



Searching NCBI Databases with Entrez

The Entrez system allows searchers to use words and phrases to construct powerful, precise searches of NCBI databases, either individually or searching across multiple databases. Many features of Entrez can be used in many or all databases, while others are specialized for specific databases.

Global Query

Search across all Entrez databases by following the “All Databases” link from the NCBI homepage. This is a quick way to search NCBI content, but the search interface lacks many of the features listed below.

Limits

The Limits tab is different for each database and provides an easy way to focus your search. Click the tab to see the options for the database you are using.

- e.g. limit to a particular species or clade in Gene, limit to mRNA in Nucleotide, or limit to a particular chromosome in OMIM.

Boolean Operators

Use the upper case Boolean operators AND, OR and NOT in conjunction with parentheses to narrow or expand your search.

- e.g. **breast cancer AND (brca1 OR brca2)**

Search Fields

Databases consist of “records” and “fields.” Records represent genes, proteins, journal articles or other objects depending on the database. Each record is composed of fields that describe the object. Fields can include Title, Accession Number, Organism, Author and more, depending on the record. Using search “tags” to specify fields allows you to increase search precision, for example **mouse[ORGN] AND cancer[DIS]**

Some Common Search Fields

Field Name	Field Tag	Database Examples	Features and Examples
Accession number	[ACCN]	Gene, Nucleotide, Protein, Structure, SNP, Probe	Searches sequence accession numbers for nucleic acids and proteins. Use a colon to search a range of accession numbers.
Organism	[ORGN]	Gene, Nucleotide, Protein, Structure, EST, GSS, Probe	Use either common names or scientific names.
Creation Date	[CDAT]	All	Date the record was created. Use a colon to search for a range of dates, e.g. 2003/15/01:2004/15/01[CDAT] . Month and day are optional.
Gene Name	[GENE NAME]	Gene, Nucleotide, Protein, OMIM, Probe, UniGene	Retrieves your search term as the exact gene name. Use a * to truncate your search; e.g. lrh*[GENE NAME] retrieves LRH1, LRHA, LRHR, etc.
Disease Name	[DIS]	Gene, OMIM, Probe, UniGene	Searches for the name of a disease or phenotype associated with genetic mutations.
Gene Ontology	[GO]	Gene, SNP, UniGene, Probe	Searches for the term in Gene Ontology annotations.
Molecular Weight	[MOLWT]	Protein	Use a colon to indicate a range of molecular weights; e.g. 1500:1550[MOLWT] .
Sequence Length	[SLEN]	Gene, Nucleotide, Protein	Use a colon to indicate a range of sequence lengths; e.g. 900:1000[SLEN] .

Indexes

Many databases use indexes to control for synonyms (e.g. common and scientific names of organisms). To see if there is a term for your search in an index, use the Preview/Index tab. Select a search field from the pull-down menu and type your term in the box, then click “Index”. You’ll see an alphabetical list of terms in the index, with a number in parentheses that indicates the number of records in the database with that index term assigned. You can add an index term to your search by highlighting it and clicking AND, OR or NOT, then clicking Go. Some fields that have indexes are Gene Name, Disease/Phenotype, and Organism.

Using Truncation and Synonyms to Expand Field Searches

Search for variants of a word or phrase by incorporating synonyms or related terms with OR and by using Entrez's truncation symbol * (an asterisk).

- e.g. **pseudopod* OR filopod*** will retrieve records with any of the following:
pseudopod, pseudopodia, pseudopodium, filopod, filopodia, filopodium, etc.

Properties and Filters

In addition to search fields like [ACCN] and [ORGN], Entrez databases use properties and filters. These search features limit searches in many different ways depending on the database. Some examples are searching in Gene to retrieve only records that have a link to Protein, or a searching in Nucleotide to retrieve only tRNA molecule records. Use the Preview/Index tab to view the index for the search field [FILTER] or [PROPERTIES] to see what is available.

Some Examples of Properties and Filters

Search	Databases	Features and Examples
gene nucleotide[FILTER]	Gene	Gene records with links to Nucleotide records
genotype protein coding[PROPERTIES]	Gene	Gene records for protein coding genes
biomol trna[PROPERTIES]	Nucleotide	Nucleotide records for tRNA molecules
uncultured[FILTER]	Nucleotide	Nucleotide records for sequences from uncultured microorganisms
gene in plasmid[PROPERTIES]	Protein	Protein records in which the coding gene is on a plasmid
protein homologene[FILTER]	Protein	Protein records with links to the Homologene database

Details

Some databases use "Automatic Term Mapping" for your searches. The Details tab allows you to see how your term has been mapped and make any adjustments necessary

- e.g. the Details tab reveals that a search for "human" in the Gene database automatically searches the Organism field for *Homo sapiens*

History

The History tab displays all of your recent searches in chronological order. Use the History tab to rerun, combine or modify previous searches. Searches are lost after 8 hours of inactivity on NCBI unless they are saved to a myNCBI account.

Display and Send to

The Display drop-down menu allows you to view your search results in different formats depending on the database. Typically, displays are available that show record summaries, links to other databases, and sequence data. Some databases have specialized displays; such as the Gene Table display in Entrez Gene, which provides a graphical overview of the gene and includes intron and exon information.

The Send to drop-down menu allows you to send your results (in your chosen Display format) to a printer, an email address, a text file

The Clipboard

The Clipboard temporarily saves citations from one search or several searches in one place. To send search results to the Clipboard, click on the check boxes to the left of the citations and then select Clipboard from the Send to pull-down menu.

- If you do not check off citations, Entrez will place your entire search (up to 500 items) on the Clipboard.
- Citations saved on the Clipboard are lost after eight hours of inactivity in NCBI.
- To open the Clipboard, click on the Clipboard Tab (found below the Query Box). You can reformat citations (and LinkOut), and also print, save, or email search results from the Clipboard.

MyNCBI

MyNCBI allows you to save results and search strategies indefinitely, as well as set up email alerts and change displays to your preferences. After registering, you can access your results and preferences at any computer you use to access NCBI databases.