# **Resource Summary Report**

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# **Phenologs**

RRID:SCR\_005529

Type: Tool

## **Proper Citation**

Phenologs (RRID:SCR\_005529)

#### **Resource Information**

URL: http://www.phenologs.org/

**Proper Citation:** Phenologs (RRID:SCR\_005529)

**Description:** Database for identifying orthologous phenotypes (phenologs). Mapping between genotype and phenotype is often non-obvious, complicating prediction of genes underlying specific phenotypes. This problem can be addressed through comparative analyses of phenotypes. We define phenologs based upon overlapping sets of orthologous genes associated with each phenotype. Comparisons of >189,000 human, mouse, yeast, and worm gene-phenotype associations reveal many significant phenologs, including novel non-obvious human disease models. For example, phenologs suggest a yeast model for mammalian angiogenesis defects and an invertebrate model for vertebrate neural tube birth defects. Phenologs thus create a rich framework for comparing mutational phenotypes, identify adaptive reuse of gene systems, and suggest new disease genes. To search for phenologs, go to the basic search page and enter a list of genes in the box provided, using Entrez gene identifiers for mouse/human genes, locus ids for yeast (e.g., YHR200W), or sequence names for worm (e.g., B0205.3). It is expected that this list of genes will all be associated with a particular system, trait, mutational phenotype, or disease. The search will return all identified model organism/human mutational phenotypes that show any overlap with the input set of the genes, ranked according to their hypergeometric probability scores. Clicking on a particular phenolog will result in a list of genes associated with the phenotype, from which potential new candidate genes can identified. Currently known phenotypes in the database are available from the link labeled "Find phenotypes", where the associated gene can be submitted as queries, or alternately, can be searched directly from the link provided.

Abbreviations: Phenologs

Synonyms: phenologs.org, Phenologs - Systematic discovery of non-obvious disease

models and candidate genes

Resource Type: database, data or information resource

**Defining Citation:** PMID:20308572

Keywords: gene, phenotype, ortholog, genotype, human, mouse, yeast, worm

Funding: Texas Advanced Research Program;

Welch Foundation; Packard Fellowship; March of Dimes;

Texas Institute for Drug and Diagnostic Development;

NSF; NIH; NIGMS

**Resource Name:** Phenologs

Resource ID: SCR\_005529

Alternate IDs: nlx\_144624

**Record Creation Time:** 20220129T080230+0000

**Record Last Update:** 20250517T055711+0000

### **Ratings and Alerts**

No rating or validation information has been found for Phenologs.

No alerts have been found for Phenologs.

#### Data and Source Information

Source: SciCrunch Registry

### **Usage and Citation Metrics**

We found 4 mentions in open access literature.

**Listed below are recent publications.** The full list is available at NIF.

Kachroo AH, et al. (2022) Humanized yeast to model human biology, disease and evolution. Disease models & mechanisms, 15(6).

Wangler MF, et al. (2017) Drosophila and genome-wide association studies: a review and resource for the functional dissection of human complex traits. Disease models & mechanisms, 10(2), 77.

Segura-Cabrera A, et al. (2013) A viral-human interactome based on structural motif-domain interactions captures the human infectome. PloS one, 8(8), e71526.

Godwin J, et al. (2012) Nonapeptides and social behavior in fishes. Hormones and behavior, 61(3), 230.