Resource Summary Report

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WEGO - Web Gene Ontology Annotation Plot

RRID:SCR_005827
Type: Tool

Proper Citation

WEGO - Web Gene Ontology Annotation Plot (RRID:SCR_005827)

Resource Information

URL: http://wego.genomics.org.cn/cgi-bin/wego/index.pl

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Description: Web Gene Ontology Annotation Plot (WEGO) is a simple but useful tool for plotting Gene Ontology (GO) annotation results. Different from other commercial software for chart creating, WEGO is designed to deal with the directed acyclic graph (DAG) structure of GO to facilitate histogram creation of GO annotation results. WEGO has been widely used in many important biological research projects, such as the rice genome project and the silkworm genome project. It has become one of the useful tools for downstream gene annotation analysis, especially when performing comparative genomics tasks. Platform: Online tool

Abbreviations: WEGO

Synonyms: BGI WEGO - Web Gene Ontology Annotation Plotting, Web Gene Ontology Annotation Plot

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

Defining Citation: PMID:16845012

Keywords: visualization, gene ontology, gene, annotation, comparative genomics, histogram, directed acyclic graph, genomics, genome, ontology or annotation visualization, bio.tools

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Availability: Free for academic use

Resource Name: WEGO - Web Gene Ontology Annotation Plot

Resource ID: SCR_005827

Alternate IDs: biotools:wego, nlx_149334

Alternate URLs: https://bio.tools/wego

Record Creation Time: 20220129T080232+0000

Record Last Update: 20250420T015526+0000

Ratings and Alerts

No rating or validation information has been found for WEGO - Web Gene Ontology Annotation Plot.

No alerts have been found for WEGO - Web Gene Ontology Annotation Plot.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 383 mentions in open access literature.

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

Bhatia N, et al. (2024) Transcriptome analysis reveals genes associated with late blight resistance in potato. Scientific reports, 14(1), 15501.

Suppiyar V, et al. (2024) Genome-wide identification and expression analysis of the SET domain-containing gene family in potato (Solanum tuberosum L.). BMC genomics, 25(1), 442.

Song YY, et al. (2024) A novel Trichinella spiralis serine proteinase disrupted gut epithelial barrier and mediated larval invasion through binding to RACK1 and activating MAPK/ERK1/2 pathway. PLoS neglected tropical diseases, 18(1), e0011872.

Ma XY, et al. (2024) Transcriptome analysis of Gossypium hirsutum cultivar Zhongzhimian No.2 uncovers the gene regulatory networks involved in defense against Verticillium dahliae. BMC plant biology, 24(1), 457.

Miranda J, et al. (2024) First neurotranscriptome of adults Tambaquis (Colossoma macropomum) with characterization and differential expression between males and females. Scientific reports, 14(1), 3130.

Petijová L, et al. (2024) In silico prediction of polyketide biosynthetic gene clusters in the genomes of Hypericum-borne endophytic fungi. BMC genomics, 25(1), 555.

Wang M, et al. (2024) Exploring the potential of Paris polyphylla var. yunnanensis pollen manipulation in modifying seed dormancy. Frontiers in plant science, 15, 1389357.

Wu L, et al. (2023) CD146-positive adipose-derived stem cells subpopulation enriched by albumin magnetic sphere ameliorates knee osteoarthritis pain and promotes cartilage repair. Journal of orthopaedic surgery and research, 18(1), 969.

Chen L, et al. (2023) Genome-wide identification of WD40 transcription factors and their regulation of the MYB-bHLH-WD40 (MBW) complex related to anthocyanin synthesis in Qingke (Hordeum vulgare L. var. nudum Hook. f.). BMC genomics, 24(1), 166.

Yang Y, et al. (2022) Metagenomic and metatranscriptomic analyses reveal minor-yet-crucial roles of gut microbiome in deep-sea hydrothermal vent snail. Animal microbiome, 4(1), 3.

Wang Z, et al. (2022) Taurine metabolism is modulated in Vibrio-infected Penaeus vannamei to shape shrimp antibacterial response and survival. Microbiome, 10(1), 213.

Sun YL, et al. (2022) Identification and Characterization of Chemosensory Receptors in the Pheromone Gland-Ovipositor of Spodoptera frugiperda (J. E. Smith). Insects, 13(5).

Lee KW, et al. (2022) Developmental Transcriptome Analysis of Red-Spotted Apollo Butterfly, Parnassius bremeri. International journal of molecular sciences, 23(19).

He QR, et al. (2021) The natural product trienomycin A is a STAT3 pathway inhibitor that exhibits potent in vitro and in vivo efficacy against pancreatic cancer. British journal of pharmacology, 178(12), 2496.

Vangelisti A, et al. (2021) LTR-retrotransposon dynamics in common fig (Ficus carica L.) genome. BMC plant biology, 21(1), 221.

Hussain T, et al. (2021) Combined Transcriptome and Proteome Analysis to Elucidate Salt Tolerance Strategies of the Halophyte Panicum antidotale Retz. Frontiers in plant science, 12, 760589.

Du N, et al. (2021) Adult astrocytes from reptiles are resistant to proinflammatory activation via sustaining Vav1 expression. The Journal of biological chemistry, 296, 100527.

Huang HJ, et al. (2021) Identification of Riptortus pedestris Salivary Proteins and Their Roles in Inducing Plant Defenses. Biology, 10(8).

Cárcamo de la Concepción M, et al. (2021) De novo sequencing and analysis of the transcriptome of two highbush blueberry (Vaccinium corymbosum L.) cultivars 'Bluecrop' and 'Legacy' at harvest and following post-harvest storage. PloS one, 16(8), e0255139.

Sharma S, et al. (2021) Exploring the edible gum (galactomannan) biosynthesis and its regulation during pod developmental stages in clusterbean using comparative transcriptomic approach. Scientific reports, 11(1), 4000.