

Resource Summary Report

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genomics Workbench

RRID:SCR_013599

Type: Tool

Proper Citation

genomics Workbench (RRID:SCR_013599)

Resource Information

URL: <http://www.geworkbench.org>

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Description: geWorkbench (genomics Workbench) is a Java-based open-source platform for integrated genomics. Using a component architecture it allows individually developed plug-ins to be configured into complex bioinformatic applications. At present there are more than 70 available plug-ins supporting the visualization and analysis of gene expression and sequence data. Example use cases include: * loading data from local or remote data sources. * visualizing gene expression, molecular interaction networks, protein sequence and protein structure data in a variety of ways. * providing access to client- and server-side computational analysis tools such as t-test analysis, hierarchical clustering, self organizing maps, regulatory networks reconstruction, BLAST searches, pattern/motif discovery, etc. * validating computational hypothesis through the integration of gene and pathway annotation information from curated sources as well as through Gene Ontology enrichment analysis. geWorkbench is the Bioinformatics platform of MAGNet, the National Center for the Multi-scale Analysis of Genomic and Cellular Networks (one of the 7 National Centers for Biomedical Computing funded through the NIH Roadmap). Additionally, geWorkbench is supported by caBIG, NCI's cancer Biomedical Informatics Grid initiative.

Synonyms: geWorkbench

Resource Type: software application, data analysis software, software resource, data processing software, data visualization software

Funding: NIH ;
caBIG

Resource Name: genomics Workbench

Resource ID: SCR_013599

Alternate IDs: nif-0000-00306

Record Creation Time: 20220129T080317+0000

Record Last Update: 20260729T044334+0000

Ratings and Alerts

No rating or validation information has been found for genomics Workbench.

No alerts have been found for genomics Workbench.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 25 mentions in open access literature.

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

Lee DY, et al. (2023) Cyclosporin A inhibits prostate cancer growth through suppression of E2F8 transcription factor in a MELK-dependent manner. *Oncology reports*, 50(6).

Baßler K, et al. (2023) Identification of the novel FOXP3-dependent Treg cell transcription factor MEOX1 by high-dimensional analysis of human CD4+ T cells. *Frontiers in immunology*, 14, 1107397.

Pillai M, et al. (2021) Systems-level network modeling deciphers the master regulators of phenotypic plasticity and heterogeneity in melanoma. *iScience*, 24(10), 103111.

Lee S, et al. (2021) Transcriptome Analysis of the Anti-TGF- β Effect of Schisandra chinensis Fruit Extract and Schisandrin B in A7r5 Vascular Smooth Muscle Cells. *Life (Basel, Switzerland)*, 11(2).

Guo L, et al. (2020) A Systematic Analysis Revealed the Potential Gene Regulatory Processes of ATRA-Triggered Neuroblastoma Differentiation and Identified a Novel RA Response Sequence in the NTRK2 Gene. *BioMed research international*, 2020, 6734048.

Zamani-Ahmadm Mahmudi M, et al. (2019) Development of a Reproducible Prognostic Gene Signature to Predict the Clinical Outcome in Patients with Diffuse Large B-Cell Lymphoma. *Scientific reports*, 9(1), 12198.

Caja L, et al. (2018) Snail regulates BMP and TGF- β pathways to control the differentiation status of glioma-initiating cells. *Oncogene*, 37(19), 2515.

Jang W, et al. (2017) Mechanical cue-induced YAP instructs Skp2-dependent cell cycle exit and oncogenic signaling. *The EMBO journal*, 36(17), 2510.

Liu K, et al. (2017) DNA repair and replication links to pluripotency and differentiation capacity of pig iPS cells. *PloS one*, 12(3), e0173047.

Zamani-Ahmadmahmudi M, et al. (2017) Prognostic efficacy of the human B-cell lymphoma prognostic genes in predicting disease-free survival (DFS) in the canine counterpart. *BMC veterinary research*, 13(1), 17.

Piccaluga PP, et al. (2016) Virus-encoded microRNA contributes to the molecular profile of EBV-positive Burkitt lymphomas. *Oncotarget*, 7(1), 224.

Qu K, et al. (2016) Integrative genomic analysis by interoperation of bioinformatics tools in GenomeSpace. *Nature methods*, 13(3), 245.

Lee S, et al. (2016) Geraniol suppresses prostate cancer growth through down-regulation of E2F8. *Cancer medicine*, 5(10), 2899.

Yin X, et al. (2016) Insights into the Mechanisms Underlying Ultraviolet-C Induced Resveratrol Metabolism in Grapevine (*V. amurensis* Rupr.) cv. "Tonghua-3". *Frontiers in plant science*, 7, 503.

Yue H, et al. (2016) De novo Assembly and Characterization of the Transcriptome of Broomcorn Millet (*Panicum miliaceum* L.) for Gene Discovery and Marker Development. *Frontiers in plant science*, 7, 1083.

Qiao J, et al. (2015) Filamin C, a dysregulated protein in cancer revealed by label-free quantitative proteomic analyses of human gastric cancer cells. *Oncotarget*, 6(2), 1171.

Yepes S, et al. (2015) Regulatory network reconstruction reveals genes with prognostic value for chronic lymphocytic leukemia. *BMC genomics*, 16, 1002.

Piccaluga PP, et al. (2015) IFI16 Expression Is Related to Selected Transcription Factors during B-Cell Differentiation. *Journal of immunology research*, 2015, 747645.

Zamani-Ahmadmahmudi M, et al. (2015) Reconstruction of canine diffuse large B-cell lymphoma gene regulatory network: detection of functional modules and hub genes. *Journal of comparative pathology*, 152(2-3), 119.

Kim T, et al. (2015) A basal-like breast cancer-specific role for SRF-IL6 in YAP-induced cancer stemness. *Nature communications*, 6, 10186.