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#!/usr/bin/perl -w
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use strict;  
use warnings;
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sub find_pattern{  
    my($pattern, $file)=@_  
    my @gene_ids;  
    my @gene_sequences;  
  
    if(-e "$file"){  
        open("IN", "< $file");  
        my $idx_seq=-1;  
        while(my $line=<IN>){  
            chomp($line);  
            $line=~s/ //g;  
            if($line eq "") {next;}  
            if($line=~/^>(.)//){  
                $idx_seq++;  
                push(@gene_ids, $1);  
                next;  
            }  
            $gene_sequences[$idx_seq].=$line;  
        }  
        close(IN);  
  
        for(my $i=0;$i<=$#gene_sequences;$i++){  
            print "$gene_ids[$i]";  
            my $offset=0;  
            do{  
                my $substring=substr $gene_sequences[$i], $offset, length($pattern);  
                if($substring eq $pattern){  
                    print ",";  
                    print $offset+1;  
                }  
                $offset++;  
            }  
            while(($offset+length($pattern))<=length($gene_sequences[$i]));  
            print "\n";  
        }  
    }  
    else{print ":: $file does not exist\n";}  
}  
  
if($#ARGV !=1){  
    print ":: Usage $0 <pattern> <file>\n";  
    exit();  
}  
  
&find_pattern($ARGV[0], $ARGV[1]);
```