

Resource Summary Report

Generated by SPARC SAWG on Aug 9, 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: analysis service resource, data analysis service, production service resource, service resource

Defining Citation: [PMID:24451213](https://pubmed.ncbi.nlm.nih.gov/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 [SPARC SAWG](#) .

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.