Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 15, 2025

Computational Biology and Functional Genomics Laboratory at Harvard

RRID:SCR_010240
Type: Tool

Proper Citation

Computational Biology and Functional Genomics Laboratory at Harvard (RRID:SCR_010240)

Resource Information

URL: http://compbio.dfci.harvard.edu/

Proper Citation: Computational Biology and Functional Genomics Laboratory at Harvard (RRID:SCR_010240)

Description: A computational biology laboratory that builds and redistributes genetic software tools.

Synonyms: Quackenbush Lab

Resource Type: software resource

Funding:

Resource Name: Computational Biology and Functional Genomics Laboratory at Harvard

Resource ID: SCR_010240

Alternate IDs: nlx_156871

Record Creation Time: 20220129T080257+0000

Record Last Update: 20250410T065952+0000

Ratings and Alerts

No rating or validation information has been found for Computational Biology and Functional

Genomics Laboratory at Harvard.

No alerts have been found for Computational Biology and Functional Genomics Laboratory at Harvard.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 221 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Zheng X, et al. (2023) Hydrogen Sulfide Alleviates Cadmium Stress by Enhancing Photosynthetic Efficiency and Regulating Sugar Metabolism in Wheat Seedlings. Plants (Basel, Switzerland), 12(13).

Kim OT, et al. (2017) Characterization of the Asiatic Acid Glucosyltransferase, UGT73AH1, Involved in Asiaticoside Biosynthesis in Centella asiatica (L.) Urban. International journal of molecular sciences, 18(12).

Karaki L, et al. (2016) Genome-wide analysis identifies gain and loss/change of function within the small multigenic insecticidal Albumin 1 family of Medicago truncatula. BMC plant biology, 16, 63.

Liu X, et al. (2015) De Novo Sequencing and Analysis of the Safflower Transcriptome to Discover Putative Genes Associated with Safflor Yellow in Carthamus tinctorius L. International journal of molecular sciences, 16(10), 25657.

Galeano E, et al. (2015) Large-scale transcriptional profiling of lignified tissues in Tectona grandis. BMC plant biology, 15, 221.

Vitali V, et al. (2015) Root hydraulic conductivity and adjustments in stomatal conductance: hydraulic strategy in response to salt stress in a halotolerant species. AoB PLANTS, 7.

Gy?rffy B, et al. (2015) Dynamic classification using case-specific training cohorts outperforms static gene expression signatures in breast cancer. International journal of cancer, 136(9), 2091.

Hu H, et al. (2015) Bioinformatics analysis of small RNAs in pima (Gossypium barbadense L.). PloS one, 10(2), e0116826.

Gil-Quintana E, et al. (2015) Medicago truncatula and Glycine max: Different Drought Tolerance and Similar Local Response of the Root Nodule Proteome. Journal of proteome research, 14(12), 5240.

Teng W, et al. (2014) ALY proteins participate in multifaceted Nep1Mo-triggered responses in Nicotiana benthamiana and Arabidopsis thaliana. Journal of experimental botany, 65(9), 2483.

Galli V, et al. (2014) Identifying microRNAs and transcript targets in Jatropha seeds. PloS one, 9(2), e83727.

Duarte J, et al. (2014) Transcriptome sequencing for high throughput SNP development and genetic mapping in Pea. BMC genomics, 15, 126.

Sebastiana M, et al. (2014) Oak root response to ectomycorrhizal symbiosis establishment: RNA-Seq derived transcript identification and expression profiling. PloS one, 9(5), e98376.

Mishima K, et al. (2014) Transcriptome sequencing and profiling of expressed genes in cambial zone and differentiating xylem of Japanese cedar (Cryptomeria japonica). BMC genomics, 15, 219.

Nemri A, et al. (2014) The genome sequence and effector complement of the flax rust pathogen Melampsora lini. Frontiers in plant science, 5, 98.

Obulkasim A, et al. (2014) stepwiseCM: An R Package for Stepwise Classification of Cancer Samples Using Multiple Heterogeneous Data Sets. Cancer informatics, 13, 1.

Zhao Z, et al. (2014) Bioinformatics analysis of alternative polyadenylation in green alga Chlamydomonas reinhardtii using transcriptome sequences from three different sequencing platforms. G3 (Bethesda, Md.), 4(5), 871.

Zhang H, et al. (2014) Identification, expression and interaction analyses of calcium-dependent protein kinase (CPK) genes in canola (Brassica napus L.). BMC genomics, 15, 211.

Sun Y, et al. (2014) Identification and functional analysis of mitogen-activated protein kinase kinase kinase (MAPKKK) genes in canola (Brassica napus L.). Journal of experimental botany, 65(8), 2171.

Wey-Fabrizius AR, et al. (2014) Transcriptome data reveal Syndermatan relationships and suggest the evolution of endoparasitism in Acanthocephala via an epizoic stage. PloS one, 9(2), e88618.