

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

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: 20260829T182545+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 294 mentions in open access literature.

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

Furukawa T, et al. (2026) Patient-derived orthotopic xenograft models recapitulate the peritoneal dissemination of pancreatic cancer and delineate its transcriptional and regulatory programs. *Journal of experimental & clinical cancer research* : CR, 45(1).

Müller F, et al. (2026) CITED2 is a druggable epigenetic switch coupling neuronal maturation to regenerative decline. *EMBO molecular medicine*, 18(4), 1174.

Ko DK, et al. (2026) A tissue-resolved, network-based transcriptomic framework for abiotic stress responses in sorghum. *The Plant journal : for cell and molecular biology*, 126(1), e70834.

Fitzgerald E, et al. (2026) Astrocyte fatty acid metabolism as a driver of risk for major depressive disorder. *Nature communications*, 17(1).

Chopra A, et al. (2026) The epitranscriptomic m6A RNA modification modulates the synapse in ageing and in a mouse model of synucleinopathy. *NPJ Parkinson's disease*, 12(1).

Taslim C, et al. (2026) RNA-SeqEZPZ: a point-and-click pipeline for comprehensive transcriptomics analysis with interactive visualizations. *GigaScience*, 15.

Jin M, et al. (2026) Chimeric brain models to study human glial-neuronal and macroglial-microglial interactions. *Cell reports*, 45(1), 116794.

Verdin E, et al. (2026) CD38 Inhibition Ameliorates Age-Related Cognitive Decline via a Choroid Plexus-Cerebrospinal Fluid-Hippocampus Axis. *Research square*.

Michael Deans PJ, et al. (2026) Functional implications of polygenic risk for schizophrenia in human neurons. *Nature communications*, 17(1), 1355.

Khouri-Farah N, et al. (2026) Gene expression dynamics of human and mouse craniofacial development at the single-cell level. *Nature communications*, 17(1).

Morlion A, et al. (2026) Patient-specific alterations in blood plasma cfRNA profiles enable accurate classification of cancer patients and controls. *Communications medicine*, 6(1).

Hughes JB, et al. (2026) DNA damage drives a unique, Alzheimer's disease-relevant senescent state in neurons. *bioRxiv : the preprint server for biology*.

O'Chan JC, et al. (2026) Dopamine drives persistent remodelling of the maternal brain. *Nature*, 654(8118), 465.

Singh PN, et al. (2026) Multiomic analyses delineate human neuroendocrine tumor cell states in relation to normal enteroendocrine cell ontogeny. *The Journal of clinical investigation*, 136(13).

Liu H, et al. (2026) C9orf72 hexanucleotide repeat RNA drives transcriptional dysregulation through genome-wide DNA:RNA hybrid G-quadruplexes. *Neuron*, 114(6), 1045.

Doser RL, et al. (2026) Mitochondrial double-stranded RNA accumulation in brain aging and Alzheimer's disease. *bioRxiv : the preprint server for biology*.

Wong JP, et al. (2026) NF- κ B and STAT3 signaling uniquely stratify survival in female glioblastoma patients. *iScience*, 29(2), 114761.

Laroche VT, et al. (2026) Epigenomic subtypes of late-onset Alzheimer's disease reveal distinct microglial signatures. *Acta neuropathologica*, 151(1).

Sichlinger L, et al. (2026) Schizophrenia risk gene ZNF804A controls ribosome localization and synaptogenesis in developing human neurons. *Science advances*, 12(21), eaea0755.

Liu M, et al. (2026) Differential physiological responses and transcriptome co-expression networks of salt-tolerant and salt-sensitive foxtail millet (*Setaria italica* (L.)) under salt stress. *Frontiers in plant science*, 17, 1772695.