# Using the caBIO Home Page Freestyle Lexical Mine to Find Compounds and Diseases Associated with a Gene

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**Need Additional Help?**

If you need additional support, please contact Application Support.

**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.

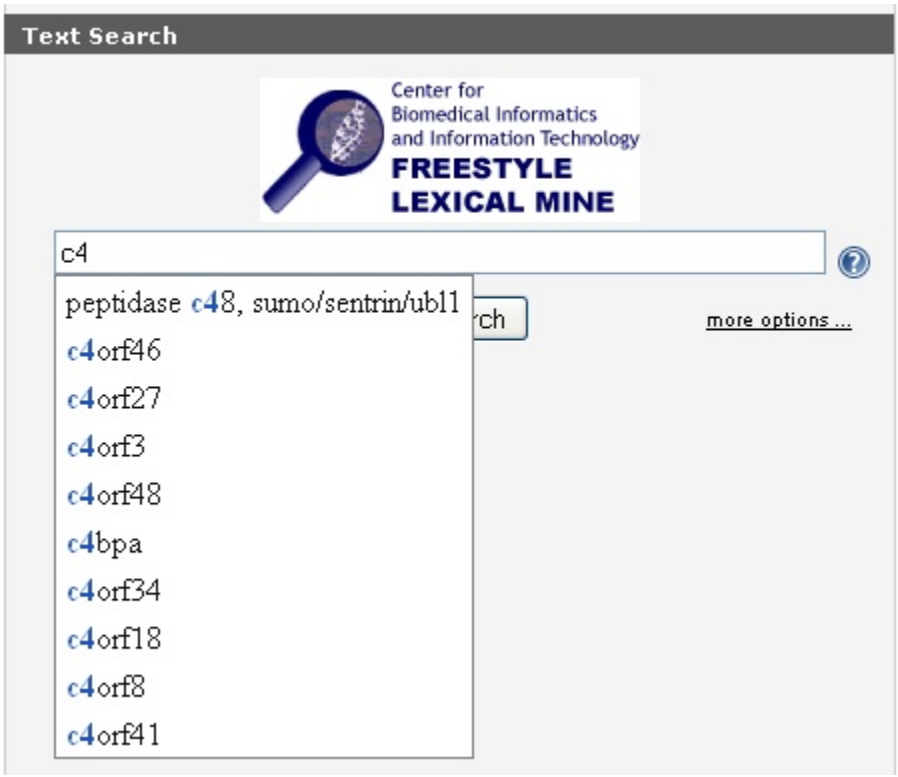
**Having Trouble Reading the Text?**

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 .

## Searching for Diseases and Compounds Associated with a Gene

To use the caBIO Home Page Freestyle Lexical Mine tool to find diseases and pharmacological substances that are associated with a gene, begin typing the HUGO gene name

into the search field. Because the Freestyle Lexical Mine suggests caBIO terms that match the characters you have entered, it is relatively easy to find a gene term that matches your desired gene concept.




If you would like to search for any gene that contains a string use the special character "*." For example, "C4BPA" would only return objects with attributes that match this exact gene, but "C4BP*" will retrieve objects with attributes containing "C4BPA" and "C4BPB."

After entering a search term (1), click the Submit button (2) to retrieve results. Although you may limit your search by clicking on the `more options ...` link, this is not required (3).

> **Tip**
>
> If you have cannot find an appropriate search term, click the `Contact Us` link for help.

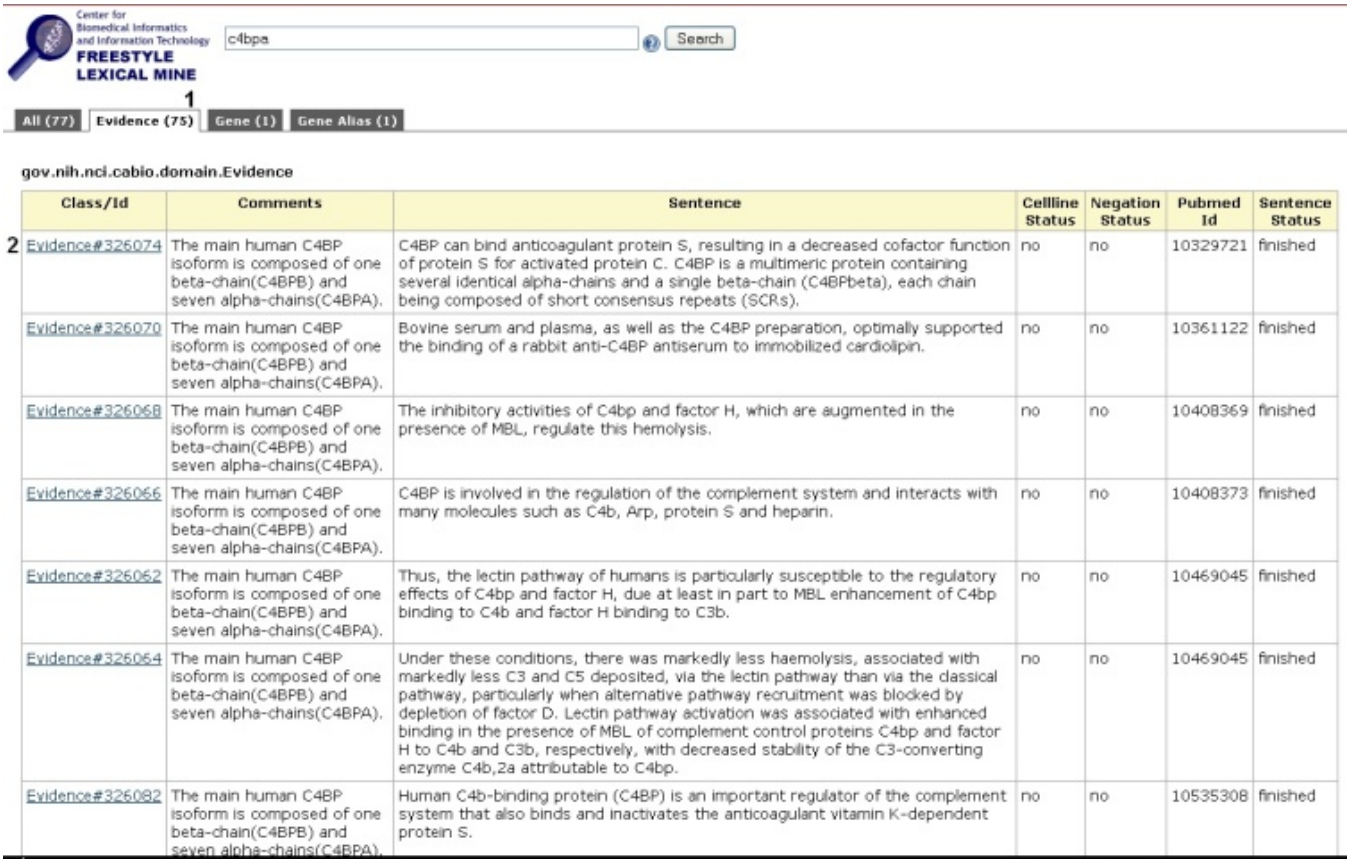

# Search Results

The caBIO Home Page Freestyle Lexical Mine will retrieve objects that match your gene search term. These objects are grouped by type, which are shown as tabs at the top of the results page. To view diseases and compounds that are associated with your gene search term, click the Evidence tab at the top of the page (1).

Each row in the Evidence results table is a truncated view of an `Evidence` object (that is, not all attributes and methods are shown on this page), where the columns include:

- the class and identifier (`Class/Id`),
- evidence of the gene-disease or gene-compound association (`Sentence`),
- whether the evidence was collected from experiments involving cell lines ( `Cellline Status` ),
- whether the evidence is negative (that is, gene X is not associated with disease or compound Y; `Negation Status` ),
- the PubMed identifier for the abstract from which the evidence was extracted (`Pubmed Id`), and
- whether the status of the sentence ( `Sentence Status` ).

For additional information on these attributes, refer to the section Data, Metadata, and Annotations.




| Class/Id | Comments | Sentence | Cellline Status | Negation Status | Pubmed Id | Sentence Status |
|---|---|---|---|---|---|---|
| Evidence#326074 | The main human C4BP isoform is composed of one beta-chain(C4BPB) and seven alpha-chains(C4BPA). | C4BP can bind anticoagulant protein S, resulting in a decreased cofactor function of protein S for activated protein C. C4BP is a multimeric protein containing several identical alpha-chains and a single beta-chain (C4BPbeta), each chain being composed of short consensus repeats (SCRs). | no | no | 10329721 | finished |
| Evidence#326070 | The main human C4BP isoform is composed of one beta-chain(C4BPB) and seven alpha-chains(C4BPA). | Bovine serum and plasma, as well as the C4BP preparation, optimally supported the binding of a rabbit anti-C4BP antiserum to immobilized cardiolipin. | no | no | 10361122 | finished |
| Evidence#326068 | The main human C4BP isoform is composed of one beta-chain(C4BPB) and seven alpha-chains(C4BPA). | The inhibitory activities of C4bp and factor H, which are augmented in the presence of MBL, regulate this hemolysis. | no | no | 10408369 | finished |
| Evidence#326066 | The main human C4BP isoform is composed of one beta-chain(C4BPB) and seven alpha-chains(C4BPA). | C4BP is involved in the regulation of the complement system and interacts with many molecules such as C4b, Arp, protein S and heparin. | no | no | 10408373 | finished |
| Evidence#326062 | The main human C4BP isoform is composed of one beta-chain(C4BPB) and seven alpha-chains(C4BPA). | Thus, the lectin pathway of humans is particularly susceptible to the regulatory effects of C4bp and factor H, due at least in part to MBL enhancement of C4bp binding to C4b and factor H binding to C3b. | no | no | 10469045 | finished |
| Evidence#326064 | The main human C4BP isoform is composed of one beta-chain(C4BPB) and seven alpha-chains(C4BPA). | Under these conditions, there was markedly less haemolysis, associated with markedly less C3 and C5 deposited, via the lectin pathway than via the classical pathway, particularly when alternative pathway recruitment was blocked by depletion of factor D. Lectin pathway activation was associated with enhanced binding in the presence of MBL of complement control proteins C4bp and factor H to C4b and C3b, respectively, with decreased stability of the C3-converting enzyme C4b,2a attributable to C4bp. | no | no | 10469045 | finished |
| Evidence#326082 | The main human C4BP isoform is composed of one beta-chain(C4BPB) and seven alpha-chains(C4BPA). | Human C4b-binding protein (C4BP) is an important regulator of the complement system that also binds and inactivates the anticoagulant vitamin K-dependent protein S. | no | no | 10535308 | finished |

# Finding Diseases or Compounds Associated with the Evidence

To discover which disease and/or compound associated with each piece of evidence, click on the `Class/Id` link for the desired object. This will open the full `Evidence` type object. Scroll over to the right, and click on `getGeneFunctionAssociationCollection` method link (1) to view the `Gene Disease Association` and/or `Gene Agent Association` type objects. The `GeneFunctionAssocation` type object has a role attribute that contains Role Codes or Role Details that describe the nature of the gene-disease and gene-compound relationship, as well as a notation that the Cancer Gene Index is the source of these data.

> **Tip**
>
> Although the Cancer Gene Index refers to pharmacological substances as "compounds" or even "drugs," caBIO and the NCI Thesaurus use "agents" to refer to this concept.

The following subsections provide step-by-step guidance on how to find #disease terms or #compound terms.

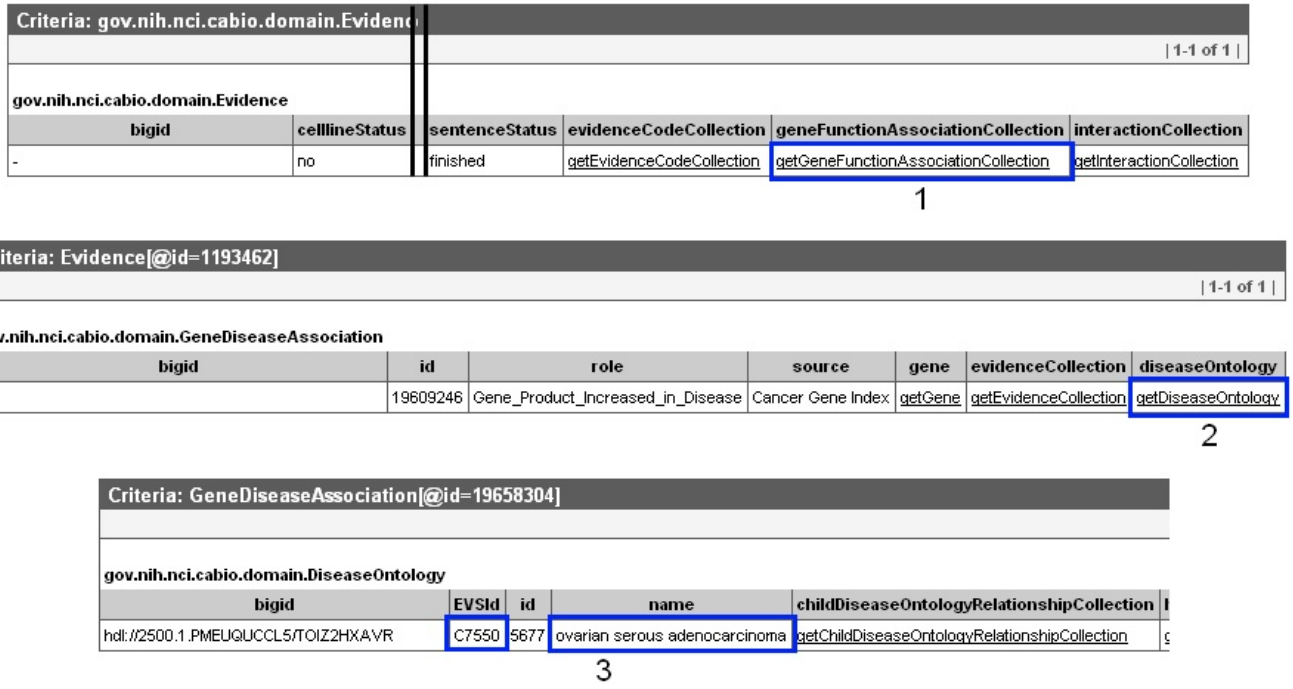
## Finding Disease Terms

To view associated disease terms that are linked to the `Gene Disease Association` type object, click on the `getDiseaseOntology` link (2) to access the related `DiseaseOntology` object (bottom panel). This `DiseaseOntology` object contains the disease name and EVS Identifier in the `name` and `EVSid` columns (3), for example, for the disease associated with the gene of interest and a specific piece of evidence.

> **Warning**
>
> If you do not want to spend time navigating through the caBIO object model for candidate gene-disease associations that were found to be false positives, select only `Evidence` objects where the `Sentence Status` is `finished` and the `Negation Status` is `no`.

> **Note**
>
> A single piece of evidence may have multiple Role Codes and Role Details describing the gene-disease association.

To explore additional diseases associated with the gene term of interest, navigate back to the evidence page and repeat this process.



Criteria: gov.nih.nci.cabio.domain.Evidenc

| 1-1 of 1 |

gov.nih.nci.cabio.domain.Evidence

| bigid | celllineStatus | sentenceStatus | evidenceCodeCollection | geneFunctionAssociationCollection | interactionCollection |
|---|---|---|---|---|---|
| - | no | finished | getEvidenceCodeCollection | getGeneFunctionAssociationCollection | getInteractionCollection |

1

Criteria: Evidence[@id=1193462]

| 1-1 of 1 |

gov.nih.nci.cabio.domain.GeneDiseaseAssociation

| bigid | id | role | source | gene | evidenceCollection | diseaseOntology |
|---|---|---|---|---|---|---|
| - | 19609246 | Gene_Product_Increased_in_Disease | Cancer Gene Index | getGene | getEvidenceCollection | getDiseaseOntology |

2

Criteria: GeneDiseaseAssociation[@id=19658304]

gov.nih.nci.cabio.domain.DiseaseOntology

| bigid | EVSId | id | name | childDiseaseOntologyRelationshipCollection |
|---|---|---|---|---|
| hdl://2500.1.PMEUQUCCL5/TOIZ2HXAVR | C7550 | 5677 | ovarian serous adenocarcinoma | getChildDiseaseOntologyRelationshipCollection |

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> **Be Careful**
>
> If you find yourself in a part of the object model that you do not understand or if you get confused, stop and navigate your web browser back to the search results page with the Evidence tab.

For your reference, the subset of caBIO classes that are related to the Cancer Gene Index are shown here.The full model is available on the caBIO gForge page, but you must have the Enterprise Architect

modeling tool to view this file.

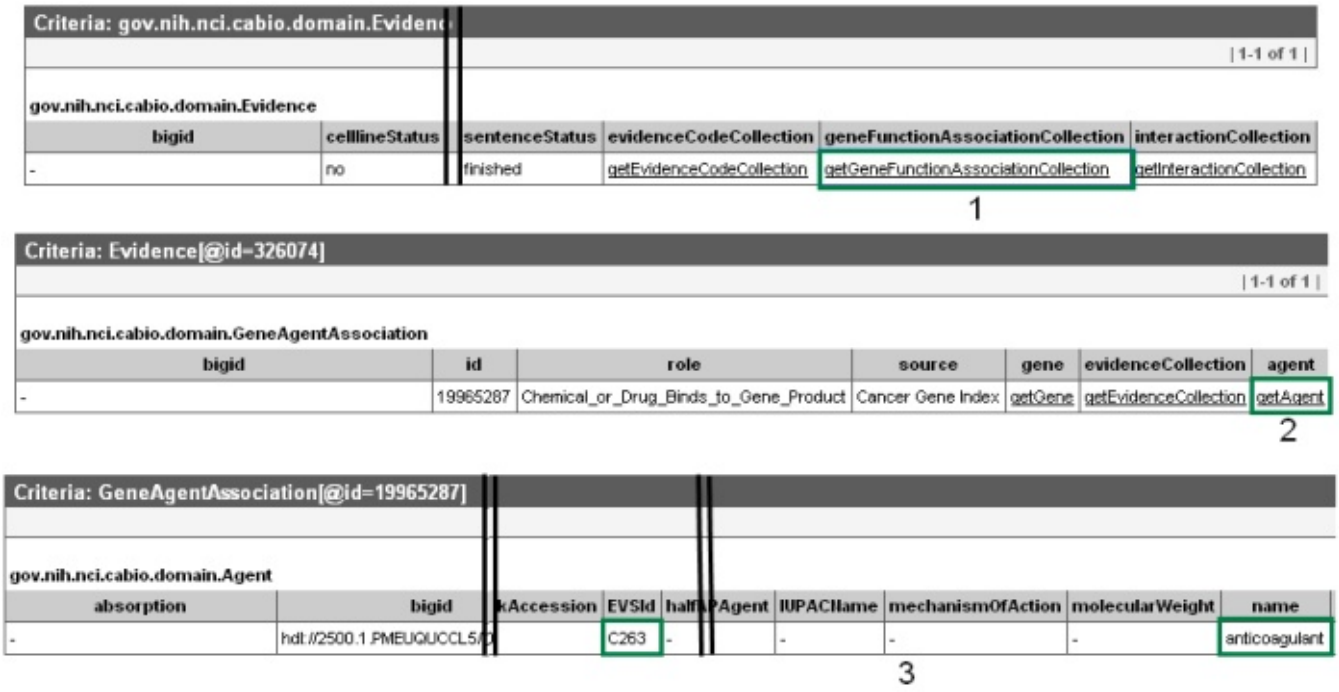
## Finding Compound Terms

Evidence may also be associated with compounds. To view associated compound terms that are linked to any `Gene Agent Association` type object, click on the `getAgent` link (2) to access the related `Agent` object (bottom panel). This object contains the compound name and EVS Identifier in the `name` and `EVSid` columns (3), for example, for the compound associated with the gene of interest and a specific piece of evidence.

> **Warning**
>
> If you do not want to spend time navigating through the caBIO object model for candidate gene-compound associations that were found to be false positives, select only `Evidence` objects where the `Sentence Status` is `finished` and the `Negation Status` is no.

> **Note**
>
> A single piece of evidence may have multiple Role Codes and Role Details describing the gene-compound association.

To explore additional compounds associated with the gene term of interest, navigate back to the evidence page and repeat this process.




**Be Careful**

If you find yourself in a part of the object model that you do not understand or if you get confused, stop and navigate your web browser back to the search results page with the Evidence tab.

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