Resource Summary Report

Generated by NIF on Apr 23, 2025

SwissRegulon

RRID:SCR_005333
Type: Tool

Proper Citation

SwissRegulon (RRID:SCR_005333)

Resource Information

URL: http://swissregulon.unibas.ch/fcgi/sr/swissregulon

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Description: A database of genome-wide annotations of regulatory sites. The predictions are based on Bayesian probabilistic analysis of a combination of input information including: * Experimentally determined binding sites reported in the literature. * Known sequence-specificities of transcription factors. * ChIP-chip and ChIP-seq data. * Alignments of orthologous non-coding regions. Predictions were made using the PhyloGibbs, MotEvo, IRUS and ISMARA algorithms developed in their group, depending on the data available for each organism. Annotations can be viewed in a Gbrowse genome browser and can also be downloaded in flat file format.

Abbreviations: SwissRegulon

Synonyms: SwissRegulon Database

Resource Type: data or information resource, database

Defining Citation: PMID:23180783, PMID:17130146

Keywords: genome, binding site, transcription factor, genome-wide annotation, annotation, chip-chip, chip-seq, non-coding region, promoter, motif, transcript, regulatory motif, genome browser, FASEB list

Funding:

Availability: Acknowledgement requested

Resource Name: SwissRegulon

Resource ID: SCR_005333

Alternate IDs: nif-0000-03524, OMICS_00543

Record Creation Time: 20220129T080229+0000

Record Last Update: 20250422T055234+0000

Ratings and Alerts

No rating or validation information has been found for SwissRegulon.

No alerts have been found for SwissRegulon.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 43 mentions in open access literature.

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

Williquett J, et al. (2024) AMPK-SP1-Guided Dynein Expression Represents a New Energy-Responsive Mechanism and Therapeutic Target for Diabetic Nephropathy. Kidney360, 5(4), 538.

Ren X, et al. (2023) High throughput PRIME editing screens identify functional DNA variants in the human genome. bioRxiv : the preprint server for biology.

Pastore SF, et al. (2023) Neuronal transcription of autism gene PTCHD1 is regulated by a conserved downstream enhancer sequence. Scientific reports, 13(1), 20391.

Chen SA, et al. (2023) Gene-by-environment interactions are pervasive among natural genetic variants. Cell genomics, 3(4), 100273.

Liu D, et al. (2022) circKCNN2 suppresses the recurrence of hepatocellular carcinoma at least partially via regulating miR-520c-3p/methyl-DNA-binding domain protein 2 axis. Clinical and translational medicine, 12(1), e662.

Ajore R, et al. (2022) Functional dissection of inherited non-coding variation influencing multiple myeloma risk. Nature communications, 13(1), 151.

Cheng X, et al. (2022) Identification of potential functional variants and genes at 18q21.1 associated with the carcinogenesis of colorectal cancer. PLoS genetics, 18(2), e1010050.

Freddolino PL, et al. (2021) Dynamic landscape of protein occupancy across the Escherichia coli chromosome. PLoS biology, 19(6), e3001306.

Kang HG, et al. (2021) Genetic variants in histone modification regions are associated with the prognosis of lung adenocarcinoma. Scientific reports, 11(1), 21520.

Duran-Lozano L, et al. (2021) Germline variants at SOHLH2 influence multiple myeloma risk. Blood cancer journal, 11(4), 76.

Morello G, et al. (2021) Transcriptional Profiles of Cell Fate Transitions Reveal Early Drivers of Neuronal Apoptosis and Survival. Cells, 10(11).

Greulich F, et al. (2021) The glucocorticoid receptor recruits the COMPASS complex to regulate inflammatory transcription at macrophage enhancers. Cell reports, 34(6), 108742.

Ducoli L, et al. (2021) LETR1 is a lymphatic endothelial-specific lncRNA governing cell proliferation and migration through KLF4 and SEMA3C. Nature communications, 12(1), 925.

Yang W, et al. (2019) Three novel genetic variants in NRF2 signaling pathway genes are associated with pancreatic cancer risk. Cancer science, 110(6), 2022.

Li S, et al. (2019) Stable enhancers are active in development, and fragile enhancers are associated with evolutionary adaptation. Genome biology, 20(1), 140.

Franzén O, et al. (2019) PanglaoDB: a web server for exploration of mouse and human single-cell RNA sequencing data. Database : the journal of biological databases and curation, 2019.

Weger BD, et al. (2019) The Mouse Microbiome Is Required for Sex-Specific Diurnal Rhythms of Gene Expression and Metabolism. Cell metabolism, 29(2), 362.

Chiu HS, et al. (2018) Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. Cell reports, 23(1), 297.

Klein AP, et al. (2018) Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. Nature communications, 9(1), 556.

Mermet J, et al. (2018) Clock-dependent chromatin topology modulates circadian transcription and behavior. Genes & development, 32(5-6), 347.