Resource Summary Report

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EISEN LAB

RRID:SCR_013508
Type: Tool

Proper Citation

EISEN LAB (RRID:SCR_013508)

Resource Information

URL: http://eisenlab.org/

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Description: Welcome to Michael Eisens lab in the Howard Hughes Medical Institute (HHMI) at University of California at Berkeley (UCB) and the Lawrence Berkeley National Lab (LBNL). We are part of the Department of Molecular and Cell Biology of UCB and the Genomics Division of LBNL, and the. We are located in Stanley Hall on the Berkeley campus.Our lab applies computational and experimental genomic approaches to study how genome sequences specify organismal form and function. We are particularly interested in the regulation of gene expression, and focus on how the information that specifies when and where genes are expressed is encoded in genome sequences, the role that regulated gene expression plays in animal development and the response of microbes to their environments, and how variation in and evolution of gene expression contributes to phenotypic variation and the remarkable diversity of life on Earth. This site contains a more detailed description of our research projects, an introduction to members of the lab, reprints of all of our publications, free downloadable and web-based software. Sponsor. Experimental work described here was supported by a Howard Hughes Medical Institute Investigator award to MBE and by National Institutes of Health (NIH) grant GM704403 to MBE and MDB. Computational analyses were supported in by NIH grant HG002779 to MBE. Work at Lawrence Berkeley National Laboratory was conducted under Department of Energy contract DE-AC02-05CH11231. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Synonyms: EISEN LAB

Resource Type: data or information resource, organization portal, portal, laboratory portal

Resource Name: EISEN LAB

Resource ID: SCR_013508

Alternate IDs: nif-0000-30508

Old URLs: http://rana.lbl.gov/EisenSoftware.htm

Record Creation Time: 20220129T080316+0000

Record Last Update: 20260729T044331+0000

Ratings and Alerts

No rating or validation information has been found for EISEN LAB.

No alerts have been found for EISEN LAB.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 143 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Kim Y, et al. (2021) Adenine base editing and prime editing of chemically derived hepatic progenitors rescue genetic liver disease. Cell stem cell, 28(9), 1614.

Santha S, et al. (2020) Mutant Kras as a Biomarker Plays a Favorable Role in FL118-Induced Apoptosis, Reactive Oxygen Species (ROS) Production and Modulation of Survivin, Mcl-1 and XIAP in Human Bladder Cancer. Cancers, 12(11).

Meng Z, et al. (2016) Antiretroviral Therapy Normalizes Autoantibody Profile of HIV Patients by Decreasing CD33?CD11b?HLA-DR? Cells: A Cross-Sectional Study. Medicine, 95(15), e3285.

Oshida K, et al. (2016) Chemical and Hormonal Effects on STAT5b-Dependent Sexual Dimorphism of the Liver Transcriptome. PloS one, 11(3), e0150284.

Nightingale S, et al. (2016) CSF/plasma HIV-1 RNA discordance even at low levels is associated with up-regulation of host inflammatory mediators in CSF. Cytokine, 83, 139.

Oshida K, et al. (2016) Disruption of STAT5b-Regulated Sexual Dimorphism of the Liver Transcriptome by Diverse Factors Is a Common Event. PloS one, 11(3), e0148308.

Ito T, et al. (2016) Loss of YAP1 defines neuroendocrine differentiation of lung tumors. Cancer science, 107(10), 1527.

Chao WS, et al. (2016) Phytohormone balance and stress-related cellular responses are involved in the transition from bud to shoot growth in leafy spurge. BMC plant biology, 16, 47.

Oeser ML, et al. (2016) Dynamic Sumoylation of a Conserved Transcription Corepressor Prevents Persistent Inclusion Formation during Hyperosmotic Stress. PLoS genetics, 12(1), e1005809.

Lee HS, et al. (2015) Abasic pivot substitution harnesses target specificity of RNA interference. Nature communications, 6, 10154.

Lee JG, et al. (2015) A draft map of rhesus monkey tissue proteome for biomedical research. PloS one, 10(5), e0126243.

Nagel S, et al. (2015) Aberrant expression of homeobox gene SIX1 in Hodgkin lymphoma. Oncotarget, 6(37), 40112.

Pampalakis G, et al. (2015) Distinct cholesterogenic and lipidogenic gene expression patterns in ovarian cancer - a new pool of biomarkers. Genes & cancer, 6(11-12), 472.

Lin J, et al. (2015) Osteopontin (OPN/SPP1) isoforms collectively enhance tumor cell invasion and dissemination in esophageal adenocarcinoma. Oncotarget, 6(26), 22239.

Narayan A, et al. (2015) High-throughput RNA profiling via up-front sample parallelization. Nature methods, 12(4), 343.

Sakhinia E, et al. (2015) Expression profiling of microarray gene signatures in acute and chronic myeloid leukaemia in human bone marrow. Iranian journal of pediatric hematology and oncology, 5(1), 27.

Alves MM, et al. (2015) PAK2 is an effector of TSC1/2 signaling independent of mTOR and a potential therapeutic target for Tuberous Sclerosis Complex. Scientific reports, 5, 14534.

Zhang L, et al. (2015) Proteins S100A8 and S100A9 are potential biomarkers for renal cell carcinoma in the early stages: results from a proteomic study integrated with bioinformatics analysis. Molecular medicine reports, 11(6), 4093.

O'Leary K, et al. (2015) Identification of Endoglin as an epigenetically regulated tumour-suppressor gene in lung cancer. British journal of cancer, 113(6), 970.

Arish N, et al. (2015) Overexpression of Telomerase Protects Human and Murine Lung Epithelial Cells from Fas- and Bleomycin-Induced Apoptosis via FLIP Upregulation. PloS one, 10(5), e0126730.