ZFIN NEWS

The Zebrafish Information Network

http://zfin.org

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Name That Gene -
The Zebrafish Nomenclature Committee provides advice and approval for gene and mutant names

The rapidly expanding wealth of zebrafish genetic and genomic information makes it essential to give unique and meaningful names to every zebrafish gene. Good nomenclature practices foster unambiguous communication within the research community and make electronic data retrieval much easier and more efficient.

The Zebrafish Nomenclature Committee maintains guidelines for naming genes and mutants. These conventions are based on input from the zebrafish community and on the rules applied to naming human and mouse genes. ZFIN serves as the central location for obtaining information and advice about how to name your newly discovered gene or mutant.

Before you publish...
We encourage you to consult the committee at nomenclature@zfin.org before publishing new gene names. ZFIN also has a mechanism for registered users to reserve names for newly discovered mutants. The committee reviews these names to ensure that they conform to accepted conventions and then gives provisional approval that reserves the name until the mutant is published.

You may request the committee to approve names for cloned genes as well. Names and symbols are reserved in ZFIN and, at your request, may be done so anonymously until publication.

You can review the nomenclature guidelines at http://zfin.org/zf_info/nomen.html.

ZFIN curators continuously review zebrafish gene names to consolidate multiple names of the same gene, to assign uniform names to all gene family members, and to clarify the relationships between genes in zebrafish, mammals, and other vertebrates. These reviews often require BLAST and mapping analysis. The approved name and all other previous names of all published zebrafish genes are shown on ZFIN.

About us...
The zebrafish nomenclature committee was appointed at the Cold Spring Harbor Laboratory meeting several years ago and has participated in the International Nomenclature Workshops. We have published guidelines in *Trends in Genetics* (Genetic Nomenclature Guide, 1998). These are updated periodically and are listed on ZFIN.

The current members of the committee are Marc Ekker, Mary Mullins, John Postlethwait, and Monte Westerfield. In addition, a member of the ZFIN curation staff is designated as nomenclature coordinator on a rotating basis and fields questions and requests from the research community.

Analysis Tools for sequences in ZFIN

ZFIN has implemented easier access to a variety of sequence analysis tools on Gene, Marker and Clone pages. These tools are available for each sequence, listed in a pulldown menu in the far right column of the "sequence information" section of each page. When only one analysis tool is available for a sequence, a button replaces the pulldown menu.

Analysis tools available for sequences in ZFIN include:

NCBI BLAST
The Basic Local Alignment Search Tool (BLAST) is used to compare nucleotide or amino acid sequences for identity and similarity with other sequences. Selecting this tool opens a search form for a BLAST analysis at the National Center for Biotechnology Information (NCBI). The sequence accession number of interest is automatically added to the search form for your convenience. Just select your search options and click the BLAST! button on the NCBI page.

Thanks to all who completed the ZFIN User Survey! There's still time to make your voice heard!
ZFIN User Survey

(continued from page 1)

Ensembl

Selecting this tool opens a search form for a BLAST analysis at The Wellcome Trust Sanger Institute's Ensembl BLASTView resource. The sequence accession number of interest is automatically added to the search form for your convenience. Just select your search options and click the RUN button near the bottom of the Sanger BLASTView page.

Mega BLAST

Mega BLAST is a BLAST algorithm that more efficiently handles longer nucleotide sequences. Selecting this tool opens a search form for a Mega BLAST analysis at NCBI. The sequence accession number of interest is automatically added to the search form for your convenience. Just select your search options and click the BLAST! button on the NCBI page.

SIB BLAST

Selecting this tool runs an amino acid sequence BLAST analysis at Swiss Institute of Bioinformatics (SIB). The results are automatically displayed on the SIB page.

UCSC BLAT

The Blast-Like Alignment Tool (BLAT) is a genome browser that displays the sequence of interest in the context of other genome features such as known genes from a number of species, other nucleotide sequences, and gene prediction models. Selecting this tool runs a BLAT analysis against the November 2003 assembly at the University of California, Santa Cruz (UCSC) Genome Bioinformatics Site. The results are automatically displayed on the UCSC page. ☚

Expression Data in ZFIN

Determining when and where a gene is expressed is invaluable to understanding its role in development and disease. Whole mount *in situ* hybridization of mRNA is the most common method employed to visualize these data. As of January 2005 ZFIN has 3,791 genes with images of expression (Table 1). Much of these data are available for otherwise uncharacterized genes. As of January 31, 2005, 1,000 expression patterns were available for otherwise uncharacterized genes.

What expression images are available?
Currently, all expression images are obtained from researchers who have made special arrangements to submit their data directly to ZFIN. Several groups submitted small scale expression studies with 323 genes linked to expression patterns (Kudoh *et al*. 2001, Rhinn *et al*. 2003 and Chen and Kimelman 2003). The vast majority of expression data with images has been submitted by the Thisse lab (Thisse et al. 2001 and Thisse et al. 2004). We are currently working with the Talbot Lab to make data available from their large-scale screen later this year. If you are interested in submitting data to ZFIN, please contact us at zfinadmn@zfin.org.

How is expression data derived?
The methodology for the *in situs* is detailed in the various publications. There are two different types of data available from the Thisse lab. Data submitted prior to Sept. 2004 characterize genes expressed in a spatially regulated manner

Table 1: Expression Patterns

Total expression patterns	3,796
Named Genes with expression	1,440
Unnamed cDNAs with expression	1,027
ESTs with expression	1,329

with probes designated "cb". Multiple images covering a range of stages are available for each gene studied. Recent data are from high throughput experiments and are designated as "fast release". Between 400 and 500 expression patterns are released each month. The probes used in these experiments are derived either from the NCBI zebrafish full length cDNA collection, (ZGC http://zgc.nci.nih.gov/), or the NCBI zebrafish EST collection, (IMAGE clones http://image.llnl.gov/) and are indicated by their prefix of "ZGC" or "IMAGE". These data show the expression patterns for all probes even if there is no spatial restriction of the expression pattern. When the expression is unrestricted, a single image containing multiple embryos at a range of developmental stages is shown. Multiple images are created at relevant stages for genes with interesting expression.

How can I find these data?
These data are available only in ZFIN, and can be accessed either through the Anatomy browser or the Expression search form. The Anatomy browser is useful to identify which genes are expressed in a specific anatomical structure. The Expression search also allows query for expression in a particular structure, as well as expression in a particular gene, a particular stage, or for expression in a mutant background of interest. (Also see ZFIN News Summer 2004 for more information on these tools). ☚

ZGC & Zebrafish Genome Annotation Update

Full length cDNA clones from the Zebrafish Gene Collection (ZGC) continue to be incorporated into ZFIN weekly. Many of these sequences are curated and associated with their encoding genes. Nomenclature for these genes are continually revised and updated as information from orthologous and paralagous sequences become available. In addition, many of the ZGC clones also contain expression data generated from the large scale *in situ* hybridization screen at the Thisse's Laboratory.

ZFIN is also involved in a joint effort with the Sanger Institute to manually annotate the zebrafish genome. ZFIN provides nomenclature for Sanger annotated gene structures as well as the integration of these genes with expression, gene ontology and phenotype from primary literature and other data sources. All annotated genes and clones in ZFIN contain reciprocal links with the Vega zebrafish genome browser, providing ZFIN users with an entry into the zebrafish genome.

Table 2: Current statistics for ZFIN data (as of January 31, 2005)

Genes, Alleles & GO (Gene Ontology):	
Genes	16,916
Alleles	2,850
ESTs	13,190
Genes with GO Annotations	7,291
Genomics:	
Full length ZGC cDNA clones	6,057
ZFIN Genes associated w/ZGC cDNA clones	5,332
Sanger annotated genomic clones	662
ZFIN genes associated w/Sanger annotated genes	2,130
Expression & Phenotypes:	
Expression Pattern Images	23,646
ZFIN Genes with Expression Patterns	4,322
Anatomical Structures with Expression	252
Community Information:	
Publications	5,879
Researchers	3,192
Laboratories	397

Get Connected! Subscribe to the Zebrafish Newsgroup

Are you looking for a place to exchange information and share ideas with other zebrafish researchers? Well, we can help you with that! The zebrafish newsgroup is moderated through ZFIN, and is, perhaps, the best kept secret in the zebrafish research community. The zebrafish newsgroup has the potential to be a valuable means of communicaton for the community. Of course, the more subscribers, the more valuable it will be! Currently, fewer than 10% of ZFIN users are subscribed to the newsgroup, and an average of only 12 messages are posted per month.

Recent topics on the newsgroup include: protocols and techniques, water quality and disease issues, and information on suppliers, job openings and funding opportunities. We encourage you to get connected with your colleagues through the zebrafish newsgroup. See http://zfin.org/zf_info/news/newsgroup.html for information on subscribing and options for accessing the newsgroup (this link is also available from the ZFIN home page under "Information and News"). Questions? Contact Sherry at zfinadmn@zfin.org.

Sehen wir euch in Dresden? *Register now & submit abstracts for the* 2005 European Zebrafish Genetics & Development Meeting*!*