

Resource Summary Report

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BioToolBox

RRID:SCR_015696

Type: Tool

Proper Citation

BioToolBox (RRID:SCR_015696)

Resource Information

URL: <http://search.cpan.org/dist/Bio-ToolBox/lib/Bio/ToolBox.pm>

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Description: Tools for querying and analysis of genomic data. These libraries provide a useful interface for working with bioinformatic data. Many bioinformatic data analysis revolves around working with tables of information, including lists of genomic annotation (genes, promoters, etc.) or defined regions of interest (epigenetic enrichment, transcription factor binding sites, etc.). This library works with these tables and provides a set of common tools for working with them. Opening and saving common tab-delimited text formats Support for BED, GFF, VCF, narrowPeak files Scoring intervals with datasets from microarray and sequencing ChIPSeq, RNASeq, microarray expression Support for Bam, BigWig, BigBed, wig, and USeq data formats Intersection with other known annotation Works with any genomic annotation in GTF, GFF3, and UCSC formats The libraries provide a unified and integrated approach to analyses. In many cases, they provide an abstraction layer over a variety of different specialized BioPerl and related modules. Instead of writing numerous scripts specialized for each data format (wig, bigWig, Bam), one script can now work with any data format.

Resource Type: software library, software resource, software toolkit

Resource Name: BioToolBox

Resource ID: SCR_015696

Record Creation Time: 20220129T080327+0000

Record Last Update: 20260808T190231+0000

Ratings and Alerts

No rating or validation information has been found for BioToolBox.

No alerts have been found for BioToolBox.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Shukla PK, et al. (2023) Structure and functional determinants of Rad6-Bre1 subunits in the histone H2B ubiquitin-conjugating complex. *Nucleic acids research*, 51(5), 2117.

Orstad G, et al. (2022) FoxA1 and FoxA2 control growth and cellular identity in NKX2-1-positive lung adenocarcinoma. *Developmental cell*, 57(15), 1866.

Connell Z, et al. (2022) The interaction between the Spt6-tSH2 domain and Rpb1 affects multiple functions of RNA Polymerase II. *Nucleic acids research*, 50(2), 784.

Wike CL, et al. (2021) Chromatin architecture transitions from zebrafish sperm through early embryogenesis. *Genome research*, 31(6), 981.

Clapier CR, et al. (2020) Cancer-Associated Gain-of-Function Mutations Activate a SWI/SNF-Family Regulatory Hub. *Molecular cell*, 80(4), 712.

Larrimore KE, et al. (2020) Aneuploidy-induced proteotoxic stress can be effectively tolerated without dosage compensation, genetic mutations, or stress responses. *BMC biology*, 18(1), 117.

Parnell EJ, et al. (2020) Ash1 and Tup1 dependent repression of the *Saccharomyces cerevisiae* HO promoter requires activator-dependent nucleosome eviction. *PLoS genetics*, 16(12), e1009133.

Schlichter A, et al. (2020) Specialization of the chromatin remodeler RSC to mobilize partially-unwrapped nucleosomes. *eLife*, 9.

Geoghegan G, et al. (2019) Targeted deletion of Tcf7l2 in adipocytes promotes adipocyte hypertrophy and impaired glucose metabolism. *Molecular metabolism*, 24, 44.

Sharma A, et al. (2019) Common genetic variants associated with Parkinson's disease display widespread signature of epigenetic plasticity. *Scientific reports*, 9(1), 18464.

McLain AT, et al. (2018) The evolution of CpG density and lifespan in conserved primate and mammalian promoters. *Aging*, 10(4), 561.

Sdano MA, et al. (2017) A novel SH2 recognition mechanism recruits Spt6 to the doubly phosphorylated RNA polymerase II linker at sites of transcription. *eLife*, 6.

Brown JK, et al. (2017) Molecular diagnostic development for begomovirus-betasatellite complexes undergoing diversification: A case study. *Virus research*, 241, 29.

Ramakrishnan S, et al. (2016) Counteracting H3K4 methylation modulators Set1 and Jhd2 co-regulate chromatin dynamics and gene transcription. *Nature communications*, 7, 11949.

Bolli MH, et al. (2016) Novel S1P1 receptor agonists - Part 5: From amino-to alkoxy-pyridines. *European journal of medicinal chemistry*, 115, 326.

Parnell TJ, et al. (2015) The chromatin remodelers RSC and ISW1 display functional and chromatin-based promoter antagonism. *eLife*, 4, e06073.

Potok ME, et al. (2013) Reprogramming the maternal zebrafish genome after fertilization to match the paternal methylation pattern. *Cell*, 153(4), 759.