Module 3: Genes and Sequences (NCBI)

ii - Does My Gene Have Known Homologs/Orthologs?

Aims

- Introduce tools to mine homology data
- Suggest ways to identify homologs
- Provide alternative ways to navigate
- Show examples of pre-computed homology comparisons

Introduction

You can mine the pre-computed sequence comparisons identifying putative orthologs (highly similar sequences across genomes) in Homologene. Begin your search for homologs by submitting a search on the Entrez home page (http://www.ncbi.nlm.nih.gov/gquery/gquery.fcgi) or by navigating to Homologene (http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=homologene) to view results or submit a text query against the Homologene database. You can also following Links to Homologene from related records in other Entrez databases, such as Entrez Gene or UniGene.

Pre-computed protein comparisons are also available for each protein in Entrez Protein in the BLink (BLAST Link) database. You can view a graphical display of similar proteins by following the BLink link from any Entrez protein record. On the BLink page you can view a blast2 alignment between your protein and each protein identified by BLink as highly similar. Scroll down the list of Protein Descriptions to view the protein names for these proteins.

Homologs can also be identified through cross-species BLAST searches, as described in Module 2_iv.

Since homologs often share similar naming conventions, querying Entrez Gene with a gene name or gene symbol may yield homologous gene records, as seen in the exercise in Module3 i.

Additionally, you can determine if a curated homolog has been identified for a zebrafish gene by following the link to ZFIN found on Entrez Gene and UniGene pages.

Cross-species genome comparisons may also be used to identify homologs. For example, mouse homlogs for human genes can be putatively identified based on the placement of mouse genes on the human genome. To see these comparative maps for human, mouse and rat, navigate to the Map Viewer home page (http://www.ncbi.nlm.nih.gov/mapview/), choose one of these organisms and select a chromosome to view. The "Maps & Options" button will provide a pop-up window where you can then add maps from human or rat to the mouse Map Viewer page. See Module2_iii to view the zebrafish Map Viewer page. Zebrafish Map Viewer does not currently include comparative maps.

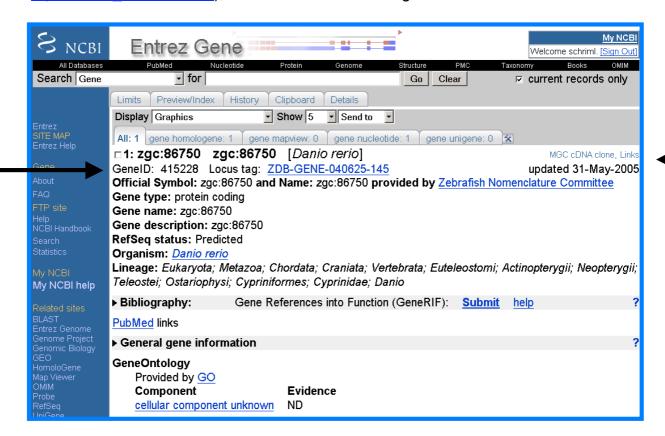
Exercises

1. Homologene: Identify putative homologs based on sequence similarity using pre-computed comparisons in Homologene.

- 2. BLink: Identify putative homologs in other fish species.
- **1. Homologene:** Identify putative homologs based on sequence similarity using pre-computed comparisons in Homologene.

Starting with an anonymous Entrez Gene record, zgc:86750 (GeneID:415228,

http://ww.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene&cmd=Retrieve&dopt=Graphics&list_uids=415228), follow the link to Homologene.

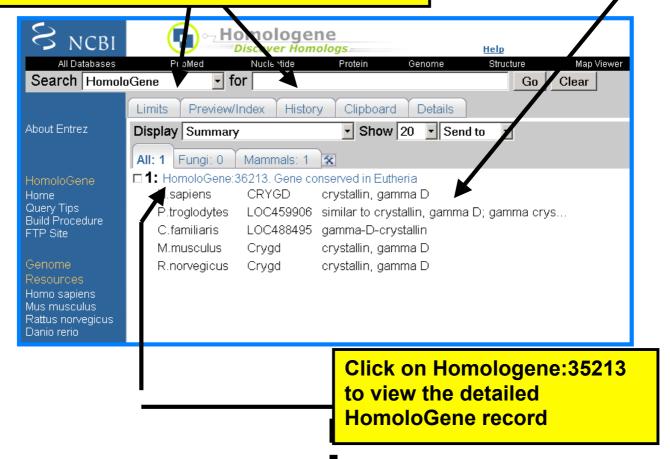




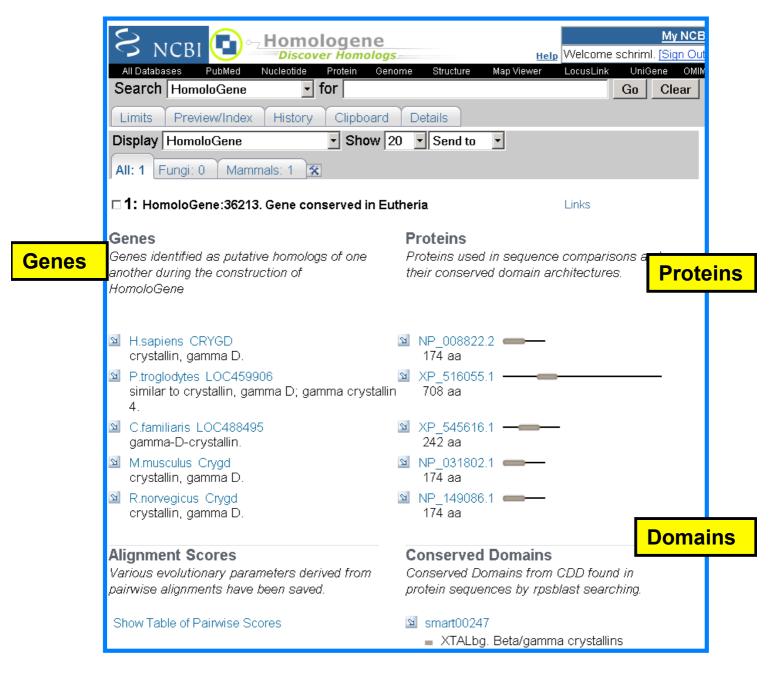
Click on Homologene link to view results of pre-computed sequence comparisons

You can also submit a text search against the Homologene database from any Entrez page

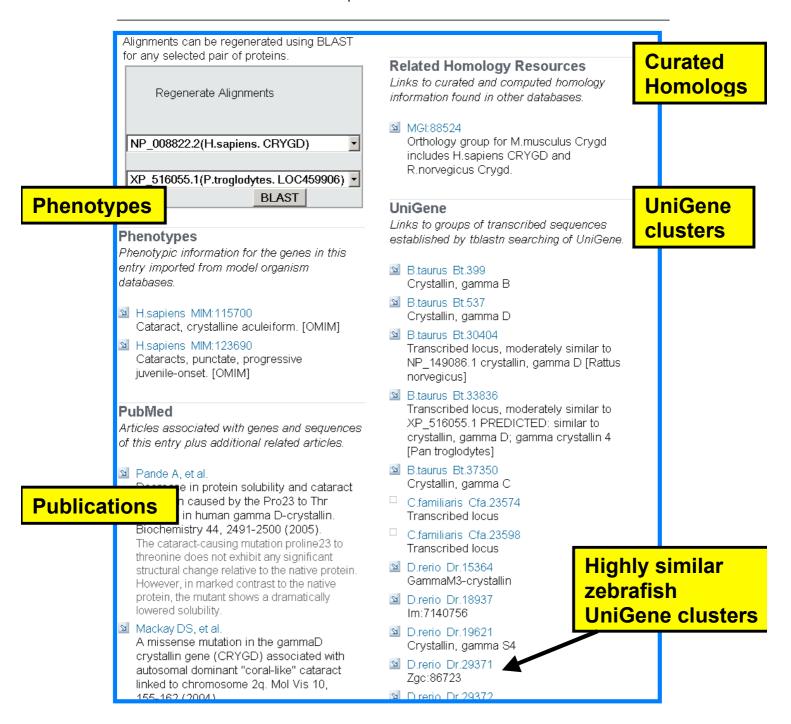
View Homologene record links to zgc:86750



- View related Genes, their Proteins, related Phenotypes and PubMed entries
- View conserved domains identified in these proteins
- View curated homology data
- View related UniGene clusters







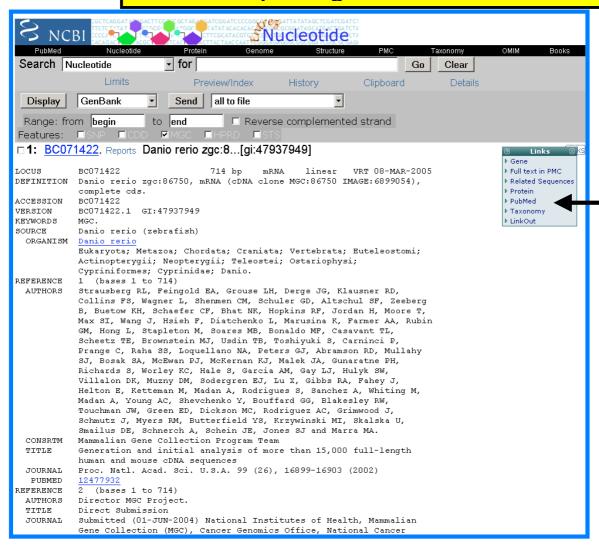
Homologene comparisons have shown that the Entrez Gene zgc:86723 record is highly similar to members of the gamma crystallin gene family.

2. BLink: Identify putative homologs in other fish species. Begin your search from mRNA accession.

For example: BC071422

(http://www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?val=BC071422.1

Click on the Links menu and select 'Protein' to go to the corresponding Entrez Protein record



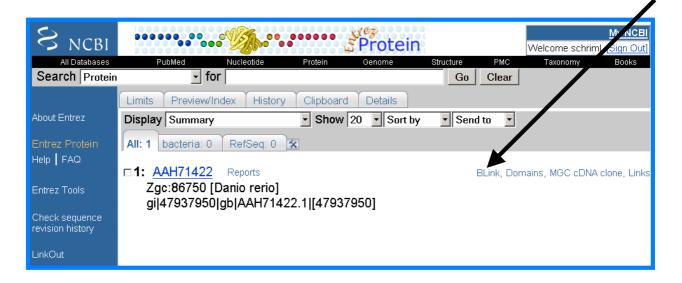
To navigate to the corresponding Entrez
Protein record: first scroll down the page to
the Protein Link



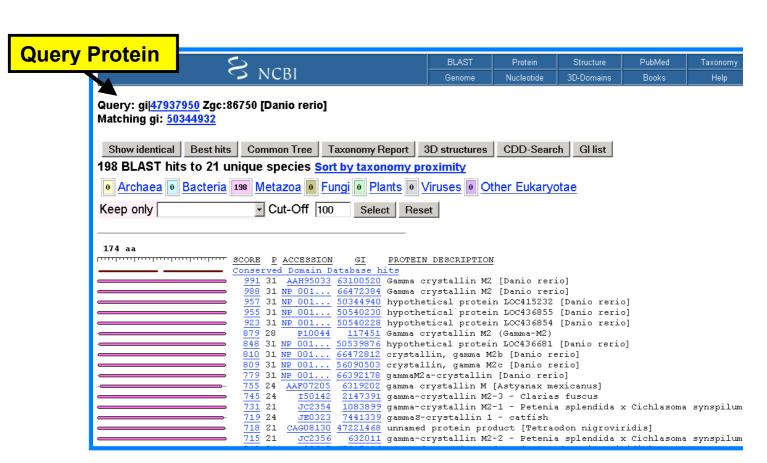
Now click on the Protein Link

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Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 56 Row: g Column: 20
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 47937949.
FEATURES
                     Location/Qualifiers
                     1..714
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                     /mol_type="mRNA"
                     /db_xref="taxon: 7955"
                     /clone="MGC:86750 IMAGE:6899054"
                     /tissue_type="Embryo, 7 different stages (from just
                     fertilized embryos to 72 hours just hatched baby fish)"
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                     /lab host="DH10B"
                     /note="Vector: pDNR-LIB"
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                     /db xref="GeneID:415228"
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                     67..591
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                     MYEMMDDCDNIMNRYRMSHCQSCHVMDGHWLFYDQPNYRGRMWHFGPGQYRNFSNYGG
                     MRFMSMRRIMDSWY"
ORIGIN
        1 caacacagaa aatcagtttc agcttctcct ttgtgcaatc accaagggtc agctaaagta
       61 accatgatgg gcaaggtcat cttctacgag gacagaaact tccagggtcg ctcttatgag
      121 tgtatgggag actgtggtga cttctcctcc tacatgaatc gctgtcactc ttgcagagtg
      181 gagagoggot gotggatgat gtacgaccaa accaactaca tgggaagtgg atatttotto
      241 aggaggggag agtatgctga ttacatgtct atgtttggaa tgaacaactg catcaggtcc
      301 tgccgtatga tccccatgta caggggatcc tacagaatga ggatctacga gagggacaac
      361 ttcatgggtc agatgtacga gatgatggat gactgtgaca acatcatgaa ccgttaccgc
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Navigate to BLink by the provided link



- View the graphical display of protein hits
- Click on the BLAST score to see the alignment
- Click on the Accession to go to the Entrez Protein record
- Scroll down the Protein Descriptions to protein names
- Click on "Show identical" to include all identical hits in the display
- Click on "Best hits" to view the hits grouped by organism
- Click on "Conserved Domain Database hits" to view domain details



BLink has identified highly similar proteins in several fish including: zebrafish, Mexican tetra, whitespotted clarias, catfish and freshwater pufferfish