

Resource Summary Report

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LABRAT

RRID:SCR_025006

Type: Tool

Proper Citation

LABRAT (RRID:SCR_025006)

Resource Information

URL: <https://github.com/TaliaferroLab/LABRAT>

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Description: Software application to quantify usage of alternative polyadenylation and cleavage sites in RNAseq data and identify genes whose usage of these sites varies across experimental conditions.

Synonyms: Lightweight Alignment Based Resolution of Alternative Three prime ends

Resource Type: software application, software resource, source code

Defining Citation: [DOI:10.1186/s12864-021-07781-1](https://doi.org/10.1186/s12864-021-07781-1)

Keywords: quantify usage, alternative polyadenylation, cleavage sites, RNAseq data, identify genes,

Funding: NIGMS R35 GM118051;
NIGMS R35 GM133885;
NIGMS T32 GM008730;
RNA Bioscience Initiative at the University of Colorado Anschutz Medical Campus

Availability: Free, Available for download, Freely available

Resource Name: LABRAT

Resource ID: SCR_025006

License: MIT license

Record Creation Time: 20240214T050222+0000

Record Last Update: 20260821T194303+0000

Ratings and Alerts

No rating or validation information has been found for LABRAT.

No alerts have been found for LABRAT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Wong CH, et al. (2024) Genome-scale requirements for dynein-based transport revealed by a high-content arrayed CRISPR screen. The Journal of cell biology, 223(5).