

Resource Summary Report

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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 analytics software, data processing software, software application, software resource

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: 20260905T133052+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 67 mentions in open access literature.

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

Cai Y, et al. (2026) EIF5A Couples Translational Control With Transcriptional Reprogramming Through Chromocenter Reorganization During Spermiogenesis. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(9), e17423.

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.

Kerstens M, et al. (2026) A PLETHORA3/7 transcription factor shapes cucumber shoot architecture. *The New phytologist*, 250(1), 230.

Di Bartolomei G, et al. (2026) Dilated cardiomyopathy-associated RNA-binding motif protein 20 regulates long pre-mRNAs in neurons. *eLife*, 14.

Abdelfattah N, et al. (2026) Male-biased Yap1-Cd276/B7-H3 axis for immune evasion in medulloblastoma. *Cancer cell*, 44(4), 760.

Vuong TT, et al. (2026) DNA Methyltransferase Inhibition Prevents Platinum-Induced Ovarian Cancer Stem Cell Enrichment. *Cancer research communications*, 6(7), 1721.

Kosiński JG, et al. (2025) Characterization of bacterial intrinsic transcription terminators identified with TERMITE-a novel method for comprehensive analysis of Term-seq data. *Nucleic acids research*, 53(12).

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

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.

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.

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

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

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*.

Chang Y, et al. (2024) Drought-responsive dynamics of H3K9ac-marked 3D chromatin interactions are integrated by OsbZIP23-associated super-enhancer-like promoter regions in rice. *Genome biology*, 25(1), 262.

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.