Alternate front-end code documentation

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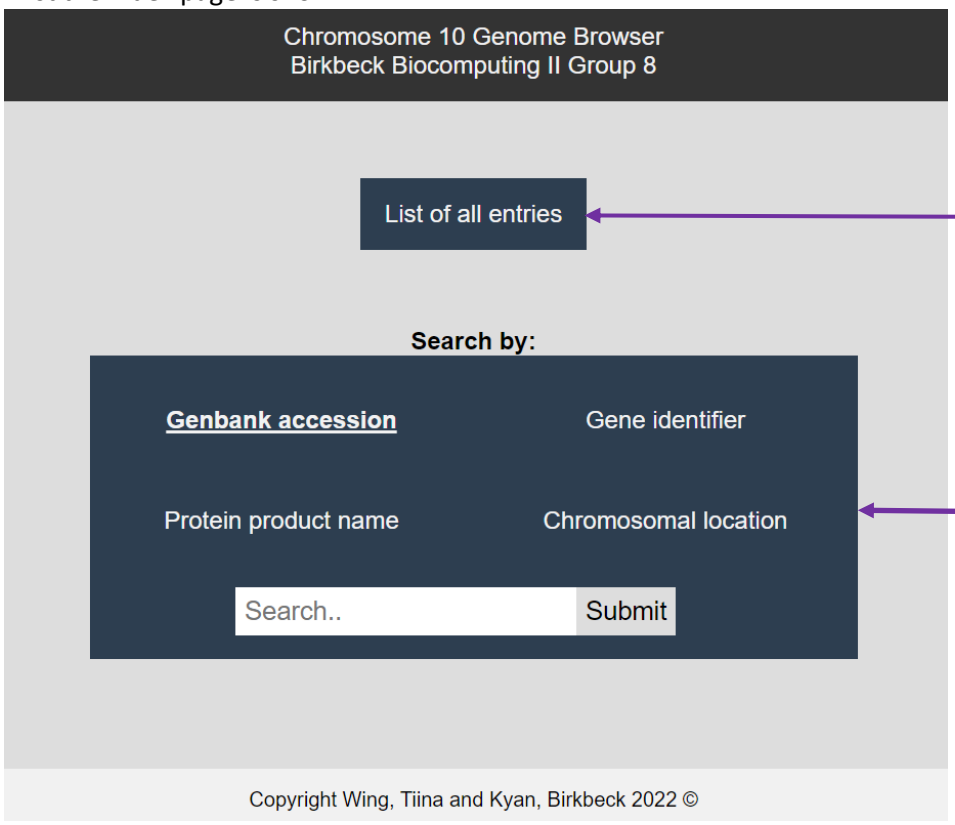
The website can be accessed from the following address:

https://student.cryst.bbk.ac.uk/~kk004/biocomp2demo/

First the index page is shown:



Clicking on the "List of all entries" link calls the listall.cgi script to produce a list of all entries

Alternatively, you can search for a specific entry. This is done by first selecting one of the four search options. Then enter the search text and press the enter-key or click on "Submit". This sends the form data to the search.cgi script.

Here is the "list of entries" page produced by the listall.cgi:

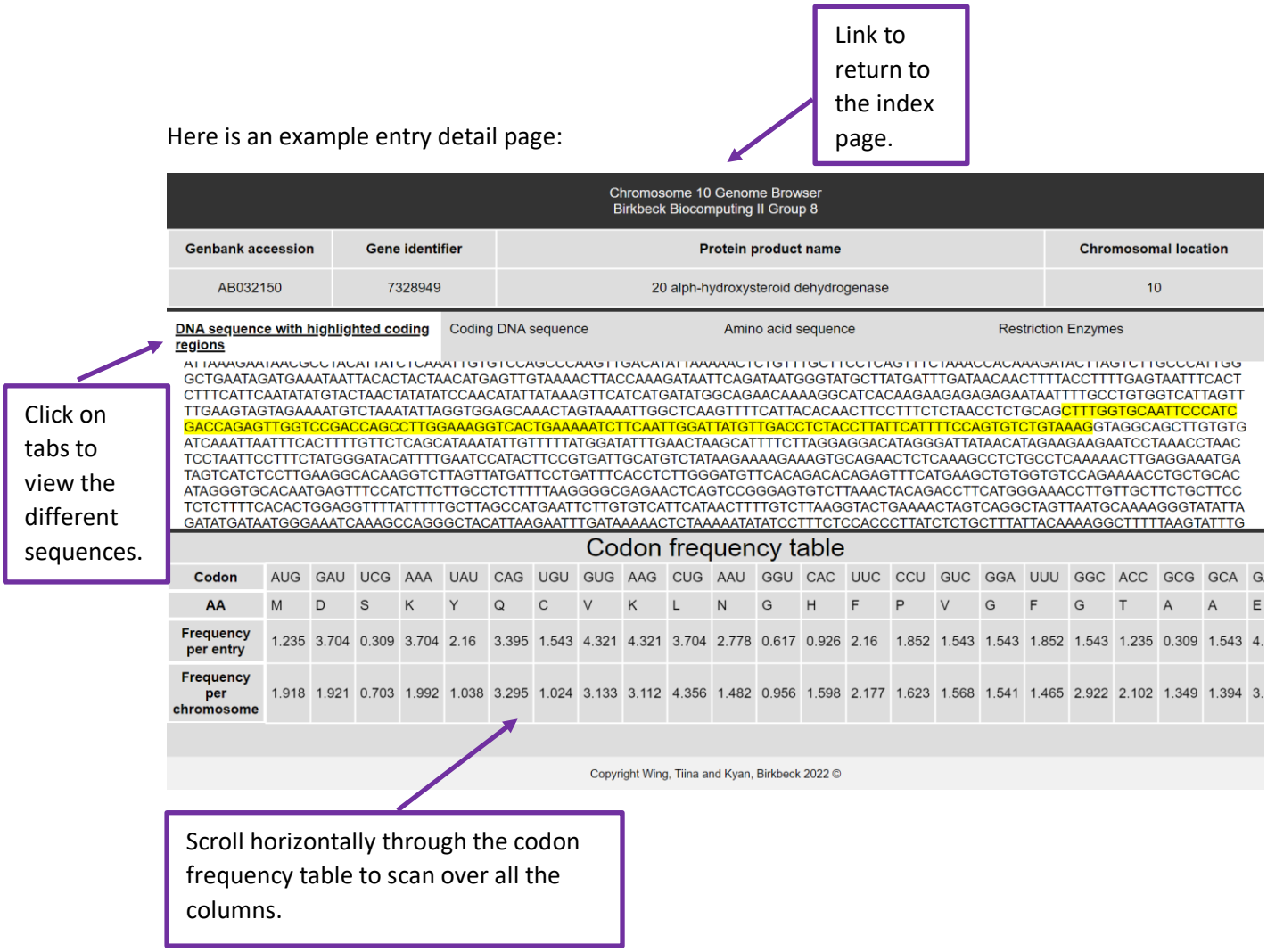
Clicking on the header to return to the index page.

Click on the link in the genbank accession to call the search.cgi script and view the details page for the entry.

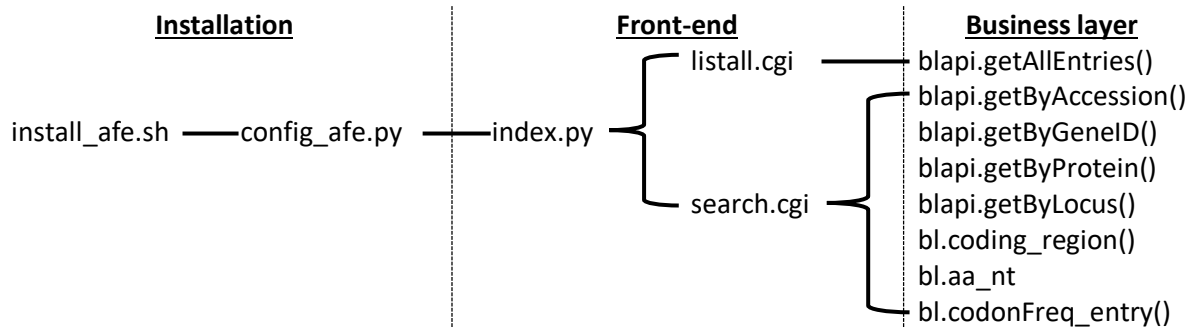
Chromosome 10 Genome Browser
Birkbeck Biocomputing II Group 8

Genbank accession	Gene identifier	Protein product name	Chromosomal location
AB032150	7328949	20 alph-hydroxysteroid dehydrogenase	10
AB032153	60391440	bile acid-binding protein	10
AB032157	60391441	prostaglandin F synthase	10
AB032163	60391442	dihydrodiol dehydrogenase 4	10
AB033920	60391447	fatty acid coenzyme A ligase 5	10q25.1-q25.2

Here is an example entry detail page:



Call routine:



install_afe.sh - This program is run in the command-line to create the directories for the website to be run.

config_afe.py - Contains information on the website url and cgi script locations.

index.py - Prints the index.html page

search.cgi - Takes the form data from the index page and uses the business layer to produce a details page for an entry. Or creates a table list of entries if there are multiple results.

listall.cgi - Formats output from the business layer into an html table of all the entries.