

Resource Summary Report

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Alliance of Genome Resources

RRID:SCR_015850

Type: Tool

Proper Citation

Alliance of Genome Resources (RRID:SCR_015850)

Resource Information

URL: <http://www.alliancegenome.org/>

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Description: Organization that aims to develop and maintain sustainable genome information resources to promote understanding of the genetic and genomic basis of human biology, health, and disease. The Alliance is composed of FlyBase, Mouse Genome Database (MGD), the Gene Ontology Consortium (GOC), Saccharomyces Genome Database (SGD), Rat Genome Database (RGD), WormBase, and the Zebrafish Information Network (ZFIN).

Synonyms: The Alliance

Resource Type: access service resource, consortium, data or information resource, organization portal, portal, service resource

Keywords: gene ontology, human biology, genome, organism model, gene ontology consortium, FASEB list, DRKB

Funding: NHGRI U41HG02223E;
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Resource Name: Alliance of Genome Resources

Resource ID: SCR_015850

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260903T235336+0000

Ratings and Alerts

No rating or validation information has been found for Alliance of Genome Resources .

No alerts have been found for Alliance of Genome Resources .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 87 mentions in open access literature.

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

Laulederkind SJF, et al. (2026) Mapping of EFO terms from the GWAS catalog data to multiple ontologies at the Rat Genome Database. Database : the journal of biological databases and curation, 2026.

Horecka I, et al. (2026) Expanding TheCellMap.org to visualize a genome-scale genetic interaction network for a human cell line. bioRxiv : the preprint server for biology.

Khvorykh GV, et al. (2026) Abundance of Inflammatory Response Genes Among Cardiovascular Disease and Ischemic Stroke Genes. International journal of molecular sciences, 27(10).

Wood V, et al. (2026) Empowering biological knowledgebases: advances in human-in-the-loop AI-driven literature curation. Bioinformatics advances, 6(1), vbag028.

Flores-Iga G, et al. (2026) Capsaicin responses in Drosophila: Exploring the possibility of establishing a new Non-TRPV1 model. Biochemistry and biophysics reports, 45, 102515.

Zhao X, et al. (2026) Leveraging PANoptosis-associated genes for unraveling implication of decidualization deficiency in pre-eclampsia via transcriptome data and experiment validation. Frontiers in cell and developmental biology, 14, 1677798.

Garapati PV, et al. (2026) Comprehensive annotation of the enzymes of Drosophila melanogaster. G3 (Bethesda, Md.), 16(2).

Shen Y, et al. (2026) Genome-wide reconstruction of the intrinsic apoptosis pathway in Haemonchus contortus. BMC genomics, 27(1).

Huynh L, et al. (2026) Canonical and noncanonical Hippo signaling in C. elegans. Genetics, 233(1).

Smith JR, et al. (2025) Standardized pipelines support and facilitate integration of diverse datasets at the Rat Genome Database. Database : the journal of biological databases and curation, 2025.

Jhaveri N, et al. (2025) Heat tolerance and genetic adaptations in Caenorhabditis briggsae: insights from comparative studies with Caenorhabditis elegans. Genetics, 230(2).

Tian R, et al. (2025) Cetacean loss of the master adipose tissue regulator β 3-adrenergic receptor may underlie their thick blubber and an Oligocene radiation and dispersal. *Nature communications*, 16(1), 9235.

Pfister JA, et al. (2025) *C. elegans* SSNA-1 is required for the structural integrity of centrioles and bipolar spindle assembly. *Nature communications*, 16(1), 5220.

Pazour GJ, et al. (2025) Cilia.Pro database of ciliary proteins from vertebrates, *Chlamydomonas*, and *Caenorhabditis*. *Molecular biology of the cell*, 36(9), mr8.

Perez SM, et al. (2025) Utilizing *C. elegans* Spermatogenesis and Fertilization Mutants as a Model for Human Disease. *Journal of developmental biology*, 13(1).

Wang J, et al. (2025) p21, ccng1, foxo3b, and fbxw7 contribute to p53-dependent cell cycle arrest. *iScience*, 28(6), 112558.

Tackie E, et al. (2025) Whole Exome Sequencing Uncovers Genetic Syndromes Associated with Orofacial Clefts presenting with Limb abnormalities in a Sub-Saharan African cohort. *Research square*.

Huynh L, et al. (2025) *Caenorhabditis elegans* Uses Canonical and Non-canonical Hippo signaling. *bioRxiv : the preprint server for biology*.

Djeghmoum Y, et al. (2025) Donor transcription suppresses D-loops in cis and promotes genome stability. *The EMBO journal*, 44(19), 5595.

Plaisancié J, et al. (2024) Structural Variant Disrupting the Expression of the Remote FOXC1 Gene in a Patient with Syndromic Complex Microphthalmia. *International journal of molecular sciences*, 25(5).