

Resource Summary Report

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YuGene

RRID:SCR_006023

Type: Tool

Proper Citation

YuGene (RRID:SCR_006023)

Resource Information

URL: <http://cran.r-project.org/web/packages/YuGene/>

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Description: Software providing a simple method for comparison of gene expression generated across different experiments, and on different platforms; that does not require global renormalization, and is not restricted to comparison of identical probes. YuGene works on a range of microarray dataset distributions, such as between manufacturers. The resulting output allows direct comparisons of gene expression between experiments and experimental platforms.

Synonyms: YuGene: A simple approach to scale gene expression data derived from different platforms for integrated analyses

Resource Type: software resource

Defining Citation: [PMID:24667244](#)

Keywords: standalone software, mac os x, unix/linux, windows, r

Availability: GNU General Public License, v2, v3

Resource Name: YuGene

Resource ID: SCR_006023

Alternate IDs: OMICS_04030

Record Creation Time: 20220129T080233+0000

Record Last Update: 20260905T132545+0000

Ratings and Alerts

No rating or validation information has been found for YuGene.

No alerts have been found for YuGene.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Su Y, et al. (2026) The Sig27 multigene stratifies breast cancer fatality risk via reflecting tumor-associated immune suppressive features. *Translational oncology*, 69, 102820.

Tyshkovskiy A, et al. (2026) Universal transcriptomic hallmarks of mammalian ageing and mortality. *Nature*, 654(8117), 173.

Hernández-Arciga U, et al. (2025) Mutation in IR or IGF1R produces features of long-lived mice while maintaining metabolic health. *JCI insight*, 10(24).

Mitchell W, et al. (2024) The mitochondrial-targeted peptide therapeutic elamipretide improves cardiac and skeletal muscle function during aging without detectable changes in tissue epigenetic or transcriptomic age. *bioRxiv : the preprint server for biology*.

Junet V, et al. (2021) CuBlock: a cross-platform normalization method for gene-expression microarrays. *Bioinformatics (Oxford, England)*, 37(16), 2365.

Hsu YH, et al. (2020) Functional Gene Clusters in Global Pathogenesis of Clear Cell Carcinoma of the Ovary Discovered by Integrated Analysis of Transcriptomes. *International journal of environmental research and public health*, 17(11).

Tajti F, et al. (2020) A Functional Landscape of CKD Entities From Public Transcriptomic Data. *Kidney international reports*, 5(2), 211.

Patel H, et al. (2020) Working Towards a Blood-Derived Gene Expression Biomarker Specific for Alzheimer's Disease. *Journal of Alzheimer's disease : JAD*, 74(2), 545.

Chen J, et al. (2020) Downregulation of the circadian rhythm regulator HLF promotes multiple-organ distant metastases in non-small cell lung cancer through PPAR/NF- κ B signaling. *Cancer letters*, 482, 56.

Chen J, et al. (2020) LINC00173.v1 promotes angiogenesis and progression of lung squamous cell carcinoma by sponging miR-511-5p to regulate VEGFA expression. *Molecular cancer*, 19(1), 98.

Merve A, et al. (2019) c-MYC overexpression induces choroid plexus papillomas through a T-cell mediated inflammatory mechanism. *Acta neuropathologica communications*, 7(1),

Cheng Y, et al. (2019) Identification of candidate diagnostic and prognostic biomarkers for pancreatic carcinoma. *EBioMedicine*, 40, 382.

Zhang X, et al. (2017) Phospholipid Phosphatase 4 promotes proliferation and tumorigenesis, and activates Ca^{2+} -permeable Cationic Channel in lung carcinoma cells. *Molecular cancer*, 16(1), 147.

Hartung F, et al. (2017) A core program of gene expression characterizes cancer metastases. *Oncotarget*, 8(60), 102161.

Rohart F, et al. (2017) MINT: a multivariate integrative method to identify reproducible molecular signatures across independent experiments and platforms. *BMC bioinformatics*, 18(1), 128.

Brinkley JF, et al. (2016) The FaceBase Consortium: a comprehensive resource for craniofacial researchers. *Development (Cambridge, England)*, 143(14), 2677.