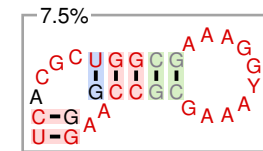




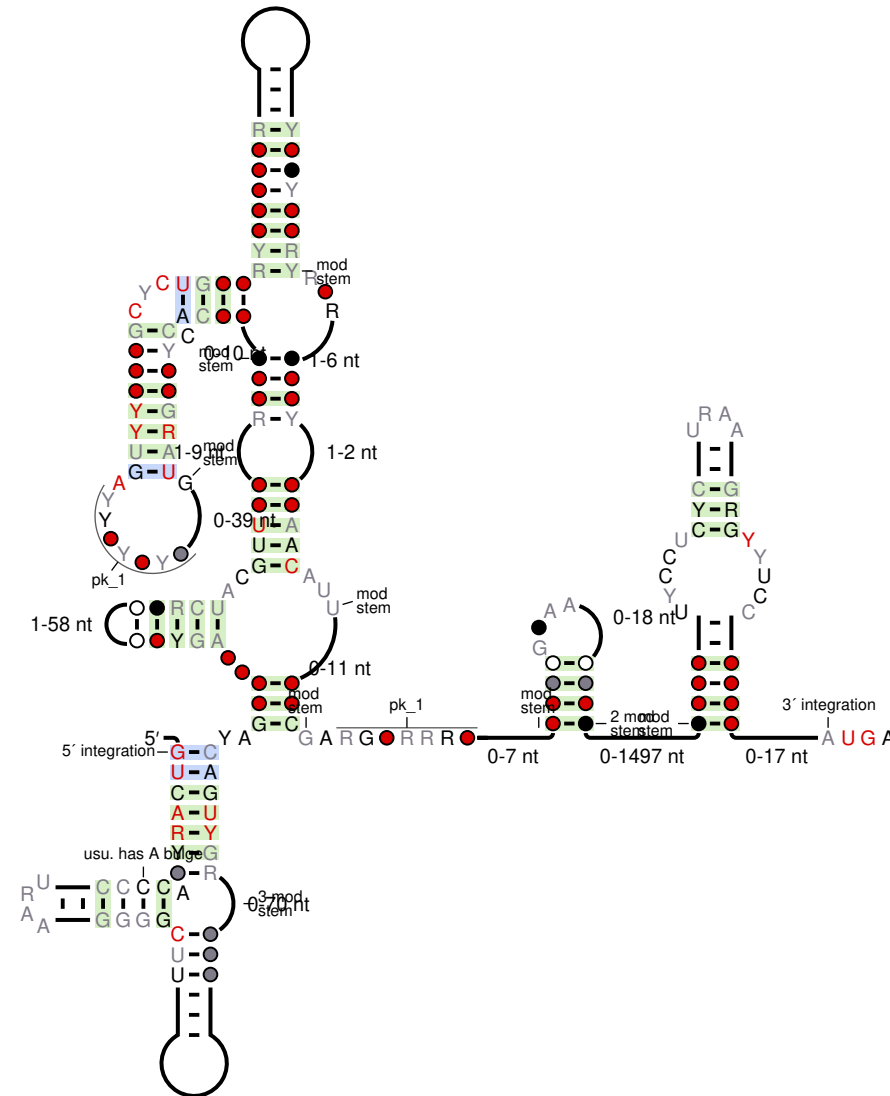
WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

### HEARO-RYGCAA.cons

subfam\_weight=0.0745961

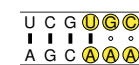


### HEARO.cons

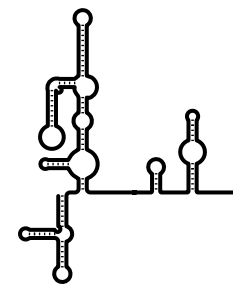


### HEARO.cons NZ\_ABYK01000021.1/61949-61536 pknot=1

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.

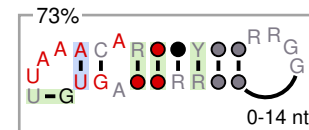


### HEARO.cons skeleton-with-bp



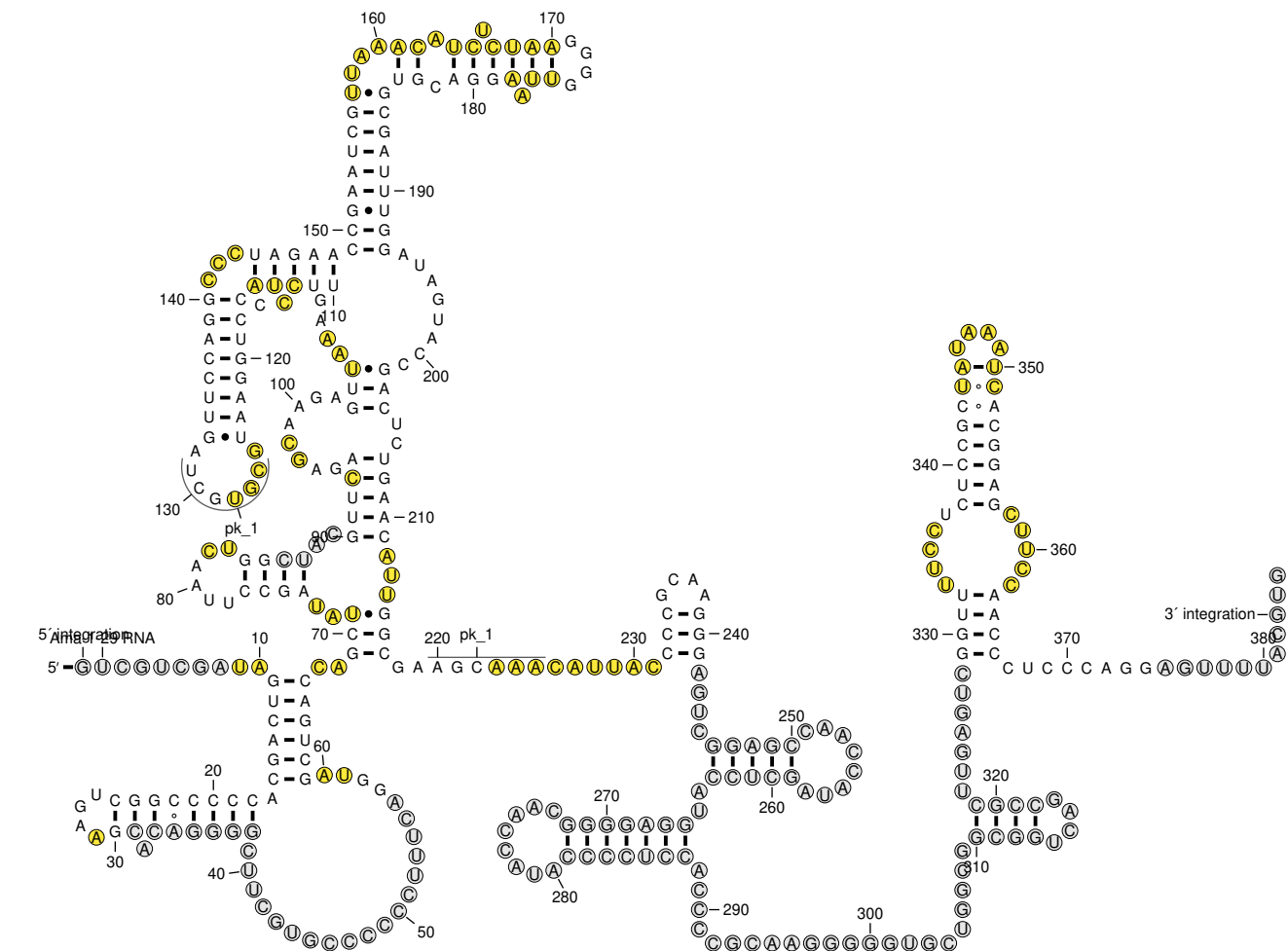
### HEARO-UAA.cons

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







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:

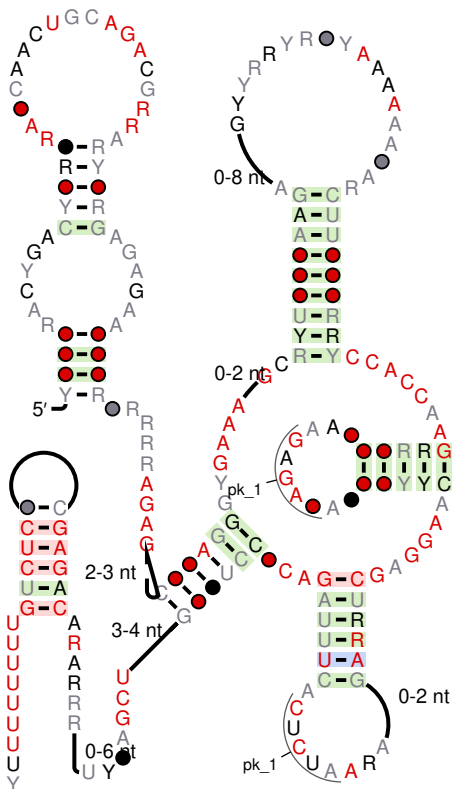
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation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

IMES-1-pknot.cons  
 subfam\_weight=1

G-C  
 A-U  
 G-C  
 A-U  
 ●-A

IMES-1.cons

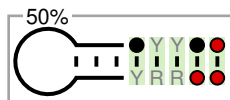


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

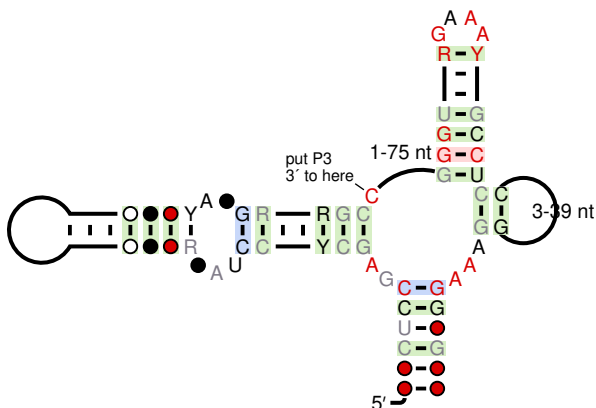
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation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

Moco-withP3.cons  
 subfam\_weight=0.496344



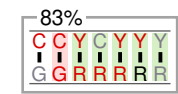
Moco.cons



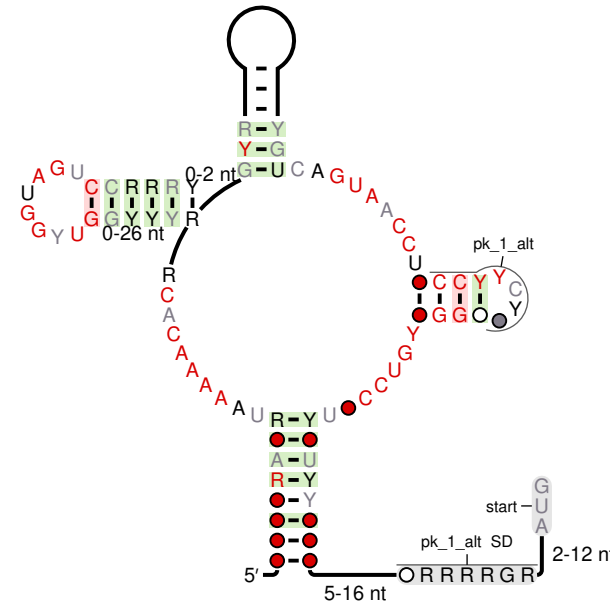


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

yjdF-AUG.cons  
subfam\_weight=0.832593

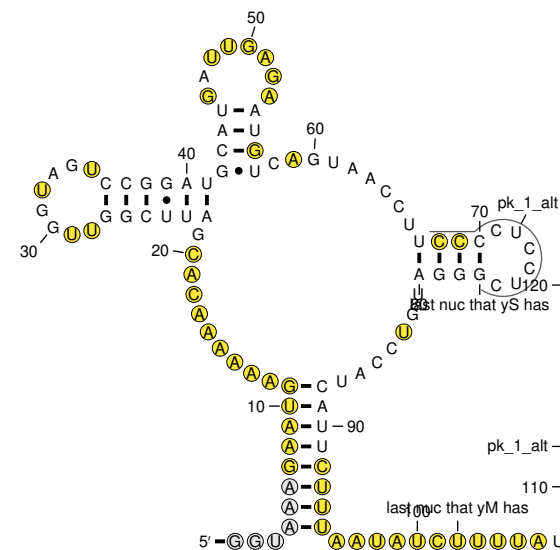


yjdF.cons

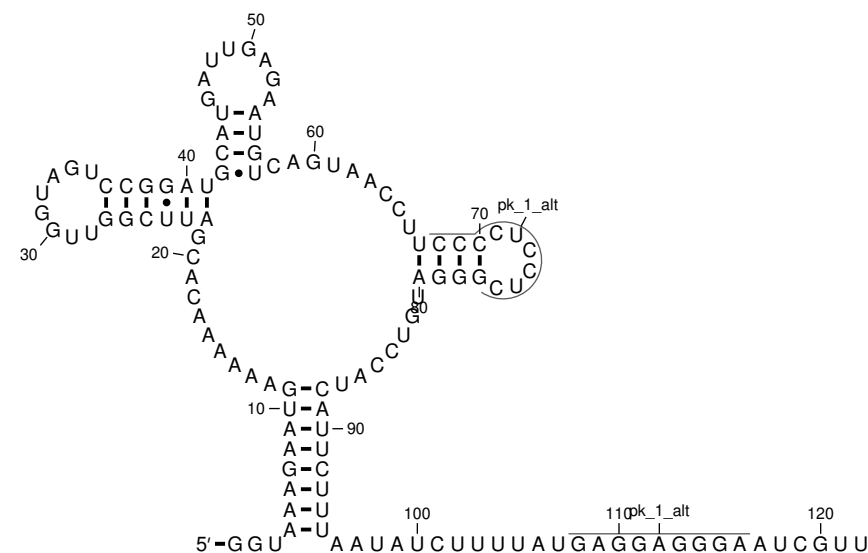


yjdF.cons NC\_000964.2/1274965-1275471:L

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:S

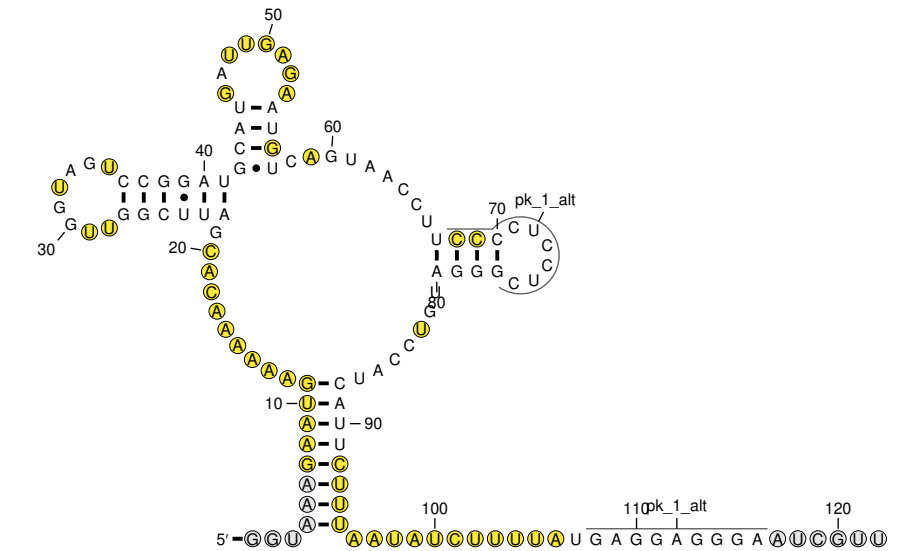


yjdF-altstem.cons  
subfam\_weight=1



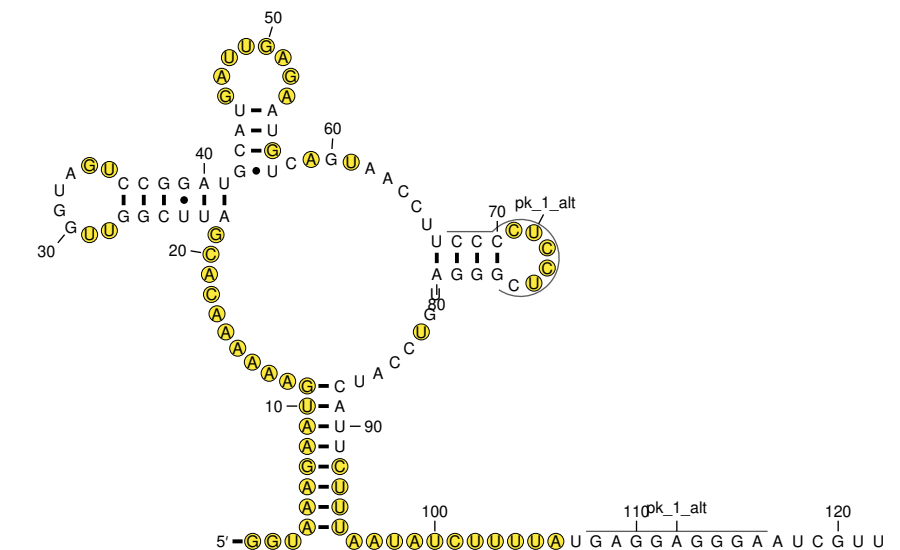
yjdF.cons NC\_000964.2/1274965-1275471

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.



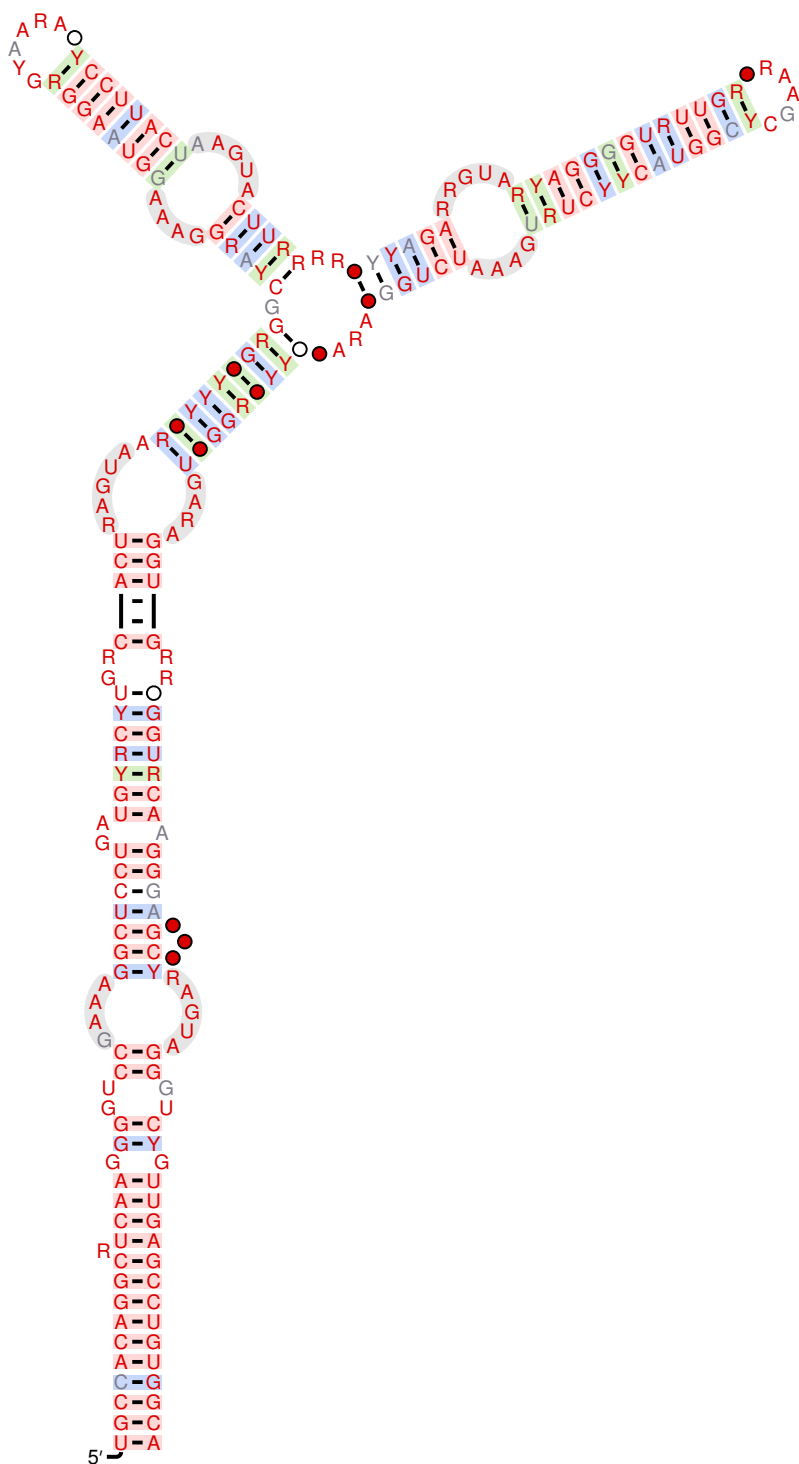
yjdF.cons NC\_000964.2/1274965-1275471:M

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.



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

Dictyoglomi-1.cons

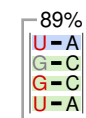




"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation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

manA-pknot1.cons  
subfam weight=0.891987

subfam weight=0.891987



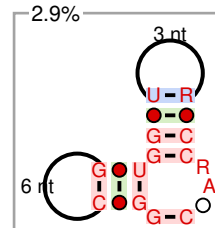
manA-pknot2.cons

subfam weight=1



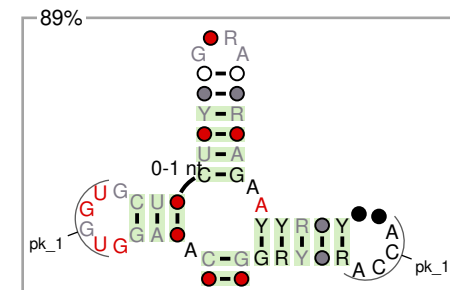
manA-var1.cons

subfam\_weight=0.028518



manA-var2.cons

subfam\_weight=0.891987

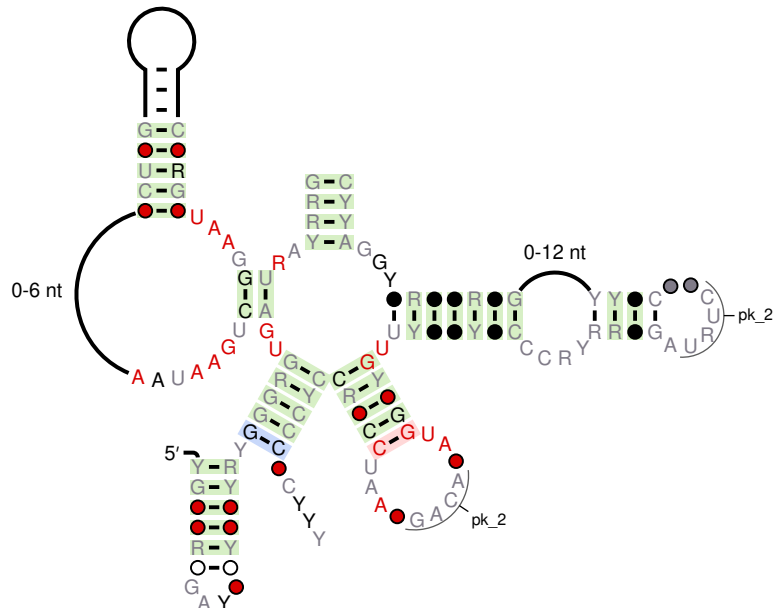


manA-var3.cons

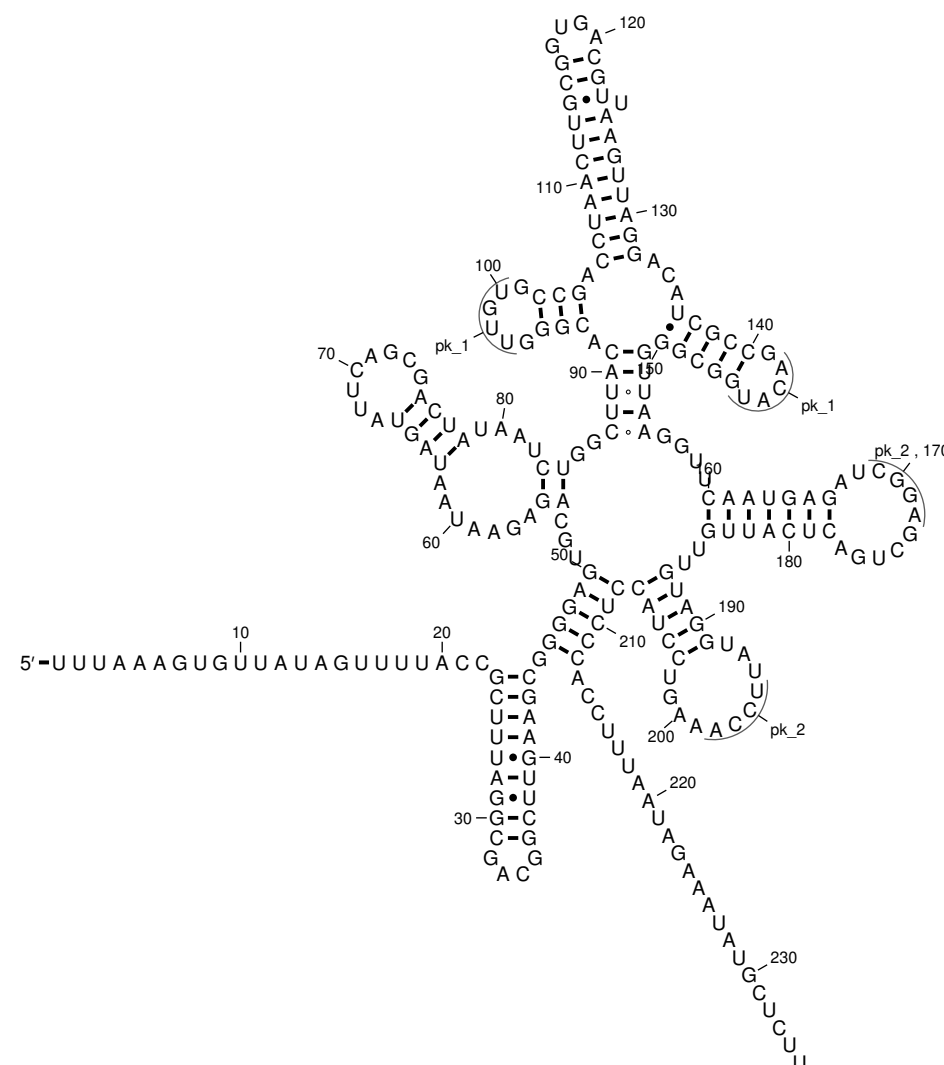
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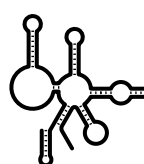
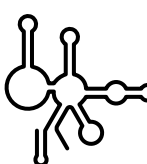
manA.cons



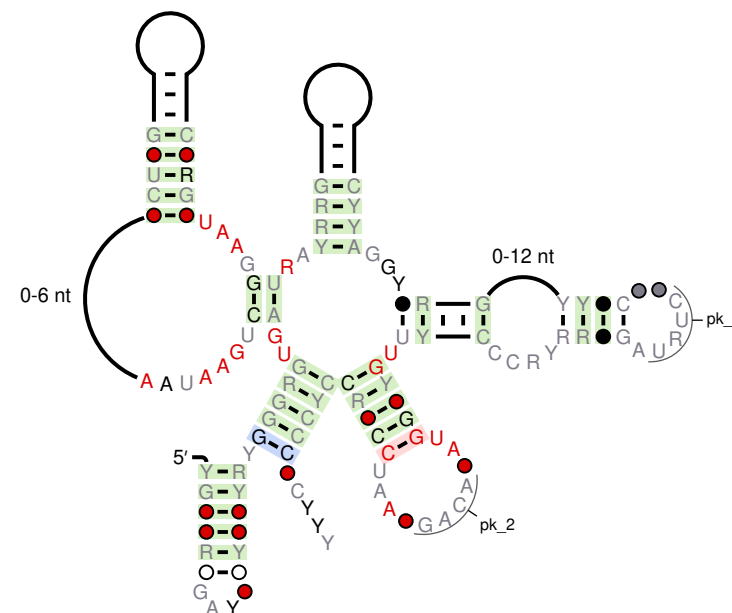
manA.cons NZ AAOJ01000001.1/468755-469351



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



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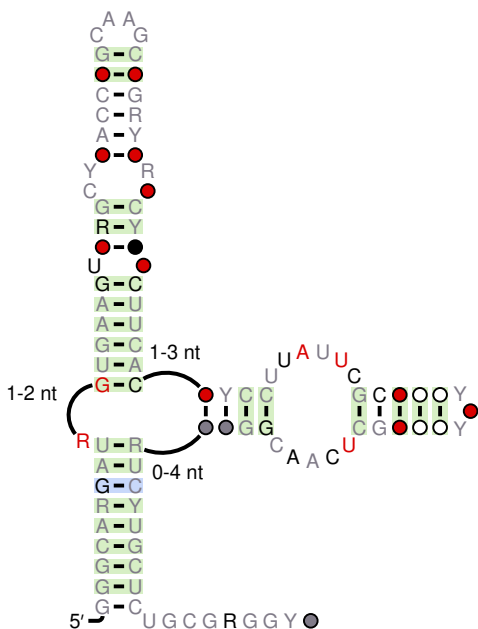


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

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

traJ-II.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:

"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."

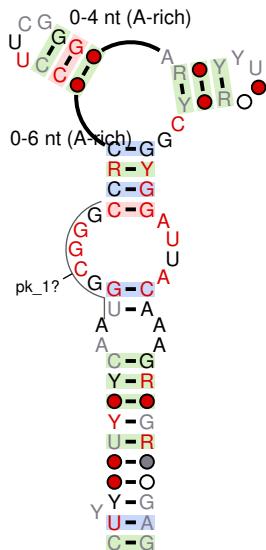
To disable this warning, run r2r with --disable-usage-warning

## Bacteroidales-1-pknot.cons

subfam\_weight=1



## Bacteroidales-1.cons



5'-AGCCG<sup>Y</sup>AYY●RYURGAUYGGGARACUCAUCA—CGGAGAOAA<sup>G</sup>●CUCAA<sup>A</sup>AUCYUGUY<sup>Y</sup>●CGGAGUUU●RYCRYAUC●●YRGUGCGGCU

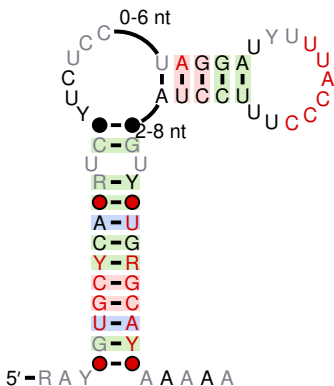
11-17 nt

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:

"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

potC.cons

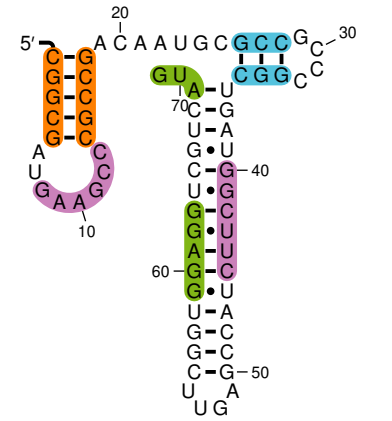




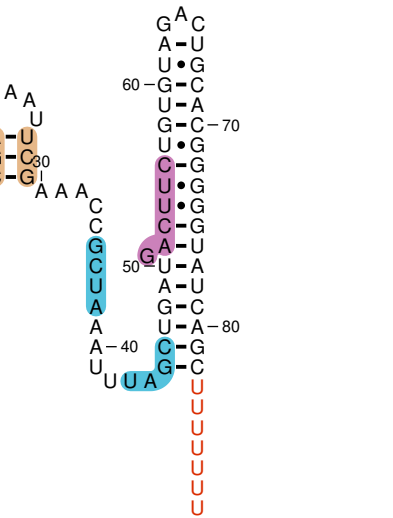


WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg and Breaker, 2011 wrote: "This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation can result from an incorrect alignment of sequences, or from alignments of sequences that do not function as structured RNAs. Unfortunately, there is no accepted method to assign confidence that entirely eliminates the need to analyze the full alignment." To disable this warning, run r2r with --disable-usage-warning

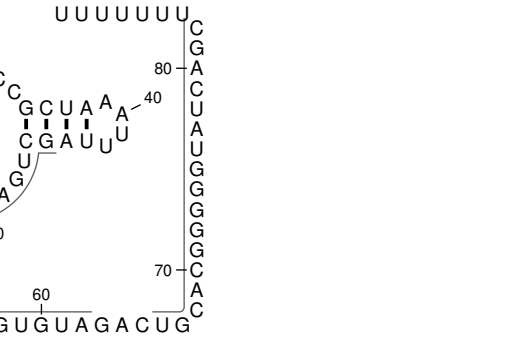
crcB NC\_008578.1/805741-806202 alt-struct=2



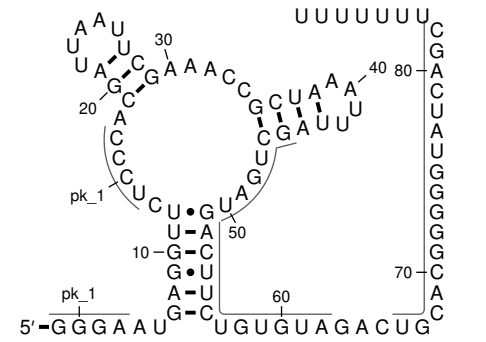
crcB NZ\_ABYJ01000311.1/4968-4495 alt-struct=2



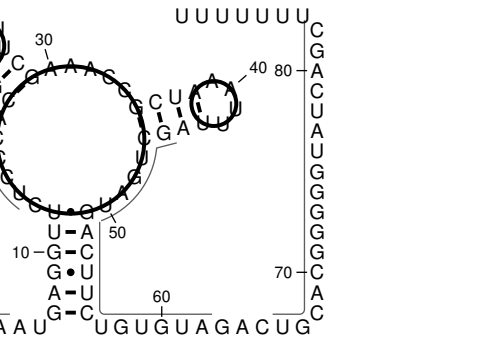
crcB NZ\_ABYJ01000311.1/4968-4495 no-shading=1



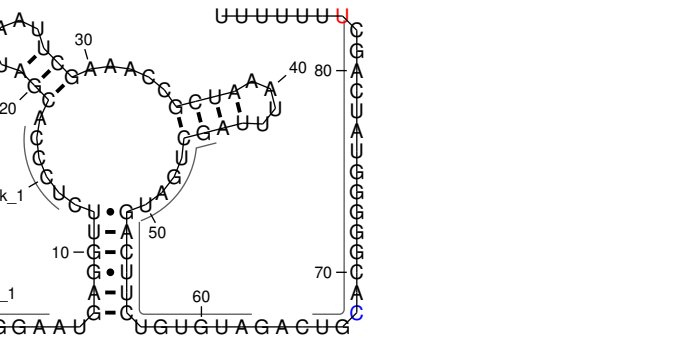
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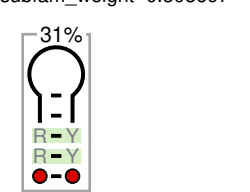
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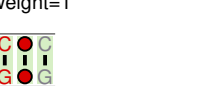
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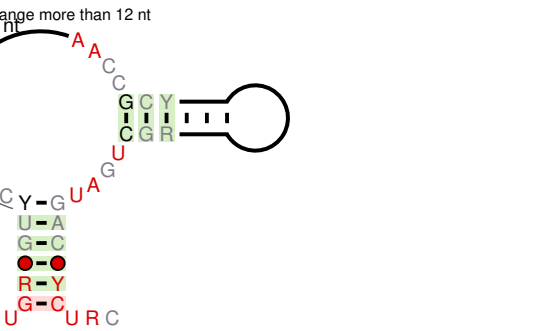
crcB-P2.cons



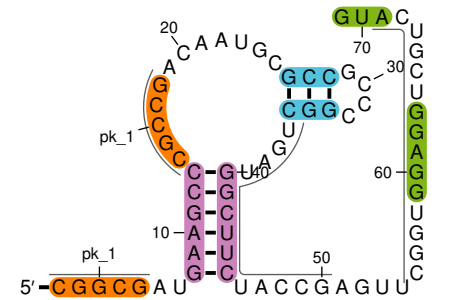
crcB-pknot1.cons



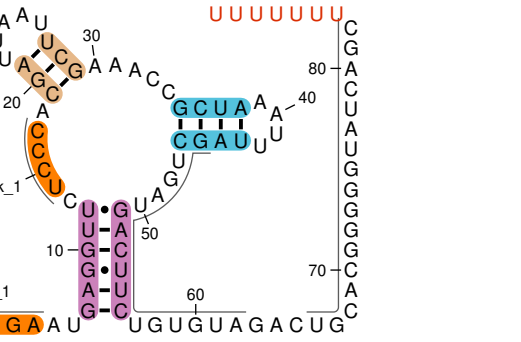
crcB.cons



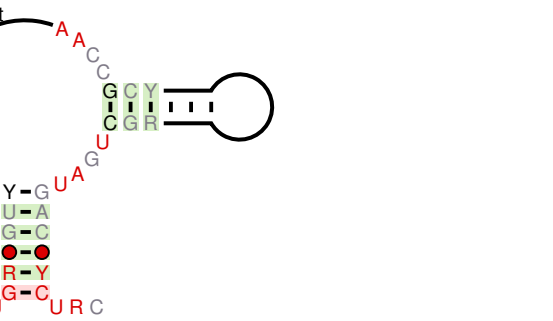
crcB.cons NC\_008578.1/805741-806202



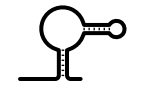
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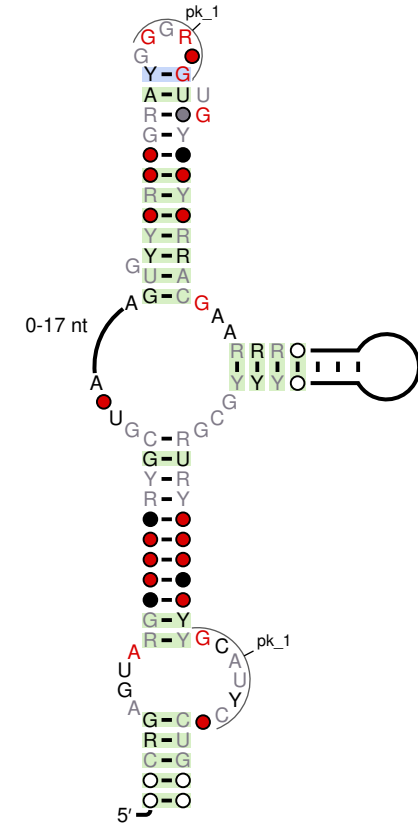
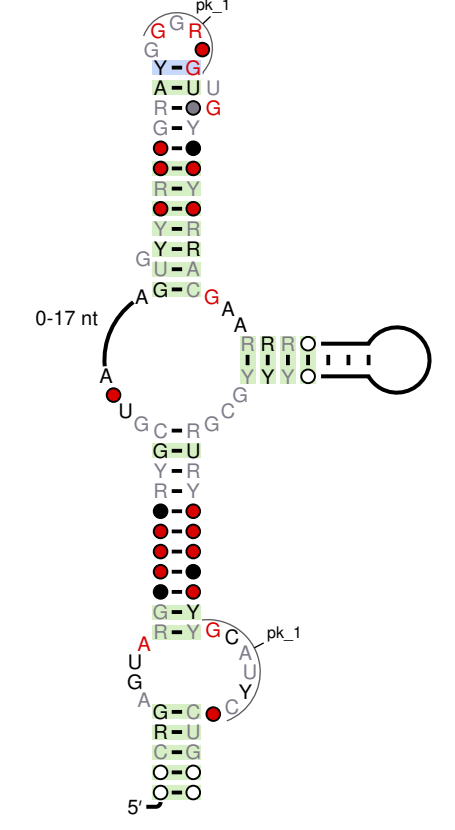
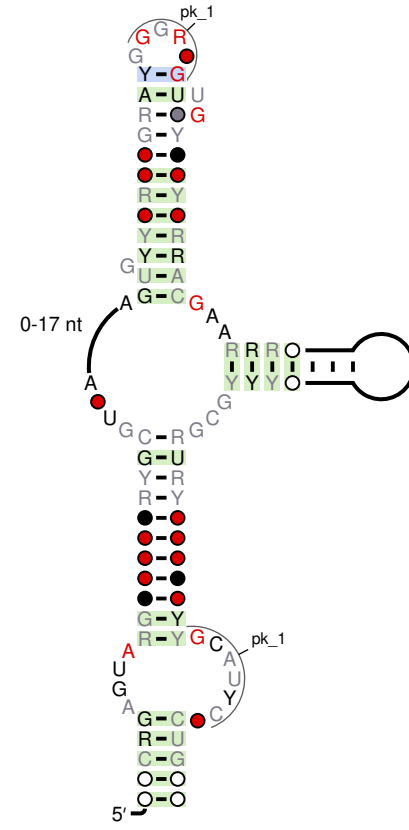
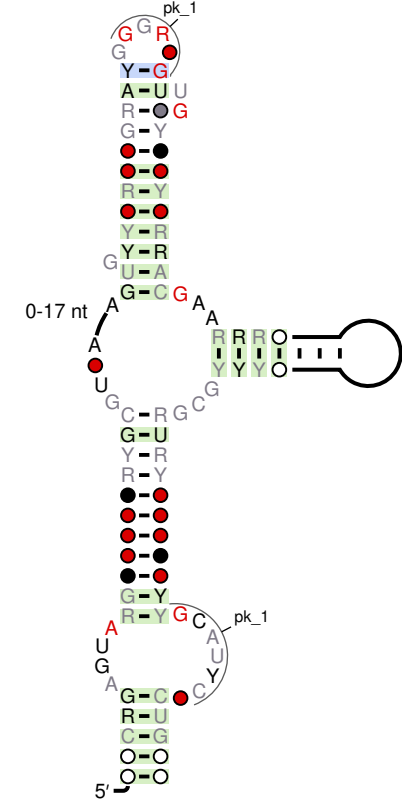
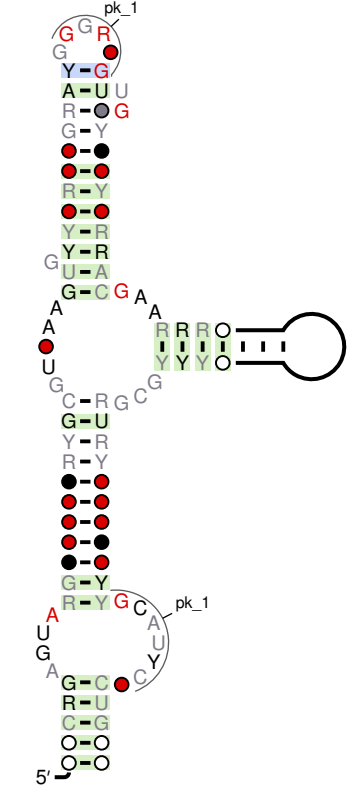
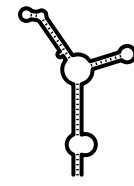
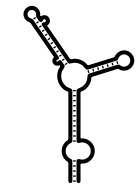
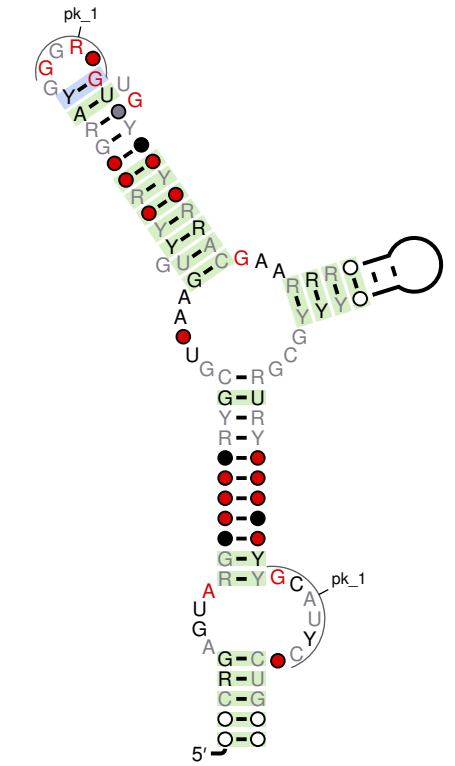
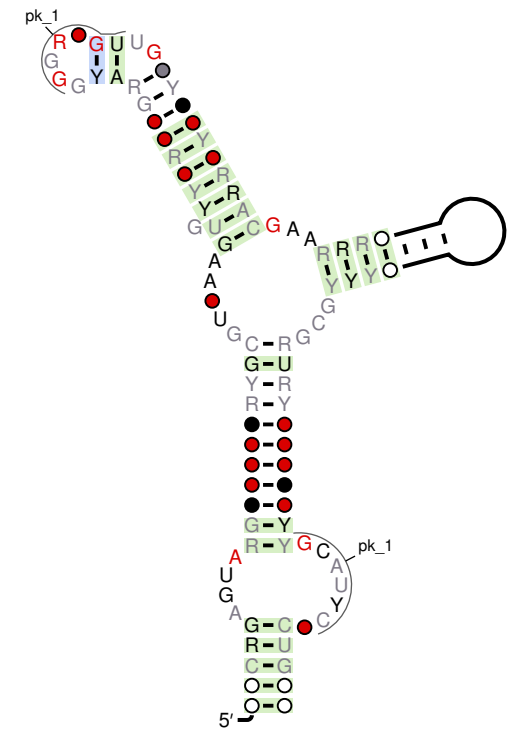
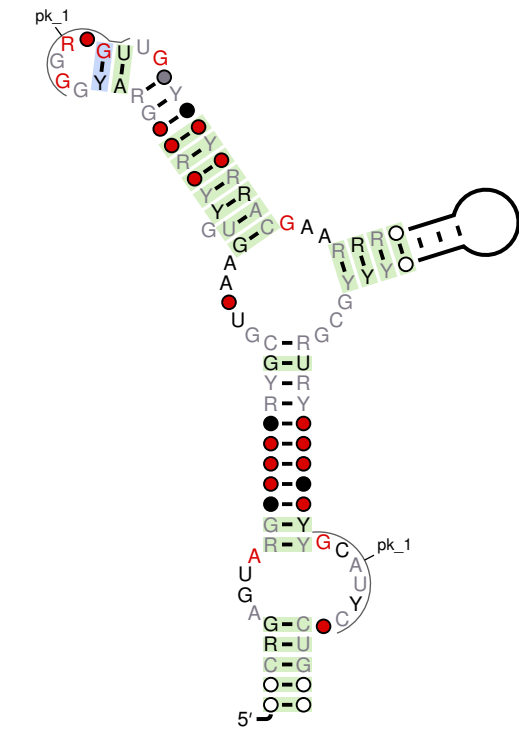


crcB.cons R2R-paper=1



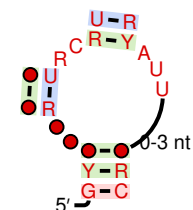
crcB.cons skeleton-with-bp



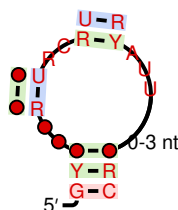


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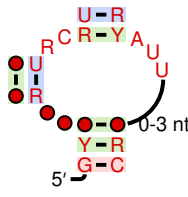
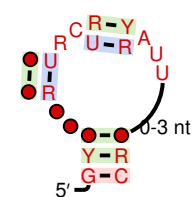
demo-multistem.cons



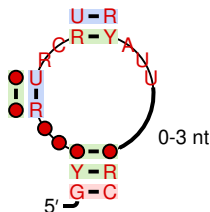
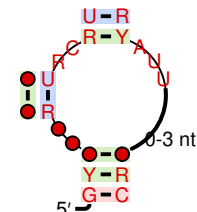
demo-multistem.cons circle=1



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



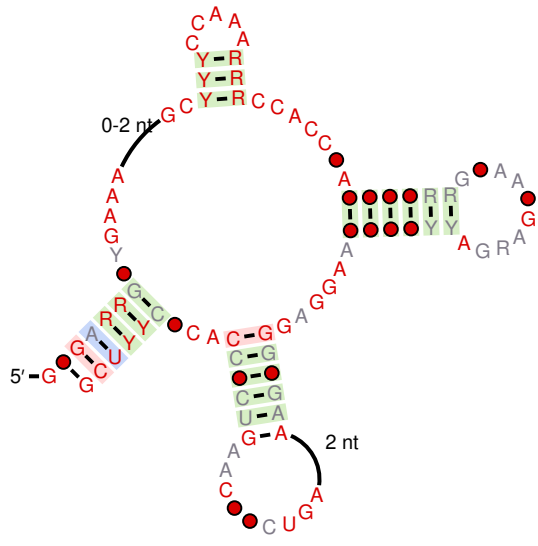
demo-multistem.cons solver1=1 demo-multistem.cons solver2=1



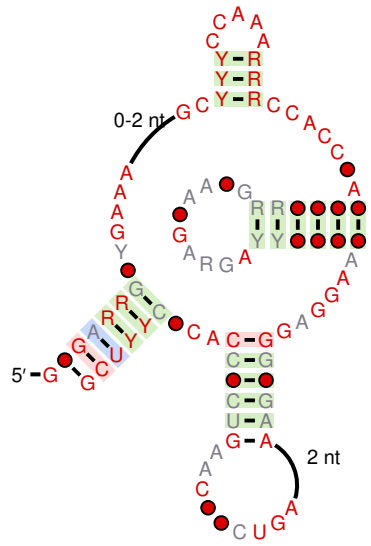
WARNING: R2R is not intended to evaluate evidence for covariation or RNA structure where this is in question. It is not appropriate to use R2R's covariation markings to declare that there is evidence of structural conservation within an alignment. R2R is a drawing program. As the original paper, Weinberg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

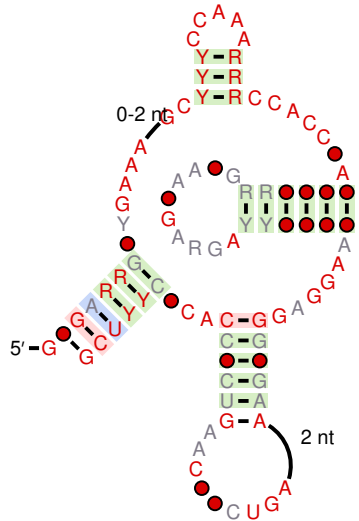
demo-multistem-IMES-1.cons



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

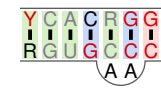


demo-multistem-IMES-1.cons solver=2

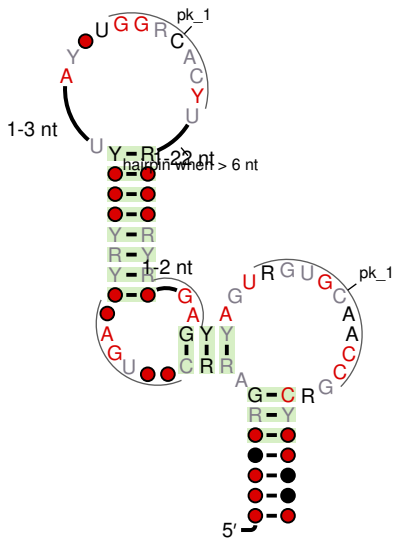


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To disable this warning, run r2r with --disable-usage-warning

c-di-GMP-II-pknot.cons  
subfam\_weight=1

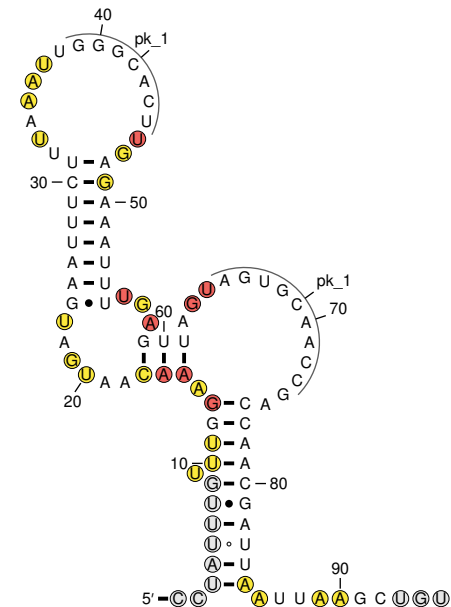


c-di-GMP-II.cons



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.

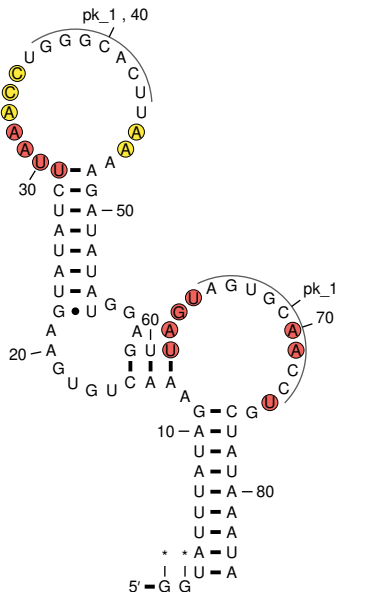


c-di-GMP-II.cons skeleton-with-bp



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.



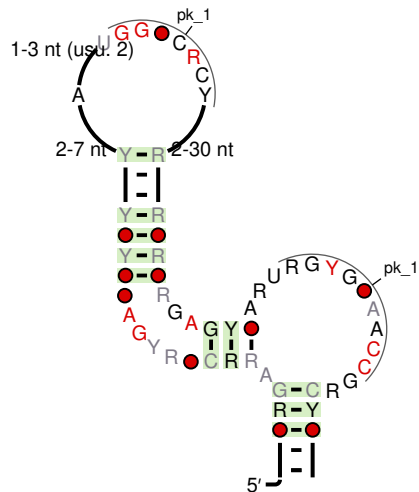


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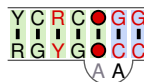
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To disable this warning, run r2r with --disable-usage-warning

c-di-GMP-II-update.cons



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



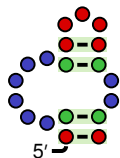
c-di-GMP-II-update.cons skeleton-with-bp



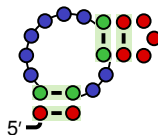
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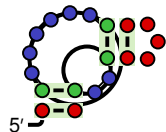
solver-formulation1-1.cons



solver-formulation1-1.cons solver=1



solver-formulation1-1.cons solver=2

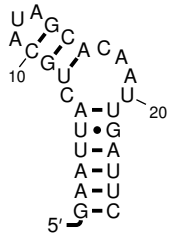


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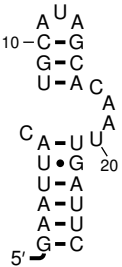
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation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

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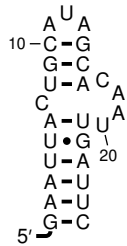
uneven-internal-loop seq layout=anyangle



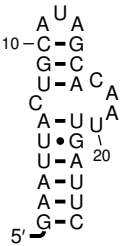
uneven-internal-loop seq layout=broken-left



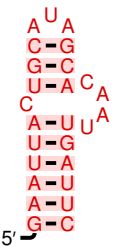
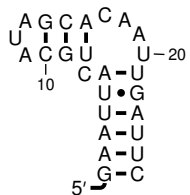
uneven-internal-loop seq layout=default



uneven-internal-loop seq layout=left-turn



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

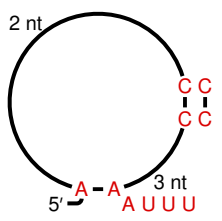


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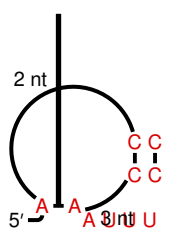
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation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

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

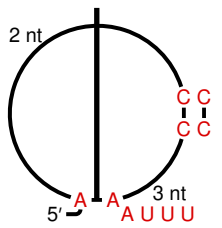
TestAngularAlignment.cons



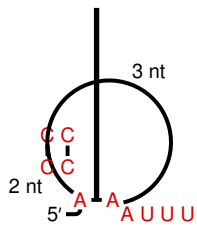
TestAngularAlignment.cons alignangle=-32



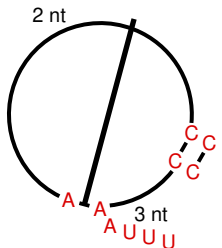
TestAngularAlignment.cons alignangle=-45



TestAngularAlignment.cons alignangle=45



TestAngularAlignment.cons rots0=-15







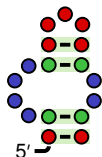
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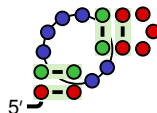
Unfortunately, there is no accepted method to assign confidence that entirely eliminates the need to analyze the full alignment."

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

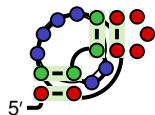
solver-formulation2-1.cons



solver-formulation2-1.cons solver=1



solver-formulation2-1.cons solver=2

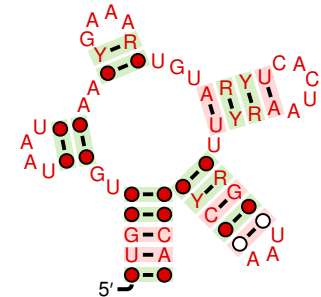


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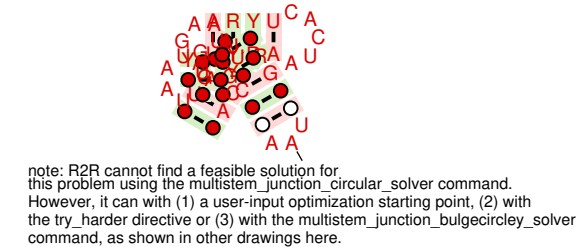
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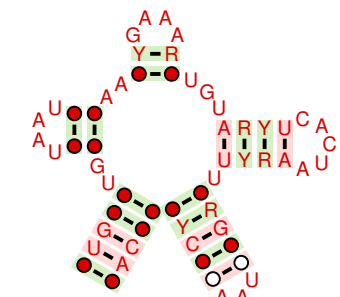
demo-multistem-manA.cons



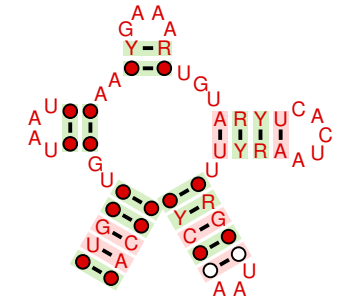
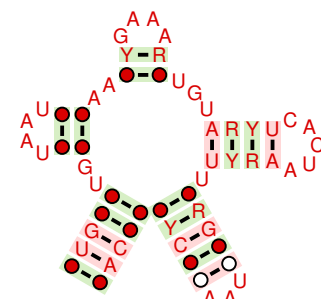
demo-multistem-manA.cons solver=1



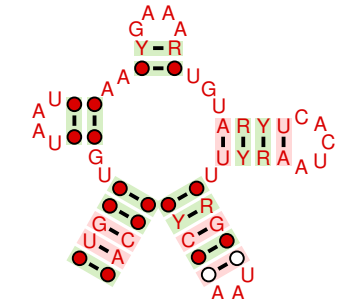
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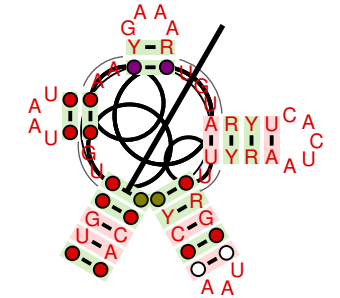
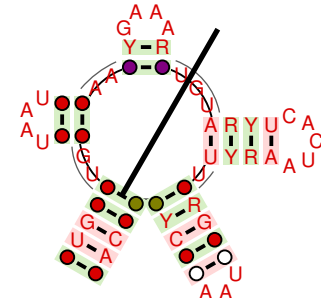
demo-multistem-manA.cons solver=1tryharderdemo-multistem-manA.cons solver=2



demo-multistem-manA.cons solver=3



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

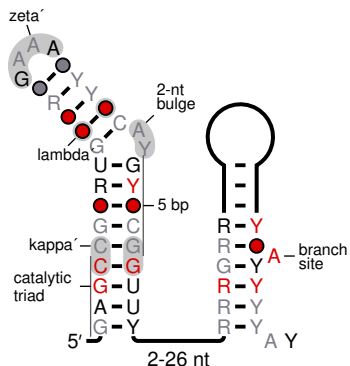


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To disable this warning, run r2r with  
 --disable-usage-warning

group-II-DV-DVI.cons

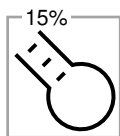


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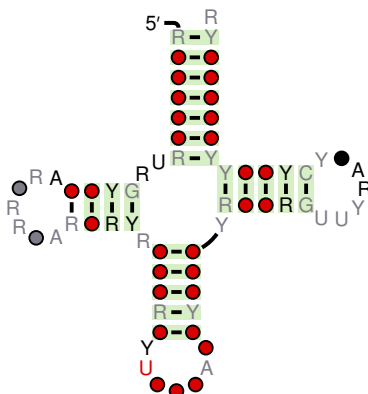
"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation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

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 --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

