

Supplementary Materials

Predicted Fold-backs

Fold-back secondary structures were predicted with the computer program RNAfold, using the Zuker algorithm (6, 7). The cloned RNA (or a predicted homolog) was folded with flanking sequence in two contexts, either 70 nt of upstream sequence with 15 nt of downstream sequence, or 15 nt of upstream sequence with 70 nt of downstream sequence. Optimal folds, as predicted by RNAfold, can be viewed using the links of Supplemental Table 1. To determine the chance occurrence of predicted fold-back structures within the *C. elegans* genome, 1000 genomic segments 22 nt in length were randomly selected and folded as for the cloned RNAs and their homologs. Less than 5% of these randomly generated segments resided within a sequence context that might have been scored as a plausible miRNA fold-back structure.

Supplemental Table 1. Table of links to predicted fold-back structures for miRNAs from <i>C.elegans</i> and other animals.			
<i>C. elegans</i>	<i>C. briggsae</i>	<i>D. melanogaster</i>	<i>H. sapiens</i>
let-7	let-7	let-7	let-7
lin-4	lin-4		
miR-1	miR-1	miR-1	miR-1
miR-2	miR-2	miR-2	
miR-34	miR-34	miR-34	miR-34
mir-35	miR-35:miR-41		
miR-36	" —		
miR-37	" —		
miR-38	" —		
miR-39	" —		
miR-40	" —		
miR-41	" —		
miR-42	miR-42		
miR-43	miR-43		
miR-44	miR-44		
miR-45	miR-45		
miR-46	miR-46		
miR-47	miR-47		

miR-48	miR-48		
miR-49	miR-49		
miR-50	miR-50		
miR-51	miR-51		
miR-52	miR-52		
miR-53			
miR-54	miR-54:miR-56		
miR-55	"		
miR-56	"		
miR-57	miR-57		
miR-58	miR-58		
miR-59	miR-59		
miR-60	miR-60	miR-60	miR-60
miR-61	miR-61		
miR-62	miR-62		
miR-63			
miR-64			
miR-65	miR-65		
miR-66			
miR-67	miR-67		
miR-68			
miR-69			
miR-70	miR-70		
miR-71	miR-71		
miR-72			
miR-73	miR-73		
miR-74	miR-74		

miR-75	miR-75		
miR-76	miR-76		
miR-77	miR-77		
miR-78			
miR-79	miR-79	miR-79	
miR-80	miR-80		
miR-81	miR-81		
miR-82	miR-82		
miR-83	miR-83		
miR-84	miR-84	miR-84	miR-84
miR-85	miR-85		
miR-86	miR-86		

Methods for Cloning miRNAs.

Total RNA was extracted from a flash-frozen pellet of mixed-stage wild-type N2-strain nematodes by using the Tri-Reagent protocol (Molecular Research Center, Inc.). Extracted RNA (500 µg) was combined with trace amounts of 5′-³²P-labeled RNA standards, AGCGUGUAGGGAUCCAAA and GGCCAACGUUCUCAACAAUAGUG++, 18 and 24-26 nt in length, respectively (where the length heterogeneity of the second standard was due to 0, 1, or 2 nontemplated nucleotides added during in vitro transcription, indicated by ++). RNA was then electrophoresed through a single 1.5 mm x 23 mm lane on a 15% polyacrylamide, 8 M urea gel. A gel fragment spanning both the 18 nt and 24-26 nt internal standards was excised, and RNA was eluted and ethanol-precipitated in siliconized tubes, with 20 µg of glycogen as carrier. Gel-purified 18-26 nt RNA (less than 1 µg) was incubated with 40 mM pre-adenylylated 3′-adaptor oligonucleotide, 50 mM HEPES pH 8.3, 10 mM MgCl₂, 3.3 mM dithiothreitol, 10 mg/mL BSA, 8.3% glycerol and 1 U/mL T4 RNA ligase (Amersham Pharmacia Biotech) in a 20 µl reaction at 22°C for 2 hours. The body of the 3′-adaptor oligonucleotide, a DNA oligo, pCTGTAGGCACCATCAATx (p, phosphate; x, O-C3 linker, which blocks the 3′-terminus, preventing it from participating in ligation) was synthesized by standard phosphoramidite chemistry, then activated by adenylation with adenosine 5′-phosphorimidazolide (2) and gel purified prior to use. The T4 RNA ligase reaction was purified on a 10% sequencing gel, by using the ligated forms of the standards as a guide, then added to a second T4 RNA ligase reaction, like the first except ATP (0.4 mM) was included, and a 5′-adaptor oligonucleotide, ATCGTtaggcaccugaaa (Dharmacon Research; uppercase, DNA; lowercase RNA) replaced the 3′-adaptor oligonucleotide. The ligated products from the second ligation reaction were gel-purified, excising the gel fragment spanning the doubly ligated standards. Based on the ligation efficiencies of the internal standards, the overall ligation efficiencies of *C. elegans* RNAs are estimated to have ranged from 30-90%, depending upon how well the *C. elegans* sequences matched the preferences of T4 RNA ligase (3). One quarter of the gel-purified doubly ligated RNA was used in a standard 50 µl reverse transcription (RT) reaction (SuperScript II, Gibco BRL) with the RT primer, ATTGATGGTGCCTACAG. The cDNA was amplified by PCR, using the RT primer and a completely DNA version of the 5′-adaptor oligo. PCR product was phenol-extracted, ethanol-precipitated, and then digested with Ban I (NEB), a restriction enzyme that cuts the non-palindromic sites present in the 3′ and 5′ adaptor oligos. After further phenol extraction and ethanol precipitation, the digested products were concatemerized with T4 DNA ligase (NEB). Concatemers ranging from 200-600 bp were isolated from a low-melt agarose gel, processed with Taq polymerase, and cloned into the pCR2.1-TOPO vector using the TOPO TA cloning kit (Invitrogen), as similarly described (1). PCR products spanning the insert were directly submitted for sequencing (Research Genetics, Inc.).

Sequences Not Matching *C. elegans* or *E. coli*

Fourty-four clones that did not match *C. elegans* or *E. coli* genomic sequences. Eleven matched the two oligoribonucleotides used as internal standards to follow the progress of the cloning. The remaining clones might represent RNAs of fungal contaminants, *C. elegans* RNAs processed or edited beyond recognition, or portions of the *C. elegans* genome that have not been sequenced. None matched *C. elegans* mitochondrial sequence. A few *C. elegans* clones were not perfect matches to the *C. elegans* genomic sequence. These single-nucleotide mismatches were attributed to errors introduced by reverse transcription or PCR, and were ignored if the other clones for the same miRNA matched the genomic sequence. When there were no other clones, the location of the mismatch is indicated by a lower-case nucleotide in Table 1. Two clones for miR-47 and one clone for miR-58 had an untemplated U at their 3' terminus, and one clone for miR-57 had an untemplated A at its 5' terminus.

Methods for Developmental Northern

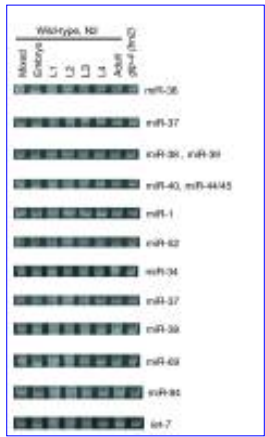
Eggs were harvested from gravid wild-type N2-strain nematodes by the standard bleaching method, and were hatched at 20°C without food for 20 hours, leading to arrest in early L1. Upon feeding, worms were allowed to grow at 20°C and harvested at specific time intervals based on inspection of P cell and vulval development to obtain synchronized cultures of L1, L2, L3, L4 and young adult worms. Gravid adult *glp-4 (bn2ts)* worms were first cultured at the permissive temperature (15°C), and were then bleached to harvest eggs. These eggs were then cultured at the non-permissive temperature (25°C) to adults. Total RNA was extracted as described for the cloning protocol and separated on a denaturing 15% polyacrylamide gel, with about 30 µg of RNA loaded per lane. RNA was electrophoretically transferred to Zeta-Probe GT membranes (BioRad) or GeneScreen Plus membranes (NEN) as indicated in Supplemental Table 2. A marker lane containing radiolabeled RNAs was also electrophoresed and transferred to the membranes. Membranes were baked and crosslinked as described (4), and hybridization and washing conditions were as prescribed for oligonucleotide probes by the ZetaProbe membrane manual. The oligonucleotides used as probes are listed in Supplemental Table 2. Probes were designed based on their predicted melting temperatures (5), and all probes were hybridized and washed at 50°C. Blots were analyzed by phosphorimaging (BAS2000, FujiMed). The miR-35—41 consensus probes were used as specificity controls. They did not match any miRNAs of the miR-35—41 cluster but instead corresponded to the miR-35—41 consensus sequence. The absence of signal from these control probes indicated that there was little if any cross-hybridization among probes matching members of the cluster.

Supplemental Table 2. Membranes and probes used for Northern analysis.

miRNA	Membrane	Probe
miR-1	Zeta-Probe GT	TACATACTTCTTTACATTCCA
miR-34	GeneScreen Plus	CAACCAGCTAACCACACTGC
miR-35	Zeta-Probe GT	ACTGCTAGTTTCCACCC
miR-36	Zeta-Probe GT	CATGCGAATTTTCACCCGG
miR-37	Zeta-Probe GT	ACTGCAAGTGTTACCCCG
miR-38	Zeta-Probe GT	ACTCCAGTTTTTCTCCC
miR-39	Zeta-Probe GT	CAAGCTGATTACACCCGGT
miR-40	Zeta-Probe GT	TTAGCTGATGTACACCCGG
miR-41	Zeta-Probe GT	TAGGTGATTTTTCACCCGG
miR-42	Zeta-Probe GT	CTGTAGATGTAAACCCGGTG
miR-43	GeneScreen Plus	GCGACAGCAAGTAACTGTGATA
miR-44/45	Zeta-Probe GT	AGCTGAATGTGTCTCTAGT
miR-46/47	GeneScreen Plus	TGAAGAGAGCGACTCCATGA

miR-52	Zeta-Probe GT	AGCACGGAAACATATGTACGGGTG
miR-56	GeneScreen Plus	CTCAGCGGAAACATTACGGGTA
miR-56*	GeneScreen Plus	TACAACCCAAAATGGATCCGCCA
miR-61	GeneScreen Plus	GATGAGTAACGGTTCTAGTCA
miR-62	GeneScreen Plus	CTGTAAGCTAGATTACATATCA
miR-68	GeneScreen Plus	TCTACACTTTTGAGTCTTCGA
miR-69	GeneScreen Plus	TCTACACTTTTTAATTTTCGA
miR-80	GeneScreen Plus	TCGGCTTTCAACTAATGATCTCA
miR-84	GeneScreen Plus	TACAATATTACATACTACCTCA
miR-35—41 consensus1	Zeta-Probe GT	AATGCTAATTTTCACCCGGT
miR-35—41 consensus2	Zeta-Probe GT	ATTGCTAATTTTCACCCGGT
let-7	GeneScreen Plus	ACTATACAACCTACTACCTCA

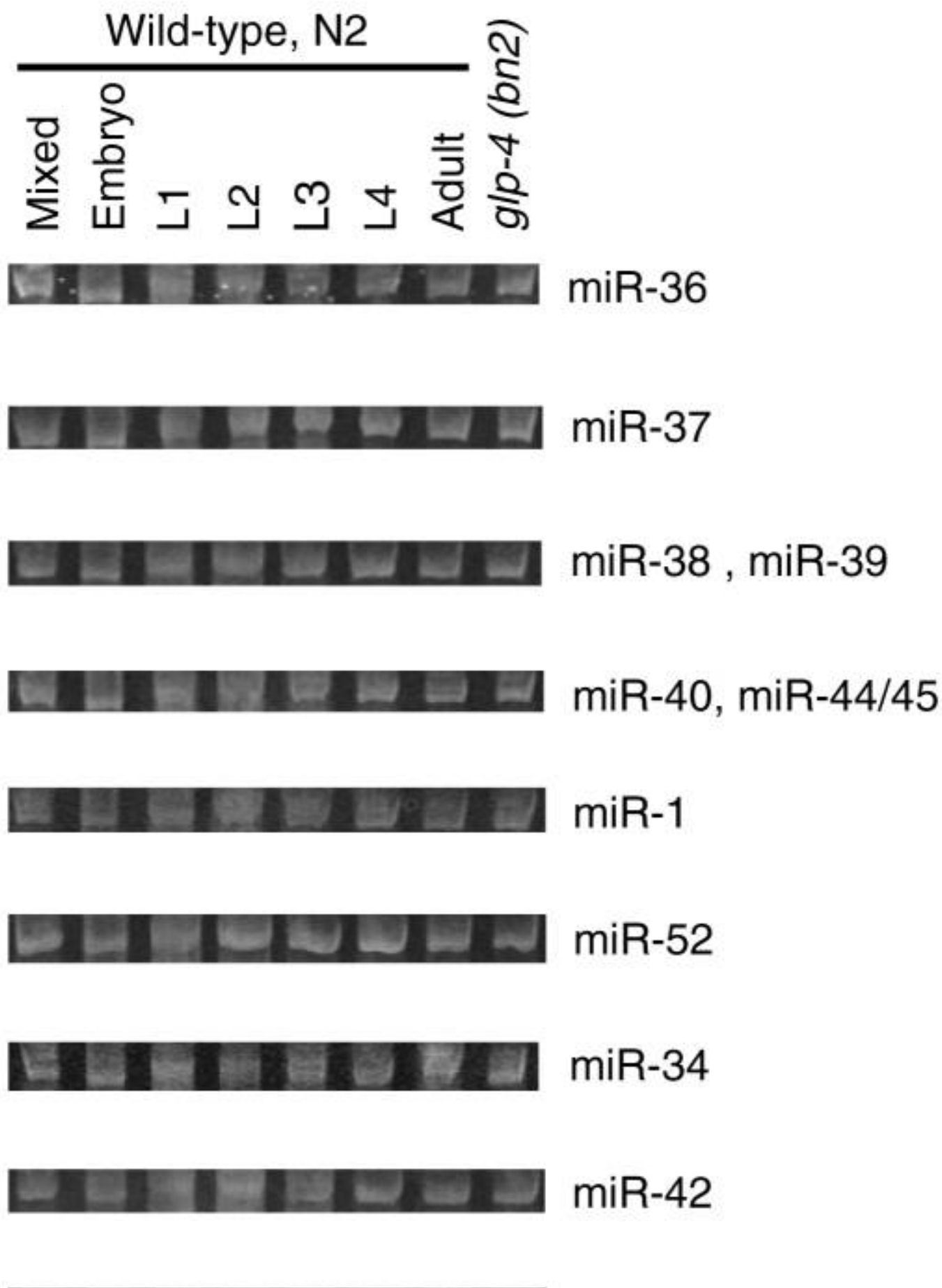
Supplemental Figure 1. 5S rRNA bands, used as loading controls for Northern blots.



[Full Size Version](#)

References

1. S. M. Elbashir, W. Lendeckel, T. Tuschl, *Genes Dev* **15**, 188-200 (2001).
2. P. J. Unrau, D. P. Bartel, *Nature* **395**, 260-3 (1998).
3. E. Romaniuk, L. W. McLaughlin, T. Neilson, P. J. Romaniuk, *Eur J Biochem* **125**, 639-43 (1982).
4. R. C. Lee, R. L. Feinbaum, V. Ambros, *Cell* **75**, 843-54 (1993).
5. N. Sugimoto, et al., *Biochemistry* **34**, 11211-6 (1995).
6. D. H. Mathews, J. Sabina, M. Zuker, D. H. Turner, *J Mol Biol* **288**, 911-40 (1999).
7. I. L. Hofacker, et al., *Monatshefte f. Chemie* **125**, 167-188 (1994).





miR-43



miR-69

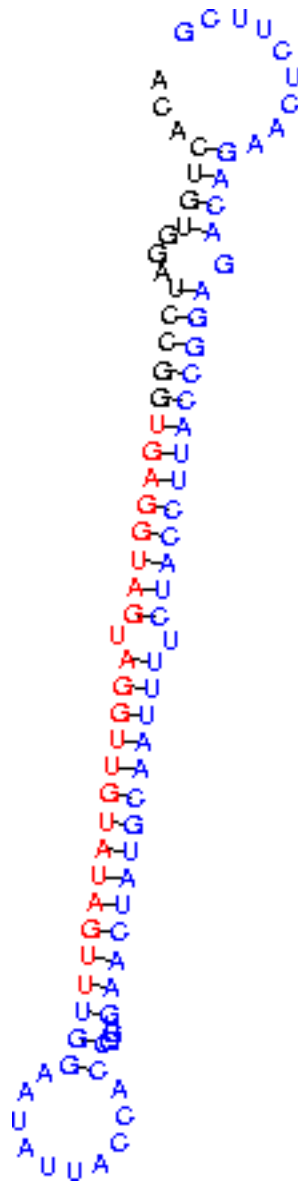


miR-84



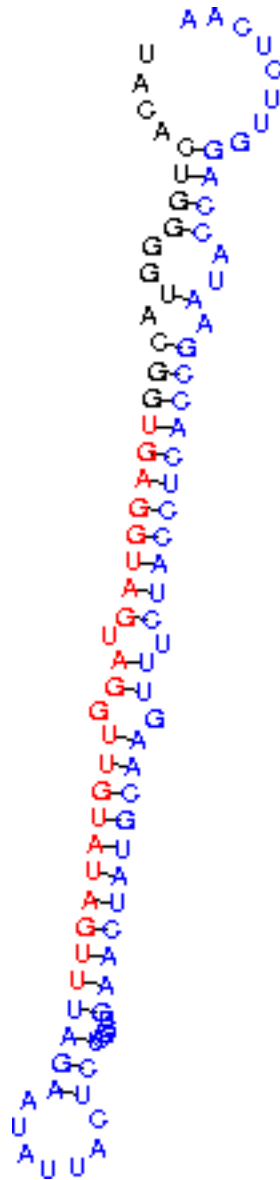
let-7

let-7



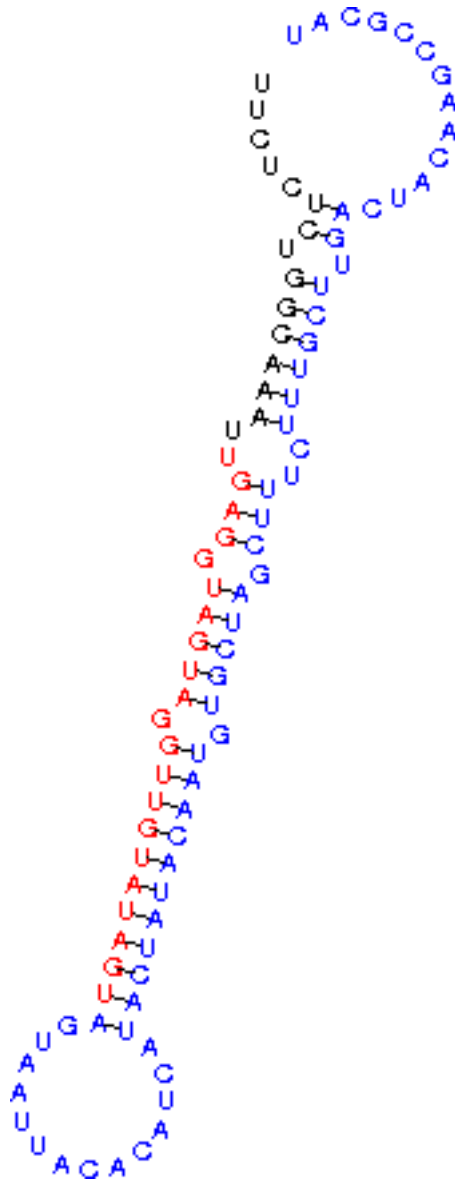
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of let-7 in *C. briggsae*



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of let-7 in *D. melanogaster*



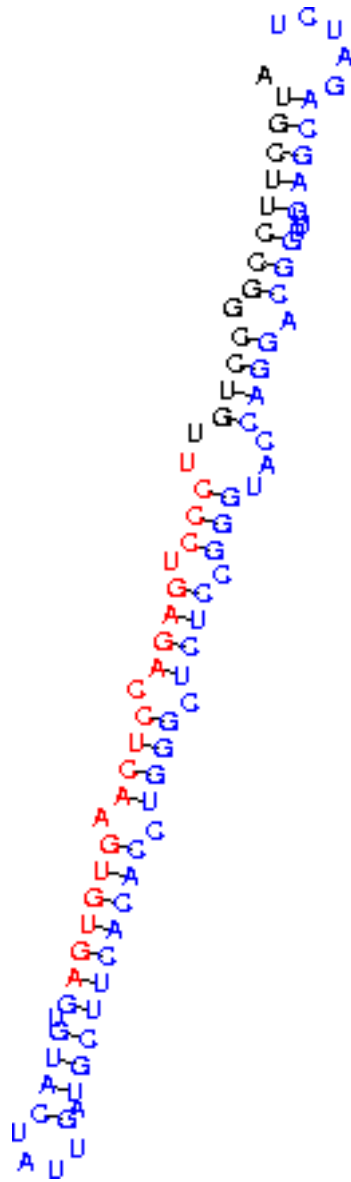
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potential ortholog of let-7 in *H. sapiens*



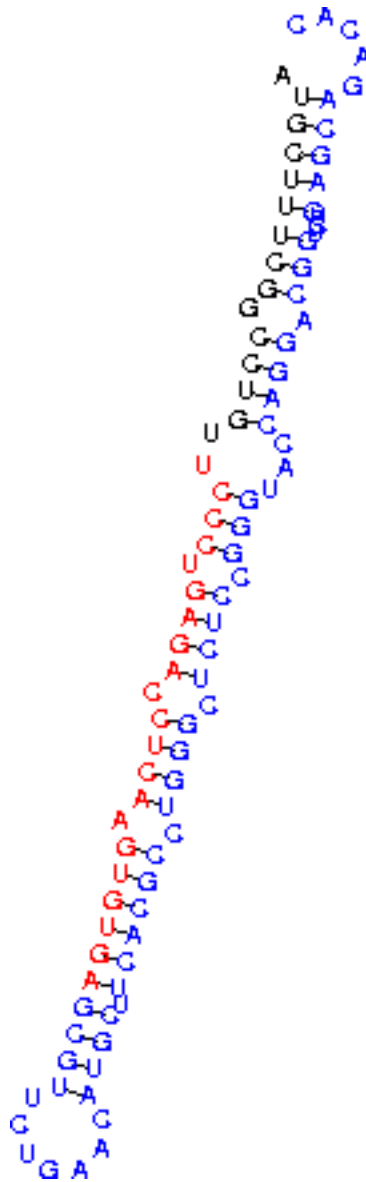
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lin-4



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

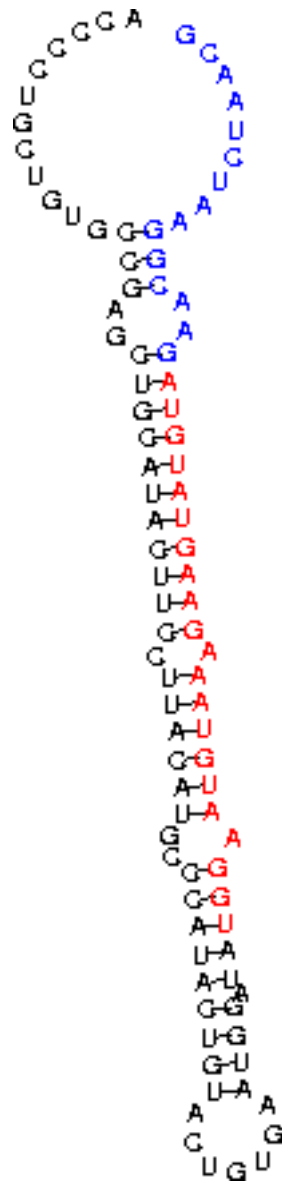
potential ortholog of lin-4 in *C. briggsae*



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

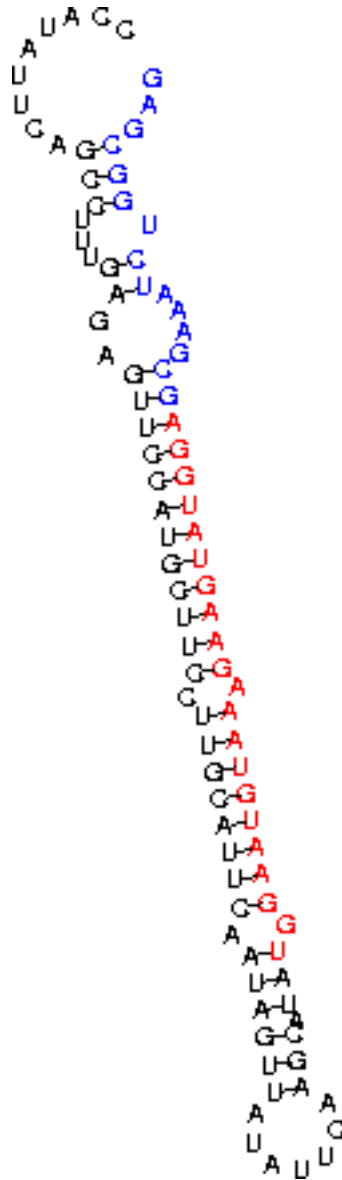
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-1 in *C. briggsae*



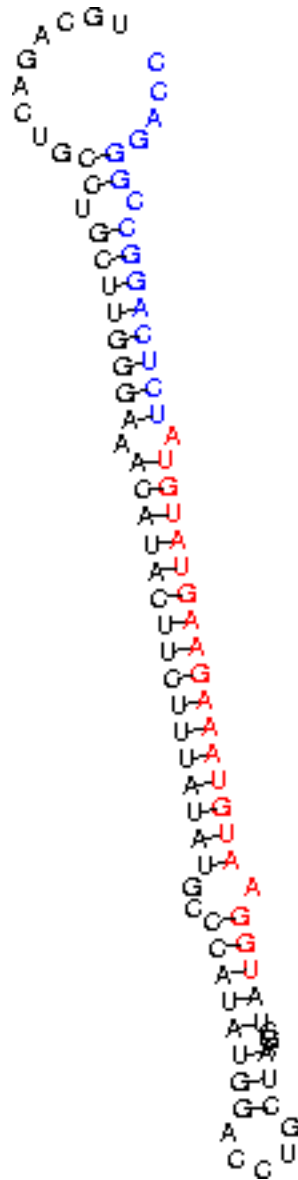
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-1 in *D. melanogaster*



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-1 in *H. sapiens*



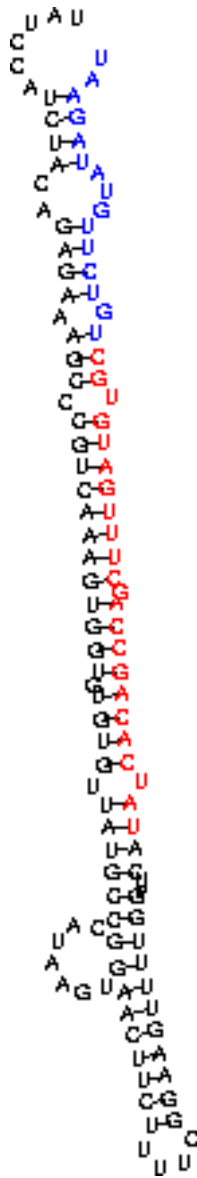
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miR-2



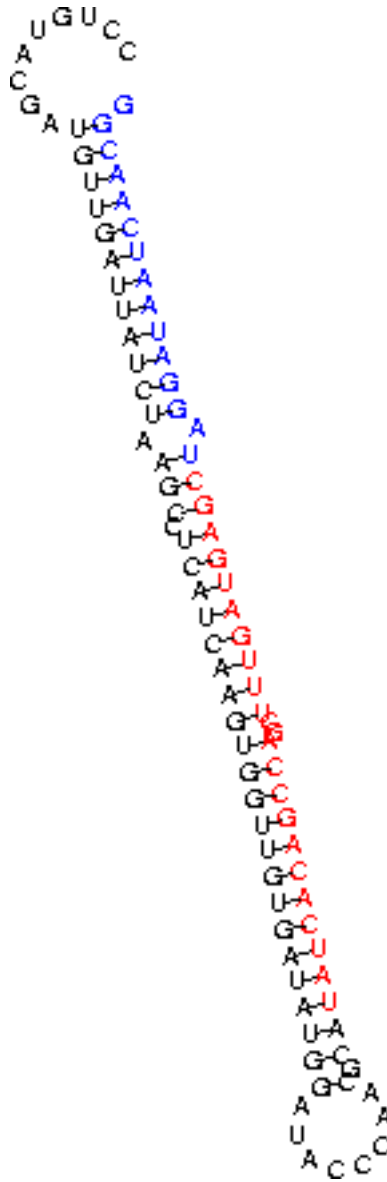
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-2 in *C. briggsae*



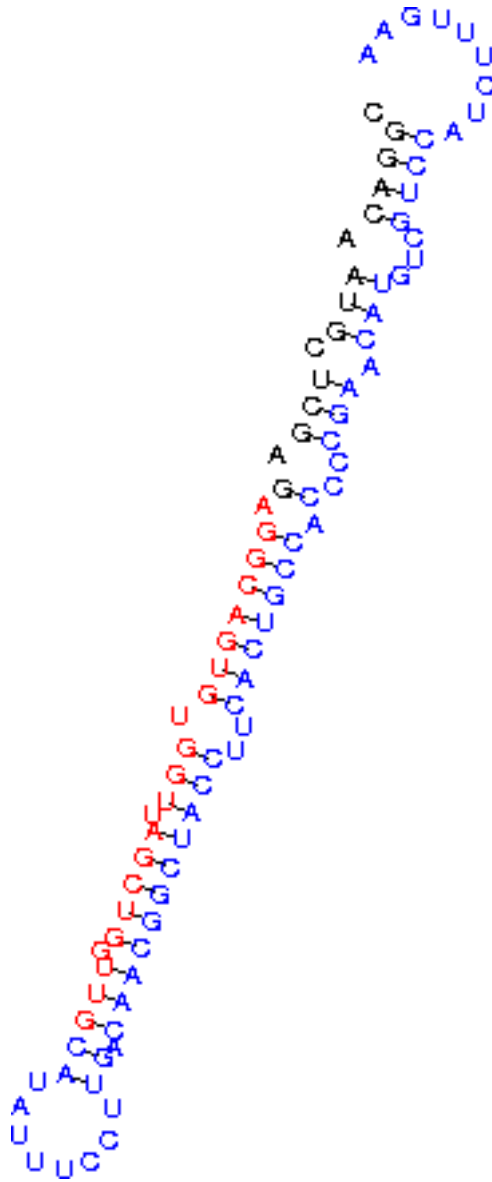
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potential ortholog of miR-2 in *D. melanogaster*



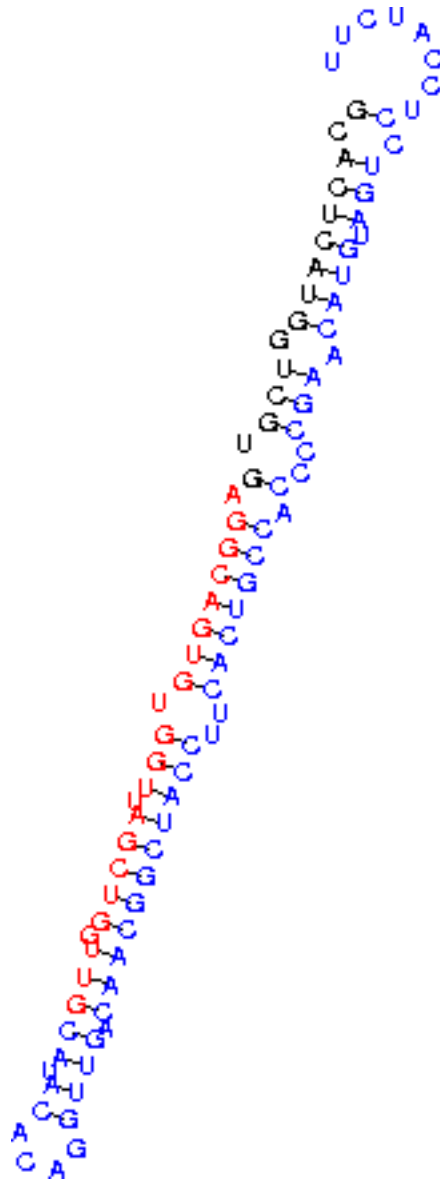
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miR-34



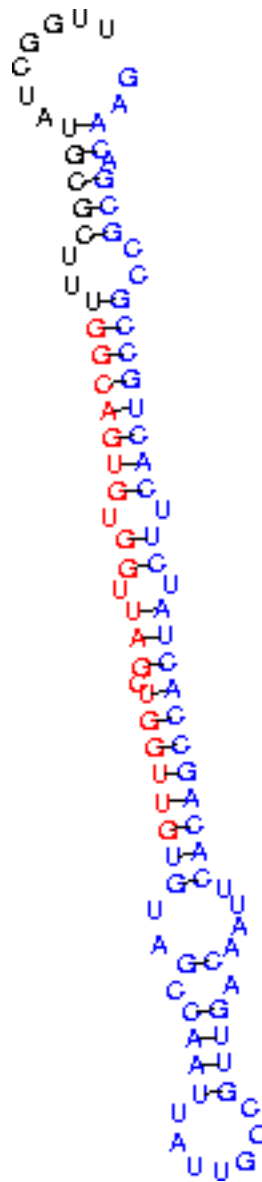
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-34 in *C. briggsae*



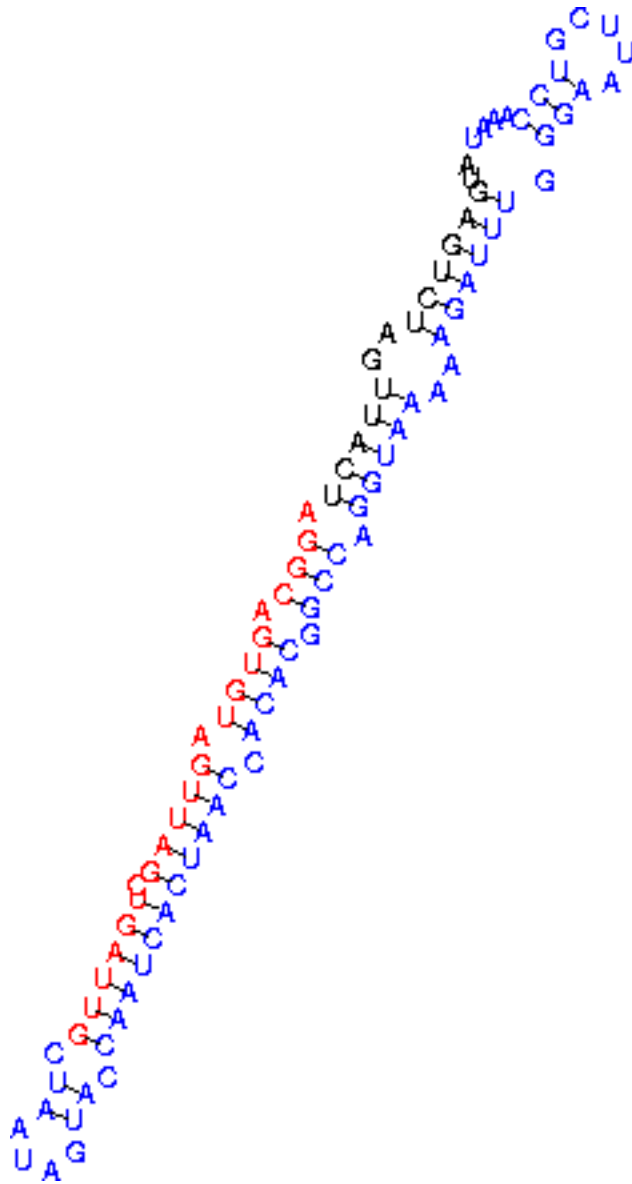
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-34 in *D. melanogaster*



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-34 in *H. sapiens*



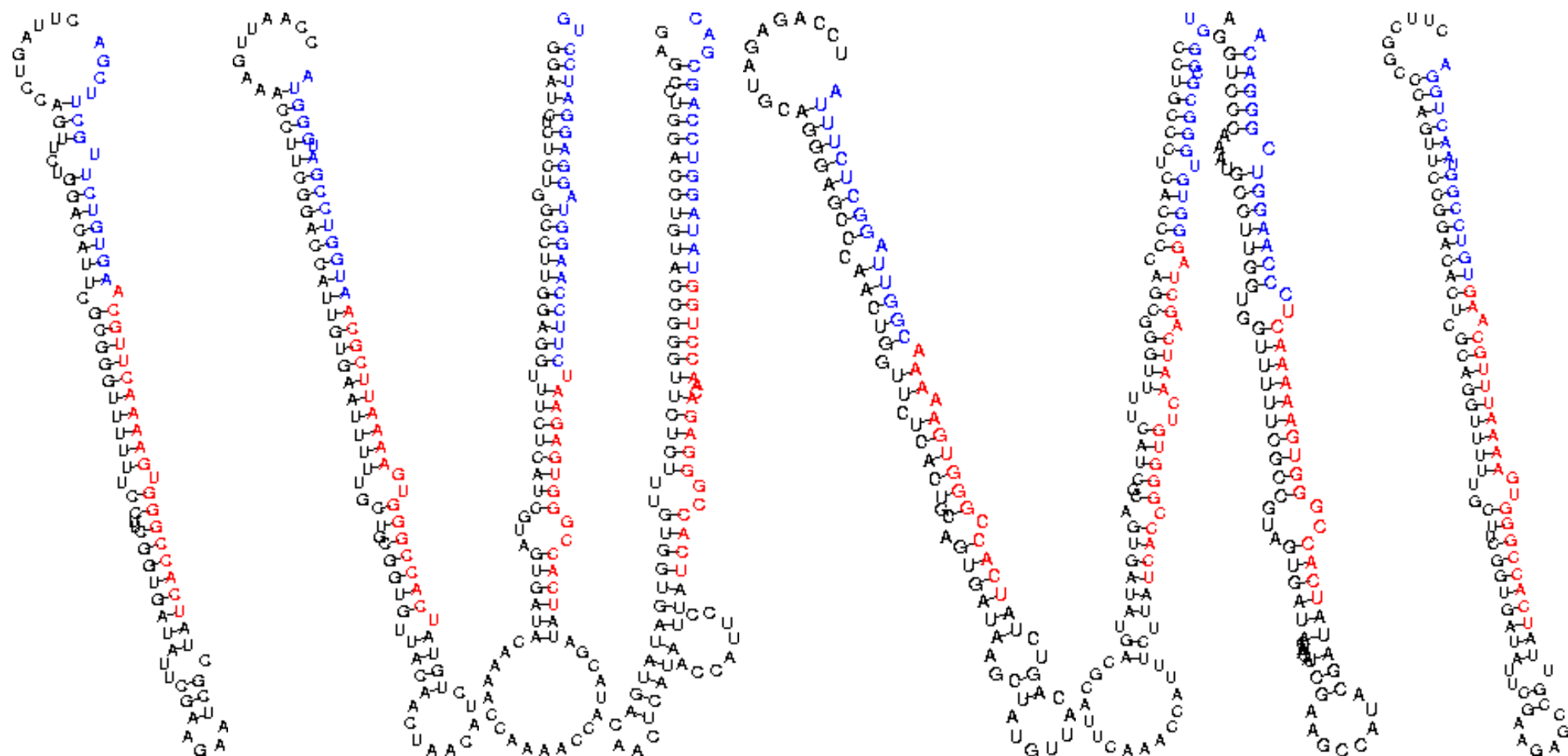
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

mir-35



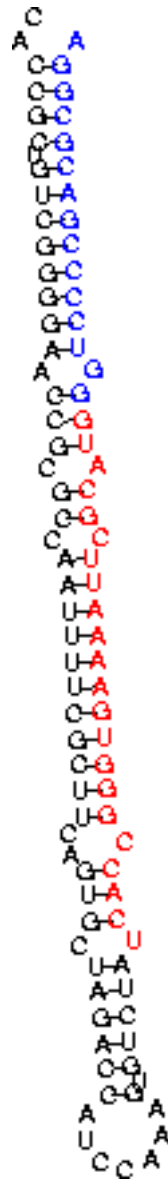
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-35 to miR-41 cluster in *C. briggsae*



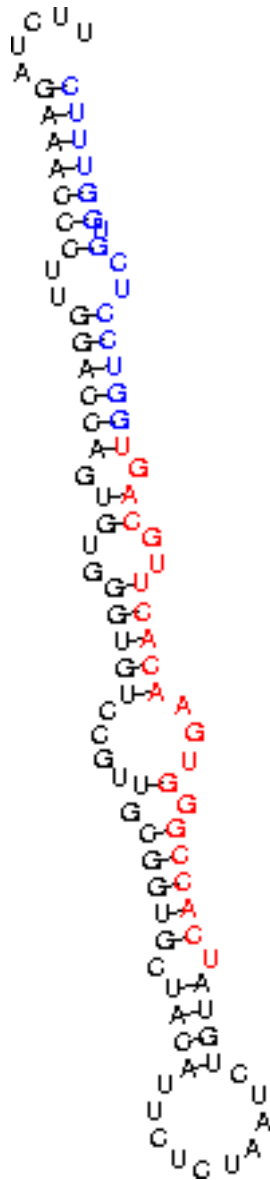
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-36



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-37

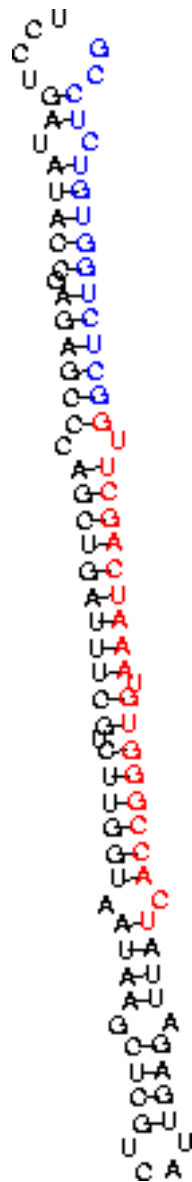


(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

U¹ G² U³
G⁴ U⁵ A⁶ G⁷ C⁸ U⁹ A¹⁰ G¹¹ C¹² U¹³ G¹⁴ C¹⁵ U¹⁶ A¹⁷ G¹⁸ C¹⁹ U²⁰ G²¹ C²² U²³ A²⁴ G²⁵ C²⁶ U²⁷ G²⁸ C²⁹ U³⁰ A³¹ G³² C³³ U³⁴ G³⁵ C³⁶ U³⁷ A³⁸ G³⁹ C⁴⁰ U⁴¹ G⁴² C⁴³ U⁴⁴ A⁴⁵ G⁴⁶ C⁴⁷ U⁴⁸ G⁴⁹ C⁵⁰ U⁵¹ A⁵² G⁵³ C⁵⁴ U⁵⁵ G⁵⁶ C⁵⁷ U⁵⁸ A⁵⁹ G⁶⁰ C⁶¹ U⁶² G⁶³ C⁶⁴ U⁶⁵ A⁶⁶ G⁶⁷ C⁶⁸ U⁶⁹ G⁷⁰ C⁷¹ U⁷² A⁷³ G⁷⁴ C⁷⁵ U⁷⁶ G⁷⁷ C⁷⁸ U⁷⁹ A⁸⁰ G⁸¹ C⁸² U⁸³ G⁸⁴ C⁸⁵ U⁸⁶ A⁸⁷ G⁸⁸ C⁸⁹ U⁹⁰ G⁹¹ C⁹² U⁹³ A⁹⁴ G⁹⁵ C⁹⁶ U⁹⁷ G⁹⁸ C⁹⁹ U¹⁰⁰ A¹⁰¹ G¹⁰² C¹⁰³ U¹⁰⁴ G¹⁰⁵ C¹⁰⁶ U¹⁰⁷ A¹⁰⁸ G¹⁰⁹ C¹¹⁰ U¹¹¹ G¹¹² C¹¹³ U¹¹⁴ A¹¹⁵ G¹¹⁶ C¹¹⁷ U¹¹⁸ G¹¹⁹ C¹²⁰ U¹²¹ A¹²² G¹²³ C¹²⁴ U¹²⁵ G¹²⁶ C¹²⁷ U¹²⁸ A¹²⁹ G¹³⁰ C¹³¹ U¹³² G¹³³ C¹³⁴ U¹³⁵ A¹³⁶ G¹³⁷ C¹³⁸ U¹³⁹ G¹⁴⁰ C¹⁴¹ U¹⁴² A¹⁴³ G¹⁴⁴ C¹⁴⁵ U¹⁴⁶ G¹⁴⁷ C¹⁴⁸ U¹⁴⁹ A¹⁵⁰ G¹⁵¹ C¹⁵² U¹⁵³ G¹⁵⁴ C¹⁵⁵ U¹⁵⁶ A¹⁵⁷ G¹⁵⁸ C¹⁵⁹ U¹⁶⁰ G¹⁶¹ C¹⁶² U¹⁶³ A¹⁶⁴ G¹⁶⁵ C¹⁶⁶ U¹⁶⁷ G¹⁶⁸ C¹⁶⁹ U¹⁷⁰ A¹⁷¹ G¹⁷² C¹⁷³ U¹⁷⁴ G¹⁷⁵ C¹⁷⁶ U¹⁷⁷ A¹⁷⁸ G¹⁷⁹ C¹⁸⁰ U¹⁸¹ G¹⁸² C¹⁸³ U¹⁸⁴ A¹⁸⁵ G¹⁸⁶ C¹⁸⁷ U¹⁸⁸ G¹⁸⁹ C¹⁹⁰ U¹⁹¹ A¹⁹² G¹⁹³ C¹⁹⁴ U¹⁹⁵ G¹⁹⁶ C¹⁹⁷ U¹⁹⁸ A¹⁹⁹ G²⁰⁰ C²⁰¹ U²⁰² G²⁰³ C²⁰⁴ U²⁰⁵ A²⁰⁶ G²⁰⁷ C²⁰⁸ U²⁰⁹ G²¹⁰ C²¹¹ U²¹² A²¹³ G²¹⁴ C²¹⁵ U²¹⁶ G²¹⁷ C²¹⁸ U²¹⁹ A²²⁰ G²²¹ C²²² U²²³ G²²⁴ C²²⁵ U²²⁶ A²²⁷ G²²⁸ C²²⁹ U²³⁰ G²³¹ C²³² U²³³ A²³⁴ G²³⁵ C²³⁶ U²³⁷ G²³⁸ C²³⁹ U²⁴⁰ A²⁴¹ G²⁴² C²⁴³ U²⁴⁴ G²⁴⁵ C²⁴⁶ U²⁴⁷ A²⁴⁸ G²⁴⁹ C²⁵⁰ U²⁵¹ G²⁵² C²⁵³ U²⁵⁴ A²⁵⁵ G²⁵⁶ C²⁵⁷ U²⁵⁸ G²⁵⁹ C²⁶⁰ U²⁶¹ A²⁶² G²⁶³ C²⁶⁴ U²⁶⁵ G²⁶⁶ C²⁶⁷ U²⁶⁸ A²⁶⁹ G²⁷⁰ C²⁷¹ U²⁷² G²⁷³ C²⁷⁴ U²⁷⁵ A²⁷⁶ G²⁷⁷ C²⁷⁸ U²⁷⁹ G²⁸⁰ C²⁸¹ U²⁸² A²⁸³ G²⁸⁴ C²⁸⁵ U²⁸⁶ G²⁸⁷ C²⁸⁸ U²⁸⁹ A²⁹⁰ G²⁹¹ C²⁹² U²⁹³ G²⁹⁴ C²⁹⁵ U²⁹⁶ A²⁹⁷ G²⁹⁸ C²⁹⁹ U³⁰⁰ G³⁰¹ C³⁰² U³⁰³ A³⁰⁴ G³⁰⁵ C³⁰⁶ U³⁰⁷ G³⁰⁸ C³⁰⁹ U³¹⁰ A³¹¹ G³¹² C³¹³ U³¹⁴ G³¹⁵ C³¹⁶ U³¹⁷ A³¹⁸ G³¹⁹ C³²⁰ U³²¹ G³²² C³²³ U³²⁴ A³²⁵ G³²⁶ C³²⁷ U³²⁸ G³²⁹ C³³⁰ U³³¹ A³³² G³³³ C³³⁴ U³³⁵ G³³⁶ C³³⁷ U³³⁸ A³³⁹ G³⁴⁰ C³⁴¹ U³⁴² G³⁴³ C³⁴⁴ U³⁴⁵ A³⁴⁶ G³⁴⁷ C³⁴⁸ U³⁴⁹ G³⁵⁰ C³⁵¹ U³⁵² A³⁵³ G³⁵⁴ C³⁵⁵ U³⁵⁶ G³⁵⁷ C³⁵⁸ U³⁵⁹ A³⁶⁰ G³⁶¹ C³⁶² U³⁶³ G³⁶⁴ C³⁶⁵ U³⁶⁶ A³⁶⁷ G³⁶⁸ C³⁶⁹ U³⁷⁰ G³⁷¹ C³⁷² U³⁷³ A³⁷⁴ G³⁷⁵ C³⁷⁶ U³⁷⁷ G³⁷⁸ C³⁷⁹ U³⁸⁰ A³⁸¹ G³⁸² C³⁸³ U³⁸⁴ G³⁸⁵ C³⁸⁶ U³⁸⁷ A³⁸⁸ G³⁸⁹ C³⁹⁰ U³⁹¹ G³⁹² C³⁹³ U³⁹⁴ A³⁹⁵ G³⁹⁶ C³⁹⁷ U³⁹⁸ G³⁹⁹ C⁴⁰⁰ U⁴⁰¹ A⁴⁰² G⁴⁰³ C⁴⁰⁴ U⁴⁰⁵ G⁴⁰⁶ C⁴⁰⁷ U⁴⁰⁸ A⁴⁰⁹ G⁴¹⁰ C⁴¹¹ U⁴¹² G⁴¹³ C⁴¹⁴ U⁴¹⁵ A⁴¹⁶ G⁴¹⁷ C⁴¹⁸ U⁴¹⁹ G⁴²⁰

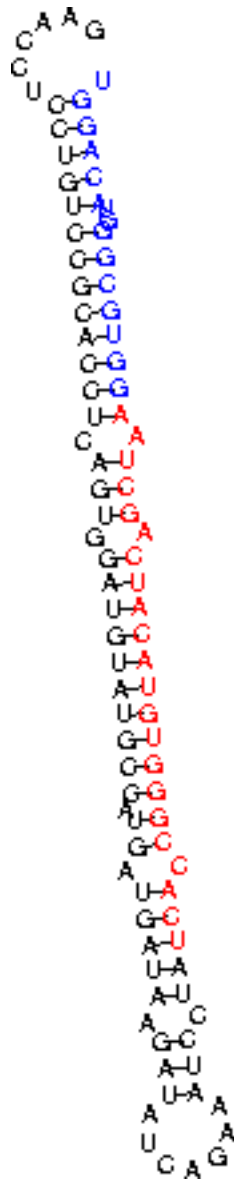
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-39



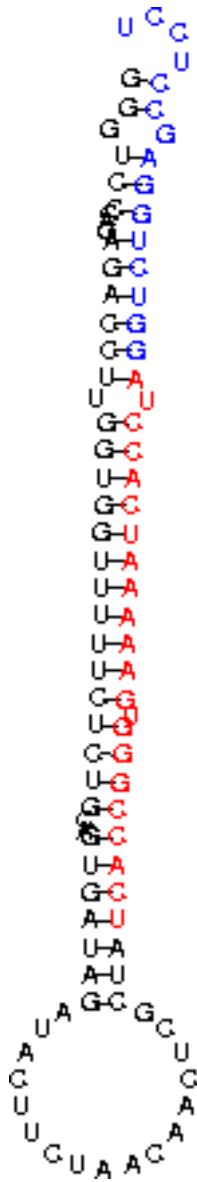
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-40



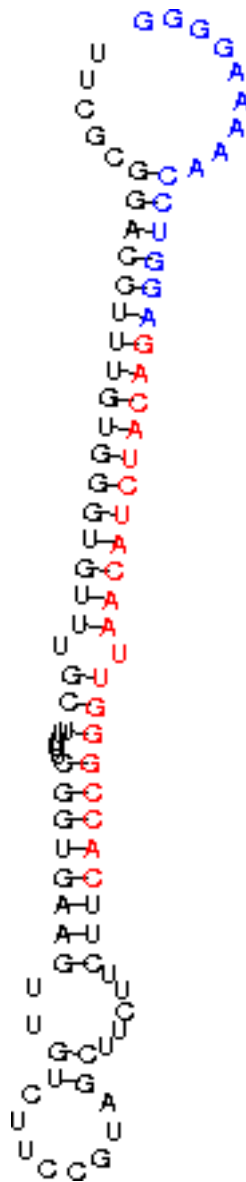
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-41



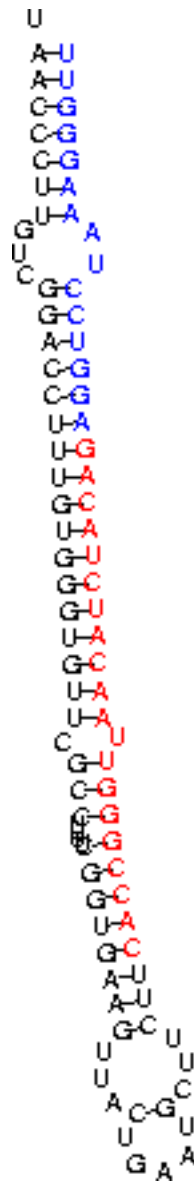
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-42



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-42 in *C. briggsae*

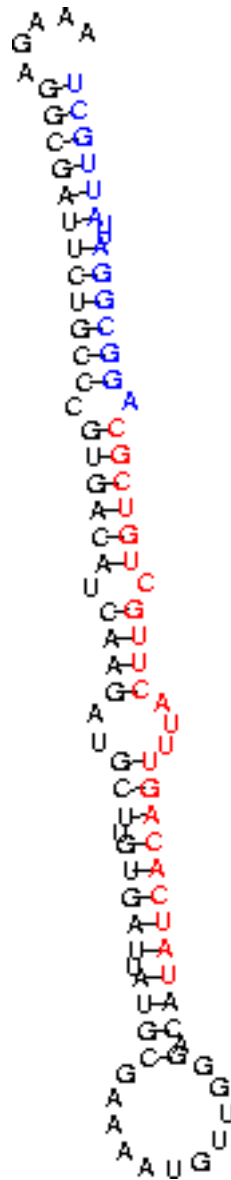


(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

The diagram illustrates the secondary structure of the 16S rRNA of *E. coli*. It is a large, complex molecule with a length of 1629 nucleotides. The structure is characterized by a high degree of base pairing, forming a series of stems and loops. The sequence is written in a circular fashion, with the 5' end at the top and the 3' end at the bottom. The bases are color-coded: U (blue), A (green), G (red), and C (black). The structure shows a variety of base pairs, including Watson-Crick base pairs (A-U, G-C) and non-Watson-Crick base pairs (G-U, U-U, A-A, C-C). The overall structure is a compact, globular fold with a central core and several peripheral loops and bulges.

(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-43 in *C. briggsae*



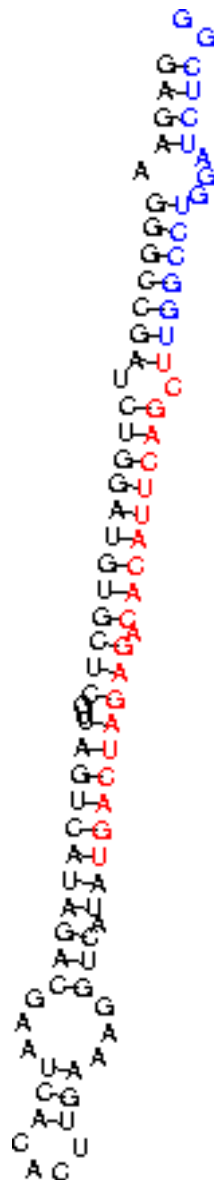
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-44



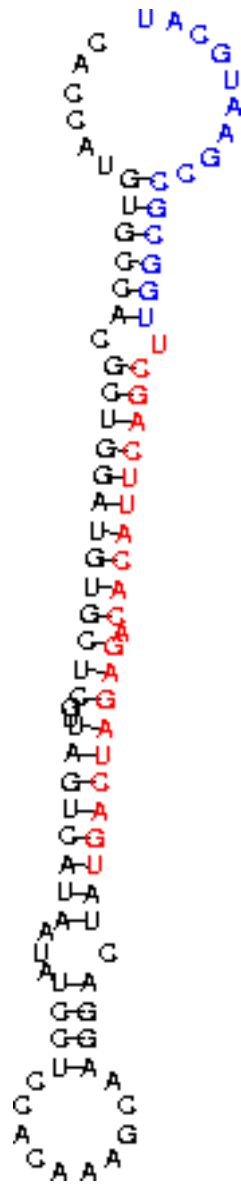
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-44 in *C. briggsae*



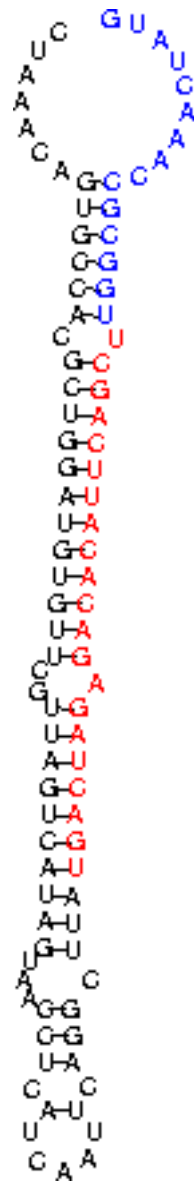
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-45



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

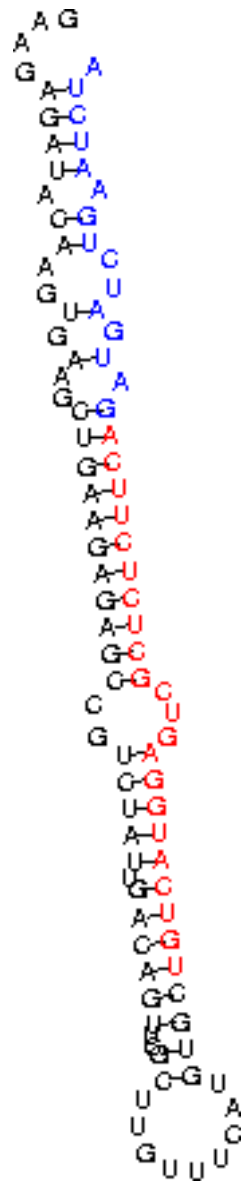
potential ortholog of miR-45 in *C. briggsae*



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-46 in *C. briggsae*

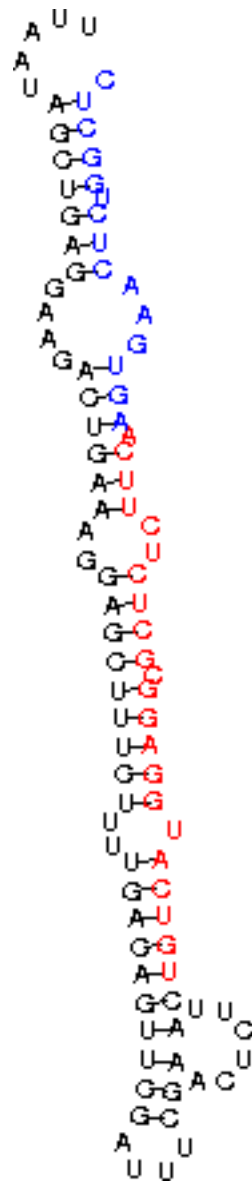


(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

Diagram illustrating the secondary structure of the 16S rRNA of *E. coli*. The structure is a complex of stems and loops, with base pairing indicated by lines connecting complementary bases (A-U, G-C).

(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-47 in *C. briggsae*



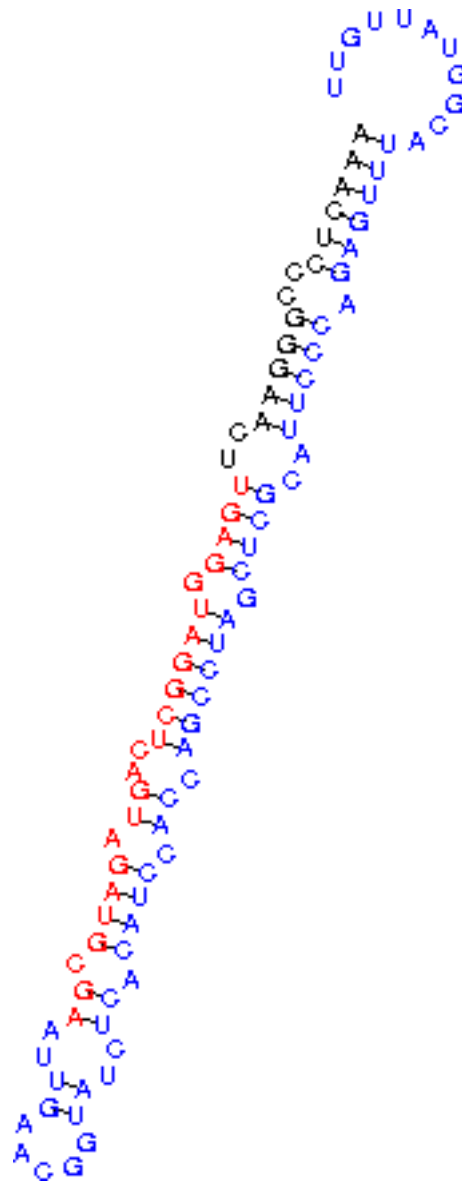
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-86 in *C. briggsae*



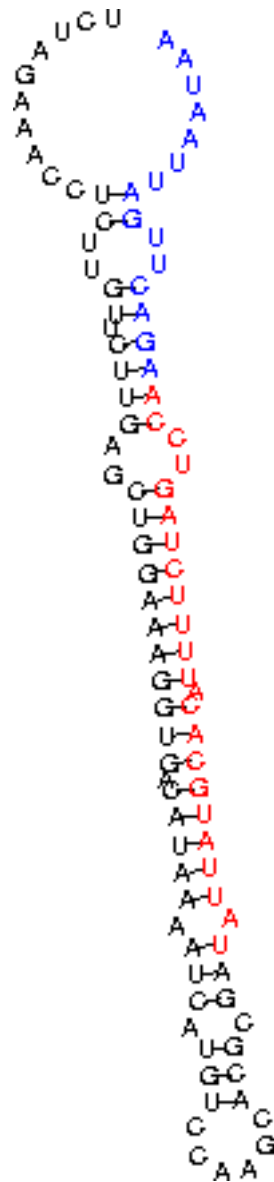
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-48



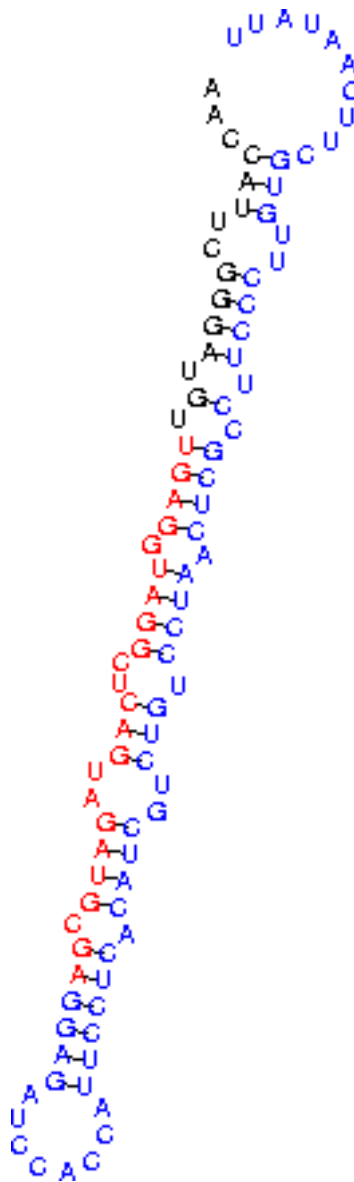
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-60 in *C. briggsae*



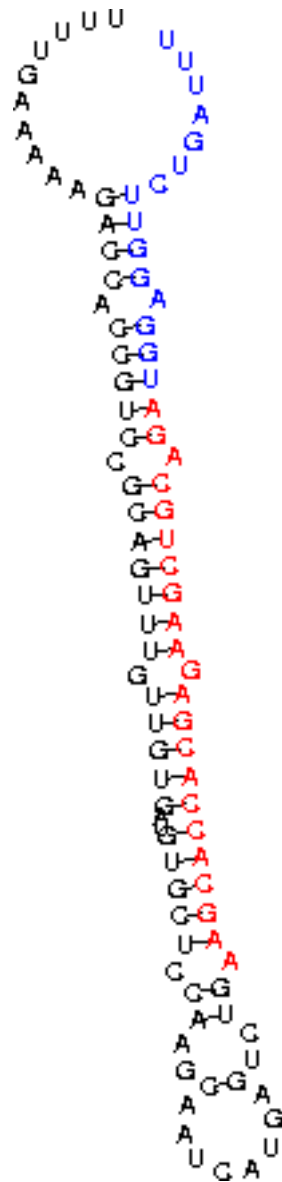
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-48 in *C. briggsae*



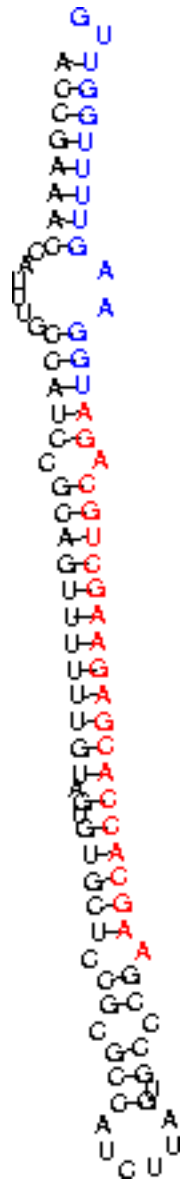
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-49



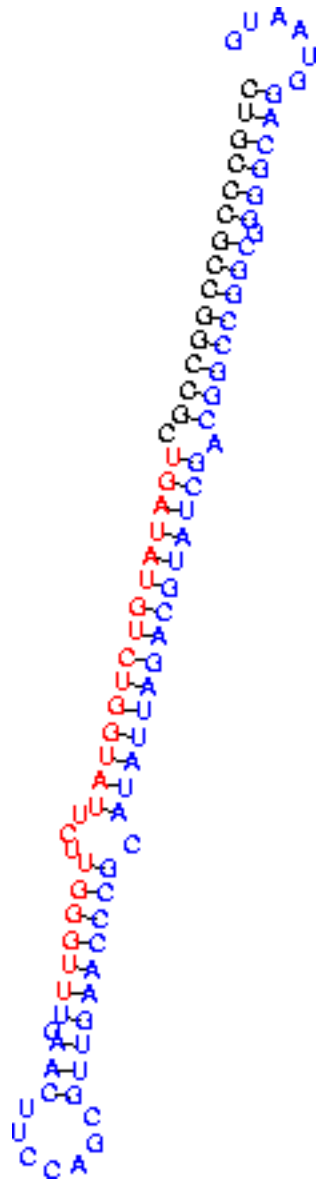
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-49 in *C. briggsae*



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-50



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

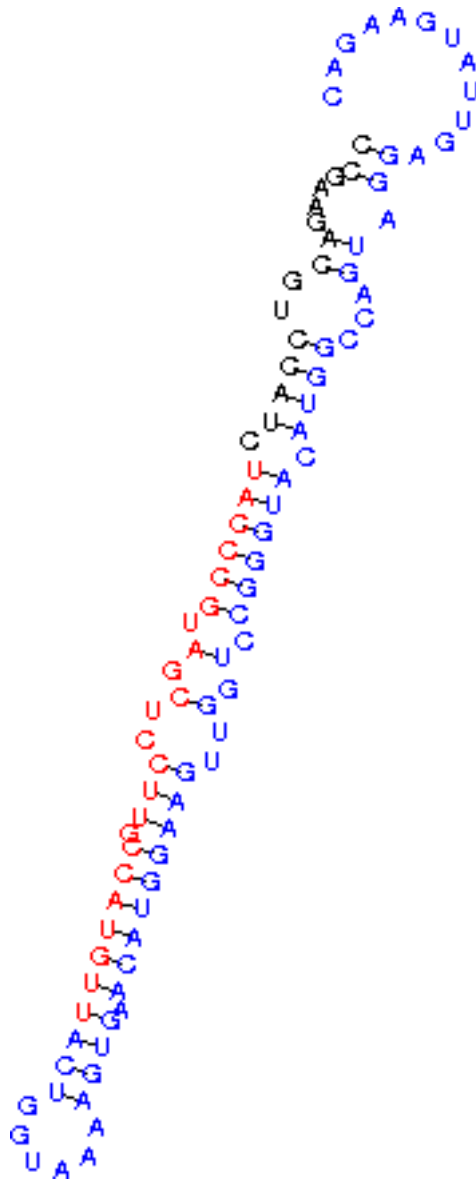
potential ortholog of miR-50 in *C. briggsae*



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

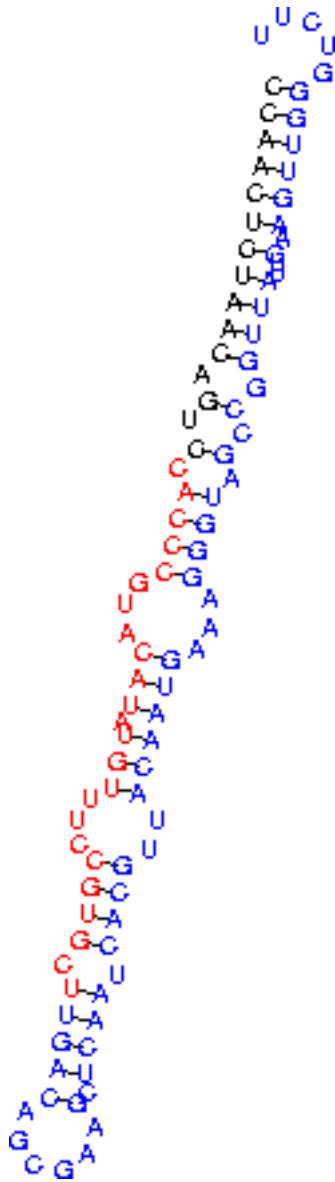
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-51 in *C. briggsae*



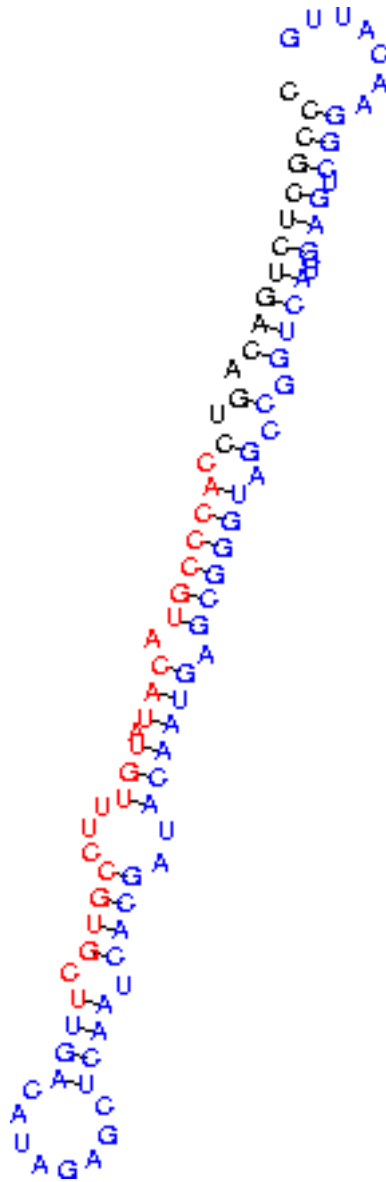
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-52



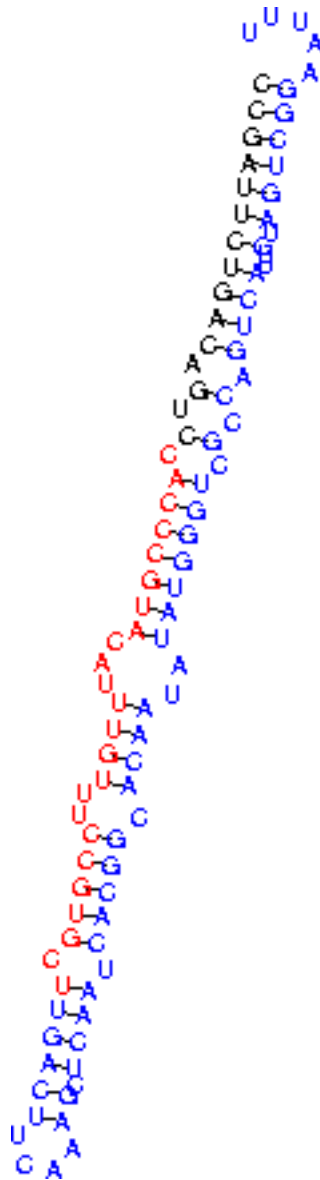
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-52 in *C. briggsae*



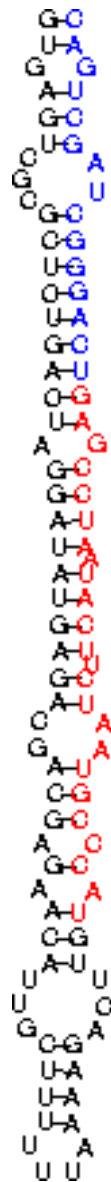
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-53



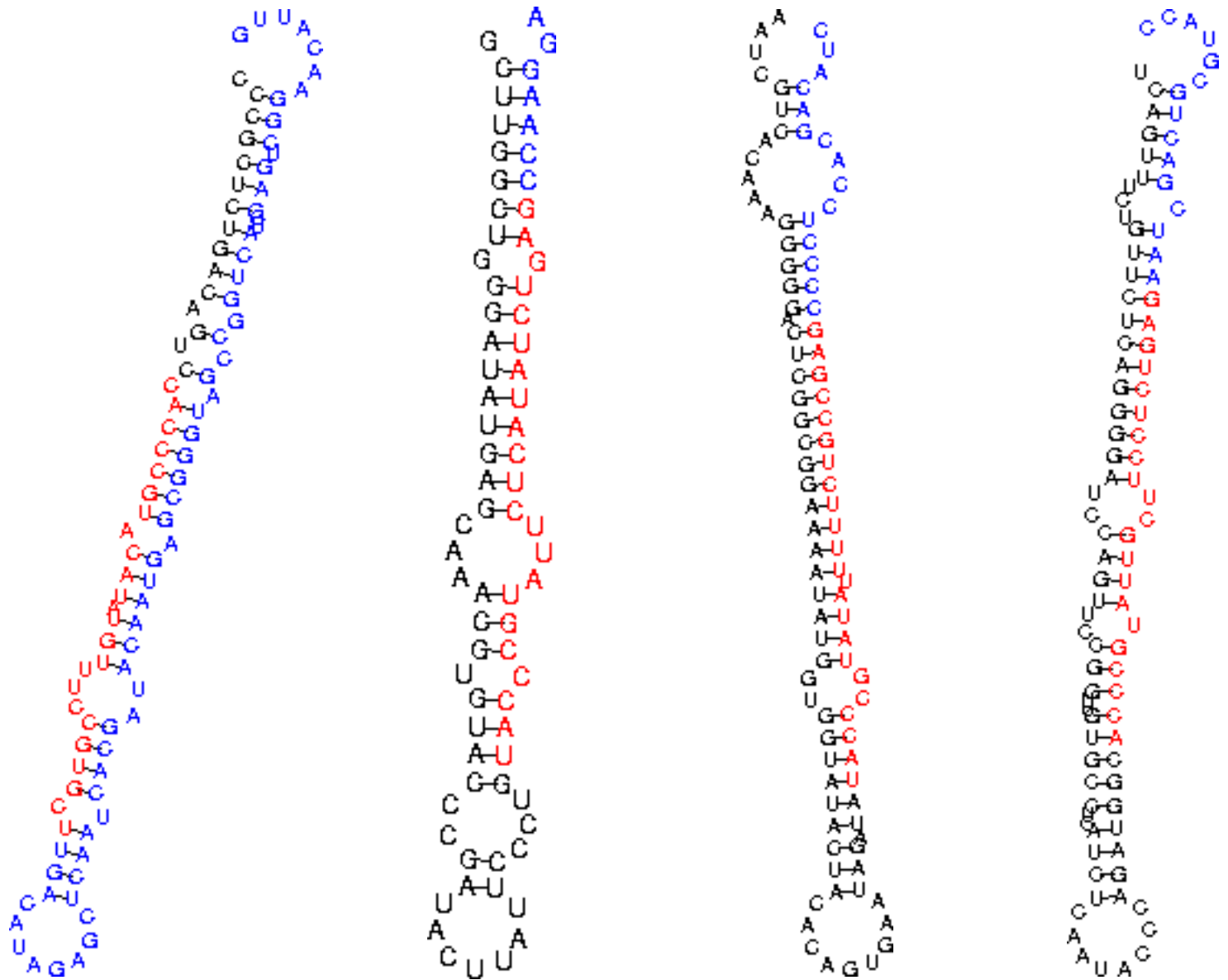
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-54



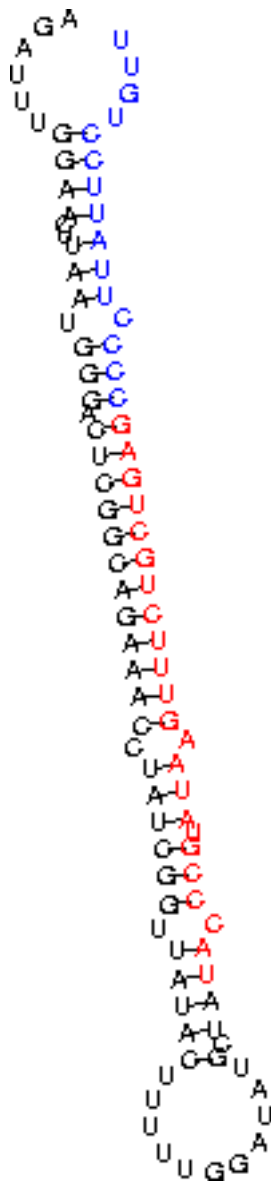
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-54 to miR-56 cluster in *C. briggsae*



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-55



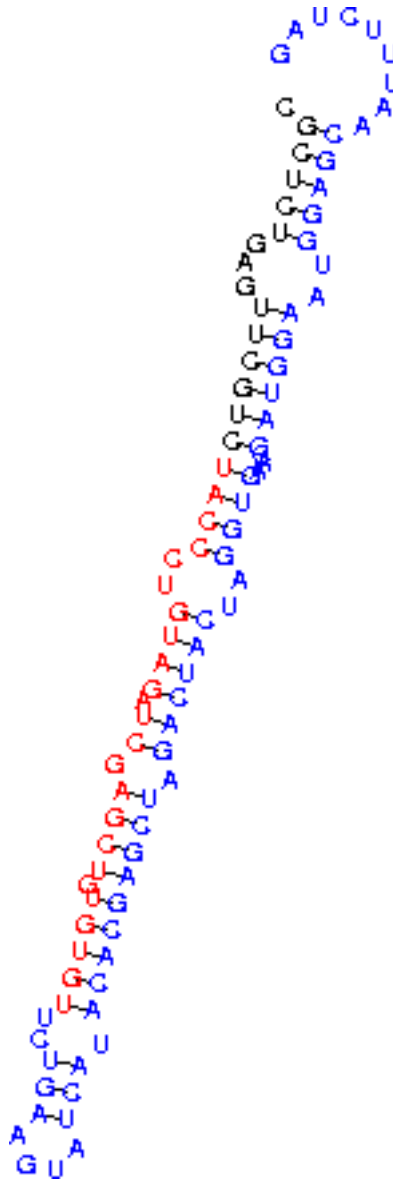
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

Diagram illustrating the secondary structure of the 16S rRNA of *E. coli*. The structure is a complex of stems and loops, with base pairing indicated by lines connecting complementary bases (A-U, G-C).

(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

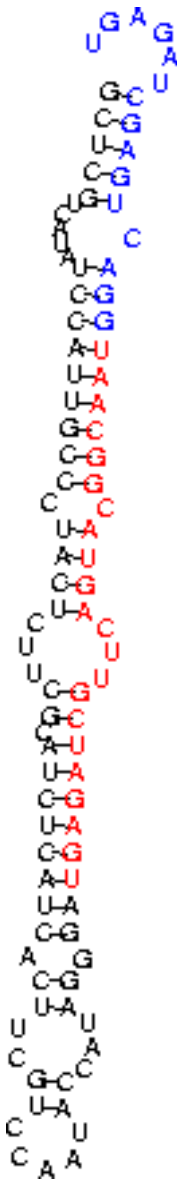
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-57 in *C. briggsae*



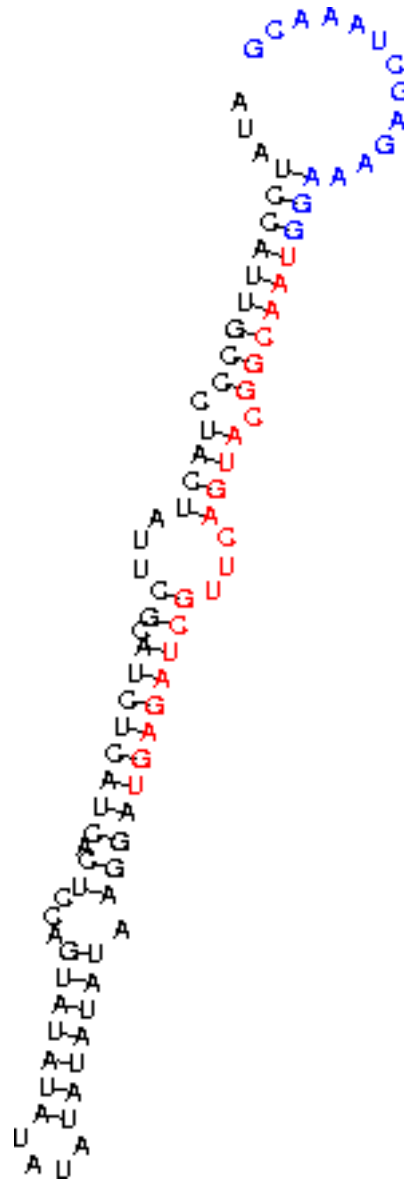
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-58



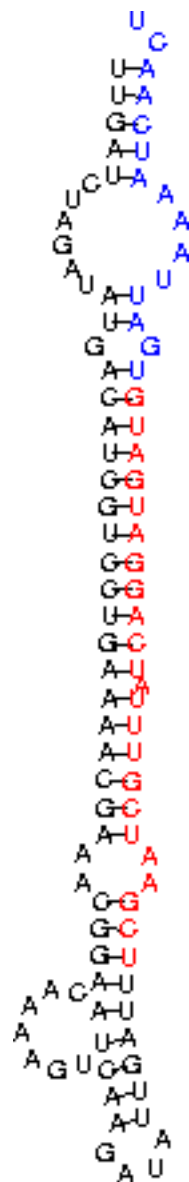
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-58 in *C. briggsae*



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-59



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

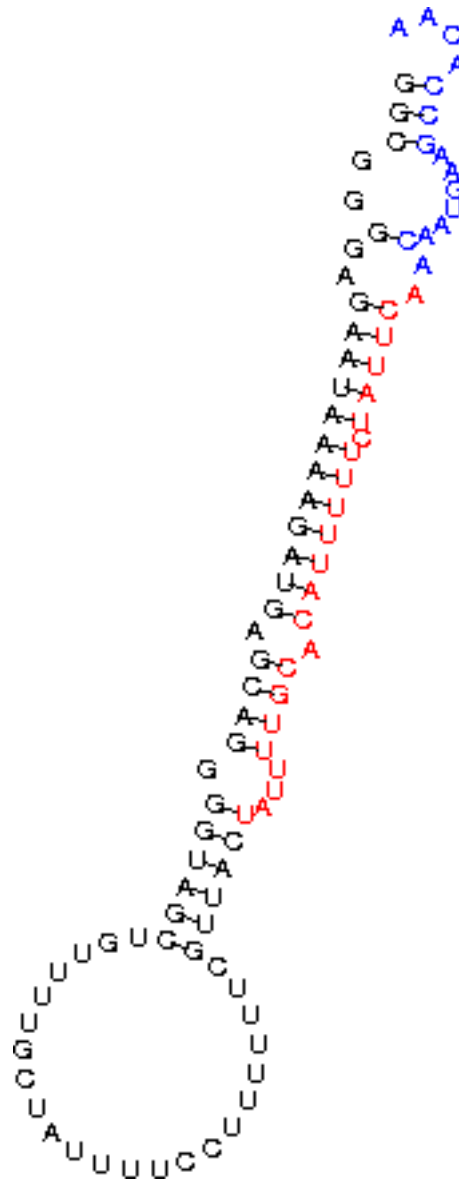
potential ortholog of miR-59 in *C. briggsae*



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

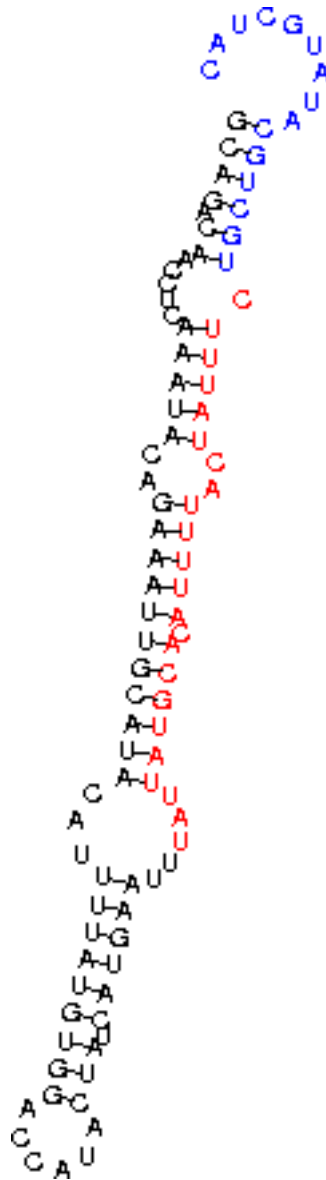
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-60 in *D. melanogaster*



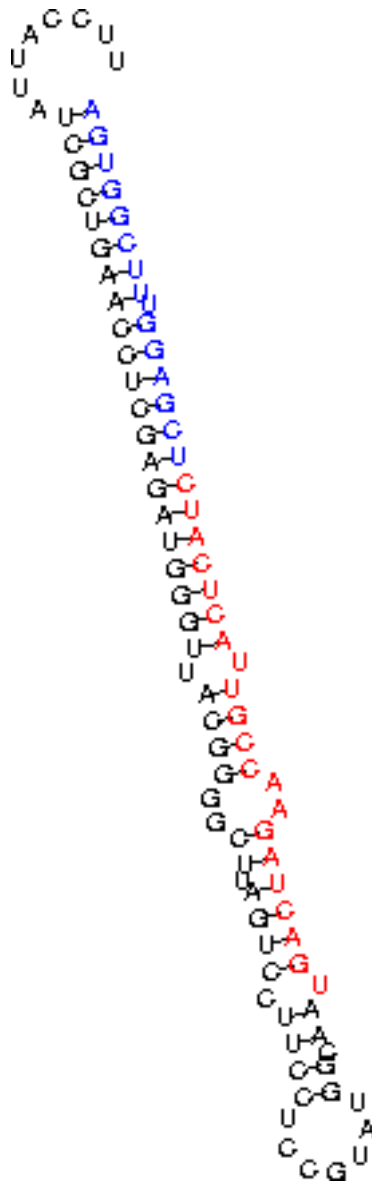
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-60 in *H. sapiens*



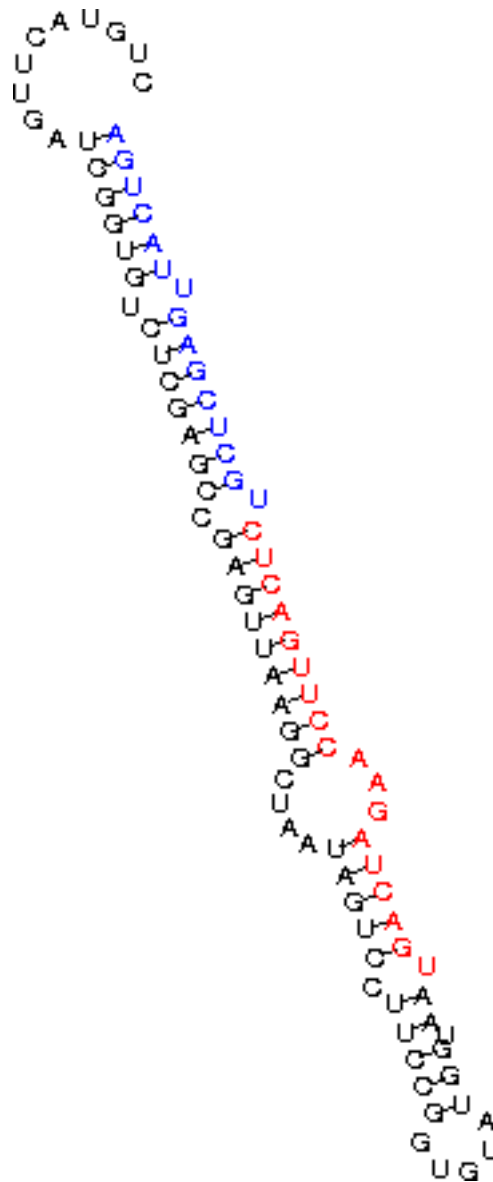
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-61



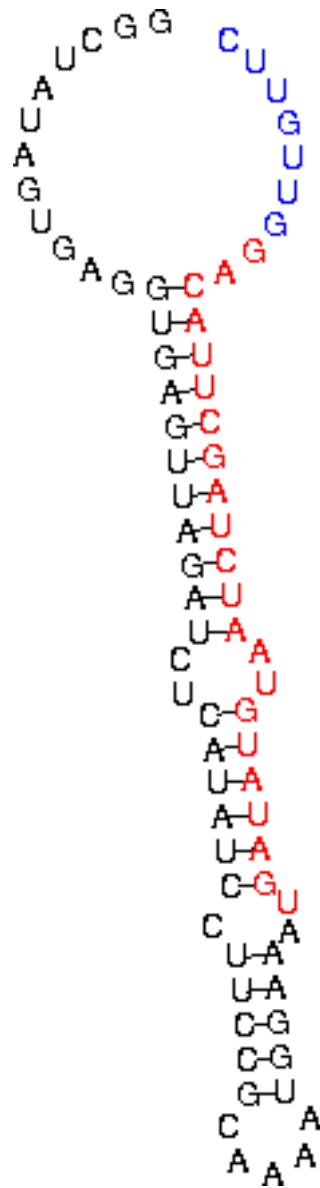
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-61 in *C. briggsae*



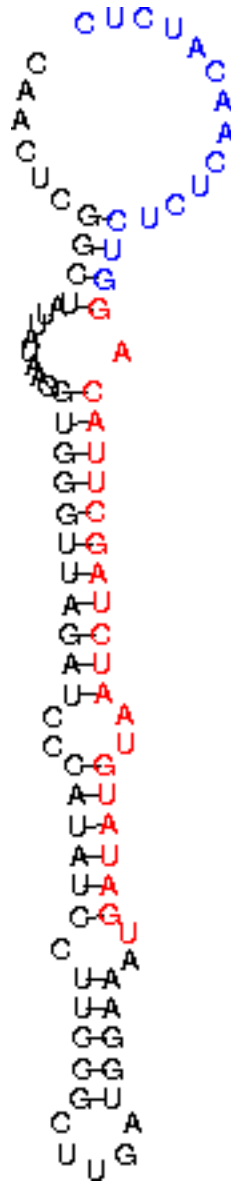
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-62



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-62 in *C. briggsae*

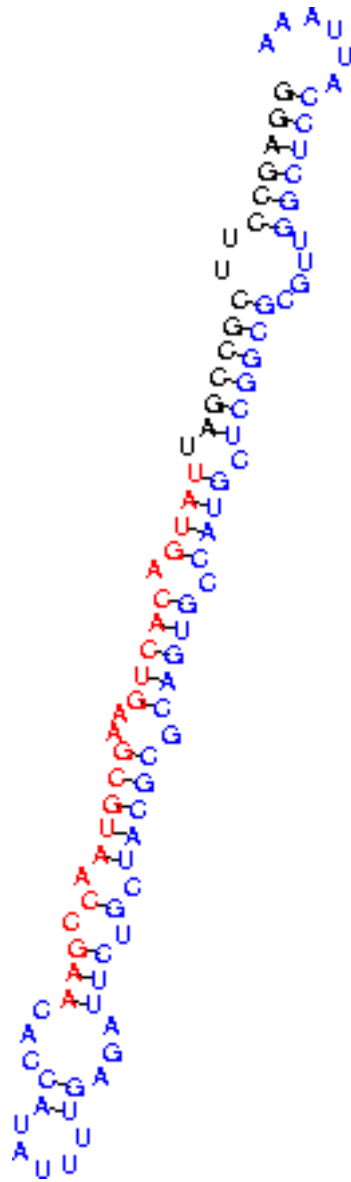


(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

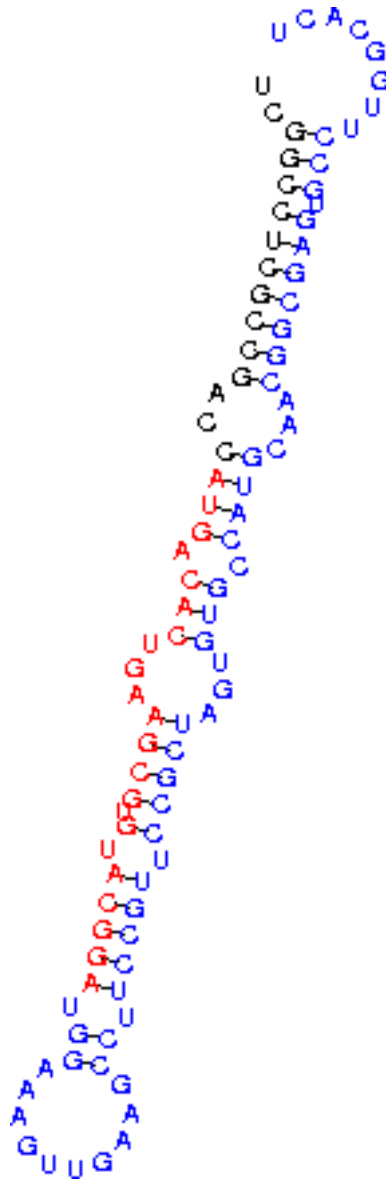
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-65



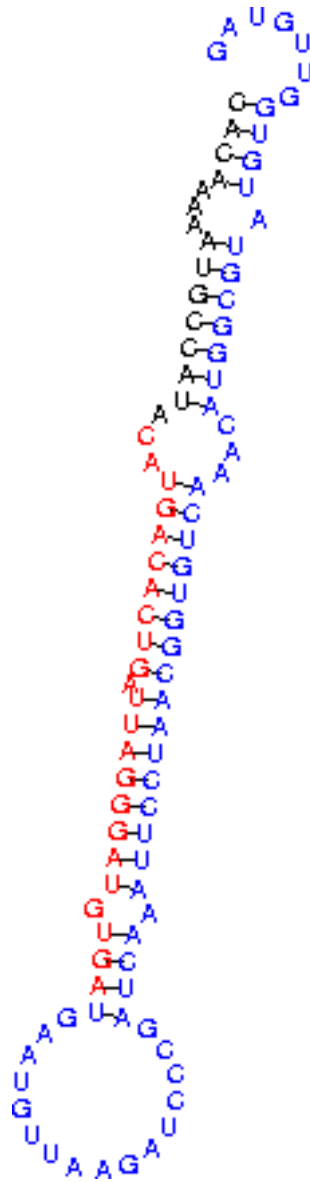
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-65 in *C. briggsae*



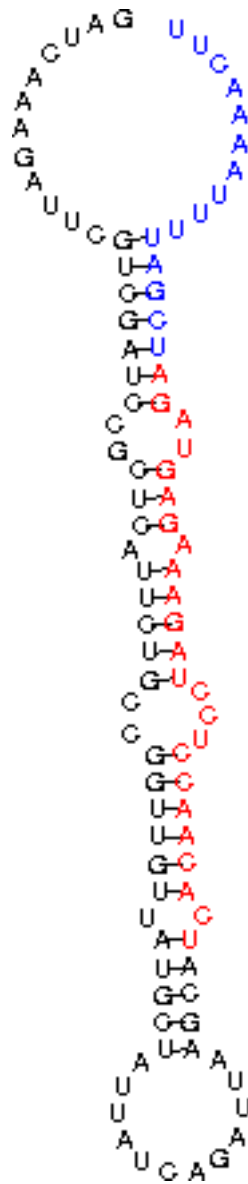
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-66



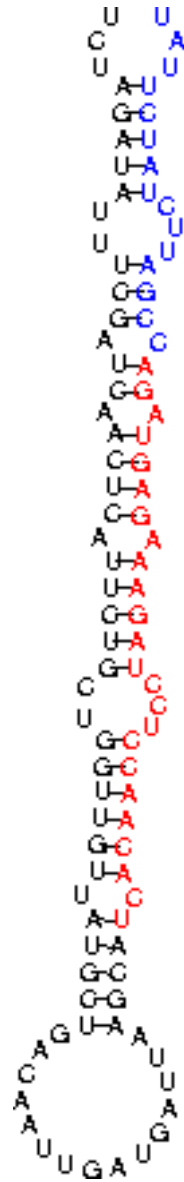
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-67



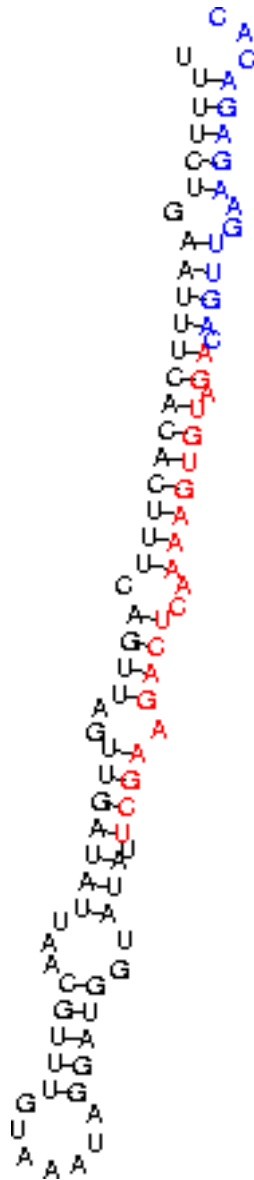
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-67 in *C. briggsae*



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

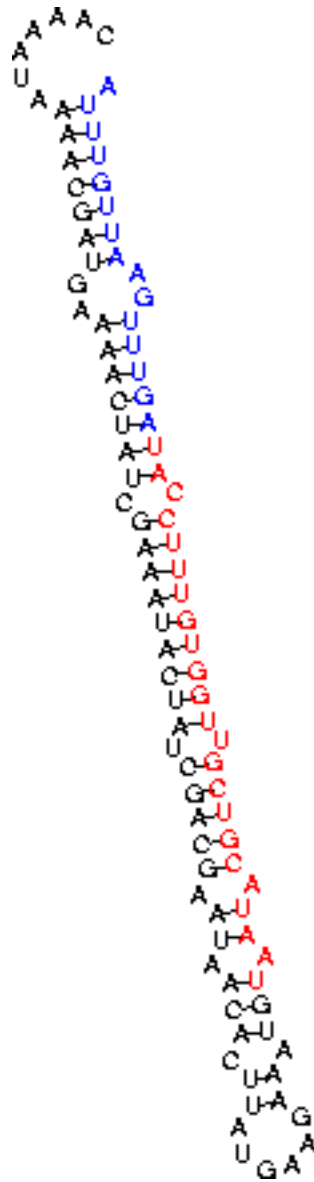
miR-68



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

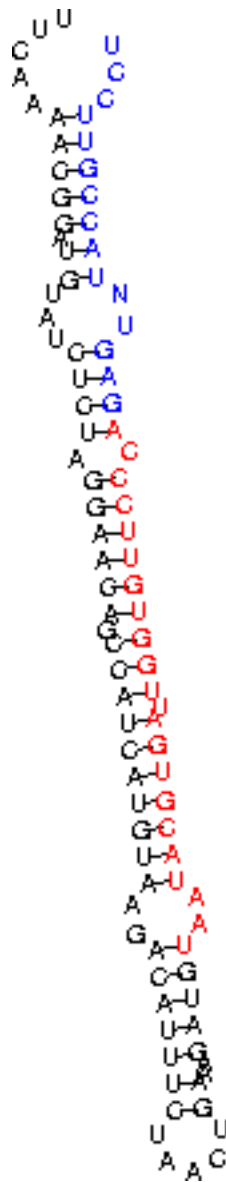
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-70



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-70 in *C. briggsae*

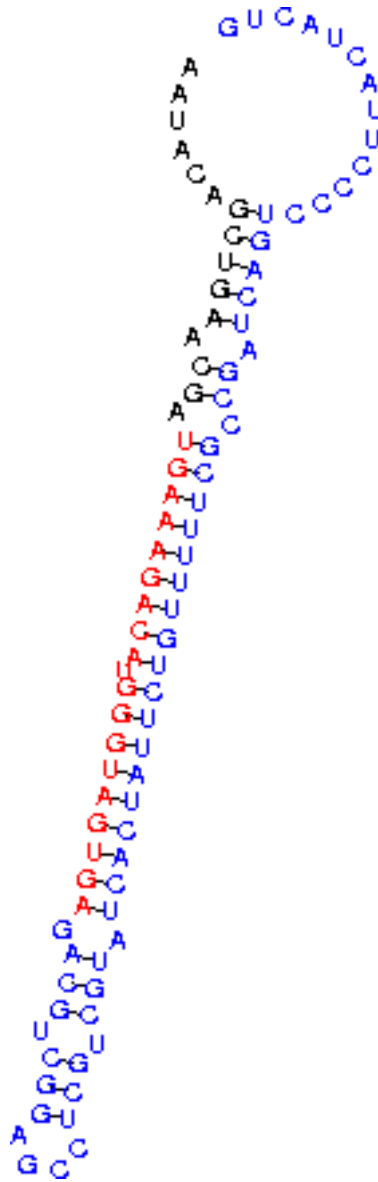


(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

Secondary structure diagram of the 16S rRNA gene from *Escherichia coli*. The diagram illustrates the complex folding of the RNA molecule, showing various stem-loops and bulges. The sequence is written vertically on the right side of the diagram, with nucleotides color-coded to match the base pairing lines (red for A-U, blue for U-A, green for G-C, and black for C-G).

(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

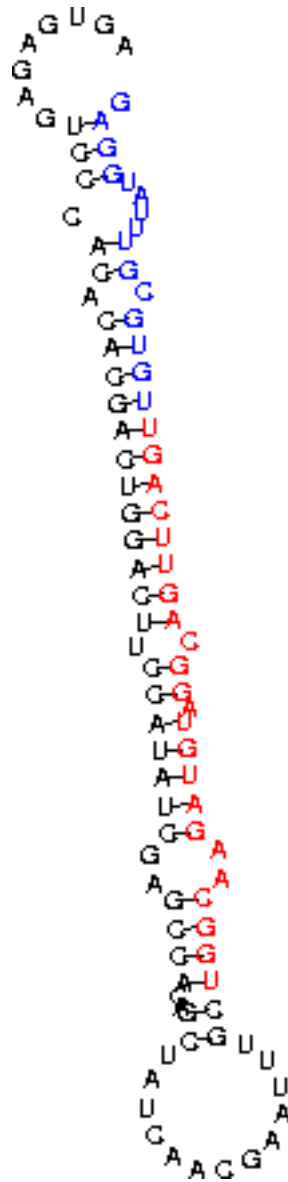
potential ortholog of miR-71 in *C. briggsae*



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

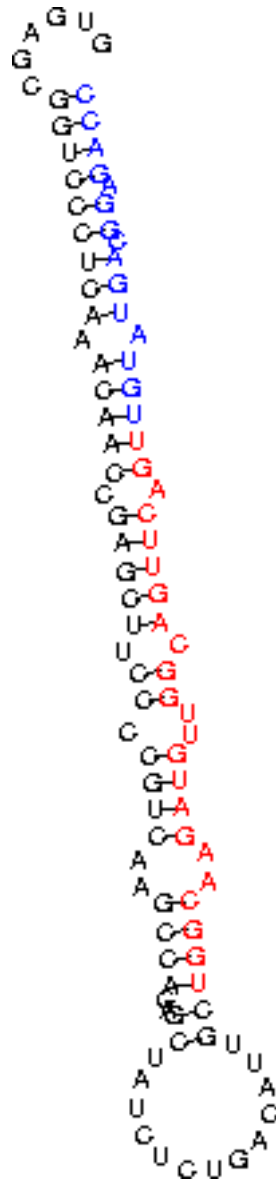
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-73



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-73 in *C. briggsae*

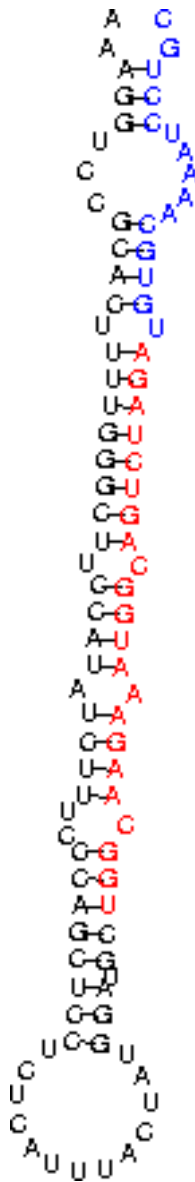


(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

The diagram illustrates the secondary structure of the 16S rRNA of *Escherichia coli*. It shows a complex arrangement of stems and loops. The sequence is written vertically, with bases connected by lines representing base pairs. The structure is highly conserved and plays a crucial role in the function of the ribosome. The diagram uses color coding: blue for certain base pairs, red for others, and black for the remaining bases, likely indicating different structural or functional regions.

(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-74 in *C. briggsae*



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-75



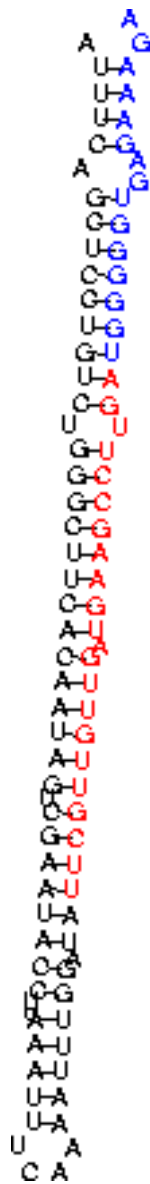
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-75 in *C. briggsae*



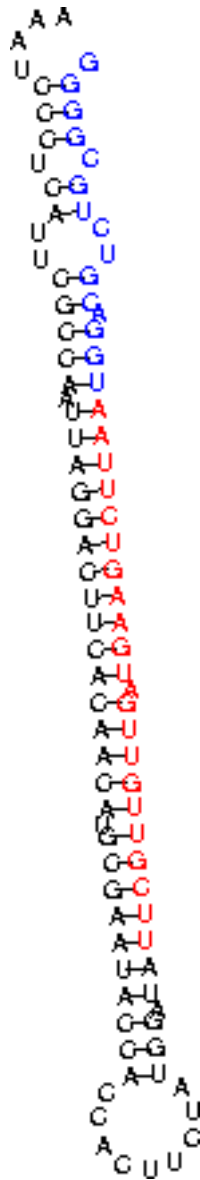
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-76



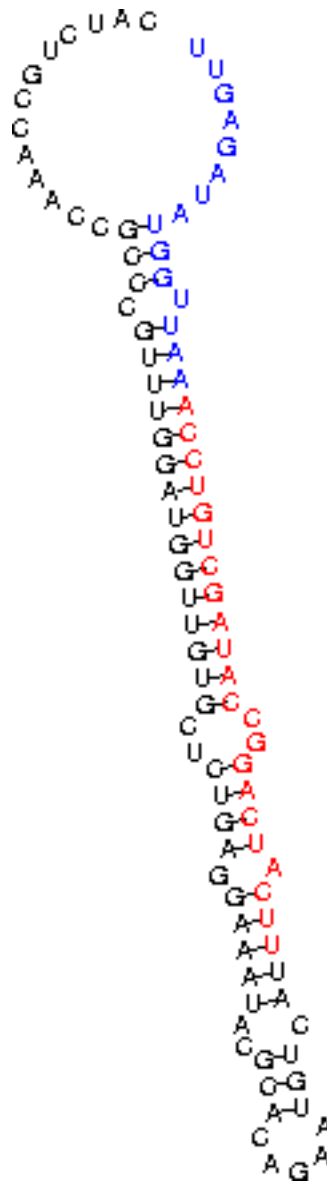
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-76 in *C. briggsae*



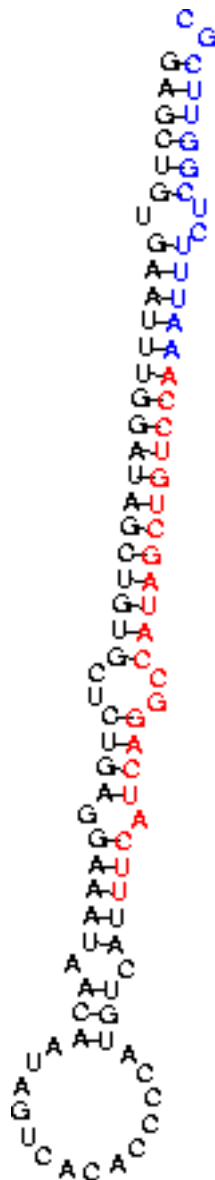
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-77



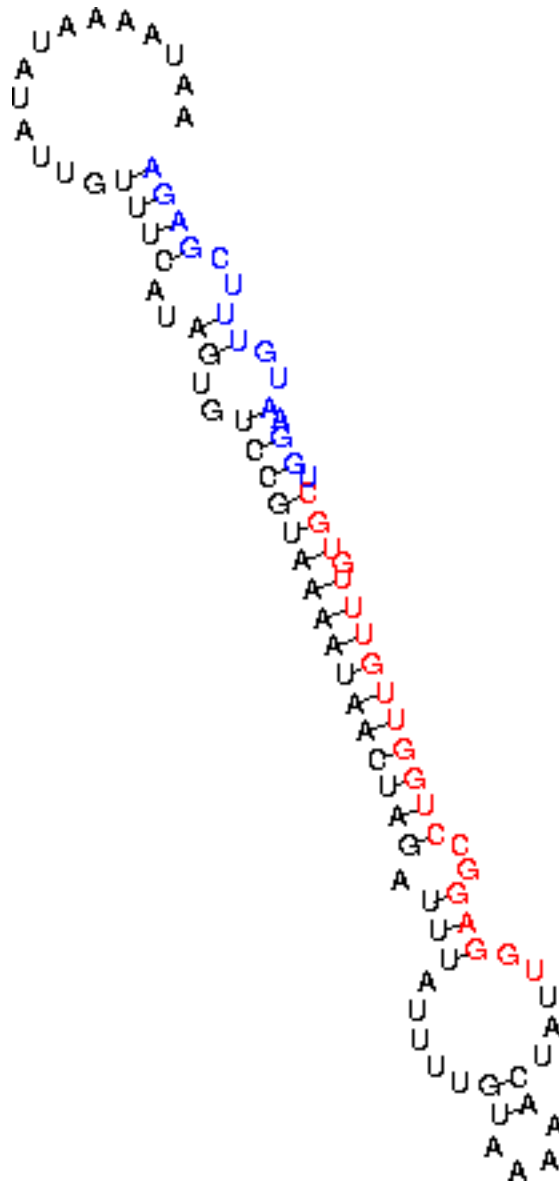
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-77 in *C. briggsae*



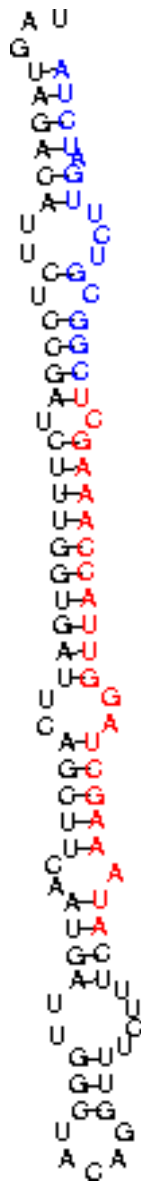
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-78



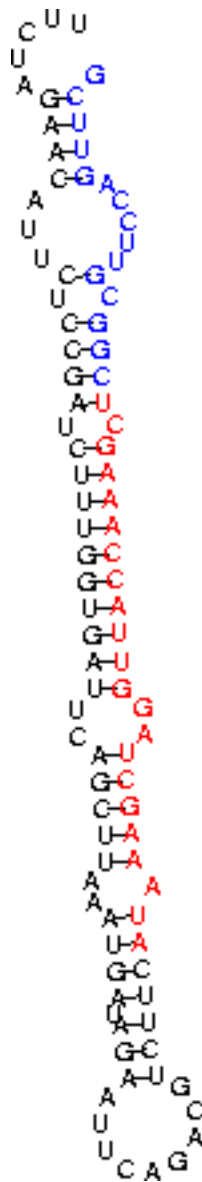
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-79



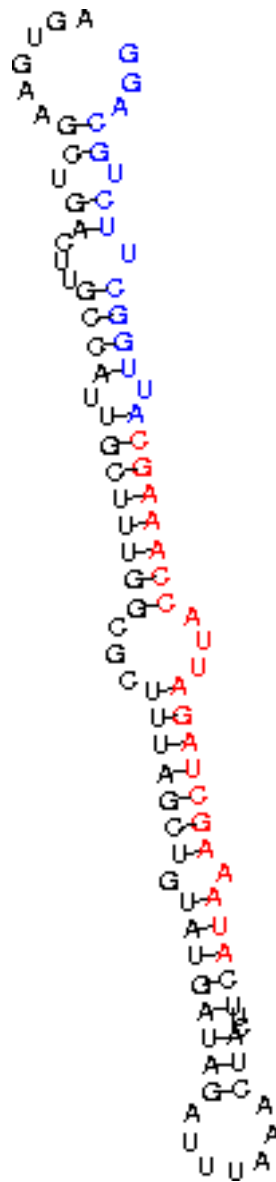
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-79 in *C. briggsae*



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

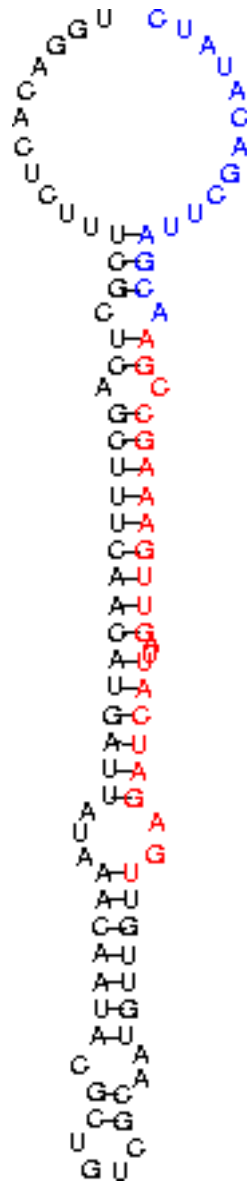
potential ortholog of miR-79 in *D. melanogaster*



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

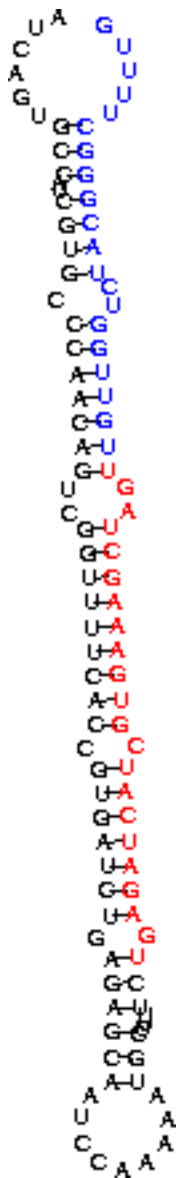
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-80 in *C. briggsae*



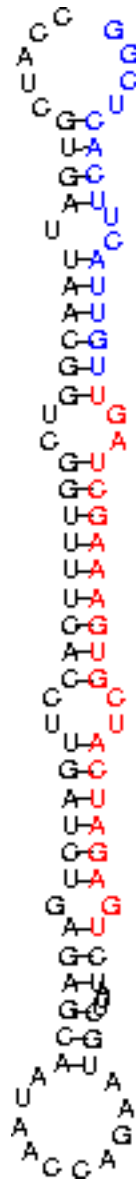
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-81



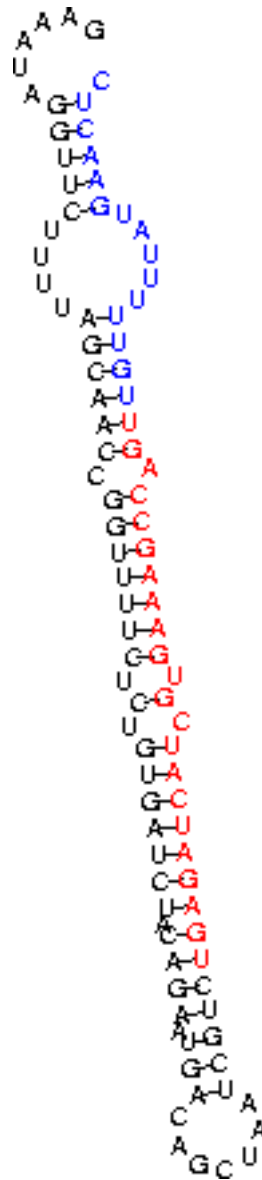
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-81 in *C. briggsae*



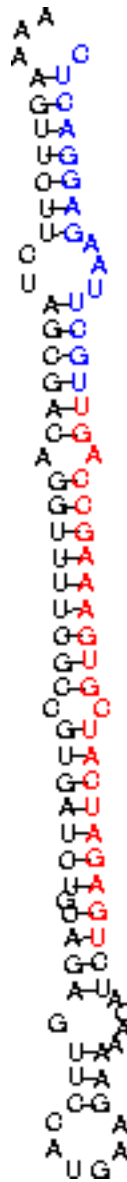
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-82



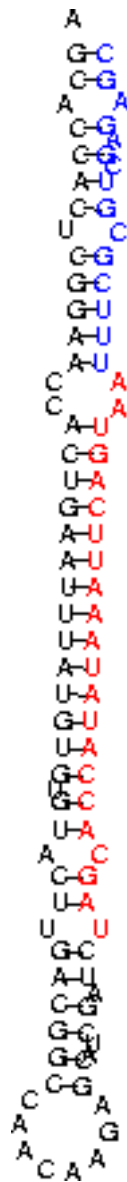
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-82 in *C. briggsae*



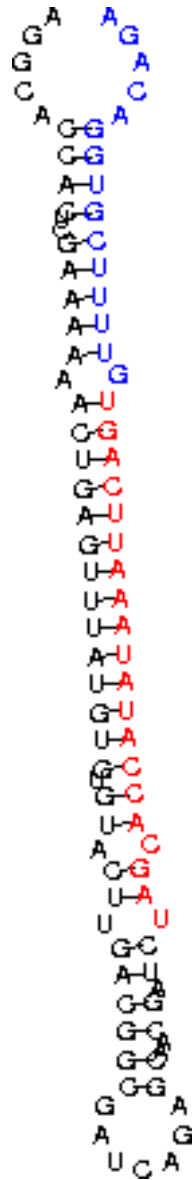
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-83



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-83 in *C. briggsae*



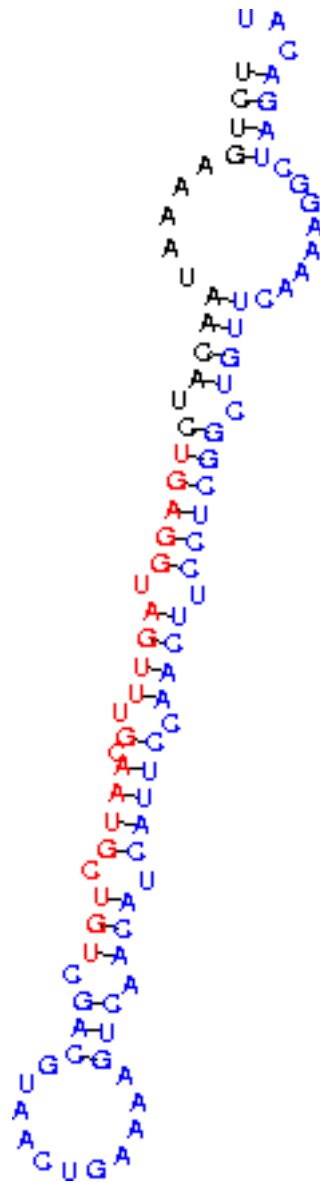
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

miR-84



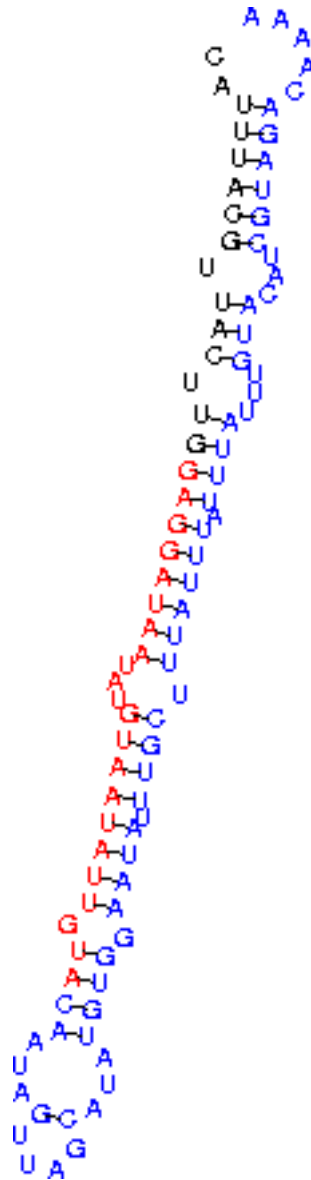
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-84 in *C. briggsae*



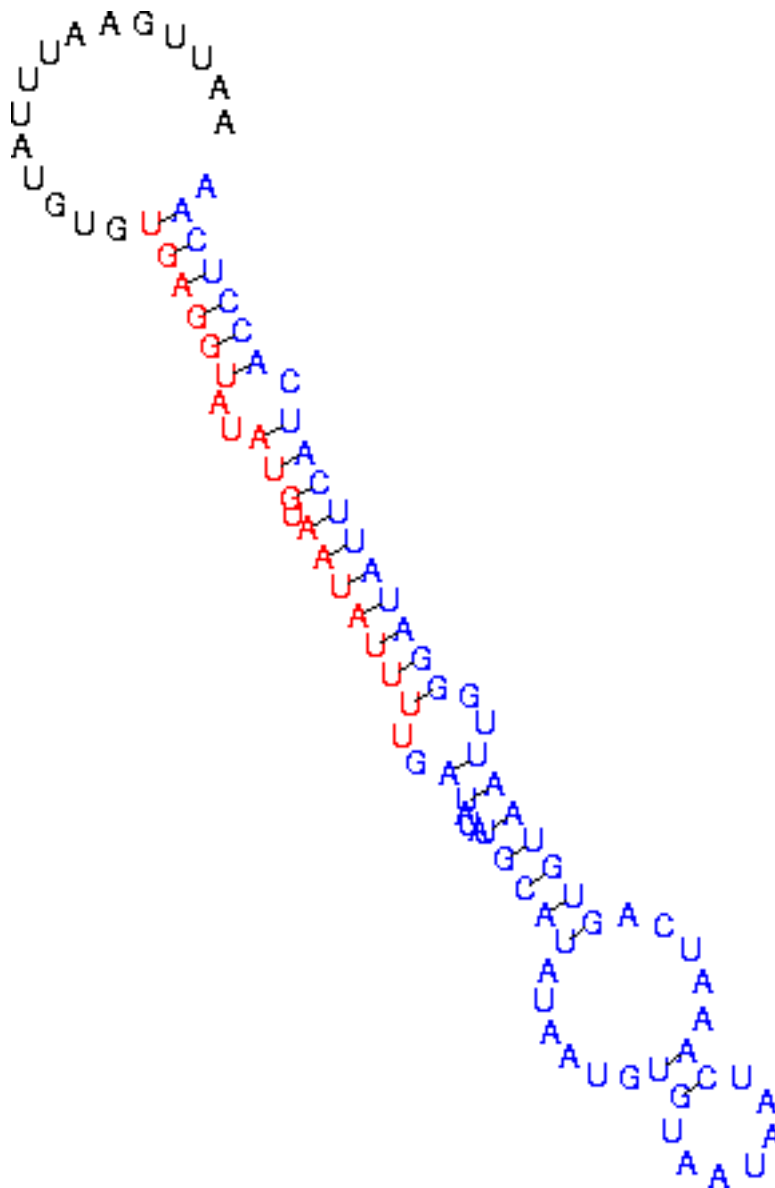
(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-84 in *D. melanogaster*



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-84 in *H. sapiens*



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

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

(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

potential ortholog of miR-85 in *C. briggsae*



(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)

(miRNA sequence is shown in red, 5' sequence is shown in black, and 3' sequence is shown in blue.)