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#!/usr/bin/python3
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"""
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Version: 1.0
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Date: 02/05/2022
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```
This CGI script obtains all the entries from the BL layer and formats them for  
HTML display as a table
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"""
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```
# 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 blapi_dummy # Import the Business Logic API
```

```
import htmlutils # Import HTML utilities
```

```
import config # Import configuration information (e.g. URLs)
```

```
import cgi
```

```
form = cgi.FieldStorage()
```

```
ac = str(form.getvalue('ac'))
```

```
gi = str(form.getvalue('gi'))
```

```
ppn = str(form.getvalue('ppn'))
```

```
entries = blapi_dummy.getAllEntries()
```

```
html = htmlutils.header()
```

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

```
html += "<tr><th style='background-color: gold'>Accession Number</th>"
```

```
html += "<th style='background-color: darkseagreen'>Gene ID</th>"
```

```
html += "<th style='background-color: salmon'>Protein Product Name</th>"
```

```
html += "<th style='background-color: skyblue'>Chromosomal Location</th></tr>\n"
```

```
if 'ac' not in form and 'gi' not in form and 'ppn' not in form:
```

```
    for d in entries:
```

```
        html += "<tr><td>" + "<a href='" + config.searchurl + "?ac=" + d.get('acc') + "'>" +  
d.get('acc') + "</a>" + "</td>"
```

```
        html += "<td>" + d.get('gene_id') + "</td>"
```

```
        html += "<td>" + d.get('ppn') + "</td>"
```

```
        html += "<td>" + d.get('chrom_loc') + "</td></tr>"
```

```
if 'ac' in form:
```

```
    for d in entries:
```

```
        if d.get('acc') == ac:
```

```
            html += "<tr><td>" + "<a href='" + config.searchurl + "?ac=" + d.get('acc') + "'>" +  
d.get('acc') + "</a>" + "</td>"
```

```
            html += "<td>" + d.get('gene_id') + "</td>"
```

```
            html += "<td>" + d.get('ppn') + "</td>"
```

```
            html += "<td>" + d.get('chrom_loc') + "</td></tr>"
```

```
elif 'gi' in form:
```

```
    for d in entries:
```

```
        if d.get('gene_id') == gi:
```

```
            html += "<tr><td>" + "<a href='" + config.searchurl + "?ac=" + d.get('acc') + "'>" +  
d.get('acc') + "</a>" + "</td>"
```

```
            html += "<td>" + d.get('gene_id') + "</td>"
```

```
            html += "<td>" + d.get('ppn') + "</td>"
```

```
            html += "<td>" + d.get('chrom_loc') + "</td></tr>"
```

```

elif 'ppn' in form:
    for d in entries:
        if d.get('ppn') == ppn:
            html += "<tr><td>" + "<a href='" + config.searchurl + "?ac=" + d.get('acc') + "'>" +
d.get('acc') + "</a>" + "</td>"
            html += "<td>" + d.get('gene_id') + "</td>"
            html += "<td>" + d.get('ppn') + "</td>"
            html += "<td>" + d.get('chrom_loc') + "</td></tr>"

html += " </table>\n"
html += htmlutils.footer()

```