

Resource Summary Report

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GeneOverlap

RRID:SCR_018419

Type: Tool

Proper Citation

GeneOverlap (RRID:SCR_018419)

Resource Information

URL: <https://rdr.io/bioc/GeneOverlap/man/GeneOverlap.html>

Proper Citation: GeneOverlap (RRID:SCR_018419)

Description: Software package to test and visualize gene overlaps. Given two gene lists, tests significance of their overlap in comparison with genomic background.

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

Keywords: Test gene overlap, visualize gene overlap, gene list, overlap significance test, comparison with genomic background

Availability: Free, Available for download, Freely available

Resource Name: GeneOverlap

Resource ID: SCR_018419

License: GPL-3

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260728T043545+0000

Ratings and Alerts

No rating or validation information has been found for GeneOverlap.

No alerts have been found for GeneOverlap.

Data and Source Information

Usage and Citation Metrics

We found 260 mentions in open access literature.

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

Sun J, et al. (2025) An integrated framework for functional dissection of variable expressivity in genetic disorders. medRxiv : the preprint server for health sciences.

Pelletier JM, et al. (2025) Dissecting the cellular architecture and genetic circuitry of the soybean seed. Proceedings of the National Academy of Sciences of the United States of America, 122(1), e2416987121.

Takao S, et al. (2025) Epigenetic mechanisms controlling human leukemia stem cells and therapy resistance. Nature communications, 16(1), 3196.

Alaiz-Noya M, et al. (2025) Neuronal type-specific modulation of cognition and AP-1 signaling by early-life rearing conditions. Nature communications, 16(1), 9710.

Nayak PK, et al. (2025) Transcriptome profiling of tendon fibroblasts at the onset of embryonic muscle contraction reveals novel force-responsive genes. eLife, 14.

Raun N, et al. (2025) Trithorax regulates long-term memory in Drosophila through epigenetic maintenance of mushroom body metabolic state and translation capacity. PLoS biology, 23(1), e3003004.

Saxe R, et al. (2025) Hierarchical Lineage Tracing Reveals Diverse Pathways of AML Treatment Resistance. bioRxiv : the preprint server for biology.

Lai KO, et al. (2025) Age-Dependent Regulation of Hippocampal Inflammation by the Mitochondrial Translocator Protein in Mice. Aging cell, 24(6), e70039.

Huang J, et al. (2025) Model-to-crop conserved NUE Regulons enhance machine learning predictions of nitrogen use efficiency. The Plant cell, 37(5).

Butler MLMD, et al. (2025) Repeated head trauma causes neuron loss and inflammation in young athletes. Nature, 647(8088), 228.

Galvan B, et al. (2025) Subversion of mRNA degradation pathways by EWSR1::FLI1 represents a therapeutic vulnerability in Ewing sarcoma. Nature communications, 16(1), 6537.

He X, et al. (2025) The single-cell atlas of short-chain fatty acid receptors in human and mice hearts. Frontiers in immunology, 16, 1538384.

Gehlhausen JR, et al. (2025) Cutaneous Lupus Features Specialized Stromal Niches and Altered Retroelement Expression. The Journal of investigative dermatology, 145(12), 3011.

Rickle A, et al. (2025) More than meets the eye: mutation of the white gene in *Drosophila* has broad phenotypic and transcriptomic effects. *Genetics*, 230(3).

Marianski K, et al. (2025) Whole-exome sequencing in children with dyslexia implicates rare variants in *CLDN3* and ion channel genes. *Human genetics*, 145(1), 2.

Alsema AM, et al. (2025) Schizophrenia-associated changes in neuronal subpopulations in the human midbrain. *Brain : a journal of neurology*, 148(4), 1374.

Berezovsky A, et al. (2025) Impact of developmental state, p53 status, and interferon signaling on glioblastoma cell response to radiation and temozolomide treatment. *PloS one*, 20(2), e0315171.

Guo Y, et al. (2025) snCED-seq: high-fidelity cryogenic enzymatic dissociation of nuclei for single-nucleus RNA-seq of FFPE tissues. *Nature communications*, 16(1), 4101.

de Silva K, et al. (2025) Shining light on *Arabidopsis* regulatory networks integrating nitrogen use and photosynthesis. *The Plant journal : for cell and molecular biology*, 122(3), e70211.

Ueda Y, et al. (2025) Comparative Transcriptome Reveals ART1-Dependent Regulatory Pathways for Fe Toxicity Response in Rice Roots. *Physiologia plantarum*, 177(4), e70398.