Resource Summary Report

Generated by dkNET on Sep 2, 2026

Cscan

RRID:SCR_006756
Type: Tool

Proper Citation

Cscan (RRID:SCR_006756)

Resource Information

URL: http://159.149.160.51/cscan/

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Description: Data resource that includes a large collection of genome-wide ChIP-Seq experiments performed on transcription factors (TFs), histone modifications, RNA polymerases and others. Enriched peak regions from the ChIP-Seq experiments are crossed with the genomic coordinates of a set of input genes, to identify which of the experiments present a statistically significant number of peaks within the input genes' loci. The input can be a cluster of co-expressed genes, or any other set of genes sharing a common regulatory profile. Users can thus single out which TFs are likely to be common regulators of the genes, and their respective correlations. Also, by examining results on promoter activation, transcription, histone modifications, polymerase binding and so on, users can investigate the effect of the TFs (activation or repression of transcription) as well as of the cell or tissue specificity of the genes' regulation and expression.

Abbreviations: Cscan

Resource Type: analysis service resource, data analysis service, data or information resource, database, production service resource, service resource

Defining Citation: PMID:22669907

Keywords: regulator, gene, genome-wide chip-seq, chip-seq, gene, genome

Availability: Free

Resource Name: Cscan

Resource ID: SCR_006756

Alternate IDs: OMICS_00529

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260829T182241+0000

Ratings and Alerts

No rating or validation information has been found for Cscan.

No alerts have been found for Cscan.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Lu Z, et al. (2024) Assessing next-generation sequencing-based computational methods for predicting transcriptional regulators with query gene sets. Briefings in bioinformatics, 25(5).

Bai J, et al. (2019) Mitochondrial metabolic study guided by proteomics analysis in hepatocellular carcinoma cells surviving long-term incubation with the highest dose of sorafenib. Aging, 11(24), 12452.

Sweeney T, et al. (2016) The application of transcriptomic data in the authentication of beef derived from contrasting production systems. BMC genomics, 17(1), 746.

Sommer F, et al. (2015) Site-specific programming of the host epithelial transcriptome by the gut microbiota. Genome biology, 16(1), 62.