```python
#!/usr/bin/python3
"""
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This CGI script obtains all the entries from the BL layer and formats them for
HTML display as a table
"""


# Add the bl sub-directory to the module path
# and the directory above to import the config file
import sys
sys.path.insert(0, "../bl/")
sys.path.insert(0, "../")

import cgi        # Import the CGI module
import blapi_dummy      # Import the Business Logic API
import htmlutils  # Import HTML utilities
import config     # Import configuration information (e.g. URLs)

form = cgi.FieldStorage()
accession = str(form.getvalue('ac'))
codon_count_table = blapi_dummy.codon_count(accession)
dna_string = blapi_dummy.CDS_DNA_string(accession)
se_string = blapi_dummy.sticky_ends_inplace(accession)
exons = blapi_dummy.exon_string(accession)


html = htmlutils.header()
html += "<h1>Detailed Genbank Results</h1>\n"
html += '  <table border="5">\n'

html += "<tr><th style='background-color: gold' td>Result of search for Accession Number :  </td>" + "<td>" + accession + "</td></tr>"

html += "<tr><th style='background-color: salmon' td>Protein Product Name: </td>" + "<td>" + blapi_dummy.ppn(accession) + "</td></tr>"

html += "<tr><th style='background-color: darkseagreen' td>Gene ID: </td>" + "<td>"  + blapi_dummy.gene_id(accession) + "</td></tr>"

html += "<tr><th style='background-color: skyblue' td>Chromosomal Location: </td>" + "<td>" + blapi_dummy.chrom_loc(accession) + "</td></tr>"

html += "<tr><th style='background-color: cadetblue' td>CDS AA String: </td>" + "<td>"  + blapi_dummy.CDS_aa_string(accession) + "</td></tr>"

html += "  </table>\n"

#dna string details

html += "<h3>CDS DNA String</h3>\n"

html += '  <table>\n'

html += '<tr>'
for n in dna_string:
    html += "<td>" + n + "</td>"
html += "</tr>"
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```python
html += '<tr>'
for se in se_string:
    html += "<td>" + se + "</td>"
html += "</tr>"
html += '<tr>'
for n in exons:
    html += "<td>" + n + "</td>"
html += "</tr>"
html += "  </table>\n"


#Codon counting

html += "<h3>Codon Frequency in CDS DNA String</h3>\n"

html += '  <table border="5">\n'

html += '<tr>'

x = 0
for codon in codon_count_table:
    if x % 10 == 0:
        html += "</tr>"
        html += "<tr>"
    html += "<td>" + codon + "</td>"
    x += 1
html += "</tr>"
html += "  </table>\n"

html += "Key: <br>"
html += "Count of Codons in genbank entry (1st Number) <br>"
html += "% of codon found in entry (1st percentage) <br>"
html += "% of codon found across all chromosome coding regions in database (2nd percentage)
<br>"

html += htmlutils.footer()

print(html)
```