Resource Summary Report

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L1000 Fireworks Display

RRID:SCR_016175
Type: Tool

Proper Citation

L1000 Fireworks Display (RRID:SCR_016175)

Resource Information

URL: http://amp.pharm.mssm.edu/l1000fwd/

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Description: Web application that provides interactive visualization of drug and small-molecule induced gene expression signatures. L1000FWD enables coloring of signatures by different attributes such as cell type, time point, concentration, as well as drug attributes such as MOA and clinical phase.

Abbreviations: L1000FWD

Synonyms: L1000FWD: Large-scale Visualization of Drug-Induced Transcriptomic Signatures

Resource Type: software application, data processing software, web application, software resource, data visualization software

Defining Citation: PMID:29420694

Keywords: drug, small molecule, gene, expression, signature, moa, clinical, phase

Availability: Freely available, Free, Available for download

Resource Name: L1000 Fireworks Display

Resource ID: SCR_016175

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260804T043618+0000

Ratings and Alerts

No rating or validation information has been found for L1000 Fireworks Display.

No alerts have been found for L1000 Fireworks Display.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Lu J, et al. (2025) Identification of key genes regulating colorectal cancer stem cell characteristics by bioinformatics analysis. Medicine, 104(22), e40910.

Liu Z, et al. (2025) Proteomic analysis reveals chromatin remodeling as a potential therapeutical target in neuroblastoma. Journal of translational medicine, 23(1), 234.

Ge J, et al. (2024) New HCC Subtypes Based on CD8 Tex-Related lncRNA Signature Could Predict Prognosis, Immunological and Drug Sensitivity Characteristics of Hepatocellular Carcinoma. Journal of hepatocellular carcinoma, 11, 1331.

El-Aarag SA, et al. (2022) Identifying potential novel insights for COVID-19 pathogenesis and therapeutics using an integrated bioinformatics analysis of host transcriptome. International journal of biological macromolecules, 194, 770.

Vagapova ER, et al. (2021) Viral fibrotic scoring and drug screen based on MAPK activity uncovers EGFR as a key regulator of COVID-19 fibrosis. Scientific reports, 11(1), 11234.

Ma P, et al. (2020) Target RNA modification for epigenetic drug repositioning in neuroblastoma: computational omics proximity between repurposing drug and disease. Aging, 12(19), 19022.

Fang J, et al. (2020) Regulatory Master Genes Identification and Drug Repositioning by Integrative mRNA-miRNA Network Analysis for Acute Type A Aortic Dissection. Frontiers in pharmacology, 11, 575765.

Cao MD, et al. (2020) Identification of Osteosarcoma Metastasis-Associated Gene Biomarkers and Potentially Targeted Drugs Based on Bioinformatic and Experimental Analysis. OncoTargets and therapy, 13, 8095.

Li YL, et al. (2020) Identification of Subtype-Specific Metastasis-Related Genetic Signatures in Sarcoma. Frontiers in oncology, 10, 544956.

Gu L, et al. (2020) Identification and clinical validation of metastasis-associated biomarkers based on large-scale samples in colon-adenocarcinoma. Pharmacological research, 160, 105087.

Mofers A, et al. (2020) Identification of proteasome inhibitors using analysis of gene expression profiles. European journal of pharmacology, 889, 173709.

Yang X, et al. (2019) Novel drug candidate for the treatment of several soft?tissue sarcoma histologic subtypes: A computational method using survival?associated gene signatures for drug repurposing. Oncology reports, 41(4), 2241.

Torre D, et al. (2018) BioJupies: Automated Generation of Interactive Notebooks for RNA-Seq Data Analysis in the Cloud. Cell systems, 7(5), 556.

Liu TP, et al. (2018) Systematic polypharmacology and drug repurposing via an integrated L1000-based Connectivity Map database mining. Royal Society open science, 5(11), 181321.