

Resource Summary Report

Generated by [NIF](#) on Apr 17, 2025

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.

Abbreviations: GeneTrail

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

Funding:

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: 20250417T065241+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 101 mentions in open access literature.

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

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.

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-Wuerttemberg, 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.

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.

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.

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

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.

Henn D, et al. (2023) Cas9-mediated knockout of *Ndr2* enhances the regenerative potential of dendritic cells for wound healing. *Nature communications*, 14(1), 4729.

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.

Nelke C, et al. (2023) Senescent fibro-adipogenic progenitors are potential drivers of pathology in inclusion body myositis. *Acta neuropathologica*, 146(5), 725.

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.

Diener C, et al. (2023) Time-resolved RNA signatures of CD4+ T cells in Parkinson's disease. *Cell death discovery*, 9(1), 18.

Hart M, et al. (2023) miR-34a-5p as molecular hub of pathomechanisms in Huntington's disease. *Molecular medicine (Cambridge, Mass.)*, 29(1), 43.

Christofyllakis K, et al. (2023) Vitamin D Enhances Immune Effector Pathways of NK Cells Thus Providing a Mechanistic Explanation for the Increased Effectiveness of Therapeutic Monoclonal Antibodies. *Nutrients*, 15(16).

Prasad K, et al. (2022) The SARS-CoV-2 targeted human RNA binding proteins network biology to investigate COVID-19 associated manifestations. *International journal of biological macromolecules*, 217, 853.