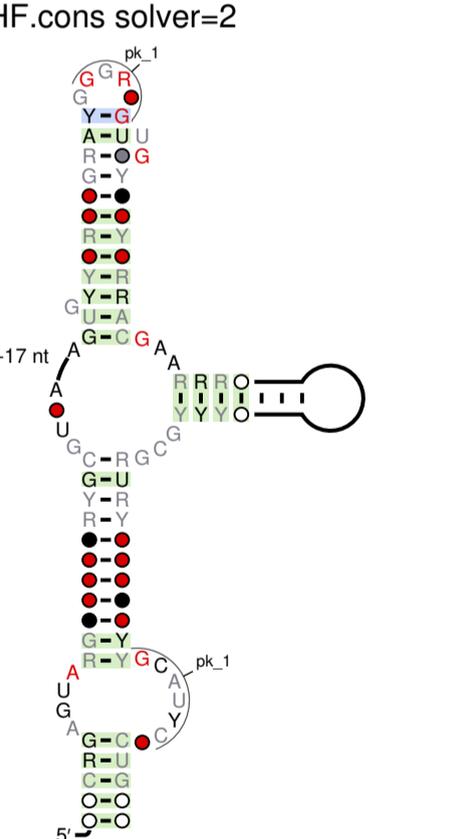
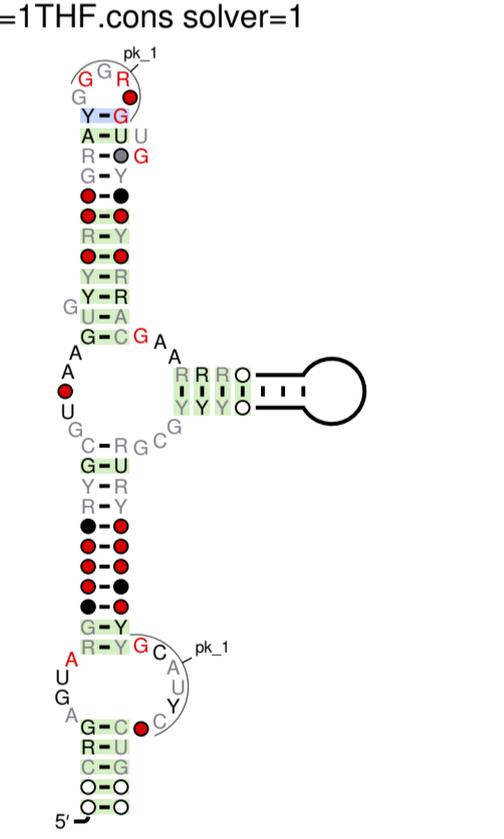
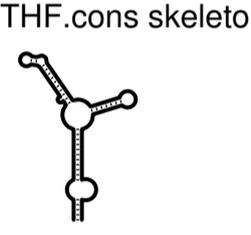
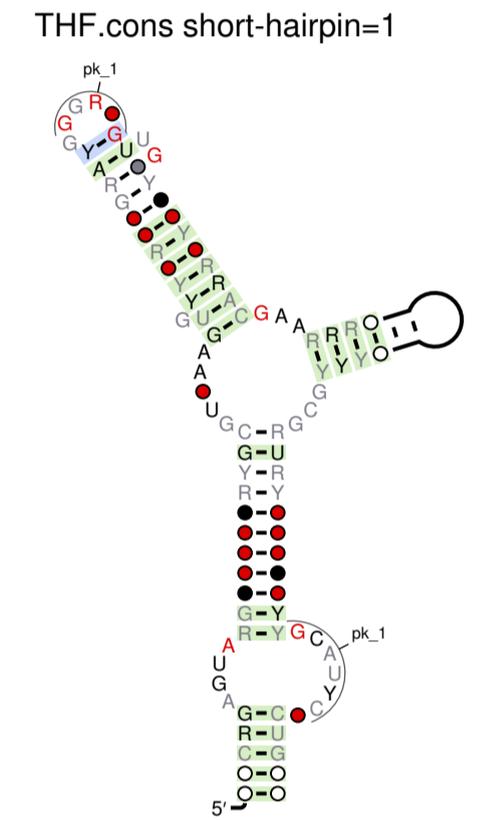
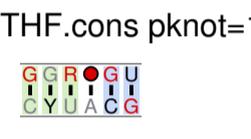
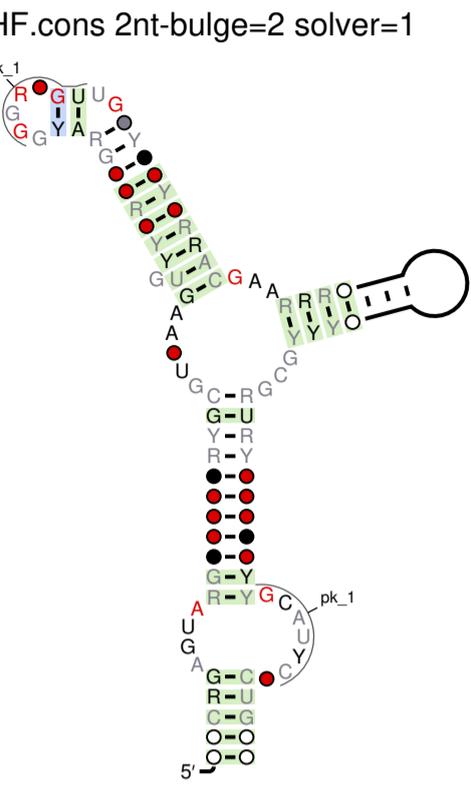
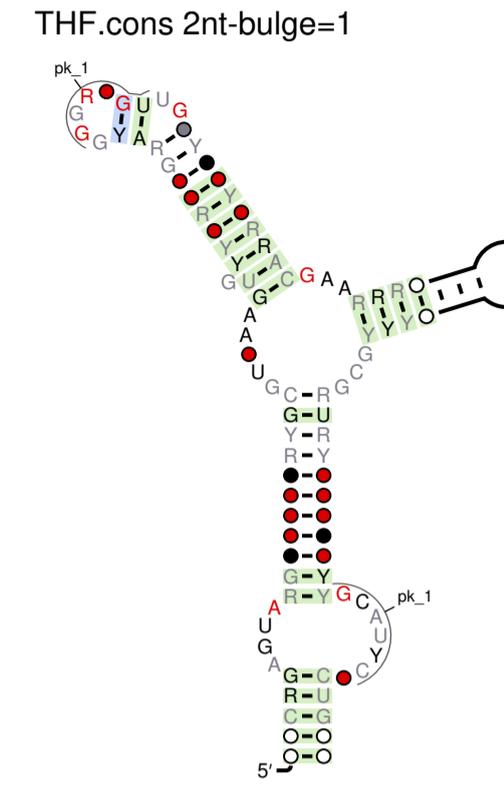
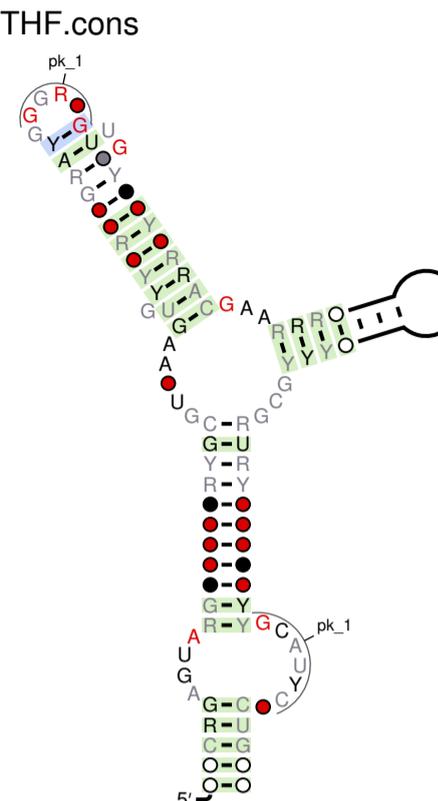
crcB.cons R2R-paper=1



crcB.cons skeleton-with-bp

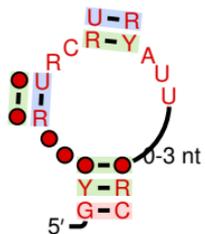


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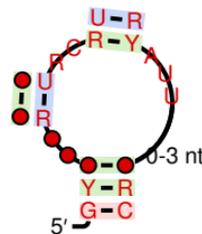


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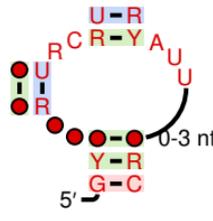
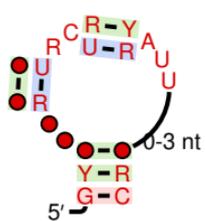
demo-multistem.cons



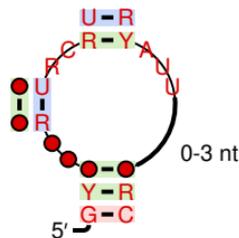
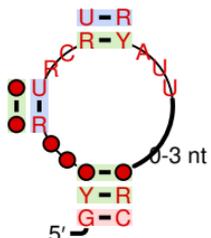
demo-multistem.cons circle=1



demo-multistem.cons flipstem=1 demo-multistem.cons manual=1



demo-multistem.cons solver1=1 demo-multistem.cons solver2=1

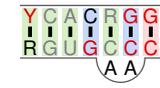


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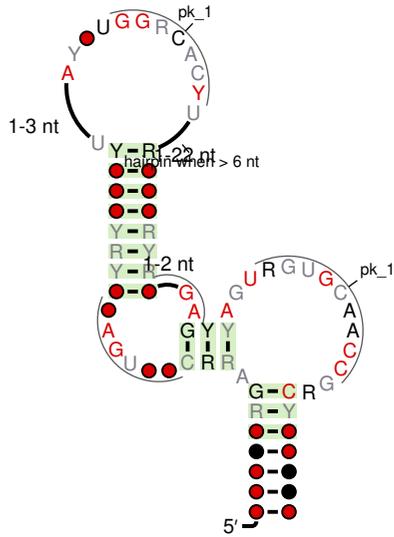
To disable this warning, run r2r with --disable-usage-warning

c-di-GMP-II-pknot.cons

subfam_weight=1



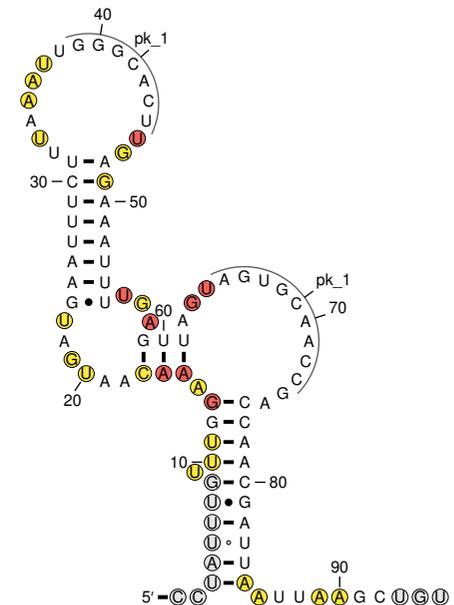
c-di-GMP-II.cons



c-di-GMP-II.cons NC_003030.1/648383-648856

Shrinking nucs & bonds using nucShrinkWithCircleNuc and pairBondScaleWithOneSeq because circle_nuc or #=GR ... CLEAVAGE was used To disable this warning message:

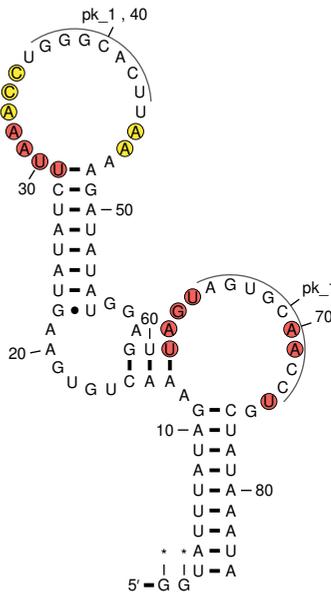
#=GF R2R SetDrawingParam nucShrinkWithCircleNuc 1 drawingParams.pairBondScaleWithCircleNuc 1 drawingParams.pairBondScaleWithCircleNuc 1 See note1 in manual for more information.



c-di-GMP-II.cons NC_009089.1/3801245-3800770

Shrinking nucs & bonds using nucShrinkWithCircleNuc and pairBondScaleWithOneSeq because circle_nuc or #=GR ... CLEAVAGE was used To disable this warning message:

1#=GF R2R SetDrawingParam nucShrinkWithCircleNuc 1 drawingParams.pairBondScaleWithCircleNuc 1 drawingParams.pairBondScaleWithCircleNuc 1 See note1 in manual for more information.



c-di-GMP-II.cons skeleton-with-bp



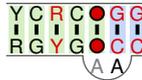
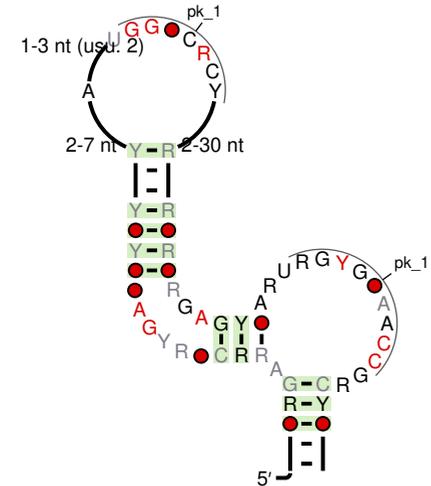
WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg and Breaker, 2011 wrote:

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To disable this warning, run r2r with --disable-usage-warning

c-di-GMP-II-update.cons

c-di-GMP-II-update.cons pknot=1



c-di-GMP-II-update.cons skeleton-with-bp



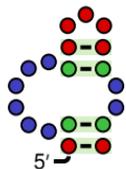
WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg and Breaker, 2011 wrote:

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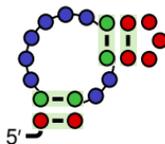
Unfortunately, there is no accepted method to assign confidence that entirely eliminates the need to analyze the full alignment."

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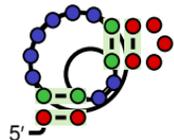
solver-formulation1-1.cons



solver-formulation1-1.cons solver=1



solver-formulation1-1.cons solver=2

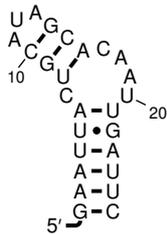


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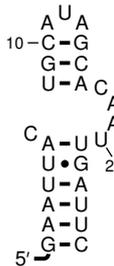
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation can result from an incorrect alignment of sequences, or from alignments of sequences that do not function as structured RNAs. Unfortunately, there is no accepted method to assign confidence that entirely eliminates the need to analyze the full alignment."

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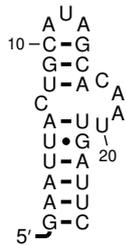
uneven-internal-loop seq layout=anyangle



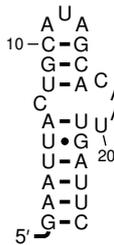
uneven-internal-loop seq layout=broken-left



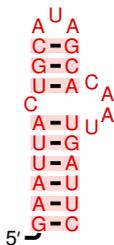
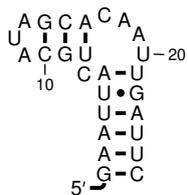
uneven-internal-loop seq layout=default



uneven-internal-loop seq layout=left-turn



uneven-internal-loop seq layout=left-turn-multistemuneven-internal-loop.cons

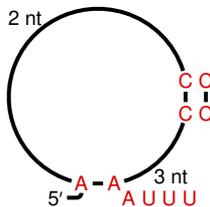


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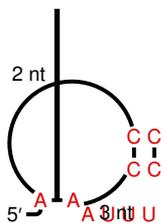
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation can result from an incorrect alignment of sequences, or from alignments of sequences that do not function as structured RNAs. Unfortunately, there is no accepted method to assign confidence that entirely eliminates the need to analyze the full alignment."

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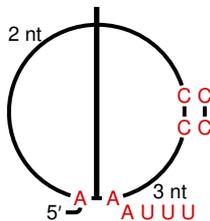
TestAngularAlignment.cons



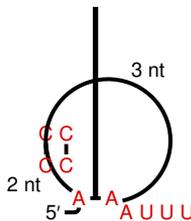
TestAngularAlignment.cons alignangle=-32



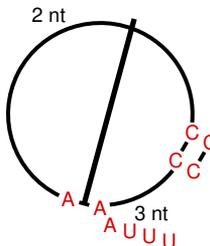
TestAngularAlignment.cons alignangle=-45



TestAngularAlignment.cons alignangle=45



TestAngularAlignment.cons rots0=-15

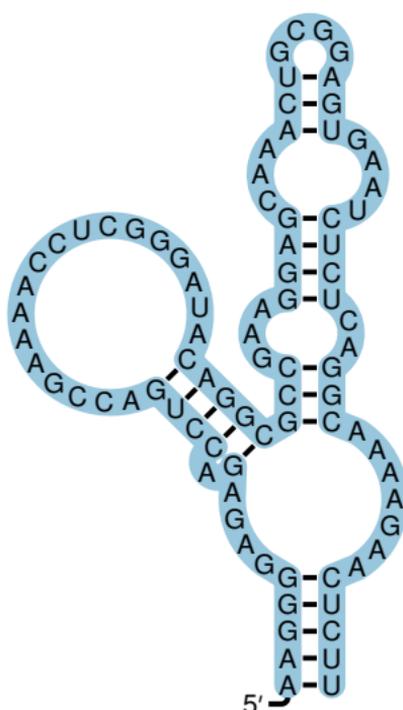


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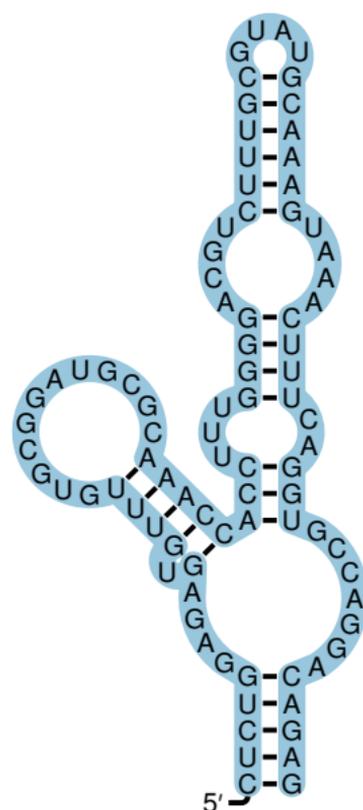
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation can result from an incorrect alignment of sequences, or from alignments of sequences that do not function as structured RNAs. Unfortunately, there is no accepted method to assign confidence that entirely eliminates the need to analyze the full alignment."

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--disable-usage-warning

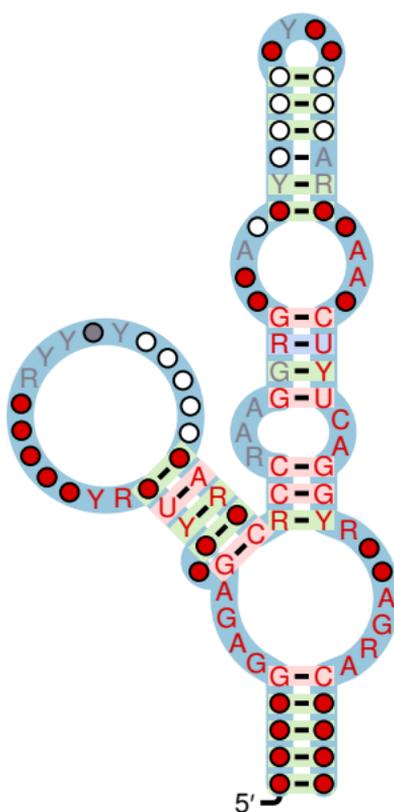
two-glycine Bsu-1



two-glycine Bsu-2



two-glycine.cons



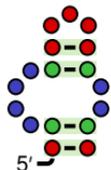
WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg and Breaker, 2011 wrote:

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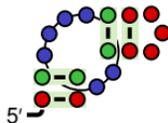
Unfortunately, there is no accepted method to assign confidence that entirely eliminates the need to analyze the full alignment."

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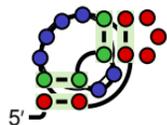
solver-formulation2-1.cons



solver-formulation2-1.cons solver=1



solver-formulation2-1.cons solver=2

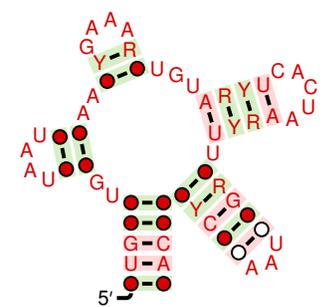


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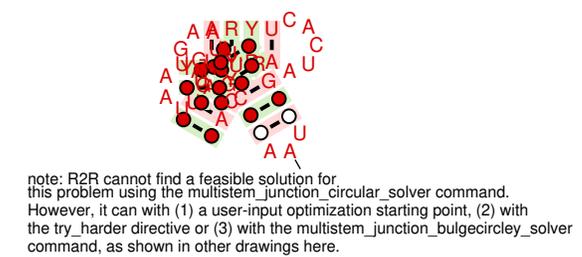
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation can result from an incorrect alignment of sequences, or from alignments of sequences that do not function as structured RNAs. Unfortunately, there is no accepted method to assign confidence that entirely eliminates the need to analyze the full alignment."

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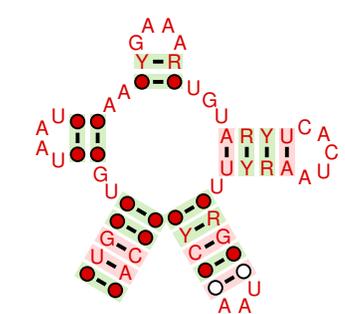
demo-multistem-manA.cons



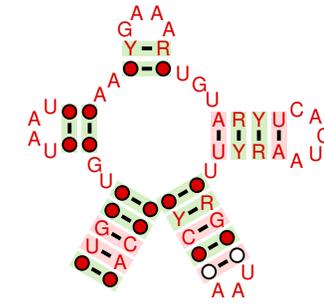
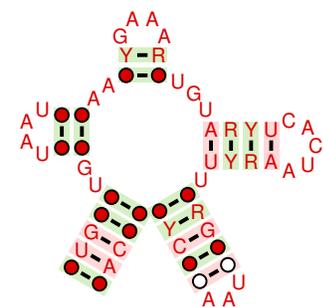
demo-multistem-manA.cons solver=1



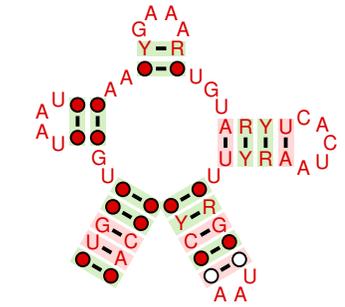
demo-multistem-manA.cons solver=1 explicitinitial



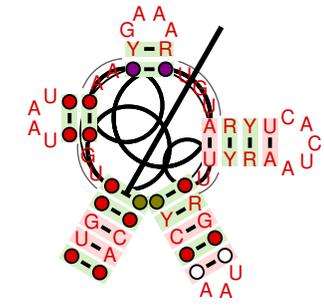
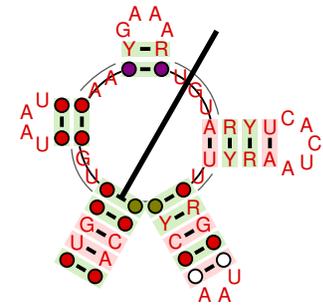
demo-multistem-manA.cons solver=1 tryharder demo-multistem-manA.cons solver=2



demo-multistem-manA.cons solver=3



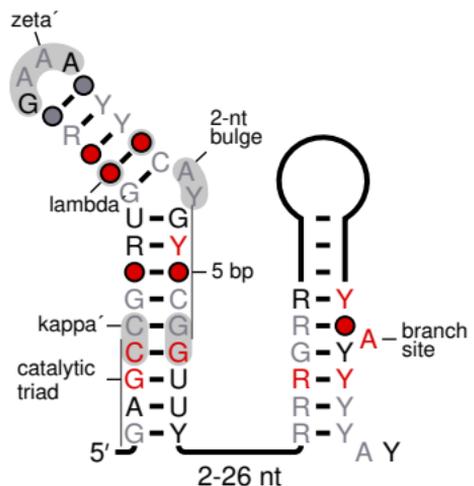
demo-multistem-manA.cons solver=3 annot=1 demo-multistem-manA.cons solver=3 annot=1 fewiters=1



WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg and Breaker, 2011 wrote: "This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation can result from an incorrect alignment of sequences, or from alignments of sequences that do not function as structured RNAs. Unfortunately, there is no accepted method to assign confidence that entirely eliminates the need to analyze the full alignment."

To disable this warning, run r2r with
 --disable-usage-warning

group-II-DV-DVI.cons

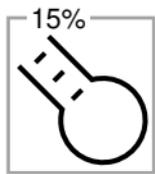


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg and Breaker, 2011 wrote:

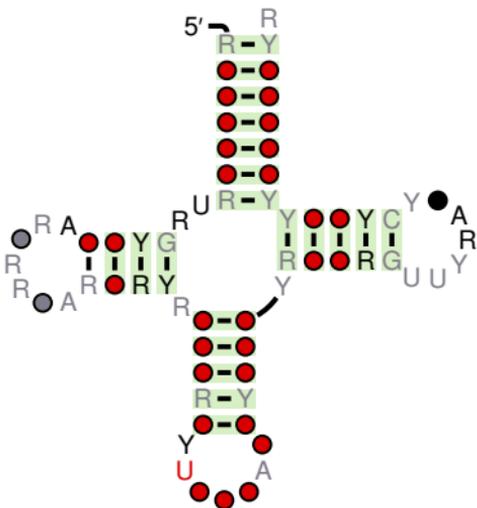
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation can result from an incorrect alignment of sequences, or from alignments of sequences that do not function as structured RNAs. Unfortunately, there is no accepted method to assign confidence that entirely eliminates the need to analyze the full alignment."

To disable this warning, run r2r with
 --disable-usage-warning

tRNA-var.cons
 subfam_weight=0.154412



tRNA.cons



tRNA.cons skeleton-with-bp



WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg and Breaker, 2011 wrote:

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To disable this warning, run r2r with
 --disable-usage-warning

U1.cons

