

Resource Summary Report

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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 processing software, software application, data analysis software, 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

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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 35 mentions in open access literature.

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

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).

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.

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

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

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).

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

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.

Schwich OD, et al. (2021) SRSF3 and SRSF7 modulate 3'UTR length through suppression or activation of proximal polyadenylation sites and regulation of CFIm levels. *Genome biology*, 22(1), 82.

Liu Q, et al. (2021) Repressing Ago2 mRNA translation by Trim71 maintains pluripotency through inhibiting let-7 microRNAs. *eLife*, 10.

Monzón-Casanova E, et al. (2021) Essential requirement for polypyrimidine tract binding proteins 1 and 3 in the maturation and maintenance of mature B cells in mice. *European journal of immunology*, 51(9), 2266.

Gong C, et al. (2021) Sequential inverse dysregulation of the RNA helicases DDX3X and DDX3Y facilitates MYC-driven lymphomagenesis. *Molecular cell*, 81(19), 4059.