

# Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

## Newtomics

RRID:SCR\_006073

Type: Tool

### Proper Citation

Newtomics (RRID:SCR\_006073)

### Resource Information

**URL:** <http://newt-omics.mpi-bn.mpg.de/index.php>

**Proper Citation:** Newtomics (RRID:SCR\_006073)

**Description:** Newt-omics is a database, which enables researchers to locate, retrieve and store data sets dedicated to the molecular characterization of newts. Newt-omics is a transcript-centered database, based on an Expressed Sequence Tag (EST) data set from the newt, covering ~50,000 Sanger sequenced transcripts and a set of high-density microarray data, generated from regenerating hearts. Newt-omics also contains a large set of peptides identified by mass spectrometry, which was used to validate 13,810 ESTs as true protein coding. Newt-omics is open to implement additional high-throughput data sets without changing the database structure. Via a user-friendly interface Newt-omics allows access to a huge set of molecular data without the need for prior bioinformatical expertise. The newt *Notophthalmus viridescens* is the master of regeneration. This organism is known for more than 200 years for its exceptional regenerative capabilities. Newts can completely replace lost appendages like limb and tail, lens and retina and parts of the central nervous system. Moreover, after cardiac injury newts can rebuild the functional myocardium with no scar formation. To date only very limited information from public databases is available. Newt-Omics aims to provide a comprehensive platform of expressed genes during tissue regeneration, including extensive annotations, expression data and experimentally verified peptide sequences with yet no homology to other publicly available gene sequences. The goal is to obtain a detailed understanding of the molecular processes underlying tissue regeneration in the newt, that may lead to the development of approaches, efficiently stimulating regenerative pathways in mammals. \* Number of contigs: 26594 \* Number of est in contigs: 48537 \* Number of transcripts with verified peptide: 5291 \* Number of peptides: 15169

**Abbreviations:** Newt-Omics

**Synonyms:** newt db, Newt database

**Resource Type:** analysis service resource, data analysis service, data or information resource, database, production service resource, service resource

**Defining Citation:** [PMID:22039101](#)

**Keywords:** gene expression, regeneration, annotation, expression data, peptide sequence, gene sequence, tissue regeneration, newt, pathway, mammal, blast, contigs, peptide, tissue, microarray, heart, lens, dorsal, ventral, transcript, functional annotation, molecular process, model organism, expressed sequence tag, sequence, mass spectrometry, protein, bio.tools

**Funding:** Hessian Ministry for Science and Art

**Availability:** To be used only for research and educational purposes. Any reproduction or use for commercial purpose is prohibited without the prior express written permission of the MPI for heart and lung research.

**Resource Name:** Newtomics

**Resource ID:** SCR\_006073

**Alternate IDs:** nlx\_151479, biotools:newt-omics

**Alternate URLs:** <https://bio.tools/newt-omics>

**Record Creation Time:** 20220129T080234+0000

**Record Last Update:** 20260903T234830+0000

---

## Ratings and Alerts

No rating or validation information has been found for Newtomics.

No alerts have been found for Newtomics.

---

## Data and Source Information

**Source:** [SciCrunch Registry](#)

---

## Usage and Citation Metrics

We found 1 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

Lu S, et al. (2019) Bichirs employ similar genetic pathways for limb regeneration as are used in lungfish and salamanders. Gene, 690, 68.