

LATEST Gene Models & NEW Gene Pages

Genome improvement is a major goal of Xenbase, and we have devoted a large amount of effort to this task over the past year. Manual curation and analyses have resulted in many new gene pages and many more updates to gene models and gene nomenclature. In particular, the assignment of *X. laevis* homeologues to the L and S sub-genomes is vastly improved. In summary:

- The JBrowse genome browser was updated with the latest gene models for *X. laevis* (v9.2) and *X. tropicalis* (v. 9.2).
- *X. tropicalis* 9.1 Genome Annotation.
 - Total named models: 22,658 (66.24%), increase of 4,383
 - Models with *provisional* names: 3,931
 - Models with updated names: 5,554 (16.2%)
- *X. laevis* 9.2 Genome Annotation.
 - Total named models: 32,538 (63.7%), increase of 10,545
 - Models with *provisional* names: 7,067
 - *Models with updated names: 12,510 (24.5%)*
- Manual annotation of *X. tropicalis*, *X. laevis.L* and *X. laevis.S* gene models has resulted in:
 - [665 new](#) gene pages.
 - 950+ genes have updated gene symbols.
 - 2,200+ genes with updated Entrez assignments.
 - *X. tropicalis* has 16,338 genes (an increase of 554).
 - *X. laevis* has 24,345 genes (*.L and .S combined; an increase of 861*).

Note: *X. tropicalis* v9.1 is now available on [Ensembl](#), a genome browser that supports multiple vertebrate genomes for comparative genomics, evolution, sequence variation and transcriptional regulation. http://uswest.ensembl.org/Xenopus_tropicalis/Info/Index

NEW GEO & SRA RNA-Seq and ChIP-Seq data now on Xenbase

Xenbase has developed a suite of tools, interfaces and data processing pipelines that transform ChIP-Seq and RNA-Seq data from the NCBI Gene Expression Omnibus (GEO), into deeply integrated gene expression and chromatin data, mapping all aligned reads to the most recent *Xenopus* genomes on JBrowse. The GEO pipelines are continuously monitored for issues and bugs, and we plan to release stable, bug-free versions every 3 months. The code is open access (GNU General Public License v3.0) and available on [GitLab](#) and [GitHub](#).

Full details of the Xenbase GEO pipeline and data processing are given in this *in press* article: [Xenbase: Deep integration of GEO & SRA RNA-Seq and ChIP-Seq data in a model organism database](#). Fortriede et al 2019. Nucleic Acid Research:

Note: ChIP-Seq and RNA-Seq data that has been deposited with the EMBL-EBI *is* shared with the NCBI's BIOPROject database, but that this data *does not* migrate automatically to GEO, and therefore Xenbase will *not* be able to automatically process and display your RNA-seq or ChIP-seq data. Authors need to resubmit both metadata and processed data directly to GEO. [Click here for instructions](#) on how to get NGS data from EMBL-EBI into the GEO-Xenbase pipeline.

NEW [GEO data Video-Tutorials](#)

Learn how to navigate GEO data on Xenbase via our new video tutorials:

- [GEO Data Simple Search](#) Basic search options, GSE page, and loading tracks to JBrowse.
- [GEO Data Advanced Search](#): Advanced filter options for experimental conditions and assay.
- [Navigating a GSE Page](#): GEO series pages, sample table (the control vs treatment), how to load into JBrowse, view the Differentially Expressed Genes (DEG) tables and download .

2019 Xenbase Survey

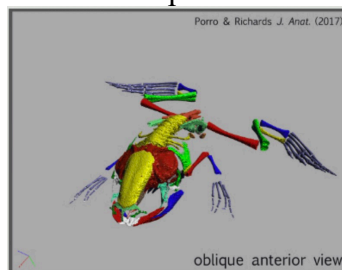
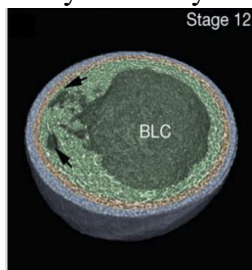
Xenbase exists solely to support the *Xenopus* research community- we need and value your feedback! Please take our quick, [10-question survey](#) about the new GEO data on JBrowse and other Xenbase features. Use this URL to access the survey: <https://www.surveymonkey.com/r/LYZ6L9L>

Xenbase Grant Renewal

The P41 grant that supports Xenbase ends in 2020, and we will submit a grant renewal in January 2020 to the NICHD to continue Xenbase funding for 2020-2025. If Xenbase is essential for your research, please consider writing a **Letter of Support** to be included with our grant renewal. You can leave your name and email in Question 7 of the survey OR email us at xenbase@ucalgary.ca. We will get back to you!

Anatomy Atlas-2 new modules.

- Movies of the *in vivo* time-lapse phase-contrast X-ray microtomography of [gastrulating *Xenopus*](#) embryos from Moosmann et. al (2013) (doi:10.1038/nature12116).
- Gross anatomy of [adult *Xenopus*](#), created by contrast-enhanced computed tomography, including rotating views of skeleton, musculature and nervous system, and all of the annotated figures from the 2017 J. Anatomy article by Laura Porro & Christopher Richards.



The goal of building the *Xenopus* Anatomy Atlas is to provide a comprehensive resource of reference images, videos and 3D models for use by students, teachers and researchers.

If you have a collection of images to share, please contact us at xenbase@ucalgary.ca.

[microPublication Biology](#) (μ Pub for short)

μ Pub is a publishing platform to share single, validated results that include novel, negative and/or reproduced results, as well as findings which may lack a broader scientific narrative. μ Pub articles are **open-access**, **peer-reviewed**, have a **DOI** and **indexed in PMC Europe**. μ Pub is widely used in the *C. elegans* and *Drosophila* communities and is an especially accessible format to quickly publish student research. *Xenopus* researchers can submit papers here: <https://www.micropublication.org/submit.html>.