

# Choosing Genes

## Choosing Genes

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 calIntegrator pulls identified genes into the application for analysis.
  1. Click **bioDBnet**.
  2. Enter **Search Terms**. Note that calIntegrator can perform a search on a partial HUGO symbol. For example, as search using **ACH \*** would 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 (calIntegrator) 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.

bioDBnet Biological Database Network Search

Search Terms (comma separated): BRCA\* in Gene Symbols

Select Taxon: Human

☐ Show only genes that are part of this study

☐ Case Sensitive Search

Search

5 gene(s) found.

<input checked="" type="checkbox"/> Gene Id	Symbol	Taxon	Description	Gene Aliases
<input checked="" type="checkbox"/> 672	BRCA1	human	breast cancer 1, early onset	PSCP,RNF53,IRIS,PNUA4,BRCA1,BRCC1,PPP1R53,BROV...
<input checked="" type="checkbox"/> 675	BRCA2	human	breast cancer 2, early onset	FAD,FANCD,RP11-298P3.4,BRCC2,FACD,GLM3,FAD1,FAN...
<input checked="" type="checkbox"/> 8068	BRCA1A	human	Breast cancer, 11;22 translocation associated	
<input checked="" type="checkbox"/> 60500	BRCA3	human	breast cancer 3	BRCA3
<input checked="" type="checkbox"/> 394269	BRCA1P1	human	BRCA1 pseudogene 1	pseudo-BRCA1,LBRCA1,PsiBRCA1

Use Genes



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.

For Annotation For Gene Expression For Queries and Saved Lists

Gene Expression Based Kaplan-Meier Survival Plots

1.) Gene Symbol: CDH13,FAEP3,HAND1,HA

CGAP

- **Gene List**– This link locates gene lists saved in calIntegrator.
  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 calIntegrator but does provide information about the gene(s) whose names you entered.