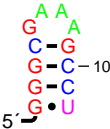


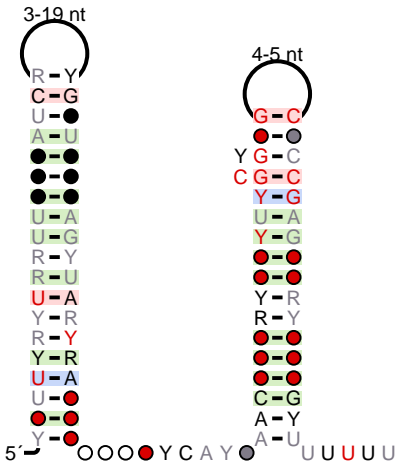
# 1ZIF



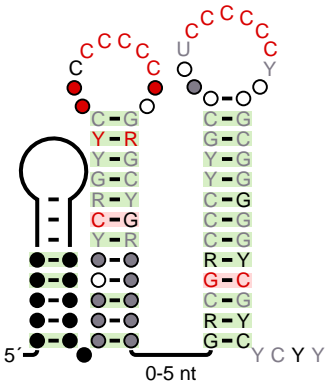
# 1ZIF seq



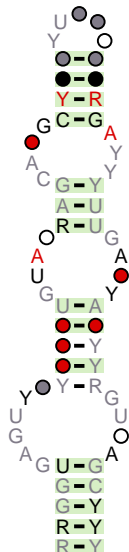
# 23S-methyl



6C

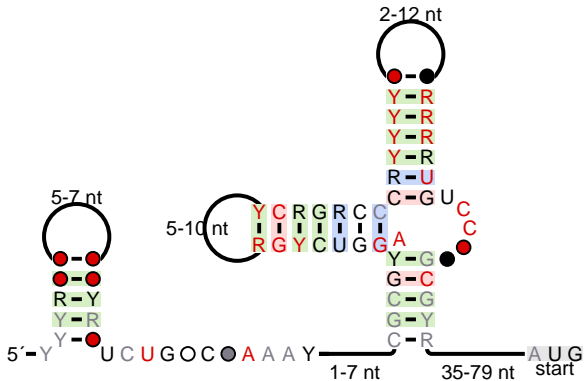


# 6S-flavo

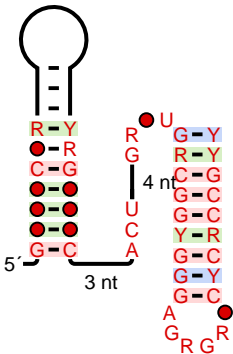


5'-ACUC AAC OO A U U U R R A A A C Y U G U U R G G A G U U U A-3'

# ATPC



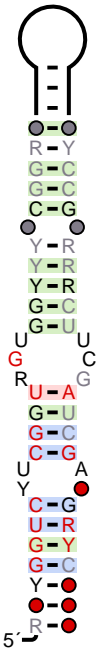
# Acido-1



# Acido-Lenti-1

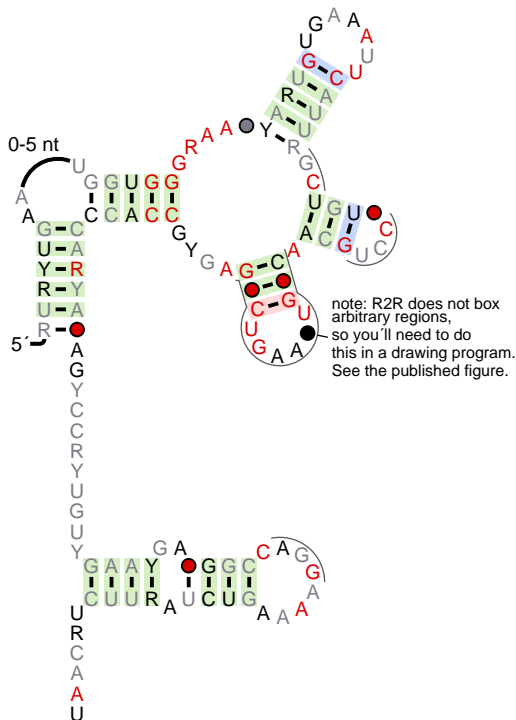


# Actino-pnp



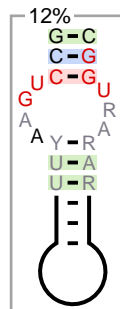


# AdoCbl-variant



# AdoCbl-variant-p7

subfam\_weight=0.115058



# AdoCbl-variant-pknot1

subfam\_weight=1

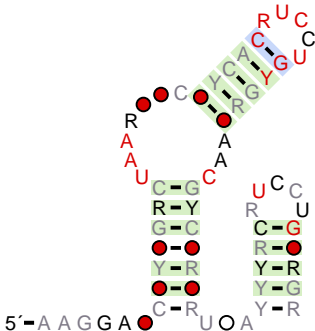


# AdoCbl-variant-pknot2

subfam\_weight=1

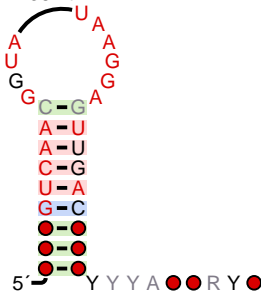


# Bacillaceae-1

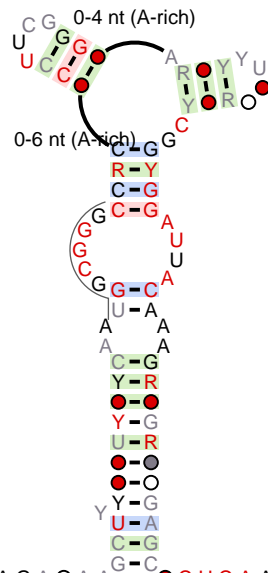


# Bacillus-plasmid

11-38 nt



# Bacteroidales-1



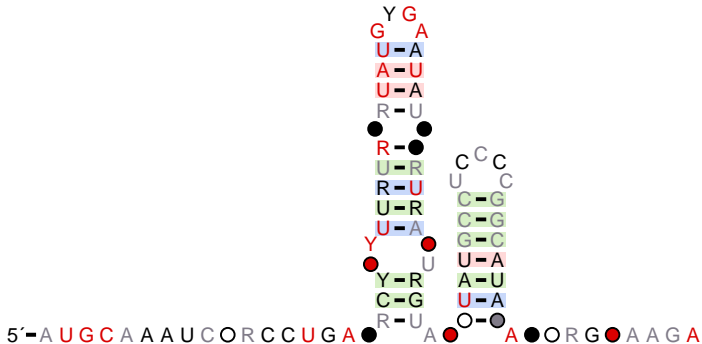
5'-AGCCGYAYY●RYURGAUYGGARACUCAUCA—11-17 nt—CCGAGAOAA●CUCAAAU CYUGUY●Y●CGGAGUUU●RYCRYAUC●●YRGUGC GGCU

## Bacteroidales-1-pknot

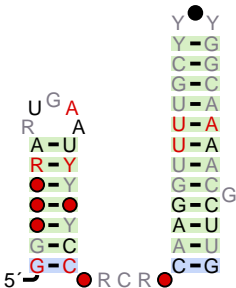
subfam\_weight=1



# Bacteroides-1

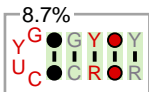
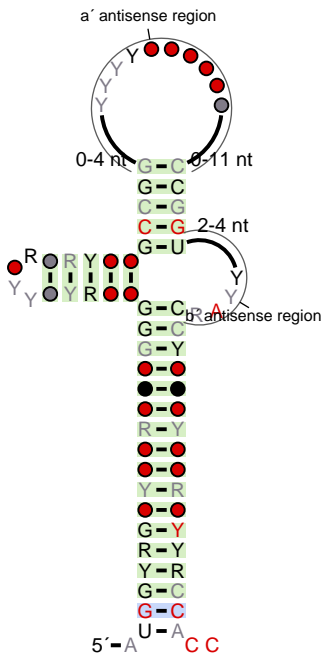


# Bacteroides-2



# C4

C4-CUNG  
subfam\_weight=0.0870331



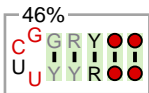
# C4-GNRA

subfam\_weight=0.209657

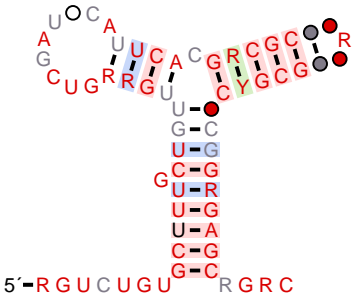


# C4-UNCG

subfam\_weight=0.459042

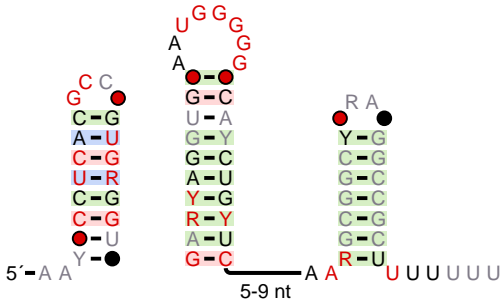


COG2252





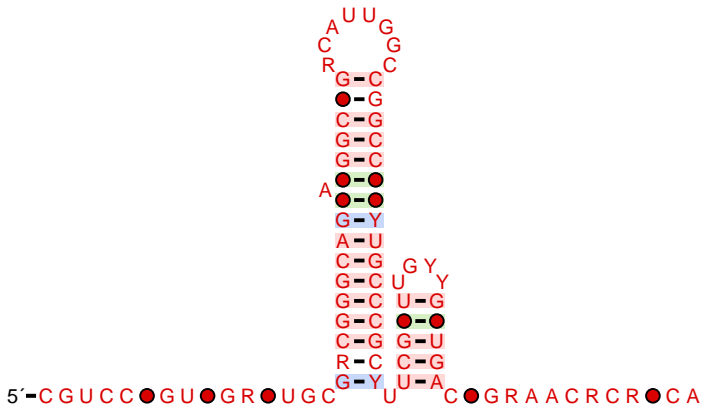
# Chlorobi-1



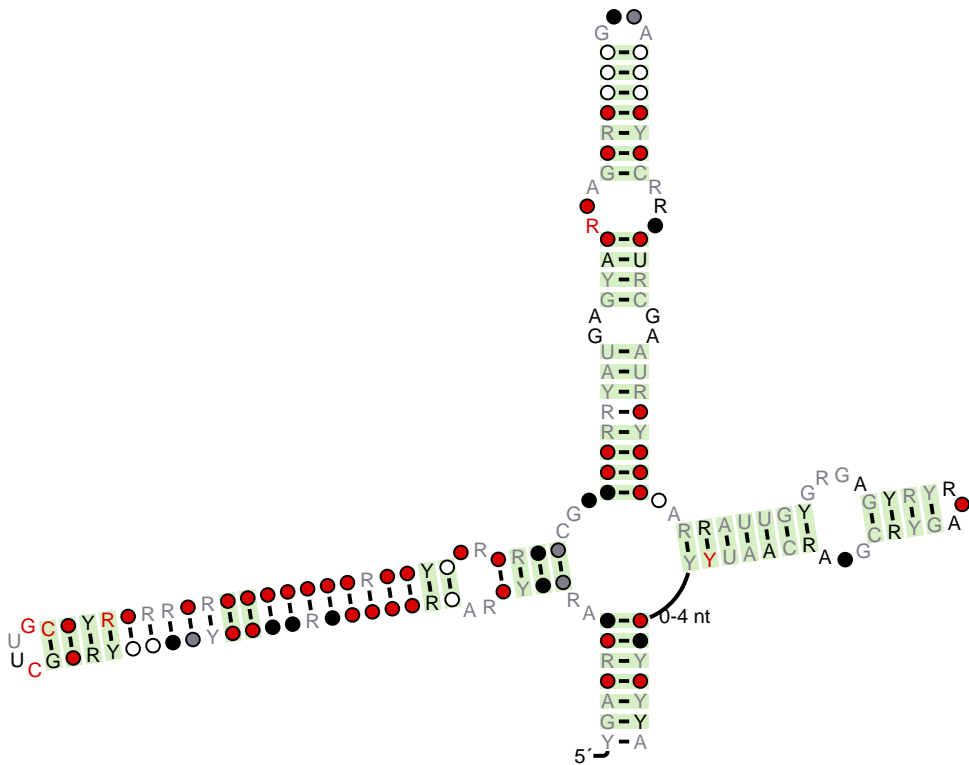
# Chlorobi-RRM



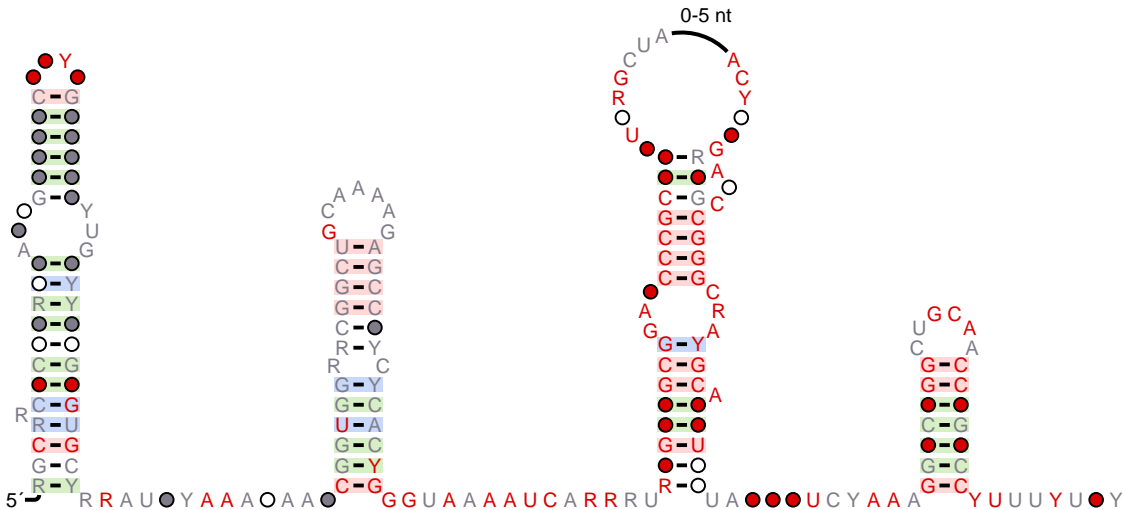
# Chloroflexi-1



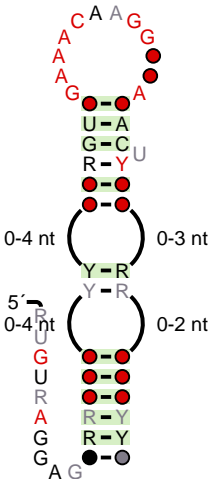
# Clostridiales-1



# Collinsella-1



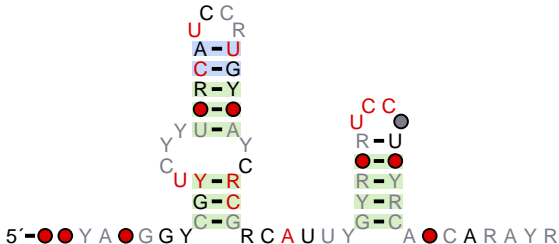
# Cyano-1



# Cyano-2

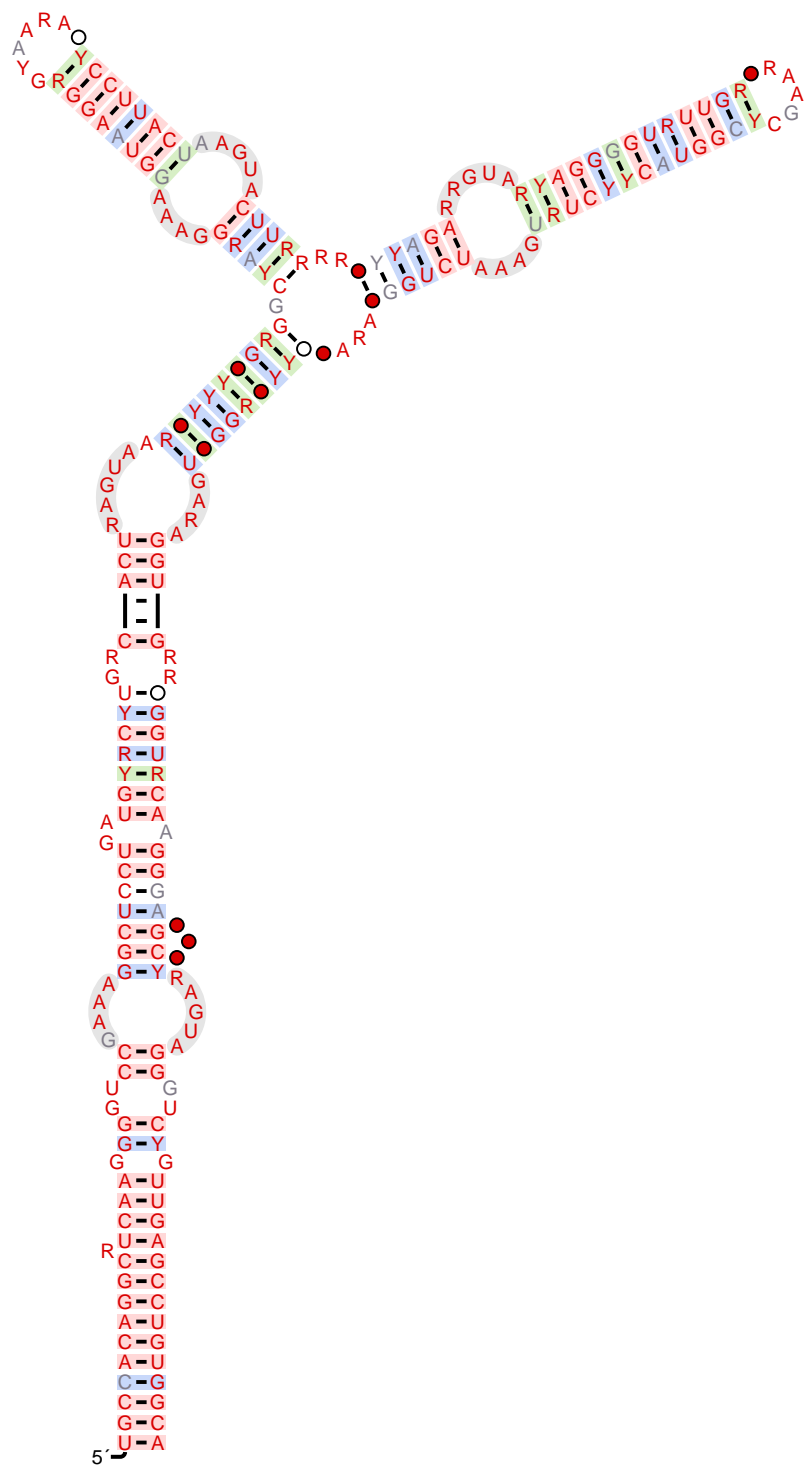


# Desulfotalea-1

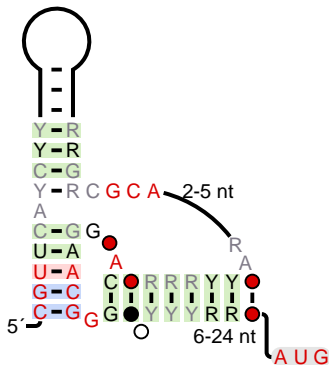




# Dictyoglomi-1



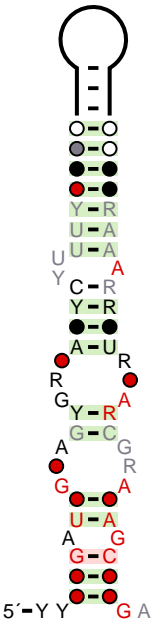
# Downstream-peptide



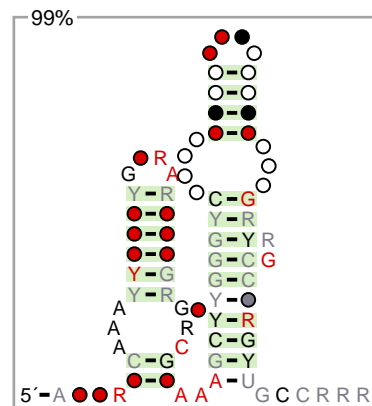
# Downstream-peptide skeleton-with-bp



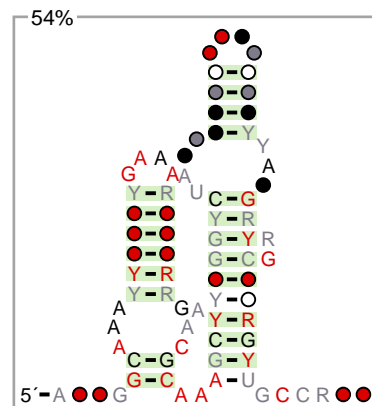
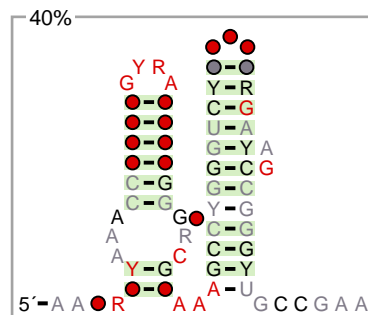
# Flavo-1



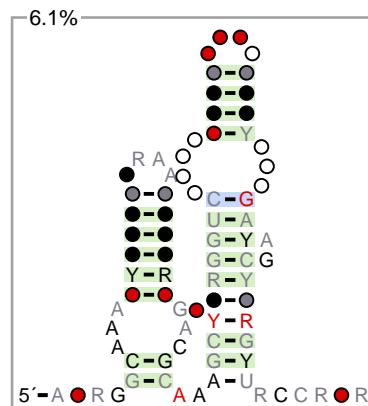
**GEMM-BP**  
subfam\_weight=0.990787

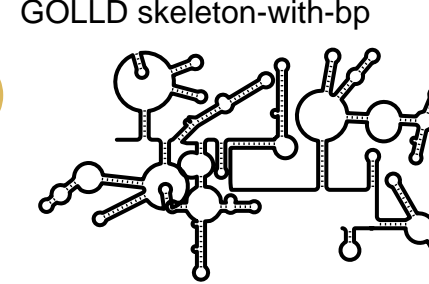
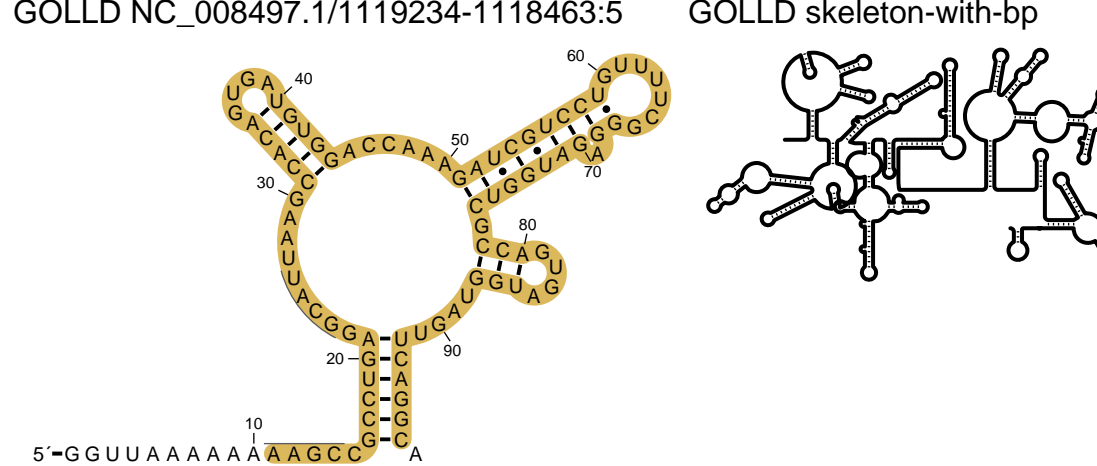
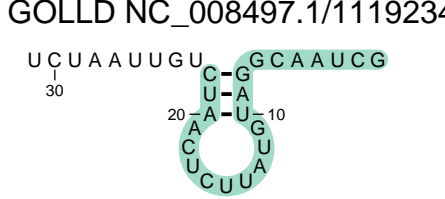
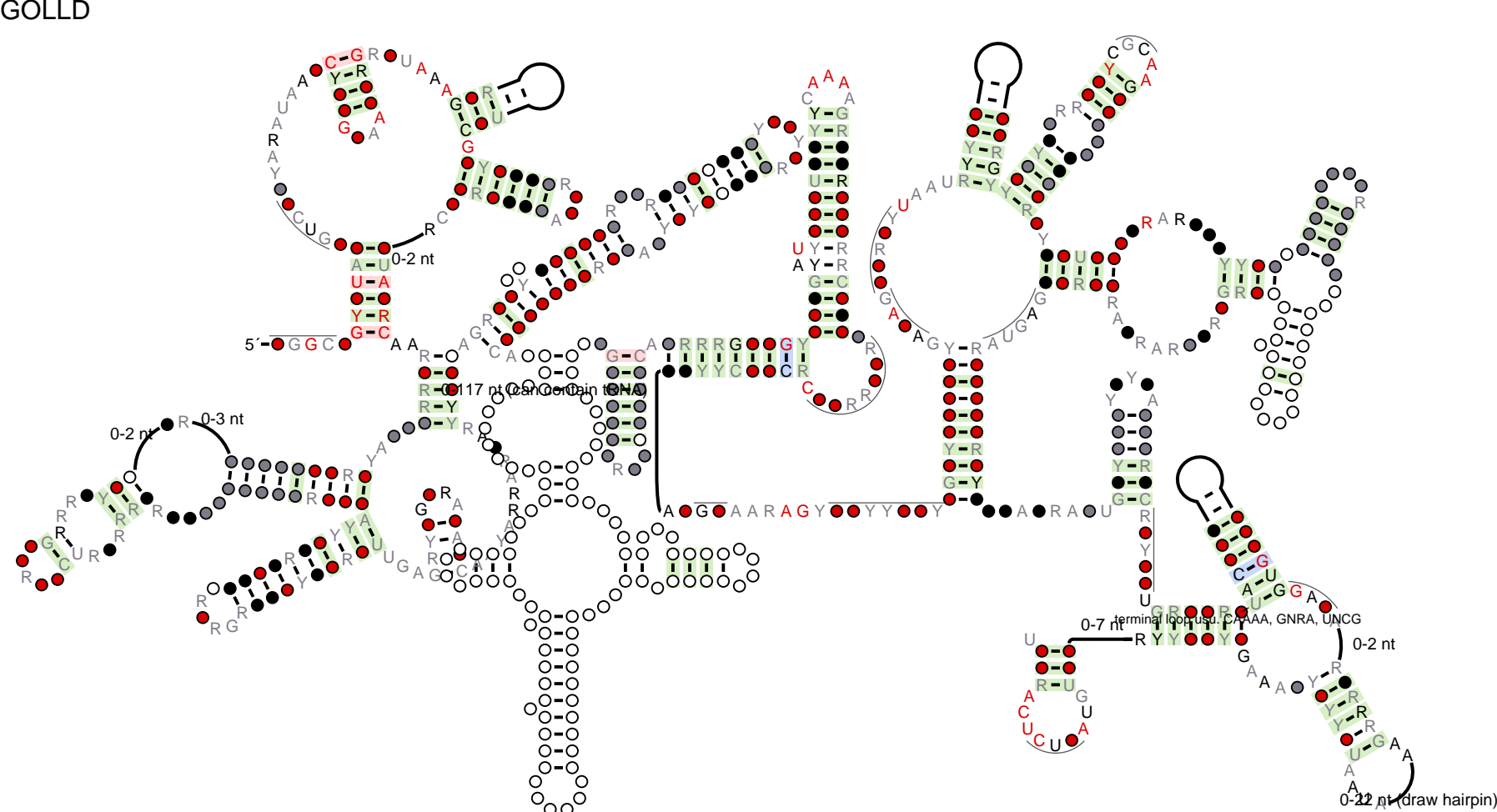


**GEMM-RXGRRA**  
subfam\_weight=0.542566

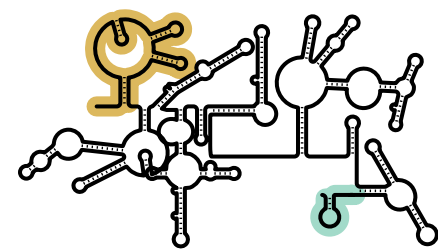


**GEMM-other**  
subfam\_weight=0.0608549

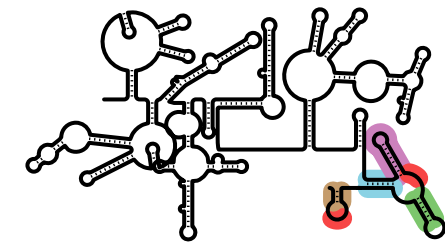




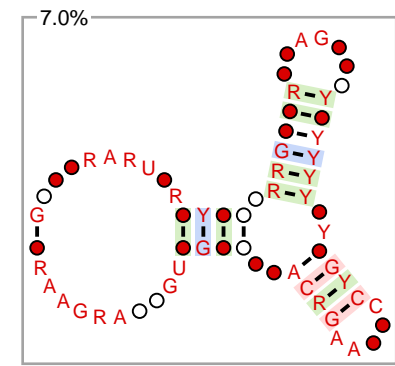
GOLLD skeleton-with-bp RACE-skeleton=1



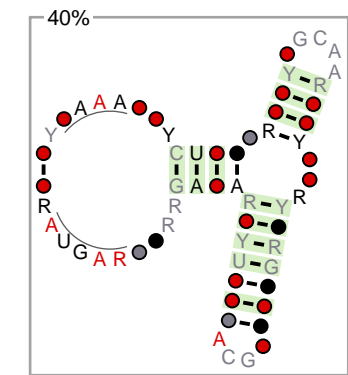
GOLLD skeleton-with-bp align-skeleton=1



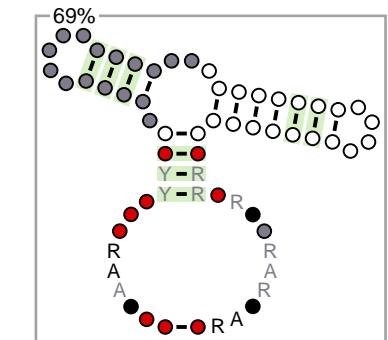
GOLLD-3vp12  
subfam\_weight=0.0697332



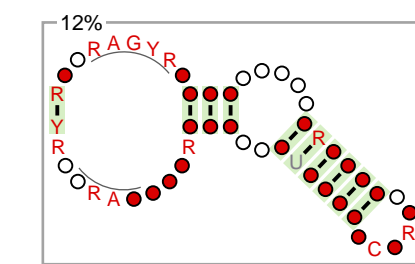
GOLLD-3vp23  
subfam\_weight=0.401602



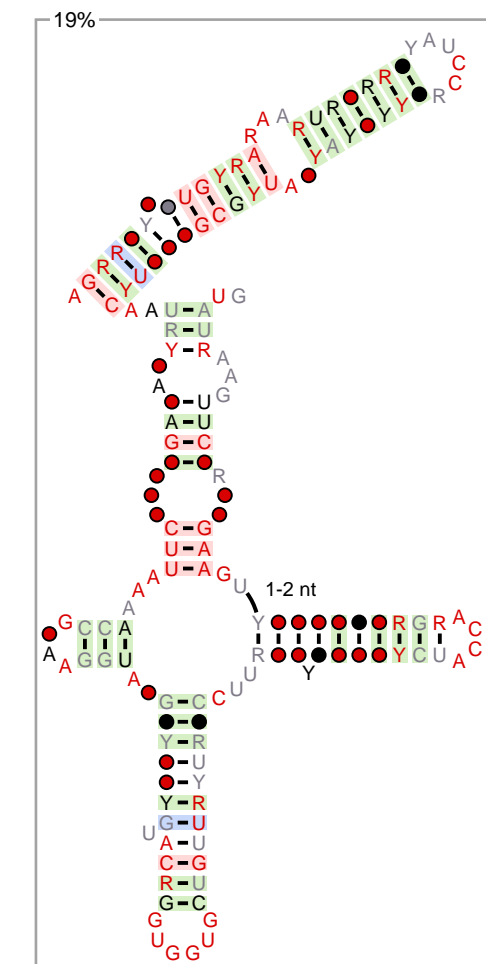
GOLLD-3vpnottruncated  
subfam\_weight=0.889503



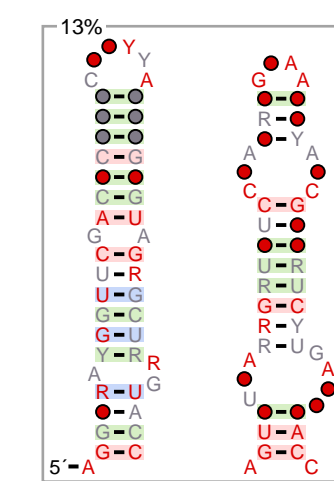
GOLLD-3vp1  
subfam\_weight=0.118998



GOLLD-d3classic  
subfam\_weight=0.192877



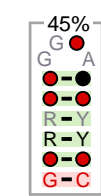
GOLLD-d3justone  
subfam\_weight=0.139952



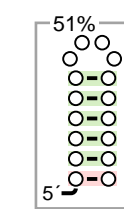
GOLLD-d3valid  
subfam\_weight=0.020029



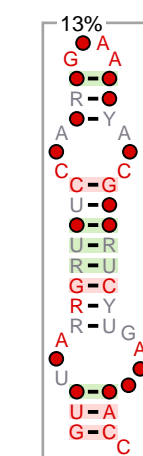
GOLLD-p-1  
subfam\_weight=0.452781



GOLLD-p-1-surround  
subfam\_weight=0.509432



GOLLD-p-2  
subfam\_weight=0.133952



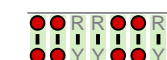
GOLLD-pknot1  
subfam\_weight=1



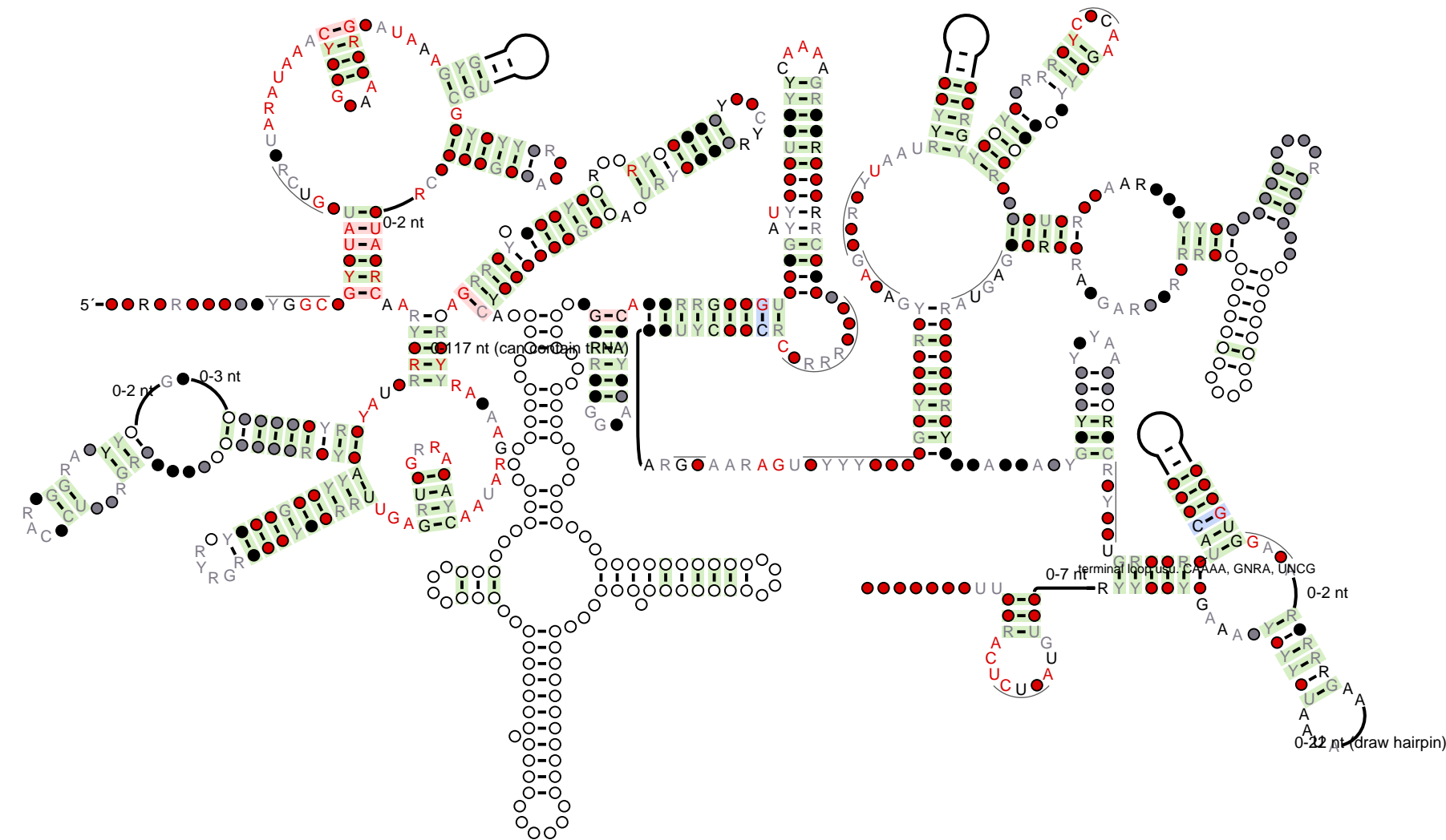
GOLLD-pknot5  
subfam\_weight=1



GOLLD-pknot2  
subfam\_weight=1



GOLLD-skipbadd2



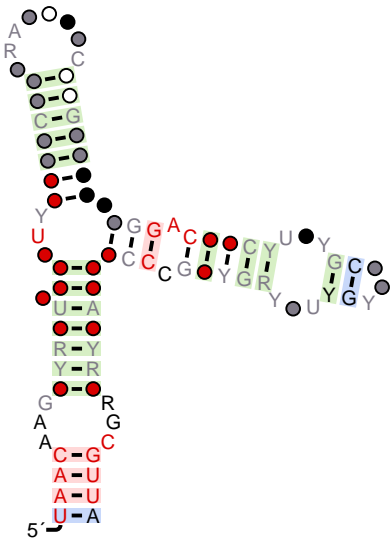
GOLLD-pknot3  
subfam\_weight=1



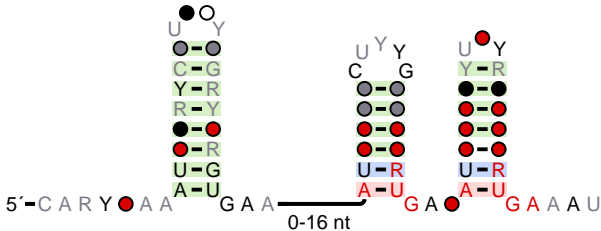
GOLLD-pknot4  
subfam\_weight=1



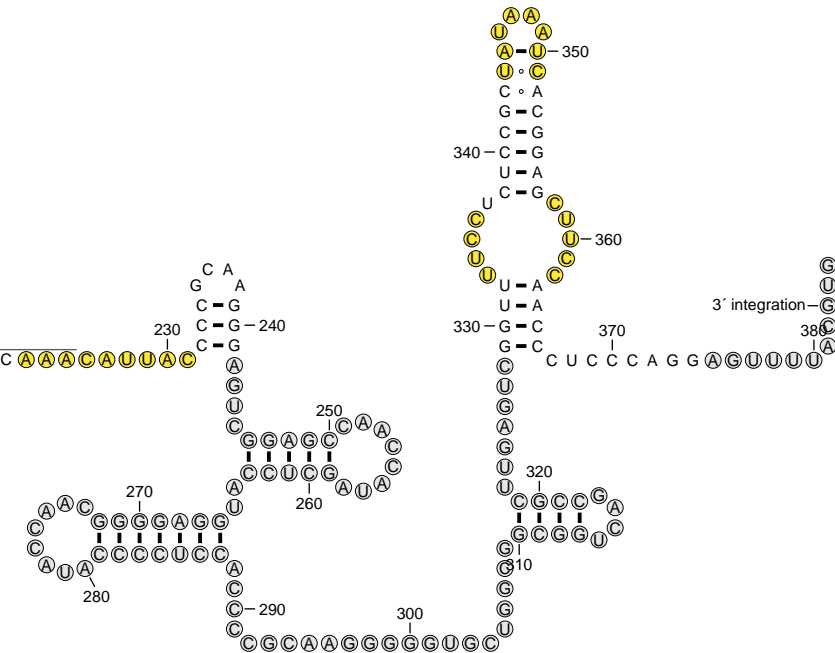
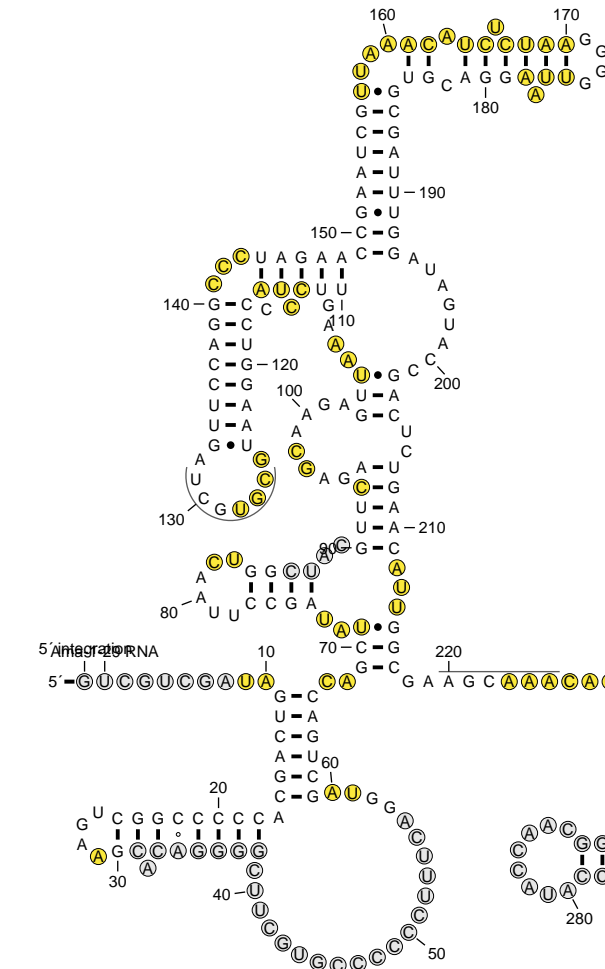
# Gamma-cis-1



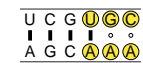
# Gut-1



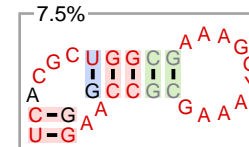
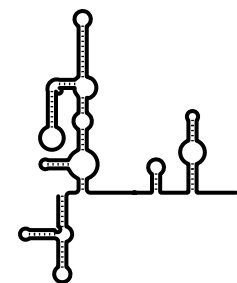
Shrinking nucs & bonds using  
 nucShrinkWithCircleNuc and pairBondScaleWithOneSeq  
 because circle\_nuc or #=GR ... CLEAVAGE was used  
 Set these vars to 1 using SetDrawingParam  
 to disable. See note1 in manual.



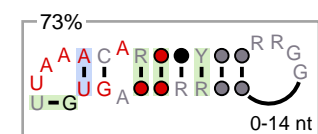
Shrinking nucs & bonds using  
nucShrinkWithCircleNuc and pairBondScaleWithOneSeq  
because circle\_nuc or !=GR ... CLEAVAGE was used  
Set these vars to 1 using SetDrawingParam  
to disable. See note1 in manual.



subfam\_weight=0.0745961

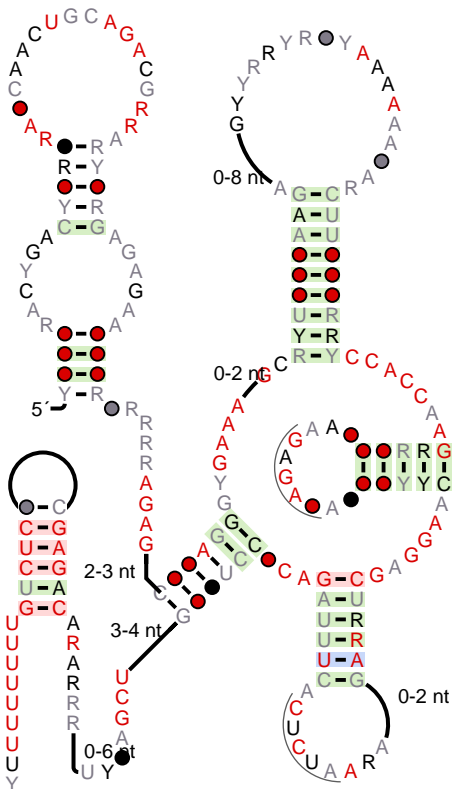


HEARU-UAA  
subfam\_weight=0.732286



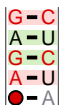


# IMES-1

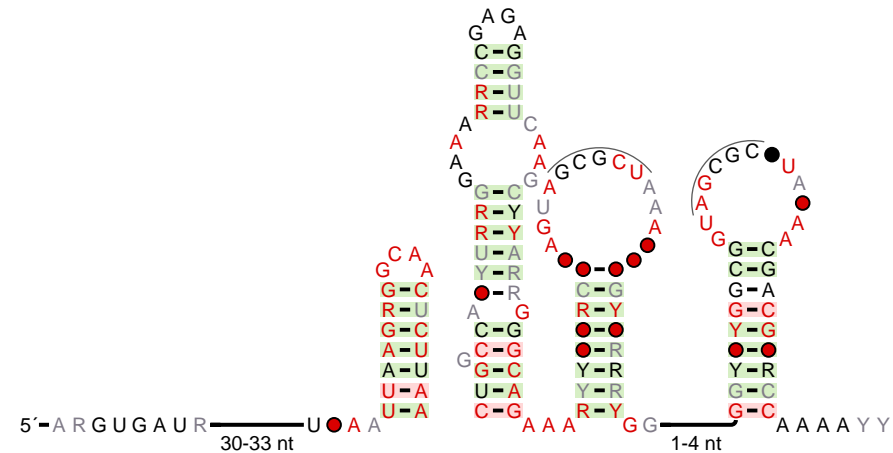


## IMES-1-pknot

subfam\_weight=1



IMES-2

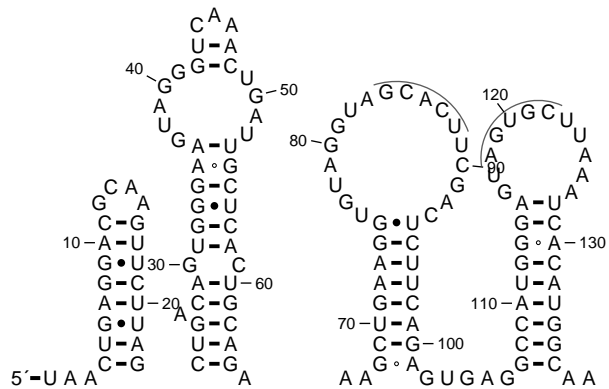


IMES-2-pknot

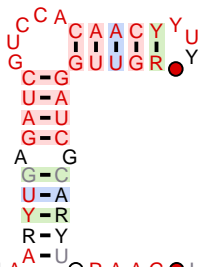
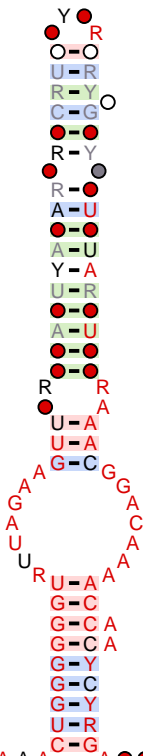
subfam\_weight=1



IMES-2 NZ\_GG704932.1/1211227-1211368

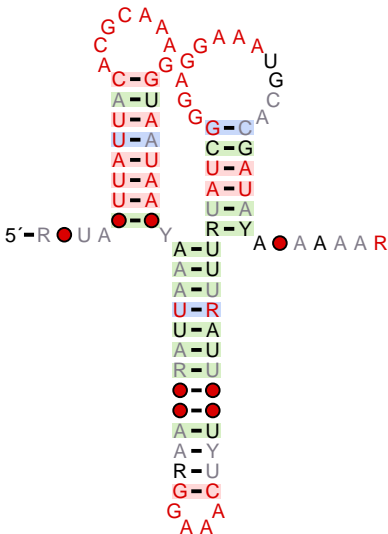


# IMES-3

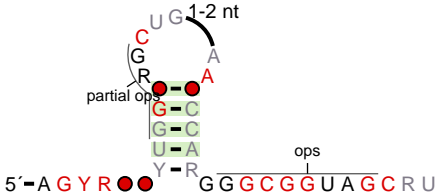


5'-AGGAUAAA AA AUA A-3'

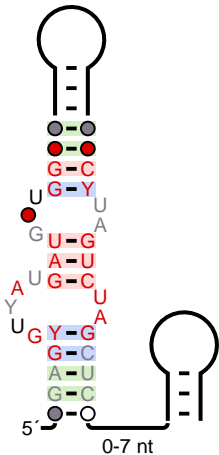
# IMES-4



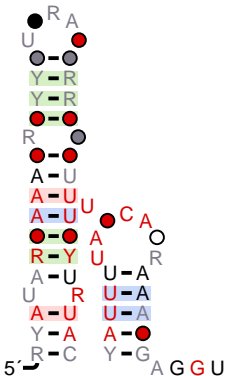
# JUMPstart



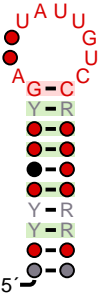
# L17DE



# Lacto-int

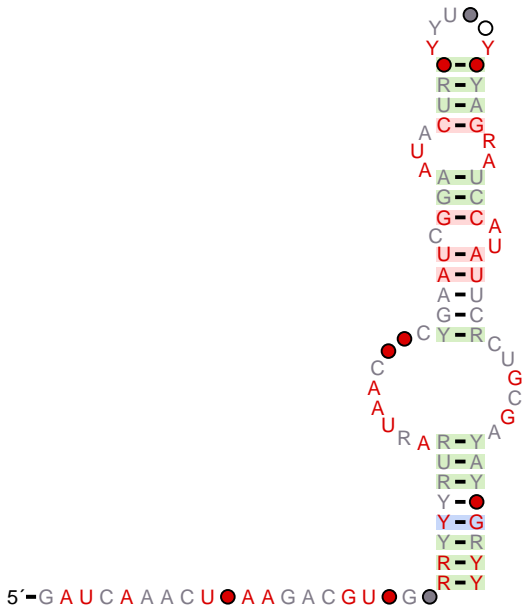


# Lacto-rpoB





# Lacto-usp

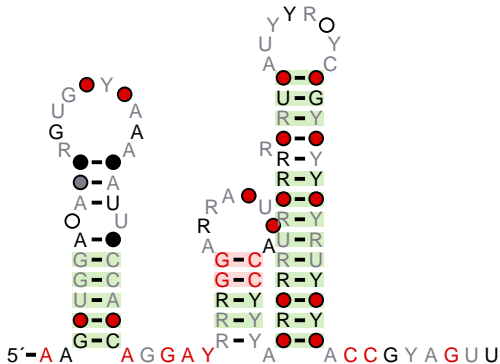


# MAEB

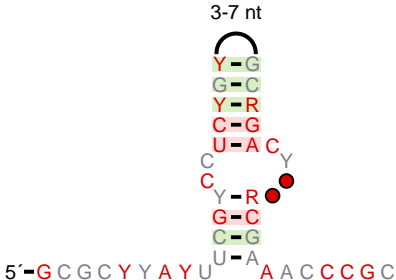


5'-G C A U G G G A C

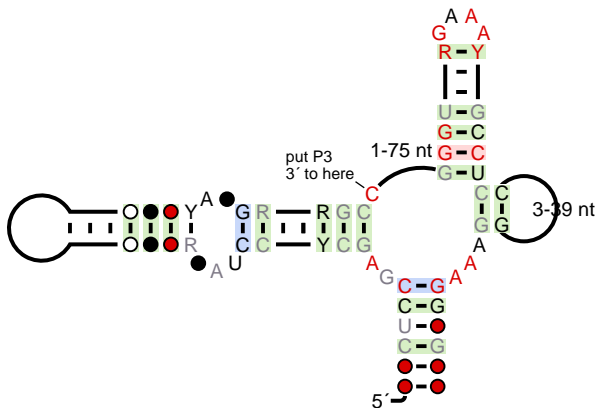
# Methylobacterium-1



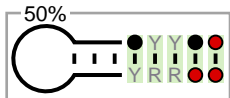
# Moco-II



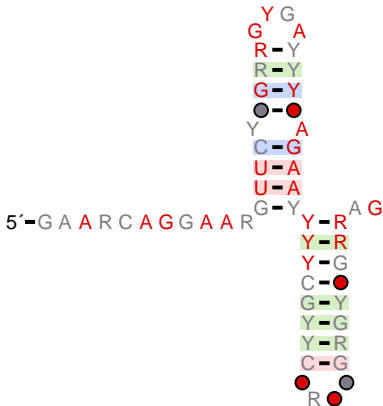
# Moco



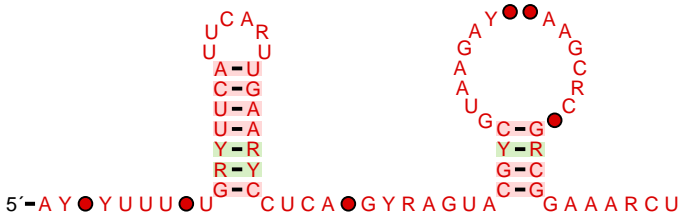
**Moco-withP3**  
subfam\_weight=0.496344



# Nitrosococcus-1



# Ocean-V

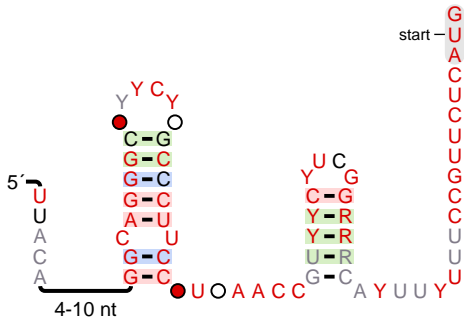


# Ocean-VI

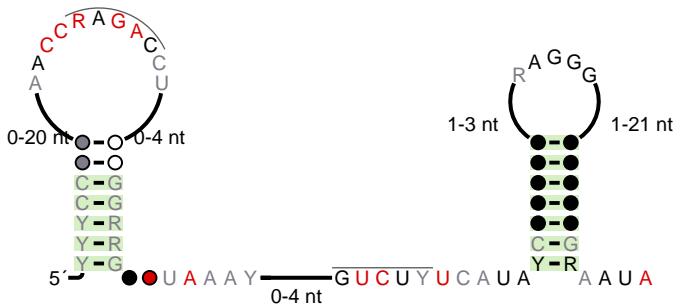




# PhotoRC-I



# PhotoRC-II

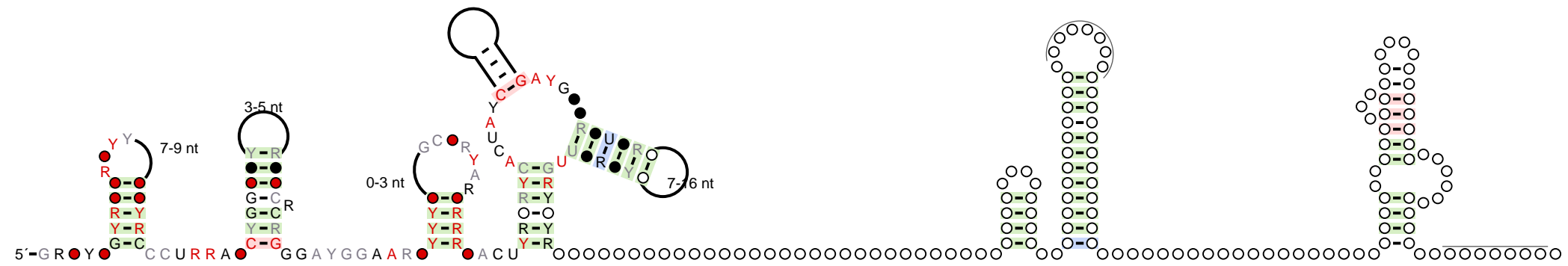


# PhotoRC-II-pknot

subfam\_weight=1

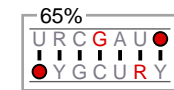


# Polynucleobacter-1



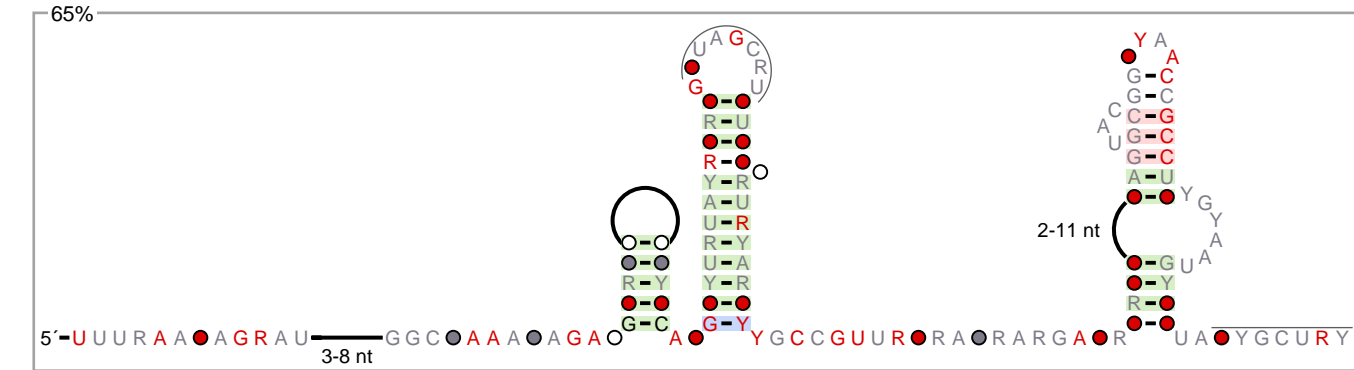
## Polynucleobacter-1-tailpknot

subfam\_weight=0.652083

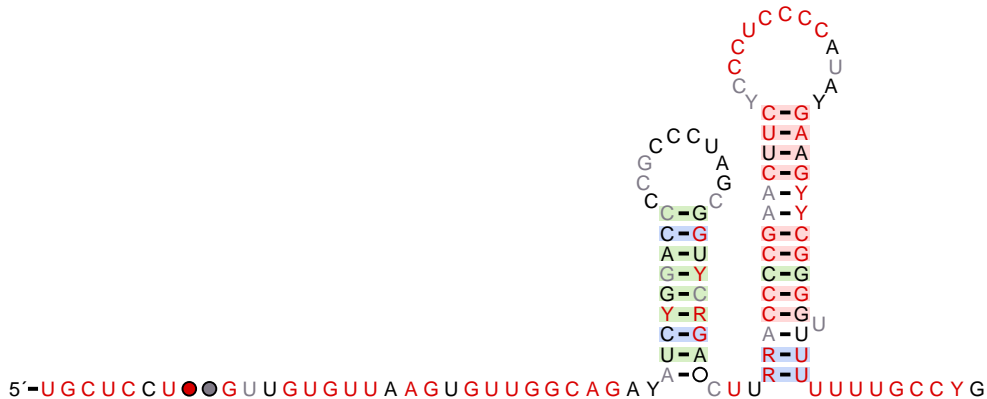


## Polynucleobacter-1-tail

subfam\_weight=0.652083



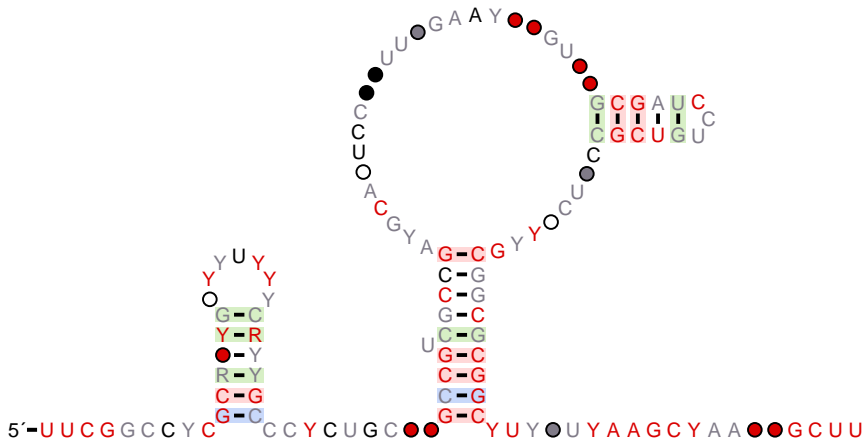
# Pseudomonon-1



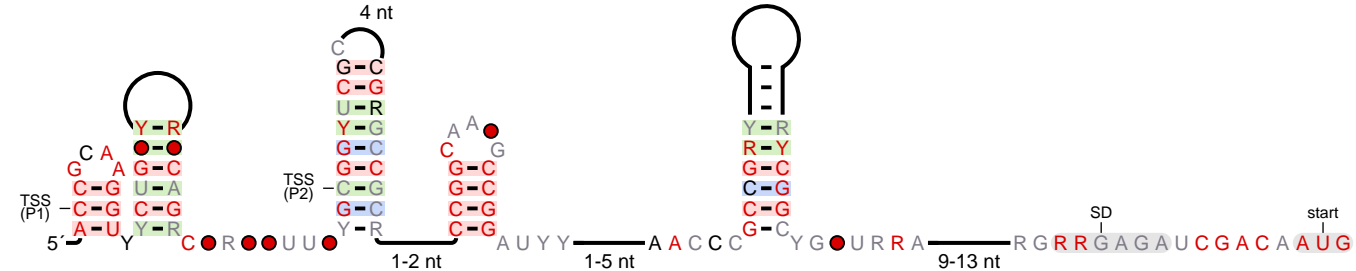
# Pseudomon-2



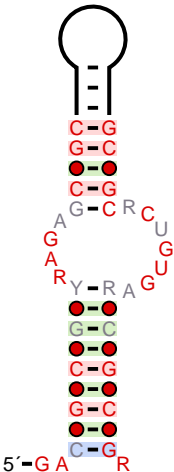
# Pseudomonon-Rho



# Pseudomonas groES

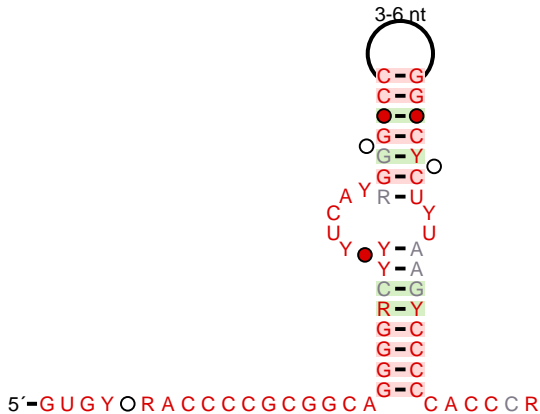


# Pyrobac-1

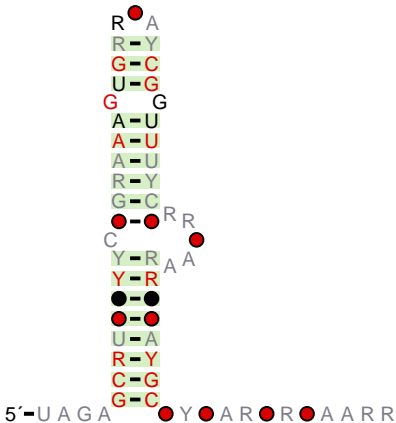




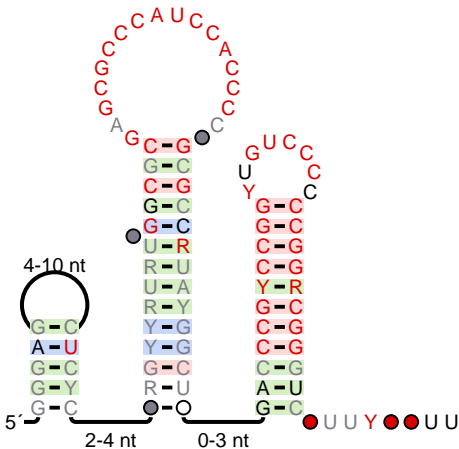
# Pyrobac-HINT



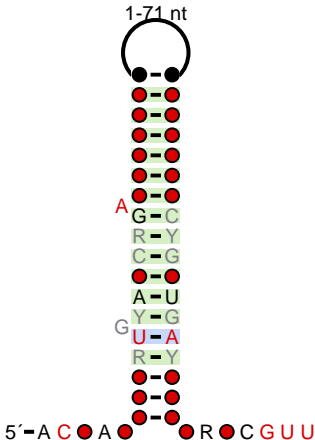
# Rhizobiales-1



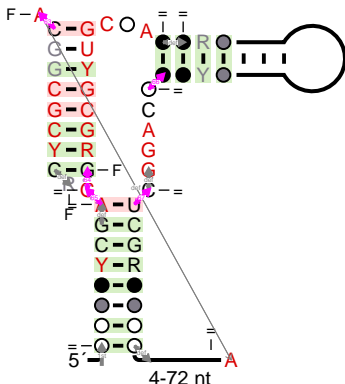
## Rhizobiales-2



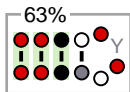
# Rhodopirellula-1



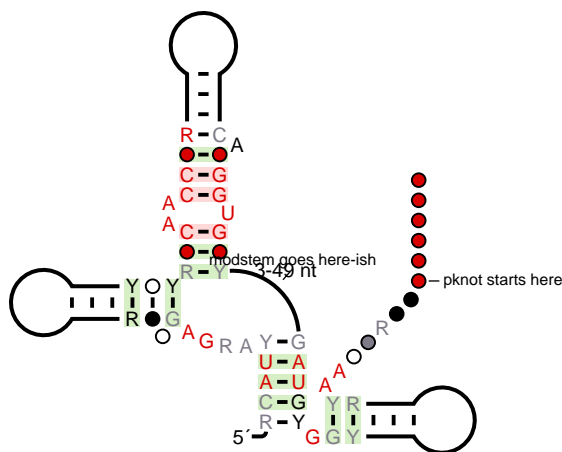
## SAH showPlace=1



## subfam\_weight=0.632009



# SAM-I-IV-variant



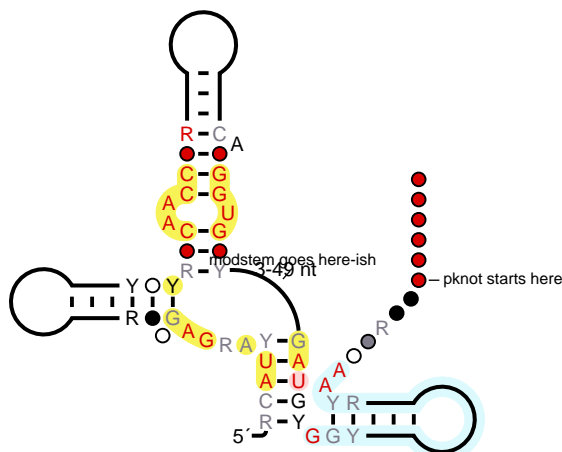
# SAM-I-IV-variant-PKNOT2

subfam\_weight=1

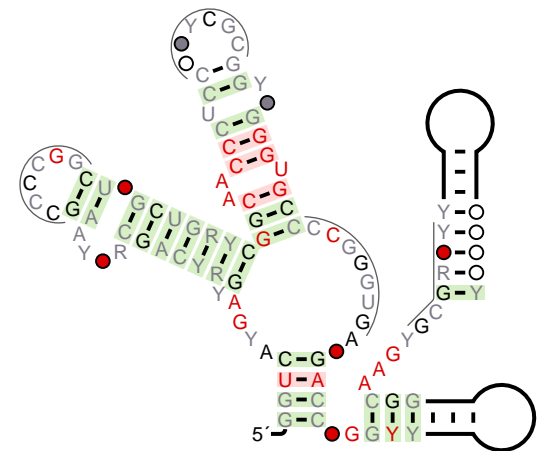


# SAM-I-IV-variant-resemblance

subfam\_weight=1

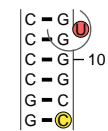


SAM-IV

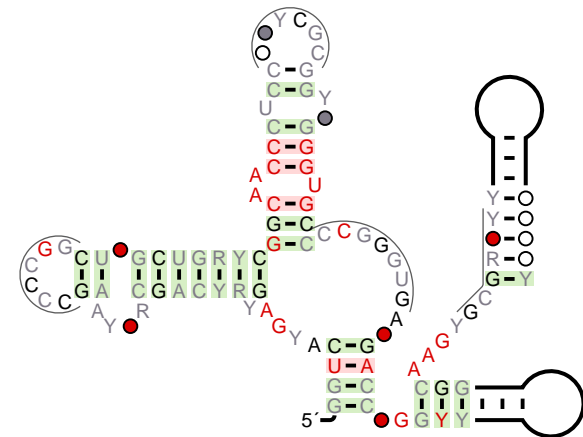


SAM-IV NC\_003888.3/2308784-2308334 pseudoknot=1

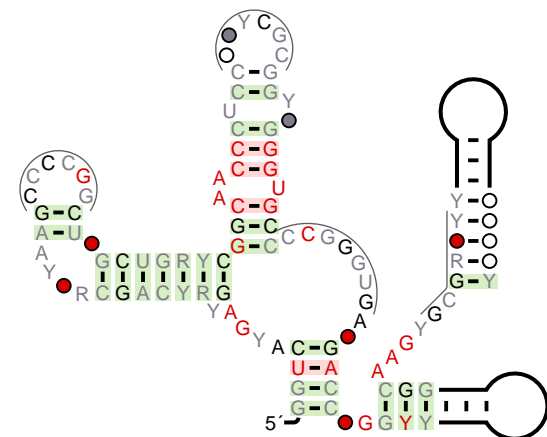
Shrinking nucs & bonds using  
nucShrinkWithCircleNuc and pairBondScaleWithOneSeq  
because circle\_nuc or #=GR ... CLEAVAGE was used  
Set these vars to 1 using SetDrawingParam  
to disable. See note1 in manual.



SAM-IV multistem=original



SAM-IV multistem=original internalloop=turn

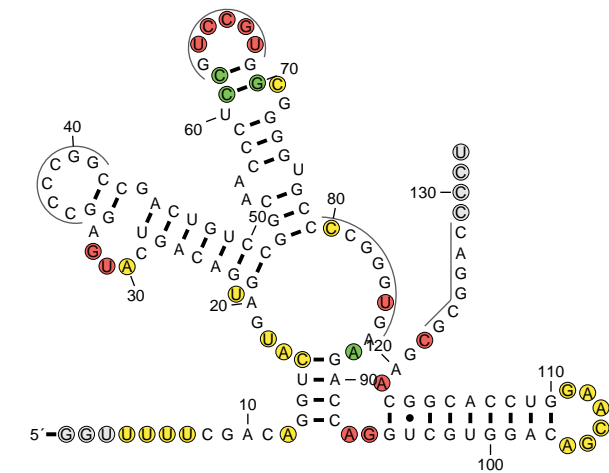


SAM-IV pseudoknot=2



SAM-IV NC\_003888.3/2308784-2308334

Shrinking nucs & bonds using  
nucShrinkWithCircleNuc and pairBondScaleWithOneSeq  
because circle\_nuc or #=GR ... CLEAVAGE was used  
Set these vars to 1 using SetDrawingParam  
to disable. See note1 in manual.

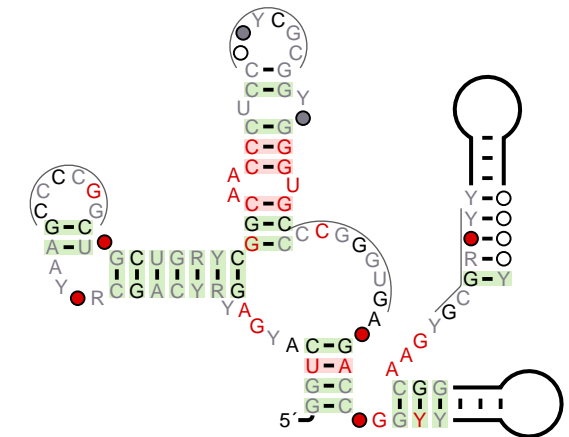


SAM-IV NC\_003888.3/2308784-2308334 pseudoknot=2

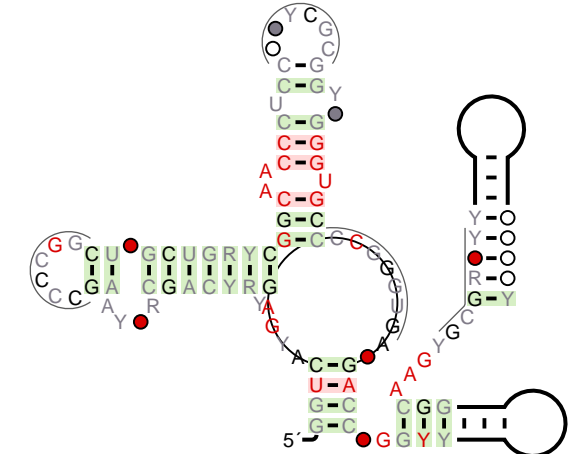
Shrinking nucs & bonds using  
nucShrinkWithCircleNuc and pairBondScaleWithOneSeq  
because circle\_nuc or #=GR ... CLEAVAGE was used  
Set these vars to 1 using SetDrawingParam  
to disable. See note1 in manual.



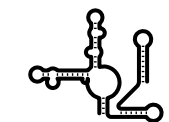
SAM-IV multistem=original internalloop=solver



SAM-IV multistem=solver

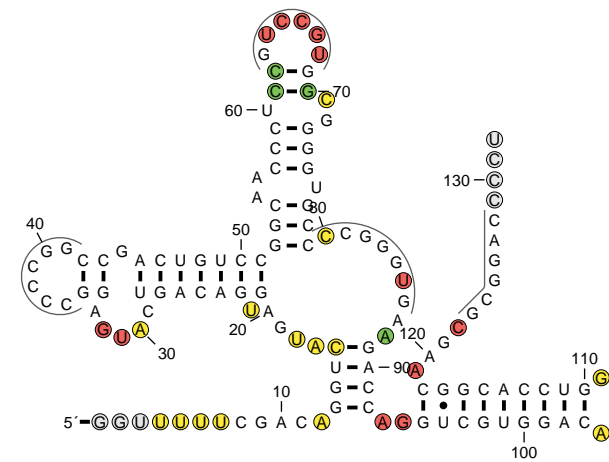


SAM-IV skeleton-with-bp

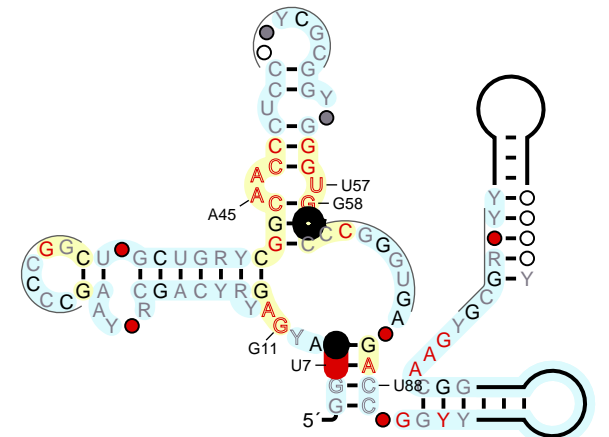


SAM-IV NC\_003888.3/2308784-2308334 multistem=original

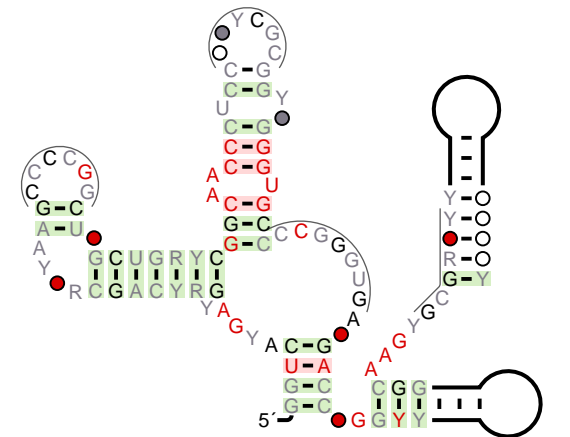
Shrinking nucs & bonds using  
nucShrinkWithCircleNuc and pairBondScaleWithOneSeq  
because circle\_nuc or #=GR ... CLEAVAGE was used  
Set these vars to 1 using SetDrawingParam  
to disable. See note1 in manual.



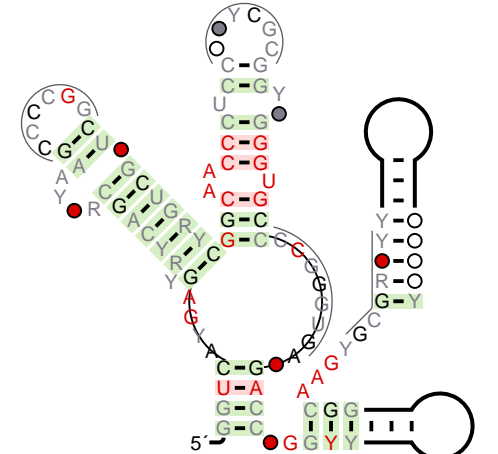
SAM-IV Weinberg2008-Fig1=1



SAM-IV multistem=original internalloop=solver2

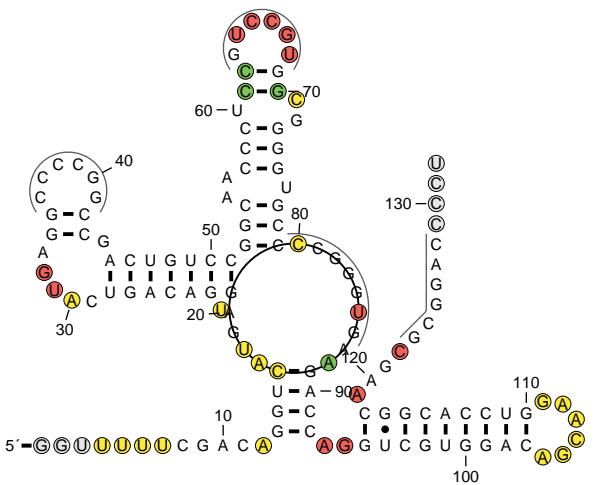


SAM-IV multistem=solver2

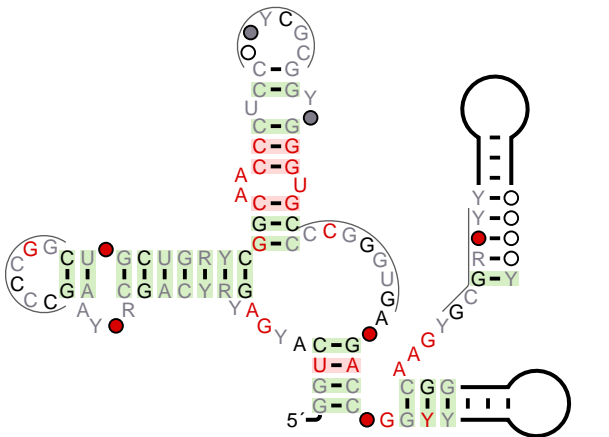


SAM-IV NC\_003888.3/2308784-2308334 multistem=solver internalloop=solver2

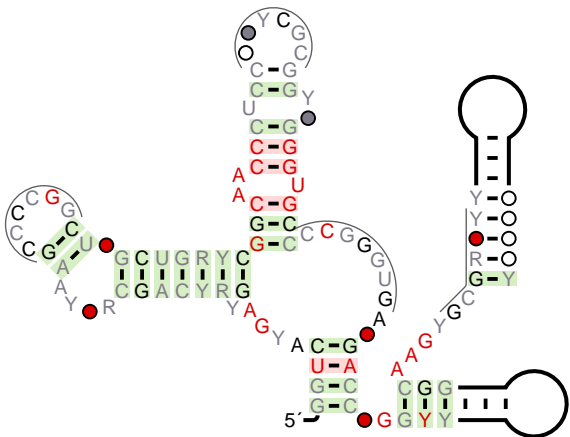
Shrinking nucs & bonds using  
nucShrinkWithCircleNuc and pairBondScaleWithOneSeq  
because circle\_nuc or #=GR ... CLEAVAGE was used  
Set these vars to 1 using SetDrawingParam  
to disable. See note1 in manual.



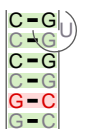
SAM-IV multistem=bulgey



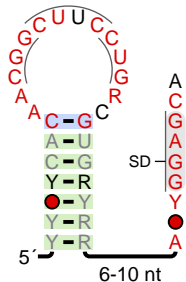
SAM-IV multistem=original internalloop=solver3



SAM-IV pseudoknot=1

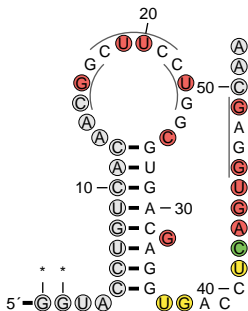


# SAM-SAH



# SAM-SAH NZ\_AAYC01000001.1/141950-142398

Shrinking nucs & bonds using  
 nucShrinkWithCircleNuc and pairBondScaleWithOneSeq  
 because circle\_nuc or #=GR ... CLEAVAGE was used  
 Set these vars to 1 using SetDrawingParam  
 to disable. See note1 in manual.



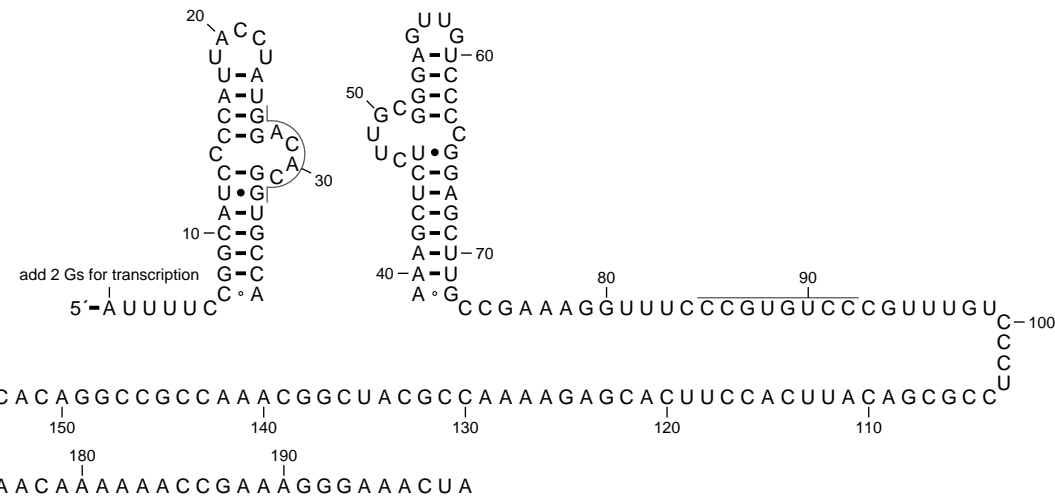
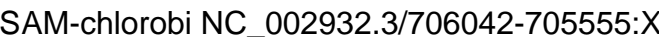
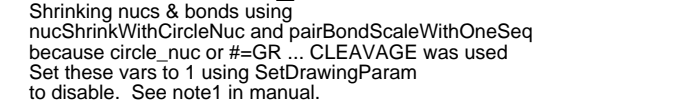
# SAM-SAH skeleton-with-bp SAM-SAH-pknot1

subfam\_weight=1

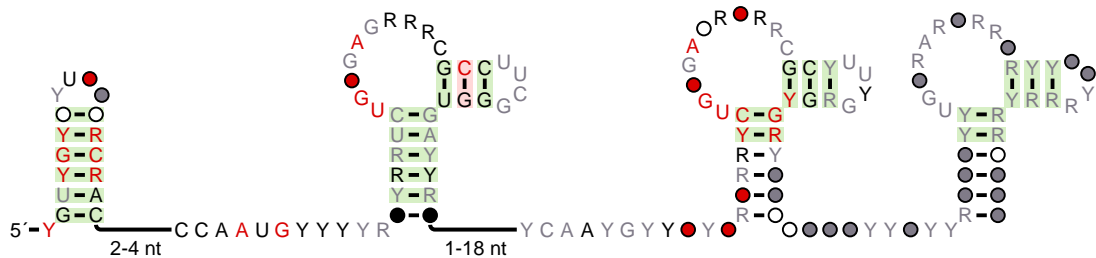




SAM-chlorobi NC\_002932.3/706042-705555:S

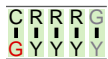


# STAXI



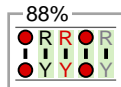
# STAXI-pknot1

subfam\_weight=1



## STAXI-pknot3

subfam\_weight=0.882988

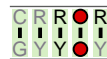


## STAXI skeleton-with-bp

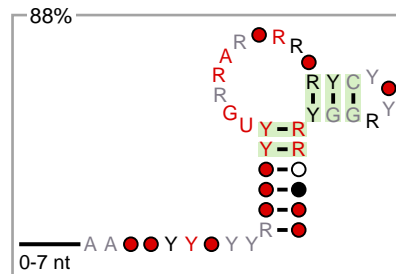


## STAXI-pknot2

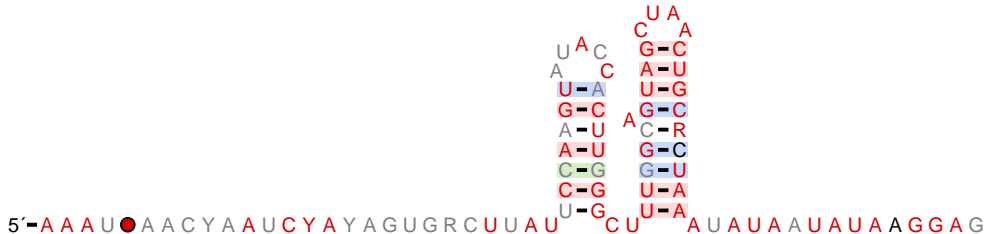
subfam\_weight=1

STAXI-unit3  
subfam\_weight 0.8

subfam\_weight=0.882988



# ScRE

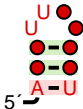


# ScriptInputExample

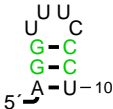
A

C C C G U U G  
A  
G  
U G

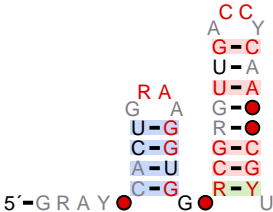
# SmallWithCovary



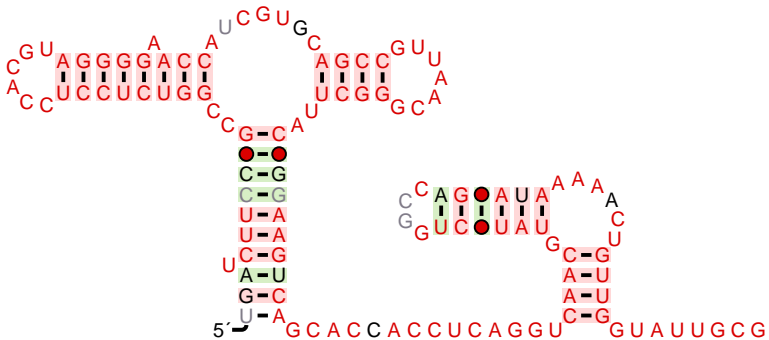
# SmallWithCovary 5



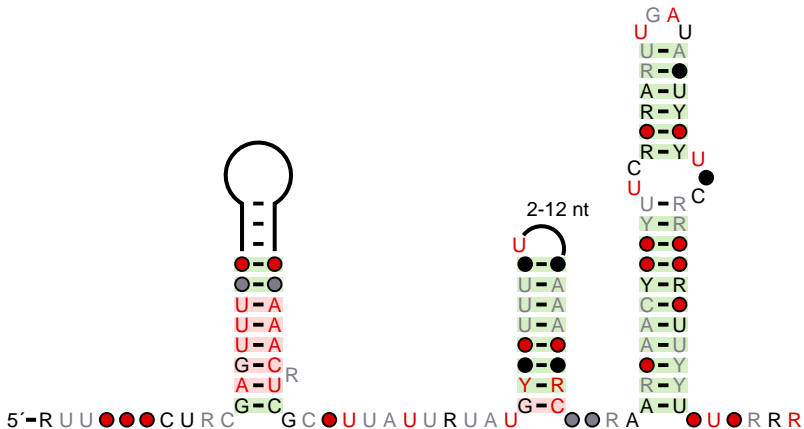
# Soil-1



# Solibacter-1

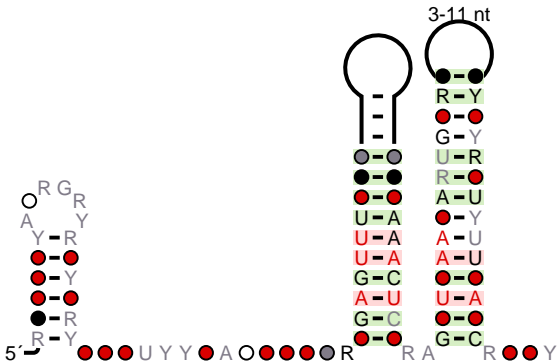


TD-1

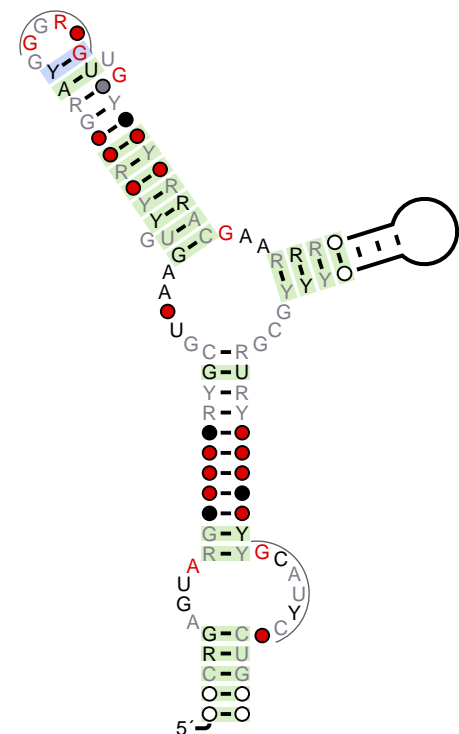




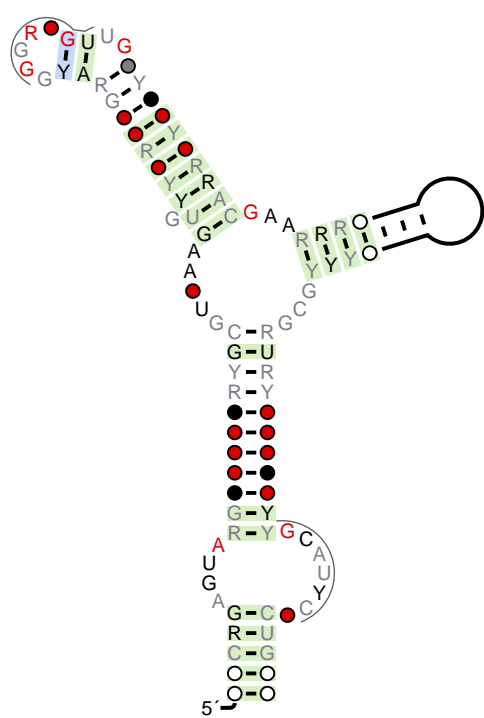
# TD-2



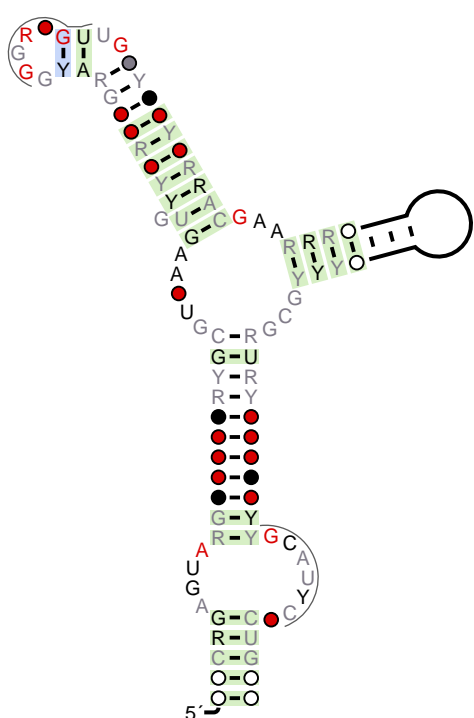
THF



THF 2nt-bulge=1



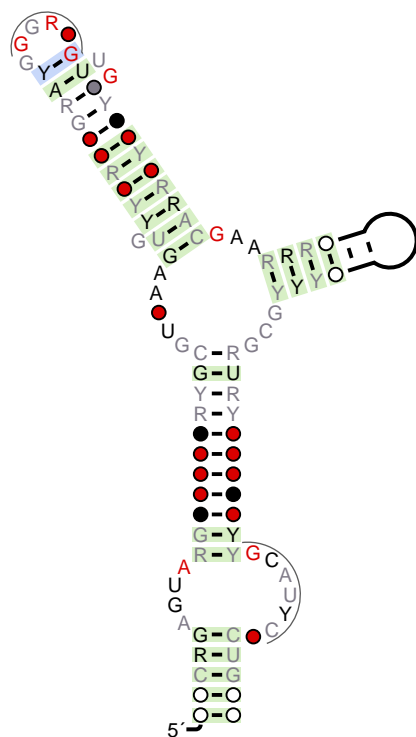
THF 2nt-bulge=2 solver=1



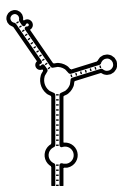
THF pknot=1



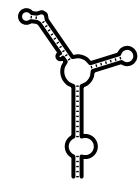
THF short-hairpin=1



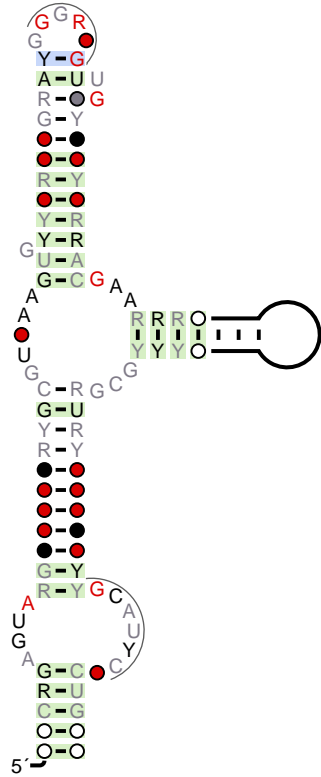
THF skeleton-with-bp



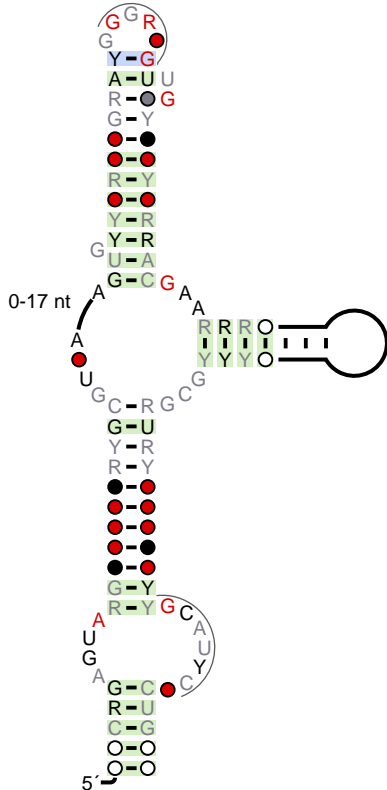
THF skeleton-with-bp 2nt-bulge=1



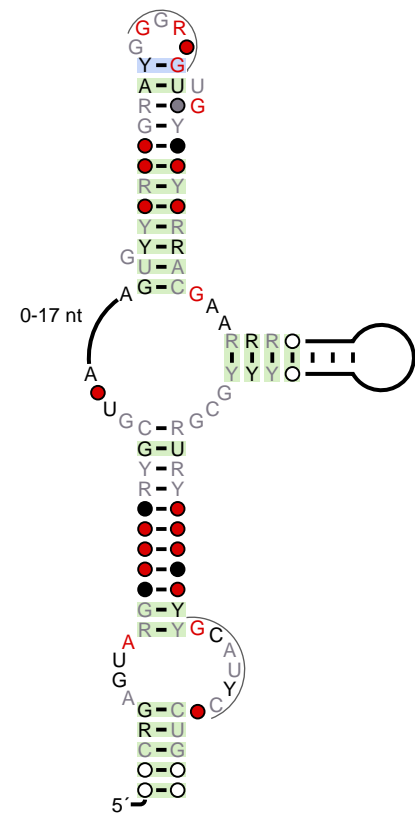
THF solver=1



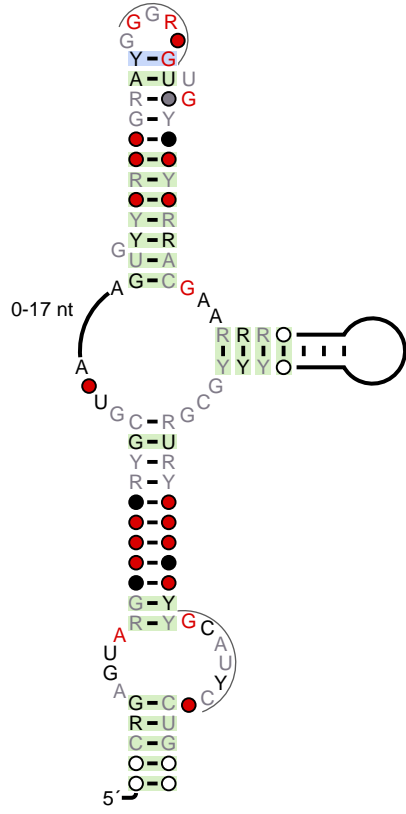
THF solver=2



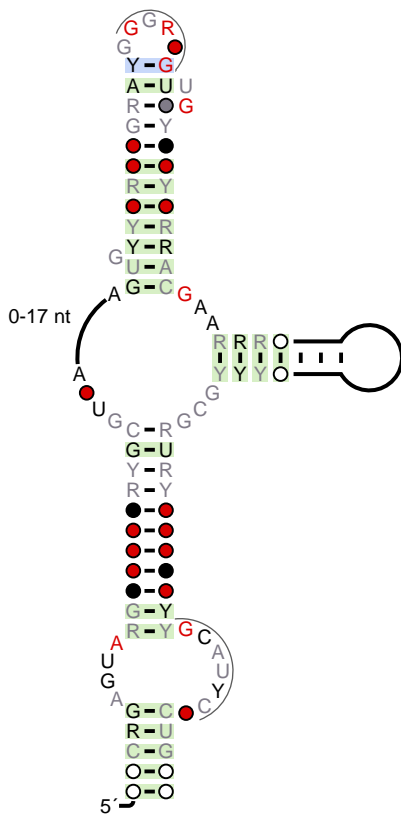
THF solver=2 align-with-circle=1



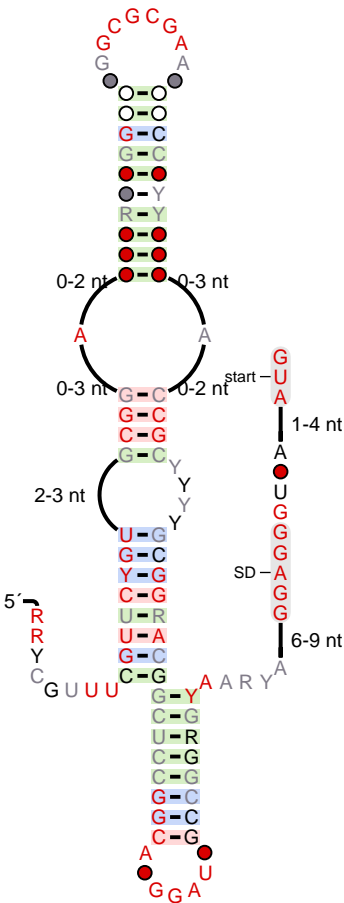
THF solver=3



THF solver=3 align-with-circle=1



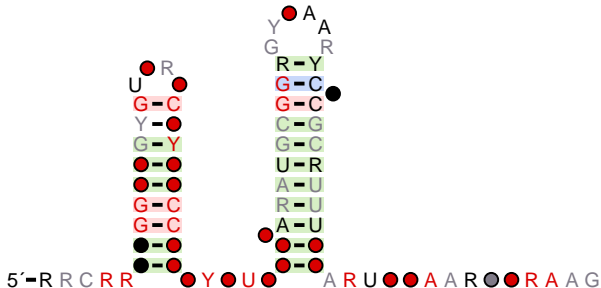
# Termite-flg



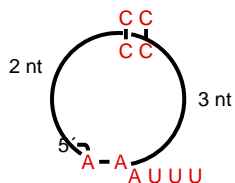
# Termite-flg skeleton-with-bp



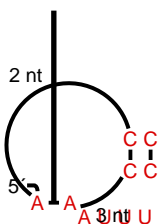
# Termite-leu



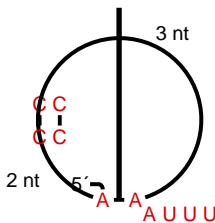
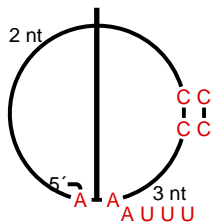
TestAngularAlignment



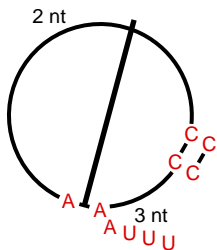
TestAngularAlignment alignangle=-32



TestAngularAlignment alignangle=-45TestAngularAlignment alignangle=45



TestAngularAlignment rots0=-15



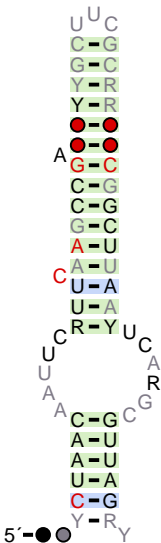
# TestColumnNumbers

pos 0

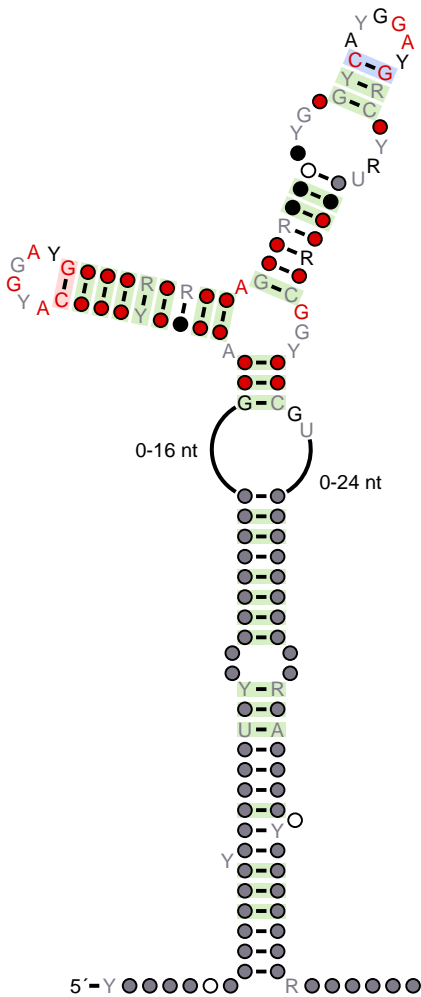
pos 6



# Transposase-resistance



TwoAYGGAY



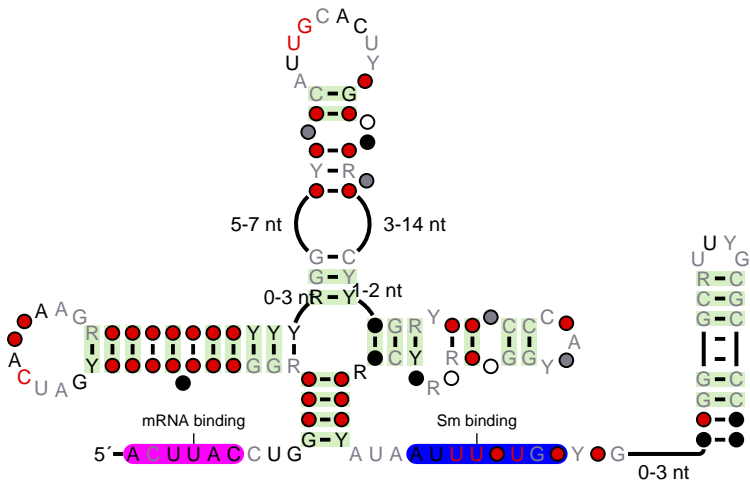


# TwoBasePairs

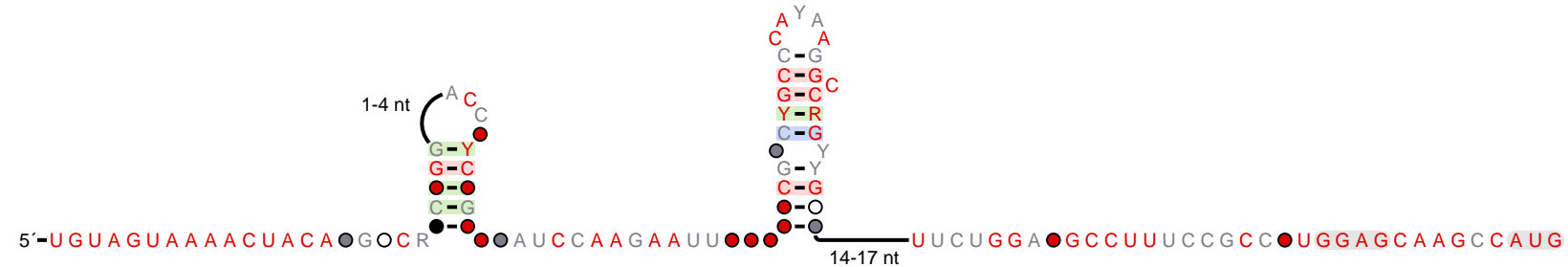


# TwoBasePairs seq

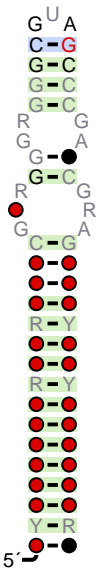




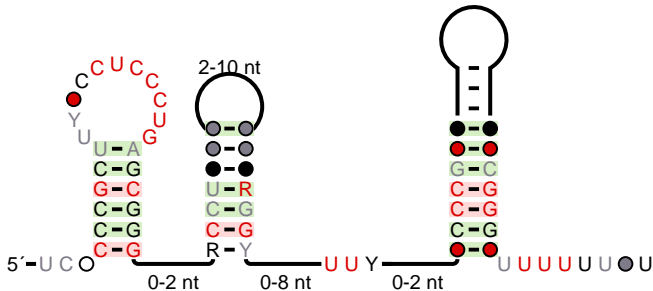
aceE



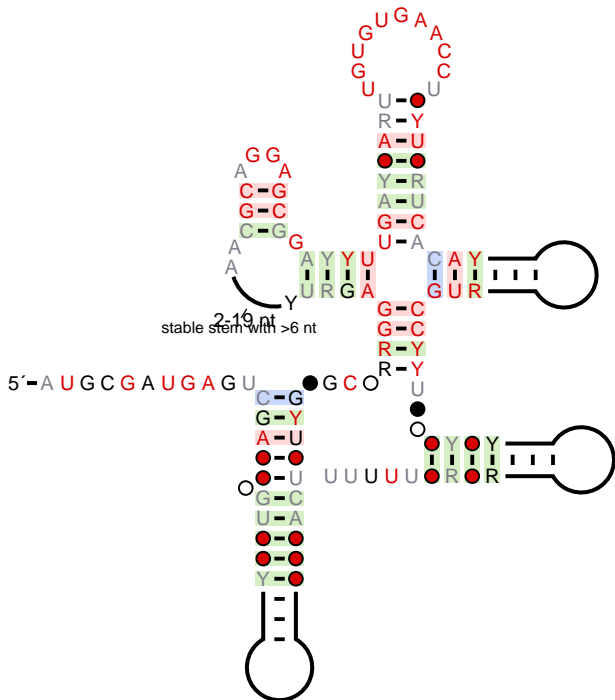
# alpha-transposase



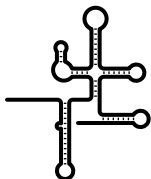
# anti-hemB



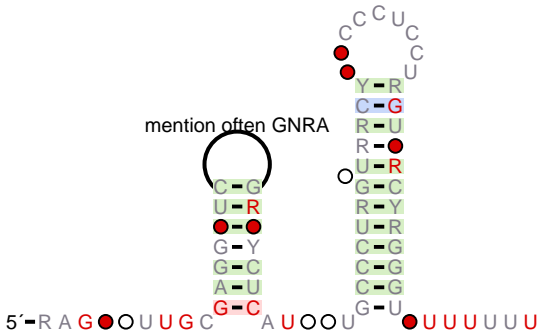
asd



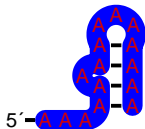
asd skeleton-with-bp



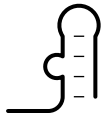
atoC



backbone-path1

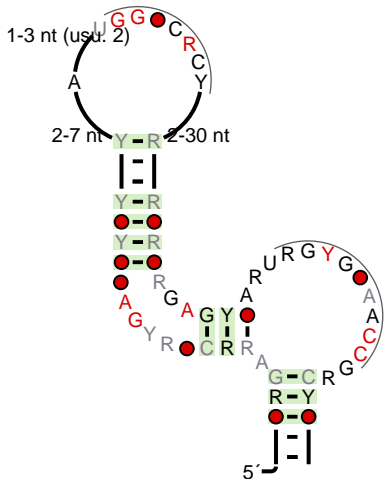


backbone-path1 skeleton-with-bp

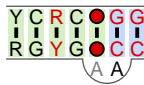




c-di-GMP-II-update



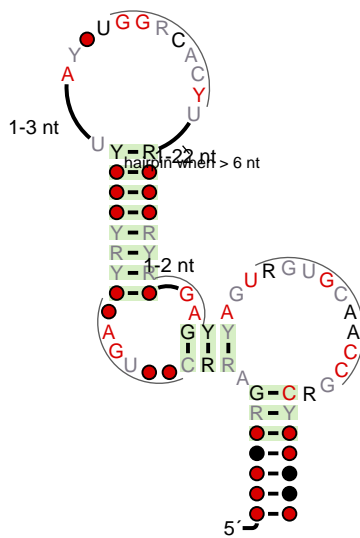
c-di-GMP-II-update pknot=1



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

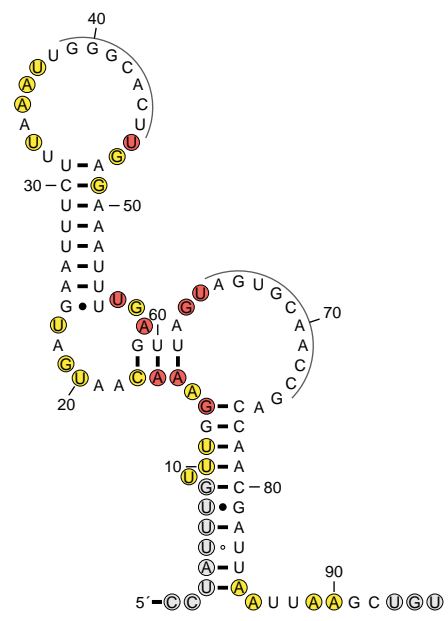


# c-di-GMP-II



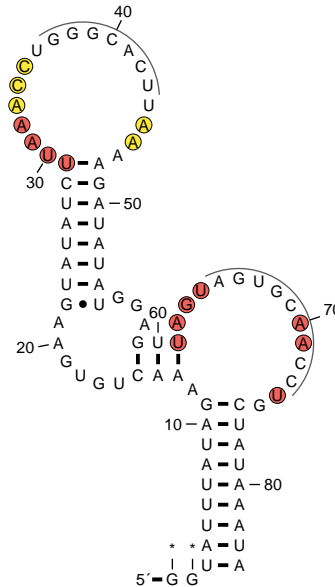
# c-di-GMP-II NC\_003030.1/648383-648856

Shrinking nucs & bonds using  
nucShrinkWithCircleNuc and pairBondScaleWithOneSeq  
because circle\_nuc or !=GR ... CLEAVAGE was used  
Set these vars to 1 using SetDrawingParam  
to disable. See note1 in manual.



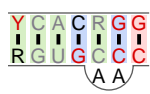
# c-di-GMP-II NC\_009089.1/3801245-3800770c-di-GMP-II skeleton-with-bp

Shrinking nucs & bonds using  
nucShrinkWithCircleNuc and pairBondScaleWithOneSeq  
because circle\_nuc or !=GR ... CLEAVAGE was used  
Set these vars to 1 using SetDrawingParam  
to disable. See note1 in manual.

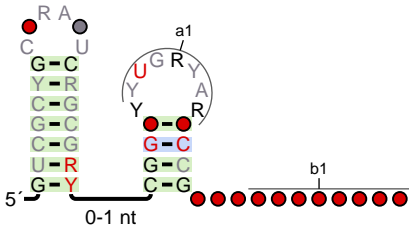


# c-di-GMP-II-pknot

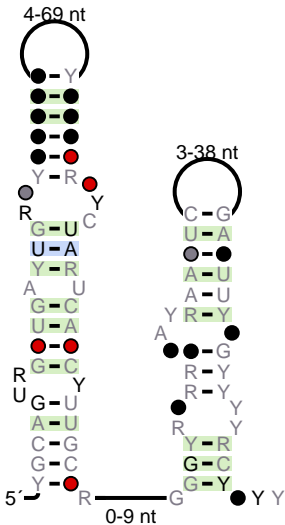
subfam\_weight=1



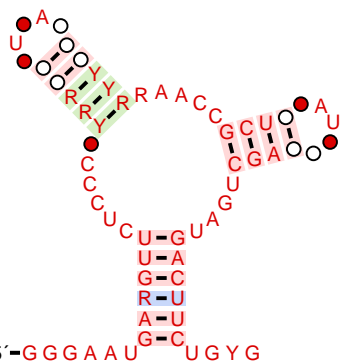
c4-a1b1



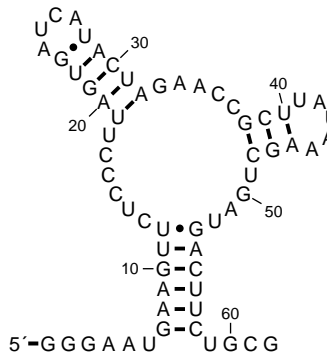
# COCCUS-1



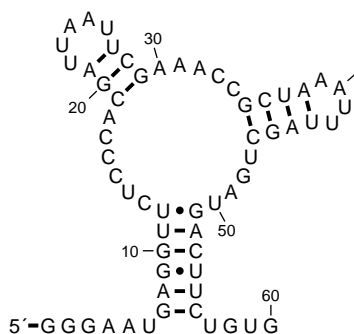
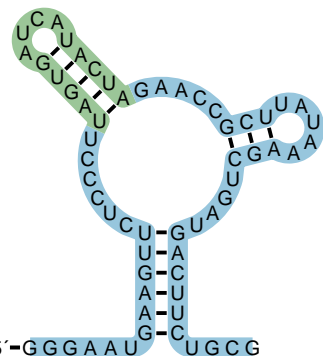
consensus-of-2



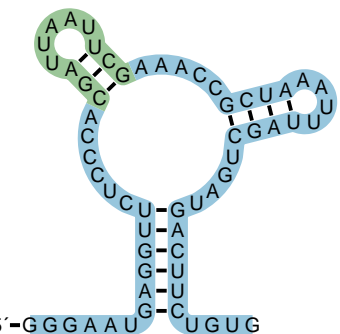
consensus-of-2 NZ\_AAXB02000001.1/235534-236009



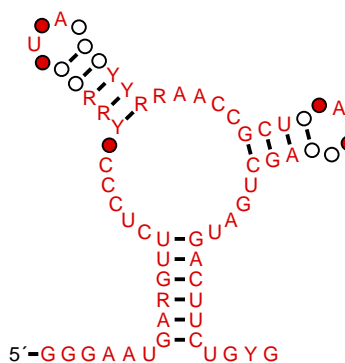
consensus-of-2 NZ\_AAXB02000001.1/235534-236009 LIX2010=1consensus-of-2 NZ\_ABYJ01000311.1/4968-4495



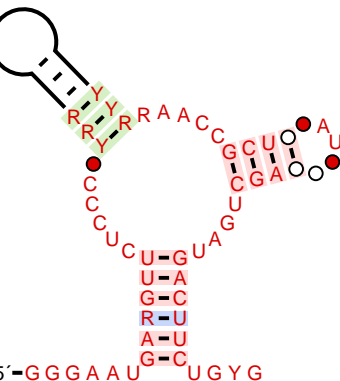
consensus-of-2 NZ\_ABYJ01000311.1/4968-4495 LIX2010=1



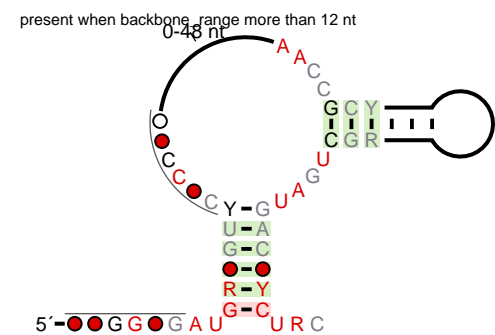
consensus-of-2 plain=1



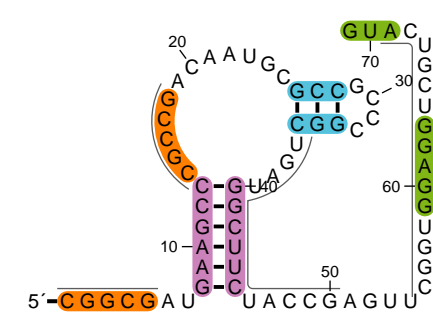
consensus-of-2 variables=1



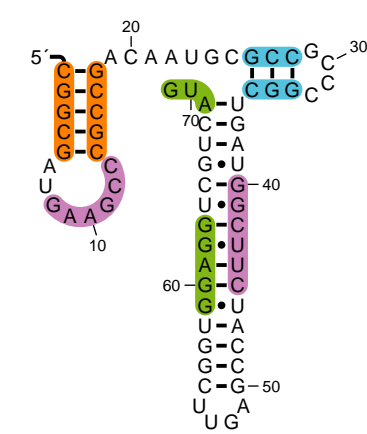
crcB



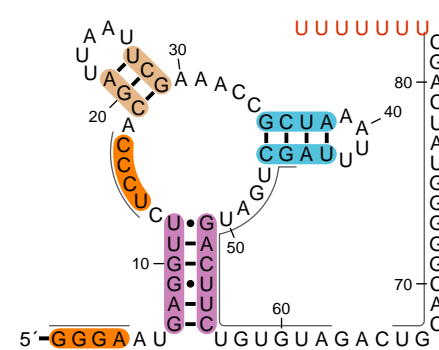
crcB NC\_008578.1/805741-806202



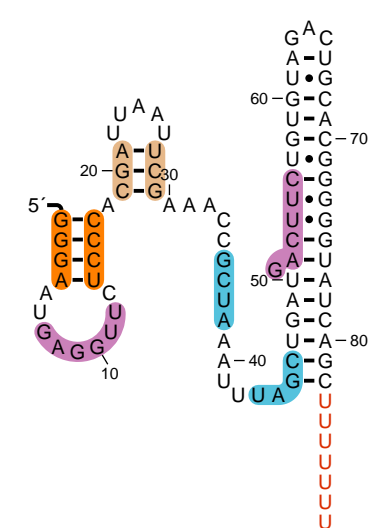
crcB NC\_0085741-806202 alt-struct=2



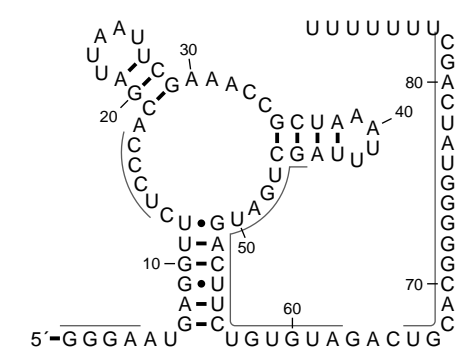
crcB NZ\_ABYJ01000311.1/4968-4495



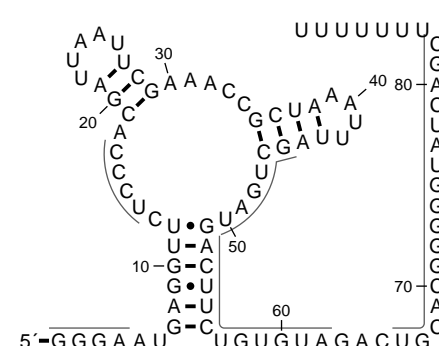
crcB NZ\_ABYJ01000311.1/4968-4495 alt-struct=2



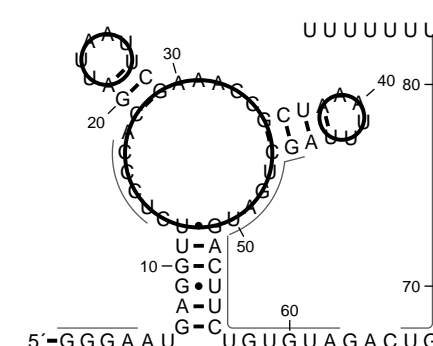
crcB NZ\_ABYJ01000311.1/4968-4495 no-shading=1



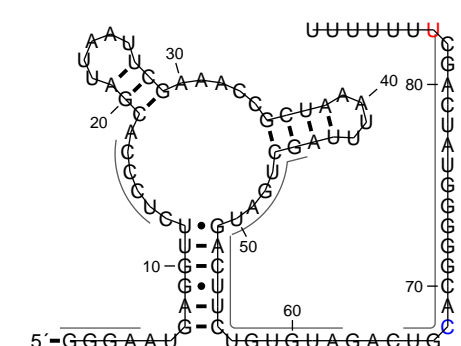
crcB NZ\_ABYJ01000311.1/4968-4495 no-shading=1 anyangle=1



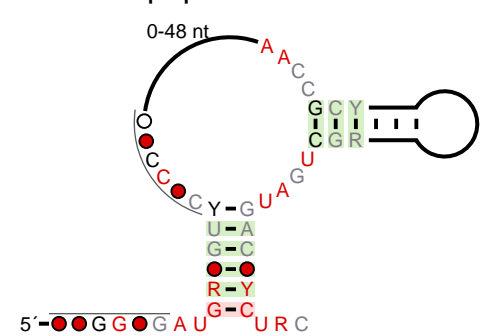
crcB NZ\_ABYJ01000311.1/4968-4495 no-shading=1 anyangle=1 drawcirc=1



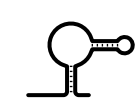
crcB NZ\_ABYJ01000311.1/4968-4495 no-shading=1 anyangle=1 drawedges=1



crcB R2R-paper=1



crcB skeleton-with-bp



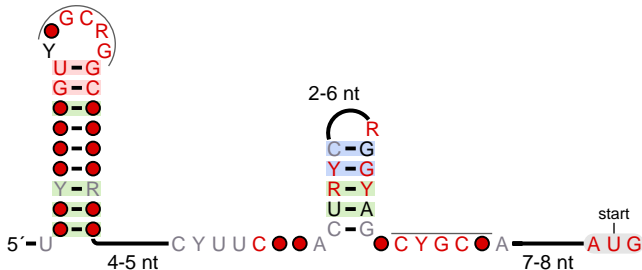
crcB-pknot1  
subfam\_weight=1



crcB-P2  
subfam\_weight=0.308697



# cyano-30S

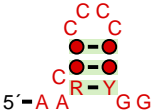


# cyano-30S-pknot

subfam\_weight=1

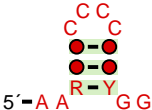


# demo-breakpair-fix1

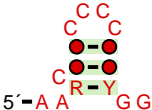




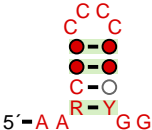
# demo-breakpair-fix2



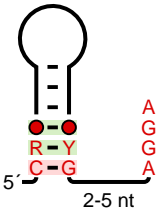
# demo-breakpair-fix3



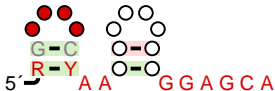
# demo-breakpair-fix4



# demo-contrived



# demo-modular



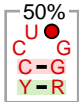
# demo-modular-GNRA

subfam\_weight=0.230158



# demo-modular-OPT

subfam\_weight=0.5

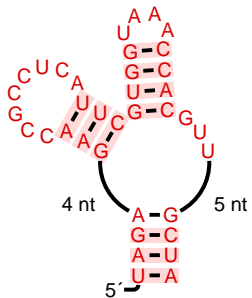


# demo-modular-UNCG

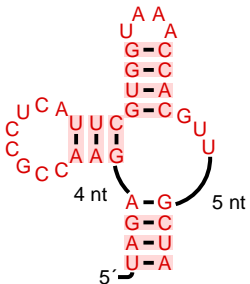
subfam\_weight=0.269842



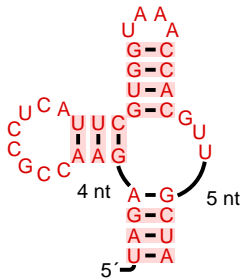
demo-multistem-HEARO2



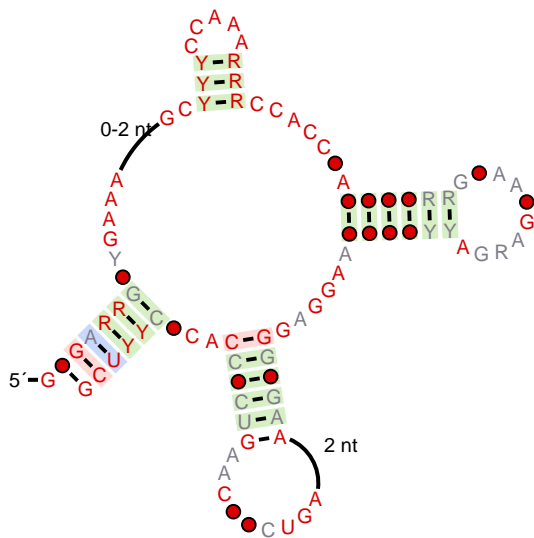
demo-multistem-HEARO2 solver=1



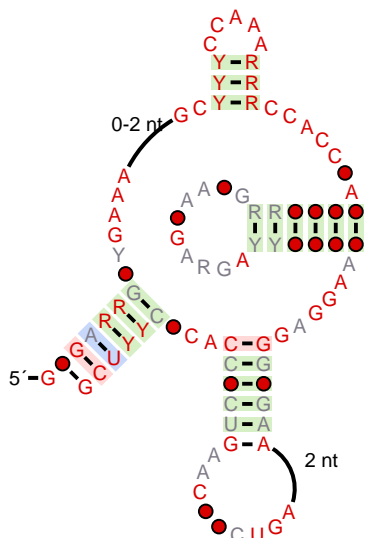
demo-multistem-HEARO2 solver=2



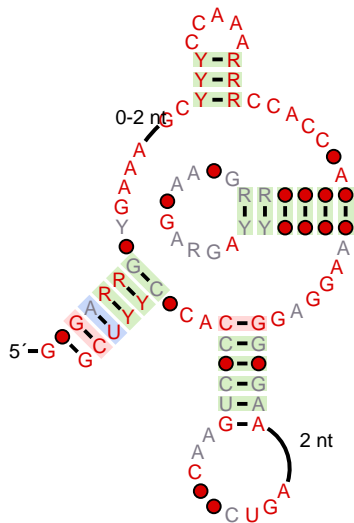
demo-multistem-IMES-1



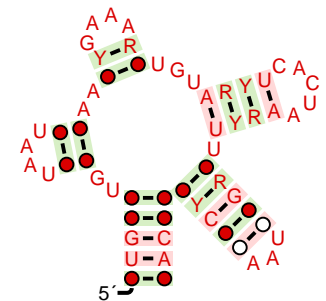
demo-multistem-IMES-1 solver=1



demo-multistem-IMES-1 solver=2



demo-multistem-manA

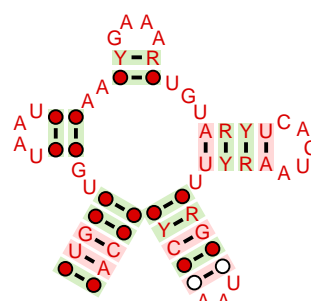


demo-multistem-manA solver=1

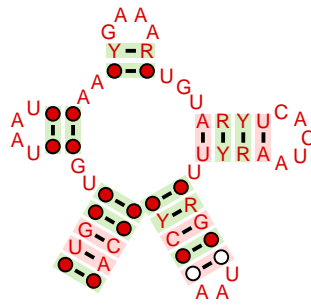
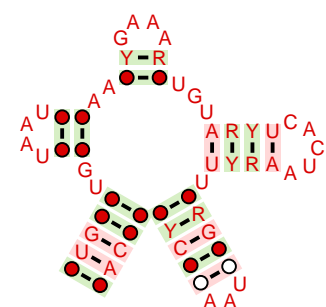


note: R2R cannot find a feasible solution for this problem using the multistem\_junction\_circular\_solver command. However, it can with (1) a user-input optimization starting point, (2) with the try\_harder directive or (3) with the multistem\_junction\_bulgecircle\_solver command, as shown in other drawings here.

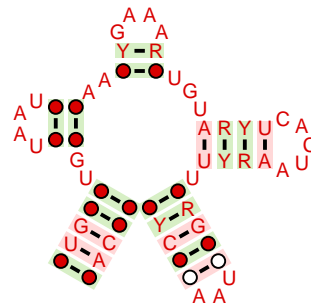
demo-multistem-manA solver=1 explicitinitial



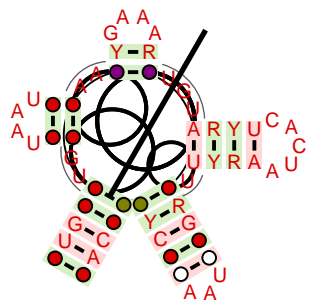
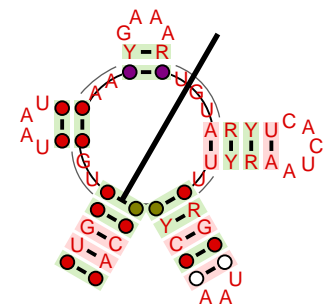
demo-multistem-manA solver=1tryharderdemo-multistem-manA solver=2



demo-multistem-manA solver=3

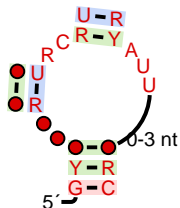


demo-multistem-manA solver=3 annot=1 demo-multistem-manA solver=3 annot=1 fewiters=1

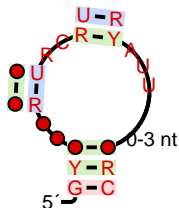




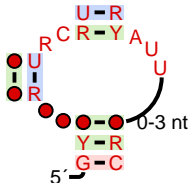
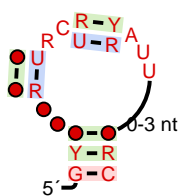
demo-multistem



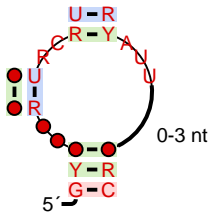
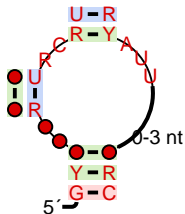
demo-multistem circle=1



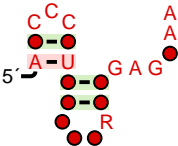
demo-multistem flipstem=1 demo-multistem manual=1



demo-multistem solver1=1 demo-multistem solver2=1



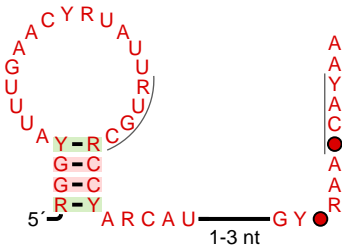
# demo-pe



demo-pknot-callout-ifdef pknot=1



# demo-pknot-callout

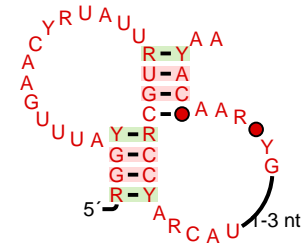


# demo-pknot-callout-pknot

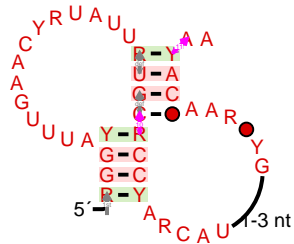
subfam\_weight=1



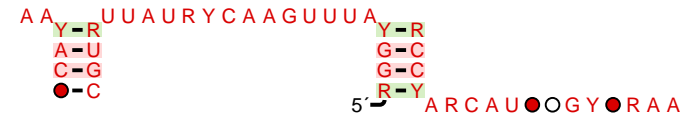
demo-pknot-inline



demo-pknot-inline debug\_place\_explicit=1



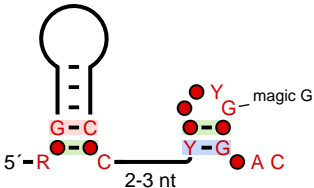
demo-pknot-inline default=1



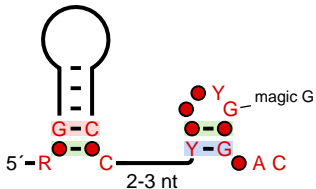
demo-pknot-inline default=1 labelnucs=1



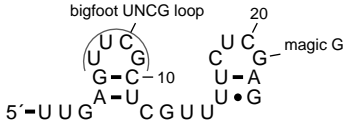
demo1-ii



demo1-iii



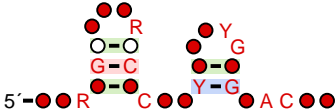
demo1-iii bigfoot



demo1-iii skeleton-with-bp

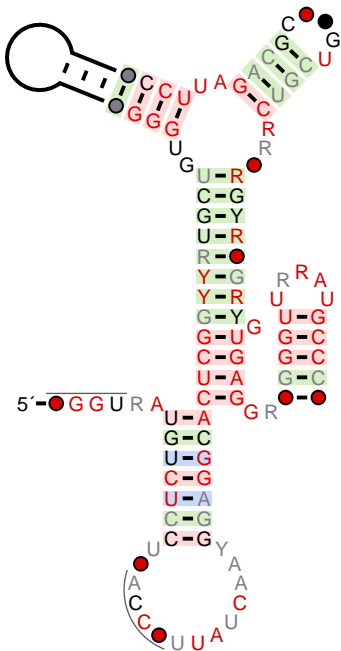


demo1





epsC



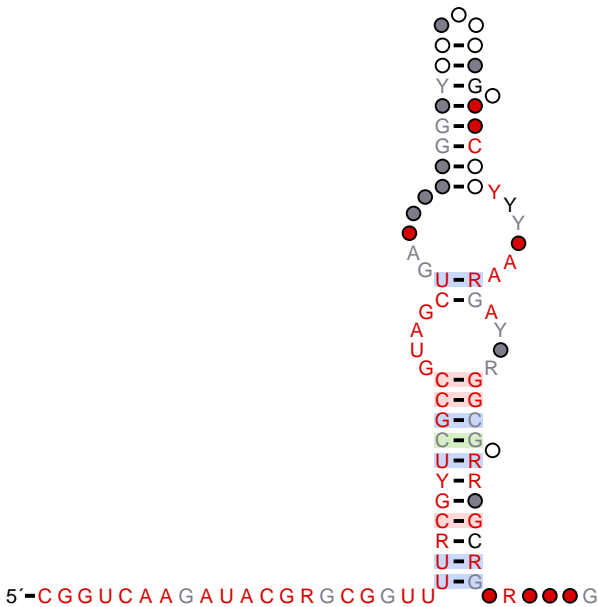
epsC-pknot  
subfam\_weight=1



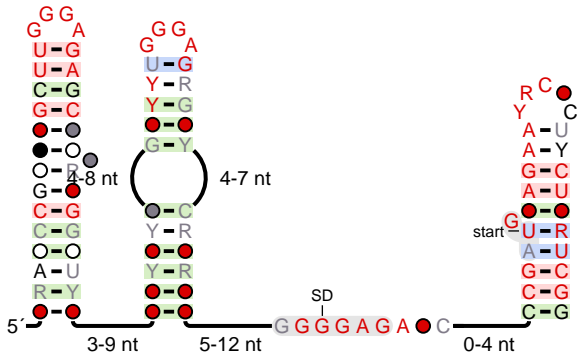
# excisionase



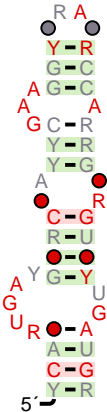
fixA



# flg-Rhizobiales

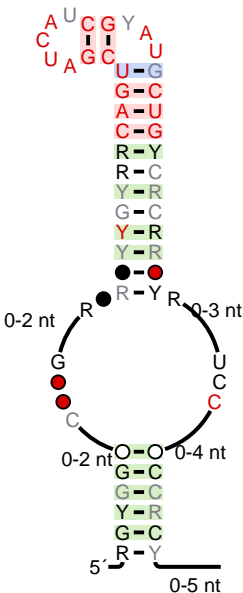


flpD



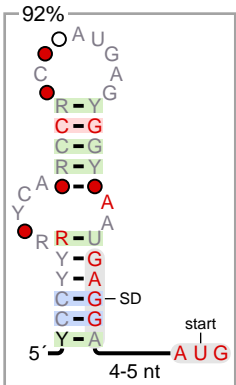
# g150

# gabT



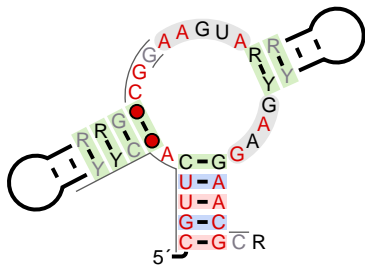
# gabT-P2

subfam\_weight=0.915134



glnA

glnA skeleton-with-bp



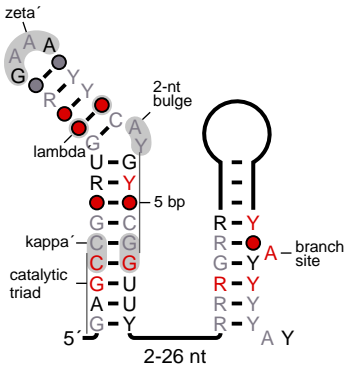
glnA-pknot

subfam\_weight=1

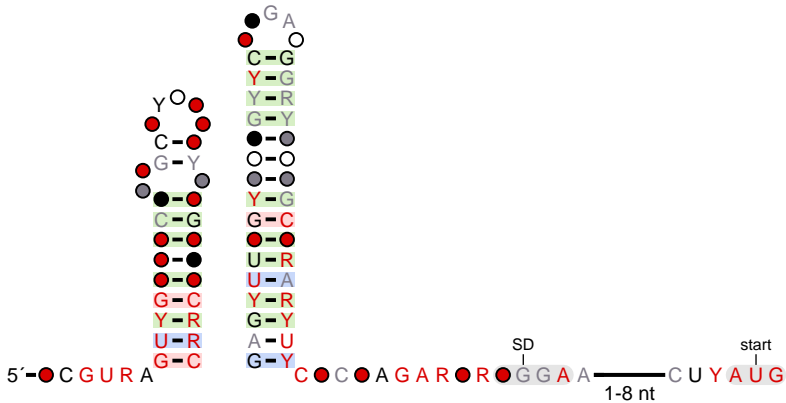




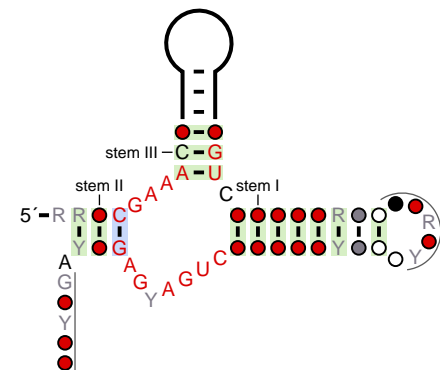
# group-II-DV-DVI



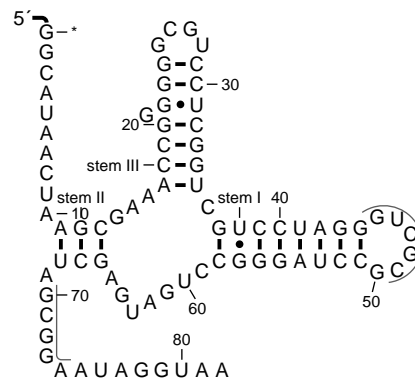
# gyrA



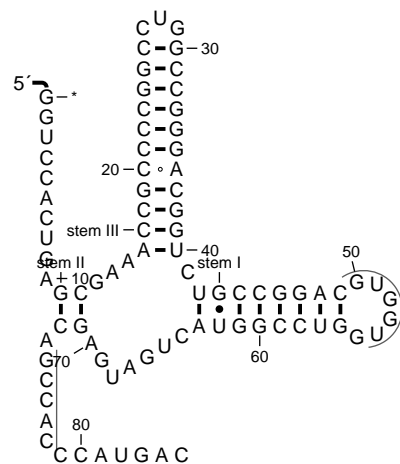
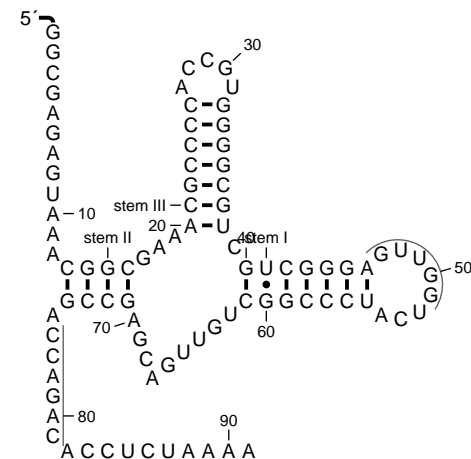
hammerhead-typell



hammerhead-typell NC\_003062.1/1182082-1182558



hammerhead-typell NC\_003345.1/10184-10663hammerhead-typell NC\_009818.1/8209-8688

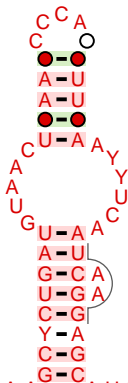


hammerhead-typell-pknot

subfam\_weight=1



hopC



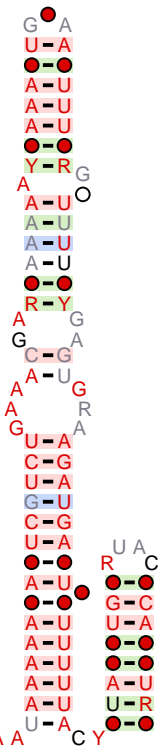
5'-YYAYAA A U C C C A U U G A Y A A G G A A A Y ● A U G

icd



5'-A ● YUGACGUC ● ACUGRUGCAYCCA

# lactis-plasmid



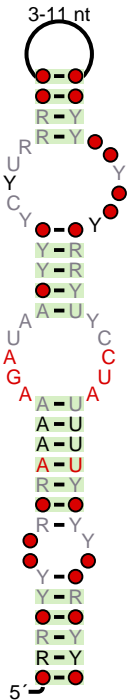
5'-C C A A A A A

C Y

lacto-1



# lacto-2

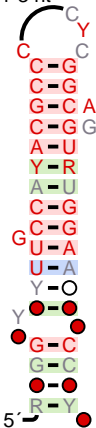




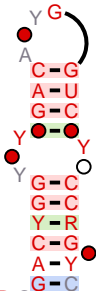
5'-A A U A A ●●●●● A A ●●● G A G G ●●● C ●●● R A <sup>A=U</sup> <sup>G=C</sup> ●●● G G R C G U C U U U U U

# livK

1-3 nt



2-3 nt



Int



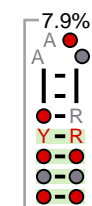
manA skeleton-with-bp varhairpin=1 var-right-stem=1



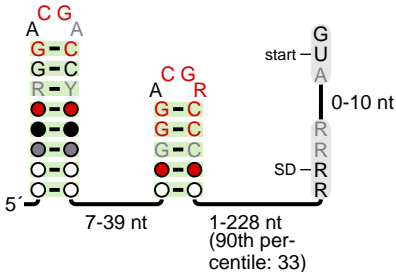
manA-pknot2  
subfam\_weight=1



manA-var3  
subfam\_weight=0.0794949



# mini-ykkC

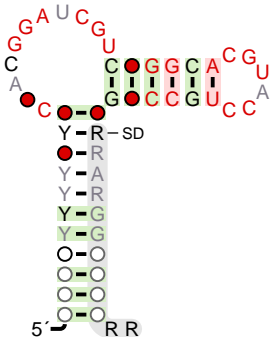


mraW

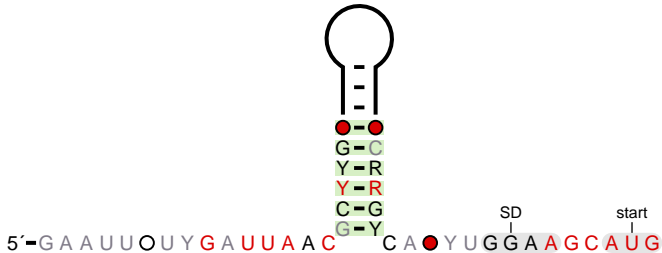


5' ↘

msik

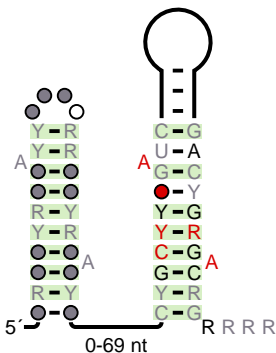


nuoG



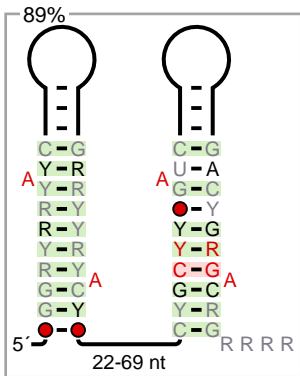


pan



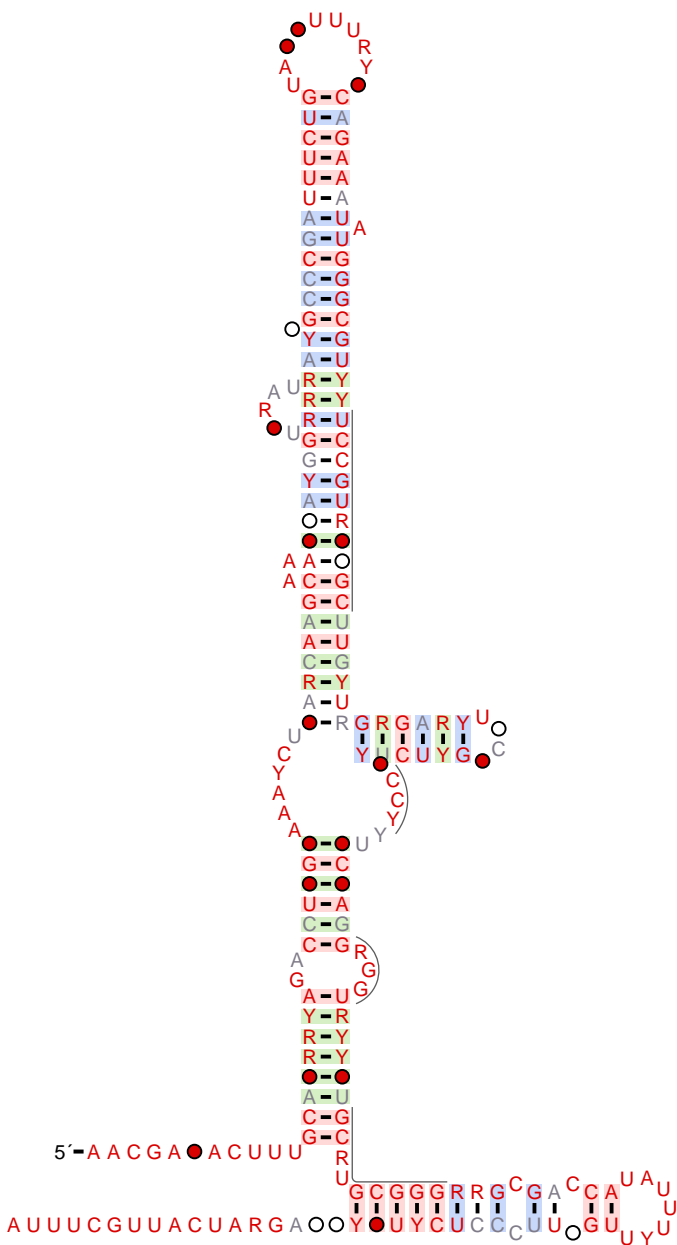
pan-two

subfam\_weight=0.893289



pedo-repair-p1  
subfam\_weight=1

subfam\_weight=1

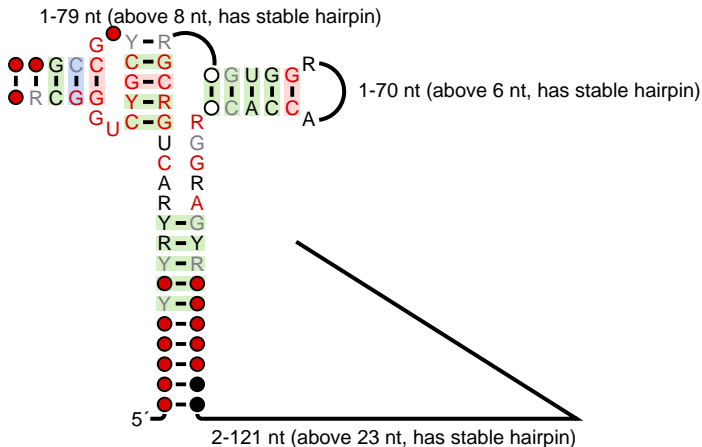


pedo-repair-p2

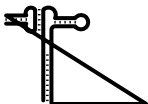
subfam\_weight=1



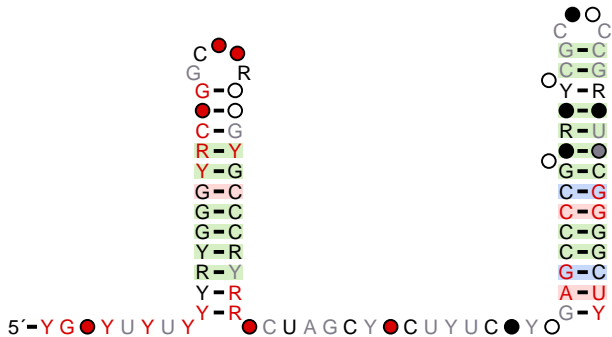
pfl



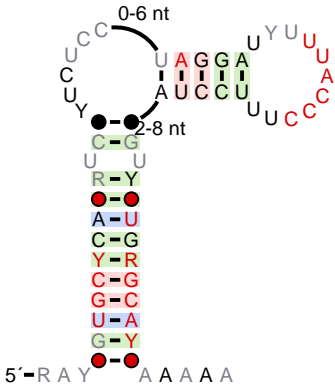
pfl skeleton-with-bp



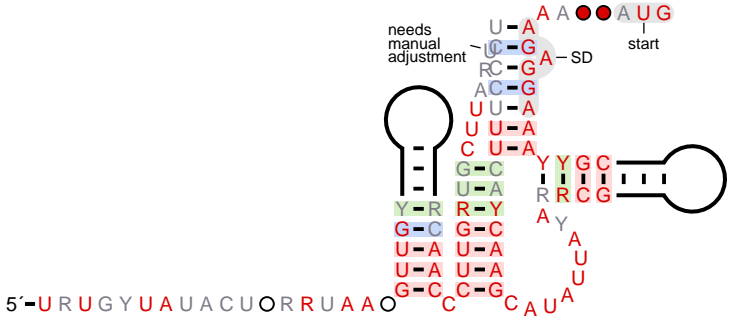
pheA



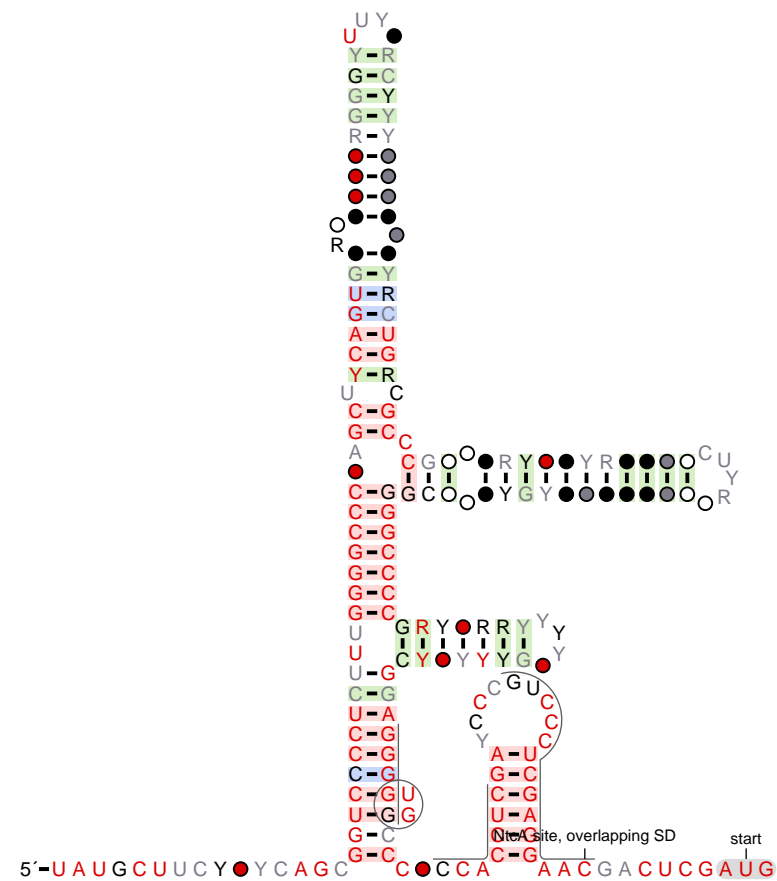
## potC



preQ1-II



psaA



psaA-cung2

subfam\_weight=0.164709

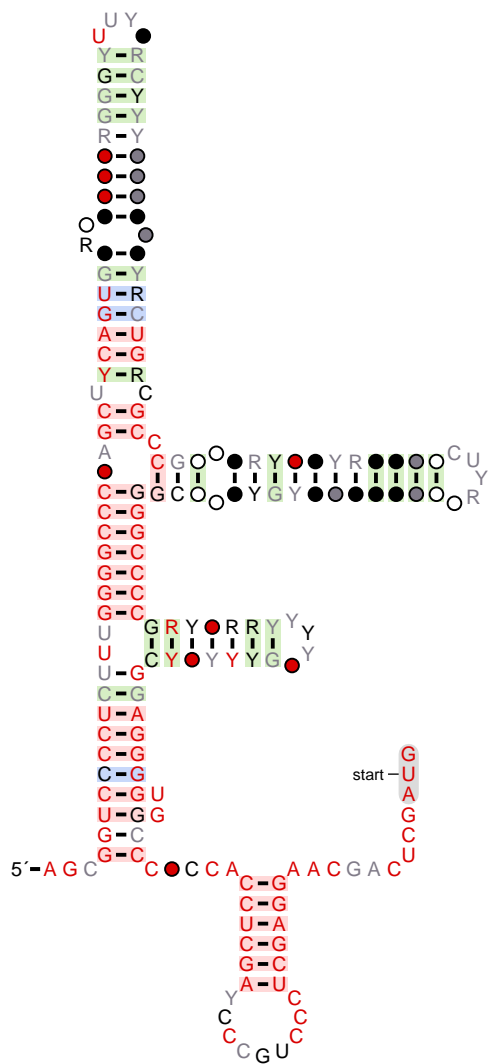


psaA-uncg1

subfam\_weight=0.611264



psaA R2R-paper=1



psaA-cung3

subfam\_weight=0.0980232

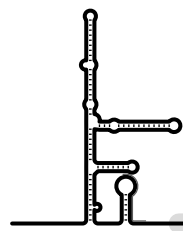


psaA-uncg2

subfam\_weight=0.163149

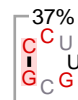


psaA skeleton-with-bp



psaA-cyygn2

subfam\_weight=0.374591

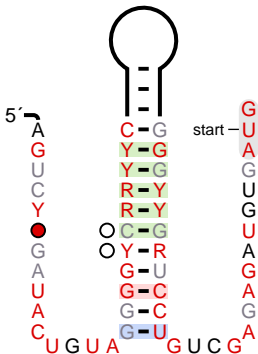


psaA-uncg3

subfam\_weight=0.430613



psbNH





purD



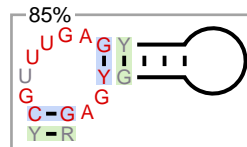
purD-MODSTEM2

subfam\_weight=0.148241



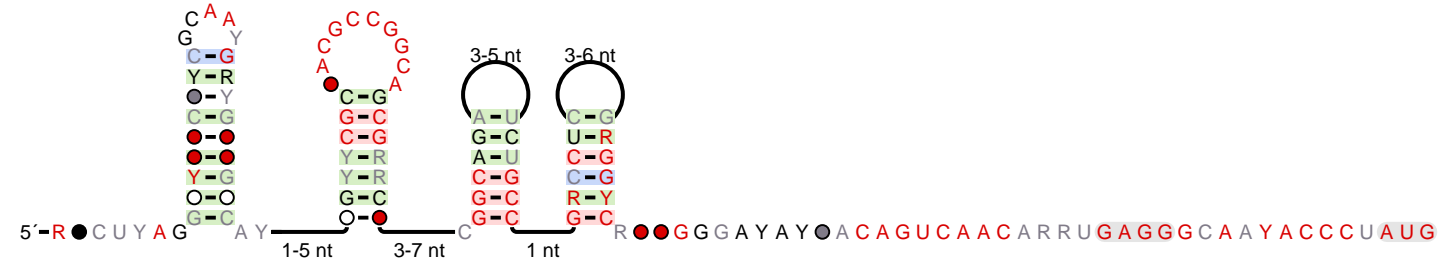
## purD-MODSTEM

subfam\_weight=0.851759

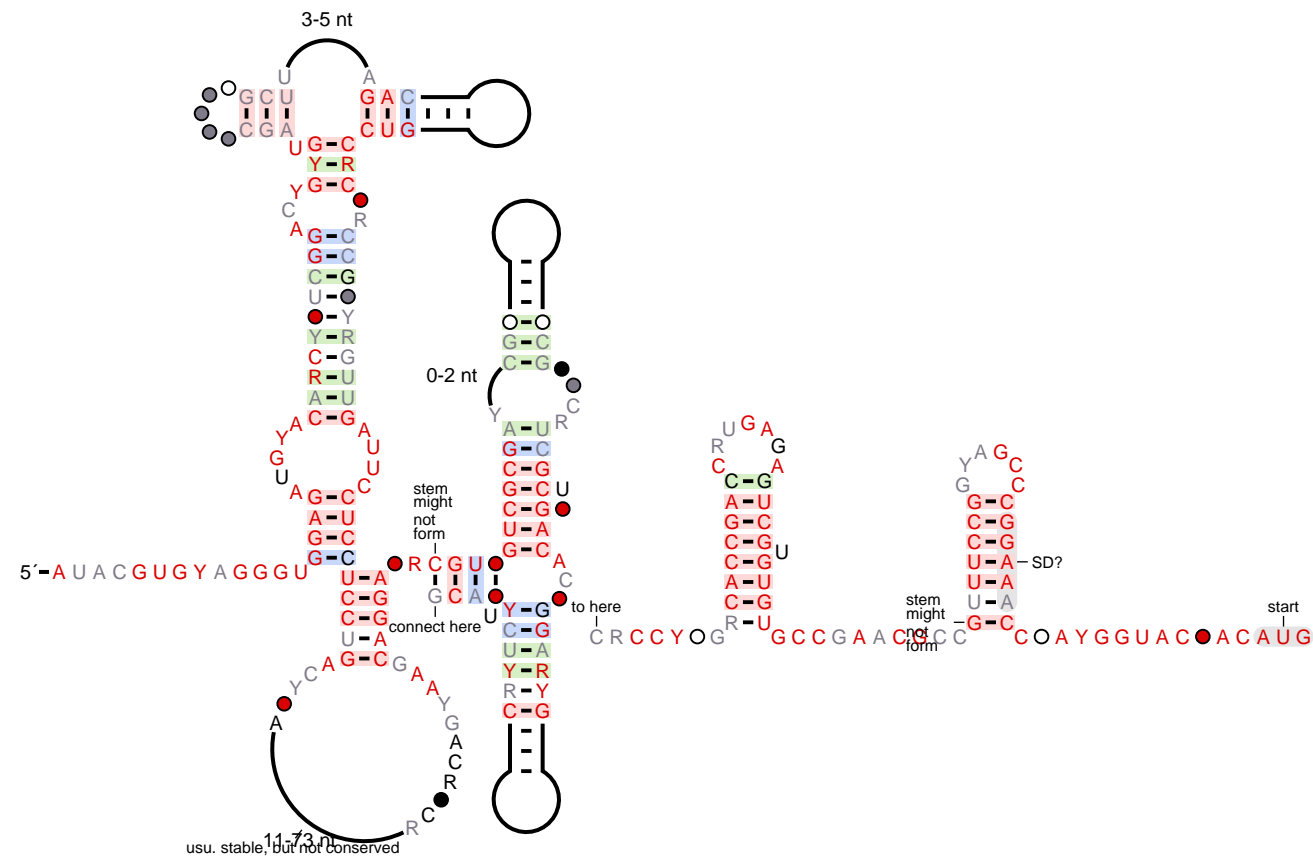
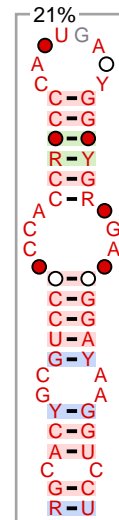




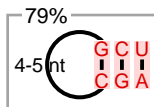
rnf



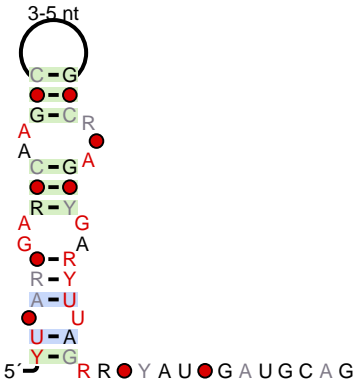
rne-II-O1  
subfam\_weight=0.21294



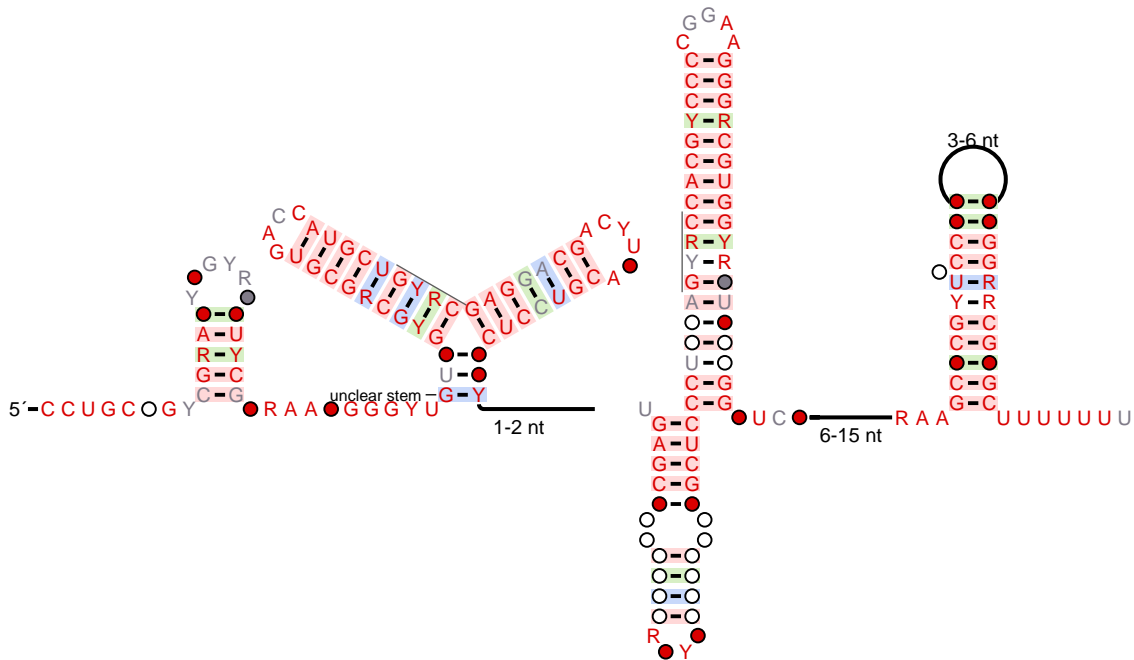
rne-II-O2  
subfam\_weight=0.78706

usu. stable, but not conserved<sup>11-73 nt</sup>

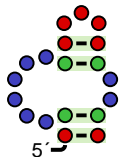
# sanguinis-hairpin



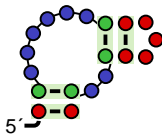
sbcd



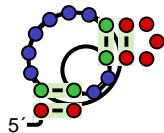
solver-formulation1-1



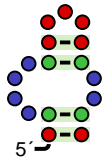
solver-formulation1-1 solver=1



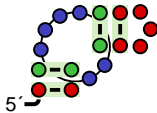
solver-formulation1-1 solver=2



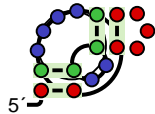
solver-formulation2-1



solver-formulation2-1 solver=1



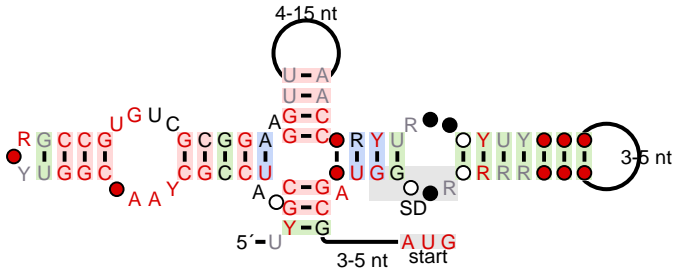
solver-formulation2-1 solver=2







# sucA

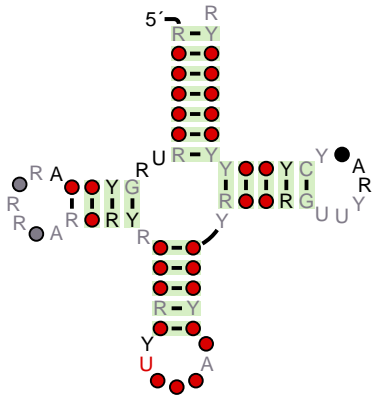


sucC



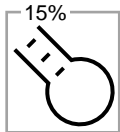
tRNA	tRNA skeleton-with-bp
	

tRNA skeleton-with-bp

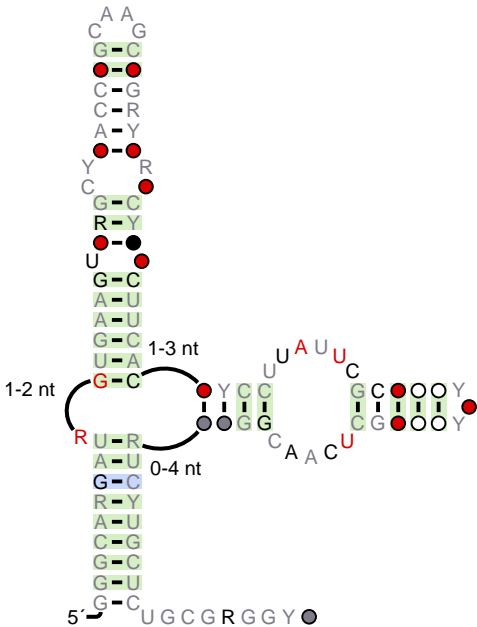


tRNA-var

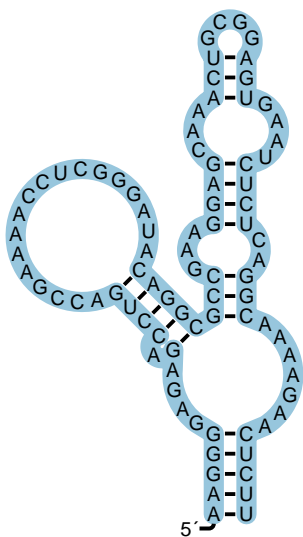
subfam\_weight=0.154412



## traJ-II

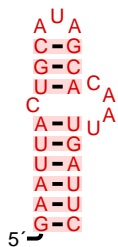


two-glycine Bsu-1

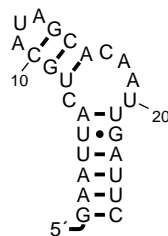


The diagram illustrates the cloverleaf secondary structure of a tRNA molecule. The structure is composed of several stems and loops. The acceptor stem is at the top, followed by the D arm, the anticodon arm, and the T arm. The anticodon is 3'-UAC-5'. The structure is color-coded: blue for the stems and red for the loops.

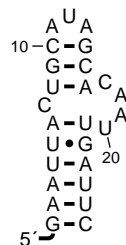
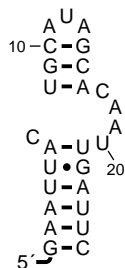
uneven-internal-loop



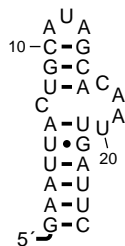
uneven-internal-loop seq layout=anyangle



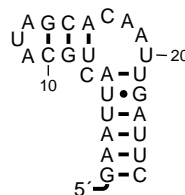
uneven-internal-loop seq layout=broken-leftuneven-internal-loop seq layout=default



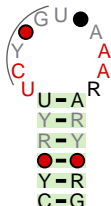
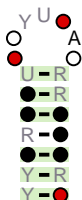
uneven-internal-loop seq layout=left-turn



uneven-internal-loop seq layout=left-turn-multistem



wcaG



5'-G U U U U G G U G C G G A C C Y R G U U U U G G C G ● G C

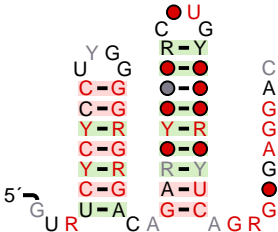
wcaG-pknot

subfam\_weight=1

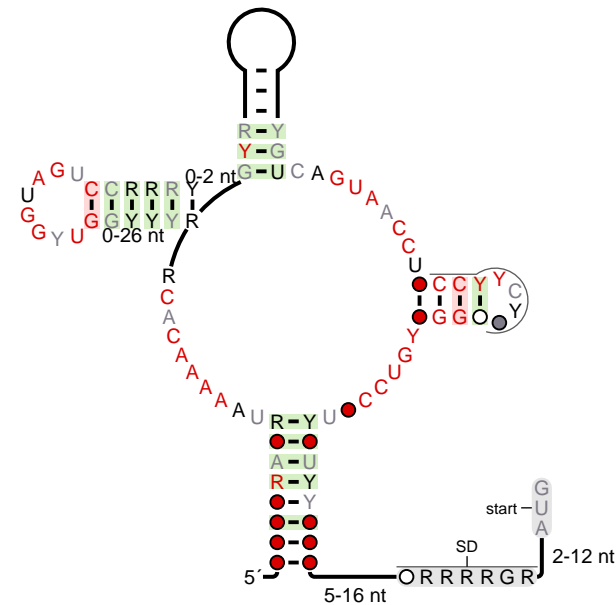




whalefall-1

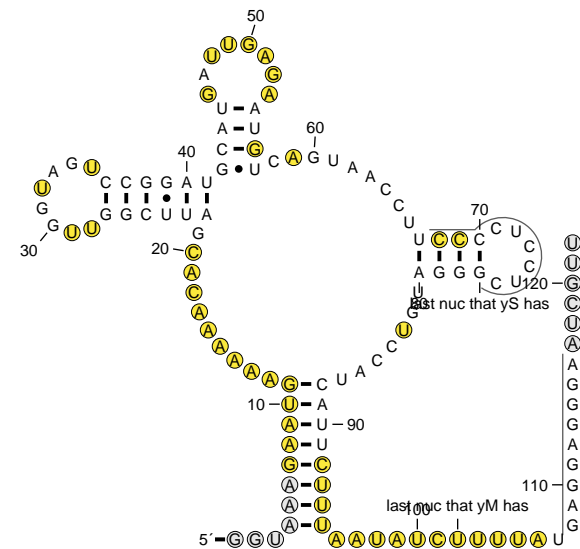


yjdF

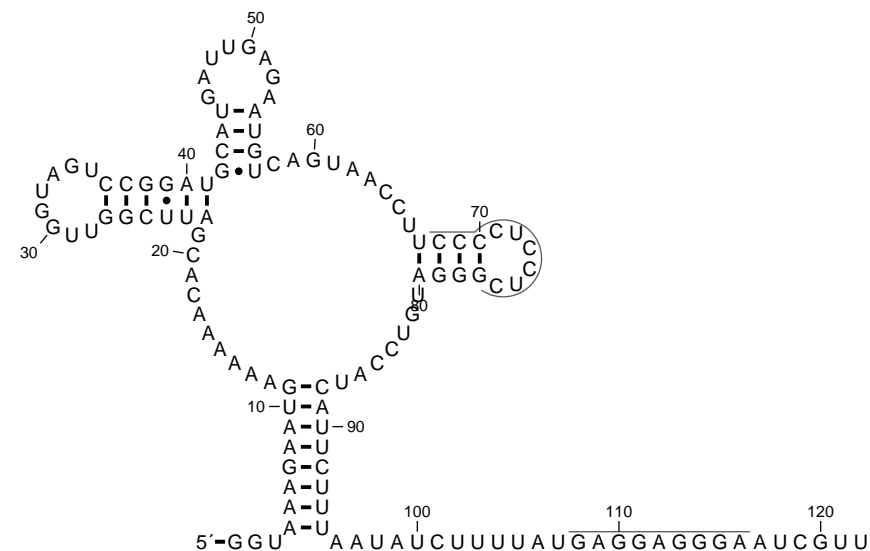


yjdF NC\_000964.2/1274965-1275471:L

Shrinking nucs & bonds using  
nucShrinkWithCircleNuc and pairBondScaleWithOneSeq  
because circle\_nuc or #=GR ... CLEAVAGE was used  
Set these vars to 1 using SetDrawingParam  
to disable. See note1 in manual.



yjdF NC\_000964.2/1274965-1275471:S

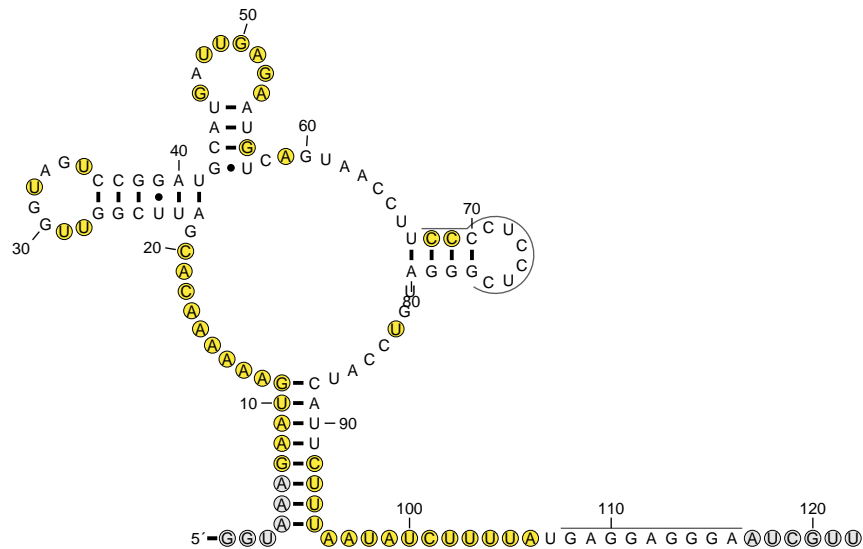


yjdF-altstem  
subfam\_weight=1



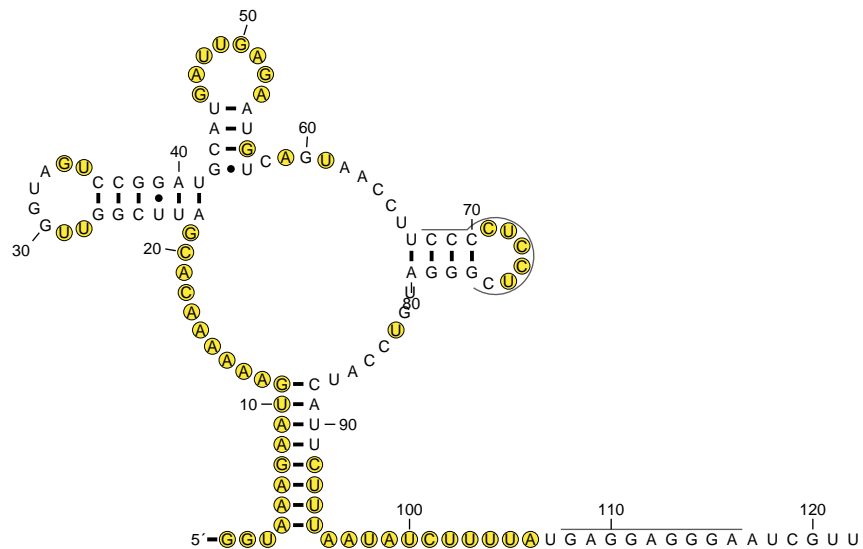
yjdF NC\_000964.2/1274965-1275471

Shrinking nucs & bonds using  
nucShrinkWithCircleNuc and pairBondScaleWithOneSeq  
because circle\_nuc or #=GR ... CLEAVAGE was used  
Set these vars to 1 using SetDrawingParam  
to disable. See note1 in manual.



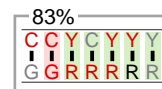
yjdF NC\_000964.2/1274965-1275471:M

Shrinking nucs & bonds using  
nucShrinkWithCircleNuc and pairBondScaleWithOneSeq  
because circle\_nuc or #=GR ... CLEAVAGE was used  
Set these vars to 1 using SetDrawingParam  
to disable. See note1 in manual.

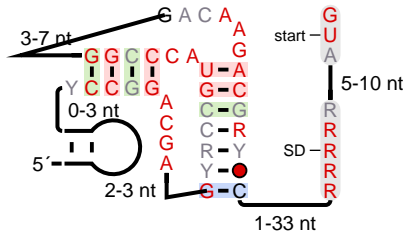


yjdF-AUG

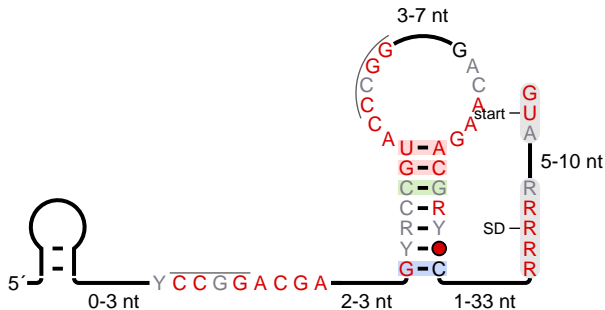
subfam\_weight=0.832593



ykkC-III



ykkC-III callout-style=1



ykkC-III debug\_place\_explicit=trueykkC-III pseudoknot=1

