

Resource Summary Report

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ShinyGO

RRID:SCR_019213

Type: Tool

Proper Citation

ShinyGO (RRID:SCR_019213)

Resource Information

URL: <http://bioinformatics.sdstate.edu/go/>

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Description: Software graphical gene set enrichment tool for animals and plants. Graphical web application to gain insights from gene sets. Features include graphical visualization of enrichment results and gene characteristics, and application program interface access to KEGG and STRING for retrieval of pathway diagrams and protein-protein interaction networks.

Synonyms: ShinyGO 0.77, ShinyGO 0.80, Shiny Gene Ontology, ShinyGO v0.61

Resource Type: data access protocol, software resource, web service

Defining Citation: [PMID:31882993](#)

Keywords: Graphical gene set enrichment, animal gene, plant gene, graphical visualization, enrichment results, gene characteristics, pathway diagrams retrieval, protein interaction network, bio.tools

Resource Name: ShinyGO

Resource ID: SCR_019213

Alternate IDs: biotools:ShinyGO

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

Record Creation Time: 20220129T080344+0000

Record Last Update: 20260829T182558+0000

Ratings and Alerts

No rating or validation information has been found for ShinyGO.

No alerts have been found for ShinyGO.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1213 mentions in open access literature.

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

Ríos-Ortiz A, et al. (2026) Integrative transcriptomic and physiological assessment of nanoencapsulated carvacrol and thymol oil as an antioxidant in thermal-stressed white shrimp (*Litopenaeus vannamei*). *Veterinary research communications*, 50(2), 126.

Chen J, et al. (2026) G9a-mediated H3K9me2 orchestrates intestinal epithelial regeneration through epigenetic silencing of cell cycle-related genes. *Nature communications*, 17(1).

Biswas S, et al. (2026) A tryptophan-phenylalanine binding motif for the histone methyltransferases MLL4 and MLL3. *The Journal of biological chemistry*, 302(3), 111189.

Hitti E, et al. (2026) Profound alterations of cancer transcriptomes by the RNase L inhibitor ABCE1 through the modulation of UU/UA-dinucleotide rich transcript abundance. *RNA biology*, 23(1), 1.

Leroux C, et al. (2026) Exploring the role of food-source microRNAs as potential nutritional bioactives in humans. *NPJ science of food*, 10(1), 50.

Alqarni AO, et al. (2026) Phytosulfokine signalling blocks mycotoxin toxicity in *Arabidopsis* and mediates suppression of cell death activated by bacterial microbe-associated molecular patterns. *The New phytologist*, 249(5), 2515.

Feldmann JW, et al. (2026) Aging changes the mechanism that underlies JAK2 modulation of neutrophil function. *Journal of immunology (Baltimore, Md. : 1950)*, 215(3).

Utami N, et al. (2026) Integrative Computational and Transcriptional Analysis of NF- κ B and HIF-1 α Modulation Following Doxorubicin Treatment in Triple-Negative Breast Cancer Cells. *Journal of experimental pharmacology*, 18, 576572.

Bastakis E, et al. (2026) The *Aspergillus nidulans* transcription factor SclB governs the transition from vegetative to asexual development. *mBio*, 17(4), e0348825.

Shah VJ, et al. (2026) Targeting ubiquitin signaling vulnerabilities in KEAP1-inactivated lung cancer. *The EMBO journal*, 45(9), 3276.

Zerouak N, et al. (2026) Vitamin D Modulates Humoral Responses to SARS-CoV-2 Vaccination in Autoimmune Thyroiditis: An Endocrine-Immune Perspective Supported by Network Pharmacology, Molecular Docking, and Molecular Dynamics Simulations. *International journal of molecular sciences*, 27(5).

Karousa MM, et al. (2026) Chrysopogon zizanioides (Vetiver) Essential Oil from Qatar Targets AKT1 and STAT3 in Colorectal and Lung Cancer: GC-MS Profiling, In Vitro Antiproliferative Activity, and In Silico Analyses. *Plants (Basel, Switzerland)*, 15(5).

Kim SM, et al. (2026) The C2H2-type zinc finger protein SIHair5 acts as a regulatory node coordinating trichome development and leaf morphogenesis in tomato. *Plant cell reports*, 45(4).

Greco S, et al. (2026) Diagnostic potential of circular RNAs in carotid atherosclerotic plaque vulnerability. *Non-coding RNA research*, 18, 118.

Fu Y, et al. (2026) Metabolic profiling of the TME uncovers the contrasting impacts of CKMT2 and PDE2A in CRC progression and therapeutic response. *Frontiers in pharmacology*, 17, 1732137.

Sun YS, et al. (2026) CXCL10 as a migration-associated biomarker in oral squamous cell carcinoma. *BMC oral health*, 26(1).

Johnson C, et al. (2026) Comparative liver proteome analysis of feedlot steer calves reveals growth trait-specific pathways influenced by calving season. *Journal of animal science and biotechnology*, 17(1).

Varghese S, et al. (2026) Integrative Analysis of Post-Translational Modifications Identifies a PTM-Enriched Regulatory Core in Human Metabolic Enzymes. *Metabolites*, 16(3).

Gorbea C, et al. (2026) A viral noncoding RNA is a master regulator of gene expression that defines host cell identity and function. *Nucleic acids research*, 54(9).

Rasetto NB, et al. (2026) Cell-state mapping reveals a reversible neuroblast accumulation in the aging mouse hippocampus. *bioRxiv : the preprint server for biology*.