

Resource Summary Report

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BIIT - Bioinformatics Algorithmics and Data Mining Group

RRID:SCR_005690

Type: Tool

Proper Citation

BIIT - Bioinformatics Algorithmics and Data Mining Group (RRID:SCR_005690)

Resource Information

URL: <https://biit.cs.ut.ee/>

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Description: The Bioinformatics, Algorithmics, and Data Mining group BIIT lead by prof. Jaak Vilo is a joint research group between the Department of Computer Science (University of Tartu), Quretec, and the Estonian Biocenter. Our main research topics and capabilities include the gene regulation, gene expression data analysis, biological data mining, systems biology, combinatorial pattern matching, developing software for biomedical research databases, as well as partnering in stem cell and cancer related projects. Software * MEM - Multi-Experiment-Matrix -- large-scale gene expression data queries and mining (Genome Biology 2009) * g:Profiler family of tools for functional assessment of gene groups, gene ID mappings, orthology and expression similarity searches. (NAR web server issue 2007) * KEGGanim - visualisation of high-throughput data on biological pathway charts (Bioinformatics, 2007) * GraphWeb - a tool for mining large biological networks (NAR Web server issue 2008) * FunGenES data atlas * More software tools

Abbreviations: BIIT Research group

Synonyms: BIIT - Bioinformatics Algorithmics Data Mining Group, BIIT Group - Institute of Computer Science

Resource Type: data or information resource, department portal, organization portal, portal, software application, software resource, text-mining software

Keywords: gene regulation, gene expression, data analysis, biological, data mining, systems biology, combinatorial pattern matching, software, biomedical research, stem cell, cancer

Resource Name: BIIT - Bioinformatics Algorithmics and Data Mining Group

Resource ID: SCR_005690

Alternate IDs: nlx_149141

Old URLs: <http://biit.cs.ut.ee/about/main>

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260905T132540+0000

Ratings and Alerts

No rating or validation information has been found for BIIT - Bioinformatics Algorithmics and Data Mining Group.

No alerts have been found for BIIT - Bioinformatics Algorithmics and Data Mining Group.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Dcunha R, et al. (2025) Enhanced cell survival in prepubertal testicular tissue cryopreserved with membrane lipids and antioxidants rich cryopreservation medium. Cell and tissue research, 399(1), 97.

Karimi HZ, et al. (2025) Proteasomes accumulate in the plant apoplast where they participate in microbe-associated molecular pattern (MAMP)-triggered pathogen defense. Nature communications, 16(1), 1634.

Gomes-Gonçalves A, et al. (2025) Lactic Acid Influences Iron Assimilation by a Fungal Pathogen via the Iron Reductive Uptake Pathway. MicrobiologyOpen, 14(6), e70167.

Chen KE, et al. (2025) Streamline Protocol for Arabidopsis Apoplastic Fluid Isolation Enables a Detailed Proteomic View of the Plant Extracellular Space. Plant direct, 9(7), e70087.

Masliantsev K, et al. (2025) Hippo pathway effectors are associated with glioma patient survival, control cell proliferation and sterol metabolism through TEAD3. Brain pathology (Zurich, Switzerland), 35(6), e70021.

Zheng X, et al. (2025) Global research landscape and hotspots for ferroptosis in glioma: A comprehensive bibliometric and visual analysis. Heliyon, 11(3), e42242.

Wang J, et al. (2023) Genetic diversity, population structure, and selective signature of sheep in the northeastern Tarim Basin. *Frontiers in genetics*, 14, 1281601.

Xu K, et al. (2022) SLC22A8: An indicator for tumor immune microenvironment and prognosis of ccRCC from a comprehensive analysis of bioinformatics. *Medicine*, 101(37), e30270.

Brito C, et al. (2021) Unraveling the Relevance of ARL GTPases in Cutaneous Melanoma Prognosis through Integrated Bioinformatics Analysis. *International journal of molecular sciences*, 22(17).

Nelson DR, et al. (2021) Large-scale genome sequencing reveals the driving forces of viruses in microalgal evolution. *Cell host & microbe*, 29(2), 250.