

Resource Summary Report

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

GeneTrail

RRID:SCR_006250

Type: Tool

Proper Citation

GeneTrail (RRID:SCR_006250)

Resource Information

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

Proper Citation: GeneTrail (RRID:SCR_006250)

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 cleavage 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, data analysis service, production service resource, 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 cleavage 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: 20260904T000154+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 114 mentions in open access literature.

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

Leroux C, et al. (2026) Exploring the role of food-source microRNAs as potential nutritional bioactives in humans. NPJ science of food, 10(1), 50.

Jiang K, et al. (2026) The Histone Modifier KANSL2 Is an Actionable Biomarker in Multiple Myeloma. Molecular cancer therapeutics, 25(6), 1016.

Hellkamp M, et al. (2026) Targeting metabolic dependencies to reverse chemoradiotherapy resistance in colorectal cancer. Journal of experimental & clinical cancer research : CR, 45(1).

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

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).

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

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.

Ruskovska T, et al. (2024) Integrated Analysis of Genomic and Genome-Wide Association Studies Identified Candidate Genes for Nutrigenetic Studies in Flavonoids and Vascular Health: Path to Precision Nutrition for (Poly)phenols. *Nutrients*, 16(9).

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).

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.

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

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

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.

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

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.

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.