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 microarry, 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 enrichement 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 application, software resource

Defining Citation: PMID:20513647

Keywords: analysis, alternative splicing, microarray, calculate, pathway, ontology, domain, microrna, targeting, splicing, microarry, 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: 20260912T200229+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 86 mentions in open access literature.

Listed below are recent publications. The full list is available at SPARC SAWG .

Radke MH, et al. (2026) RBM20 isoform regulation by independent transcription start sites adapts alternative splicing in development and disease. Nature communications, 17(1).

Malysheva V, et al. (2026) High-resolution promoter interaction analysis implicates genes involved in the activation of Type 3 Innate Lymphoid Cells in autoimmune disease risk. bioRxiv : the preprint server for biology.

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.

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

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. Molecular & cellular proteomics : MCP, 22(12), 100678.

Tominaga K, et al. (2023) Tip60/KAT5 Histone Acetyltransferase Is Required for Maintenance and Neurogenesis of Embryonic Neural Stem Cells. International journal of molecular sciences, 24(3).

Chimote AA, et al. (2023) Immune and ionic mechanisms mediating the effect of dexamethasone in severe COVID-19. Frontiers in immunology, 14, 1143350.

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).

Oria M, et al. (2022) Premature Neural Progenitor Cell Differentiation Into Astrocytes in Retinoic Acid-Induced Spina Bifida Rat Model. Frontiers in molecular neuroscience, 15, 888351.