

Resource Summary Report

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Genevestigator

RRID:SCR_002358

Type: Tool

Proper Citation

Genevestigator (RRID:SCR_002358)

Resource Information

URL: <https://www.genevestigator.com/gv/>

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Description: A high performance search engine for gene expression that integrates thousands of manually curated public microarray and RNAseq experiments and nicely visualizes gene expression across different biological contexts (diseases, drugs, tissues, cancers, genotypes, etc.). There are two basic analysis approaches: # for a gene of interest, identify which conditions affect its expression. # for condition(s) of interest, identify which genes are specifically expressed in this/these conditions. Genevestigator builds on the deep integration of data, both at the level of data normalization and on the level of sample annotations. This deep integration allows scientists to ask new types of questions that cannot be addressed using conventional tools.

Abbreviations: Genevestigator

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

Keywords: gene, genetic, animal, development, disease, meta-analysis, regulation, stage, microarray, rnaseq, visualization, gene expression, disease, drug, tissue, cancer, genotype, pharma, biomedical, conditions, genotype, anatomy, neoplasm, chemical, hormone, infection, model organism, organ, cell type, cell line, target, biomarker, similarity, FASEB list

Availability: 4 products:, Free, Free for academic use, Account required, Paid subscription, Local installation

Resource Name: Genevestigator

Resource ID: SCR_002358

Alternate IDs: nif-0000-21172, OMICS_00763

Record Creation Time: 20220129T080213+0000

Record Last Update: 20260829T182118+0000

Ratings and Alerts

No rating or validation information has been found for Genevestigator.

No alerts have been found for Genevestigator.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 407 mentions in open access literature.

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

Dotson BR, et al. (2026) Streptomyces Volatiles Alter Auxin/Cytokinin Signaling, Root Architecture, and Growth Rate in Arabidopsis thaliana via Signaling Through the KISS ME DEADLY Gene Family. Plants (Basel, Switzerland), 15(1).

Wu X, et al. (2025) Genome-wide identification of WRKY gene family and expression analysis of key WRKY genes in response to Fusarium solani infection in Lycium barbarum. Frontiers in plant science, 16, 1543373.

Tenhaken V, et al. (2025) The MAP kinase negative regulator DUSP2 (dual specificity phosphatase 2) is controlled by oncogenic microRNA cluster miR-17-92, miR-106a-363 and miR-106b-25. BMC cancer, 25(1), 1020.

Yang H, et al. (2025) Redirecting E3 ubiquitin ligases for targeted protein degradation with heterologous recognition domains. The Journal of biological chemistry, 301(1), 108077.

Buoso E, et al. (2025) Disruption of Epithelial Barrier Integrity via Altered GILZ/c-Rel/RACK1 Signaling in Inflammatory Bowel Disease. Journal of Crohn's & colitis, 19(1).

Ceccarelli S, et al. (2025) Toll-Like Receptor 4 and 8 are Overexpressed in Lung Biopsies of Human Non-small Cell Lung Carcinoma. Lung, 203(1), 38.

Sudharson S, et al. (2025) Transcriptomic Profiles of the Nasal Mucosa Following Birch Pollen Provocation Differ Between Birch Pollen-Allergic and Non-Allergic Individuals. Allergy, 80(6), 1757.

Guillou MC, et al. (2025) Phytocytokine genes newly discovered in Malus domestica and their regulation in response to Erwinia amylovora and acibenzolar-S-methyl. The plant genome, 18(1), e20540.

- Singh A, et al. (2024) Comparative analysis of IRE1s in plants: insights into heat stress adaptation in *Triticum aestivum*. *BMC plant biology*, 24(1), 1083.
- Rivière Q, et al. (2024) Effects of light regimes on circadian gene co-expression networks in *Arabidopsis thaliana*. *Plant direct*, 8(8), e70001.
- Bläsius K, et al. (2024) Pathological mutations reveal the key role of the cytosolic iRhom2 N-terminus for phosphorylation-independent 14-3-3 interaction and ADAM17 binding, stability, and activity. *Cellular and molecular life sciences : CMLS*, 81(1), 102.
- Saleki K, et al. (2024) Matrix metalloproteinase/Fas ligand (MMP/FasL) interaction dynamics in COVID-19: An in silico study and neuroimmune perspective. *Heliyon*, 10(10), e30898.
- Faustino M, et al. (2024) OsTH1 is a key player in thiamin biosynthesis in rice. *Scientific reports*, 14(1), 13591.
- Zhang W, et al. (2024) SA and NHP glucosyltransferase UGT76B1 affects plant defense in both SID2- and NPR1-dependent and independent manner. *Plant cell reports*, 43(6), 149.
- Zhou LZ, et al. (2024) The RALF signaling pathway regulates cell wall integrity during pollen tube growth in maize. *The Plant cell*, 36(5), 1673.
- Du B, et al. (2024) Genome-wide screening of meta-QTL and candidate genes controlling yield and yield-related traits in barley (*Hordeum vulgare* L.). *PloS one*, 19(5), e0303751.
- Maruszczak KK, et al. (2024) Structure prediction analysis of human core TIM23 complex reveals conservation of the protein translocation mechanism. *FEBS open bio*, 14(10), 1656.
- Adejumo IO, et al. (2024) Hypothetical proteins of chicken-isolated *Limosilactobacillus reuteri* subjected to in silico analyses induce IL-2 and IL-10. *Genes & nutrition*, 19(1), 21.
- Aksoy E, et al. (2024) Genome-wide characterization and expression analysis of GATA transcription factors under combination of light wavelengths and drought stress in potato. *Plant direct*, 8(4), e569.
- Masum AA, et al. (2024) Methylglyoxal detoxifying gene families in tomato: Genome-wide identification, evolution, functional prediction, and transcript profiling. *PloS one*, 19(6), e0304039.