Resource Summary Report

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Babelomics

RRID:SCR_002969
Type: Tool

Proper Citation

Babelomics (RRID:SCR_002969)

Resource Information

URL: http://babelomics.bioinfo.cipf.es

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Description: An integrative platform for the analysis of transcriptomics, proteomics and genomic data with advanced functional profiling. Version 4 of Babelomics integrates primary (normalization, calls, etc.) and secondary (signatures, predictors, associations, TDTs, clustering, etc.) analysis tools within an environment that allows relating genomic data and/or interpreting them by means of different functional enrichment or gene set methods. Such interpretation is made not only using functional definitions (GO, KEGG, Biocarta, etc.) but also regulatory information (from Transfac, Jaspar, etc.) and other levels of regulation such as miRNA-mediated interference, protein-protein interactions, text-mining module definitions and the possibility of producing de novo annotations through the Blast2GO system . Babelomics has been extensively re-engineered and now it includes the use of web services and Web 2.0 technology features, a new user interface with persistent sessions and a new extended database of gene identifiers. In this release GEPAS and Babelomics have integrated into a unique web application with many new features and improvements: * Data input: import and quality control for the most common microarray formats * Normalization and base calling: for the most common expression, tiling and SNP microarrays (Affymetrix and Agilent). * Transcriptomics: diverse analysis options that include well established as well as novel algorithms for normalization, gene selection, class prediction, clustering and time-series analysis. * Genotyping: stratification analysis, association, TDT. * Functional profiling: functional enrichment and gene set enrichment analysis with functional terms (GO, KEGG, Biocarta, etc.), regulatory (Transfac, Jaspar, miRNAs, etc.), text-mining, derived bioentities, protein-protein interaction analysis. * Integrative analysis: Different variables can be related to each other (e.g. gene expression to gnomic copy number) and the results subjected to functional analysis. Platform: Online tool

Abbreviations: Babelomics

Synonyms: Babelomics 4: Gene Expression and Functional Profiling Analysis Suite, Babelomics 4

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

Defining Citation: PMID:20478823, PMID:18515841, PMID:16845052, PMID:14990455, PMID:15980512, PMID:17478504

Keywords: platform, analysis, transcriptomics, proteomics, genomics, normalization, clustering, gene, mirna, protein, interaction, text mining, genotyping, bioentity, functional profiling, statistical analysis, functional annotation, regulatory motif, microarray, fatigo, biclustering, networkminer, gepas, gene expression, FASEB list

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Spanish Ministry of Science and Innovation CEN-2008-1002;
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Instituto de Salud Carlos III

Availability: Free for academic use, Account required

Resource Name: Babelomics

Resource ID: SCR_002969

Alternate IDs: OMICS_00748, nif-0000-30144

Alternate URLs: http://www.fatigo.org/, http://www.gepas.org/, http://babelomics3.bioinfo.cipf.es

Old URLs: http://www.babelomics.org

Record Creation Time: 20220129T080216+0000

Record Last Update: 20250418T055009+0000

Ratings and Alerts

No rating or validation information has been found for Babelomics.

No alerts have been found for Babelomics.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 135 mentions in open access literature.

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

Kumar R, et al. (2024) Advances in genomic tools for plant breeding: harnessing DNA molecular markers, genomic selection, and genome editing. Biological research, 57(1), 80.

Galmés S, et al. (2023) KLB and NOX4 expression levels as potential blood-based transcriptional biomarkers of physical activity in children. Scientific reports, 13(1), 5563.

Fernández-Barroso MÁ, et al. (2022) Understanding the role of myoglobin content in Iberian pigs fattened in an extensive system through analysis of the transcriptome profile. Animal genetics, 53(3), 352.

Rosina M, et al. (2022) Ejection of damaged mitochondria and their removal by macrophages ensure efficient thermogenesis in brown adipose tissue. Cell metabolism, 34(4), 533.

Rodríguez N, et al. (2022) Gene expression study in monocytes: evidence of inflammatory dysregulation in early-onset obsessive-compulsive disorder. Translational psychiatry, 12(1), 134.

Moreno AD, et al. (2022) Insights into cell robustness against lignocellulosic inhibitors and insoluble solids in bioethanol production processes. Scientific reports, 12(1), 557.

Eren Gozel H, et al. (2021) A novel insight into differential expression profiles of sporadic cerebral cavernous malformation patients with different symptoms. Scientific reports, 11(1), 19351.

Lizamore D, et al. (2021) Elevated transcription of transposable elements is accompanied by het-siRNA-driven de novo DNA methylation in grapevine embryogenic callus. BMC genomics, 22(1), 676.

Potrony M, et al. (2021) DNA Repair and Immune Response Pathways Are Deregulated in Melanocyte-Keratinocyte Co-cultures Derived From the Healthy Skin of Familial Melanoma Patients. Frontiers in medicine, 8, 692341.

Hernández RB, et al. (2021) Manganese-Induced Neurotoxicity through Impairment of Cross-Talk Pathways in Human Neuroblastoma Cell Line SH-SY5Y Differentiated with Retinoic Acid. Toxics, 9(12).

Yang LY, et al. (2021) Exerting the Appropriate Application of Methylprednisolone in Acute Spinal Cord Injury Based on Time Course Transcriptomics Analysis. International journal of molecular sciences, 22(23).

Hervás-Salcedo R, et al. (2021) Enhanced anti-inflammatory effects of mesenchymal stromal cells mediated by the transient ectopic expression of CXCR4 and IL10. Stem cell research & therapy, 12(1), 124.

Mendaza S, et al. (2021) A DNA Methylation-Based Gene Signature Can Predict Triple-Negative Breast Cancer Diagnosis. Biomedicines, 9(10).

Fernández-Barroso MÁ, et al. (2020) Differences in the Loin Tenderness of Iberian Pigs Explained through Dissimilarities in Their Transcriptome Expression Profile. Animals : an open access journal from MDPI, 10(9).

Hulatt CJ, et al. (2020) Proteomic and Transcriptomic Patterns during Lipid Remodeling in Nannochloropsis gaditana. International journal of molecular sciences, 21(18).

Caballero-Campo P, et al. (2020) Gene transcription profiling of astheno- and normo-zoospermic sperm subpopulations. Asian journal of andrology, 22(6), 608.

Romdhane L, et al. (2020) The morbid cutaneous anatomy of the human genome revealed by a bioinformatic approach. Genomics, 112(6), 4232.

González-Alonso P, et al. (2020) The Hippo Pathway Transducers YAP1/TEAD Induce Acquired Resistance to Trastuzumab in HER2-Positive Breast Cancer. Cancers, 12(5).

Boumendil C, et al. (2019) Nuclear pore density controls heterochromatin reorganization during senescence. Genes & development, 33(3-4), 144.

Mato A, et al. (2019) The first evidence of global meat phosphoproteome changes in response to pre-slaughter stress. BMC genomics, 20(1), 590.