

Stratagene's High-Specificity Primer Design Guidelines

Note: This information is provided free of charge to our customers in order to provide consistent quality service and allow for the greatest specificity possible for miRNA detection.

Step 1. Obtain miRNA Sequence Information

- Download the most recent update of mature miRNA sequences (mature.fa "Fasta format sequences of all mature miRNA sequences") from the Sanger database at <http://microrna.sanger.ac.uk/sequences/ftp.shtml>. The following screen will appear:

miRBase Sequence Download	
Go to the FTP site	
Previous releases	
README	Release notes - read these first!
miRNA.dat	all published miRNA data in EMBL format
hairpin.fa	Fasta format sequences of all miRNA hairpins
mature.fa	Fasta format sequences of all mature miRNA sequences
maturestar.fa	Fasta format sequences of all minor miR* sequences
miRNA.diff	Changes between the last release and this
miRNA.dead	List of entries that have been removed from the database
miFam.dat	Family classification of miRNA hairpin sequences

- Extract the file and then open with Microsoft Word

Step 2. Identify Species Specific Information

- Remove all non-specific target species information

For example:

For human sequence (hsa) specific information, delete all non-human miRNA information

Step 5. Convert RNA to DNA

- Change the **U** in the desired miRNA sequence to **T** (convert RNA to DNA).
- We recommend that you **highlight** the nucleotides that are not the same as the desired miRNA in **red** or some other distinguishable color for easier identification.

Step 6. Identify Nucleotides

- Identify a nucleotide position close to the 3' end that has the lowest nucleotide identity with the other miRNA – make sure that there is at least **1** nucleotide in the remaining portion of the sequences that is not the same – delete the nucleotides 3' of this position.

***Note:** Nucleotides do not have to be deleted – this is only performed to increase specificity when needed*

- Avoid relying upon a **G:T** or **T:T** mismatch for specificity as they are not easily discriminated
- **C:A** mismatches are most easily discriminated

Step 7. Calculate T_m

- Determine the estimated T_m of the remaining desired miRNA.

***Note:** You can use the standard T_m calculators of your oligo house. For example, if using Integrated DNA Technologies website use the default settings to estimate the T_m.*

Step 8. Adjust the T_m

- You now need to adjust the T_m of the sequence in order to obtain a T_m in the appropriate range of **50°C to 55°C**. This temperature range provides for greater

specificity.

- Add one or more **G** to the 5' end of the remaining desired miRNA to adjust the T_m to **50°C -55°C**.
- The minimum length before adding G's should not be less than 15 nucleotides.
Note: *You may determine that there may be more than one sequence for your desired miRNA primer.*

Step 9. Order Sequences

- Design and order your primer(s). Order more if needed. In some cases you will determine one or more sequences that are projected to provide the desired specificity.
Note: *HPLC purification is required for highest consistency and sensitivity*
- Order synthetic miRNA templates of the desired miRNA(s) from your standard oligo supplier and any other closely related miRNA(s). You will want to test empirically for specificity.