

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

PIPE-CLIP

RRID:SCR_005820

Type: Tool

Proper Citation

PIPE-CLIP (RRID:SCR_005820)

Resource Information

URL: <http://pipeclip.qbrc.org/>

Proper Citation: PIPE-CLIP (RRID:SCR_005820)

Description: A Galaxy framework-based online pipeline for reliable analysis of data generated by three types of CLIP-seq protocols: HITS-CLIP, PAR-CLIP and iCLIP. It provides both data processing and statistical analysis to determine candidate cross-linking regions, which are comparable to those regions identified from the original studies or using existing computational tools., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: PIPE-CLIP

Synonyms: PIPE-CLIP: a comprehensive online tool for CLIP-seq data analysis

Resource Type: service resource, production service resource, analysis service resource, data analysis service

Defining Citation: [PMID:24451213](#)

Keywords: clip-seq, python, bioinformatics, r, high-throughput sequencing, rna-binding protein, rna

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: PIPE-CLIP

Resource ID: SCR_005820

Alternate IDs: OMICS_02254

Alternate URLs: <https://github.com/QBRC/PIPE-CLIP>

Record Creation Time: 20220129T080232+0000

Ratings and Alerts

No rating or validation information has been found for PIPE-CLIP.

No alerts have been found for PIPE-CLIP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 10 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Bauriedl S, et al. (2020) The minimal meningococcal ProQ protein has an intrinsic capacity for structure-based global RNA recognition. Nature communications, 11(1), 2823.

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

Sethuraman S, et al. (2018) Computational analysis of ribonomics datasets identifies long non-coding RNA targets of γ -herpesviral miRNAs. Nucleic acids research, 46(16), 8574.

Holmqvist E, et al. (2018) Global Maps of ProQ Binding In Vivo Reveal Target Recognition via RNA Structure and Stability Control at mRNA 3' Ends. Molecular cell, 70(5), 971.

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

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

Dang Y, et al. (2016) Antisense transcription licenses nascent transcripts to mediate transcriptional gene silencing. Genes & development, 30(21), 2417.

Reyes-Herrera PH, et al. (2014) Computational Methods for CLIP-seq Data Processing. Bioinformatics and biology insights, 8, 199.

Chen B, et al. (2014) PIPE-CLIP: a comprehensive online tool for CLIP-seq data analysis. Genome biology, 15(1), R18.

Attar N, et al. (2014) The RBPome: where the brains meet the brawn. Genome biology, 15(1), 402.