

Resource Summary Report

Generated by [ASWG](#) on Aug 4, 2026

IDR

RRID:SCR_017237

Type: Tool

Proper Citation

IDR (RRID:SCR_017237)

Resource Information

URL: <https://github.com/nboley/idr>

Proper Citation: IDR (RRID:SCR_017237)

Description: Software R package to measure reproducibility of findings identified from replicate experiments and to provide highly stable thresholds based on reproducibility.

Synonyms: Irreproducible Discovery Rate

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

Defining Citation: [DOI:10.1214/11-AOAS466](https://doi.org/10.1214/11-AOAS466)

Keywords: measure, reproducibility, finding, identified, replicate, irreproducible, discovery, rate

Availability: Free, Available for download, Freely available

Resource Name: IDR

Resource ID: SCR_017237

Alternate URLs: <https://CRAN.R-project.org/package=idr>

License: GPL v3

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260804T043649+0000

Ratings and Alerts

No rating or validation information has been found for IDR.

No alerts have been found for IDR.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 55 mentions in open access literature.

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

Kerstens M, et al. (2026) PLETHORAs shape Arabidopsis phyllotaxis through modulation of patterning robustness and accelerated inflorescence development. *The New phytologist*, 249(1), 495.

Yeki S, et al. (2026) Sex-Specific doublesex Regulation Targeting the Color-Patterning Gene h Underlies the Evolution of Wing Sexual Dimorphism in the Harlequin Ladybug *Harmonia axyridis*. *Evolution & development*, 28(1), e70028.

Liu N, et al. (2025) Comprehensive co-expression network reveals the fine-tuning of ASHSFA2c in balancing drought tolerance and growth in oat. *Communications biology*, 8(1), 393.

Vasseur L, et al. (2025) Derepression of the epithelial transcription factor GRHL2 promotes direct hepatocyte-to-cholangiocyte transdifferentiation. *PLoS biology*, 23(12), e3003547.

Qu X, et al. (2025) Charting the regulatory landscape of TP53 on transposable elements in cancer. *Genome research*, 35(6), 1456.

Tallan A, et al. (2025) Highly quantitative measurement of differential protein-genome binding with PerCell chromatin sequencing. *Cell reports methods*, 5(6), 101052.

Tobias IC, et al. (2025) A Sox2 enhancer cluster regulates region-specific neural fates from mouse embryonic stem cells. *G3 (Bethesda, Md.)*, 15(4).

Dalal K, et al. (2025) Interpreting regulatory mechanisms of Hippo signaling through a deep learning sequence model. *Cell genomics*, 5(4), 100821.

Tingvall-Gustafsson J, et al. (2025) Chromatin interaction-based annotation of regulatory elements reveals dynamic promoter-enhancer interactions in lymphocyte development. *iScience*, 28(7), 112855.

Courret C, et al. (2024) Turnover of retroelements and satellite DNA drives centromere reorganization over short evolutionary timescales in *Drosophila*. *PLoS biology*, 22(11), e3002911.

Kosiński JG, et al. (2024) Characterization of bacterial intrinsic transcription terminators identified with TERMITE - a novel method for comprehensive analysis of Term-seq data. *bioRxiv : the preprint server for biology*.

Holub AS, et al. (2024) START domains generate paralog-specific regulons from a single network architecture. *Nature communications*, 15(1), 9861.

Papadopoulos D, et al. (2024) The MYCN oncoprotein is an RNA-binding accessory factor of the nuclear exosome targeting complex. *Molecular cell*, 84(11), 2070.

Kaplan SJ, et al. (2024) CRISPR screening uncovers a long-range enhancer for ONECUT1 in pancreatic differentiation and links a diabetes risk variant. *Cell reports*, 43(8), 114640.

Wang R, et al. (2023) Multiomic analysis of cohesin reveals that ZBTB transcription factors contribute to chromatin interactions. *Nucleic acids research*, 51(13), 6784.

Traunmüller L, et al. (2023) A cell-type-specific alternative splicing regulator shapes synapse properties in a trans-synaptic manner. *Cell reports*, 42(3), 112173.

Garske KM, et al. (2023) Increased body mass index is linked to systemic inflammation through altered chromatin co-accessibility in human preadipocytes. *Nature communications*, 14(1), 4214.

Cheng J, et al. (2023) Dynamic chromatin architectures provide insights into the genetics of cattle myogenesis. *Journal of animal science and biotechnology*, 14(1), 59.

Loganathan R, et al. (2022) Ribbon boosts ribosomal protein gene expression to coordinate organ form and function. *The Journal of cell biology*, 221(4).

Turner DJ, et al. (2022) A functional screen of RNA binding proteins identifies genes that promote or limit the accumulation of CD138+ plasma cells. *eLife*, 11.