Choosing Genes

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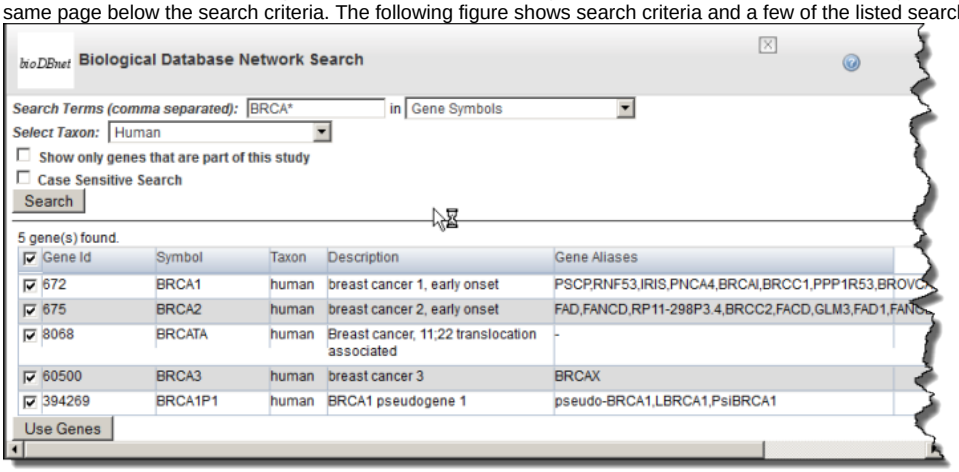
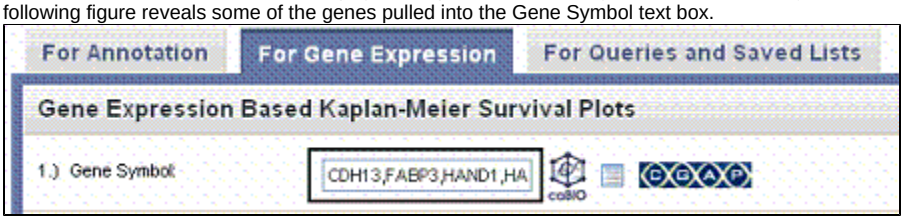
To obtain gene names for a gene expression search or analysis, use one of the following three methods described in this section: bioDBnet, Gene List or CGAP.

- **bioDBnet**– This link searches bioDBnet for gene IDs, symbols or genes within pathways. Then caIntegrator pulls identified genes into the application for analysis.
    1. Click **bioDBnet**.
    2. Enter **Search Terms**. Note that caIntegrator can perform a search on a partial HUGO symbol. For example, as search using ***ACH **** woul d find matches with 'achalasia' and 'arachidonate'.
    3. Select if you want to search in **Gene IDs**, **Gene Symbols, Gene Aliases, Pathways** (from the drop-down list), or **Search Pathways for Genes**.
        - **Gene IDs** searches the exact gene ID(s) you enter.
        - **Gene Symbols** searches only the Unigene and HUGO gene symbols in bioDBnet.
        - **Gene Aliases** searches for one or more gene symbols which are synonymous for the current gene symbol.
        - **Pathways** searches only the pathway names in bioDBnet.
        - **Search Pathways for Genes** searches for pathways containing gene(s) you specify for the search.
    4. Select **Show only genes that are part of this (caIntegrator) study** or **Case Sensitive Search** if either of these criteria are to be applied to the search. (By default, the search is case insensitive.)
    5. Choose the **Taxon** from the drop-down list and click **Search.** (The Taxon criterion defaults to Human.) The search results display on the same page below the search criteria. The following figure shows search criteria and a few of the listed search results.



    6. In the search results, use the check boxes to identify the genes whose symbols you want to use in the gene expression analysis.
    7. Click **Use Genes** at the bottom of the page. This pulls the checked genes into the Gene Symbol text box on the Criteria tab. The following figure reveals some of the genes pulled into the Gene Symbol text box.



- **Gene List**– This link locates gene lists saved in caIntegrator.
    1. Click the Genes List icon ( ) to open a Gene List Picker dialog. For more information, see Creating a Gene or Subject List.
       If a GISTIC analysis has been run, you may see the following options:
        - GISTIC Amplified genes is a list of gene symbols in which the corresponding regions of the genome are significantly amplified.
        - GISTIC Deleted genes is a list of gene symbols in which the corresponding regions of the genome are significantly deleted.
    2. In the drop-down menu that lists previously saved gene lists, select a gene list. In the list that appears, use the check boxes to identify the genes whose symbols you want to use in the gene expression analysis.
    3. Click **Use Genes** at the bottom of the dialog. This pulls the checked genes into the Search Criteria tab.
- **CGAP** – Use this directory to identify genes. Before clicking the CGAP icon ( ) you must enter gene symbols in the text box. This link does not pull anything into caIntegrator but does provide information about the gene(s) whose names you entered.