BIOCOMPUTING II

GROUP PROJECT

CODE

Name- Shaikh Mohammad Faizan

Email:faizanshaikh1897@gmail.com

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Link to the browser:

student.cryst.bbk.ac.uk/~sm004/wb.html

The whole code

```
<!-- @author: Mohammad Faizan
html for intiial view of webpage
<!DOCTYPE html>
<html lang="en">
<head>
<meta charset="UTF-8">
<meta name="viewport" content="width=device-width, initial-scale=1">
<meta http-equiv="X-UA-Compatible" content="ie=edge">
<style>
[data-tab-content] {
 display: none;
/* display selected/active tab contents*/
.active[data-tab-content] {
 display: block;
body {
 padding: 0;
 margin: 0;
/* change tabs from a list to headers on page */
.tabs {
 display: flex;
 justify-content: space-around;
 list-style-type: none;
 margin: 0;
 padding: 0;
 border-bottom: 1px solid black;
/* cursor hover and tab spacing*/
.tab {
 cursor: pointer;
 padding: 10px;
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.tab.active {
 background-color: #CCC;
.tab:hover {
 background-color: #AAA;
.tab-content {
 margin-left: 20px;
 margin-right: 20px;
body {
   font: 15pt Helvetica, Arial, serif;
   background: #DADFF1;
   margin: 0px;
   padding: 5px;
/* header logo and image */
#header {display: flex;
    flex-direction: row;
     background: #333366;
h1.site_name {text-align:center;
        font: bold italic 80pt Helvetica, Arial, serif;
        color: #1E90FF;
        padding: 0px;
        margin-top: 0;
        position: relative;
        bottom:-100px;
span.site_number {color:#B222222;
.ch22{background:#333366;
   margin: 0;
   float: left;
/* formats restriction search box with */
.ecor1{width: 40%;
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height: 190px;
    float: right;
    position: relative;
    top:-30px;
    left: -20px;
#re_search_format { width: 45%;
           height: 280px;
              padding: 5px;
                background: #87CEEB;
           border: 5px solid #333366;
           float: right;}
/* Styles navigation bar */
.topnav {overflow: hidden;
     background-color: #333333;
.topnav a {float: left;
      color: #F2F2F2;
      text-align: center;
      padding: 14px 16px;
      text-decoration: none;
      font-size: 17px;
.topnav a:hover {background-color: #DDDDDD;
          color: black;
.topnav a.active {background-color: #CD5C5C;
           color: white;
/* Styles page */
#maincontent {clear:both;
        width: 60%;
        height: 50%;
        margin: 0px;
        padding: 0px;
/* Styles tables */
table {border-collapse:collapse;
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width:40%
   }
th, td {text-align:left;
       padding: 8px;
    color:#333366;
tr:nth-child(even){background-color:#F2F2F2;
th {background-color:#333366;
  color:#1E90FF;
body { clear:both;
        width: 100%;
        height: 50%;
        background: #DADFF1;
        margin: auto;
        padding: 5px;
/* Styles main heading in all tab on navigation bar*/
.main_heads {
    text-align:center;
    font: bold 30pt Helvetica, Arial, serif;
    color: #1E90FF;
    background: #333366;
    padding: 14px 16px;
    margin-top: 0px;
/* Styles all sub-headings in all tabs on navigation bar*/
.subheads {text-align:left;
    font: bold italic 15pt Helvetica, Arial, serif;
    color: #333366;
/* Styles table in glossary*/
table {border-collapse:collapse;
    width:100%;
th, td {text-align:left;
       padding: 8px;
    color:#333366;
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tr:nth-child(even){background-color:#F2F2F2;
th {background-color:#333366;
  color:#1E90FF;
/* Styles any sentence in the body*/
.body_text {text-align:left;
    font: 15pt Helvetica, Arial, serif;
    color: #333366;
    padding: 10px;
</style>
<title>Genome Browser</title>
<script src="javascript.js" defer></script> <!--javascript deferred so it happens after html is</pre>
loaded-->
</head>
<body>
<div id='header'>
<h1 class='site name'>ChromAwesome<span class='site number'>22</span></h1>
</div>
 <!--class for tabs and individual tab on webpage-->
<!--create selector that selects specific tab div ids-->
data-tab-target="#home" class="tab">Home <!--default tab-->
data-tab-target="#about" class="tab">About
data-tab-target="#search" class="tab">Search
data-tab-target="#RE" class="tab">Restriction Enzymes
data-tab-target="#analysis" class="tab">Analysis
data-tab-target="#codon" class="tab">The Codons
<a href='glossary.html'>Glossary</a>
<a href='document.html'>Documentation</a>
<a href='Team.html'>Team</a>
<!-- class for webpage tabs and data attributes to be formatted with javascript and css-->
<div id="home" data-tab-content class="main heads"> <!--default tab-->
<h2>Home</h2>
A genome browser looking at genes in human chromosome 22. 
</div>
<div id="about" data-tab-content>
```

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<h2>About</h2>
ChromAweosome 22 is a genomic browser developed as part of a collaborative project
between MSc Bioinformatics and Systems Biology students at Birkbeck, University of London.
This platform provides information on human chromosome 22 based on GRCh38 data from
GenBank.
</div>
<div id="search" data-tab-content>
<h2>Search Chromosome 22 for information about Genes using Gene Identifiers.</h2>
Search by:
<!--form calls searchdb.py, a cgi script which search for genes using the gene identifiers-->
<form method = "get" action = "/cgi-bin/cgiwrap/sm004/searchdb.py" >
<input name="data" type="text" placeholder="E.g: AB002059" size="52" required />
<!--label for gene identifier selection-->
<select name= 'pulldown'>
<optgroup label = Identifiers>
<option id = 'gi'> Gene ID </option>
<option id = 'protein'> Protein ID </option>
<option id = 'gb'> Genbanks Accession </option>
<option id = 'loc'> Chromosomal location </option>
</optgroup>
</select>
<!-- label for text box where user enters identifier-->
<input type ='text' name= 'x'/>
<input type ='submit' value= 'Search'/>
<input type ='reset' value= 'Clear'/>
</form>
</div>
<div id="RE" data-tab-content>
<h2>Search Chromosome 22 to identify location of restriction enzymes.</h2>
Search by Accession number and name of the restriction enzyme
<!--form calls searchdb.py, a cgi script which search for genes using the gene identifiers-->
<form method = "get" action = "/cgi-bin/cgiwrap/sm004/searchRE.py" >
<input name="data" type="text" placeholder="Enter Accession number and Restriction Enzyme"
size="52" required />
<input type ='submit' value= 'Search'/>
<input type ='reset' value= 'Clear'/>
</form>
To view restriction enzymes in CDS sequence of gene 
<!--form calls searchdb.py, a cgi script which search for genes using the gene identifiers-->
<form method = "get" action = "/cgi-bin/cgiwrap/sm004/searchRRE.py" >
<!-- label for text box where user enters identifier-->
<input name="data" type="text" placeholder="Enter Accession number and Restriction Enzyme
e.g. AB002059,EcoRI" size="62" required />
```

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<input type ='submit' value= 'Search'/> <input type ='reset' value= 'Clear'/>
</form>
</div>
<div id="analysis" data-tab-content>
<h2>CDS analysis.</h2>
To view marked up sequence that identifies CdS sites 
   <!--form calls searchdb.py, a cgi script which search for genes using the gene identifiers-->
<form method = "get" action ="/cgi-bin/cgiwrap/sm004/searchmarkup.py" >
  <!-- label for text box where user enters identifier-->
<input name="data" type="text" placeholder="Enter Accession number e.g. AB002059"</pre>
size="52" required />
<input type ='submit' value= 'Search'/> <input type ='reset' value= 'Clear'/>
</form>
 For CDS information 
<!--form calls searchdb.py, a cgi script which search for genes using the gene identifiers-->
<form method = "get" action ="/cgi-bin/cgiwrap/sm004/searchWmarkup.py" >
<!-- label for text box where user enters identifier-->
<input name="data" type="text" placeholder="Enter Accession number e.g. AB002059"</pre>
size="52" required />
<input type ='submit' value= 'Search'/>
<input type ='reset' value= 'Clear'/>
</form>
 To produce translated protein sequence
<!--form calls searchdb.py, a cgi script which search for genes using the gene identifiers-->
<form method = "get" action = "/cgi-bin/cgiwrap/sm004/searchPro.py">
<!-- label for text box where user enters identifier-->
<input name="data" type="text" placeholder="Enter Accession number e.g. AB002059"</pre>
size="52" required />
<input type ='submit' value= 'Search'/> <input type ='reset' value= 'Clear'/>
</form>
 To match translated protein CDS sequence with original CDS sequence
<!--form calls searchdb.py, a cgi script which search for genes using the gene identifiers-->
<form method = "get" action ="/cgi-bin/cgiwrap/sm004/searchmatch.py" >
<!-- label for text box where user enters identifier-->
<input name="data" type="text" placeholder="Enter Accession number e.g. AB002059"</pre>
size="52" required />
<input type ='submit' value= 'Search'/> <input type ='reset' value= 'Clear'/>
</form>
</div>
<div id="codon" data-tab-content>
<h2>The Codon in Chromosome 22</h2>>>
 To view codon usage frequencies 
<!--form calls searchdb.py, a cgi script which search for genes using the gene identifiers-->
<form method = "get" action ="/cgi-bin/cgiwrap/sm004/searchcodon.py" >
<!-- label for text box where user enters identifier-->
```

```
<input name="data" type="text" placeholder="Enter Accession number e.g. AB002059"
size="52" required />
<input type ='submit' value= 'Search'/> <input type ='reset' value= 'Clear'/>
</form>
Calculate codon usage frequencies in whole chromosome
<!--form calls searchdb.py, a cgi script which search for genes using the gene identifiers-->
<form method = "get" action ="/cgi-bin/cgiwrap/sm004/searchDNAcodon.py" >
<!-- label for text box where user enters identifier-->
<input type ='submit' value= 'Click to submit chromosome data'/>
</form>
</div>
```

The code is validated using validatorw3.org

