



# ZFIN NEWS

The Zebrafish Information Network

<http://zfin.org>

Volume 5, Number 1  
Spring 2008

## *In this issue:*

- *Maximizing Data Impact (pg.1)*
- *Anatomy Pages Expanded (pg.1)*
- *Full Text publications (pg.3)*
- *Morpholino Database (MODB) and ZFIN (pg.3)*
- *Microarray Data at ZFIN (pg.4)*
- *Nomenclature Guidelines Updated (pg.5)*

## ***Maximize The Impact Of Your Published Data***


---

Great care is used while conducting research. Notes are carefully taken, and results are meticulously compiled and analyzed. When writing up your results for publication, a few simple steps will maximize the impact of your hard-earned data on the wider research community.

ZFIN Curators read your publications and extract the data into the ZFIN database. We begin by connecting your published data to gene, mutant, and morpholino records in ZFIN. Our ability to do this accurately requires allele designations for mutants, line designations for transgenic fish, and sequences for genes and morpholinos. When these details are not provided, curators may need to contact authors for additional information. Although the zebrafish research community has generally been very responsive to queries, this process can significantly delay entry of your data into ZFIN and the many interlinked databases that utilize ZFIN data.

To make data more accessible to the entire research community, we recommend authors include the following details in a dedicated part of the Methods section.

- 1- allele designations for any alleles used
- 2- complete list of genes discussed (ZDB-GENE IDs would be ideal, as gene names can change)
- 3- sequence accession numbers for any genes or cloned sequences discussed in the paper
- 4- MO sequences

Including these details in your future papers will greatly enhance the impact of your data, facilitating its proper placement in the deepening ocean of integrated online biological information. Thank you! 

## ***Anatomy Pages Expanded***

---

ZFIN anatomy pages are now easier to search and more informative. The Anatomical Ontology Browser type-ahead feature now highlights your search string in a dynamically-generated list of matching terms, making searches easier to view. Ordering of results is more intuitive, with structure names that begin with your search string shown first, followed by matches to the middle of a term and ending with synonym matches.

*continued on pg. 2*

## Anatomy Pages Expanded

(continued from pg. 1)

The anatomy page has a number of new features. The first is the ability to browse the ontology through relationships to other structures. For example, on the hindbrain page, you can see that ‘hindbrain’ develops from ‘hindbrain neural tube,’ and clicking on ‘hindbrain neural tube’ will take you to the hindbrain neural tube page. In addition to structure lineages, you can explore substructures and subtypes. Click on the Relationships “about” link to learn more about how relationships between terms are defined.

<b>Name:</b> hindbrain		Your Input Welcome
Synonyms: rhombencephalon		
Definition: The most posterior of the three principal regions of the brain, forming the rhombencephalon and all or most of the metencephalon. <a href="#">Kimmel et al, 1995</a> .		
<b>Appears at</b>	<b>Evident until</b>	
<a href="#">Segmentation: 10-13 somites (14.0h-16.0h)</a>	<a href="#">Adult (90d-730d, breeding adult)</a>	
<b>Relationships</b> ( <a href="#">about</a> )		
develops from: <a href="#">hindbrain neural tube</a>		
is part of: <a href="#">brain</a>		
has parts: <a href="#">cerebellum</a> <a href="#">floor plate hindbrain</a> <a href="#">fourth ventricle</a> <a href="#">medulla oblongata</a> <a href="#">rhombic lip</a> <a href="#">rhombomere</a>		

The EXPRESSION section of the anatomy page displays information about genes expressed in the anatomical structure. The EXPRESSION section has two powerful tools to help you choose a gene probe to label a structure. “Genes with Most Figures” displays the five genes used most frequently in the literature to label the structure. “In Situ Probes” shows probes for the structure that have been highly rated by the Thisse lab in their large-scale in situ screen. Click on the “Recommended” link to learn more about the Thisse ranking system. Links at the bottom take you to a full listing of expression in a given structure.

<b>EXPRESSION</b>		
<b>Genes with Most Figures</b>		
<b>Gene Symbol</b>	<b>Figures</b>	
<a href="#">pax6a</a>	<a href="#">14 Figures</a> from 8 publications	
<a href="#">sox3</a>	<a href="#">11 Figures</a> from 2 publications	
<a href="#">pax2a</a>	<a href="#">11 Figures</a> from 9 publications	
<a href="#">mdkb</a>	<a href="#">11 Figures</a> from 2 publications	
<a href="#">sox2</a>	<a href="#">10 Figures</a> from 3 publications	
Show all <a href="#">1012 genes, 2166 figures</a> . (including substructures <a href="#">1164 genes</a> .)		
<b>In Situ Probes:</b> <a href="#">Recommended</a> by <a href="#">Thisse lab</a>		
<b>Gene Symbol</b>	<b>Probe</b>	<b>Figures</b>
<a href="#">adcyp1b</a>	<a href="#">MGC:101522</a>	<a href="#">2 Figures</a> from <a href="#">Thisse et al., 2004</a>
<a href="#">arg2</a>	<a href="#">MGC:85630</a>	<a href="#">1 Figure</a> from <a href="#">Thisse et al., 2004</a>
<a href="#">ascl1b</a>	<a href="#">eu104</a>	<a href="#">3 Figures</a> from <a href="#">Thisse et al., 2005</a>
<a href="#">atoh2b</a>	<a href="#">MGC:92543</a>	<a href="#">1 Figure</a> from <a href="#">Thisse et al., 2004</a>
<a href="#">atp1a3a</a>	<a href="#">cb705</a>	<a href="#">3 Figures</a> from <a href="#">Thisse et al., 2001</a>
Show all <a href="#">116 Probes</a>		

(continued on pg. 3)

### 8th International Meeting on Zebrafish Development and Genetics

June 25-29, 2008 - Madison, WI, USA

Important deadlines: Abstract submission, April 14, 2008; Lodging reservations, May 19, 2008.

More information is available on the website. <http://www.union.wisc.edu/zebrafish/index.html>

## Anatomy Pages Expanded

(continued from pg. 2)

PHENOTYPE affecting hindbrain				
Mutant and Transgenic Lines				
Genotype (Background)	Affected Genes	Phenotype	Figures	
<a href="#">apc<sup>m404</sup></a> (AB)	<a href="#">apc</a>	abnormal	<a href="#">1 figure</a> from 1 publication	
<a href="#">apc<sup>m491</sup></a> (AB)	<a href="#">apc</a>	abnormal	<a href="#">1 figure</a> from 1 publication	
<a href="#">apc<sup>m691</sup></a> (AB)	<a href="#">apc</a>	abnormal	<a href="#">1 figure</a> from 1 publication	
<a href="#">atf<sup>tc234b</sup></a>	<a href="#">atf</a>	abnormal	<a href="#">1 figure</a> from 1 publication	
<a href="#">atf<sup>ta1b</sup></a>	<a href="#">atf</a>	abnormal	<a href="#">1 figure</a> from 1 publication	
Show all <a href="#">186 genotypes</a> , (including substructures <a href="#">186 genotypes</a> )				
Morpholino Experiments in wild-type fish				
Target Genes	Morpholinos	Genotype	Phenotype	Data
<a href="#">rps3a</a>	<a href="#">MO1-rps3a</a>	AB	undulate	<a href="#">1 figure</a> from 1 publication
<a href="#">rps4x</a>	<a href="#">MO1-rps4x</a>	AB	opaque undulate	<a href="#">1 figure</a> from 1 publication
<a href="#">rps15a</a>	<a href="#">MO1-rps15a</a>	AB	opaque undulate	<a href="#">1 figure</a> from 1 publication
<a href="#">rps19</a>	<a href="#">MO1-rps19</a>	AB	opaque undulate	<a href="#">1 figure</a> from 1 publication
<a href="#">rps29</a>	<a href="#">MO1-rps29</a>	AB	undulate	<a href="#">2 figures</a> from 1 publication
Show all <a href="#">23 experiments</a>				
Morpholino Experiments in mutant fish				
Target Genes	Morpholinos	Genotype	Phenotype	Data
<a href="#">cyp26c1</a> , <a href="#">cyp26b1</a>	<a href="#">MO1-cyp26b1</a> , <a href="#">MO1-cyp26c1</a>	<a href="#">cyp26a1<sup>m718/m718</sup></a>	posteriorized	<a href="#">2 figures</a> from 1 publication
<a href="#">aam</a>	<a href="#">MO2-aam</a>	<a href="#">Tg(elav3:EGFP)<sup>zfs</sup></a>	[neuron] decreased number	<a href="#">1 figure</a> from 1 publication
<a href="#">cyp26b1</a>	<a href="#">MO3-cyp26b1</a>	<a href="#">Tg(isl1:GFP)<sup>mw0</sup></a>	decreased size	<a href="#">1 figure</a> from 1 publication

In the PHENOTYPE section of the anatomy page, the “Mutant and Transgenic Lines” subsection lists mutant and transgenic genotypes with phenotypes affecting the anatomical structure. Phenotypes are described using qualities from the PATO ontology, facilitating cross-species comparisons. The “Morpholinos” section shows morpholinos that affect the structure. Morphants are divided into two groups: those with a wild type background, and those with a mutant or transgenic background.

Don't see your favorite anatomy term? Request it using the “Request new Anatomical Term” link on the anatomy search page. Once in ZFIN, your anatomy term will join the Anatomical Ontology and be linked to expression and phenotype data.

## Full Text Publications

Many ZFIN pages can now take you directly to journal articles. Look for links with journal names preceded by “Full text @”, e.g. Full text @ Development. This is the full, original paper on the publisher's site, so your institution's access privileges will apply.

The direct link is made possible by the Digital Object Identifier system (DOI®) for persistent identification of content on digital networks. For more information on the DOI system, see <http://www.doi.org/index.html>

## Morpholino Database (MODB) And ZFIN

ZFIN is now linked to the morpholino database (MODB) <http://www.secretomes.umn.edu/MODB/>. A description of MODB is now published open access at: <http://www.biomedcentral.com/1471-2105/9/7> [provisional pdf]. MODB is a searchable database that currently contains basic information on over 800 morpholinos including both those with full ZFIN annotation as well as many targeted to EST sequences. Comments and questions can be sent via the website or to Stephen Ekker ([ekker.stephen@mayo.edu](mailto:ekker.stephen@mayo.edu)) or Karl Clark ([clark.karl@mayo.edu](mailto:clark.karl@mayo.edu)).

## Microarray Data At ZFIN

ZFIN has added links from individual gene pages to curated microarray data at GEO (Fig. 2) and ZF-Espresso (Fig. 3). Currently only sequences already in ZFIN have links. We will be analyzing the sequences from the Affymetrics and Compugen chips and associating those sequences with genes as time permits. In the future we will be adding links to the ArrayExpress Data Warehouse. The microarray data is only available from individual gene pages and cannot be found using the expression search form. Full experiment details can be found by following links as indicated in the captions for Fig. 2 and Fig. 3.

ZFIN ID: ZDB-GENE-010122-1

**Gene Name:** fibroblast growth factor 8 b  
**Gene Symbol:** fgf8b  
**Previous Names:** fgf17, fgf17a  
[Nomenclature History](#)  
**Note:** Reifers et al. (2000) originally reported this gene as fgf17a with synteny to Mmu Fgf17. Kikuta et al. (2007) present mapping data showing fgf17a (fgf8b) as syntenic to Hsa Chr. 1. These data, along with BLAST results, led to changing fgf17a to fgf8b.

---

**GENE EXPRESSION:** [\(current status\)](#)

**All expression data:** [8 figure\(s\)](#) from 3 publications

**Directly submitted expression data:** [6 figure\(s\) \(9 images\)](#) from Thisse *et al.*, 2005 [eu586]

**Wild Type Stages, Structures:** [Gastrula.90%-epiboly](#) (9.00h-10.00h) to [Hatching Long-pec](#) (48.00h-60.00h)  
[midbrain hindbrain boundary](#), [optic stalk](#), [unspecified](#)

**Curated microarray expression:** [GEO \(1\)](#), [ZF-Espresso \(1\)](#)

Fig. 1 Links to GEO and ZF-Espresso are at the bottom of the Gene Expression section of the Gene's information page.

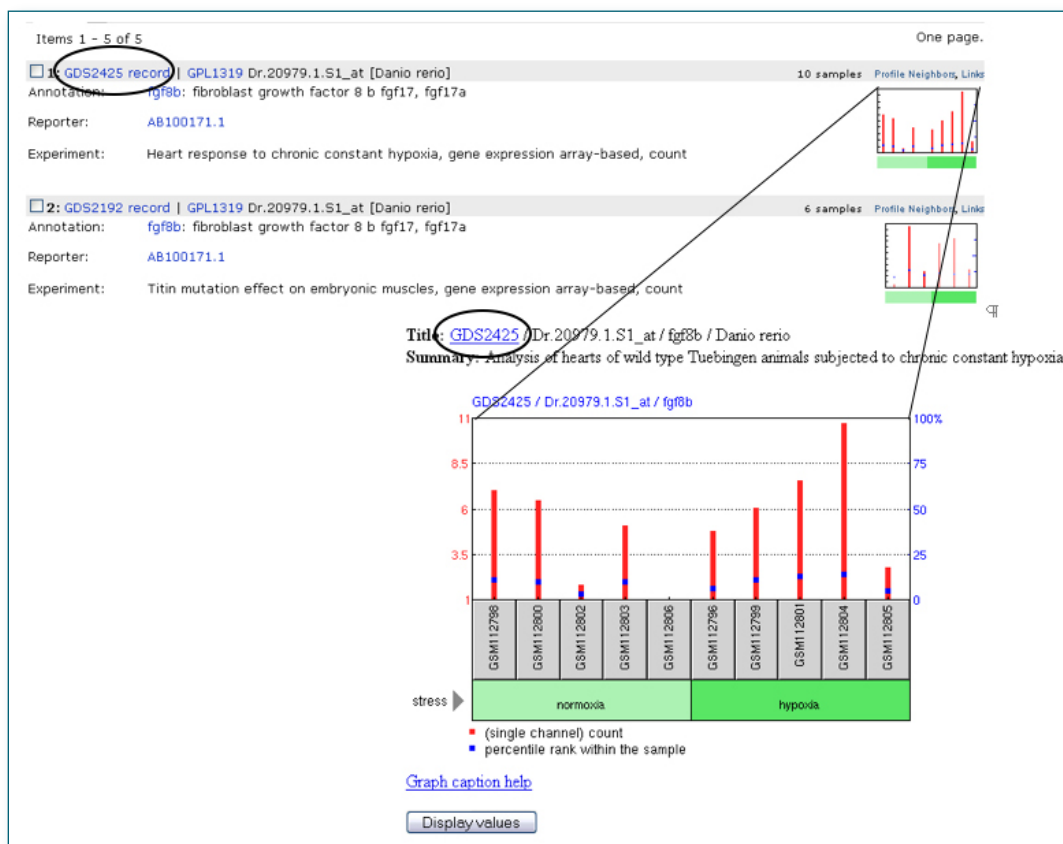


Fig. 2 Example of data from GEO. Information about the experiment and the publication are linked from the GEO experiment ID (circled).

(continued on pg. 5)



# Microarray Data At ZFIN

(continued from pg. 4)

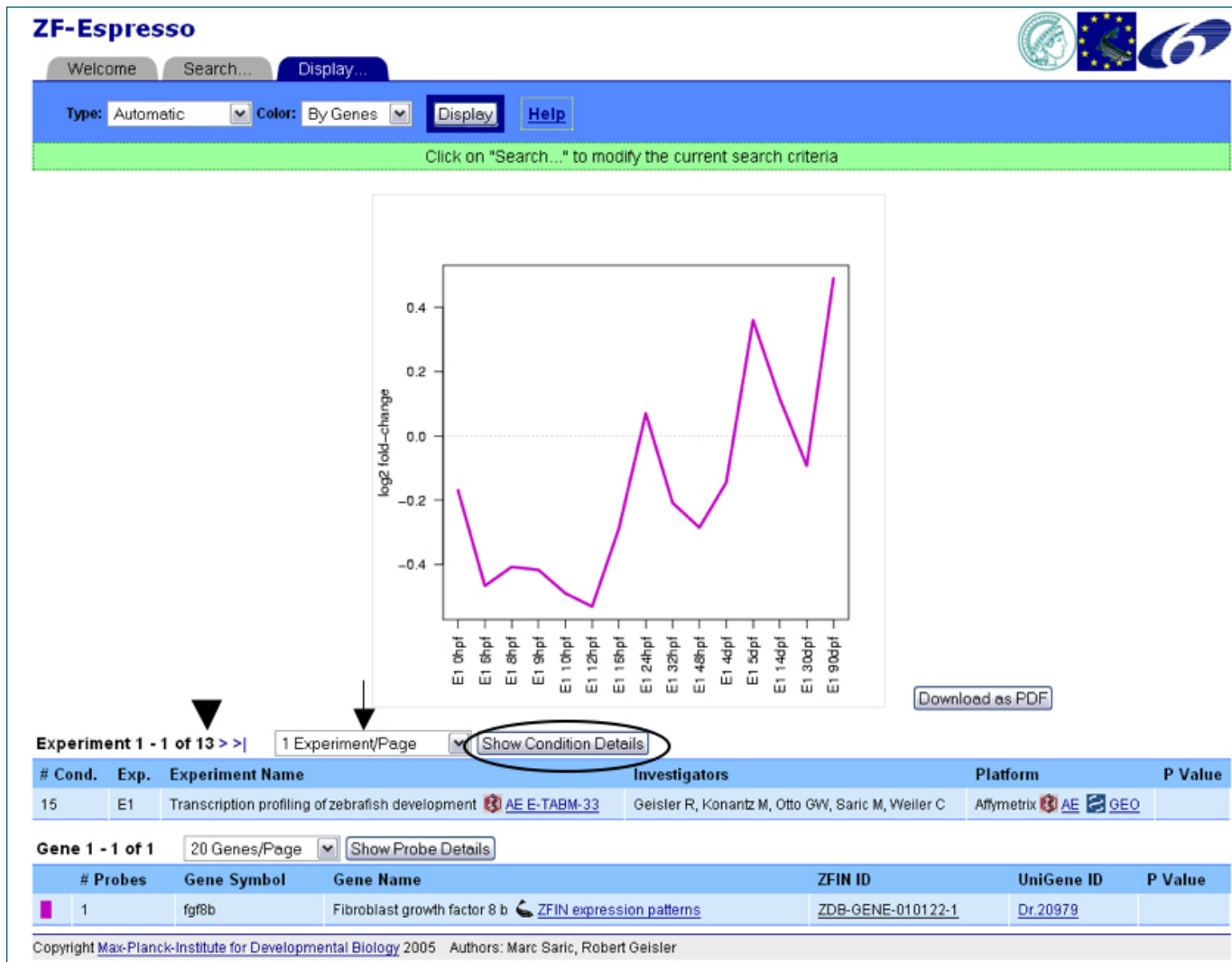


Fig. 3 Sample of data from ZF-Espresso. All data for a gene can be displayed on the same graph if the number of Experiments/Page (arrow) is selected to be greater than the total number of Experiments (arrowhead). Full information about the experiment can be obtained by clicking on the “Show Condition Details” button (circled).

## Nomenclature Guidelines Updated

Please check [http://zfin.org/zf\\_info/nomen.html](http://zfin.org/zf_info/nomen.html) for the most recent updates. If you have questions about how to apply the guidelines or would like to make sure the nomenclature for your paper is correct please email [nomenclature@zfin.org](mailto:nomenclature@zfin.org).

Share newsworthy items with your colleagues

We invite your submissions to the ZFIN Home Page News section. Contact Jonathan Knight at [zfinadmin@zfin.org](mailto:zfinadmin@zfin.org).