

Title:

From the *C.elegans* to *E.multilocularis*
——preliminary bioinformatic analysis of
miRNA-71 target gene



——Zhang Xueyong

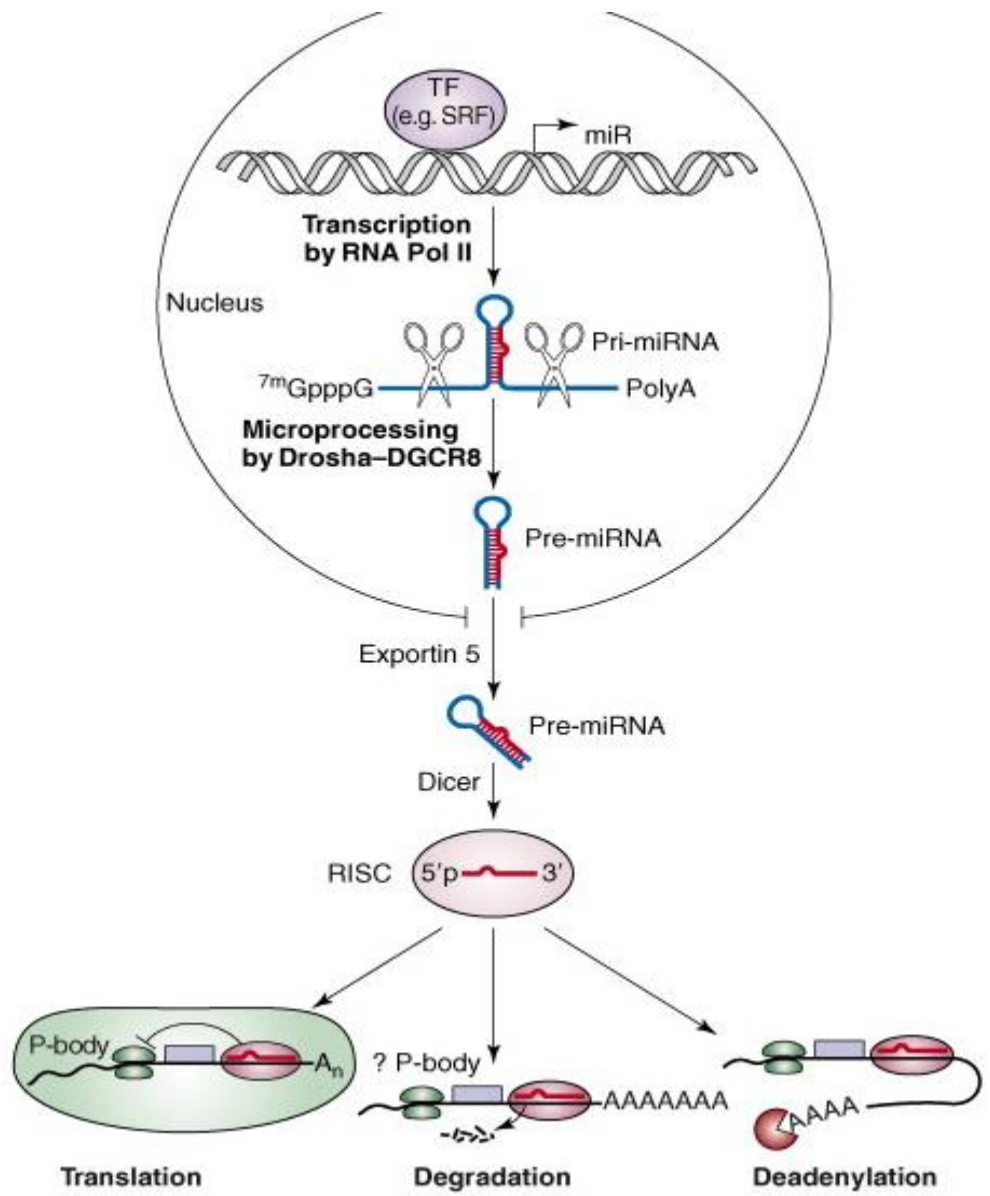
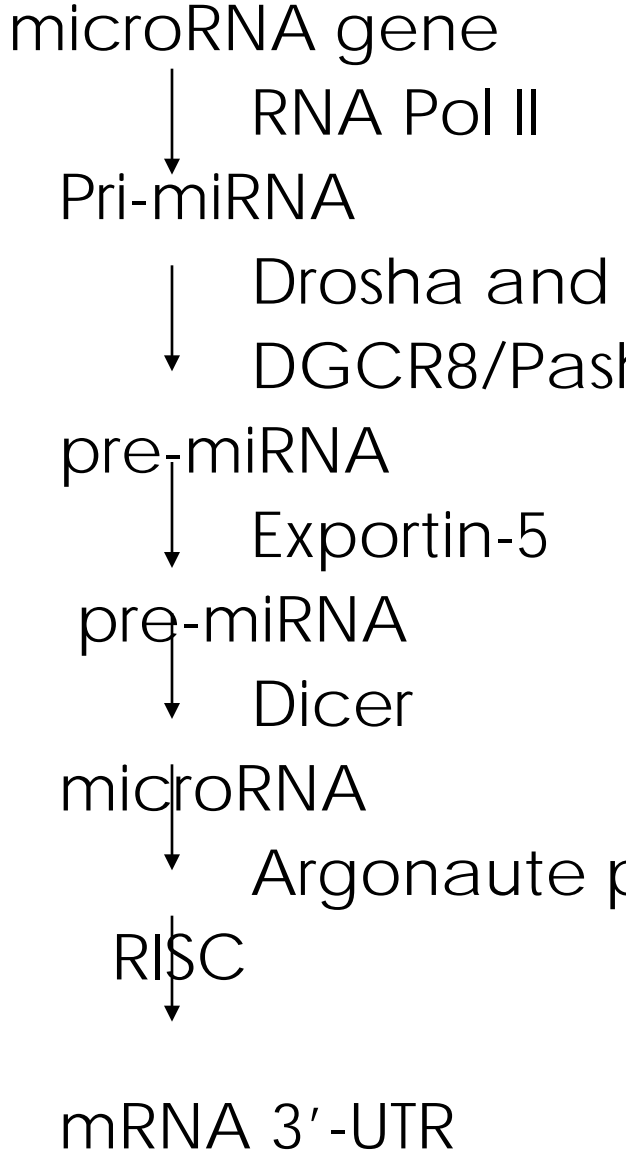
Group 7:

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Background: Origins and Mechanisms of miRNAs



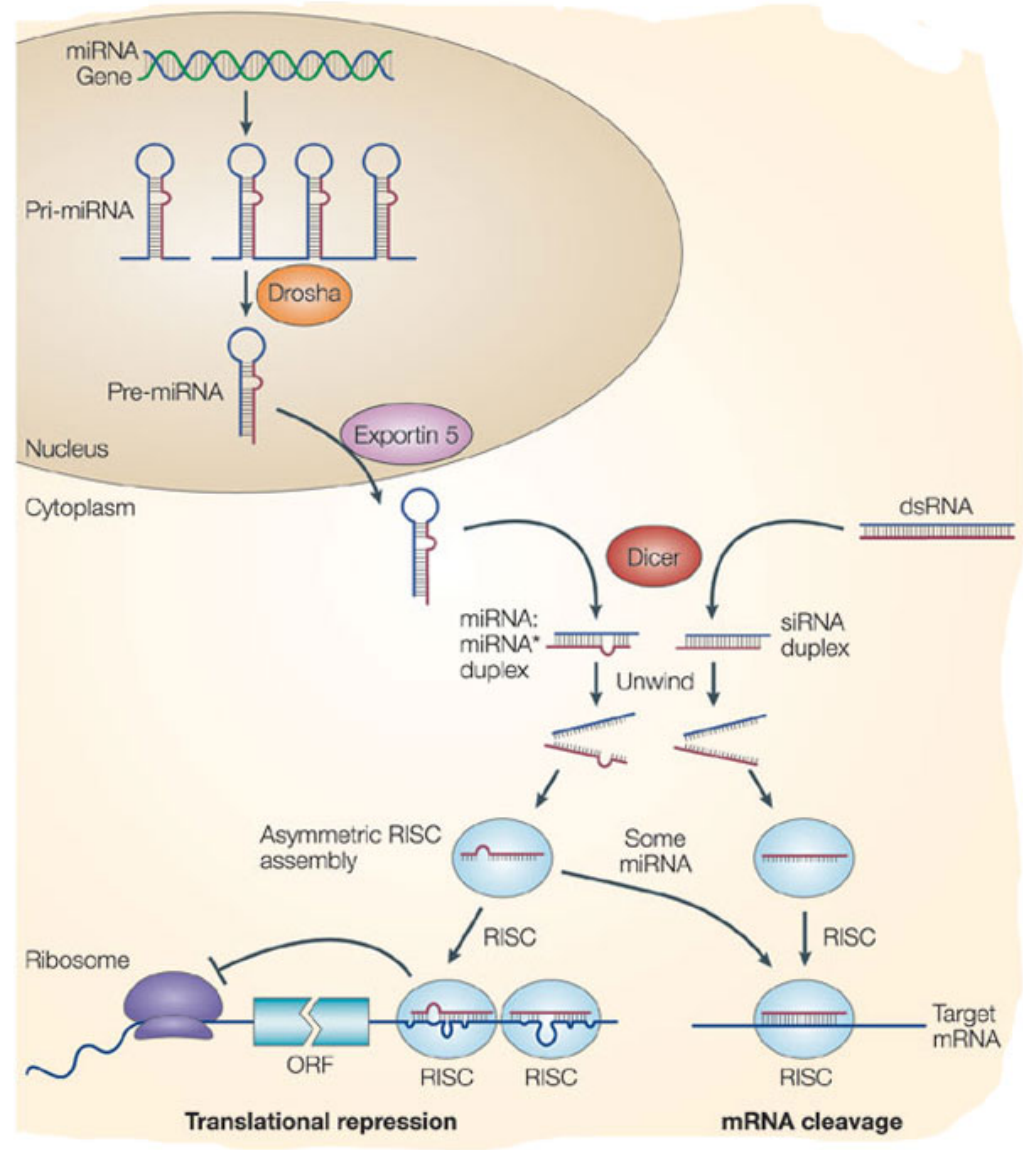
Compare siRNA and miRNA

Similarities:

- I .molecular structures are similar: Length: 21 -25bp, 5'P,3'-
- II . functions are all by the RISC
- III. effect inhibits mRNA translation activity, resulting in gene silencing.

Differences:

- I .Different biosynthetic pathway.
- II .Inhibition of translation is in different ways.
- III.Different levels of complementary bases.



A. Background:

C. elegans → *E. multilocularis*

miR mature sequence:

cel-miR-71 : UGAAAGAC **AUG** GGUAGUGAGACG

emu-mir-71: UGAAAGAC **GAU** GGUAGUGAGA

cel-miR-71 → emu-mir-71

Known target gene → unknown target gene?

B. Target gene : *tir-1*

Conserved

	predicted consequential pairing of target region
Position 106-113 of <i>tir-1</i> 3' UTR	5' ...UAUCAAAACUCCCAAUGUCUUUCA...
<i>cel-miR-71</i>	3' AGUGAUGGGUACAGAAAGU

Chromosome III: 3,869,592-3,901,466

Transcript ID: F13B10.1c



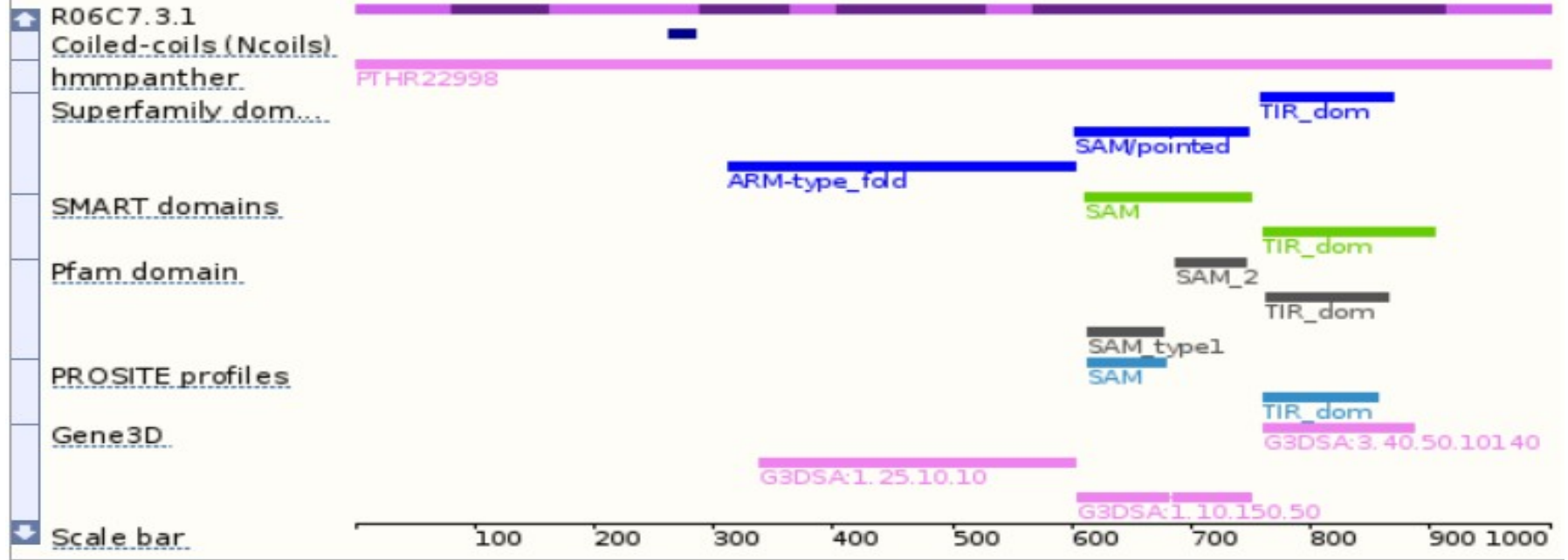
Coding exons : 9

transcript length: 3592bps

C—Protein analysis

Protein ID:F13B10.1c

Protein name: Sterile alpha and TIR motif-containing protein tir-1



SAM 1 Domain 614—678 65AA

SAM 2 Domain 684—750 67AA

TIR Domain 760—902 143AA

Function:Both innate immune response and specification ofAWC(OFF)neuron.During late embryogenesis, it acts downstream of CAMKII (unc-43) to regulate pecification of asymmetric odorant receptors in AWC(OFF) neuron via kinase signalingcascade. Also plays a central role in resistance to infection to a broad range of bacterial and fungi pathogens.

D. GENE DB—Echinococcus multilocularis Genes blast:

Pairwise Alignment Result

NAME	SCORE	IDENTITY	SIMILARY	GAPS
<u>C.elegans SAM1</u> EmuJ_001091600.1 HSP	134.0	40.0%	60.0%	3.1%
<u>C.elegans SAM2</u> EmuJ_001091600.1 HSP	86.0	26.9%	41.8%	34.3%
<u>C.elegans TIR</u> EmuJ_001091600.1 HSP	340.0	46.2%	68.5%	4.2%

Main domain regions alignment results suggest :the sequence may be in EmuJ_001091600.1 (TIR analysis)

Entry name	Organism	Length	Identity	Score
SARM1_CAEL	<u>Caenorhabditis elegans</u>	801	100.0%	752
SARM1_CAEL	<u>Caenorhabditis elegans</u>	930	100.0%	752
Q5I9W1_CAEL	<u>Caenorhabditis elegans</u>	931	100.0%	752
Q5I9W0_CAEL	<u>Caenorhabditis elegans</u>	984	100.0%	752
SARM1_CAEL	<u>Caenorhabditis elegans</u>	1,000	100.0%	752
E1G5M8_LOALO	<u>Loa loa (Eye worm)</u>	677	84.0%	632
A8Q6X5_BRUMA	<u>Brugiamalayi (worm)</u>	951	83.0%	626



Amino acid analysis:

Weblab cusp:

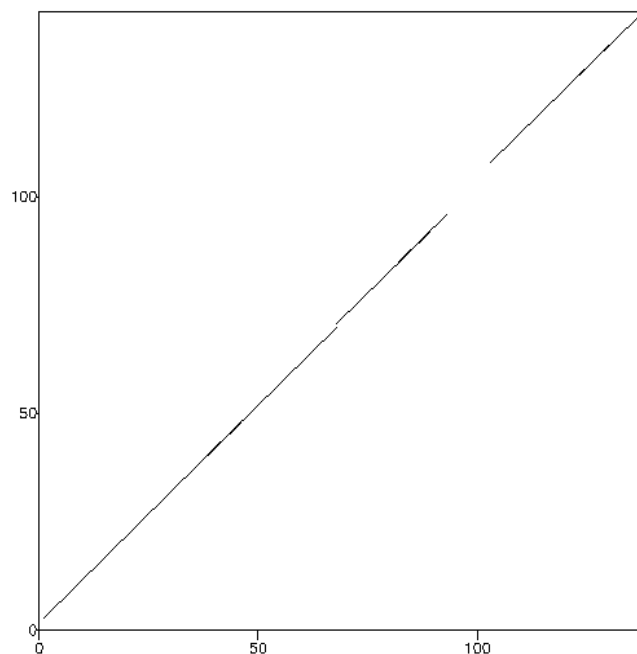
1st letter GC 50.65%

2nd letter GC 38.96%

3rd letter GC 41.46%

AA	aa	number	frequency
GAT	D	44	43.956
AAA	K	38	37.962
GAA	E	35	34.965
CAA	Q	33	32.967
AAG	K	31	30.969
...	A	29	28.971

Dotmatcher: raw::635763 vs raw::635764
(windowsize = 10, threshold = 23.00 20/06/13)

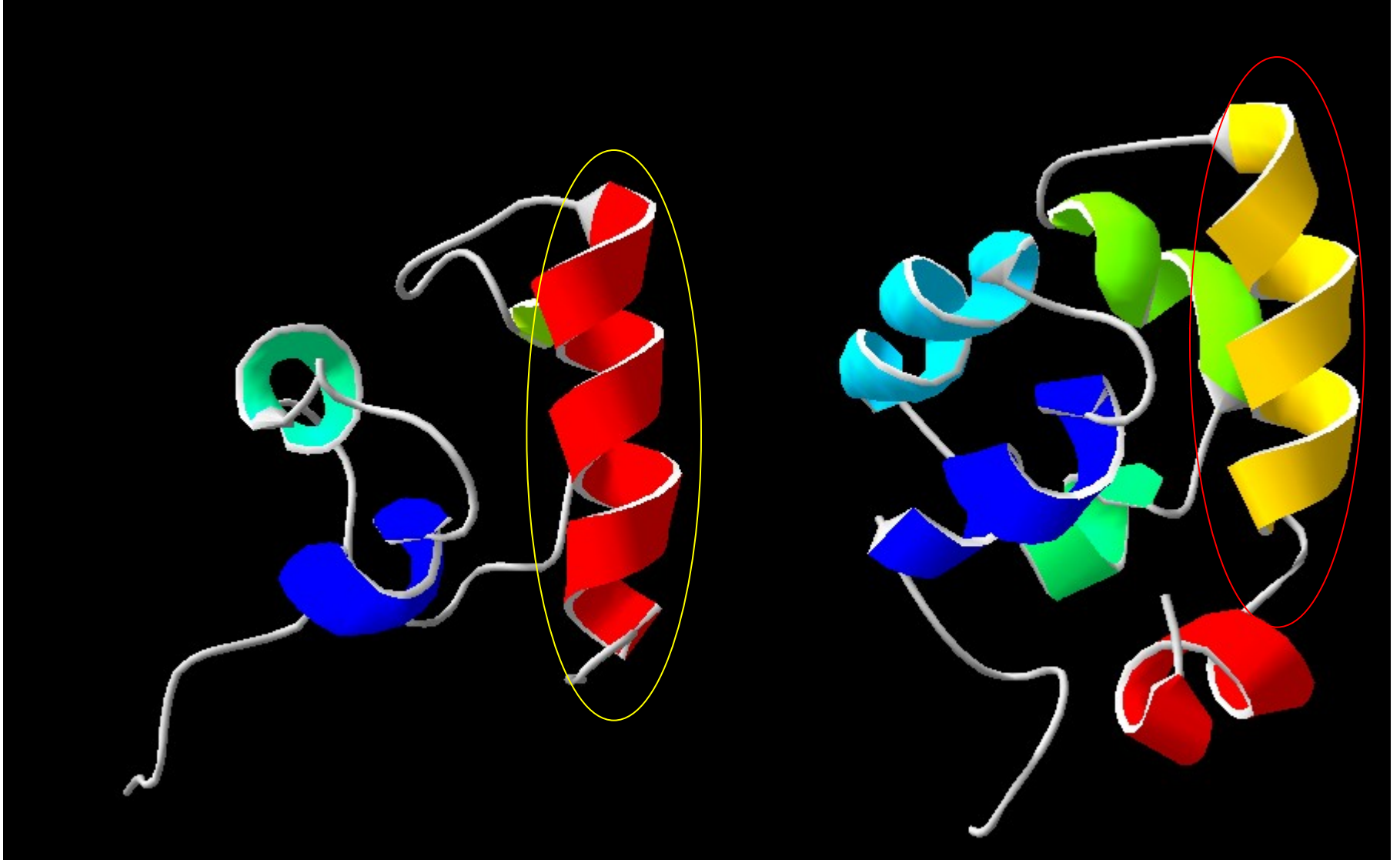


Remap: Enzymes that cut Frequency ↓

<u>BamHI</u>	4 ↓
<u>EcoRI</u>	14 ↓
<u>EcoRII</u>	24 ↓
<u>HindII</u>	30 ↓
<u>HindIII</u>	14 ↓
<u>TaqI</u>	162 ↓

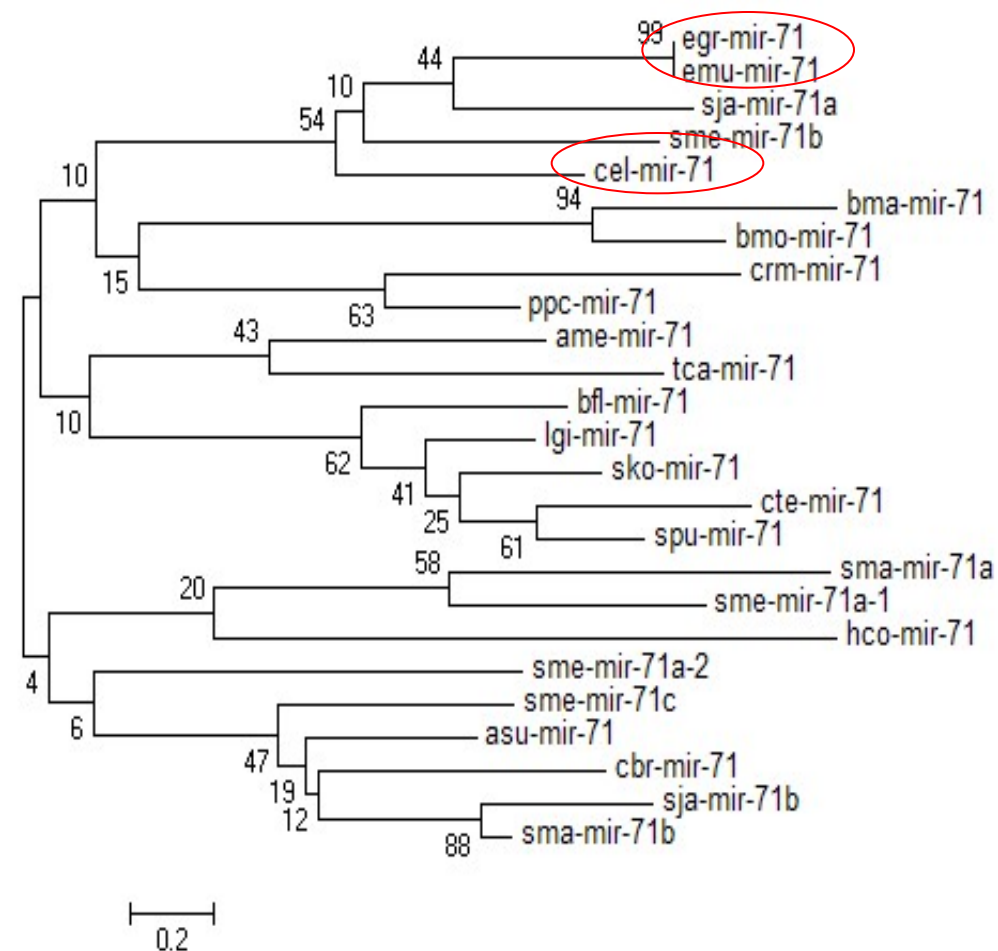
differences between TIR and prediction of Echinococcus utilocularis coding protein sequence.

SWISS-MODEL Workspace: automated model

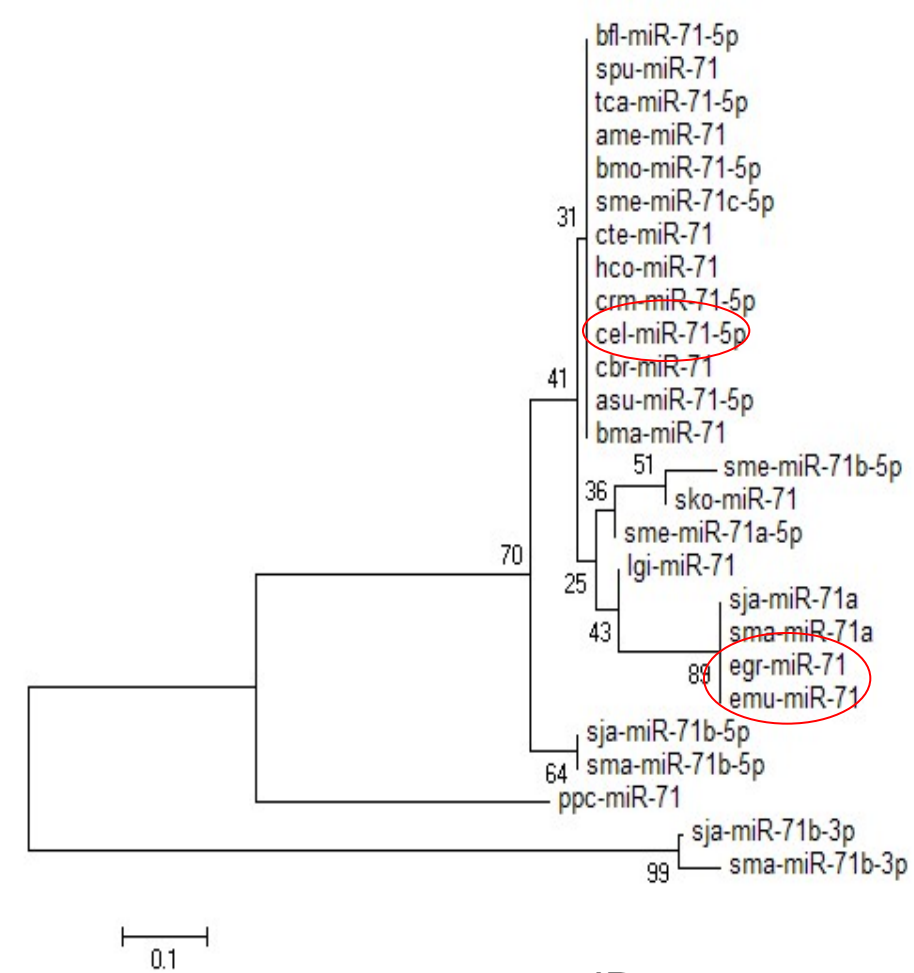




F. Evolution analysis: Pre-miR-71 and mature miR-71:



Pre-miR-71



mature miR-71

Acknowledgements:

Show our the deepest gratitude to our professor Luo.

thank my partner Jian Yingna

Wang miao Yang Xiaoyu.to show thanks to external assistant Gao Zeqian.

Preferences:

MiroRNAs: From Basic Science to Disease Biology—
—Krishnarao Appasani.

Thank you for your attention

