

my_a1.pl

DESCRIPTION

SUMMARY

This Perl program splits a sequence of DNA into the upstream and genic regions. It then performs a number of string manipulations on both those sequences. A report (see Output below) is printed.

INPUT

No input. A string of DNA is manually set in a variable.

OUTPUT

To CONSOLE (screen): A report of the first three codons and their bp locations, the upstream and genic regions and their lengths, the reverse complement of the genic portion, and the number of As and Ts in the upstream region.

AUTHORS

your name goes here

MODIFICATION HISTORY

August 4, 2009 (mdl) --

back from fishin', just getting started

August 11, 2009 (mdl) --

finished the starter kit

(add your modification dates and notes here)