Resource Summary Report

Generated by RRID on Aug 10, 2026

GenAtlas

RRID:SCR_007669
Type: Tool

Proper Citation

GenAtlas (RRID:SCR_007669)

Resource Information

URL: http://www.genatlas.org/

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Description: GENATLAS contains relevant information with respect to gene mapping and genetic diseases. GENATLAS compiles the information relevant to the mapping efforts of the Human Genome Project. This information is collected from more than 48,000 articles in the literature, collected in more than 870 reviews. The articles are daily analyzed by annotators to update the GENATLAS database. Only the objects with a known cytogenetic location are retained. GENATLAS repertories three kinds of objects Genes database (more than 21.000 entries) Phenotypes database (4104 entries , 2000 cloned) References database linked to the two previous (more than 48000 entries)

Synonyms: GenAtlas

Resource Type: data or information resource, database

Keywords: gene mapping, genetic disease, human genome project, FASEB list

Resource Name: GenAtlas

Resource ID: SCR_007669

Alternate IDs: nif-0000-02872

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260811T043313+0000

Ratings and Alerts

No rating or validation information has been found for GenAtlas.

No alerts have been found for GenAtlas.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 34 mentions in open access literature.

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

Zong N, et al. (2022) BETA: a comprehensive benchmark for computational drug-target prediction. Briefings in bioinformatics, 23(4).

Dhaliwal J, et al. (2021) Contribution of Multiple Inherited Variants to Autism Spectrum Disorder (ASD) in a Family with 3 Affected Siblings. Genes, 12(7).

Le-Niculescu H, et al. (2021) Precision medicine for mood disorders: objective assessment, risk prediction, pharmacogenomics, and repurposed drugs. Molecular psychiatry, 26(7), 2776.

Niculescu AB, et al. (2020) Blood biomarkers for memory: toward early detection of risk for Alzheimer disease, pharmacogenomics, and repurposed drugs. Molecular psychiatry, 25(8), 1651.

Gatta V, et al. (2020) Possible Correlation between Cholinergic System Alterations and Neuro/Inflammation in Multiple Sclerosis. Biomedicines, 8(6).

Kour A, et al. (2020) In silico pathway analysis based on chromosomal instability in breast cancer patients. BMC medical genomics, 13(1), 168.

Di Spirito F, et al. (2020) The Association between Periodontitis and Human Colorectal Cancer: Genetic and Pathogenic Linkage. Life (Basel, Switzerland), 10(9).

Rawoof A, et al. (2020) LeukmiR: a database for miRNAs and their targets in acute lymphoblastic leukemia. Database : the journal of biological databases and curation, 2020.

Azevedo PL, et al. (2019) Canonical WNT Signaling Pathway is Altered in Mesenchymal Stromal Cells From Acute Myeloid Leukemia Patients And Is Implicated in BMP4 Down-Regulation. Translational oncology, 12(4), 614.

Alpern D, et al. (2019) BRB-seq: ultra-affordable high-throughput transcriptomics enabled by bulk RNA barcoding and sequencing. Genome biology, 20(1), 71.

Habyarimana T, et al. (2018) CHEK2 Germ Line Mutations are Lacking among Familial and Sporadic Breast Cancer Patients in Rwanda. Asian Pacific journal of cancer prevention : APJCP, 19(2), 375.

Annese A, et al. (2018) Whole transcriptome profiling of Late-Onset Alzheimer's Disease patients provides insights into the molecular changes involved in the disease. Scientific reports, 8(1), 4282.

Yousri NA, et al. (2018) Whole-exome sequencing identifies common and rare variant metabolic QTLs in a Middle Eastern population. Nature communications, 9(1), 333.

Huang R, et al. (2017) Identification and validation of potential prognostic gene biomarkers for predicting survival in patients with acute myeloid leukemia. OncoTargets and therapy, 10, 5243.

Hendrickx DM, et al. (2017) DTNI: a novel toxicogenomics data analysis tool for identifying the molecular mechanisms underlying the adverse effects of toxic compounds. Archives of toxicology, 91(6), 2343.

Hu J, et al. (2016) Comparative transcript profiling of alloplasmic male-sterile lines revealed altered gene expression related to pollen development in rice (Oryza sativa L.). BMC plant biology, 16(1), 175.

Woon ST, et al. (2016) Comprehensive genetic testing for primary immunodeficiency disorders in a tertiary hospital: 10-year experience in Auckland, New Zealand. Allergy, asthma, and clinical immunology : official journal of the Canadian Society of Allergy and Clinical Immunology, 12, 65.

Lardo M, et al. (2015) MDR1/ABCB1 gene polymorphisms in patients with chronic myeloid leukemia. Blood research, 50(3), 154.

Singh HN, et al. (2015) Gene regulation by long purine tracks in brain related diseases. Data in brief, 5, 218.

Lin IH, et al. (2015) Hierarchical clustering of breast cancer methylomes revealed differentially methylated and expressed breast cancer genes. PloS one, 10(2), e0118453.