

caBIO Portlet Simple Search Tool

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To Print the Guide

We recommend you print one wiki page of the guide at a time. To do this, click the printer icon at the top right of the page; then from the browser File menu, choose Print. Printing multiple pages at one time is more complex. For instructions, refer to [Exporting Multiple Pages to PDF](#).



Having Trouble Reading the Text?

Resizing the text for any web page is easy. For information on how to do this in your web browser, refer to this [W3C tutorial](#) .

caBIO Portlet Simple Search Overview

caBIO is a resource that integrates biomedical data on genes, proteins, clinical protocols, disease ontologies, pharmacological agents, pathways, and other entities with annotations, controlled vocabularies, and metadata models originating from [twenty-three data sources](#), including the Cancer Gene Index, the Pathway Interaction Database, and the University of California, Santa Cruz Distributed Annotation System. You can use the Simple Search to query these data.



Note

The caBIO Portlet Simple Search tool retrieves caBIO objects that have attributes that match a gene, disease, or compound term name; however, retrieved objects are not grouped by type and you may have to scroll through dozens of search result pages to find all Cancer Gene Index-associated objects.



Warning

It is highly recommended that you use the [Cancer Gene Index Gene-Disease and Gene-Compound XML documents](#), [caBIO Portlet Templated Search](#), or even the [caBIO Portal](#) instead of the caBIO Portlet Simple Search tool. Please refer to the [documentation main page](#) to decide which of these options is best for you.

Should you still want to use the Simple Search, links to guides are given below.

caGrid Portal

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caBIO Portlet

The [caBIO portlet](#) is a portal user interface built on top of the caBIO APIs. [caBIO](#) is a repository of data useful in biomedical research, compiled from multiple primary sources.

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[Search](#)

[Advanced Options](#)

Step-by-step Guides

Should you wish to use this tool, step-by-step instructions are provided to help you find

- [genes associated with a disease](#),
- [genes associated with a compound](#), or
- [compounds and diseases associated with a gene](#).