**Project Proposal**

1. **Introduction**
   1. Many plasmid genomes are spliced and manipulated to express inserted genes which researchers test. In order to grow colonies and test these types of phenotype changes, researches cut sections of the plasmid in order to insert new genes or remove genes. They are able to do this with the use of restriction enzymes, which “digest” the DNA by cutting it at sites which hold specific nucleotide patterns.
   2. The objective of this proposal is to provide a tool which lists the compatible sites for one or several restriction enzyme of the user choice. These sites will be analyzed in conjunction with the coding regions or exons they represent. The idea is to provide the researcher with a map of the plasmid where genes can be inserted or deleted, depending on what restriction enzymes are used.
2. **Implementation**
   1. The HTML page will utilize a CSS file for visual effects, as well as Javascript widgets to improve the user interface.
   2. The user input will consist of a FASTA file with the plasmid information. The user will also select which restriction enzymes they wish to query against this plasmid. A CGI file with a connection to a database will query for the restriction enzymes and obtain their sequences. The CGI file will add CDS sequences as genes to the database as it parses the FASTA file, as well as the sites of every restriction enzyme. Once all sites of digest have been processed, it will return a list of genes which fall within the sites which can be spliced out.