

Resource Summary Report

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ngs.plot

RRID:SCR_011795

Type: Tool

Proper Citation

ngs.plot (RRID:SCR_011795)

Resource Information

URL: <https://code.google.com/p/ngsplot/>

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Description: A software program that allows you to easily visualize your next-generation sequencing (NGS) samples at functional genomic regions.

Abbreviations: ngs.plot

Synonyms: ngsplot, ngsplot - Quick mining and visualization of next-generation sequencing data by integrating genomic databases

Resource Type: software resource

Keywords: bio.tools, FASEB list

Availability: GNU General Public License, v3

Resource Name: ngs.plot

Resource ID: SCR_011795

Alternate IDs: BioTools:ngs.plot, OMICS_00922, biotools:ngs.plot

Alternate URLs: <https://bio.tools/ngs.plot>, <https://bio.tools/ngs.plot>, <https://bio.tools/ngs.plot>

Record Creation Time: 20220129T080306+0000

Record Last Update: 20260808T185959+0000

Ratings and Alerts

No rating or validation information has been found for ngs.plot.

No alerts have been found for ngs.plot.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 45 mentions in open access literature.

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

Choubey P, et al. (2026) Cohesin complex cooperates with PU.1 at super-enhancers to regulate the differentiation and identity of conventional dendritic cells. *Cell reports*, 45(5), 117331.

Kaur H, et al. (2026) Dynamicity of Topoisomerase 1 binding at super-enhancers regulates TLR-responsive gene expression program in macrophages. *Cell reports*, 45(7), 117604.

Zahavi EE, et al. (2025) Repeat-element RNAs integrate a neuronal growth circuit. *Cell*, 188(16), 4350.

Wang L, et al. (2024) T-bet deficiency and Hic1 induction override TGF- β -dependency in the formation of CD103⁺ intestine-resident memory CD8⁺ T cells. *Cell reports*, 43(6), 114258.

Feng D, et al. (2022) Chromatin organizer SATB1 controls the cell identity of CD4⁺ CD8⁺ double-positive thymocytes by regulating the activity of super-enhancers. *Nature communications*, 13(1), 5554.

Kuzin V, et al. (2022) TOP1 CAD-seq: A protocol to map catalytically engaged topoisomerase 1 in human cells. *STAR protocols*, 3(3), 101581.

Furth N, et al. (2022) H3-K27M-mutant nucleosomes interact with MLL1 to shape the glioma epigenetic landscape. *Cell reports*, 39(7), 110836.

Das SK, et al. (2022) MYC assembles and stimulates topoisomerases 1 and 2 in a "toposome". *Molecular cell*, 82(1), 140.

Akhtar J, et al. (2021) m6A RNA methylation regulates promoter- proximal pausing of RNA polymerase II. *Molecular cell*, 81(16), 3356.

Narain A, et al. (2021) Targeted protein degradation reveals a direct role of SPT6 in RNAPII elongation and termination. *Molecular cell*, 81(15), 3110.

Kuehner JN, et al. (2021) 5-hydroxymethylcytosine is dynamically regulated during forebrain organoid development and aberrantly altered in Alzheimer's disease. *Cell*

reports, 35(4), 109042.

Wiegard A, et al. (2021) Topoisomerase 1 activity during mitotic transcription favors the transition from mitosis to G1. *Molecular cell*, 81(24), 5007.

Han S, et al. (2021) Proneural genes define ground-state rules to regulate neurogenic patterning and cortical folding. *Neuron*, 109(18), 2847.

Jillson LK, et al. (2021) MAP3K7 Loss Drives Enhanced Androgen Signaling and Independently Confers Risk of Recurrence in Prostate Cancer with Joint Loss of CHD1. *Molecular cancer research : MCR*, 19(7), 1123.

Marques JG, et al. (2020) NuRD subunit CHD4 regulates super-enhancer accessibility in rhabdomyosarcoma and represents a general tumor dependency. *eLife*, 9.

Shibata S, et al. (2020) Functional interactions between Mi-2? and AP1 complexes control response and recovery from skin barrier disruption. *The Journal of experimental medicine*, 217(3).

Yang F, et al. (2020) DUX-miR-344-ZMYM2-Mediated Activation of MERV LTRs Induces a Totipotent 2C-like State. *Cell stem cell*, 26(2), 234.

Shchuka VM, et al. (2020) The pregnant myometrium is epigenetically activated at contractility-driving gene loci prior to the onset of labor in mice. *PLoS biology*, 18(7), e3000710.

Liu S, et al. (2020) Targeting DNA Methylation Depletes Uterine Leiomyoma Stem Cell-enriched Population by Stimulating Their Differentiation. *Endocrinology*, 161(10).

Akhtar J, et al. (2019) Promoter-proximal pausing mediated by the exon junction complex regulates splicing. *Nature communications*, 10(1), 521.