

Resource Summary Report

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NOISeq

RRID:SCR_003002

Type: Tool

Proper Citation

NOISeq (RRID:SCR_003002)

Resource Information

URL: <http://bioinfo.cipf.es/noiseq/doku.php?id=start>

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Description: Software used for the identification of differentially expressed genes from count data or previously normalized count data. It empirically models the noise distribution of count changes by contrasting fold-change differences (M) and absolute expression differences (D) for all the features in samples within the same condition. This reference distribution is then used to assess whether the M-D values computed between two conditions for a given gene is likely to be part of the noise or represent a true differential expression.

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

Defining Citation: [DOI:10.1101/gr.124321.111](https://doi.org/10.1101/gr.124321.111)

Keywords: differentially expressed genes, gene identification

Availability: Available for download, Acknowledgement requested

Resource Name: NOISeq

Resource ID: SCR_003002

Alternate IDs: OMICS_01311

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260808T185749+0000

Ratings and Alerts

No rating or validation information has been found for NOISeq.

No alerts have been found for NOISeq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 695 mentions in open access literature.

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

Teperino R, et al. (2026) Liver-derived Indian hedgehog (Ihh) couples fast-feed transition to thermogenic and metabolic homeostasis. *Molecular metabolism*, 106, 102339.

Joseph J, et al. (2026) Beyond dormancy: organ-specific gene regulatory networks control winter development in peach buds. *Horticulture research*, 13(2), uhaf310.

Wang K, et al. (2026) Single-nucleus multiomic profiling of the aging mouse substantia nigra reveals conserved gene alterations linked to Parkinson's disease. *Genome research*, 36(4), 849.

Singh M, et al. (2026) Endogenous retroviral elements LTR8B and MER65 rewire PSG9 regulation to control trophoblast syncytialization and pre-eclampsia risk. *Genome biology*, 27(1).

Broad S, et al. (2026) Molecular characterisation of human penile carcinoma and generation of paired epithelial primary cell lines. *Molecular oncology*, 20(2), 260.

Fagbohun OF, et al. (2026) Berry-derived gold nanoparticles induce integrated ROS-mediated apoptosis, immune modulation, and transcriptomic remodeling in 4T1 triple-negative cancer cells. *Cell death discovery*, 12(1).

Maxwell CB, et al. (2026) Harnessing New Tools for Old Challenges: Optimising Neat Plasma Proteomics with Automation and Gas-Phase Fractionation. *ACS measurement science au*, 6(1), 224.

García-Cortés D, et al. (2026) Loss of long-range co-expression is a common feature in cancer. *NPJ systems biology and applications*, 12(1).

Xiang S, et al. (2026) A pH-responsive double network hydrogel for control of tomato bacterial wilt. *Nature communications*, 17(1).

Vitale D, et al. (2026) Bile acids mediate liver-bone marrow crosstalk. *iScience*, 29(7), 116462.

Hossain M, et al. (2026) ChromAcS: an automated and flexible GUI for end-to-end reproducible ATAC-seq analysis across multiple species. *BMC bioinformatics*, 27(1).

Ceballos EG, et al. (2026) Organization of neuropeptide systems in the human brain. *Nature neuroscience*, 29(5), 1212.

Giaccari C, et al. (2026) Loss of maternal PADI6 disrupts DNA methylation and genomic imprinting maintenance in late preimplantation mouse embryos. *Epigenetics & chromatin*, 19(1).

Shastry A, et al. (2026) Confidence: a web app for cross-platform differential gene expression analysis, gene scoring, and enrichment analysis. *Scientific reports*, 16(1).

Zhang X, et al. (2026) The mechanism of dynamic equilibrium of ascorbate redox status mediated by PbrDHAR5 during scald development in pear fruit. *Molecular horticulture*, 6(1).

Córdoba-Caballero J, et al. (2026) An integrative approach to identify novel miRNA-mRNA interaction networks in LMNA-cardiomyopathy. *Scientific reports*, 16(1), 6110.

Martínez-Rodríguez P, et al. (2026) A functional betalain-producing dioxygenase in *Neolecta irregularis* reveals an expanded evolutionary origin of the pathway. *IMA fungus*, 17, e184549.

Cañas-Duarte SJ, et al. (2026) An integrative multi-omics approach points to membrane composition as a key factor in *E. coli* persistence. *PloS one*, 21(6), e0351161.

Hao LK, et al. (2026) Dual role of benzoxazinoids in plant response to combined drought stress and aphid feeding. *Plant biology (Stuttgart, Germany)*, 28(1), 45.

Wilson LS, et al. (2026) Enhancing validation of case-control omics signatures through "minimalist" single-subject analysis (N-of-1 trials): proof of concept in sepsis. *Journal of the American Medical Informatics Association : JAMIA*, 33(7), 1293.