Resource Summary Report

Generated by NIF on May 5, 2025

The Li Lab at UCSF

RRID:SCR_010269
Type: Tool

Proper Citation

The Li Lab at UCSF (RRID:SCR_010269)

Resource Information

URL: http://urogene.org/

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Description: Laboratory portal that houses the following databases. MethPrimer is a program for designing bisulfite-conversion-based Methylation PCR Primers. Currently, it can design primers for two types of bisulfite PCR: 1) Methylation-Specific PCR (MSP) and 2) Bisulfite-Sequencing PCR (BSP) or Bisulfite-Restriction PCR. CpG Island Prediction MethPrimer can also analyze input sequences for the existence of CpG islands. Human Prostate Gene Database (PGDB) is a curated and integrated database of human genes related to the prostate and prostatic diseases. Human Kidney Gene Database (KGDB) is a curated and integrated database of human genes related to the kidney and renal diseases. The Li Lab is interested in understanding how small RNA regulates gene expression at the transcriptional level by targeting gene promoter sequences, particularly how small RNA activates gene transcription, a phenomenon termed RNA activation (RNAa).

Synonyms: The Li Lab in the Department of Urology and Helen Diller Family Comprehensive Cancer Center, UCSF

Resource Type: database, data or information resource

Funding:

Resource Name: The Li Lab at UCSF

Resource ID: SCR_010269

Alternate IDs: nlx_156928

Record Creation Time: 20220129T080257+0000

Record Last Update: 20250503T060159+0000

Ratings and Alerts

No rating or validation information has been found for The Li Lab at UCSF.

No alerts have been found for The Li Lab at UCSF.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 182 mentions in open access literature.

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

Deycmar S, et al. (2024) Epigenetic MLH1 silencing concurs with mismatch repair deficiency in sporadic, naturally occurring colorectal cancer in rhesus macaques. Journal of translational medicine, 22(1), 292.

Lorenz V, et al. (2024) Glyphosate and a glyphosate-based herbicide dysregulate the epigenetic landscape of Homeobox A10 (Hoxa10) gene during the endometrial receptivity in Wistar rats. Frontiers in toxicology, 6, 1438826.

Li Q, et al. (2024) DNMT3B Alleviates Liver Steatosis Induced by Chronic Low-grade LPS via Inhibiting CIDEA Expression. Cellular and molecular gastroenterology and hepatology, 17(1), 59.

Wang J, et al. (2023) Hypermethylation-Mediated lncRNA MAGI2-AS3 Downregulation Facilitates Malignant Progression of Laryngeal Squamous Cell Carcinoma via Interacting With SPT6. Cell transplantation, 32, 9636897231154574.

Tan Y, et al. (2023) Alternative polyadenylation reprogramming of MORC2 induced by NUDT21 loss promotes KIRC carcinogenesis. JCI insight, 8(18).

Tao Y, et al. (2023) Epigenetic regulation of beta-endorphin synthesis in hypothalamic arcuate nucleus neurons modulates neuropathic pain in a rodent pain model. Nature communications, 14(1), 7234.

Gao LT, et al. (2023) Hypermethylation of the Bmp4 promoter dampens binding of HIF-1? and impairs its cardiac protective effects from oxidative stress in prenatally GC-exposed offspring. Cellular and molecular life sciences : CMLS, 80(3), 58.

Tian H, et al. (2023) PHF14 enhances DNA methylation of SMAD7 gene to promote TGF-?-driven lung adenocarcinoma metastasis. Cell discovery, 9(1), 41.

Ballesteros M, et al. (2022) DNA Methylation in Gestational Diabetes and its Predictive Value for Postpartum Glucose Disturbances. The Journal of clinical endocrinology and metabolism, 107(10), 2748.

Song B, et al. (2022) Poor semen parameters are associated with abnormal methylation of imprinted genes in sperm DNA. Reproductive biology and endocrinology : RB&E, 20(1), 155.

Gastiazoro MP, et al. (2022) Epigenetic disruption of placental genes by chronic maternal cafeteria diet in rats. The Journal of nutritional biochemistry, 106, 109015.

Khongsti K, et al. (2021) MAPK pathway and SIRT1 are involved in the down-regulation of secreted osteopontin expression by genistein in metastatic cancer cells. Life sciences, 265, 118787.

Lin M, et al. (2021) S100P contributes to promoter demethylation and transcriptional activation of SLC2A5 to promote metastasis in colorectal cancer. British journal of cancer, 125(5), 734.

Chen M, et al. (2021) Androgen receptor contributes to microglial/macrophage activation in rats with intracranial hemorrhage by mediating the JMJD3/Botch/Notch1 axis. Neuroscience letters, 765, 136283.

Gao B, et al. (2021) Identification of Feature Autophagy-Related Genes and DNA Methylation Profiles in Systemic Lupus Erythematosus Patients. Medical science monitor : international medical journal of experimental and clinical research, 27, e933425.

Yang S, et al. (2021) Epigenetically modulated miR-1224 suppresses the proliferation of HCC through CREB-mediated activation of YAP signaling pathway. Molecular therapy. Nucleic acids, 23, 944.

Pulverer W, et al. (2021) Multiplexed DNA Methylation Analysis in Colorectal Cancer Using Liquid Biopsy and Its Diagnostic and Predictive Value. Current issues in molecular biology, 43(3), 1419.

He ZH, et al. (2021) Cigarette smoke extract affects methylation status and attenuates Sca-1 expression of mouse endothelial progenitor cell in vitro. Tobacco induced diseases, 19, 08.

Shao G, et al. (2021) Methylation-dependent MCM6 repression induced by LINC00472 inhibits triple-negative breast cancer metastasis by disturbing the MEK/ERK signaling pathway. Aging, 13(4), 4962.

Huang S, et al. (2021) miR-190 promotes malignant transformation and progression of human urothelial cells through CDKN1B/p27 inhibition. Cancer cell international, 21(1), 241.