

Resource Summary Report

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AltAnalyze - Alternative Splicing Analysis Tool

RRID:SCR_002951

Type: Tool

Proper Citation

AltAnalyze - Alternative Splicing Analysis Tool (RRID:SCR_002951)

Resource Information

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

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Description: Software application for microarray, RNA-Seq and metabolomics analysis. For splicing sensitive platforms (RNA-Seq or Affymetrix Exon, Gene and Junction arrays), it will assess alternative exon (known and novel) expression along protein isoforms, domain composition and microRNA targeting. In addition to splicing-sensitive platforms, it provides comprehensive methods for the analysis of other data (RMA summarization, batch-effect removal, QC, statistics, annotation, clustering, network creation, lineage characterization, alternative exon visualization, gene-set enrichment and more). AltAnalyze can be run through an intuitive graphical user interface or command-line and requires no advanced knowledge of bioinformatics programs or scripting. Alternative regulated exons can be subsequently visualized in the context of proteins, domains and microRNA binding sites with the Cytoscape Plugin DomainGraph.

Abbreviations: AltAnalyze

Synonyms: Alternative Splicing Analysis Tool

Resource Type: software resource, software application

Defining Citation: [PMID:20513647](#)

Keywords: analysis, alternative splicing, microarray, calculate, pathway, ontology, domain, microrna, targeting, splicing, microarray, rna-seq, metabolomics, mac osx, windows, ubuntu, cross platform, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: AltAnalyze - Alternative Splicing Analysis Tool

Resource ID: SCR_002951

Alternate IDs: nif-0000-30083, OMICS_02250, biotools:altanalyze

Alternate URLs: <https://bio.tools/altanalyze>

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260801T191034+0000

Ratings and Alerts

No rating or validation information has been found for AltAnalyze - Alternative Splicing Analysis Tool.

No alerts have been found for AltAnalyze - Alternative Splicing Analysis Tool.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 81 mentions in open access literature.

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

Khan I, et al. (2025) Combinatorial therapy regimens targeting preclinical models of melanoma resistant to immune checkpoint blockade. The Journal of clinical investigation, 135(18).

Yu H, et al. (2025) The Clinical and Molecular Characterization of Distinct Subtypes in Adult T Cell Acute Lymphoblastic Leukemia. Cancer science, 116(4), 1126.

Mohamad Pakarulrazy NF, et al. (2025) Gene Expression Analysis of Papillary Thyroid Carcinoma With Lymph Node Metastasis and Radioiodine Refractivity. Cureus, 17(6), e87001.

Damen MS, et al. (2025) A shift in PKM2 oligomeric state instructs adipocyte inflammatory potential. JCI insight, 10(22).

Wu LMN, et al. (2025) Single-cell and Spatial Omics Reveals Region-Specific Plasticity and Therapeutic Vulnerabilities in Metastatic High-Risk Neuroblastoma. bioRxiv : the preprint server for biology.

Stiff A, et al. (2024) Multiomic profiling identifies predictors of survival in African American patients with acute myeloid leukemia. Nature genetics, 56(11), 2434.

Venkatasubramanian M, et al. (2024) Broad de-regulated U2AF1 splicing is prognostic and augments leukemic transformation via protein arginine methyltransferase activation. bioRxiv : the preprint server for biology.

Li G, et al. (2024) Quantifying tumor specificity using Bayesian probabilistic modeling for drug and immunotherapeutic target discovery. *Cell reports methods*, 4(11), 100900.

Rajalingam A, et al. (2023) Identification of Potential Genes and Critical Pathways in Postoperative Recurrence of Crohn's Disease by Machine Learning And WGCNA Network Analysis. *Current genomics*, 24(2), 84.

Luo Z, et al. (2023) Loss of phosphatase CTDNEP1 potentiates aggressive medulloblastoma by triggering MYC amplification and genomic instability. *Nature communications*, 14(1), 762.

Li G, et al. (2023) Quantifying tumor specificity using Bayesian probabilistic modeling for drug target discovery and prioritization. *bioRxiv : the preprint server for biology*.

Santiago JV, et al. (2023) Identification of state-specific proteomic and transcriptomic signatures of microglia-derived extracellular vesicles. *bioRxiv : the preprint server for biology*.

Santiago JV, et al. (2023) Identification of State-Specific Proteomic and Transcriptomic Signatures of Microglia-Derived Extracellular Vesicles. *Molecular & cellular proteomics : MCP*, 22(12), 100678.

Seltzer S, et al. (2023) Investigation of androgen receptor-dependent alternative splicing has identified a unique subtype of lethal prostate cancer. *Asian journal of andrology*, 25(3), 296.

Verweyen EL, et al. (2023) Population-level single-cell genomics reveals conserved gene programs in systemic juvenile idiopathic arthritis. *The Journal of clinical investigation*, 133(22).

Wu LMN, et al. (2022) Single-cell multiomics identifies clinically relevant mesenchymal stem-like cells and key regulators for MPNST malignancy. *Science advances*, 8(44), eabo5442.

Bond J, et al. (2021) A transcriptomic continuum of differentiation arrest identifies myeloid interface acute leukemias with poor prognosis. *Leukemia*, 35(3), 724.

Chlon TM, et al. (2021) Germline DDX41 mutations cause ineffective hematopoiesis and myelodysplasia. *Cell stem cell*, 28(11), 1966.

Young K, et al. (2021) Decline in IGF1 in the bone marrow microenvironment initiates hematopoietic stem cell aging. *Cell stem cell*, 28(8), 1473.

Leach DA, et al. (2021) The antiandrogen enzalutamide downregulates TMPRSS2 and reduces cellular entry of SARS-CoV-2 in human lung cells. *Nature communications*, 12(1), 4068.