

NEW [JBrowse Video-Tutorials](#)

JBrowse is the genome browser on Xenbase where you can interrogate the latest genome builds for *X. tropicalis* and *X. laevis*, transcription factor binding sites and location of morpholinos, as well as tracks for ChIP-Seq and RNA-Seq data from GEO. Learn how to navigate JBrowse via our helpful video tutorials:

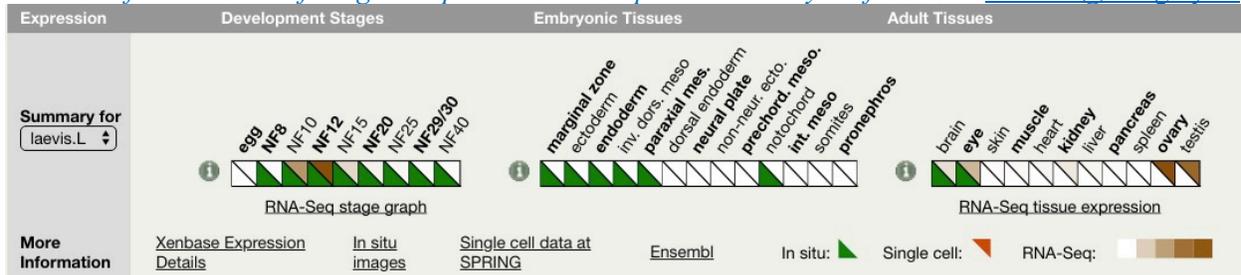
- [Introduction to JBrowse](#). How to select tracks, species, genome version and find genes.
- [JBrowse 1](#): How to view all aspects of a gene sequence (e.g., UTR, intron, CDS).
- [JBrowse 2](#): How to save track data for a particular region.
- [JBrowse 3](#): How to add custom tracks from your computer.

NEW Gene Expression ribbon

Each gene page now has a ribbon that summarizes *in situ* and RNA-Seq data for embryonic stages, embryonic tissues and adult tissues of *X. laevis* and *X. tropicalis*.

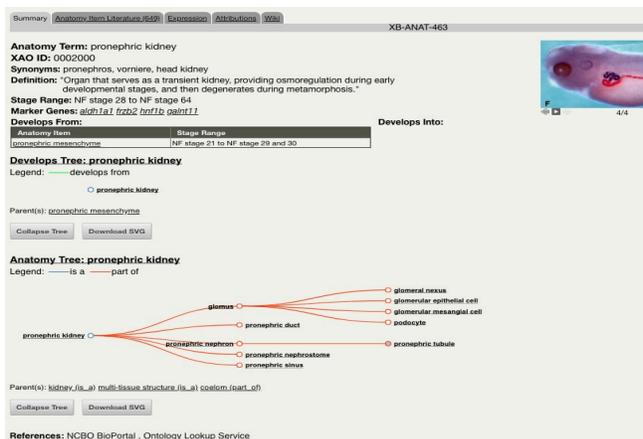
- Green represents *in situ* data from the vast collection of curated gene expression in Xenbase. Mouse over shows number of records for expression in that stage or tissue.
- Click ‘Xenbase Expression Details’ to go to the full gene expression data.
- RNA-Seq data from Sessions *et al.* 2016 (adult tissues) are shown in color gradients of TPM values in top right half of NF stage and adult tissues ribbon. Mouse over to see the TPM value for a particular tissue/stage.
- *Single-cell RNA-Seq data from Briggs et al. 2018 for embryonic tissues are coming soon, and will be shown in red. In the meantime, explore single cell data via the link to tools at SPRING.*

This is the first iteration of the gene expression ribbon-please send us your feedback: xenbase@ucalgary.ca.

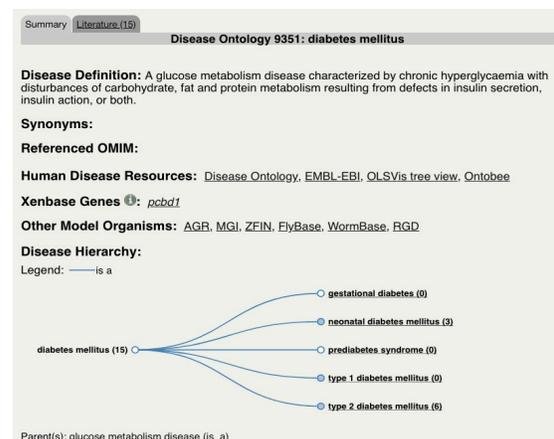


Updated Marker genes, anatomy tree and more images for [XAO anatomy pages](#) (below left)

Each anatomical term we use to describe gene expression has its own XAO page. XAO pages are useful to find out more about a structure, at what time in development it is observed, and which genes are expressed. We’re adding validated marker genes, exemplary gene expression images, and annotated diagrams as we curate new research articles and data from large screens. Let us know your favorite markers, and we’ll share your insights! Email xenbase@ucalgary.ca



Anatomy Page with marker genes list and interactive XAO tree viewer.



Disease Page with associated gene(s) and DO tree viewer (no. articles).

Disease Ontology Pages with new interactive tree viewers.

To further support human disease modeling in *Xenopus*, we have added dynamic tree viewers to the human Disease Ontology (the DO) Disease Pages.

- The ontology tree viewer shows how various diseases are related, e.g., ‘diabetes mellitus’ has five subtypes, ‘gestational’, ‘neonatal’ to ‘type 1’ and ‘type 2’ diabetes and ‘prediabetes syndrome’.
- To explore the ontology in tree-view click the nodes.
- Solid blue nodes indicate more subtypes, e.g., type1 diabetes has 24 subtypes.
- Numbers in parenthesis show the number of *Xenopus* papers that refer to that disease.
- Literature tab lists all of the articles curated for the disease.
- Genes associated with the disease are also shown, and link back to the Xenbase gene pages.

***Xenopus* Stock Center frogs all catalogued on Xenbase**

Transgenic and mutant *Xenopus* lines and wildtypes strains supplied by the NXR (USA), the NBRP (Japan) and the EXRC (Europe) are [catalogued and searchable on Xenbase](#). The stock centers hold over 130 different transgenic lines, and the NXR has developed 74 mutant lines. Many lines are shared between the centers, yet each line has a single entry on Xenbase, and carry unique RRIDs (identification numbers) depending on supplier. We encourage researchers to use the official standardized name and cite the RRID number in their papers.

[microPublication Biology](#) (μP for short)

Call for papers! μP is currently accepting single-experiment submissions of high-quality *Xenopus* research under the topics Expression patterns (RT-PCR, WISH, IHC), Phenotypic data (e.g., toxicology screens, SEM, histology), Genotypic data (CRISPR or TALEN mutants/transgenic lines), Sequence data (SNPS, polymorphisms) and Methods (new and updated protocols). Each open-access μP article is peer-reviewed, assigned a DOI, and published online as HTML and PDF. This is an especially accessible format to get student research published quickly! <https://www.micropublication.org/submit.html>

Lastly....

A new review by Xenbase, which assessed 1000+ articles, describes the breadth of recent *Xenopus*-Human disease modeling and highlights the integration of the Human Disease Ontology (DO) into Xenbase Disease Pages. Take a look! **Xenbase: Facilitating the use of *Xenopus* to Model Human Disease**. Nenni et al (2019). Front. Physiol. [doi: 10.3389/fphys.2019.00154](https://doi.org/10.3389/fphys.2019.00154).