ZFIN NEWS

The Zebrafish Information Network

http://zfin.org

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Community Wiki

We are very pleased to introduce the new ZFIN Community Wiki (http://wiki.zfin.org). Wikis allow easy creation, editing, commenting, and searching of interlinked web pages. The Community Wiki will begin with two sections – Experimental Protocols and Antibodies – more sections may be added in the future.

I. Experimental Protocols
The Protocols Wiki is divided into sections that mirror chapters of The Zebrafish Book e.g. Cellular Methods, Genetic Methods, etc. The full contents of The Zebrafish Book 5th edition have been copied to the wiki. Researchers can submit new protocols to an appropriate chapter or add comments to existing protocols.

II. Antibodies
Each antibody page in the Antibody Wiki provides a concise summary of antibody properties including host organism, recognized gene products, labeled anatomy and suppliers. You can add comments with technical tips to antibody pages or link to full protocols in the Protocols Wiki. The Antibody Wiki has been pre-populated with all the antibodies in the ZFIN antibody database. New antibodies can be added by researchers as needed.

Working in collaboration with a test group of researchers, we have customized the ZFIN Community Wiki to make it easy to use. We have chosen Confluence (http://www.atlassian.com/software/confluence/) for our wiki software, which has many attractive features including advanced search, RSS feeds, HTML/PDF/Word-format page export, and a fairly gentle learning curve for beginners.

Like any wiki, the strength of the ZFIN Community Wiki is in the people who support it - so please try it out and start contributing at http://wiki.zfin.org.   As with all ZFIN resources, we are eager to receive feedback.

ZFIN User Survey

ZFIN's competitive renewal grant will be submitted in January, 2010. Please take a moment to help us better understand your needs and plan for the future. Take the survey here.

Expand your View of Gene Function:
The Reference Genomes Project

The genomes of an increasing number of organisms from a wide range of taxa are becoming annotated with experimentally supported functional data from the Gene Ontology. As this manual annotation process progresses the potential power of comparative genomics approaches increases. There are also an increasing number of genomes from emerging model organisms that are unlikely to have expert manual curation. For these genomes, comparative genomics is an essential tool in formulating hypotheses regarding gene function. The Gene Ontology Consortium recognizes the need for comparative analysis of gene function across both expertly curated and uncurated genomes, and provides the Reference Genomes Project (RGP) to facilitate these efforts (Reference Genome Group of the Gene Ontology Consortium, 2009; http://www.geneontology.org/GO.refgenome.shtml). The RGP seeks to maximize and optimize the GO annotation of 12 key genomes from a broad taxonomic range so that those annotations may be used to effectively seed the automatic annotation efforts of other genomes. Zebrafish are included as one of the twelve Reference Genomes (Table 1, below).

Table 1
- Danio rerio (zebrafish; Zebrafish Information Network (ZFIN))
- Dictyostelium discoideum (dictyBase)
- Drosophila melanogaster (FlyBase)
- Escherichia coli (EcoliHub)
- Gallus gallus (AgBase)
- Homo sapiens (human Gene Ontology Annotation [GOA] @ EBI)
- Mus musculus (Mouse Genome Informatics)
- Rattus norvegicus (Rat Genome Database (RGD))
- Saccharomyces cerevisiae (Saccharomyces Genome Database (SGD))
- Schizosaccharomyces pombe (GeneDB S. pombe)

How Does Participation in the Reference Genomes Project Affect GO Annotation at ZFIN?

Participation in the RGP means ZFIN follows more stringent GO annotation guidelines than generally required by the Gene Ontology Consortium. For example, we make experimentally supported annotations whenever possible. These experimentally supported annotations are then available for potential propagation to related genes in other species. Also, ZFIN generally curates paper by paper whatever data those papers contain. In contrast, the Reference Genomes Project prioritizes about 20-30 gene clusters for focused GO curation each month by all members of the RGP. The clusters are selected to prioritize genes of current biological interest. The RG group has developed software to cluster genes from many organisms including the 12 reference genomes in order to determine which genes the group should curate, and also as a platform from which the transfer of annotations among the 12 reference genomes can be evaluated and executed in a phylogenetic context. For each zebrafish gene selected for curation as part of the RGP, ZFIN curators attempt to curate the GO from 100% of the papers associated with that gene. That means RGP target genes receive more comprehensive GO curation than other genes may have, both in zebrafish and any of the other Reference Genomes. To date, more than 550 zebrafish genes have been curated with more than 5350 experimentally supported GO annotations. These genes and their homologs from other species can be a rich source of cross-species functional data when the annotations are examined across the full set of Reference Genomes.

Expand your View of Gene Function:
The Reference Genomes Project *(continued from pg. 2)*

How Do I Know if a Zebrafish Gene Has Been Curated as Part of the Reference Genomes Project?

Currently, the best way to determine if a zebrafish gene has been included as part of the RGP is to search for the gene using the gene symbol from ZFIN in the gene search of AmiGO, the Gene Ontology search interface produced by the Gene Ontology Consortium (Carbon et al., 2009; http://amigo.geneontology.org/cgi-bin/amigo/go.cgi). If a gene is part of the RGP, you will see a "Ref Genome" line at the bottom of the Information block on the gene page in AmiGO (Fig. 1).

Fig. 1. The Information block from the zebrafish p2rx1 gene page in AmiGO indicates that the p2rx1 gene has been included as part of the Reference Genomes Project and that homologous genes from rat, mouse, dictyostelium, and Human have also been identified and annotated as part of this gene cluster for the Reference Genomes Project.

Alternatively you can browse the full set of annotated genes in the RGP on Amigo's All Reference Genome Homolog Sets page (Fig 2.; http://amigo.geneontology.org/cgi-bin/amigo/amigo?mode=homolset_summary). This page along with other GO tools can be found under the More Tools link at the top of AmiGO pages.

Fig. 2. A partial row from the AmiGO All Reference Genome Homolog Sets page shows the P2RX1 homolog set and the corresponding genes in Human, mouse, rat and zebrafish that have been curated with experimentally supported GO annotations from the literature. As can be observed in Figure 1, annotations also exist for Dictyostelium discoidium genes. These were left off the figure to save space.

Expand your View of Gene Function: The Reference Genomes Project (continued from pg. 3)

How Can I View the Annotations Generated by The Reference Genomes Project?

All GO annotations for zebrafish genes are found in both ZFIN (by going to the GO details that are linked from gene pages) and in AmiGO. To perform cross-species analysis of any gene, including genes selected as part of the RGP, use AmiGO. You may search by GO term or gene, and navigate the annotations and genes that have been annotated in many organisms, including the twelve reference genomes. On the All Reference Genome Homolog Sets page, clicking on the "interactive" link in the leftmost column (Fig. 2) allows you to dynamically view the annotations for the genes in that cluster from all annotated species overlaid on a graphical view of the GO ontology.

Citations:
1.   Reference Genome Group of the Gene Ontology Consortium. The Gene Ontology's Reference Genome Project: a unified framework for functional annotation across species. PLoS Comput. Biol. Jul 2009;5(7): e1000431.
2.   Carbon S, Ireland A, Mungall CJ, Shu S, Marshall B, Lewis S, AmiGO Hub, Web Presence Working Group. AmiGO: online access to ontology and annotation data. Bioinformatics. Jan 2009;25(2):288-9.

Submitting Your Unpublished Expression or Phenotype Data

ZFIN welcomes direct data submissions. If you would like to make your unpublished expression or phenotype data available to the community, you can submit this data to ZFIN using Phenote.

Phenote is advantageous because it uses ZFIN anatomy and phenotype ontology terms, so you (and ZFIN) don't have to go looking for them. It also allows basic browsing for terms, which should expedite annotation. We hope that you will find this new tool helpful for annotation of mutant phenotypes or gene expression.

Phenote allows you to save and load your expression or phenotype annotations in a tab-delimited file that can be read by Microsoft Excel.

You can download the current stable Phenote release or check out the more recent beta versions.

All your data submissions will be clearly attributed to you.

Please contact us for more information.

Mark your calendar!

The 9th International Meeting on Zebrafish Development and Genetics will take place from June 16 to June 20 at a new venue, the Overture Center for Performing Arts in Madison, WI, USA.

Transcripts

ZFIN has integrated transcript pages to support data from the whole genome sequencing and annotation effort at the Sanger Institute and to curate non-coding transcripts such as microRNAs from literature. All transcripts in ZFIN are searchable using the Genes/Markers/Clones search form. Transcripts records can also be retrieved by sequence similarity search using the BLAST tool at ZFIN.

As shown in the transcript detail page below, transcript pages include information about the sequence of transcript, associated genes and clones, and other transcripts produced by the gene. Information about the transcript type, annotation status and supporting sequences is also included.

Sequence analysis tools provide the user with the option of performing sequence searches at different databases or to download the sequence. External links to the Vega transcript and protein pages are also listed on the detail page. Transcript information is also included in the Gene Products section of the Gene page for annotated genes.

There are currently over 23,400 transcript records in ZFIN associated with over 13,500 genes. This includes 23,185 transcripts provided through data exchange with Sanger and 219 microRNA records available through literature curation and data exchange with the miRNA Registry.

PDFs Please

Due to budget constraints our library has reduced the number of journal subscriptions. This is limiting our ability to curate your articles. To address this problem we are emailing authors requesting PDFs of articles not available from our library. We do not make PDFs public. We would like to encourage everyone to publish articles open access so the research is easily available to all researchers.

We endeavor to have records for all zebrafish articles at ZFIN. If you notice we are missing an article please let us know. If an article is published in a journal that is not indexed for PubMed we are less likely to find the article. It would be very helpful if you can let us know if you publish in one of these journals. We would appreciate it if you could send a PDF of the published version at the same time.

Share newsworthy items with your colleagues

We invite your submissions to the ZFIN Home Page News section.
Contact Jonathan Knight at zfinadmn@zfin.org.