

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, service resource, web service, data access protocol

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

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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: 20260821T043033+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 34 mentions in open access literature.

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

Sabalic A, et al. (2026) Cell-type resolved transcriptional network analysis of in vivo cellular senescence following injury. PLoS computational biology, 22(6), e1014429.

Jimenez-Gracia L, et al. (2026) Interpretable inflammation landscape of circulating immune cells. Nature medicine, 32(2), 633.

Siddalingappa R, et al. (2026) Precision Medicine Gene Network Analyser: part I-cancer driver gene identification through network topology and ensemble machine learning. Genomics & informatics, 24(1).

Charest J, et al. (2026) HERMES: an open-source mining tool for open-access literature. Bioinformatics advances, 6(1), vbag058.

Mishra A, et al. (2026) A weight-sharing Bayesian neural network for consistent feature selection with applications in cancer gene expression data. BMC bioinformatics, 27(1).

Geis L, et al. (2026) Probing transcription factor subsets in gene regulatory networks. Algorithms for molecular biology : AMB, 21(1).

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

Wang Y, et al. (2025) Pan-cancer single-cell transcriptomic analysis reveals CD83 as a hallmark of tumor-associated neutrophils with senescent and pro-tumor properties. Computational and structural biotechnology journal, 27, 4615.

Hecker D, et al. (2025) Cell type-specific epigenetic regulatory circuitry of coronary artery disease loci. bioRxiv : the preprint server for biology.

Ying K, et al. (2025) Autonomous AI Agents Discover Aging Interventions from Millions of Molecular Profiles. 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.

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*.

Cao Y, et al. (2025) Uncovering hidden factors of cognitive resilience in Alzheimer's disease using a conditional-Gaussian mixture variational autoencoder. *NPJ dementia*, 1.

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.

Rivera ZAA, et al. (2024) Network Pharmacology and Molecular Docking Analysis of Morinda citrifolia Fruit Metabolites Suggest Anxiety Modulation through Glutamatergic Pathways. *Life (Basel, Switzerland)*, 14(9).