

Resource Summary Report

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[MyGene.info](#)

RRID:SCR_018660

Type: Tool

Proper Citation

MyGene.info (RRID:SCR_018660)

Resource Information

URL: <https://mygene.info/>

Proper Citation: MyGene.info (RRID:SCR_018660)

Description: Web service for querying or retrieving gene annotation data.

Resource Type: software resource, data access protocol, service resource, web service

Defining Citation: [DOI:10.1186/s13059-016-0953-9](https://doi.org/10.1186/s13059-016-0953-9)

Keywords: Querying gene, gene, annotation, gene annotation, annotation data, gene annotation data, retrieving gene annotation data, bio.tools

Funding: NHGRI U01 HG008473;
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NCI K22 CA188163;
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Scripps Translational Science Institute

Availability: Free, Freely available

Resource Name: MyGene.info

Resource ID: SCR_018660

Alternate IDs: biotools:mygene.info, BioTools:mygene.info

Alternate URLs: <https://bio.tools/mygene.info>, <https://bio.tools/mygene.info>,
<https://bio.tools/mygene.info>

Record Creation Time: 20220129T080341+0000

Record Last Update: 20260801T042836+0000

Ratings and Alerts

No rating or validation information has been found for MyGene.info.

No alerts have been found for MyGene.info.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Stikeleather R, et al. (2025) Translation Accuracy in E. coli. bioRxiv : the preprint server for biology.

Veluri R, et al. (2025) An Integrative Multitiered Computational Analysis for Better Understanding the Structure and Function of 85 Miniproteins. bioRxiv : the preprint server for biology.

Gul L, et al. (2025) Protocol for predicting host-microbe interactions and their downstream effect on host cells using MicrobioLink. STAR protocols, 6(1), 103570.

Anagho-Mattanovich M, et al. (2025) Multi-omics analysis of thermogenic lipolysis in brown adipocytes. iScience, 28(9), 113382.

Wan CY, et al. (2024) IsoVis - a webserver for visualization and annotation of alternative RNA isoforms. Nucleic acids research, 52(W1), W341.

Mancuso CA, et al. (2024) Joint representation of molecular networks from multiple species improves gene classification. PLoS computational biology, 20(1), e1011773.

Rafikova E, et al. (2024) Open Genes-a new comprehensive database of human genes associated with aging and longevity. Nucleic acids research, 52(D1), D950.

Lukauskas S, et al. (2024) Decoding chromatin states by proteomic profiling of nucleosome readers. Nature, 627(8004), 671.

Shahin-Shamsabadi A, et al. (2024) Proteomics and machine learning: Leveraging domain knowledge for feature selection in a skeletal muscle tissue meta-analysis. Heliyon, 10(24), e40772.

Tang W, et al. (2023) Single-Cell Multimodal Prediction via Transformers. ArXiv.

Lagger C, et al. (2023) scDiffCom: a tool for differential analysis of cell-cell interactions provides a mouse atlas of aging changes in intercellular communication. Nature aging, 3(11), 1446.

Salcher S, et al. (2022) High-resolution single-cell atlas reveals diversity and plasticity of tissue-resident neutrophils in non-small cell lung cancer. *Cancer cell*, 40(12), 1503.

Breidenbach JD, et al. (2022) GeneToList: A Web Application to Assist with Gene Identifiers for the Non-Bioinformatics-Savvy Scientist. *Biology*, 11(8).

Terakawa A, et al. (2022) Trans-omics analysis of insulin action reveals a cell growth subnetwork which co-regulates anabolic processes. *iScience*, 25(5), 104231.

Pavel A, et al. (2021) Integrated network analysis reveals new genes suggesting COVID-19 chronic effects and treatment. *Briefings in bioinformatics*, 22(2), 1430.

Waagmeester A, et al. (2021) A protocol for adding knowledge to Wikidata: aligning resources on human coronaviruses. *BMC biology*, 19(1), 12.

Lolansen SD, et al. (2021) Elevated CSF inflammatory markers in patients with idiopathic normal pressure hydrocephalus do not promote NKCC1 hyperactivity in rat choroid plexus. *Fluids and barriers of the CNS*, 18(1), 54.

Veldsman WP, et al. (2021) Comparative genomics of the coconut crab and other decapod crustaceans: exploring the molecular basis of terrestrial adaptation. *BMC genomics*, 22(1), 313.

Buphamalai P, et al. (2021) Network analysis reveals rare disease signatures across multiple levels of biological organization. *Nature communications*, 12(1), 6306.

Qian C, et al. (2020) A recursive framework for predicting the time-course of drug sensitivity. *Scientific reports*, 10(1), 17682.