Resource Summary Report

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Cheng Li Lab of Computational Genomics

RRID:SCR_008613
Type: Tool

Proper Citation

Cheng Li Lab of Computational Genomics (RRID:SCR_008613)

Resource Information

URL: http://www.hsph.harvard.edu/cli/complab/dchip/

Proper Citation: Cheng Li Lab of Computational Genomics (RRID:SCR_008613)

Description: Sponsor:
support is NIH grant R01 GM077122
National Institutes of Health, Claudia Adams Barr Program, and Friends of DFCI.
We are interested in how genomics changes promote cancer progression. Through collaboration with biomedical researchers, we analyze high-throughput microarray and sequencing data to study genomics, expression, and network changes in cancer cells. New methods are packaged into widely-used software such as dChip, which has been cited more than 1600 times.

Synonyms: Cheng Li Lab

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

Funding:

Resource Name: Cheng Li Lab of Computational Genomics

Resource ID: SCR_008613

Alternate IDs: nif-0000-31958

Alternate URLs: http://www.dchip.org

Record Creation Time: 20220129T080248+0000

Record Last Update: 20250517T055903+0000

Ratings and Alerts

No rating or validation information has been found for Cheng Li Lab of Computational Genomics.

No alerts have been found for Cheng Li Lab of Computational Genomics.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 31 mentions in open access literature.

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

Just U, et al. (2024) Proteomic and transcriptomic characterisation of FIA10, a novel murine leukemic cell line that metastasizes into the brain. PloS one, 19(1), e0295641.

Bolaños-Suárez V, et al. (2023) The mRNA and protein levels of the glycolytic enzymes lactate dehydrogenase A (LDHA) and phosphofructokinase platelet (PFKP) are good predictors of survival time, recurrence, and risk of death in cervical cancer patients. Cancer medicine, 12(14), 15632.

Chang YS, et al. (2023) Inhibition of the NOTCH and mTOR pathways by nelfinavir as a novel treatment for T cell acute lymphoblastic leukemia. International journal of oncology, 63(5).

Chen S, et al. (2017) Inhibition of PI3K/Akt/mTOR signaling in PI3KR2-overexpressing colon cancer stem cells reduces tumor growth due to apoptosis. Oncotarget, 8(31), 50476.

Pääkkönen V, et al. (2017) Exostosin 1 is expressed in human odontoblasts. Archives of oral biology, 80, 175.

Choi YS, et al. (2017) Mitogen- and Stress-Activated Protein Kinase 1 Regulates Status Epilepticus-Evoked Cell Death in the Hippocampus. ASN neuro, 9(5), 1759091417726607.

Hudspeth K, et al. (2016) Human liver-resident CD56(bright)/CD16(neg) NK cells are retained within hepatic sinusoids via the engagement of CCR5 and CXCR6 pathways. Journal of autoimmunity, 66, 40.

Romano O, et al. (2016) Transcriptional, epigenetic and retroviral signatures identify regulatory regions involved in hematopoietic lineage commitment. Scientific reports, 6, 24724.

Messina M, et al. (2016) Prognostic and therapeutic role of targetable lesions in B-lineage

acute lymphoblastic leukemia without recurrent fusion genes. Oncotarget, 7(12), 13886.

Zandalinas SI, et al. (2016) Activation of Secondary Metabolism in Citrus Plants Is Associated to Sensitivity to Combined Drought and High Temperatures. Frontiers in plant science, 7, 1954.

Liu X, et al. (2015) Expression Profiling Identifies Bezafibrate as Potential Therapeutic Drug for Lung Adenocarcinoma. Journal of Cancer, 6(12), 1214.

Russo MV, et al. (2015) A new mouse avatar model of non-small cell lung cancer. Frontiers in oncology, 5, 52.

Li XY, et al. (2015) MicroRNA-34a-5p enhances sensitivity to chemotherapy by targeting AXL in hepatocellular carcinoma MHCC-97L cells. Oncology letters, 10(5), 2691.

Srivastava AC, et al. (2015) Loss of function of folylpolyglutamate synthetase 1 reduces lignin content and improves cell wall digestibility in Arabidopsis. Biotechnology for biofuels, 8, 224.

Bokvaj P, et al. (2015) Transcriptome profiling of male gametophyte development in Nicotiana tabacum. Genomics data, 3, 106.

Mehrian-Shai R, et al. (2015) High metallothionein predicts poor survival in glioblastoma multiforme. BMC medical genomics, 8, 68.

Blevins R, et al. (2015) microRNAs regulate cell-to-cell variability of endogenous target gene expression in developing mouse thymocytes. PLoS genetics, 11(2), e1005020.

Tso JL, et al. (2015) Bone morphogenetic protein 7 sensitizes O6-methylguanine methyltransferase expressing-glioblastoma stem cells to clinically relevant dose of temozolomide. Molecular cancer, 14, 189.

Sarrion I, et al. (2015) Role of circulating miRNAs as biomarkers in idiopathic pulmonary arterial hypertension: possible relevance of miR-23a. Oxidative medicine and cellular longevity, 2015, 792846.

Medina-Martinez I, et al. (2014) Impact of gene dosage on gene expression, biological processes and survival in cervical cancer: a genome-wide follow-up study. PloS one, 9(5), e97842.