Resource Summary Report

Generated by dkNET on May 20, 2025

GeneMarkS-T

RRID:SCR_017648
Type: Tool

Proper Citation

GeneMarkS-T (RRID:SCR_017648)

Resource Information

URL: http://topaz.gatech.edu/GeneMark/

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Description: Software package for ab initio identification of protein coding regions in RNA transcripts. Algorithm parameters are estimated by unsupervised training which makes unnecessary manually curated preparation of training sets. Sets of assembled eukaryotic transcripts can be analyzed by modified GeneMarkS-T algorithm which part of gene prediction programs GeneMark.

Resource Type: software application, software resource, data analysis software, data processing software

Defining Citation: PMID:25870408

Keywords: Identification, protein, coding, region, RNA, transcript, gene, discovery, eukaryotic, sequence, bio.tools

Funding: NHGRI HG000783

Availability: Restricted

Resource Name: GeneMarkS-T

Resource ID: SCR_017648

Alternate IDs: biotools:GeneMarkS-t

Alternate URLs: https://bio.tools/GeneMarkS-T

License: http://topaz.gatech.edu/GeneMark/license_download.cgi

Record Creation Time: 20220129T080336+0000

Record Last Update: 20250519T204007+0000

Ratings and Alerts

No rating or validation information has been found for GeneMarkS-T.

No alerts have been found for GeneMarkS-T.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 89 mentions in open access literature.

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

Yang JT, et al. (2025) Non-adapted bacterial infection suppresses plant reproduction. Science advances, 11(2), eads7738.

Ren M, et al. (2025) Duodenal-jejunal bypass ameliorates MASLD in rats by regulating gut microbiota and bile acid metabolism through FXR pathways. Hepatology communications, 9(2).

Oriowo TO, et al. (2025) A chromosome-level, haplotype-resolved genome assembly and annotation for the Eurasian minnow (Leuciscidae: Phoxinus phoxinus) provide evidence of haplotype diversity. GigaScience, 14.

Jin Z, et al. (2024) Dapagliflozin ameliorates diabetes-induced spermatogenic dysfunction by modulating the adenosine metabolism along the gut microbiota-testis axis. Scientific reports, 14(1), 641.

Xie J, et al. (2024) Integrated multi-omics analysis of the microbial profile characteristics associated with pulmonary arterial hypertension in congenital heart disease. Microbiology spectrum, 12(12), e0180824.

Shen D, et al. (2024) Dynamics of antibiotic resistance in poultry farms via multivector analysis. Poultry science, 104(2), 104673.

Yu L, et al. (2024) Antimicrobial resistance and virulence factors analysis of a multidrug-resistant Acinetobacter baumannii isolated from chickens using whole-genome sequencing.

BMC microbiology, 24(1), 526.

Sun J, et al. (2024) Integrated meta-omics reveals the regulatory landscape involved in lipid metabolism between pig breeds. Microbiome, 12(1), 33.

Han D, et al. (2024) Metagenomics profiling of the microbial community and functional differences in solid-state fermentation vinegar starter (seed Pei) from different Chinese regions. Frontiers in microbiology, 15, 1389737.

Yan L, et al. (2024) Gut microbiota and metabolic changes in children with idiopathic short stature. BMC pediatrics, 24(1), 468.

Ding L, et al. (2024) Maternal high fat diet induces circadian clock-independent endocrine alterations impacting the metabolism of the offspring. iScience, 27(7), 110343.

Wang Y, et al. (2024) Biologic and genomic characterization of a novel virulent Aeromonas hydrophila phage phiA051, with high homology to prophages. Frontiers in veterinary science, 11, 1415685.

Xu P, et al. (2024) Characterization of a Highly Virulent Klebsiella michiganensis Strain Isolated from a Preterm Infant with Sepsis. Infection and drug resistance, 17, 4973.

Wang W, et al. (2024) A novel virus potentially evolved from the N4-like viruses represents a unique viral family: Poorviridae. Applied and environmental microbiology, 90(12), e0155924.

Cheng C, et al. (2024) A Bacillus velezensis strain isolated from oats with disease-preventing and growth-promoting properties. Scientific reports, 14(1), 12950.

Yan Z, et al. (2024) Quantitative and dynamic profiling of human gut core microbiota by real-time PCR. Applied microbiology and biotechnology, 108(1), 396.

Guo X, et al. (2024) A novel flavobacterial phage abundant during green tide, representing a new viral family, Zblingviridae. Applied and environmental microbiology, 90(7), e0036724.

Shein AMS, et al. (2024) Phage cocktail amikacin combination as a potential therapy for bacteremia associated with carbapenemase producing colistin resistant Klebsiella pneumoniae. Scientific reports, 14(1), 28992.

Liang W, et al. (2024) Identification and Genome Sequencing of Novel Virulent Strains of Xanthomonas oryzae pv. oryzae Causing Rice Bacterial Blight in Zhejiang, China. Pathogens (Basel, Switzerland), 13(12).

Wang K, et al. (2024) Contamination Characteristics of Antibiotic Resistance Genes in Multi-Vector Environment in Typical Regional Fattening House. Toxics, 12(12).