caBIO API Overview

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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 Printing multiple pages.

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 Application Programming Interfaces 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.

The caBIO APIs expose all of the Cancer Gene Index data, metadata, and annotations. Thus, you can use these APIs to evaluate the evidence from which these associations were extracted and the codes and details that describe these associations. Other annotations, such as sentence status flags, negation indicators, cell line indicators, and organism name are also available.

You may also use the APIs to uncover associations between these data and other information within caBIO (for example, protein annotations, pathway data, tissue data, or clinical protocols).

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⚠️ **Be Careful**

To effectively use the caBIO APIs, you should have some understanding of the caBIG® philosophy and a deep understanding of the caBIO object model. If you do not have this knowledge and only wish to explore Cancer Gene Index data, it is highly recommended that you start with the Gene-Disease and Gene-Compound XML. Once you become more comfortable with caBIG® technologies and practices or you would like to take full advantage of caBIO, then begin to use the APIs.

✅ **Constructing Queries**

Even with knowledge of caBIO object model, you may still need help constructing more complicated queries. For support with any of the caBIO APIs, email or telephone (1-888-478-4423) Application Support Group or join the caBIO Users listserv

For your convenience, the subset of caBIO classes that are associated with Cancer Gene Index are shown. The full model is available on the NCI SVN, but you must have the Enterprise Architect 🖼 modeling tool to view this file.

The caBIO APIs

caBIO 4.3 APIs include, but are not limited to, Java, Python, Perl, .NET, REST, REST with AJAX, and XML-HTTP. For additional information on any of these APIs, please refer to the caBIO wiki.

Sharing Your Code

As you use the caBIO APIs to explore Cancer Gene Index data, you are strongly encouraged to share your code and any related documentation on the Cancer Gene Index Parsed Data and Code wiki page.