

Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](#) on Apr 30, 2024

SPP

RRID:SCR_001790

Type: Tool

Proper Citation

SPP (RRID:SCR_001790)

Resource Information

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

Proper Citation: SPP (RRID:SCR_001790)

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

Synonyms: SPP Package

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

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

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

Funding Agency: NHGRI, NIGMS, NCRR

Availability: Open source

Resource Name: SPP

Resource ID: SCR_001790

Alternate IDs: OMICS_00425, biotools:spp

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

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 8 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

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.

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

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

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.