Resource Summary Report

Generated by NIF on May 7, 2025

FIDEA

RRID:SCR_004187
Type: Tool

Proper Citation

FIDEA (RRID:SCR_004187)

Resource Information

URL: http://www.biocomputing.it/fidea/

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Description: A web server for the functional interpretation of differential expression analysis. It can: * Calculate overrepresentation statistics using KEGG, Interpro, Gene Ontology Molecular Function, Gene Ontology Biological Process, Gene Ontology Cellular Component and GoSlim classifications; * Analyze down-regulated and up-regulated DE genes separately or together as a single set; * Provide interactive graphs and tables that can be modified on the fly according to user defined parameters; the user can set a fold change filter and interactively see the effects on the gene set under examination; * Output publication-ready plot of the graph; * Compare the results of several experiments in any combination.

Abbreviations: FIDEA

Synonyms: Functional Interpretation of Differential Expression Analysis

Resource Type: production service resource, service resource, analysis service resource, data analysis service

Defining Citation: PMID:23754850

Funding:

Availability: Public, Free, Acknowledgement requested

Resource Name: FIDEA

Resource ID: SCR_004187

Alternate IDs: OMICS_01539

Record Creation Time: 20220129T080223+0000

Record Last Update: 20250507T060222+0000

Ratings and Alerts

No rating or validation information has been found for FIDEA.

No alerts have been found for FIDEA.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Bendek MF, et al. (2023) Inverse Modulation of Aurora Kinase A and Topoisomerase II? in Normal and Tumor Breast Cells upon Knockdown of Mitochondrial ASncmtRNA. Non-coding RNA, 9(5).

Grimaldi A, et al. (2019) Microglia-Derived Microvesicles Affect Microglia Phenotype in Glioma. Frontiers in cellular neuroscience, 13, 41.

Ballarino M, et al. (2018) Deficiency in the nuclear long noncoding RNA Charme causes myogenic defects and heart remodeling in mice. The EMBO journal, 37(18).

Grassi L, et al. (2018) Dynamics of Transcription Regulation in Human Bone Marrow Myeloid Differentiation to Mature Blood Neutrophils. Cell reports, 24(10), 2784.

Fiscon G, et al. (2018) SWIM tool application to expression data of glioblastoma stem-like cell lines, corresponding primary tumors and conventional glioma cell lines. BMC bioinformatics, 19(Suppl 15), 436.

Petersen R, et al. (2017) Platelet function is modified by common sequence variation in megakaryocyte super enhancers. Nature communications, 8, 16058.

Guerrieri F, et al. (2017) Genome-wide identification of direct HBx genomic targets. BMC genomics, 18(1), 184.

Yan H, et al. (2016) Regulated Inflammation and Lipid Metabolism in Colon mRNA

Expressions of Obese Germfree Mice Responding to Enterobacter cloacae B29 Combined with the High Fat Diet. Frontiers in microbiology, 7, 1786.

Cunningham CR, et al. (2016) Type I and Type II Interferon Coordinately Regulate Suppressive Dendritic Cell Fate and Function during Viral Persistence. PLoS pathogens, 12(1), e1005356.