

Resource Summary Report

Generated by [RRID](#) on Sep 10, 2026

RAVEN

RRID:SCR_001937

Type: Tool

Proper Citation

RAVEN (RRID:SCR_001937)

Resource Information

URL: <http://burgundy.cmmmt.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., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: RAVEN

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

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

Defining Citation: [PMID:18208319](#)

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

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: RAVEN

Resource ID: SCR_001937

Alternate IDs: OMICS_01932

Record Creation Time: 20220129T080210+0000

Record Last Update: 20260905T132954+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 127 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

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.

Sertbas M, et al. (2025) Exploring Human Brain Metabolism via Genome-Scale Metabolic Modeling with Highlights on Multiple Sclerosis. *ACS chemical neuroscience*, 16(7), 1346.

Mikaeloff F, et al. (2025) Host Plasma Microenvironment in Immunometabolically Impaired HIV Infection Leads to Dysregulated Monocyte Function and Synaptic Transmission Ex Vivo. *Advanced science (Weinheim, Baden-Wurtemberg, Germany)*, 12(16), e2416453.

Liu Z, et al. (2025) Minimization of proteome reallocation explains metabolic transition in hierarchical utilization of carbon sources. *mSystems*, 10(7), e0069025.

Nguyen Chi T, et al. (2025) Circadian rhythms and the use of transfer learning for critically endangered crested argus *Rheinardia ocellata* in the Central Highlands of Vietnam: the implications for conservation. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*, 380(1928), 20240056.

León J, et al. (2025) Understanding the effects of pre-treatment and extraction methods on lipid fingerprint of cashew nut shell liquid (CNSL) by non-targeted lipidomics analysis. *Scientific reports*, 15(1), 18103.

Vayena E, et al. (2025) Metabolic network reconstruction as a resource for analyzing *Salmonella Typhimurium* SL1344 growth in the mouse intestine. *PLoS computational biology*, 21(3), e1012869.

Costa CIS, et al. (2025) Understanding rare variant contributions to autism: lessons from dystrophin-deficient model. *NPJ genomic medicine*, 10(1), 18.

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

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

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.

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

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.