Resource Summary Report

Generated by NIF on Apr 27, 2025

TileMap

RRID:SCR_001589
Type: Tool

Proper Citation

TileMap (RRID:SCR_001589)

Resource Information

URL: http://jilab.biostat.jhsph.edu/software/tilemap/index.htm

Proper Citation: TileMap (RRID:SCR_001589)

Description: Software tool for microarray tile mapping. It utilizes ChIP-chip peak calling to identify genomic loci that show transcriptional activities and transcription factor binding patterns of interest.

Synonyms: tilemapv2, TileMap Version 2

Resource Type: data processing software, data analysis software, source code, algorithm resource, software resource, software application

Defining Citation: PMID:16046496

Keywords: microarray, rna, dna, sequencing, chip, tiling, chip-chip peak calling, transcription, binding

Funding:

Availability: Available for download, Free

Resource Name: TileMap

Resource ID: SCR_001589

Alternate IDs: OMICS_00812

Record Creation Time: 20220129T080208+0000

Record Last Update: 20250426T055449+0000

Ratings and Alerts

No rating or validation information has been found for TileMap.

No alerts have been found for TileMap.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

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

Gao Z, et al. (2022) Structural and Functional Analyses of Hub MicroRNAs in An Integrated Gene Regulatory Network of Arabidopsis. Genomics, proteomics & bioinformatics, 20(4), 747.

Wang H, et al. (2016) Arabidopsis Flower and Embryo Developmental Genes are Repressed in Seedlings by Different Combinations of Polycomb Group Proteins in Association with Distinct Sets of Cis-regulatory Elements. PLoS genetics, 12(1), e1005771.

Busser BW, et al. (2015) Enhancer modeling uncovers transcriptional signatures of individual cardiac cell states in Drosophila. Nucleic acids research, 43(3), 1726.

Abou El Hassan M, et al. (2015) Cancer Cells Hijack PRC2 to Modify Multiple Cytokine Pathways. PloS one, 10(6), e0126466.

Nault R, et al. (2013) Comparison of TCDD-elicited genome-wide hepatic gene expression in Sprague-Dawley rats and C57BL/6 mice. Toxicology and applied pharmacology, 267(2), 184.

Sun Y, et al. (2010) Integration of brassinosteroid signal transduction with the transcription network for plant growth regulation in Arabidopsis. Developmental cell, 19(5), 765.

Walia H, et al. (2009) Dosage-dependent deregulation of an AGAMOUS-LIKE gene cluster contributes to interspecific incompatibility. Current biology : CB, 19(13), 1128.

Bartkuhn M, et al. (2009) Active promoters and insulators are marked by the centrosomal protein 190. The EMBO journal, 28(7), 877.