

### snoTARGET updates:

Public computational resource **snoTARGET** is a Perl script (snoTARGET.pl) that was designed to run on our web server (Linux cluster). Utilization of the cluster allowed us to make parallelization of the original **prog\_snoTARGET.pl**, and run it simultaneously on 20 CPUs. The Cluster was broken and dismantled in April 2013. Thus, this computational resource **snoTARGET** is not available for public use any longer. However, its three program scripts are open for down loading (files: [snoTARGET.pl](#), [check\\_submit.cgi](#), and [divide\\_dEID\\_character.pl](#)).

The original perl script for a single CPU usage ([prog\\_snoTARGET.pl](#)) is also available to the public. To run it on a computer with Unix environment a user should type the following command line:

```
perl prog_snoTARGET.pl argument1 argument2
```

Where `argument1` is the name of a file containing a list of snoRNA antisense elements in a FASTA format (see for example file: [Neil\\_snoRNA\\_2012.txt](#)), `argument2` is the name of the output file where the results will be printed. The program will add to this name an extension (example: `_dEID`, see below) that specifies what database has been used for the current set of computations.

#### A user should modify this program in four places:

- 1) **LINE 5:** assign a value to the variable `$prefix` (example `$prefix=5;`). In this example, this option removes first 5 nucleotides from all antisense elements (ASE) listed in the `argument1` file. So, the program begins searching for the TARGETS starting from the sixth nucleotide of the original ASE sequences.
- 2) **LINE 21:** assign a string to variable `$n`, which is a name of the Exon/Intron database file including the path to it, unless it is in the current directory: (example: `$n = '/EID/Mouse37_v2/mm37.dEID';`). This database should be in the EID format (see *Shepelev and Fedorov 2006*). These Exon-Intron databases for different species are available from our EID database (<http://bpg.utoledo.edu/~afedorov/lab/eid.html>).
- 3) **Line 24:** assign an integer number to variable `$N`, which represents the maximum number of allowed G-U pairs between the ASE and its TARGET (example: `$N =4;`).
- 4) **LINE 149:** within this line the program makes a system call invoking the `RNAcofold` program from the public **RNA Vienna** package. A user must install this `RNAcofold` program prior to use `prog_snoTARGET.pl`.

#### Optional modifications:

- 1) For sorting results by any special preferences a user should remove a comment (`#` character) from LINE 27, which activates the subroutine `&sortoutput` and simultaneously puts a comment on the next line as follows: `#@s = (0, 1, 2, 3);`
- 2) On **line 21**, a user may also assign a different string to the `$db` variable. This string will be added to the filename of the output file. Example: the `argument2` is `"test"` string and `$db = 'dEID'`. Then the output file containing the results will have the name: `"test_dEID"`.

It takes about 20 min to run this program on a regular desktop computer. A demonstration of how to run this program is available on this [video](#).