

Resource Summary Report

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SPP

RRID:SCR_001790

Type: Tool

Proper Citation

SPP (RRID:SCR_001790)

Resource Information

URL: <https://github.com/hms-dbmi/spp>

Proper Citation: SPP (RRID:SCR_001790)

Description: R analysis and processing package for Illumina platform Chip-Seq data.

Synonyms: SPP Package

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

Defining Citation: [DOI:10.1038/nbt.1508](https://doi.org/10.1038/nbt.1508)

Keywords: chip seq data, illumina, r package, bio.tools

Funding: NHGRI U01HG004258;
NIGMS R01GM082798;
NCRR UL1RR024920

Availability: Free, Available for download, Freely available

Resource Name: SPP

Resource ID: SCR_001790

Alternate IDs: OMICS_00425, biotools:spp

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

Old URLs: <https://sites.google.com/a/brown.edu/bioinformatics-in-biomed/spp-r-from-chip-seq>

Record Creation Time: 20220129T080209+0000

Record Last Update: 20260829T182103+0000

Ratings and Alerts

No rating or validation information has been found for SPP.

No alerts have been found for SPP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Qiao X, et al. (2024) Diversifying the anthracycline class of anti-cancer drugs identifies aclarubicin for superior survival of acute myeloid leukemia patients. *Molecular cancer*, 23(1), 120.

Wei H, et al. (2021) Systematic analysis of purified astrocytes after SCI unveils Zeb2os function during astrogliosis. *Cell reports*, 34(5), 108721.

Jing D, et al. (2018) Lymphocyte-Specific Chromatin Accessibility Pre-determines Glucocorticoid Resistance in Acute Lymphoblastic Leukemia. *Cancer cell*, 34(6), 906.

Goldman JA, et al. (2017) Resolving Heart Regeneration by Replacement Histone Profiling. *Developmental cell*, 40(4), 392.

Gaiti F, et al. (2017) Landscape of histone modifications in a sponge reveals the origin of animal cis-regulatory complexity. *eLife*, 6.

Chu HP, et al. (2017) TERRA RNA Antagonizes ATRX and Protects Telomeres. *Cell*, 170(1), 86.

Yu VWC, et al. (2016) Epigenetic Memory Underlies Cell-Autonomous Heterogeneous Behavior of Hematopoietic Stem Cells. *Cell*, 167(5), 1310.

Capurso D, et al. (2016) Discovering hotspots in functional genomic data superposed on 3D chromatin configuration reconstructions. *Nucleic acids research*, 44(5), 2028.

Bonhoure N, et al. (2014) Quantifying ChIP-seq data: a spiking method providing an internal reference for sample-to-sample normalization. *Genome research*, 24(7), 1157.