Resource Summary Report

Generated by dkNET on Apr 28, 2025

CLIPZ

RRID:SCR_005755
Type: Tool

Proper Citation

CLIPZ (RRID:SCR_005755)

Resource Information

URL: http://www.clipz.unibas.ch/

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on August 20,2019.Database and analysis environment for experimentally determined binding sites of RNA-binding proteins. It supports the automatic functional annotation of short reads resulting primarily from crosslinking and immunoprecipitation experiments (CLIP) performed with RNA-binding proteins in order to identify the binding sites of these proteins. The functional annotation could be also applied to short reads resulting from other types of experiments such as mRNA-Seq, Digital Gene Expression, small RNA cloning, etc. The platform enables visualization and mining of individual data sets as well as analysis involving multiple experimental data sets. The platform can support collaborative projects involving multiple users and groups of users as well as public and private datasets.

Abbreviations: CLIPZ

Resource Type: service resource, data analysis service, data or information resource, database, production service resource, analysis service resource

Defining Citation: PMID:21087992

Keywords: rna-binding protein, binding site, protein, functional annotation, cross-linking and immunoprecipitation, short read, mrna-seq, digital gene expression, small rna cloning, visualization, mining, analysis, post-transcriptional regulatory element, genome, transcript, bio.tools

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE.

Resource Name: CLIPZ

Resource ID: SCR_005755

Alternate IDs: OMICS_02256, biotools:clipz

Alternate URLs: https://bio.tools/clipz

Record Creation Time: 20220129T080232+0000

Record Last Update: 20250426T055810+0000

Ratings and Alerts

No rating or validation information has been found for CLIPZ.

No alerts have been found for CLIPZ.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 20 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Shema Mugisha C, et al. (2020) Clip for studying protein-RNA interactions that regulate virus replication. Methods (San Diego, Calif.), 183, 84.

Chalertpet K, et al. (2019) Argonaute 4 as an Effector Protein in RNA-Directed DNA Methylation in Human Cells. Frontiers in genetics, 10, 645.

Acosta-Alvear D, et al. (2018) The unfolded protein response and endoplasmic reticulum protein targeting machineries converge on the stress sensor IRE1. eLife, 7.

Bieniasz PD, et al. (2018) CLIP-related methodologies and their application to retrovirology. Retrovirology, 15(1), 35.

Paraskevopoulou MD, et al. (2018) microCLIP super learning framework uncovers functional transcriptome-wide miRNA interactions. Nature communications, 9(1), 3601.

Essig K, et al. (2017) Roquin Suppresses the PI3K-mTOR Signaling Pathway to Inhibit T

Helper Cell Differentiation and Conversion of Treg to Tfr Cells. Immunity, 47(6), 1067.

Dimitrova Y, et al. (2017) TFAP2A is a component of the ZEB1/2 network that regulates TGFB1-induced epithelial to mesenchymal transition. Biology direct, 12(1), 8.

Gumienny R, et al. (2017) High-throughput identification of C/D box snoRNA targets with CLIP and RiboMeth-seq. Nucleic acids research, 45(5), 2341.

Subasic D, et al. (2016) Post-transcriptional control of executioner caspases by RNA-binding proteins. Genes & development, 30(19), 2213.

Gruber AJ, et al. (2016) A comprehensive analysis of 3' end sequencing data sets reveals novel polyadenylation signals and the repressive role of heterogeneous ribonucleoprotein C on cleavage and polyadenylation. Genome research, 26(8), 1145.

Han Y, et al. (2016) Integrating Epigenomics into the Understanding of Biomedical Insight. Bioinformatics and biology insights, 10, 267.

Kanitz A, et al. (2015) Comparative assessment of methods for the computational inference of transcript isoform abundance from RNA-seq data. Genome biology, 16(1), 150.

Cook KB, et al. (2015) High-throughput characterization of protein-RNA interactions. Briefings in functional genomics, 14(1), 74.

Li X, et al. (2014) Finding the target sites of RNA-binding proteins. Wiley interdisciplinary reviews. RNA, 5(1), 111.

Stockinger H, et al. (2014) Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. Nucleic acids research, 42(Web Server issue), W436.

Schönemann L, et al. (2014) Reconstitution of CPSF active in polyadenylation: recognition of the polyadenylation signal by WDR33. Genes & development, 28(21), 2381.

Brümmer A, et al. (2013) Modeling the binding specificity of the RNA-binding protein GLD-1 suggests a function of coding region-located sites in translational repression. RNA (New York, N.Y.), 19(10), 1317.

Hausser J, et al. (2013) Analysis of CDS-located miRNA target sites suggests that they can effectively inhibit translation. Genome research, 23(4), 604.

Martin RC, et al. (2012) Optimal outcomes for liver-dominant metastatic breast cancer with transarterial chemoembolization with drug-eluting beads loaded with doxorubicin. Breast cancer research and treatment, 132(2), 753.

Jaskiewicz L, et al. (2012) Argonaute CLIP--a method to identify in vivo targets of miRNAs. Methods (San Diego, Calif.), 58(2), 106.