Target prediction

Science, Biology

UMUC BIOT630 Lecture 10 Exercise – " Due Version" Question a Using miRBase (http www. mirbase. org), what is the accession number for " mmu-mir-223"? Answer = The accession number for " mmu-mir-223" is MI0000703.

Question 1. b

Overlooking the record provided as your answer to Question 1. a, what " Gene Family" does " mmu-mir-223" belong to?

Answer = " mmu-mir-223" belongs to MIPF0000067; mir-223 (23 sequences) gene family.

Question 1. c

What gene does " mmu-mir-223" fall within?

Answer = The " mmu-mir-223" is an RNA gene" or a " non-coding RNA gene (ncRNA) involved in gene regulation.

Question 1. d

What type of gene feature does " mmu-mir-223" fall in?

Answer = " mmu-mir-223" is a microRNA (miRNA) gene.

Question 1. e

What is the genomic position, or coordinates, for " mmu-mir-223"?

Answer = " mmu-mir-223" can be genetically mapped to ChrX: 93438156-93438265 bp, + strand

Question 1. f

What is the " Stem-loop" sequence for " mmu-mir-223"?

Answer = The " Stem-loop" sequence for " mmu-mir-223" is:

UCUGGCCAUCUGCAGUGUCACGCUCCGUGUAUUUGACAAGCUGAGUUGGACAC
UCUGUGUGGUAGAGUGUCAGUUUGUCAAAUACCCCAAGUGUGGCUCAUGCCUA

UCAG

Question 1. g

What is the " Mature" sequence for " mmu-mir-223"?

Answer = The " Mature" sequence for " mmu-mir-223" is:

> mmu-miR-223-3p MIMAT0000665

UGUCAGUUUGUCAAAUACCCCA

> mmu-miR-223-5p MIMAT0017056

CGUGUAUUUGACAAGCUGAGUUG

Question 2. a

Using TargetScanHuman (http://www. targetscan. org/vert_50/), species set to " Mouse", and all other search criteria kept at default settings, how many " conserved targets", " conserved sites", and " poorly conserved sites" are there for " mmu-miR-223"?

Answer = There are 150 conserved targets, with a total of 154 conserved sites and 43 poorly conserved sites for " mmu-miR-223".

Question 2. b

In the target list exists " F3". What sites does " mir-223" bind in the 3' UTR for this mRNA? To answer, click on the corresponding " Site in UTR" link. Then, copy paste screen shot. The sites will be designated as outlined boxes.

Answer =

Question 2. c

Of the total number of " miR-223" binding sites that occur in the " F3" 3' UTR (see you're your answer to Question 2. b), how many are " Conserved"?

Answer = Of the total number of " miR-223" binding sites that occur in the "

F3" 3' UTR, only one is conserved.

Question 2. d

Of the " Conserved" " miR-223" binding sites in the " F3" 3' UTR, what appears to be the consensus sequence in the miRNA that binds the mRNA target sequence?

Answer = Of the " Conserved" " miR-223" binding sites in the " F3" 3' UTR, the consensus sequence in the miRNA that binds the mRNA target sequence is AACUGAC.

Question 3. a

Using your answer to Question 1. f in conjunction with Mfold (http://mfold. rna. albany. edu/? q= mfold/RNA-Folding-Form), what is the secondary structure prediction? To answer, keep all parameter settings set to default, scroll down to bottom of form and click on " Fold RNA". After, open/copy/paste the " Vienna" formatted prediction for Structure 1.

Answer =

Structure 1: Folding bases 1 to 110 of mmu-mir-223 stem-loop sequence

Initial ΔG = -44. 50

The " Vienna" formatted prediction for Structure 1 is as follows:

UCUGGCCAUCUGCAGUGUCACGCUCCGUGUAUUUGACAAGCUGAGUUGGACAC
UCUGUGUGGUAGAGUGUCAGUUUGUCAAAUACCCCAAGUGUGGCUCAUGCCUA
UCAG

.((((......(((..((((((((....((((((((((((((......

((((((((((.....))))))))))))))))))))))))))....))))))))...)))...))))(-44. 50)

Question 3. b

What does the 2D rendering for the Structure 1 prediction look like? To answer, open/copy/paste the " pdf" or " png" formatted prediction for Structure 1.

Answer = The 2D rendering for the Structure 1 prediction looks as shown below.

Question 4. a

Given the following RNA " Stem-Loop" sequence:

> What am I?

CGGGGUUGGUUGUUAUCUUUGGUUAUCUAGCUGUAUGAGUGGUGUGGAGUCU UCAUAAAGCUAGAUAACCGAAAGUAAAAAUAACCCCA

What miRNA family does the miRBase " Search" feature (http://www. mirbase. org/search. shtml) say it is likely a member of? To answer, review the search results, explore the recorded family entries in the corresponding records, report the consensus entry as your answer.

Answer = Upon search against miRNA sequences, the miRNA's are a member of " MIPF0000014; mir-9" miRNA family. The consensus sequence is: ucuuugguuaucuagcuguauga

Question 4. b

Using the same RNA " Stem-Loop" sequence in Question 4. a, what miRNA family does the Rfam " Search" feature (http://rfam. sanger. ac. uk/search) say it is likely a member of?

Answer = the miRNA's are a member of mir-9/mir-79 (RF00237) microRNA precursor family.

Question 4. c

Per your answers to Questions 4. a and 4. b, would you say Rfam and

miRBase provide similar or different results?

Answer = Definitely, both of them produce the same results.