

Resource Summary Report

Generated by [kravitz2](#) on Sep 16, 2026

iCount

RRID:SCR_016712

Type: Tool

Proper Citation

iCount (RRID:SCR_016712)

Resource Information

URL: <https://github.com/tomazc/iCount>

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Description: Software Python package for protein-RNA interaction analysis. Used for analysis of protein-RNA interactions with iCLIP sequencing data and RNA maps.

Resource Type: data analysis software, data processing software, software application, software resource

Keywords: protein, RNA, interaction, analysis, iCLIP, sequencing, data, map

Availability: Free, Available for download, Freely available, Tutorial available

Resource Name: iCount

Resource ID: SCR_016712

Alternate URLs: https://icount.readthedocs.io/en/latest/ref_python.html,
<https://hub.docker.com/r/tomazc/icount/>

License: MIT

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260912T195843+0000

Ratings and Alerts

No rating or validation information has been found for iCount.

No alerts have been found for iCount.

Data and Source Information

Usage and Citation Metrics

We found 39 mentions in open access literature.

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

Gajdušková P, et al. (2026) Phosphorylation of SF3B1 by CDK11 orchestrates spliceosome activation via SNIP1-dependent RES complex recruitment. *Nature communications*, 17(1).

Feng H, et al. (2026) Characterization of gRNA-dependent and gRNA-independent off-target binding sites of PspCas13b and RfxCas13d in mammalian cells. *Nucleic acids research*, 54(4).

Alfonso-Gonzalez C, et al. (2025) ELAV mediates circular RNA biogenesis in neurons. *Genes & development*, 39(17-18), 1064.

de Queiroz BR, et al. (2025) Axonal RNA localization is essential for long-term memory. *Nature communications*, 16(1), 2560.

Sáenz-Narciso B, et al. (2025) ZFP36-family RNA-binding proteins in regulatory T cells reinforce immune homeostasis. *Nature communications*, 16(1), 4192.

Monti M, et al. (2024) Interrogation of RNA-protein interaction dynamics in bacterial growth. *Molecular systems biology*, 20(5), 573.

Modic M, et al. (2024) Poised PABP-RNA hubs implement signal-dependent mRNA decay in development. *Nature structural & molecular biology*, 31(9), 1439.

Shi X, et al. (2024) DDX18 coordinates nucleolus phase separation and nuclear organization to control the pluripotency of human embryonic stem cells. *Nature communications*, 15(1), 10803.

Chakrabarti AM, et al. (2023) cliplotr-a comparative visualization and analysis tool for CLIP data. *RNA (New York, N.Y.)*, 29(6), 715.

Balendra R, et al. (2023) Transcriptome-wide RNA binding analysis of C9orf72 poly(PR) dipeptides. *Life science alliance*, 6(9).

Pederiva C, et al. (2023) Control of protein synthesis through mRNA pseudouridylation by dyskerin. *Science advances*, 9(30), eadg1805.

Hipke K, et al. (2023) Loss of TDP-43 causes ectopic endothelial sprouting and migration defects through increased fibronectin, vcam 1 and integrin $\alpha 4 \beta 1$. *Frontiers in cell and developmental biology*, 11, 1169962.

Mas AM, et al. (2023) ORC1 binds to cis-transcribed RNAs for efficient activation of replication origins. *Nature communications*, 14(1), 4447.

Ortega JA, et al. (2023) CLIP-Seq analysis enables the design of protective ribosomal RNA bait oligonucleotides against C9ORF72 ALS/FTD poly-GR pathophysiology. *Science advances*, 9(45), eadf7997.

West C, et al. (2023) nf-core/clipseq - a robust Nextflow pipeline for comprehensive CLIP data analysis. *Wellcome open research*, 8, 286.

Brown AL, et al. (2022) TDP-43 loss and ALS-risk SNPs drive mis-splicing and depletion of UNC13A. *Nature*, 603(7899), 131.

Salerno-Kochan A, et al. (2022) Molecular insights into RNA recognition and gene regulation by the TRIM-NHL protein Mei-P26. *Life science alliance*, 5(8).

D'Angeli V, et al. (2022) Polypyrimidine tract binding protein 1 regulates the activation of mouse CD8 T cells. *European journal of immunology*, 52(7), 1058.

Hallegger M, et al. (2021) TDP-43 condensation properties specify its RNA-binding and regulatory repertoire. *Cell*, 184(18), 4680.

Duchemin A, et al. (2021) DHX15-independent roles for TFIP11 in U6 snRNA modification, U4/U6.U5 tri-snRNP assembly and pre-mRNA splicing fidelity. *Nature communications*, 12(1), 6648.