

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: software resource, data processing software, sequence analysis software, software application, data analysis 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: 20260803T040331+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 668 mentions in open access literature.

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

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.

Sørhus E, et al. (2025) Transcriptomics uncover inhibition of repair and wound healing pathways in Atlantic halibut (*Hippoglossus hippoglossus*) after crude oil exposure. *Ecotoxicology and environmental safety*, 296, 118151.

Hu F, et al. (2025) The systemic wrinkled skin phenotype involves aberrant expression and variation of genes related to the oxidative stress and extracellular matrix in Xiang pigs. *BMC genomics*, 26(1), 1034.

Zhu S, et al. (2025) Fine-tuning of Wnt signaling by RNA surveillance factor Smg5 in the mouse craniofacial development. *iScience*, 28(3), 111972.

Wu K, et al. (2025) Continuous cell lines derived from the Asian citrus psyllid, *Diaphorina citri*, harbor viruses and *Wolbachia*. *Scientific reports*, 15(1), 124.

Rudraprasad D, et al. (2025) RNA-Sequencing Reveals the Modulation of the NLRP3 Inflammasome by miR-223-3p in Extracellular Vesicles in Bacterial Endophthalmitis. *Investigative ophthalmology & visual science*, 66(4), 53.

Fu H, et al. (2025) WIPF1 regulates stemness in small cell lung cancer. *Science progress*, 108(2), 368504251345012.

D'Amélio F, et al. (2025) Comprehensive RNA-Seq Analysis of Human Osteoclast Function in Response to *Bothrops moojeni* Venom Fractions: Pathways of Bone Resorption and Cytoskeletal Disruption. *Toxins*, 17(7).

Yheskel M, et al. (2025) Local chromatin context informs transcriptional outcomes for the histone demethylase KDM5. *Epigenetics & chromatin*, 18(1), 78.

Salatino R, et al. (2025) Cell sorting based on single nucleotide variation enables characterization of mutation-dependent transcriptome and chromatin states. *Nucleic acids research*, 53(15).

van Wilpe S, et al. (2025) Multimodal integration of blood RNA and ctDNA reflects response to immunotherapy in metastatic urothelial cancer. *JCI insight*, 10(5).

Krishnakumar H, et al. (2025) Transcriptomic profiling to investigate the therapeutic potential and medicinal properties of *Momordica cymbalaria*. *Scientific reports*, 15(1), 33882.

Ellert-Miklaszewska A, et al. (2025) 7aaRGD - a novel SPP1/integrin signaling-blocking peptide reverses immunosuppression and improves anti-PD-1 immunotherapy outcomes in experimental gliomas. *Journal of experimental & clinical cancer research : CR*, 44(1), 132.

Sierra J, et al. (2025) Apocarotenoid signaling regulates meristem activity and shapes shoot and root lateral organ formation in *Arabidopsis*. *Plant physiology*, 199(2).

Picciani N, et al. (2025) Comparative Analysis of Convergent Jellyfish Eyes Reveals Extensive Differences in Expression of Vision-Related Genes. *Ecology and evolution*, 15(7), e71784.

Pouya HSH, et al. (2025) Insights into TtCIPK gene family and its roles in durum wheat in response to PEG and ABA treatments. *Scientific reports*, 15(1), 25419.

Hernández-Eligio A, et al. (2025) The role of CsrA in controls the extracellular electron transfer and biofilm production in *Geobacter sulfurreducens*. *Frontiers in microbiology*, 16, 1534446.

Johnstone ME, et al. (2025) DEK promotes mammary hyperplasia and is associated with H3K27me3 epigenetic modifications. *Life science alliance*, 8(9).

Draper BJ, et al. (2025) Selecting differential splicing methods: Practical considerations for short-read RNA sequencing. *F1000Research*, 14, 47.

Feng Y, et al. (2025) Preventive regulation of cellular heat stress injury by mung bean polyphenols revealed by multi-omics analysis. *NPJ science of food*, 9(1), 163.