

Resource Summary Report

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Spark

RRID:SCR_006207

Type: Tool

Proper Citation

Spark (RRID:SCR_006207)

Resource Information

URL: <http://sparkinsight.org>

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Description: A clustering and visualization tool that enables the interactive exploration of genome-wide data, with a specialization in epigenomics data. Spark is also available as a service within the Epigenome toolset of the Genboree Workbench. The approach utilizes data clusters as a high-level visual guide and supports interactive inspection of individual regions within each cluster. The cluster view links to gene ontology analysis tools and the detailed region view connects to existing genome browser displays taking advantage of their wealth of annotation and functionality.

Abbreviations: Spark

Synonyms: Sparkinsight

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

Defining Citation: [PMID:22960372](#)

Keywords: epigenomics, genome browser, clustering, visualization, genome, computation, pattern discovery, cluster

Funding: Canadian Institutes of Health Research ;
Michael Smith Foundation for Health Research ;
Natural Sciences and Engineering Research Council of Canada ;
NIDA U01 DA025956;
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NHGRI HG004558

Availability: Available for download without charge. Please cite.

Resource Name: Spark

Resource ID: SCR_006207

Alternate IDs: nlx_151753

Record Creation Time: 20220129T080234+0000

Record Last Update: 20260905T132548+0000

Ratings and Alerts

No rating or validation information has been found for Spark.

No alerts have been found for Spark.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 417 mentions in open access literature.

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

Kamitaki N, et al. (2026) Human and bacterial genetic variation shape oral microbiomes and health. *Nature*, 651(8105), 429.

Bermingham CR, et al. (2026) Impact of bariatric surgery on monthly earnings and employment: a national linked data study in England, 2014-2022. *International journal of obesity* (2005), 50(3), 662.

Peng L, et al. (2026) Effects of the SPARK program on motor skills, physical fitness, and social skills in children and adolescents: a systematic review. *BMC pediatrics*, 26(1).

Kostikas K, et al. (2026) Real-Life Effectiveness of Aclidinium/Formoterol on COPD Control: The REDACT Observational Study. *International journal of chronic obstructive pulmonary disease*, 21, 611733.

Pan X, et al. (2026) An Improved Description of the Small RNA Landscape of the Human Fungal Pathogen *Aspergillus fumigatus*. *Molecular microbiology*, 125(2), 133.

Langenbacher AD, et al. (2026) Rtf1-dependent transcriptional pausing regulates cardiogenesis. *eLife*, 13.

Li Y, et al. (2026) Adding highly variable genes to spatially variable genes can improve cell type clustering performance in spatial transcriptomics data. *Bioinformatics advances*, 6(1), vbaf285.

Zapater LJ, et al. (2026) A transposase-derived gene required for human brain development. *Science advances*, 12(3), eadv7530.

Schrettenbrunner L, et al. (2026) Comprehensive mapping of the 5' and 3' untranslated regions of *Aspergillus fumigatus* reveals diverse mechanisms of mRNA processing including premature transcription termination. *RNA (New York, N.Y.)*, 32(2), 250.

Honcharuk V, et al. (2026) DeepSpaceDB: a spatial transcriptomics atlas for interactive in-depth analysis of tissues and tissue microenvironments. *Nucleic acids research*, 54(D1), D1017.

Natividad Avila M, et al. (2026) Deleterious coding variation associated with autism is shared across ancestries. *Nature medicine*, 32(4), 1519.

Wang Y, et al. (2026) A comparative study of statistical methods for identifying differentially expressed genes in spatial transcriptomics. *PLoS computational biology*, 22(2), e1013956.

Cui T, et al. (2025) SpatialRef: a reference of spatial omics with known spot annotation. *Nucleic acids research*, 53(D1), D1215.

Chen J, et al. (2025) Piwi regulates the usage of alternative transcription start sites in the *Drosophila* ovary. *Nucleic acids research*, 53(1).

Dupuis LL, et al. (2025) Factors Associated With Self-Report Symptom Screening Adherence in Pediatric Cancer Patients. *Cancer medicine*, 14(14), e71053.

Zhang Y, et al. (2025) Cancer therapy resistance from a spatial-omics perspective. *Clinical and translational medicine*, 15(7), e70396.

Tlhajoane M, et al. (2025) Interactive voice response surveys as a method for increasing the representativeness of rural respondents in a mortality mobile phone survey: Findings from Malawi. *Tropical medicine & international health : TM & IH*, 30(9), 937.

Cai Z, et al. (2025) CAD hijacks STING to impair antitumor immunity and radiotherapy efficacy of colorectal cancer. *Cell death & disease*, 16(1), 641.

Catalano Chiu S, et al. (2025) The Unseen Burden: Uncovering Shame and Its Determinants in Parkinson's Disease. *Movement disorders clinical practice*, 12(10), 1551.

Zhou D, et al. (2025) Combined therapy with DR5-targeting antibody-drug conjugate and CDK inhibitors as a strategy for advanced colorectal cancer. *Cell reports. Medicine*, 6(6), 102158.