Module 3: Genes and Sequences (NCBI)

i - How Do I Find Information About a Gene?

<u>Aims</u>

- Introduce Entrez Gene and other gene-related resources
- Suggest alternative query options
- Provide example searches by text and position
- Show additional sources of functional information in Gene records

Introduction

Information related to a gene of interest can be retrieved from NCBI databases by text, map (position) or sequence queries. Module 2_iii and Module 2_iv contain information on sequenced based searches using BLAST or position searches using Map Viewer.

Entrez Gene can be queried for genes defined by sequence or map data. Queries can be based on gene attributes such as symbols, names, accessions, publications, chromosome, model organism database identifiers (e.g. ZFINid: ZDB-GENE-040421-2), GO terms, conserved domains or E.C. numbers.

From the Entrez Gene record you can follow provided Links to other related records. You can view highly related ESTs and their expression profiles in UniGene or follow the link to Homologene to view pre-computed homology data.

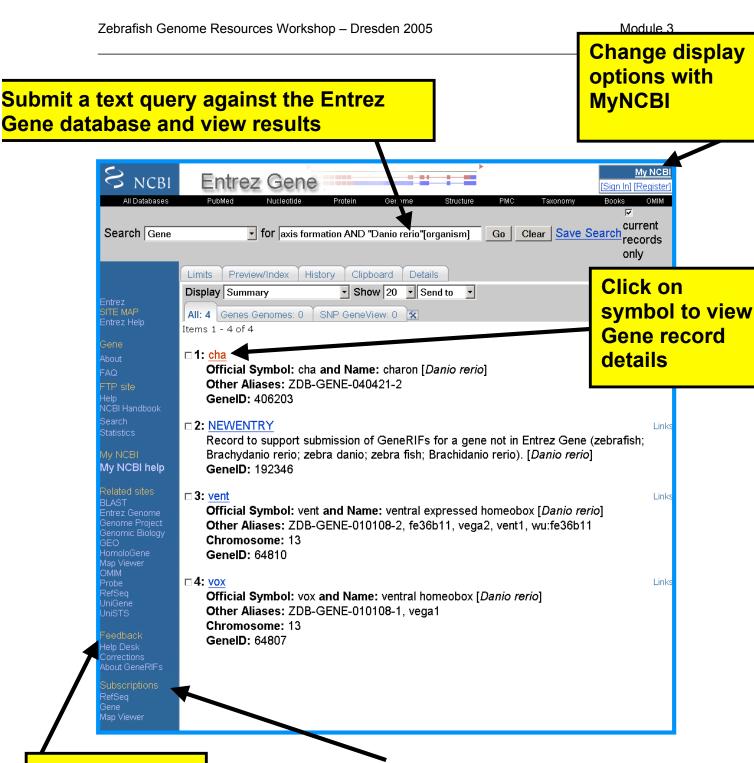
Examples:

- 1. How do I find zebrafish genes involved in axis formation?
- 2. How many vitellogenin genes are known in Gene?
- 3. How many of the zebrafish vitellogenin genes are mapped to chromosome 22 ?

To begin: navigate to the Entrez Gene home page: http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?CMD=search&DB=gene.

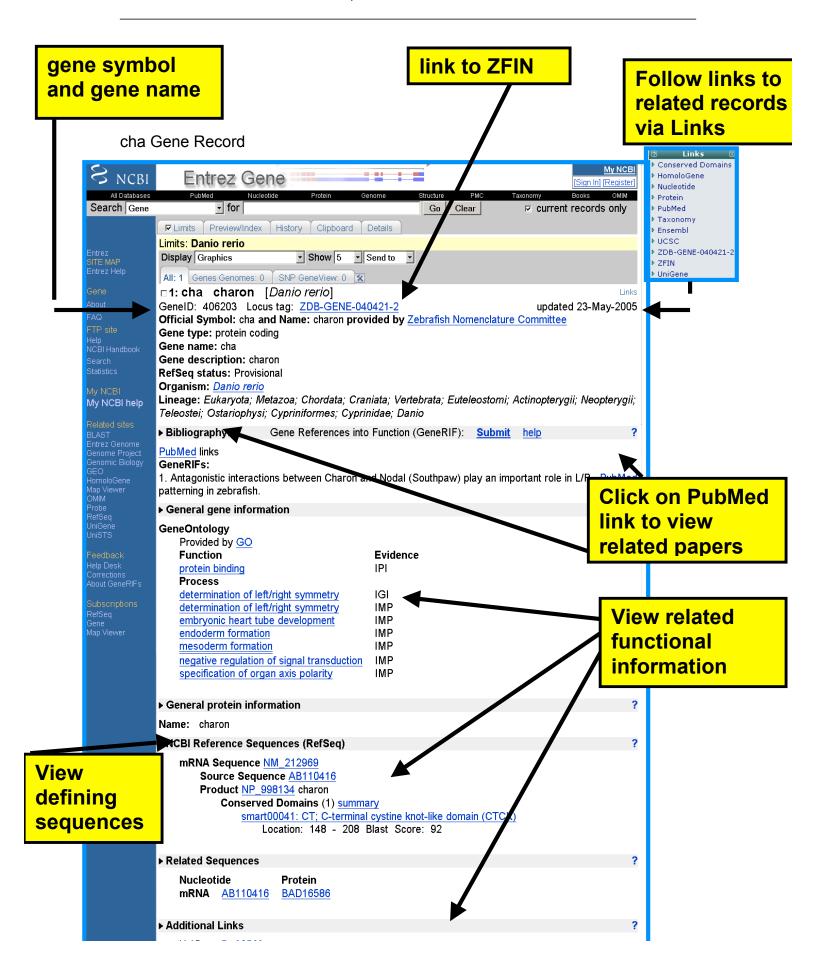
Alternatively, this query could be submitted from the Entrez home page (http://www.ncbi.nlm.nih.gov/gquery/gquery.fcgi), as demonstrated in Module1_iii, or any other Entrez page by selecting 'Gene' in the database pull-down menu from the search bar at the top of the page.

1. How do I find zebrafish genes involved in axis formation?

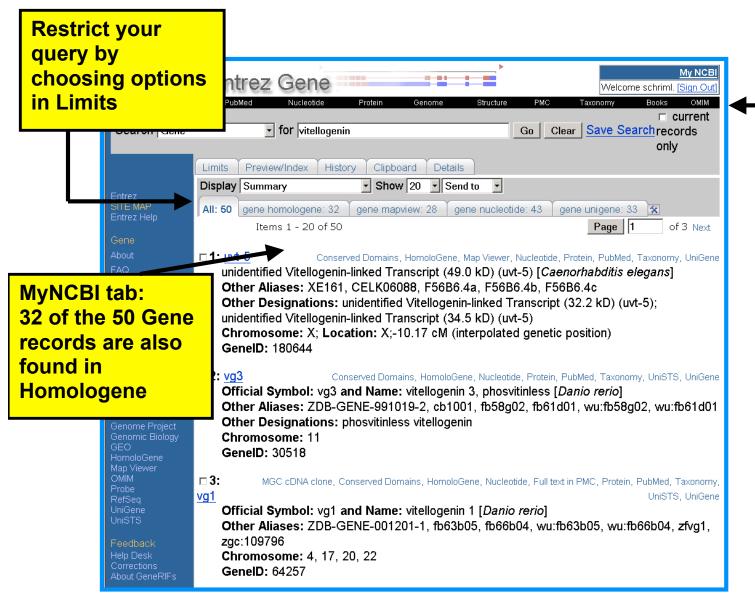


Provide feedback by following these links

Sign up for a subscription to receive updates for RefSeq, Gene or Map Viewer



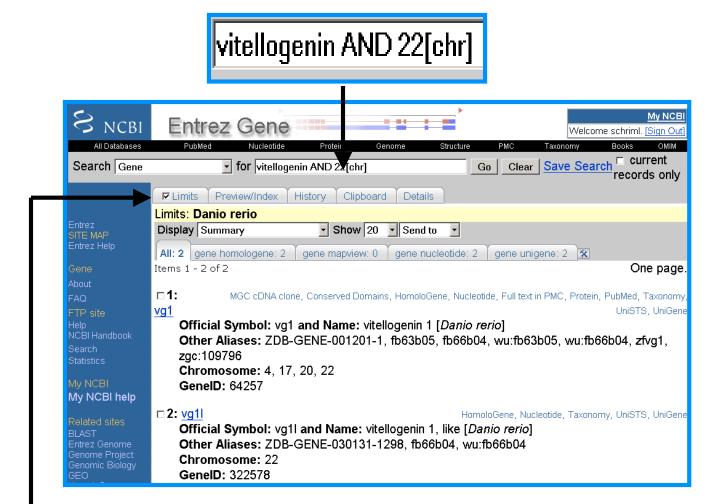
Restrict the results by adding 'AND "Danio rerio" [organism] to the search bar or click on the Entrez Limit Tab to restrict your Query by the type of Gene record, sequence, RefSeq status or organism.



Customize the output display by specifying subsets of data you want to have displayed with MyNCBI.

My NCBI is an Entrez display tool that allows you to customize the output of your queries or have your Entrez queries archived, and will send you email alerts when new results for your stored query are available.

3. How many of the zebrafish vitellogenin genes are mapped to chromosome 22 ?



Limits: restrict query by organism to retrieve Danio rerio only records