

Resource Summary Report

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SPOT - Biological prioritization after a SNP association study

RRID:SCR_005193

Type: Tool

Proper Citation

SPOT - Biological prioritization after a SNP association study (RRID:SCR_005193)

Resource Information

URL: <http://spot.cgsmd.isi.edu>

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Description: A web-based tool for using biological databases to prioritize single nucleotide polymorphisms (SNPs) after a genome-wide association study (GWAS). The site allows users to upload a list of SNPs and GWAS P-values and returns a prioritized list of SNPs using the GIN method. Users can specify candidate genes or genomic regions with custom levels of prioritization. The results can be downloaded or viewed in the browser where users can interactively explore the details of each SNP, including graphical representations of the genomic information network (GIN) method. For investigators interested in incorporating biological databases into a post-GWAS SNP selection strategy, the SPOT web tool is an easily implemented and flexible solution.

Abbreviations: SPOT

Resource Type: analysis service resource, data analysis service, production service resource, service resource

Defining Citation: [PMID:20529875](#)

Keywords: single nucleotide polymorphism, genome-wide association study, linkage disequilibrium, gene, genomic region, p-value, bio.tools, FASEB list

Resource Name: SPOT - Biological prioritization after a SNP association study

Resource ID: SCR_005193

Alternate IDs: biotools:spot, OMICS_00189

Alternate URLs: <https://bio.tools/spot>

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260905T133128+0000

Ratings and Alerts

No rating or validation information has been found for SPOT - Biological prioritization after a SNP association study.

No alerts have been found for SPOT - Biological prioritization after a SNP association study.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 512 mentions in open access literature.

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

Cairns T, et al. (2025) Uncovering the transcriptional landscape of *Fomes fomentarius* during fungal-based material production through gene co-expression network analysis. *Fungal biology and biotechnology*, 12(1), 1.

Chen L, et al. (2025) Unremodeled GPI-anchored proteins at the plasma membrane trigger aberrant endocytosis. *Life science alliance*, 8(2).

Li R, et al. (2025) Application of the 2021 AAPOS Guidelines in Clinics with Revision and Validation of SPOT Referral Criteria. *Clinical ophthalmology (Auckland, N.Z.)*, 19, 291.

McNamara KM, et al. (2025) Spermine oxidase promotes *Helicobacter pylori*-mediated gastric carcinogenesis through acrolein production. *Oncogene*, 44(5), 296.

Thomas S, et al. (2025) Characterizing safety, toxicity, and breast cancer risk reduction using a long-term fulvestrant eluting implant. *Scientific reports*, 15(1), 3028.

Lone M, et al. (2025) Antibody ligation of HLA class II induces YAP nuclear localization and formation of cytoplasmic YAP condensates in human endothelial cells. *ImmunoHorizons*, 9(3).

Strandberg J, et al. (2025) TRAIL agonists rescue mice from radiation-induced lung, skin, or esophageal injury. *The Journal of clinical investigation*, 135(5).

Lai CY, et al. (2025) CtBP1 is essential for epigenetic silencing of μ -opioid receptor genes in the dorsal root ganglion in spinal nerve ligation-induced neuropathic pain. *Neurotherapeutics : the journal of the American Society for Experimental NeuroTherapeutics*, 22(1), e00493.

Indris C, et al. (2025) Supervised and Self-Supervised Learning for Assembly Line Action Recognition. *Journal of imaging*, 11(1).

Ozcan SC, et al. (2025) RESTRICT-seq enables time-gated CRISPR screens and uncovers novel epigenetic dependencies of SCC resistance. *bioRxiv : the preprint server for biology*.

Temesgen F, et al. (2024) Utilizing multi-criteria decision-making analysis and 3D visualization techniques for dam site selection and irrigation area identification in Gedeb River, Ethiopia. *Heliyon*, 10(15), e35604.

Kroll A, et al. (2024) SPOT: A machine learning model that predicts specific substrates for transport proteins. *PLoS biology*, 22(9), e3002807.

Connors E, et al. (2024) Microbial community composition predicts bacterial production across ocean ecosystems. *The ISME journal*, 18(1).

Mushtaq I, et al. (2024) MicroRNA-452-5p regulates fibrogenesis via targeting TGF- β /SMAD4 axis in SCN5A-knockdown human cardiac fibroblasts. *iScience*, 27(6), 110084.

Thieme A, et al. (2024) Intercomparison of Same-Day Remote Sensing Data for Measuring Winter Cover Crop Biophysical Traits. *Sensors (Basel, Switzerland)*, 24(7).

Saji N, et al. (2024) Learning semantic categories of L2 verbs: The case of cutting and breaking verbs. *PloS one*, 19(1), e0296628.

Antkowiak KR, et al. (2024) A nematode model to evaluate microdeletion phenotype expression. *G3 (Bethesda, Md.)*, 14(2).

Leung AOW, et al. (2024) Suppression of apoptosis impairs phalangeal joint formation in the pathogenesis of brachydactyly type A1. *Nature communications*, 15(1), 2229.

Roberts APE, et al. (2024) Daxx mediated histone H3.3 deposition on HSV-1 DNA restricts genome decompaction and the progression of immediate-early transcription. *bioRxiv : the preprint server for biology*.

Halim A, et al. (2024) Inhibition of miR-10b treats metastatic breast cancer by targeting stem cell-like properties. *Oncotarget*, 15, 591.