

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)**