Resource Summary Report

Generated by dkNET on Apr 28, 2025

RAVEN

RRID:SCR_001937
Type: Tool

Proper Citation

RAVEN (RRID:SCR_001937)

Resource Information

URL: http://burgundy.cmmt.ubc.ca/cgi-bin/RAVEN/a?rm=home

Proper Citation: RAVEN (RRID:SCR_001937)

Description: Tool to search for putative regulatory genetic variation in your favorite gene. Single nucleotide polymorphisms (SNPs) (from dbSNP and user defined) are analyzed for overlap with potential transcription factor binding sites (TFBS) and phylogenetic footprinting using UCSC phastCons scores from multiple alignments of 8 vertebrate genomes.

Abbreviations: RAVEN

Synonyms: Regulatory analysis of Variation in Enhancers, RAVEN - Regulatory analysis of Variation in ENhancers

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

Defining Citation: PMID:18208319

Keywords: transcription factor binding site, phylogenetic footprint, regulatory sequence variation, genetic variation, in silico, regulatory sequence, FASEB list

Funding:

Resource Name: RAVEN

Resource ID: SCR_001937

Alternate IDs: OMICS_01932

Record Creation Time: 20220129T080210+0000

Record Last Update: 20250428T052913+0000

Ratings and Alerts

No rating or validation information has been found for RAVEN.

No alerts have been found for RAVEN.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 120 mentions in open access literature.

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

van Gils P, et al. (2025) Ghrelin for neuroprotection in post-cardiac arrest coma: a 1-year follow-up of cognitive and psychosocial outcomes. European heart journal. Acute cardiovascular care, 14(1), 5.

Deantas-Jahn C, et al. (2024) Metabolic modeling of Halomonas campaniensis improves polyhydroxybutyrate production under nitrogen limitation. Applied microbiology and biotechnology, 108(1), 310.

Rodriguez-Flores CJ, et al. (2024) gMCSpy: efficient and accurate computation of genetic minimal cut sets in Python. Bioinformatics (Oxford, England), 40(6).

Soommat P, et al. (2024) Light-Exposed Metabolic Responses of Cordyceps militaris through Transcriptome-Integrated Genome-Scale Modeling. Biology, 13(3).

Moon SJ, et al. (2024) Identification of high sugar diet-induced dysregulated metabolic pathways in muscle using tissue-specific metabolic models in Drosophila. bioRxiv : the preprint server for biology.

Zhang C, et al. (2024) Human-level few-shot concept induction through minimax entropy learning. Science advances, 10(16), eadg2488.

Andrabi SBA, et al. (2024) Long noncoding RNA LIRIL2R modulates FOXP3 levels and suppressive function of human CD4+ regulatory T cells by regulating IL2RA. Proceedings of the National Academy of Sciences of the United States of America, 121(23), e2315363121.

Kaushal M, et al. (2024) Reconstruction of a genome-scale metabolic model and in-silico flux

analysis of Aspergillus tubingensis: a non-mycotoxinogenic citric acid-producing fungus. Biotechnology for biofuels and bioproducts, 17(1), 70.

Kar D, et al. (2024) Creating a Modified Version of the Cambridge Multimorbidity Score to Predict Mortality in People Older Than 16 Years: Model Development and Validation. Journal of medical Internet research, 26, e56042.

Avci FG, et al. (2024) Unraveling bacterial stress responses: implications for next-generation antimicrobial solutions. World journal of microbiology & biotechnology, 40(9), 285.

Valcárcel LV, et al. (2024) An automated network-based tool to search for metabolic vulnerabilities in cancer. Nature communications, 15(1), 8685.

Akutsu M, et al. (2024) De novo sequencing allows genome-wide identification of genes involved in galactomannan synthesis in locust bean (Ceratonia siliqua). DNA research : an international journal for rapid publication of reports on genes and genomes, 31(6).

Haag C, et al. (2024) Emotional intelligence and the dark triad: a latent profile analysis to investigate the Jekyll and Hyde of the emotionally intelligent manager. Frontiers in psychology, 15, 1459997.

Hu Y, et al. (2024) PCMD: A multilevel comparison database of intra- and cross-species metabolic profiling in 530 plant species. Plant communications, 5(10), 101038.

Schiller IS, et al. (2024) A lecturer's voice quality and its effect on memory, listening effort, and perception in a VR environment. Scientific reports, 14(1), 12407.

Zhang C, et al. (2024) Yeast9: a consensus genome-scale metabolic model for S. cerevisiae curated by the community. Molecular systems biology, 20(10), 1134.

Barcia-Cruz R, et al. (2024) Phage-inducible chromosomal minimalist islands (PICMIs), a novel family of small marine satellites of virulent phages. Nature communications, 15(1), 664.

Sabatini S, et al. (2024) Hepatic glucose production rises with the histological severity of metabolic dysfunction-associated steatohepatitis. Cell reports. Medicine, 5(11), 101820.

Tec-Campos D, et al. (2023) The genome-scale metabolic model for the purple non-sulfur bacterium Rhodopseudomonas palustris Bis A53 accurately predicts phenotypes under chemoheterotrophic, chemoautotrophic, photoheterotrophic, and photoautotrophic growth conditions. PLoS computational biology, 19(8), e1011371.

Kuzmichev YV, et al. (2023) Application of ultrasensitive digital ELISA for p24 enables improved evaluation of HIV-1 reservoir diversity and growth kinetics in viral outgrowth assays. Scientific reports, 13(1), 10958.