

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

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: 20260919T195014+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 [PRECISE-TBI](#) .

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).

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

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

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.

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

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).

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).

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).

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

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

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.