

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: 20260801T190303+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 13 mentions in open access literature.

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

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).

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.

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

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.

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-??b signaling. Cancer letters, 482, 56.

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

Merve A, et al. (2019) c-MYC overexpression induces choroid plexus papillomas through a T-cell mediated inflammatory mechanism. Acta neuropathologica communications, 7(1), 95.

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

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.

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.