Resource Summary Report

Generated by dkNET on Apr 26, 2025

BAR

RRID:SCR_006748
Type: Tool

Proper Citation

BAR (RRID:SCR_006748)

Resource Information

URL: http://bar.utoronto.ca/welcome.htm

Proper Citation: BAR (RRID:SCR_006748)

Description: Web-based tools for working with functional genomics and other data, including Gene Expression and Protein Tools, Molecular Markers and Mapping Tools, and Other Genomic Tools. Most are designed with the plant (mainly Arabidopsis) researcher in mind, but a couple of them can be useful to the wider research community, e.g. Mouse eFP Browser or BlastDigester. The associated paper for most tools is available.

Abbreviations: BAR

Synonyms: Bio-Analytic Resource for Plant Biology, Bio-Analytic Resource, Bio-Analytic Resource - the BAR

Resource Type: service resource, data analysis service, data or information resource, data set, production service resource, analysis service resource

Keywords: gene expression, protein, molecular marker, mapping, tool, genomic, genomics, functional genomics, interaction, molecular interaction, protein-protein interaction, bio.tools

Funding: Canada Foundation for Innovation ;
Genome Canada

Resource Name: BAR

Resource ID: SCR_006748

Alternate IDs: nlx_152191, biotools:bioanalres_bar

Alternate URLs: https://bio.tools/bioanalres_bar

Record Creation Time: 20220129T080237+0000

Record Last Update: 20250426T055903+0000

Ratings and Alerts

No rating or validation information has been found for BAR.

No alerts have been found for BAR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 44 mentions in open access literature.

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

Dauphin BG, et al. (2024) TBL38 atypical homogalacturonan-acetylesterase activity and cell wall microdomain localization in Arabidopsis seed mucilage secretory cells. iScience, 27(5), 109666.

Yang L, et al. (2021) Global transcriptomic network of melatonin regulated root growth in Arabidopsis. Gene, 764, 145082.

Saha J, et al. (2020) Identification and characterization of differentially expressed genes in the rice root following exogenous application of spermidine during salt stress. Genomics, 112(6), 4125.

Safavi-Rizi V, et al. (2018) Divergent N Deficiency-Dependent Senescence and Transcriptome Response in Developmentally Old and Young Brassica napus Leaves. Frontiers in plant science, 9, 48.

Alam MN, et al. (2018) Transcriptomic profiling of tall fescue in response to heat stress and improved thermotolerance by melatonin and 24-epibrassinolide. BMC genomics, 19(1), 224.

Muhammad I, et al. (2018) Comparative in Silico Analysis of Ferric Reduction Oxidase (FRO) Genes Expression Patterns in Response to Abiotic Stresses, Metal and Hormone Applications. Molecules (Basel, Switzerland), 23(5).

Liu J, et al. (2018) Genome-wide screening and analysis of imprinted genes in rapeseed (Brassica napus L.) endosperm. DNA research : an international journal for rapid publication

of reports on genes and genomes, 25(6), 629.

Ogata T, et al. (2017) Virus-induced down-regulation of GmERA1A and GmERA1B genes enhances the stomatal response to abscisic acid and drought resistance in soybean. PloS one, 12(4), e0175650.

Nawkar GM, et al. (2017) In silico study on Arabidopsis BAG gene expression in response to environmental stresses. Protoplasma, 254(1), 409.

Boniecka J, et al. (2017) Within and beyond the stringent response-RSH and (p)ppGpp in plants. Planta, 246(5), 817.

Mewalal R, et al. (2016) The Arabidopsis Domain of Unknown Function 1218 (DUF1218) Containing Proteins, MODIFYING WALL LIGNIN-1 and 2 (At1g31720/MWL-1 and At4g19370/MWL-2) Function Redundantly to Alter Secondary Cell Wall Lignin Content. PloS one, 11(3), e0150254.

Hossain MR, et al. (2016) Trait Specific Expression Profiling of Salt Stress Responsive Genes in Diverse Rice Genotypes as Determined by Modified Significance Analysis of Microarrays. Frontiers in plant science, 7, 567.

Chai C, et al. (2016) Comprehensive Analysis and Expression Profiling of the OsLAX and OsABCB Auxin Transporter Gene Families in Rice (Oryza sativa) under Phytohormone Stimuli and Abiotic Stresses. Frontiers in plant science, 7, 593.

Chang YL, et al. (2016) Comprehensive Genomic Analysis and Expression Profiling of the NOX Gene Families under Abiotic Stresses and Hormones in Plants. Genome biology and evolution, 8(3), 791.

Bektas Y, et al. (2016) The Synthetic Elicitor DPMP (2,4-dichloro-6-{(E)-[(3-methoxyphenyl)imino]methyl}phenol) Triggers Strong Immunity in Arabidopsis thaliana and Tomato. Scientific reports, 6, 29554.

Hwang Y, et al. (2016) Cell wall-associated ROOT HAIR SPECIFIC 10, a proline-rich receptor-like kinase, is a negative modulator of Arabidopsis root hair growth. Journal of experimental botany, 67(6), 2007.

Shinde S, et al. (2015) Genome-wide transcriptomic analysis of the effects of sub-ambient atmospheric oxygen and elevated atmospheric carbon dioxide levels on gametophytes of the moss, Physcomitrella patens. Journal of experimental botany, 66(13), 4001.

Pradillo M, et al. (2015) Involvement of the Cohesin Cofactor PDS5 (SPO76) During Meiosis and DNA Repair in Arabidopsis thaliana. Frontiers in plant science, 6, 1034.

Wang Y, et al. (2015) Endogenous Cytokinin Overproduction Modulates ROS Homeostasis and Decreases Salt Stress Resistance in Arabidopsis Thaliana. Frontiers in plant science, 6, 1004.

Musungu B, et al. (2015) A predicted protein interactome identifies conserved global networks and disease resistance subnetworks in maize. Frontiers in genetics, 6, 201.