

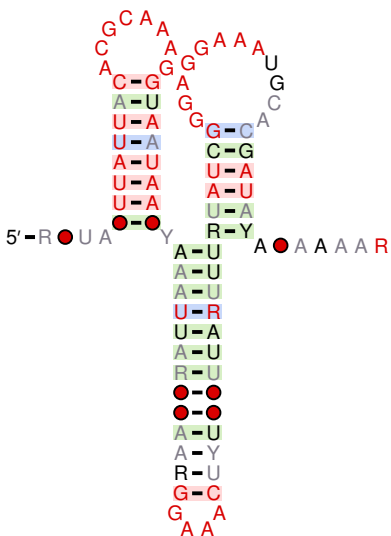


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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

IMES-4.cons



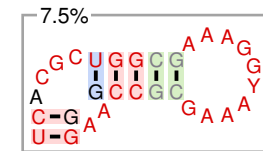
To disable this warning, run `r2r` with `--disable-usage-warning`

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

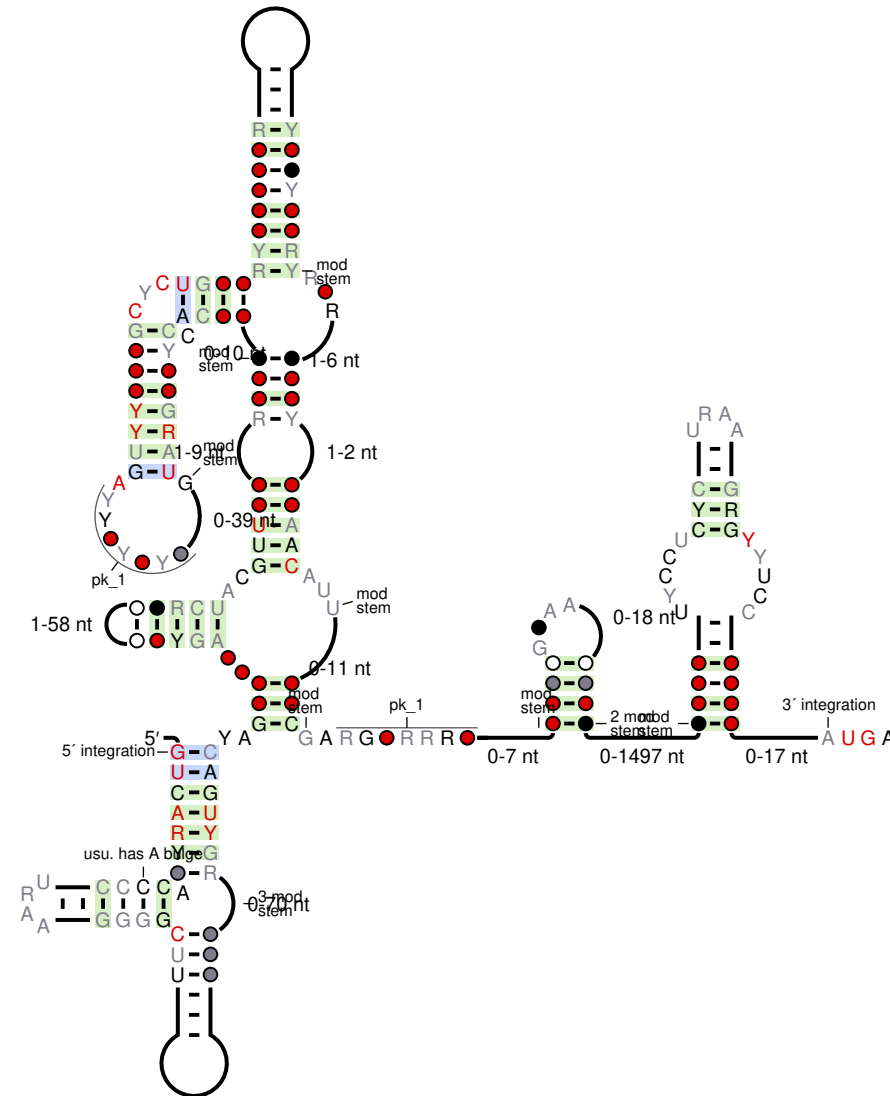
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To disable this warning, run r2r with --disable-usage-warning

HEARO-RYGCAA.cons

subfam_weight=0.0745961

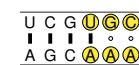


HEARO.cons

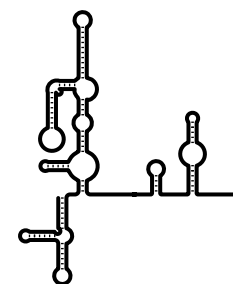


HEARO.cons NZ_ABYK01000021.1/61949-61536 pknot=1

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.

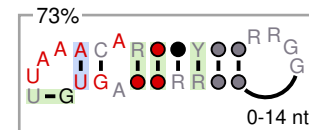


HEARO.cons skeleton-with-bp



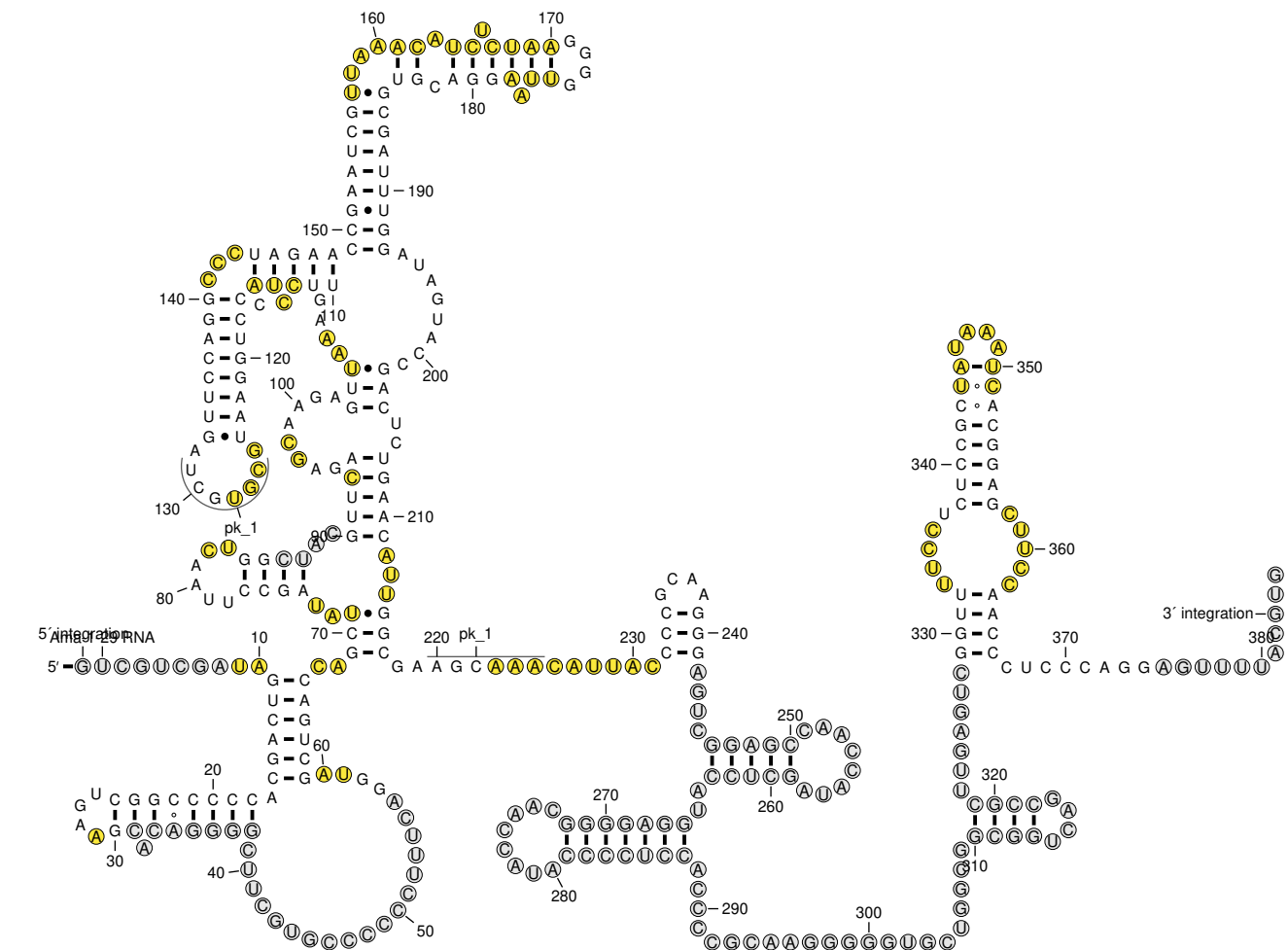
HEARO-UAA.cons

subfam_weight=0.732286



HEARO.cons NZ_ABYK01000021.1/61949-61536

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

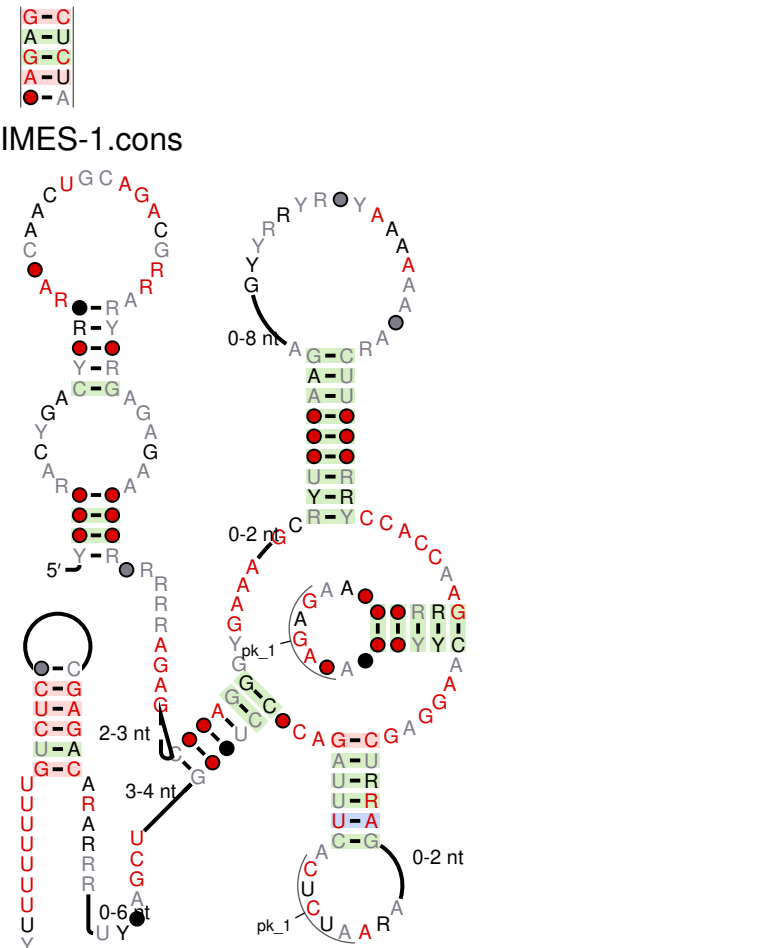


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To disable this warning, run r2r with
 --disable-usage-warning

IMES-1-pknot.cons
 subfam_weight=1

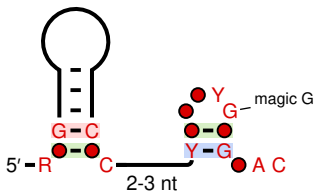


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To disable this warning, run r2r with
--disable-usage-warning

demo1-ii.cons

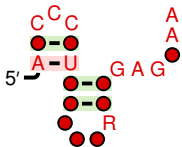


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To disable this warning, run r2r with
--disable-usage-warning

demo-pe.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:

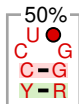
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation 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

demo-modular-GNRA.cons demo-modular-OPT.cons

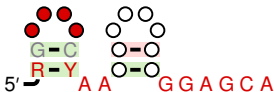
subfam_weight=0.230158

subfam_weight=0.5



demo-modular-UNCG.cons demo-modular.cons

subfam_weight=0.269842

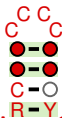


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To disable this warning, run r2r with
--disable-usage-warning

demo-breakpair-fix4.cons

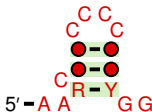


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To disable this warning, run r2r with
--disable-usage-warning

demo-breakpair-fix1.cons

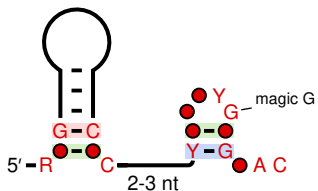


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

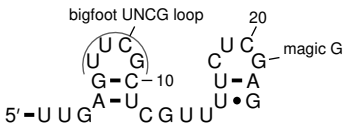
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation 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

demo1-iii.cons



demo1-iii.cons bigfoot



demo1-iii.cons skeleton-with-bp



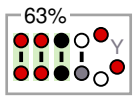
WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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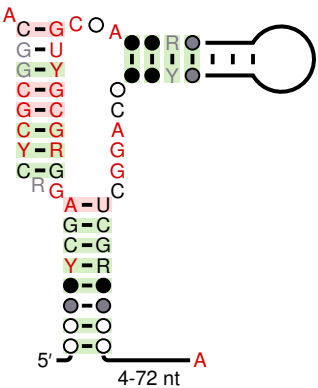
To disable this warning, run r2r with

--disable-usage-warning

SAH-P2.cons
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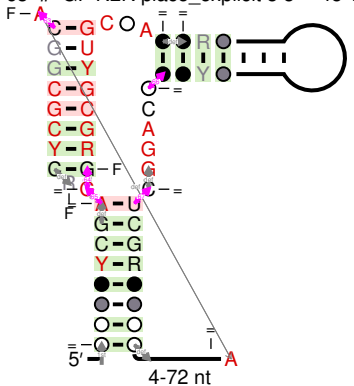


SAH.cons



SAH.cons showPlace=1

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65 #=GF R2R place_explicit 1 1-- -45 1 0 0 0 0
64 #=GF R2R place_explicit 4 4-- 0 1 0 0 0 0 f
66 #=GF R2R place_explicit 7 7-- -45 1 0 0 0 -90
67 #=GF R2R place_explicit 9 9-- +45 1 0 0 0 0
63 #=GF R2R place_explicit 8 8-- -45 1 0 0 0 0
```

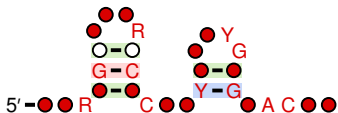


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--disable-usage-warning

demo1.cons



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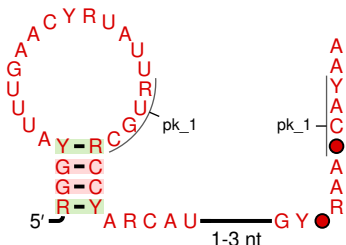
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation 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."

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

demo-pknot-callout-pknot.cons
 subfam_weight=1

R	-	Y
U	-	A
G	-	C
C	-	●

demo-pknot-callout.cons



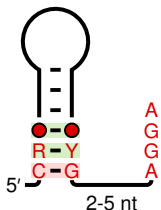
WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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To disable this warning, run r2r with

```
--disable-usage-warning
```

demo-contrived.cons



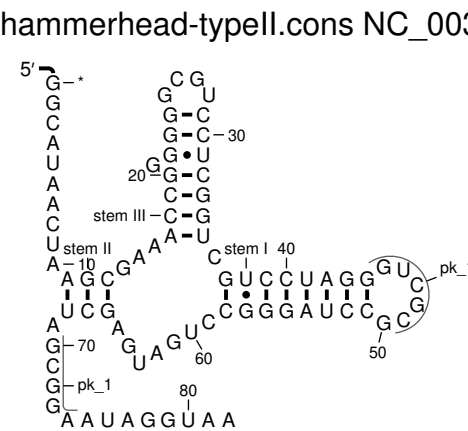
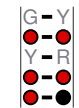
WARNING: R2R is not intended to provide evidence for covariation between RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper,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

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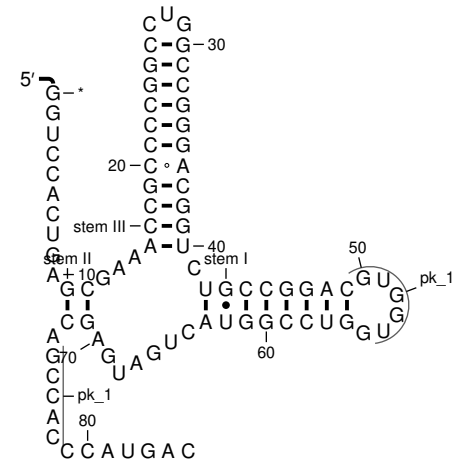
To disable this warning, run r2r with --disable-usage-warning

hammerhead-typell-pknot.cons

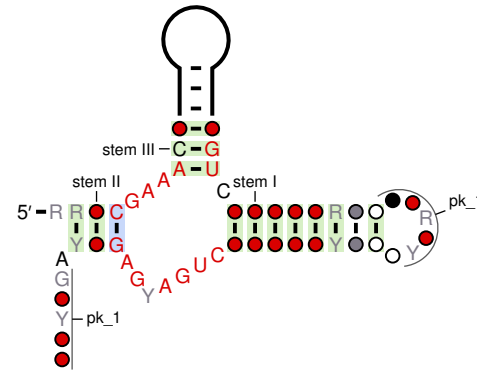
subfam_weight=1



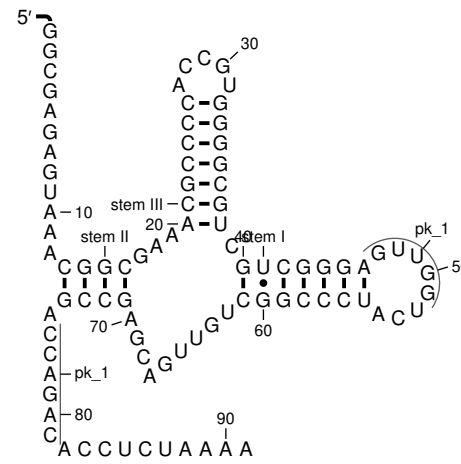
hammerhead-typell.cons NC_009818.1/8209-8688



hammerhead-typell.cons



hammerhead-typell.cons NC_003062.1/1182083-1182558hammerhead-typell.cons NC_003345.1/10184-10663

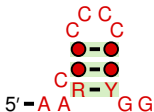


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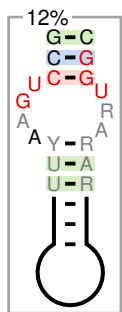
To disable this warning, run r2r with
--disable-usage-warning

demo-breakpair-fix3.cons



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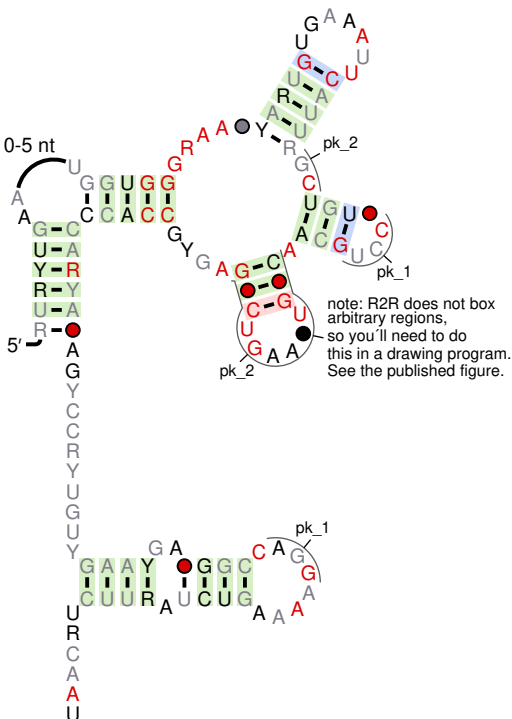
AdoCbl-variant-p7.cons
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AdoCbl-variant-pknot1.cons
 subfam_weight=1



AdoCbl-variant-pknot2.consAdoCbl-variant.cons
 subfam_weight=1

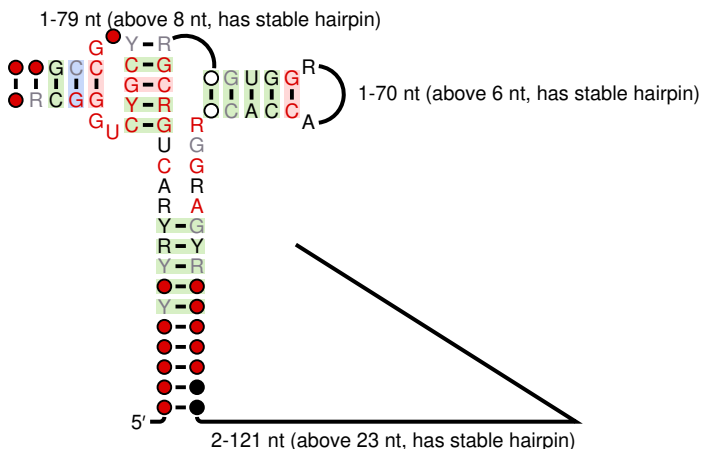


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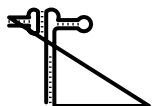
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation 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

pfl.cons



pfl.cons skeleton-with-bp



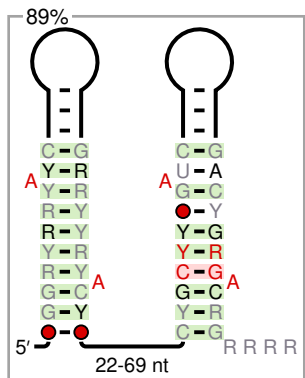
WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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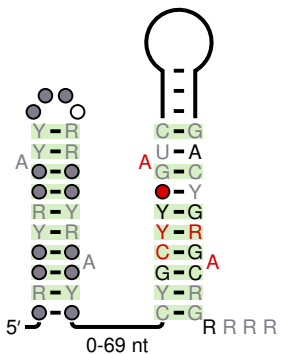
To disable this warning, run r2r with
 --disable-usage-warning

pan-two.cons

subfam_weight=0.893289



pan.cons

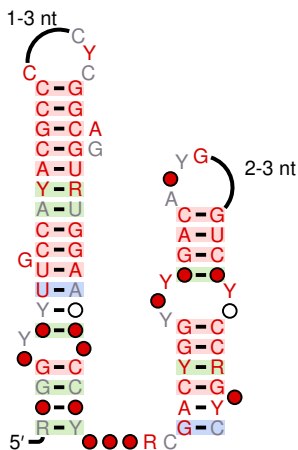


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To disable this warning, run r2r with
--disable-usage-warning

livK.cons

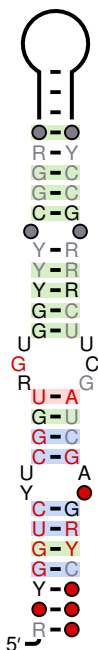


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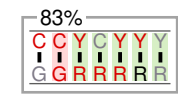
To disable this warning, run r2r with
--disable-usage-warning

Actino-pnp.cons

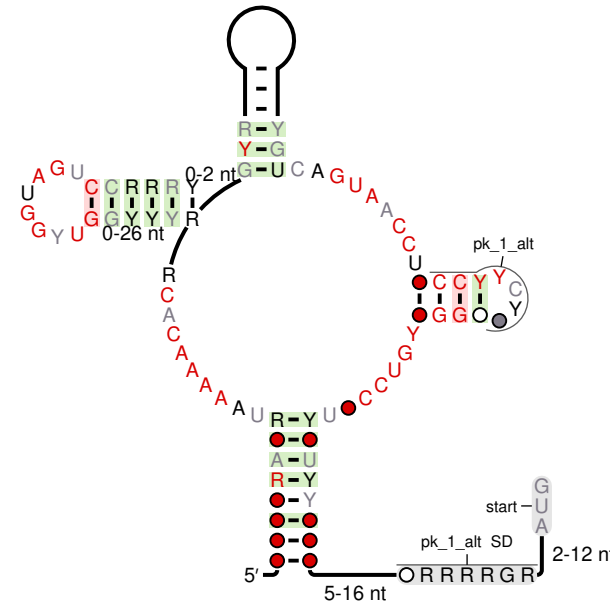


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg and Breaker, 2011 wrote:
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To disable this warning, run r2r with --disable-usage-warning

yjdF-AUG.cons
subfam_weight=0.832593



yjdF.cons

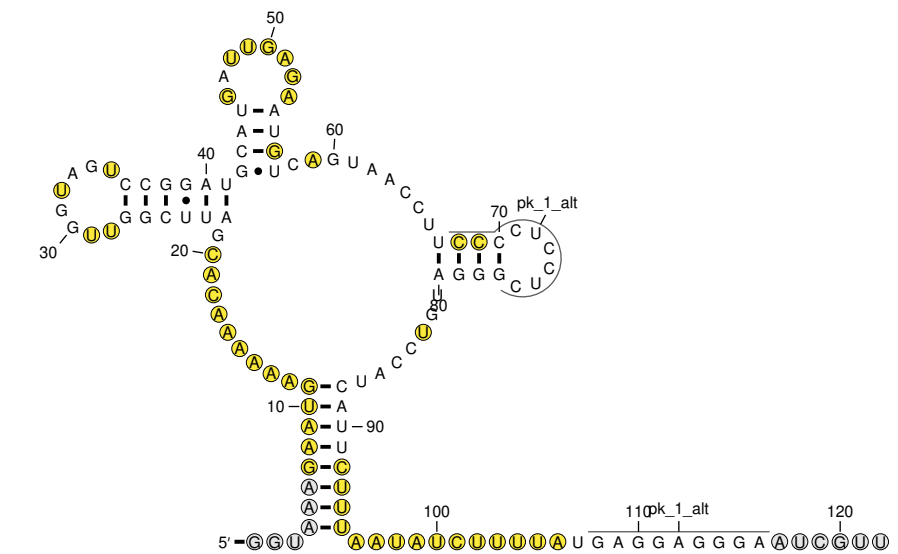


yjdF-altstem.cons
subfam_weight=1



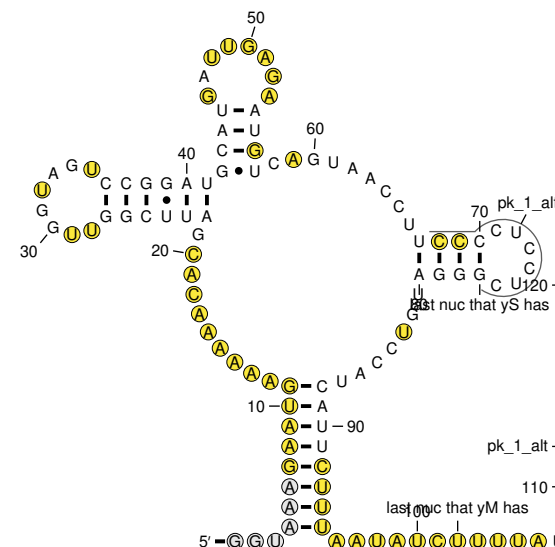
yjdF.cons NC_000964.2/1274965-1275471

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.



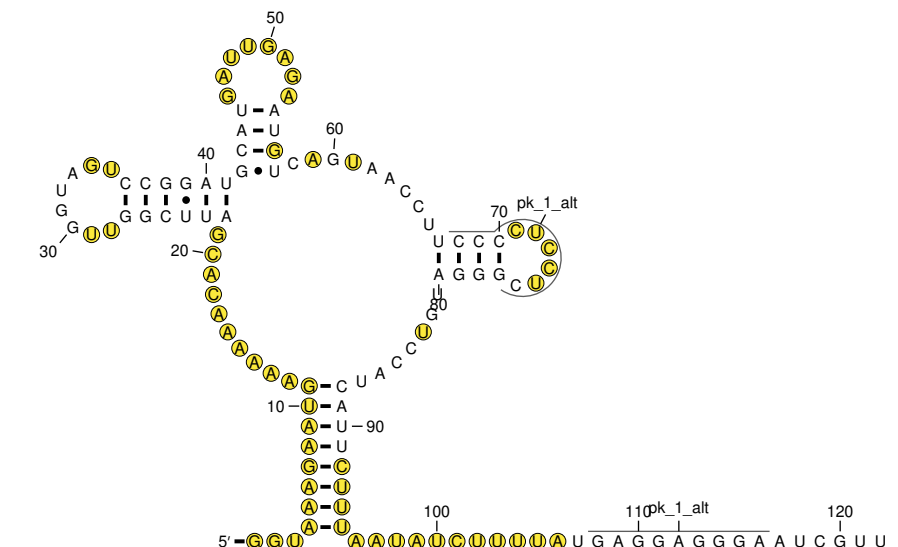
yjdF.cons NC_000964.2/1274965-1275471:L

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.

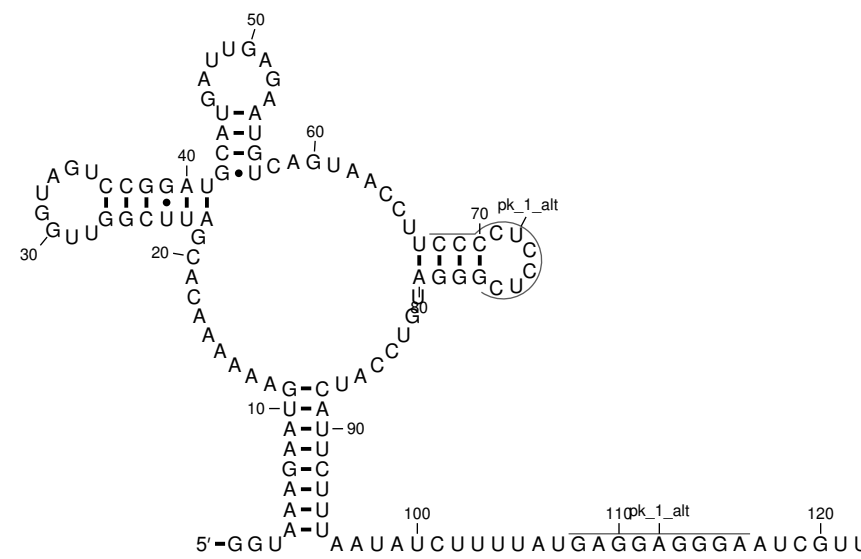


yjdF.cons NC_000964.2/1274965-1275471:M

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.



yjdF.cons NC_000964.2/1274965-1275471:S



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

Chlorobi-RRM.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

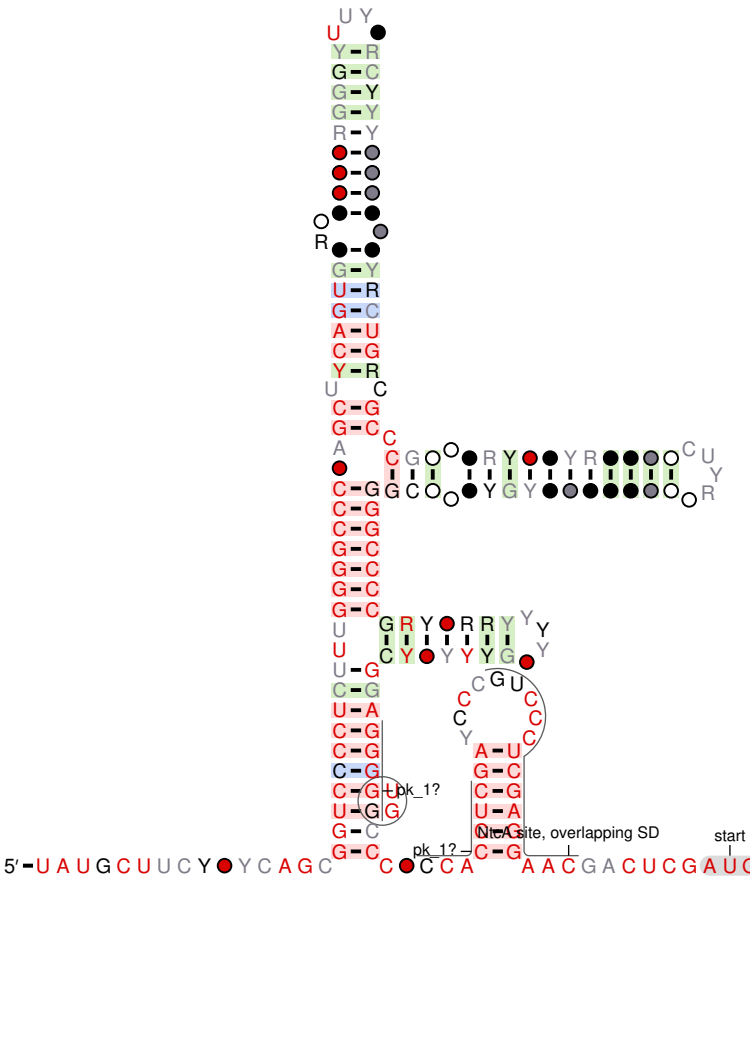
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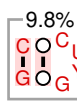
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psaA.cons



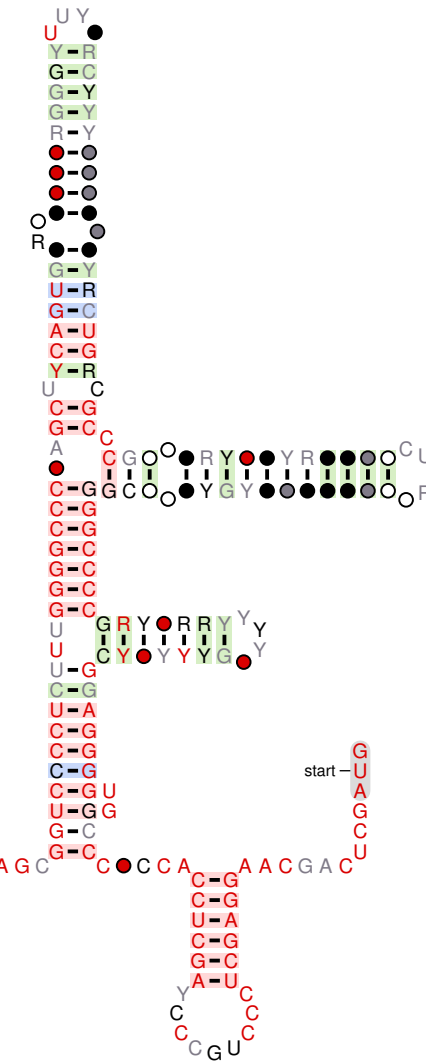
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subfam_weight=0.0980232



psaA-uncg2.cons
subfam_weight=0.163149



psaA.cons R2R-paper=1



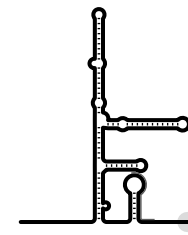
psaA-cyygn2.cons
subfam_weight=0.374591



psaA-uncg3.cons
subfam_weight=0.430613



psaA.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: "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."

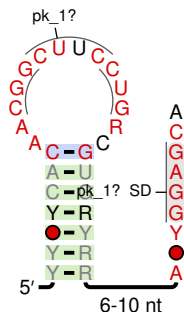
To disable this warning, run r2r with --disable-usage-warning

SAM-SAH-pknot1.cons

subfam_weight=1



SAM-SAH.cons



SAM-SAH.cons NZ_AAYC01000001.1/141950-142398

Shrinking nucs & bonds using
nucShrinkWithCircleNuc and pairBondScaleWithOneSeq

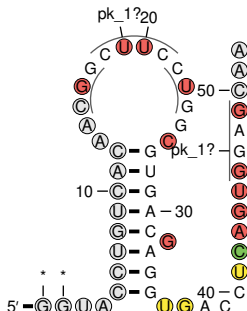
because circle_nuc or #=GR ... CLEAVAGE was used

To disable this warning message:

#=GF R2R SetDrawingParam nucShrinkWithCircleNuc 1 drawingParams.pairBondScaleWithCircleNuc 1

See note1 in manual for more information.

SAM-SAH.cons skeleton-with-bp

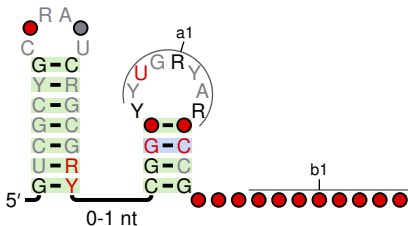


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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

c4-a1b1.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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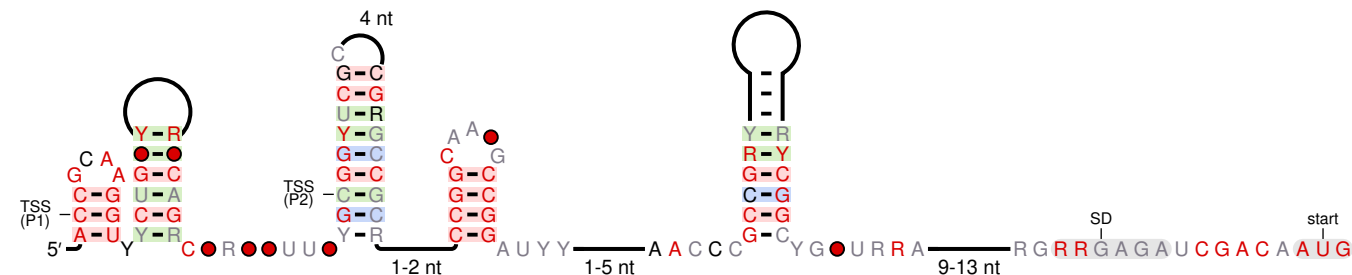
To disable this warning, run r2r with
--disable-usage-warning

Pseudomon-2.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

Pseudomonas groES.cons

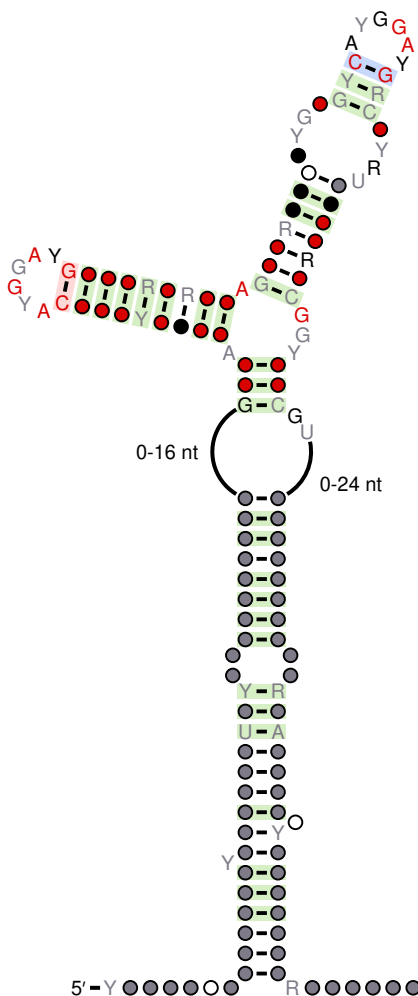


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

TwoAYGGAY.cons

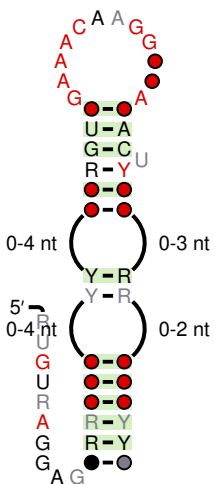


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

Cyano-1.cons

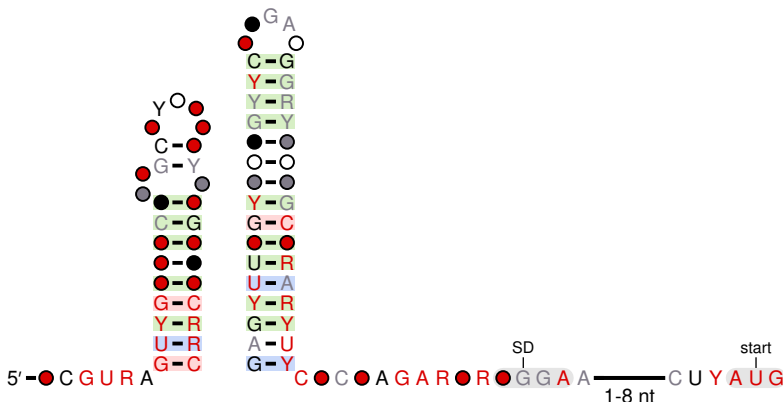


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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

gyrA.cons



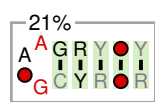
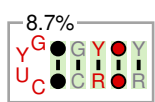
WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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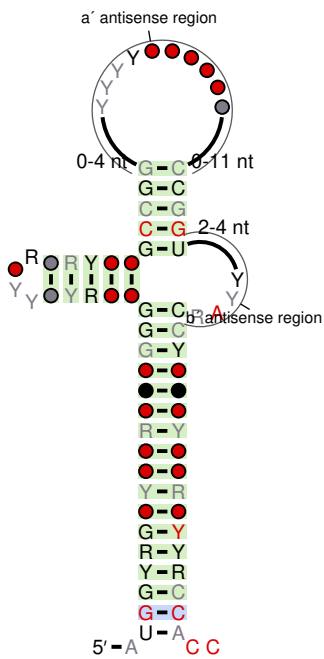
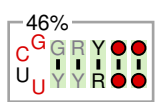
To disable this warning, run r2r with

```
--disable-usage-warning
```

C4-CUNG.cons C4-GNRA.cons
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C4-UNCG.cons C4.cons
 subfam_weight=0.459042

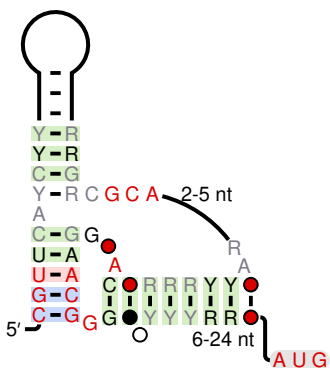


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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

Downstream-peptide.cons



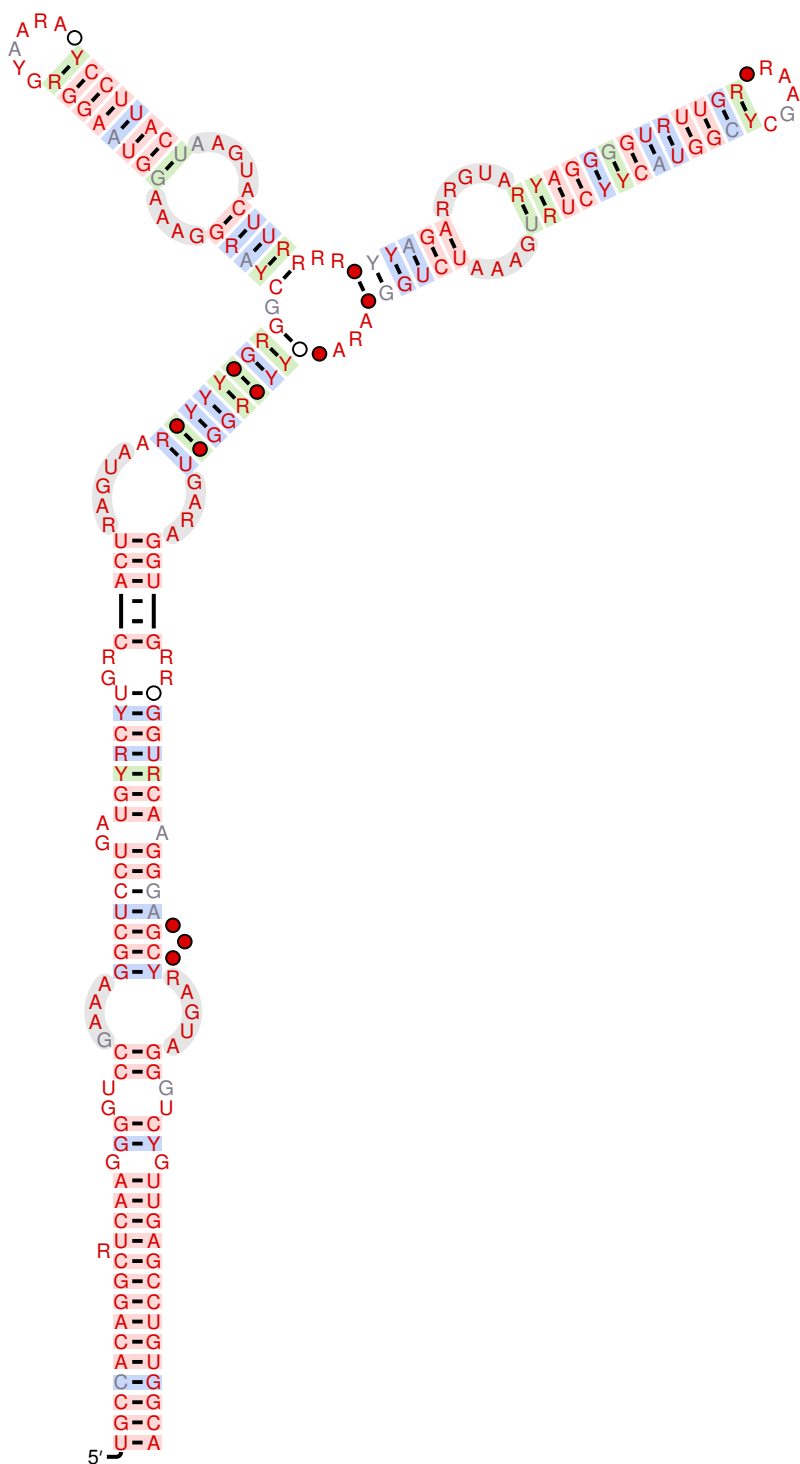
Downstream-peptide.cons skeleton-with-bp



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: "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

Dictyoglomi-1.cons

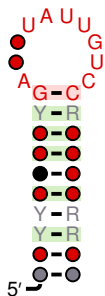


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

Lacto-rpoB.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

icd.cons

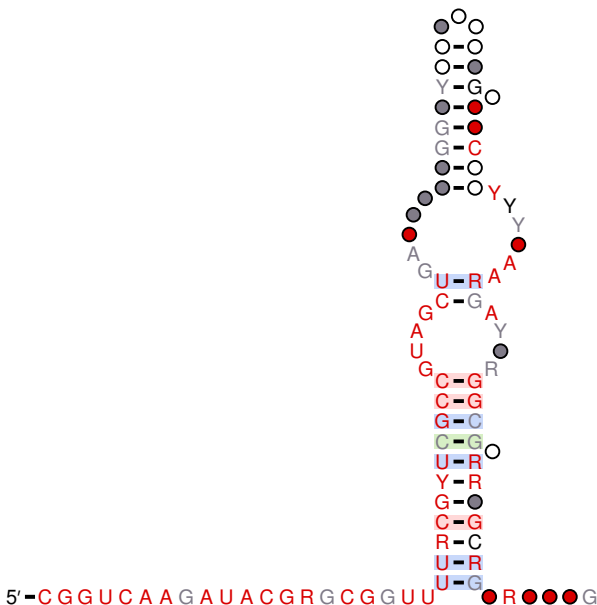


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To disable this warning, run r2r with
 --disable-usage-warning

fixA.cons



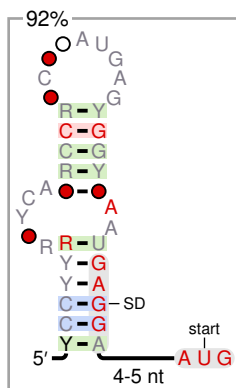
WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

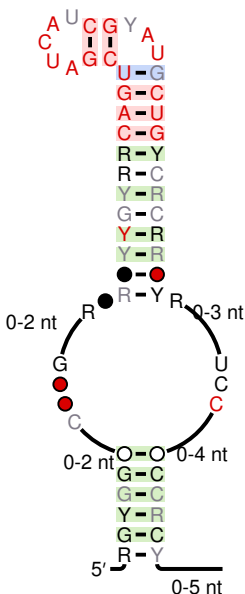
To disable this warning, run r2r with
 --disable-usage-warning

gabT-P2.cons

subfam_weight=0.915134



gabT.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

Int.cons

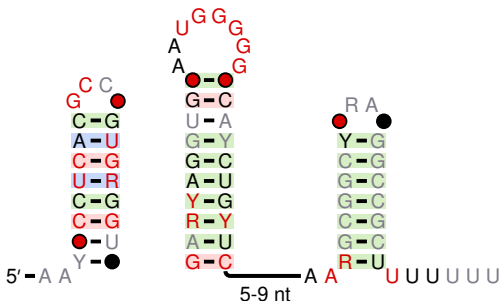


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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

Chlorobi-1.cons

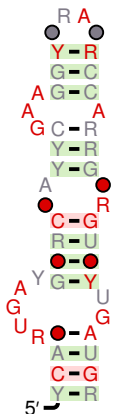


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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

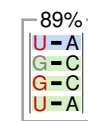
flpD.cons



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

manA-pknot1.cons

subfam_weight=0.891987



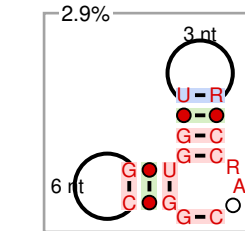
manA-pknot2.cons

subfam_weight=1



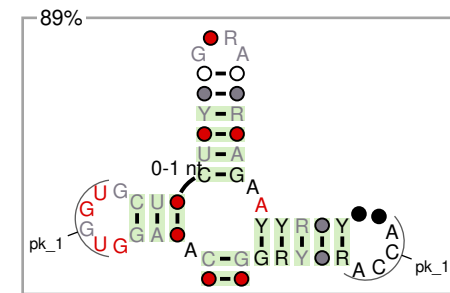
manA-var1.cons

subfam_weight=0.028518



manA-var2.cons

subfam_weight=0.891987

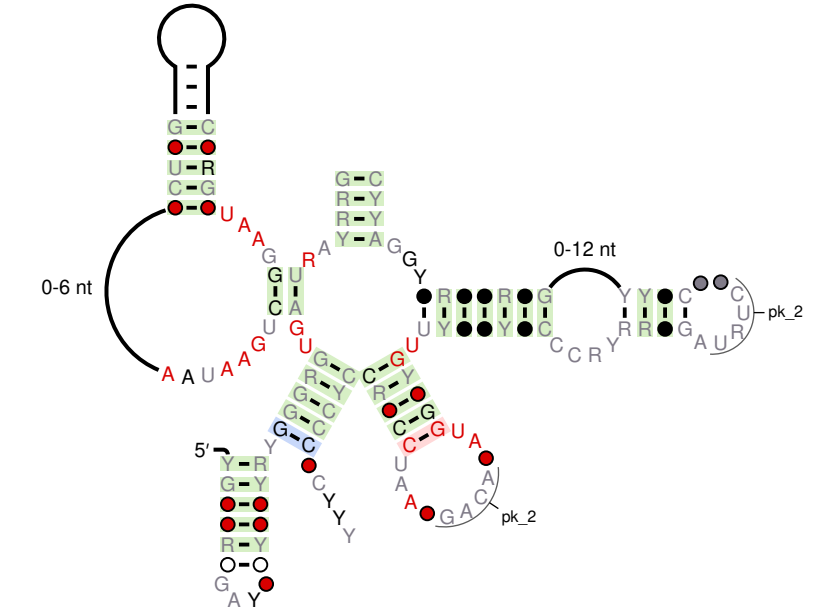


manA-var3.cons

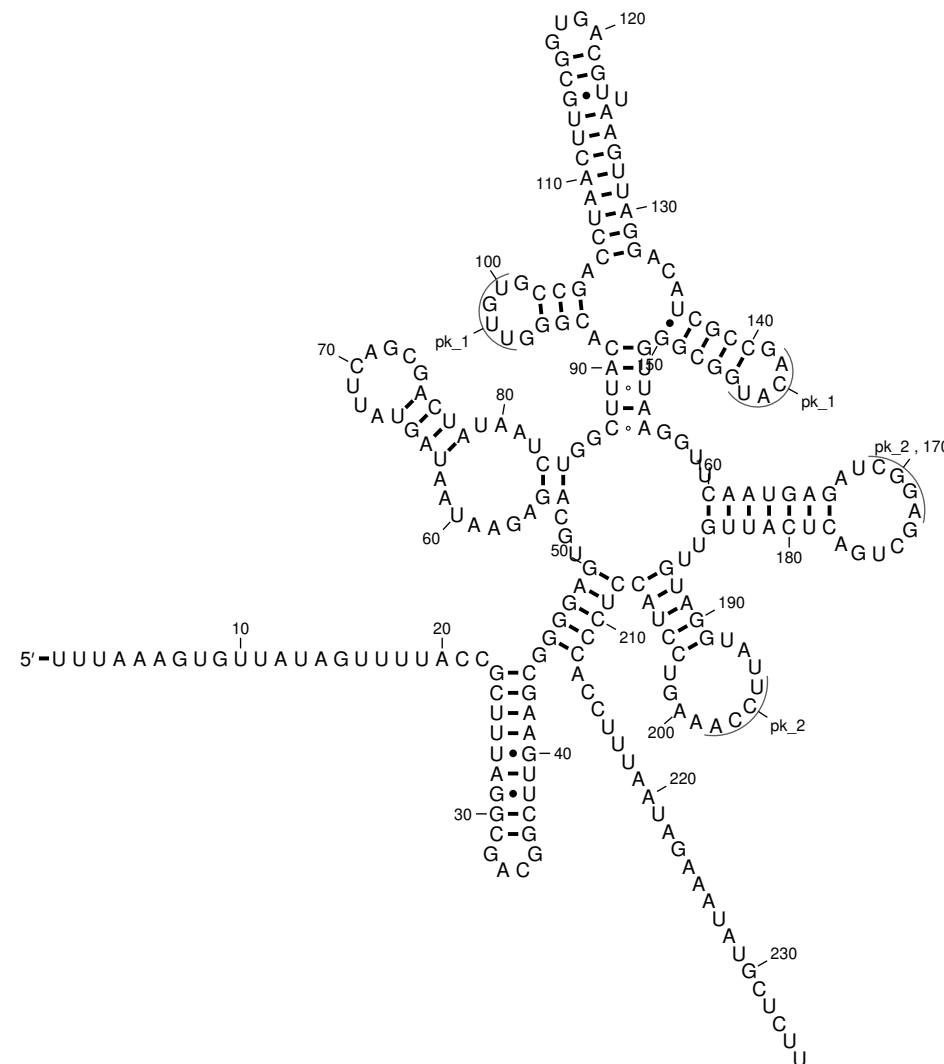
subfam_weight=0.0794949



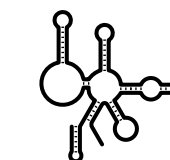
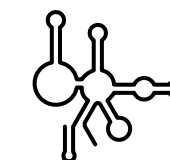
manA.cons



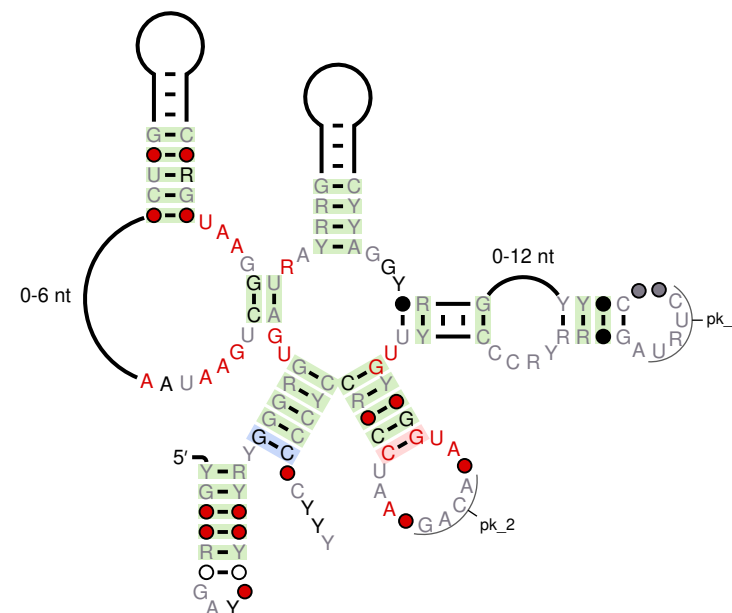
manA.cons NZ_AAOJ01000001.1/468755-469351



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

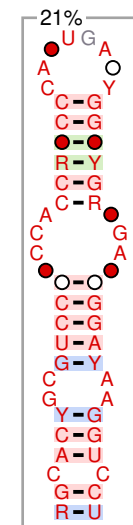


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

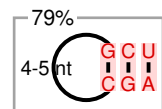
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation 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

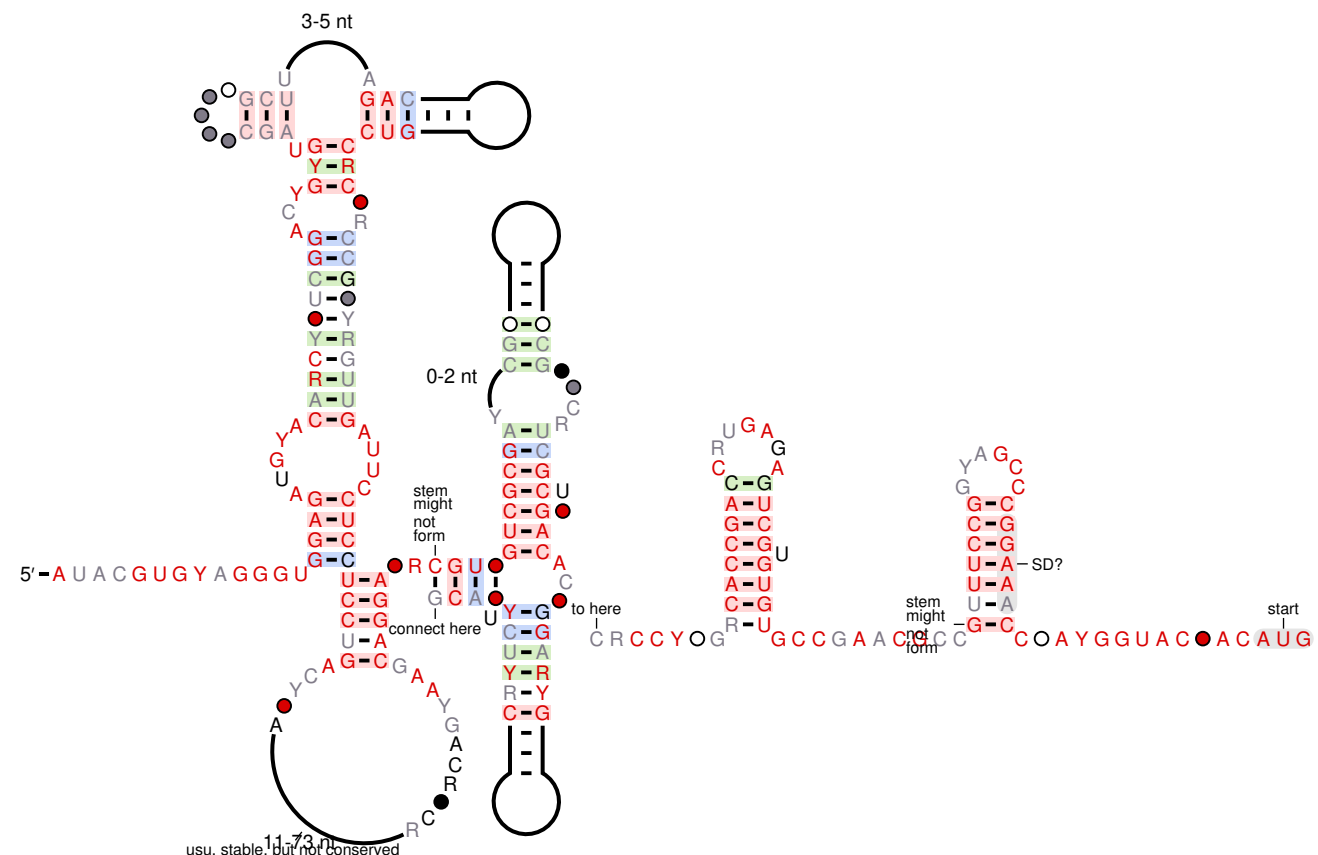
rne-II-O1.cons
subfam_weight=0.21294



rne-II-O2.cons
subfam_weight=0.78706



rne-II.cons

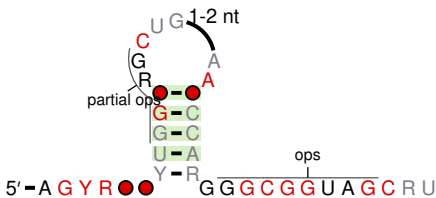


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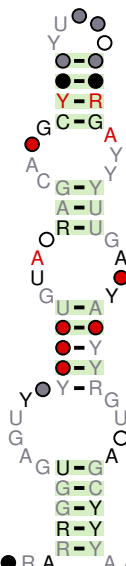
To disable this warning, run r2r with
 --disable-usage-warning

JUMPstart.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

6S-flavo.cons



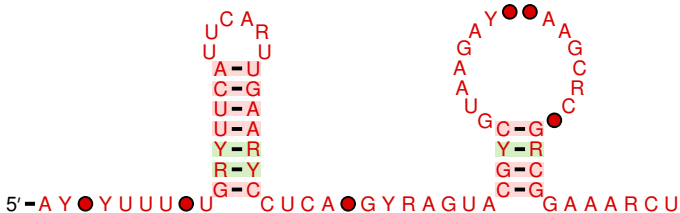
5'-ACUC AAC OOAUAUUURARA AACYUGUUUGGAGUUUA-3'

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

Ocean-V.cons



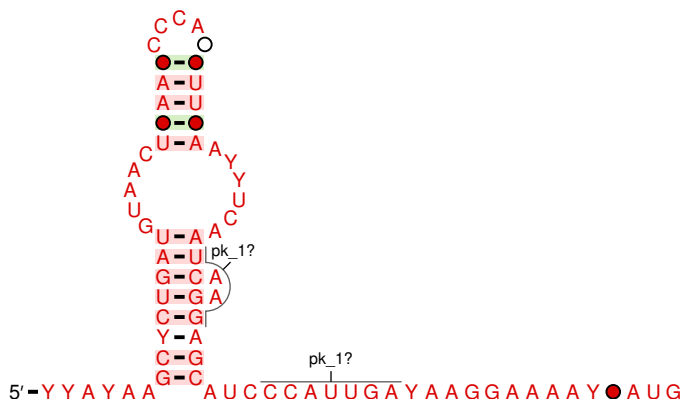
WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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To disable this warning, run r2r with

```
--disable-usage-warning
```

hopC.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

sucC.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

Cyano-2.cons



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

Acido-Lenti-1.cons

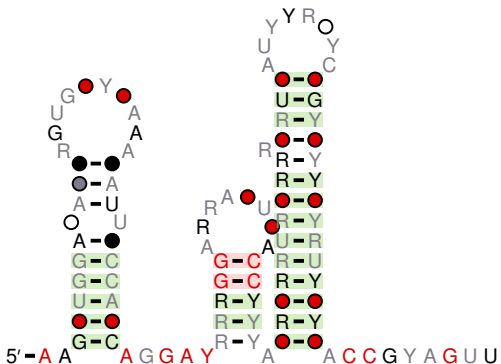


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To disable this warning, run r2r with
 --disable-usage-warning

Methylobacterium-1.cons

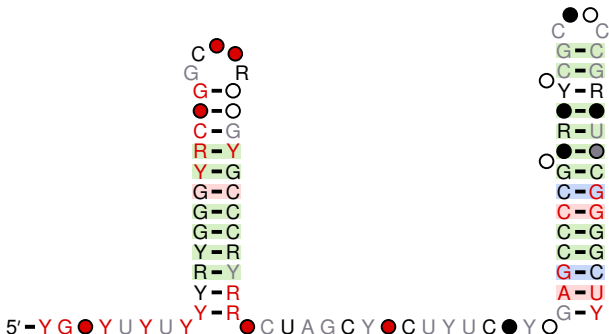


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To disable this warning, run r2r with
--disable-usage-warning

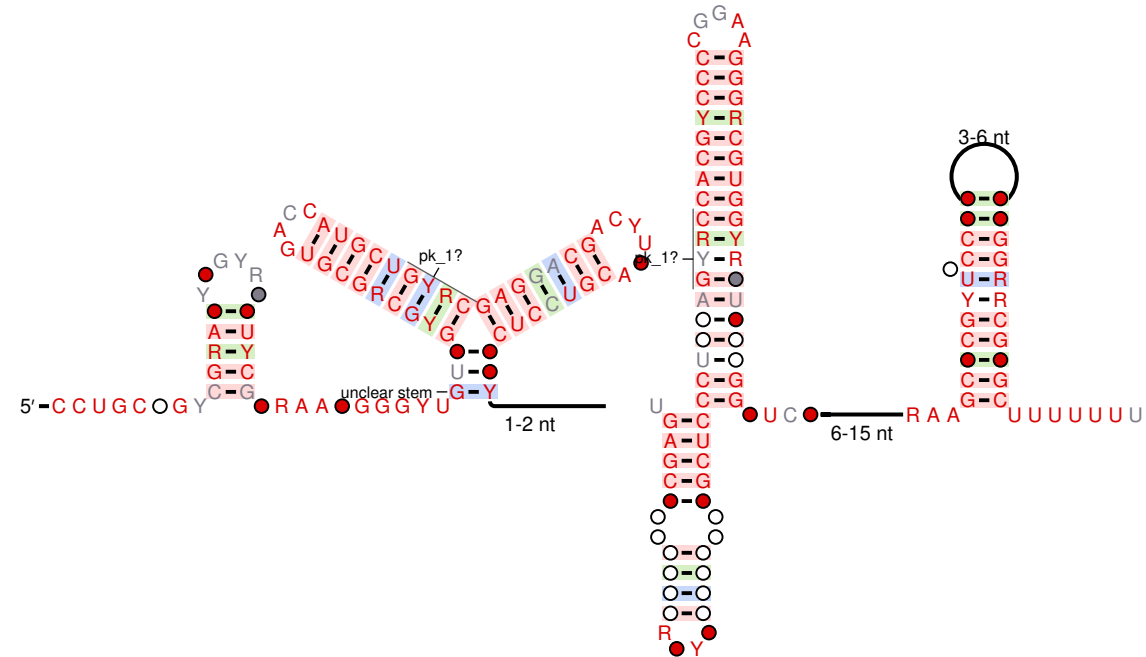
pheA.cons



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

sbcD.cons

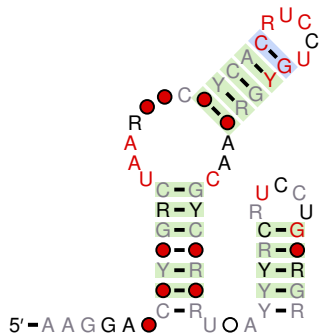


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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

Bacillaceae-1.cons

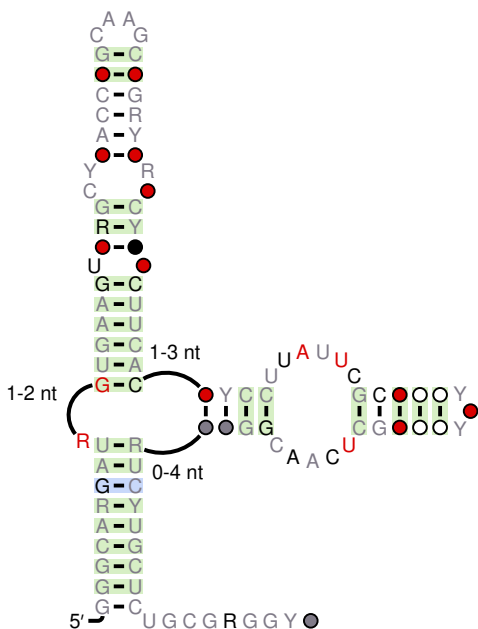


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To disable this warning, run r2r with
--disable-usage-warning

traJ-II.cons

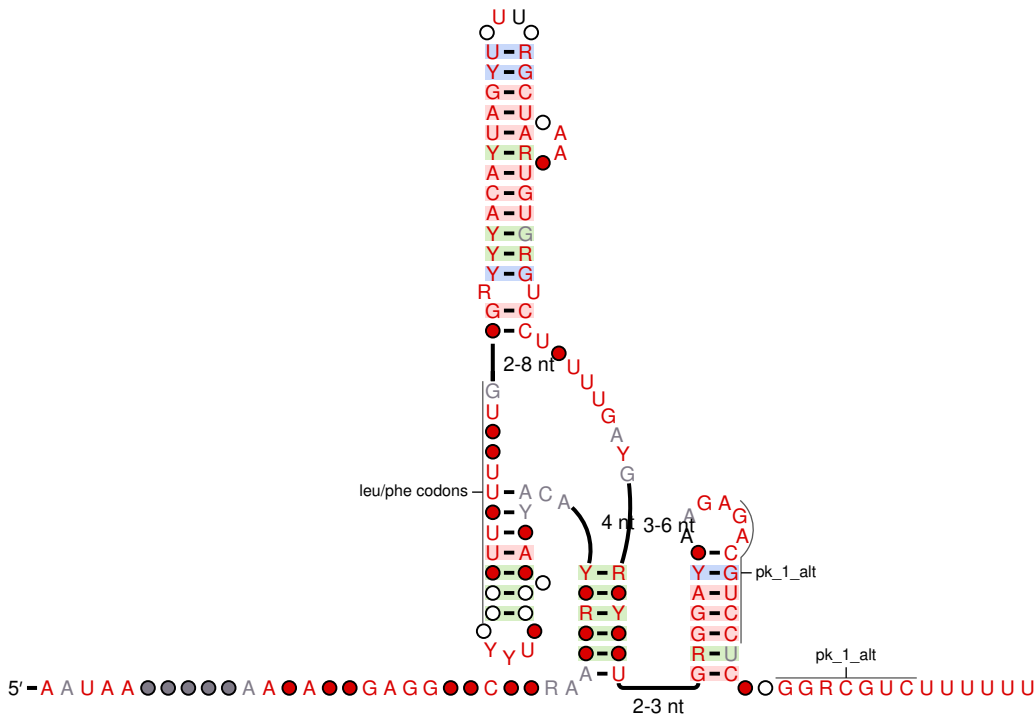


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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

leu-phe-leader.cons

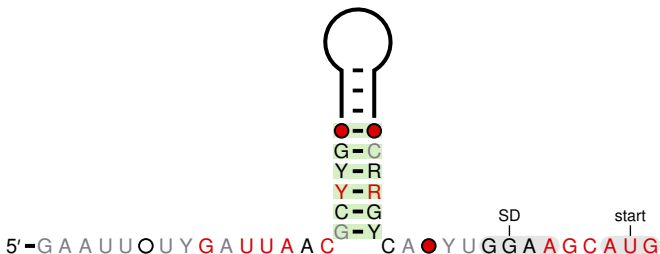


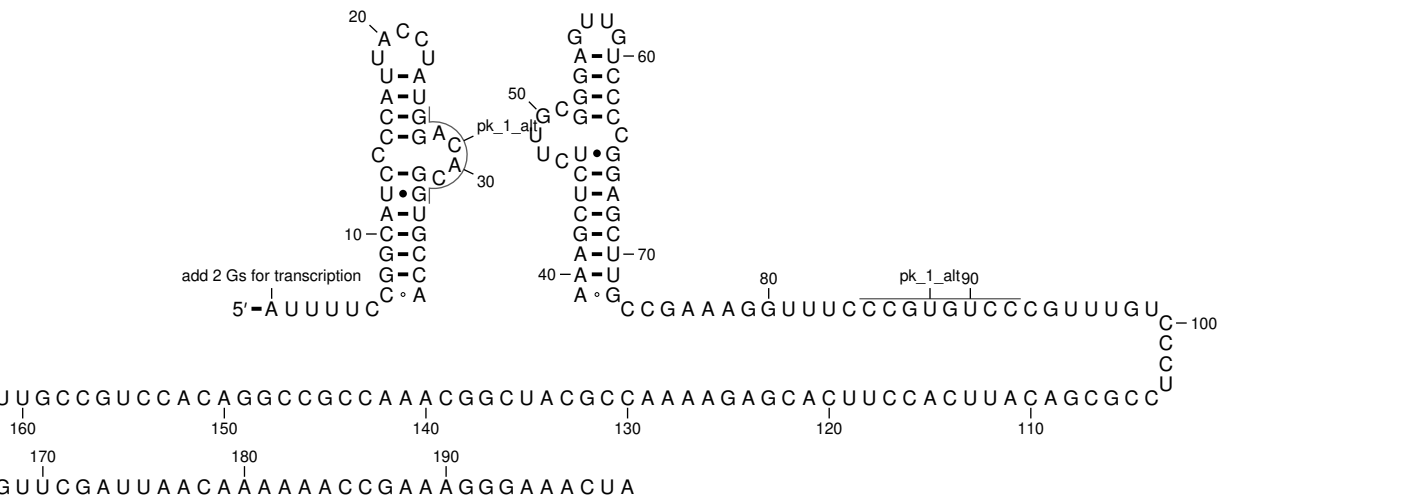
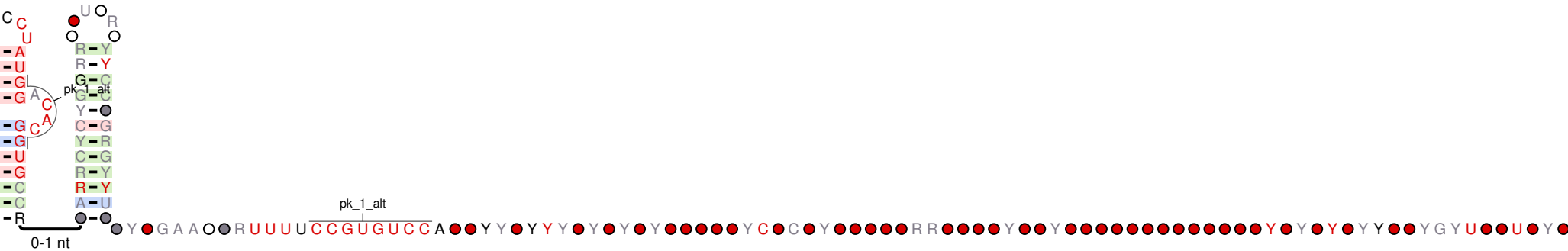
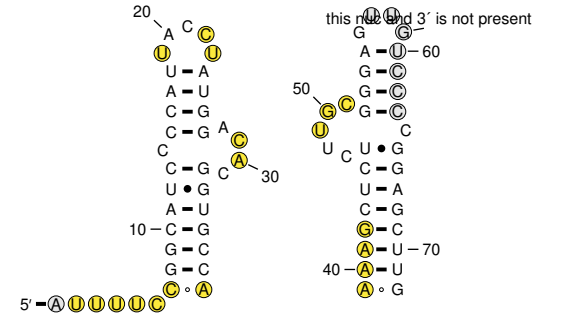
WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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

nuoG.cons



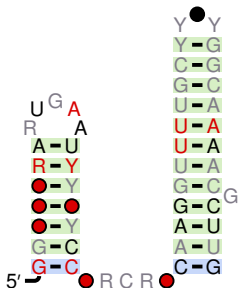


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To disable this warning, run r2r with
 --disable-usage-warning

Bacteroides-2.cons



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

Pseudomon-1.cons

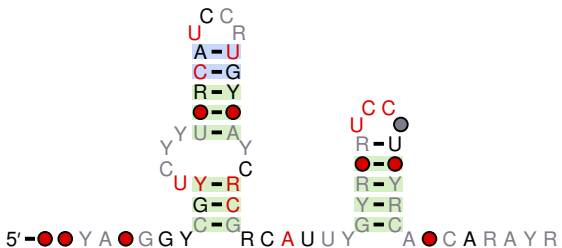


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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

Desulfotalea-1.cons



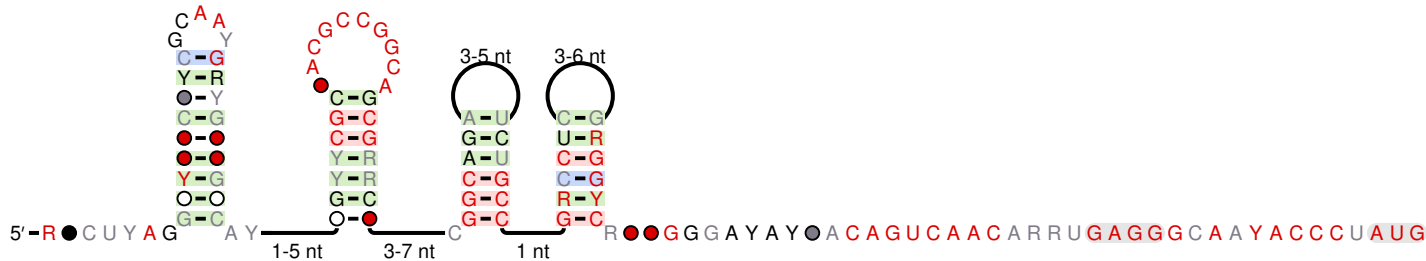
WARNING: R2R is not designed to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program.

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

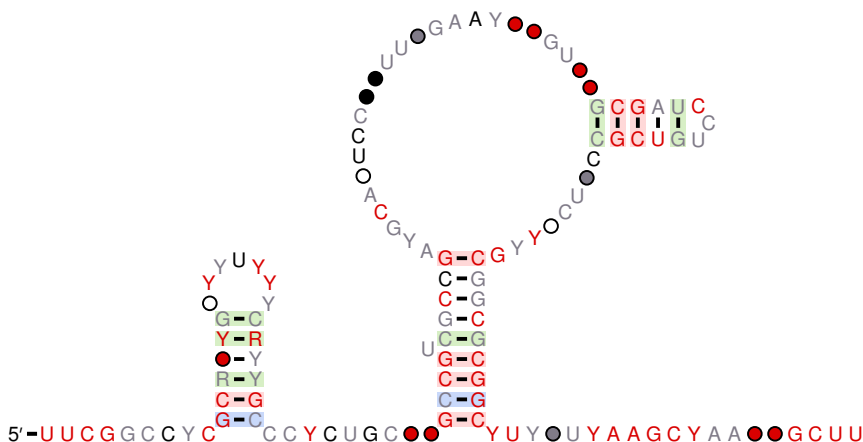
rmf.cons



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

Pseudomon-Rho.cons



WARNING: R2R is not intended to evaluate evidence for covariation in 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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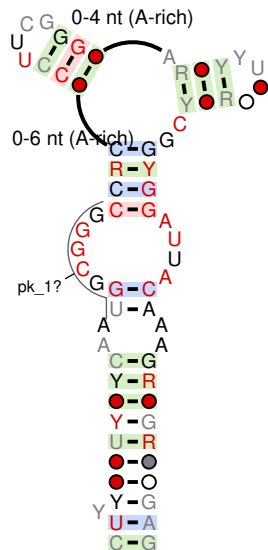
To disable this warning, run r2r with --disable-usage-warning

Bacteroidales-1-pknot.cons

subfam_weight=1



Bacteroidales-1.cons



5'-AGCCG^YAYY●RYURGAUYGGGARACUCAUCA—CGGAGAOAA^G●CUCAA^AAUCYUGUY●Y●CGGAGUUU●RYCRYAUC●●YRGUGCGGCU

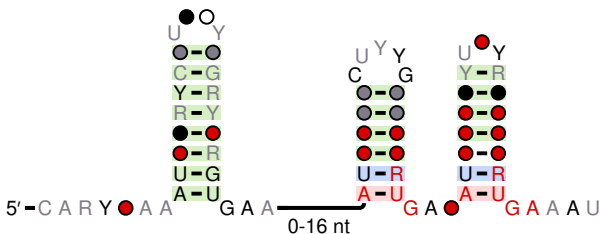
11-17 nt

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

Gut-1.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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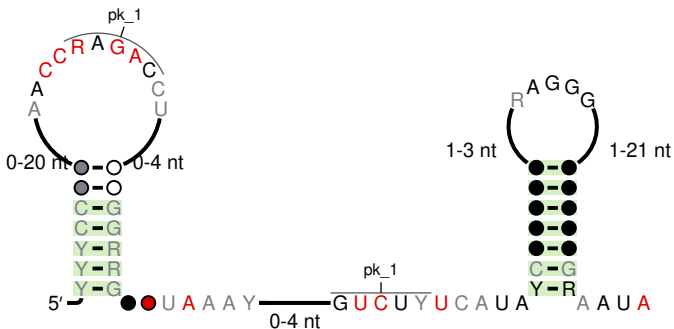
To disable this warning, run r2r with
 --disable-usage-warning

PhotoRC-II-pknot.cons

subfam_weight=1



PhotoRC-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

pedo-repair-p1.cons

subfam_weight=1

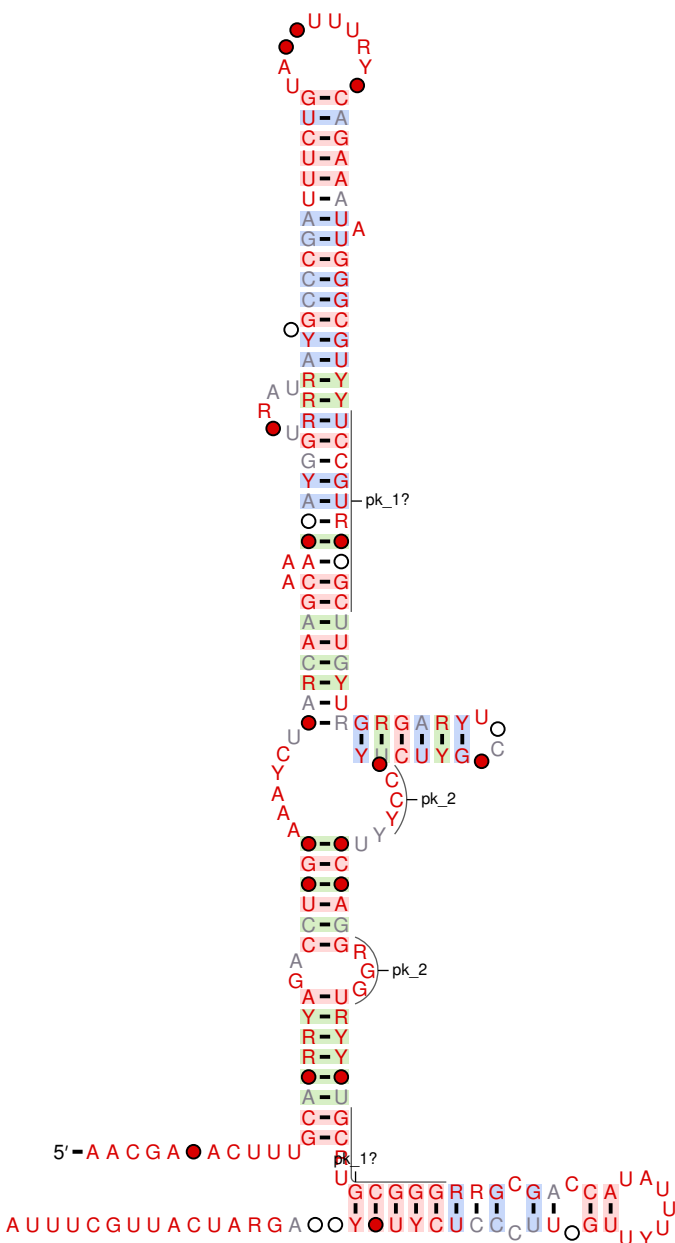


pedo-repair-p2.cons

subfam_weight=1



pedo-repair.cons

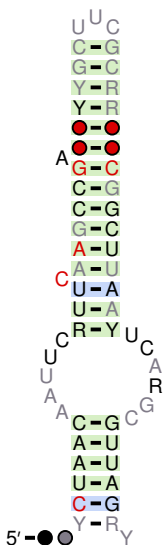


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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

Transposase-resistance.cons

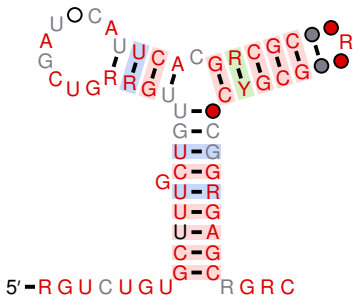


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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

COG2252.cons

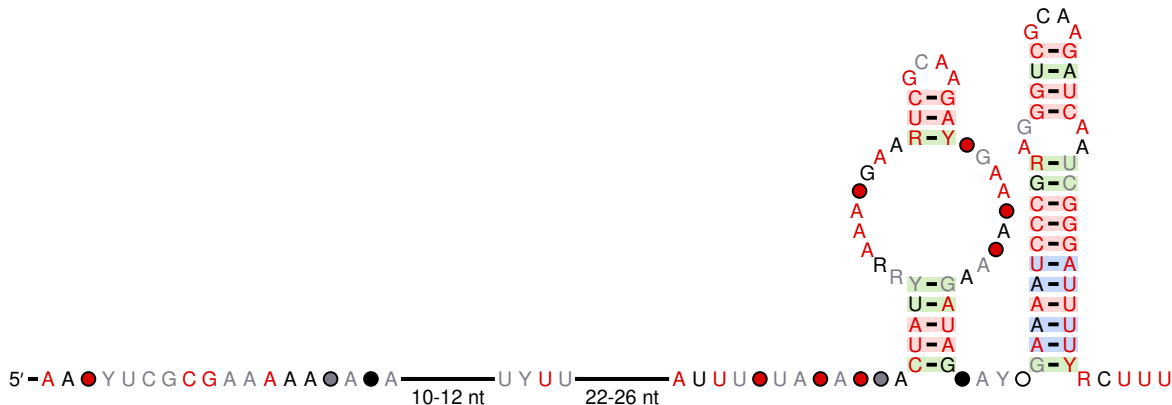


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

Ocean-VI.cons

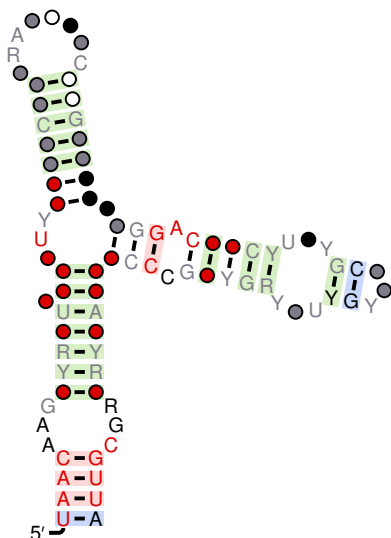


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

Gamma-cis-1.cons

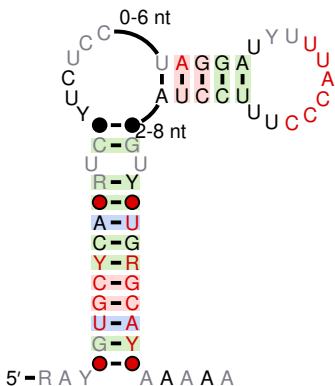


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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

potC.cons

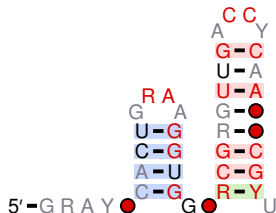


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To disable this warning, run r2r with
 --disable-usage-warning

Soil-1.cons

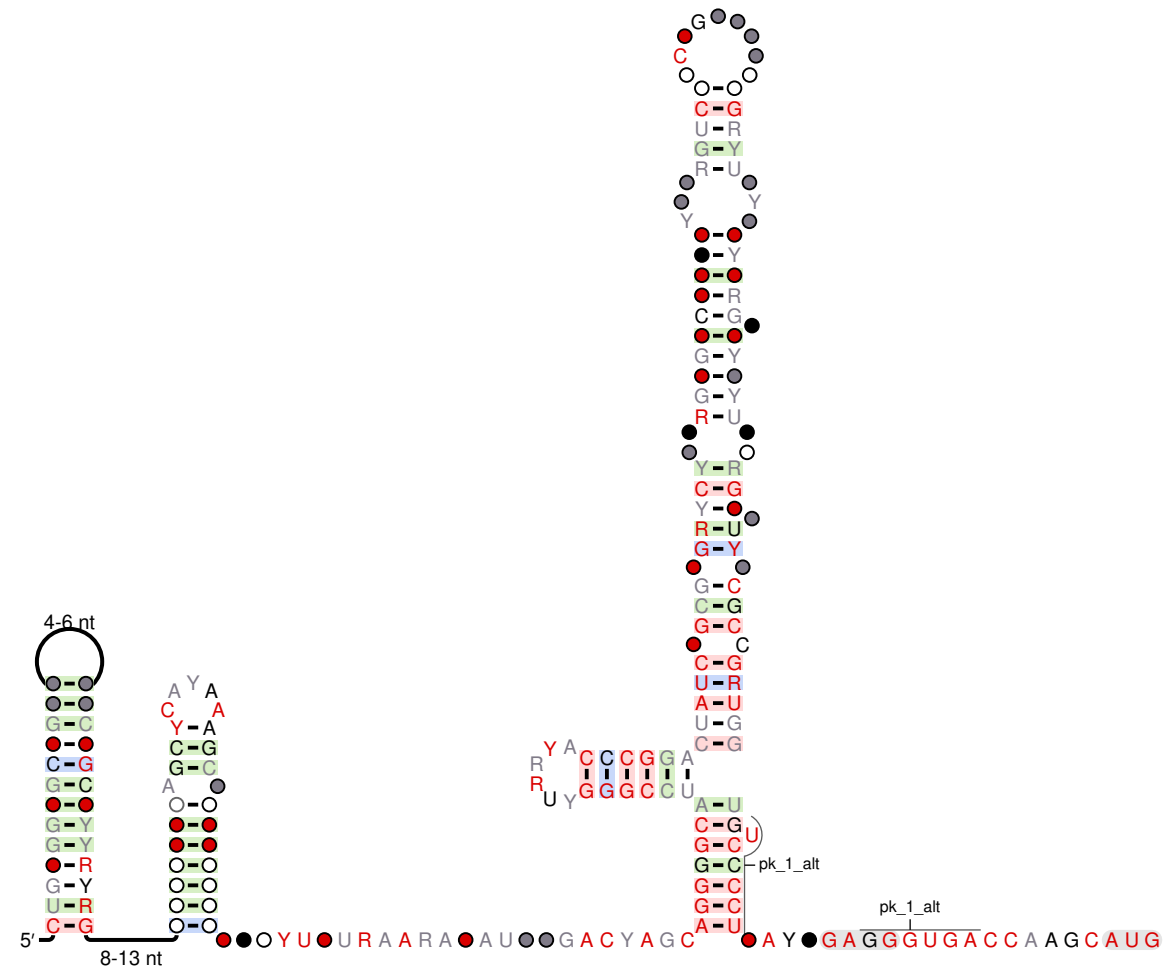


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sucA-II.cons



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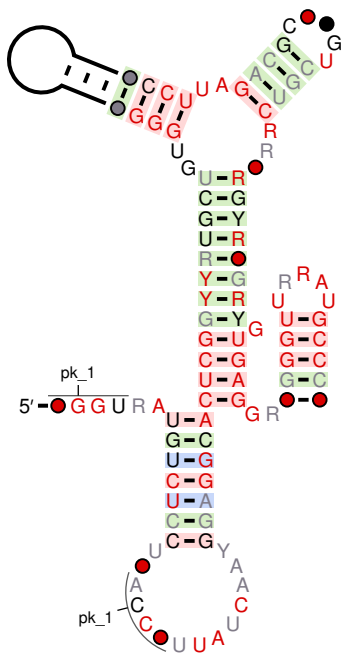
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation 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."

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

epsC-pknot.cons
 subfam_weight=1



epsC.cons

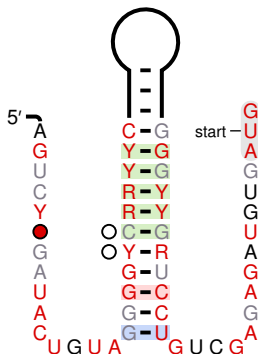


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To disable this warning, run r2r with
--disable-usage-warning

psbNH.cons



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

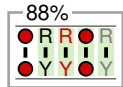
STAXI-pknot1.cons

subfam_weight=1



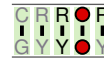
STAXI-pknot3.cons

subfam_weight=0.882988



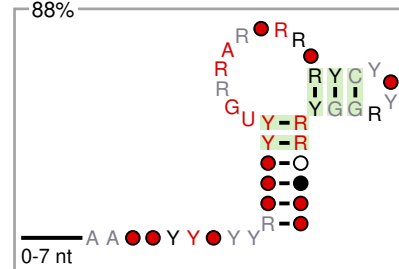
STAXI-pknot2.cons

subfam_weight=1

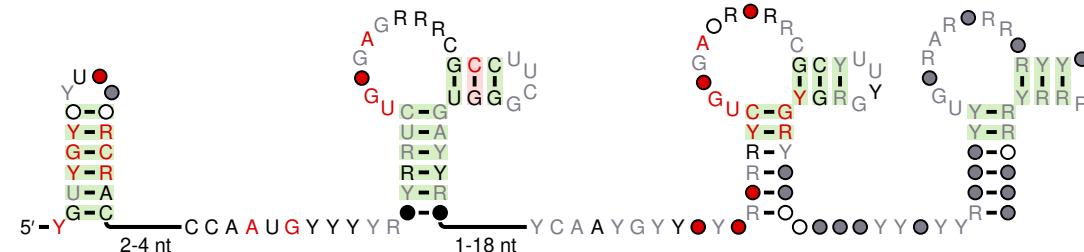


STAXI-unit3.cons

subfam_weight=0.882988



STAXI.cons



STAXI.cons skeleton-with-bp

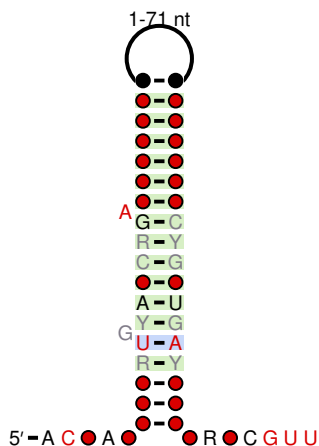


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To disable this warning, run r2r with
--disable-usage-warning

Rhodopirellula-1.cons

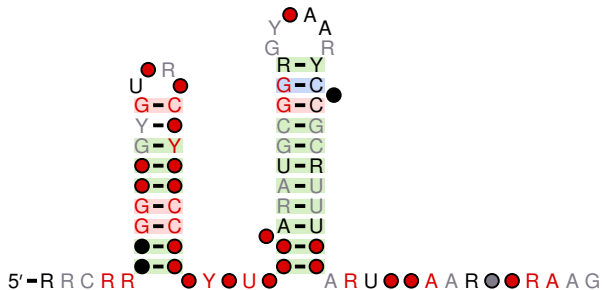


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To disable this warning, run r2r with
 --disable-usage-warning

Termite-leu.cons

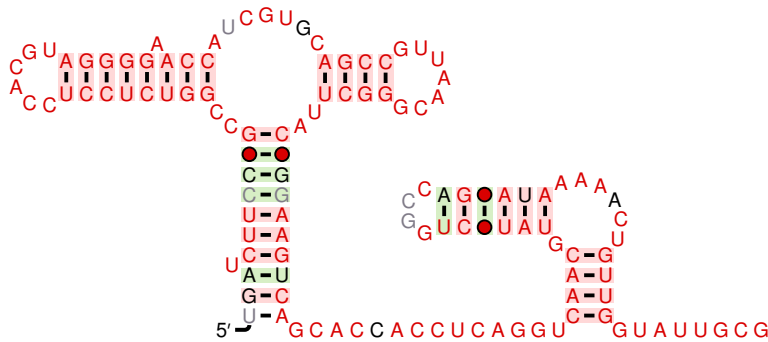


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To disable this warning, run r2r with
--disable-usage-warning

Solibacter-1.cons

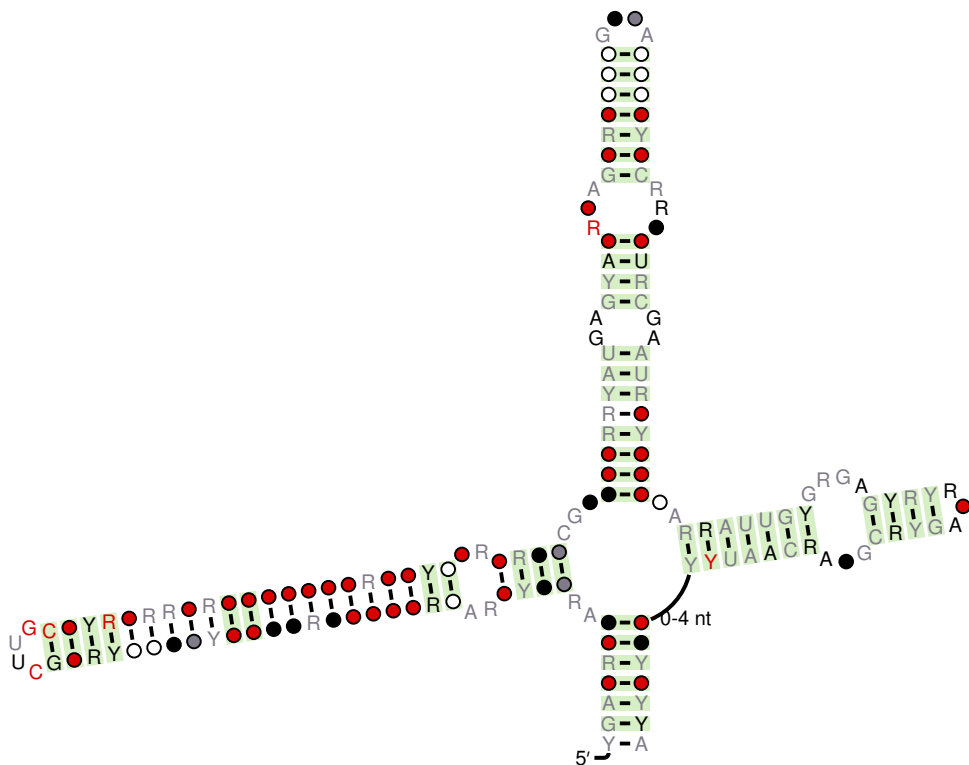


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To disable this warning, run r2r with --disable-usage-warning

Clostridiales-1.cons

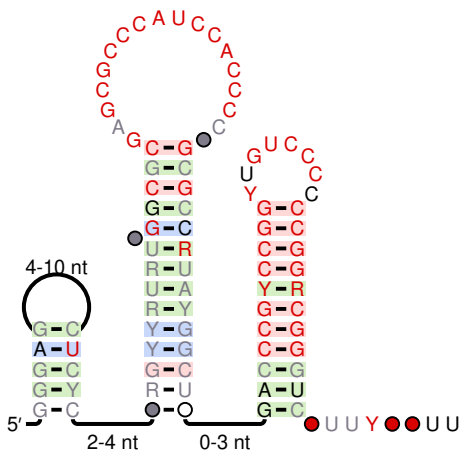


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To disable this warning, run r2r with
--disable-usage-warning

Rhizobiales-2.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:

ScRE.cons

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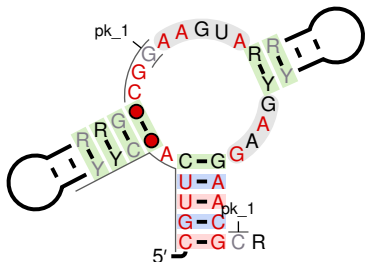
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation 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."

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

glnA-pknot.cons
 subfam_weight=1



glnA.cons



glnA.cons skeleton-with-bp

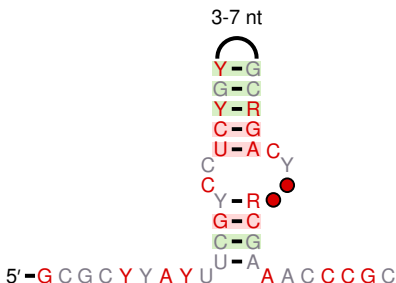


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--disable-usage-warning

Moco-II.cons

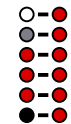


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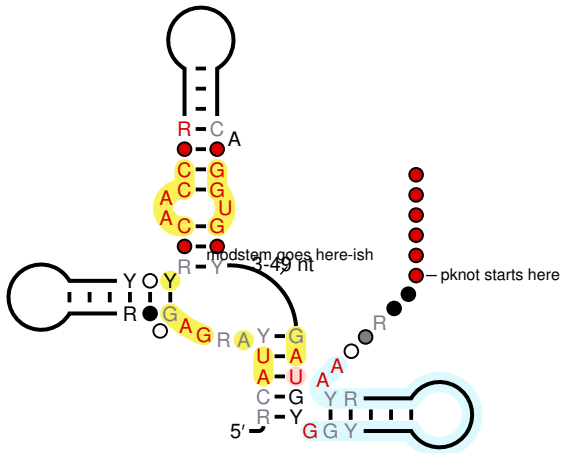
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation 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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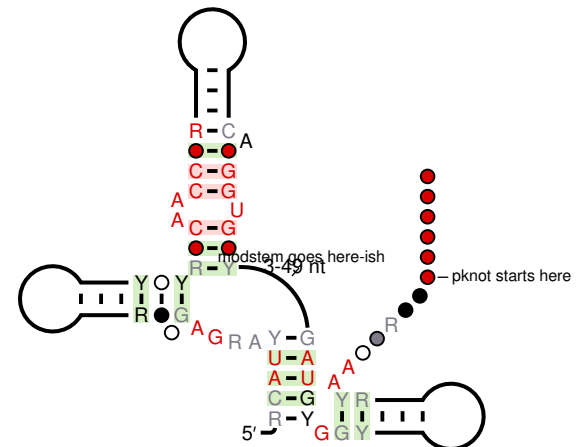
SAM-I-IV-variant-PKNOT2.cons
subfam_weight=1



SAM-I-IV-variant-resemblance.cons
subfam_weight=1



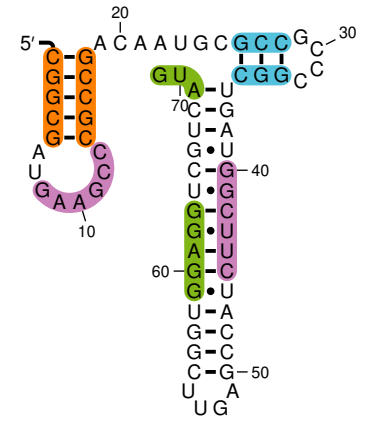
SAM-I-IV-variant.cons



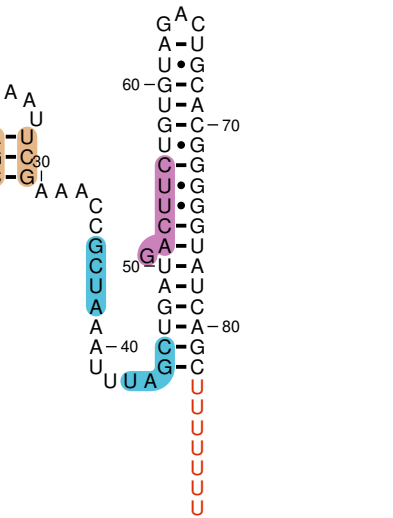
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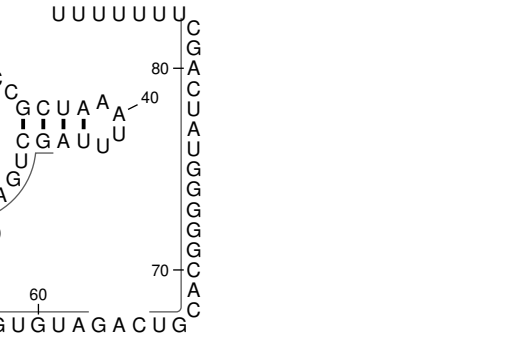
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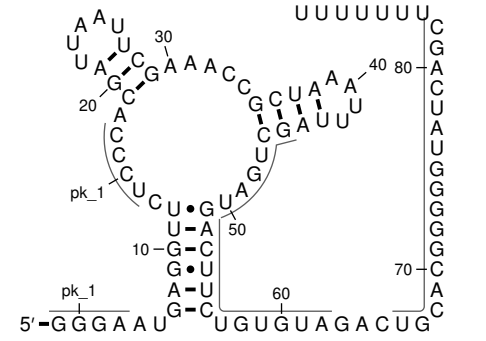
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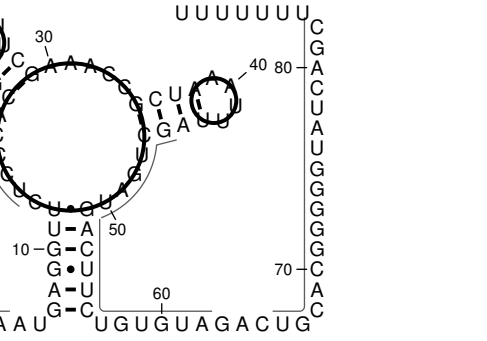
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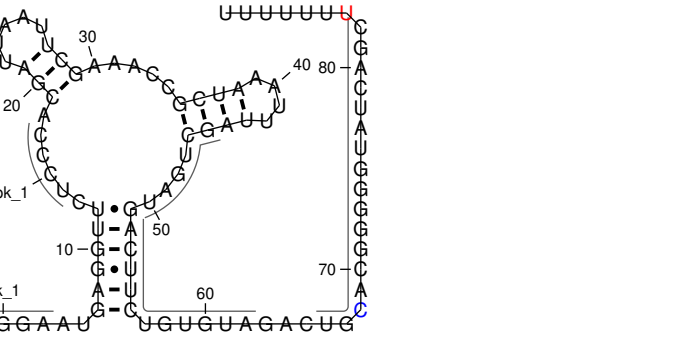
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crcB NZ_ABYJ01000311.1/4968-4495 no-shading=1 anyangle=1 drawcirc=1



crcB NZ_ABYJ01000311.1/4968-4495 no-shading=1 anyangle=1 drawedges=1



crcB-P2.cons

subfam_weight=0.308697



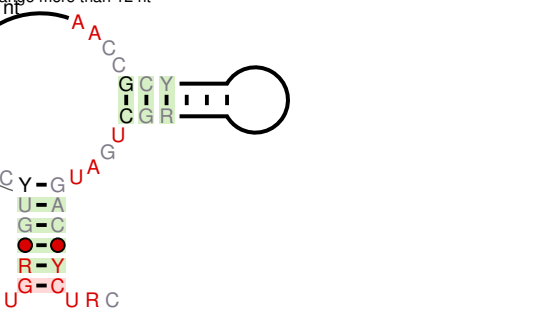
crcB-pknot1.cons

subfam_weight=1

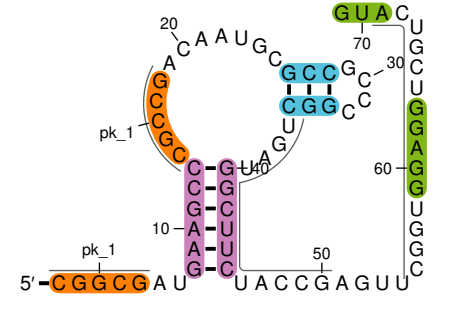


crcB.cons

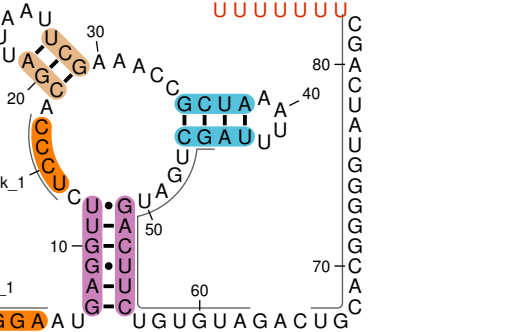
present when backbone range more than 12 nt



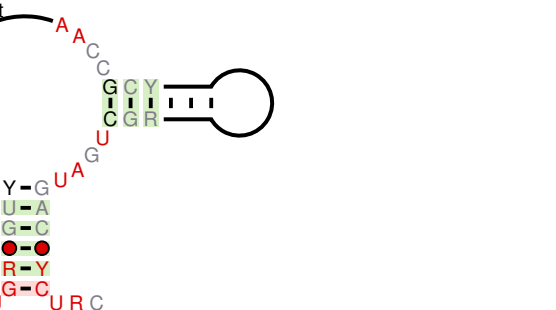
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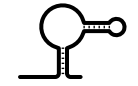
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crcB.cons R2R-paper=1

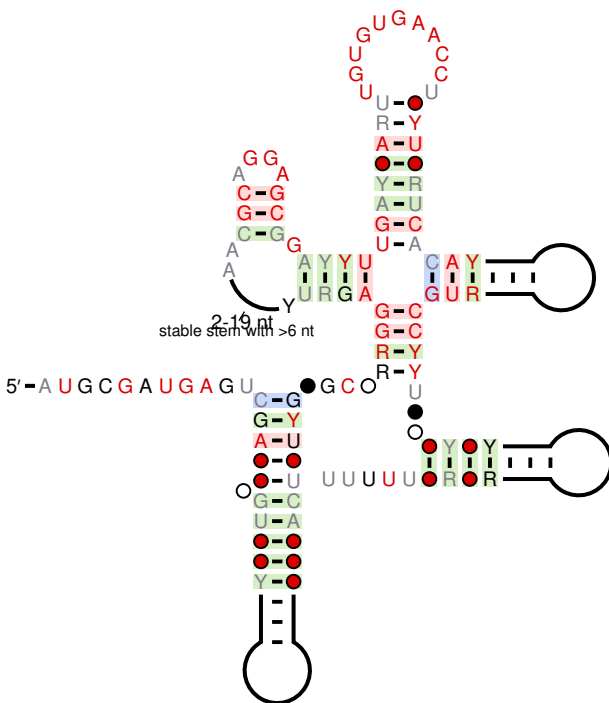


crcB.cons skeleton-with-bp

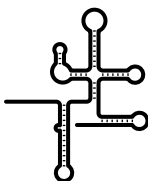


To disable this warning, run `r2r` with `--disable-usage-warning`

asd.cons



asd.cons skeleton-with-bp

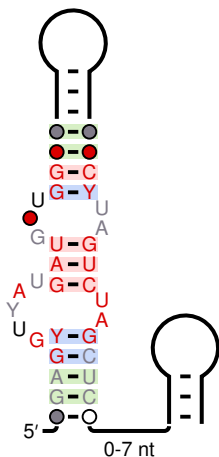


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To disable this warning, run r2r with
--disable-usage-warning

L17DE.cons

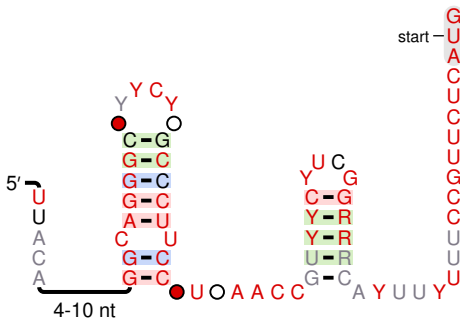


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To disable this warning, run r2r with
--disable-usage-warning

PhotoRC-I.cons

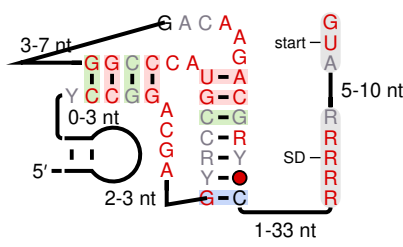


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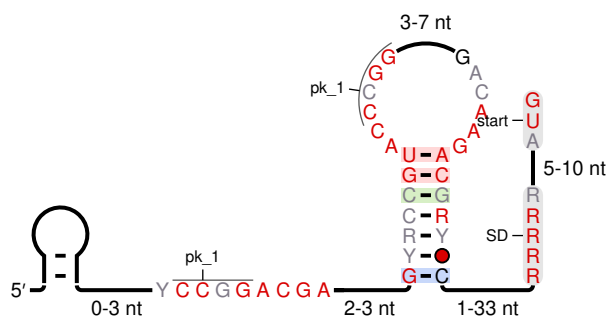
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation 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."

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

ykkC-III.cons



ykkC-III.cons callout-style=1

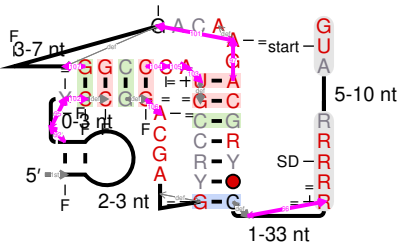


ykkC-III.cons debug_place_explicit=trueykkC-III.cons pseudoknot=1

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92  #=GF R2R place_explicit 5 5-- +45 1 0 0 0 +90
95  #=GF R2R place_explicit pe:c pe:c-- +45 1 0 0 0 +90 f
102 #=GF R2R place_explicit pe:5 pe:5-- 0 1 0 0 0 f
106 #=GF R2R place_explicit pe:3 pe:3-- +45 1 0 0 0 +90 f
103 #=GF R2R place_explicit pe:1 pe:1-- -45 1 0 0 0 -90
105 #=GF R2R place_explicit pe:2-- pe:1 0 1 0 0 0
104 #=GF R2R place_explicit pe:2 pe:2-- 0 1 0 0 0 f
107 #=GF R2R place_explicit pe:4 pe:4-- 0 1 0 0 0
101 #=GF R2R place_explicit pe:8 pe:7 -45 -1 0 -3 0 -90
97  #=GF R2R place_explicit pe:7 pe:a 0 -2 0 0 0
66  #=GF R2R place_explicit pe:S pe:S-- -45 1 0 0 0 -90

```

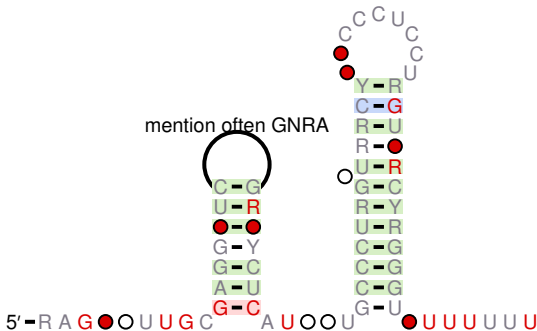


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To disable this warning, run r2r with
 --disable-usage-warning

atoC.cons

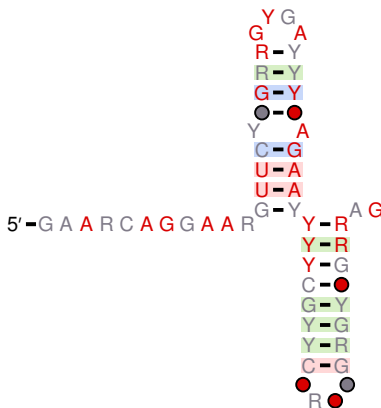


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--disable-usage-warning

Nitrosococcus-1.cons

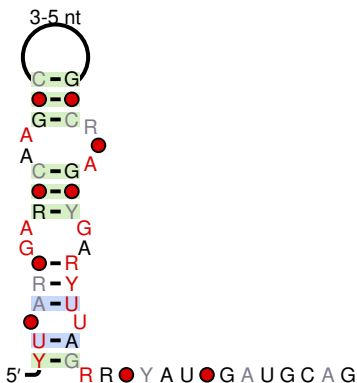


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

sanguinis-hairpin.cons



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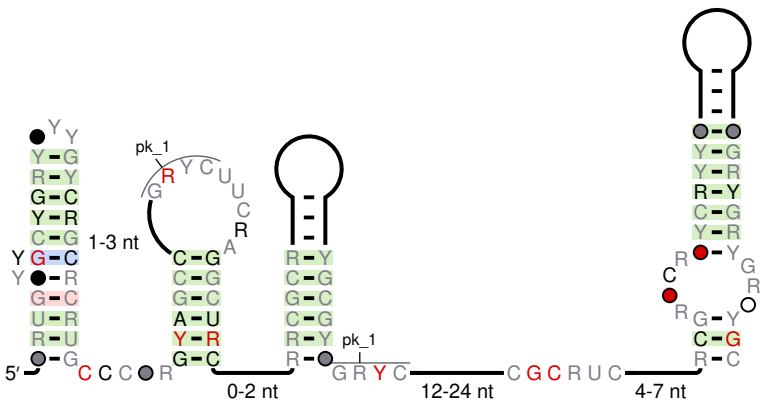
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation 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."

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

radC-pknot.cons
 subfam_weight=1



radC.cons

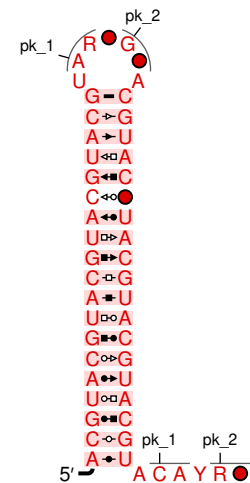


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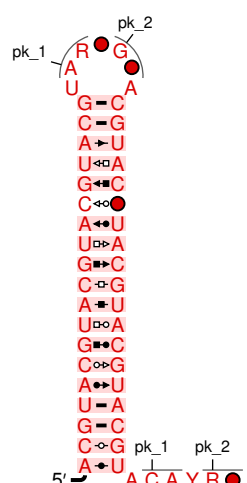
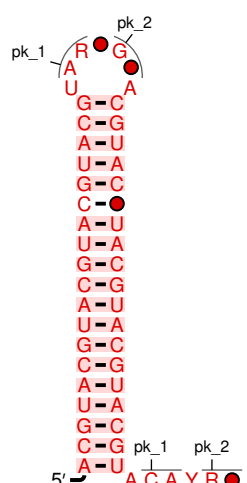
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation 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."

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

demo-leontis-westhof.cons



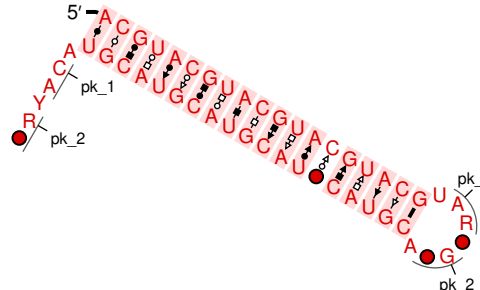
demo-leontis-westhof.cons clear_all=1 demo-leontis-westhof.cons clear_some=1



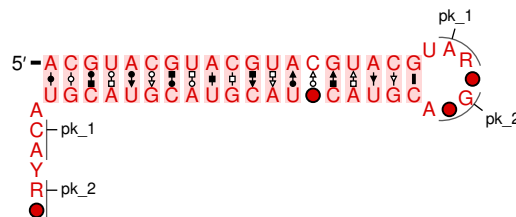
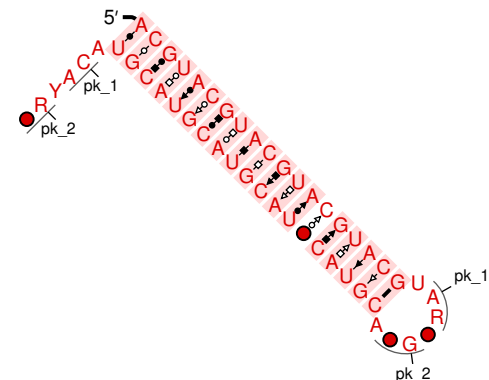
demo-leontis-westhof.cons pknot=_1 demo-leontis-westhof.cons pknot=_2



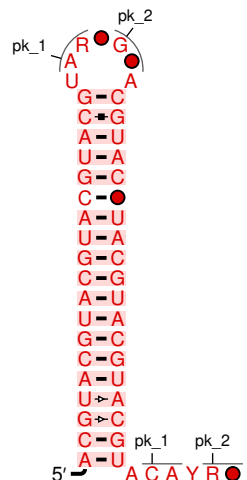
demo-leontis-westhof.cons rotate=30



demo-leontis-westhof.cons rotate=45 demo-leontis-westhof.cons rotate=90

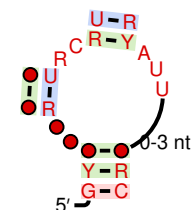


demo-leontis-westhof.cons set=1

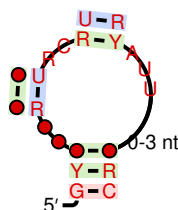


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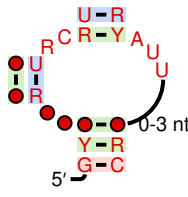
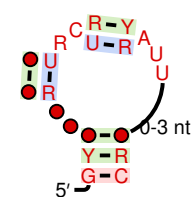
demo-multistem.cons



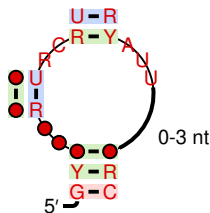
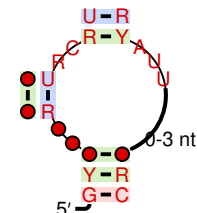
demo-multistem.cons circle=1



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



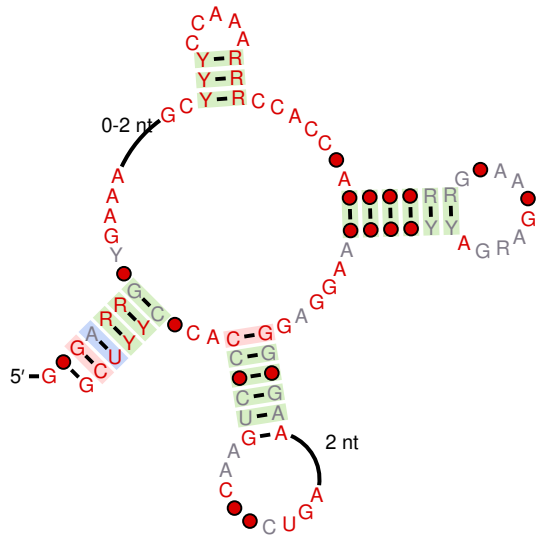
demo-multistem.cons solver1=1 demo-multistem.cons solver2=1



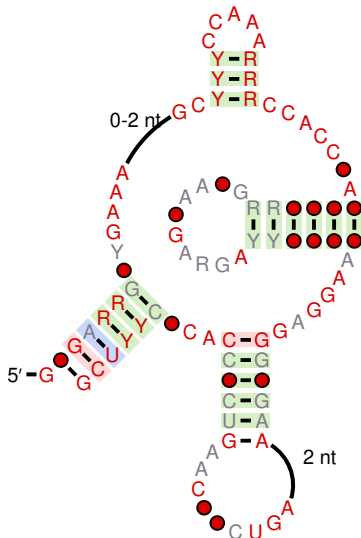
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To disable this warning, run r2r with --disable-usage-warning

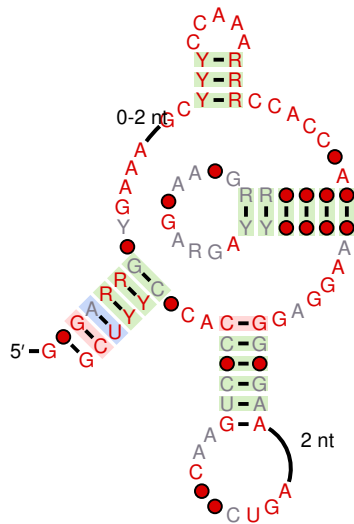
demo-multistem-IMES-1.cons



demo-multistem-IMES-1.cons solver=1



demo-multistem-IMES-1.cons solver=2

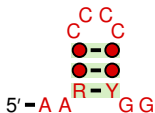


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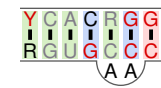
To disable this warning, run r2r with
--disable-usage-warning

demo-breakpair-fix2.cons

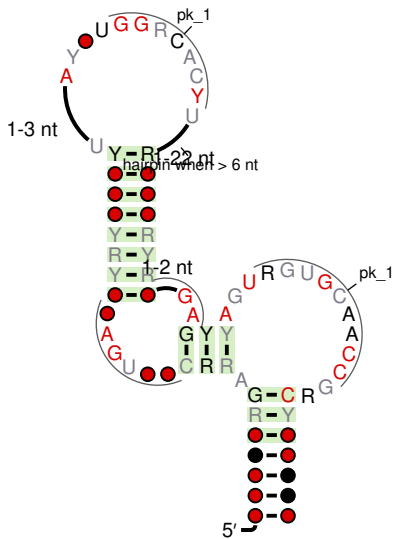


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To disable this warning, run r2r with --disable-usage-warning

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

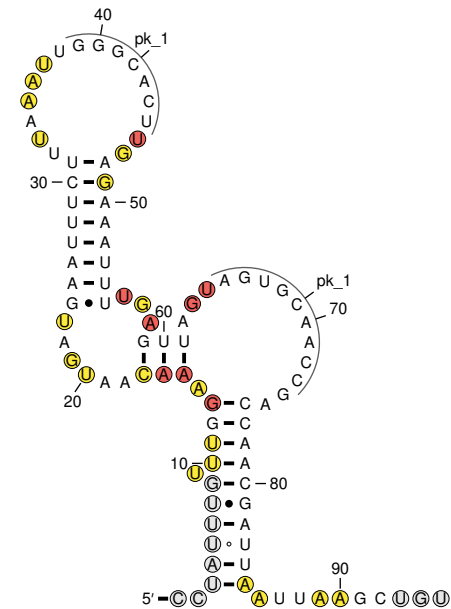


c-di-GMP-II.cons



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
See note1 in manual for more information.

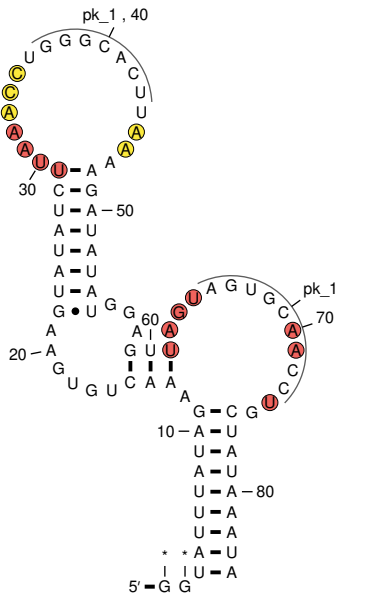


c-di-GMP-II.cons skeleton-with-bp



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
See note1 in manual for more information.

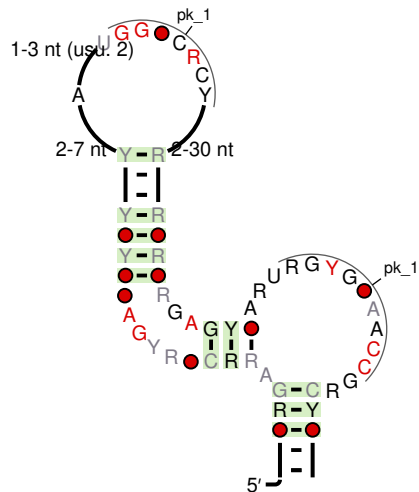


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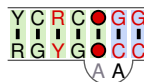
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation 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

c-di-GMP-II-update.cons



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



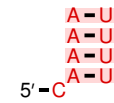
c-di-GMP-II-update.cons skeleton-with-bp



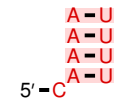
WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

test-5prime.cons



test-5prime.cons flip-angle-pair=0-0-0



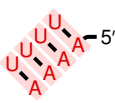
test-5prime.cons flip-angle-pair=0-0-1



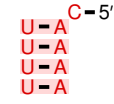
test-5prime.cons flip-angle-pair=0-135-0



test-5prime.cons flip-angle-pair=0-135-1



test-5prime.cons flip-angle-pair=0-180-0



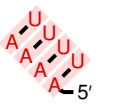
test-5prime.cons flip-angle-pair=0-180-1



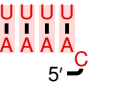
test-5prime.cons flip-angle-pair=0-225-0



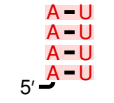
test-5prime.cons flip-angle-pair=0-225-1



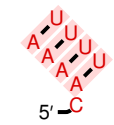
test-5prime.cons flip-angle-pair=0-270-0



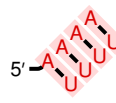
test-5prime.cons flip-angle-pair=0-270-1



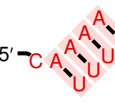
test-5prime.cons flip-angle-pair=0-315-0



test-5prime.cons flip-angle-pair=0-315-1



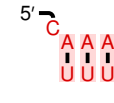
test-5prime.cons flip-angle-pair=0-45-0



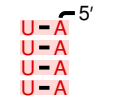
test-5prime.cons flip-angle-pair=0-45-1



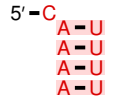
test-5prime.cons flip-angle-pair=0-90-0



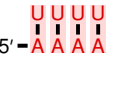
test-5prime.cons flip-angle-pair=0-90-1



test-5prime.cons flip-angle-pair=1-0-0



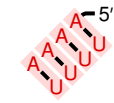
test-5prime.cons flip-angle-pair=1-0-1



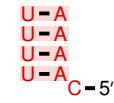
test-5prime.cons flip-angle-pair=1-135-0



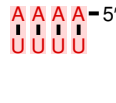
test-5prime.cons flip-angle-pair=1-135-1



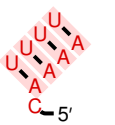
test-5prime.cons flip-angle-pair=1-180-0



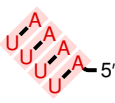
test-5prime.cons flip-angle-pair=1-180-1



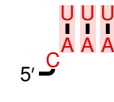
test-5prime.cons flip-angle-pair=1-225-0



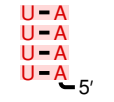
test-5prime.cons flip-angle-pair=1-225-1



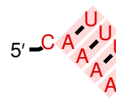
test-5prime.cons flip-angle-pair=1-270-0



test-5prime.cons flip-angle-pair=1-270-1



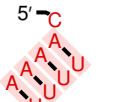
test-5prime.cons flip-angle-pair=1-315-0



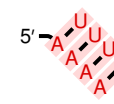
test-5prime.cons flip-angle-pair=1-315-1



test-5prime.cons flip-angle-pair=1-45-0



test-5prime.cons flip-angle-pair=1-45-1



test-5prime.cons flip-angle-pair=1-90-0



test-5prime.cons flip-angle-pair=1-90-1



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

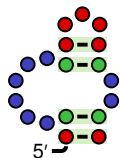
TestColumnNumbers.cons



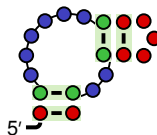
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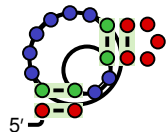
solver-formulation1-1.cons



solver-formulation1-1.cons solver=1



solver-formulation1-1.cons solver=2

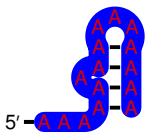


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To disable this warning, run r2r with
--disable-usage-warning

backbone-path1.cons



backbone-path1.cons skeleton-with-bp

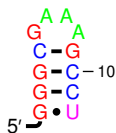


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"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence 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

1ZIF seq



1ZIF.cons

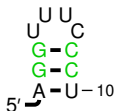


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To disable this warning, run r2r with
 --disable-usage-warning

SmallWithCovary 5



SmallWithCovary.cons

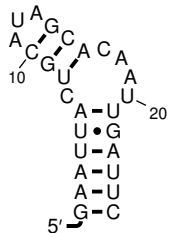


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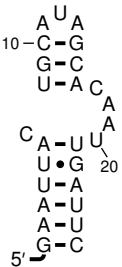
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation 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."

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

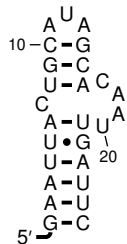
uneven-internal-loop seq layout=anyangle



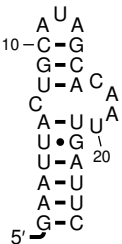
uneven-internal-loop seq layout=broken-left



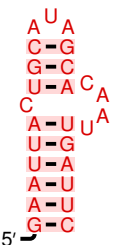
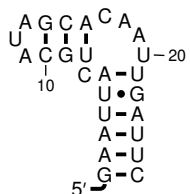
uneven-internal-loop seq layout=default



uneven-internal-loop seq layout=left-turn



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



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

TwoBasePairs seq



TwoBasePairs.cons

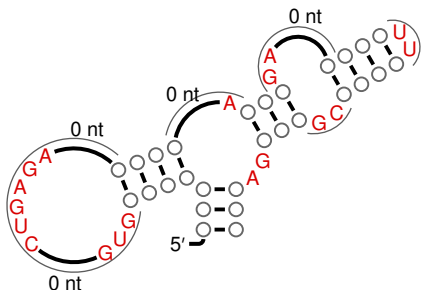


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To disable this warning, run r2r with
--disable-usage-warning

E-coli-TPP-rnamotif-descriptor.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

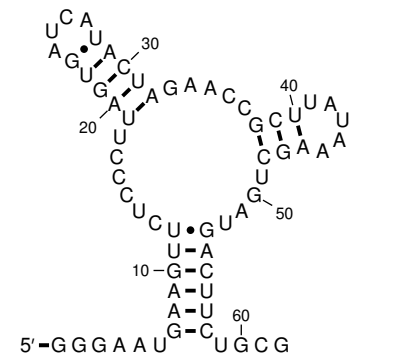
ScriptInputExample.cons

A

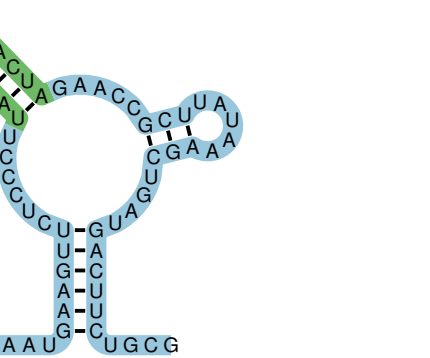


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To disable this warning, run r2r with --disable-usage-warning

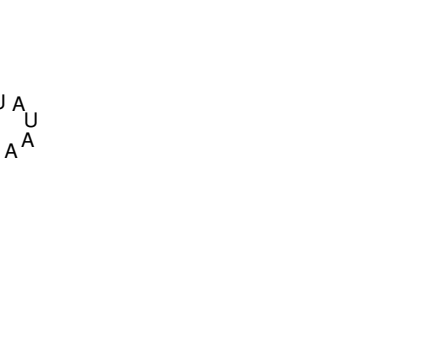
consensus-of-2 NZ_AAXB02000001.1/235534-236009



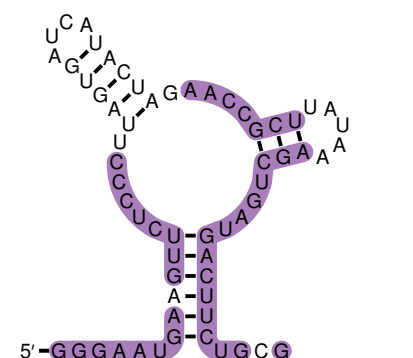
consensus-of-2 NZ_AAXB02000001.1/235534-236009 LIX2010=1 covary=1



consensus-of-2 NZ_AAXB02000001.1/235534-236009 covary=1consensus-of-2 NZ_AAXB02000001.1/235534-236009 covary=1 identity=1



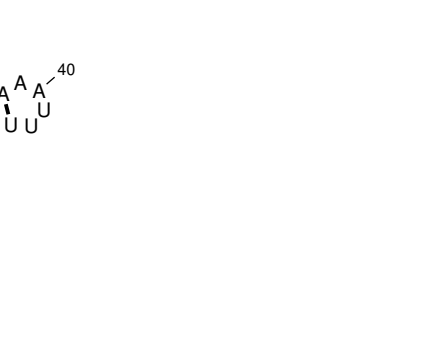
consensus-of-2 NZ_AAXB02000001.1/235534-236009 identity=1



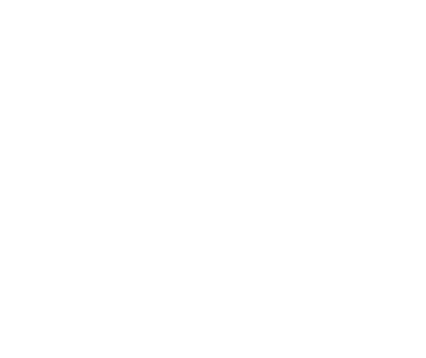
consensus-of-2 NZ_AAXB02000001.1/235534-236009 identity=1 covary=1 linear=1

5'-GGGAUGAGUUCUCCUUAAGUGAUGAUAACCGCUUAUAAAGCUGAUGACUUCUGCG

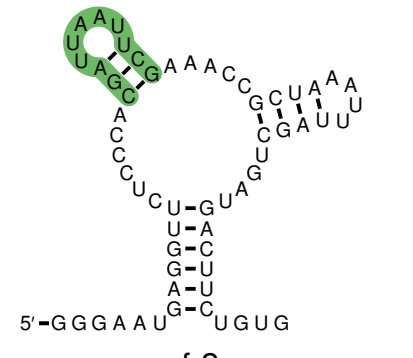
consensus-of-2 NZ_ABYJ01000311.1/4968-4495



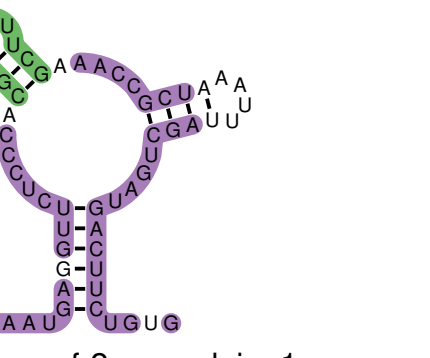
consensus-of-2 NZ_ABYJ01000311.1/4968-4495 LIX2010=1 covary=1



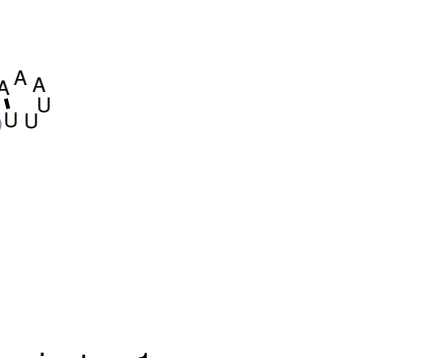
consensus-of-2 NZ_ABYJ01000311.1/4968-4495 covary=1



consensus-of-2 NZ_ABYJ01000311.1/4968-4495 covary=1 identity=1



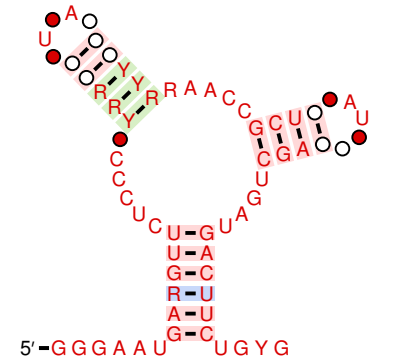
consensus-of-2 NZ_ABYJ01000311.1/4968-4495 identity=1



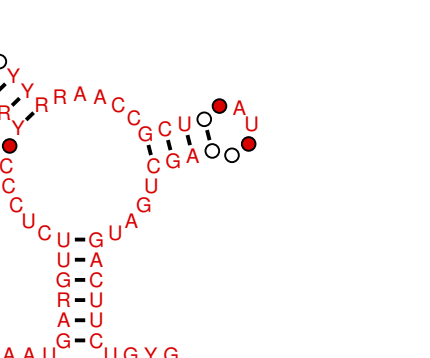
consensus-of-2 NZ_ABYJ01000311.1/4968-4495 identity=1 covary=1 linear=1

5'-GGGAUGAGUUCUCCUACGAUAUAAUUCGAACCGCUAAAUUUAGCUGAUGACUUCUGUG

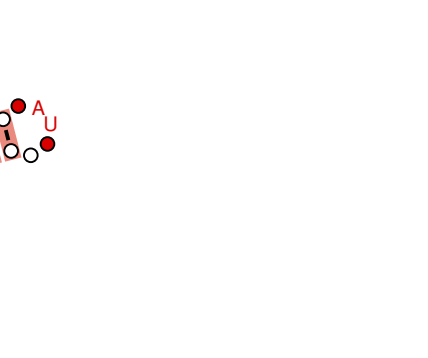
consensus-of-2.cons



consensus-of-2.cons plain=1



consensus-of-2.cons projector=1



consensus-of-2.cons variables=1



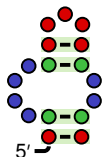
WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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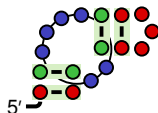
Unfortunately, there is no accepted method to assign confidence that entirely eliminates the need to analyze the full alignment."

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

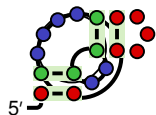
solver-formulation2-1.cons



solver-formulation2-1.cons solver=1



solver-formulation2-1.cons solver=2

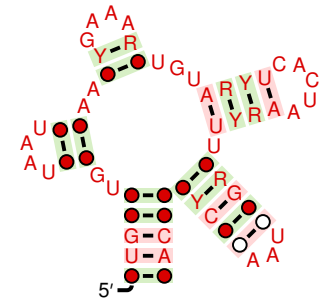


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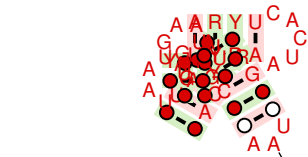
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation 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

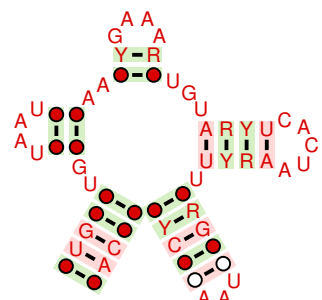


demo-multistem-manA.cons solver=1

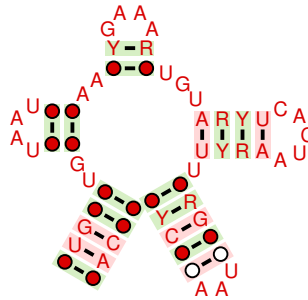
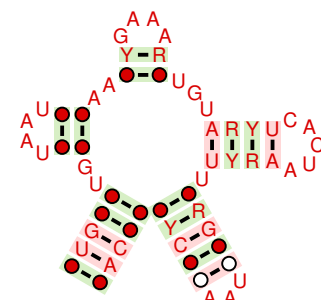


note: R2R cannot find a feasible solution for this problem using the multistem_justion_circular_solver command. However, it can with (1) a user-input optimization starting point, (2) with the try_harder directive or (3) with the multistem_justion_bulgecircley_solver command, as shown in other drawings here.

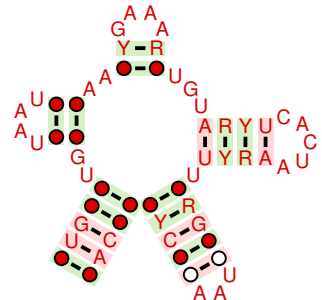
demo-multistem-manA.cons solver=1explicitinitial



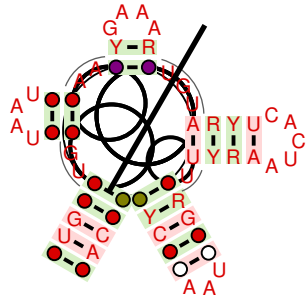
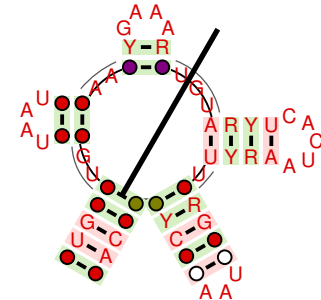
demo-multistem-manA.cons solver=1tryharderdemo-multistem-manA.cons solver=2



demo-multistem-manA.cons solver=3



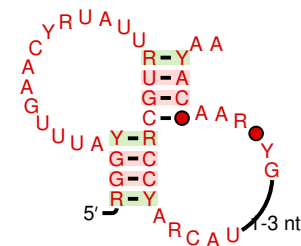
demo-multistem-manA.cons solver=3 annot=1demo-multistem-manA.cons solver=3 annot=1 fewiters=1



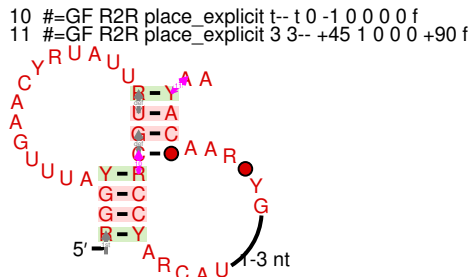
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To disable this warning, run r2r with --disable-usage-warning

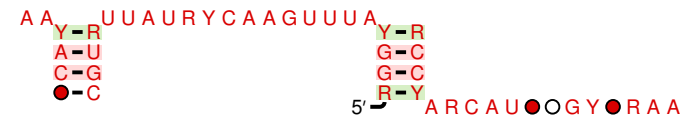
demo-pknot-inline.cons



demo-pknot-inline.cons debug_place_explicit=1



demo-pknot-inline.cons default=1



demo-pknot-inline.cons default=1 labelnucs=1

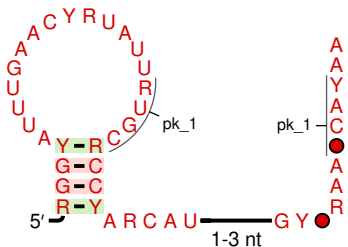


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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

demo-pknot-callout-ifdef.cons



demo-pknot-callout-ifdef.cons pknot=1

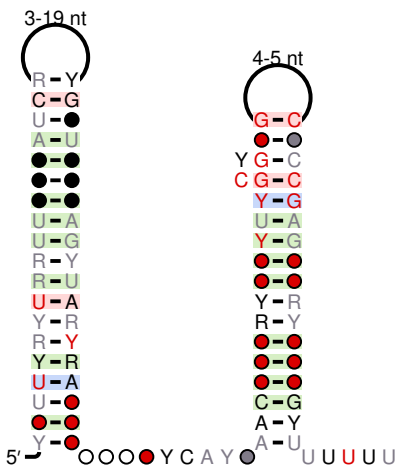


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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

23S-methyl.cons

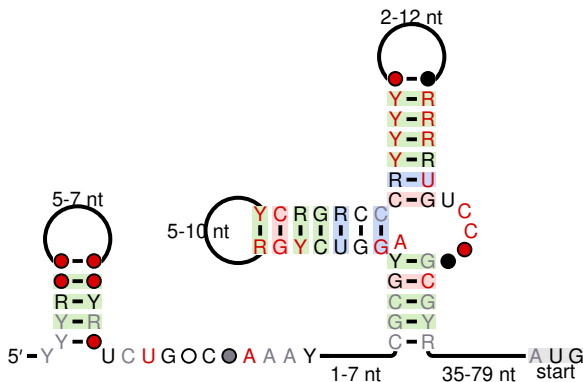


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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

ATPC.cons

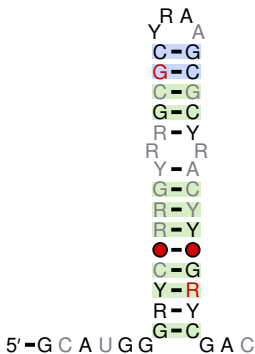


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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

MAEB.cons

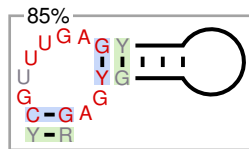


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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

purD-MODSTEM.cons
subfam_weight=0.85176



purD-MODSTEM2.cons
subfam_weight=0.14824



purD.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`

g150.cons



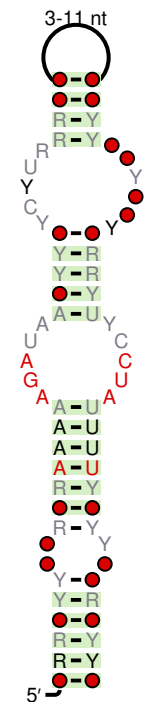
WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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To disable this warning, run r2r with

```
--disable-usage-warning
```

lacto-2.cons

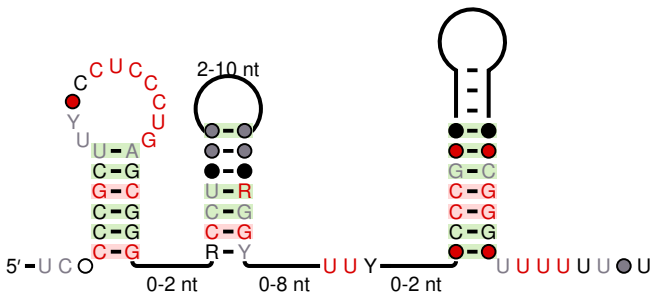


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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

anti-hemB.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

lacto-1.cons

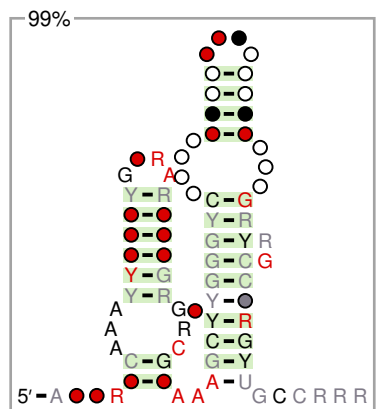


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

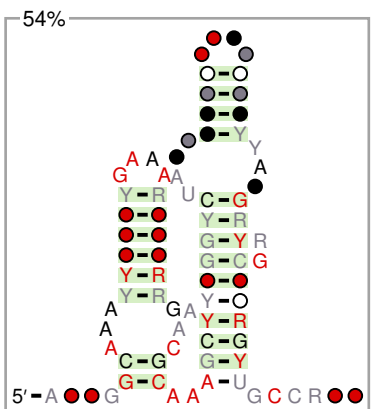
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation 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

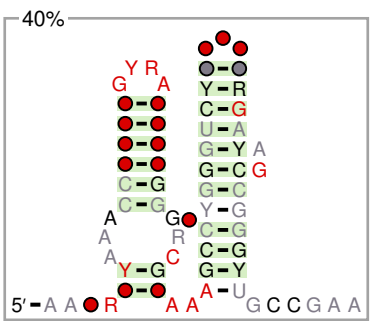
GEMM-BP.cons
subfam_weight=0.990787



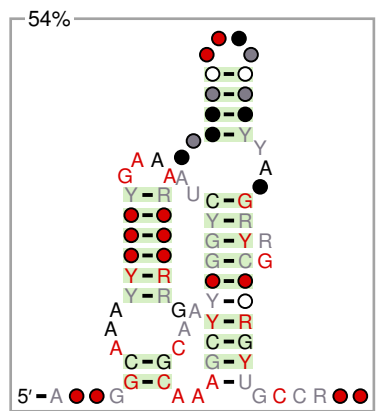
GEMM-GRRA.cons
subfam_weight=0.535756



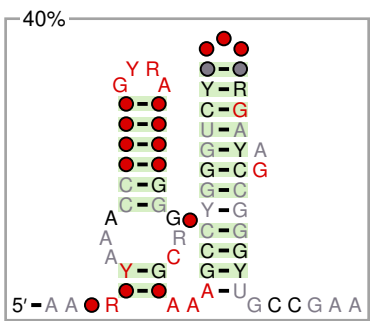
GEMM-GYRA.cons
subfam_weight=0.403389



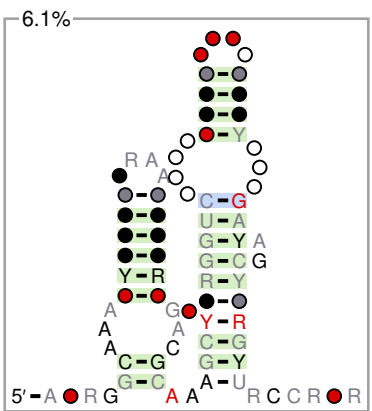
GEMM-RXGRRA.cons
subfam_weight=0.542566



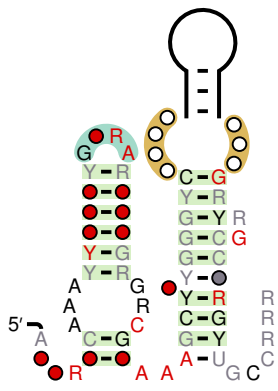
GEMM-RXGYRA.cons
subfam_weight=0.403389



GEMM-other.cons
subfam_weight=0.0608548



GEMM.cons



GEMM.cons skeleton-with-bp

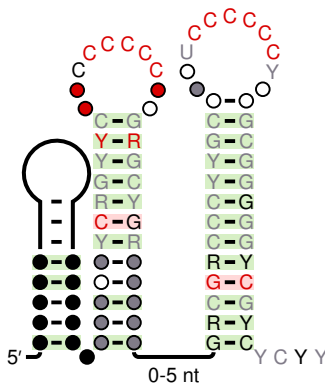


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To disable this warning, run r2r with
 --disable-usage-warning

6C.cons

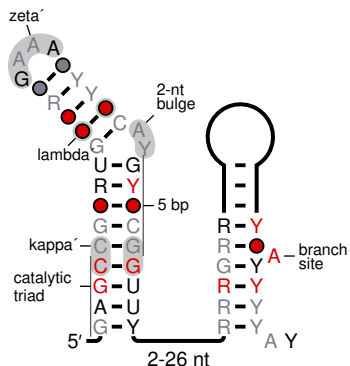


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To disable this warning, run r2r with
 --disable-usage-warning

group-II-DV-DVI.cons

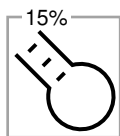


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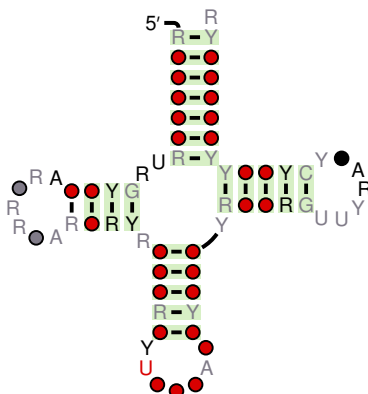
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation 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."

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

tRNA-var.cons
 subfam_weight=0.154412



tRNA.cons



tRNA.cons skeleton-with-bp



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

U1.cons

