

# Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

## 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/>

**Proper Citation:** BIIT - Bioinformatics Algorithmics and Data Mining Group (RRID:SCR\_005690)

**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, text-mining software, portal, software application, software resource, organization portal, department portal

**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:** 20260801T190257+0000

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## 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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 7 mentions in open access literature.

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

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.

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

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.

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.