Resource Summary Report

Generated by SPARC SAWG on Jul 28, 2026

GeneTrail

RRID:SCR_006250
Type: Tool

Proper Citation

GeneTrail (RRID:SCR_006250)

Resource Information

URL: http://genetrail.bioinf.uni-sb.de/

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Description: A web-based application that analyzes gene sets for statistically significant accumulations of genes that belong to some functional category. Considered category types are: KEGG Pathways, TRANSPATH Pathways, TRANSFAC Transcription Factor, GeneOntology Categories, Genomic Localization, Protein-Protein Interactions, Coiled-coil domains, Granzyme-B clevage sites, and ELR/RGD motifs. The web server provides two statistical approaches, "Over-Representation Analysis" (ORA) comparing a reference set of genes to a test set, and "Gene Set Enrichment Analysis" (GSEA) scoring sorted lists of genes., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: GeneTrail

Resource Type: analysis service resource, service resource, data analysis service, production service resource

Defining Citation: PMID:17526521

Keywords: pathway, microarray, enrichment, genomic, proteomic, function, transcription factor, genomic localization, protein-protein interaction, coiled-coil domain, granzyme-b clevage site, motif, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: GeneTrail

Resource ID: SCR_006250

Alternate IDs: biotools:genetrail, OMICS_02236

Alternate URLs: https://bio.tools/genetrail

Record Creation Time: 20220129T080235+0000

Record Last Update: 20260728T043230+0000

Ratings and Alerts

No rating or validation information has been found for GeneTrail.

No alerts have been found for GeneTrail.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 106 mentions in open access literature.

Listed below are recent publications. The full list is available at SPARC SAWG .

Raj Murthi S, et al. (2025) Contribution of hypoxia-inducible factor 1alpha to pathogenesis of sarcomeric hypertrophic cardiomyopathy. Scientific reports, 15(1), 2132.

Nastaranpour M, et al. (2025) miRNA Expression Profile in Primary Limbal Epithelial Cells of Aniridia Patients. Investigative ophthalmology & visual science, 66(1), 20.

Junyent M, et al. (2025) Unravelling Convergent Signaling Mechanisms Underlying the Aging-Disease Nexus Using Computational Language Analysis. Current issues in molecular biology, 47(3).

Caballero I, et al. (2025) Cystic fibrosis alters the structure of the olfactory epithelium and the expression of olfactory receptors affecting odor perception. Science advances, 11(9), eads1568.

Fraga LN, et al. (2025) A Global Transcriptomic Analysis Reveals Body Weight-Specific Molecular Responses to Chronic Orange Juice Consumption in Healthy Individuals. Molecular nutrition & food research, 69(24), e70299.

Grandke F, et al. (2025) A single-cell atlas to map sex-specific gene-expression changes in blood upon neurodegeneration. Nature communications, 16(1), 1965.

Xie S, et al. (2025) Development of a novel prognostic prediction model using mitochondrial-related genes and single-cell sequencing data for colorectal carcinoma. Translational gastroenterology and hepatology, 10, 65.

Eckhart L, et al. (2024) A comprehensive benchmarking of machine learning algorithms and dimensionality reduction methods for drug sensitivity prediction. Briefings in bioinformatics, 25(4).

Burattin FV, et al. (2024) LINE1 modulate human T cell function by regulating protein synthesis during the life span. Science advances, 10(41), eado2134.

Schneider C, et al. (2024) A Novel AMPK Inhibitor Sensitizes Pancreatic Cancer Cells to Ferroptosis Induction. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(31), e2307695.

Tang C, et al. (2024) Classification of distinct tendinopathy subtypes for precision therapeutics. Nature communications, 15(1), 9460.

Wagner V, et al. (2024) Characterizing expression changes in noncoding RNAs during aging and heterochronic parabiosis across mouse tissues. Nature biotechnology, 42(1), 109.

Xiao H, et al. (2024) Genetic analyses of 104 phenotypes in 20,900 Chinese pregnant women reveal pregnancy-specific discoveries. Cell genomics, 4(10), 100633.

Farrim MI, et al. (2024) Gene expression analysis reveals diabetes-related gene signatures. Human genomics, 18(1), 16.

Gioulbasani M, et al. (2024) Concomitant loss of TET2 and TET3 results in T cell expansion and genomic instability in mice. Communications biology, 7(1), 1606.

Henn D, et al. (2023) Cas9-mediated knockout of Ndrg2 enhances the regenerative potential of dendritic cells for wound healing. Nature communications, 14(1), 4729.

Yang Y, et al. (2023) Molecular characterization of extracellular vesicles derived from follicular fluid of women with and without PCOS: integrating analysis of differential miRNAs and proteins reveals vital molecules involving in PCOS. Journal of assisted reproduction and genetics, 40(3), 537.

Aljedaie MM, et al. (2023) In silico identification of human microRNAs pointing centrin genes in Leishmania donovani: Considering the RNAi-mediated gene control. Frontiers in genetics, 14, 1329339.

Dönig J, et al. (2023) Characterization of nucleolar SUMO isopeptidases unveils a general p53-independent checkpoint of impaired ribosome biogenesis. Nature communications, 14(1), 8121.

Torinsson Naluai Å, et al. (2023) Transcriptomics unravels molecular changes associated with cilia and COVID-19 in chronic rhinosinusitis with nasal polyps. Scientific reports, 13(1), 6592.