

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

Funding:

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>

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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 41 mentions in open access literature.

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

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.

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

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

Das SK, et al. (2022) MYC assembles and stimulates topoisomerases 1 and 2 in a "topoisome". 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.

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.

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

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).

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

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.

Qu Z, et al. (2019) Visual Analytics of Genomic and Cancer Data: A Systematic Review. *Cancer informatics*, 18, 1176935119835546.

Payá-Milans M, et al. (2019) Genome-wide analysis of the H3K27me3 epigenome and transcriptome in *Brassica rapa*. *GigaScience*, 8(12).

Lambert JP, et al. (2019) Interactome Rewiring Following Pharmacological Targeting of BET Bromodomains. *Molecular cell*, 73(3), 621.

Valencia AM, et al. (2019) Recurrent SMARCB1 Mutations Reveal a Nucleosome Acidic Patch Interaction Site That Potentiates mSWI/SNF Complex Chromatin Remodeling. *Cell*, 179(6), 1342.