

Resource Summary Report

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

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: 20260912T195855+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 172 mentions in open access literature.

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

Zhang J, et al. (2026) Enhancing the fiber degradation efficiency in dairy cattle rumen through engineered bacterial communities. *Microbiome*, 14(1).

Wang X, et al. (2026) Disrupted Tryptophan Metabolism Mediates Manganese-Induced Neurogenesis and Neuroinflammatory Impairments: Rescue by Exogenous Melatonin. *Environment & health (Washington, D.C.)*, 4(2), 275.

Ma W, et al. (2026) Type A and D *Clostridium perfringens* with unique genetic evolution characteristics cause mortality in juvenile Bactrian camels. *Frontiers in cellular and infection microbiology*, 16, 1787432.

Zhang Y, et al. (2026) Prevalence and mobile genetic element-mediated dissemination of antimicrobial resistance along the swine industry chain of Guizhou, China. *BMC veterinary research*, 22(1).

Li H, et al. (2026) Dysbiosis and unsustainable delayed gut microbiota development as non-invasive biomarkers for predicting autism spectrum disorder in Chinese children. *Frontiers in microbiology*, 17, 1753665.

Lu Q, et al. (2026) Genomic characterization of APEC phages and evaluation of the efficacy in reducing the loads of APEC O78 infections in chickens. *Frontiers in microbiology*, 17, 1670169.

Gu T, et al. (2026) Genomic characteristics and drug resistance phenotype of *Levyella massiliensis* isolated from blood. *BMC microbiology*, 26(1).

Serna-García R, et al. (2026) Harnessing Biogas into High-Value Chemicals: The Role of Algal-Methanotrophic Co-Cultures. *Marine drugs*, 24(2).

Yuan G, et al. (2026) Shading affects the nitrogen cycling process and plant nitrogen uptake by altering the rhizosphere microbial community. *Frontiers in plant science*, 17, 1780344.

Naitchede LHS, et al. (2026) Microbial community characterization in semi-hydroponic systems of Starbor kale (*Brassica oleracea* L.) grown under normal gravity and simulated microgravity. *Current research in microbial sciences*, 10, 100592.

Kong Y, et al. (2026) Prebiotics as adjunctive treatment ameliorates DSS-induced colitis and gut microbiota. *Microbiology spectrum*, 14(1), e0150225.

Ge G, et al. (2026) Isolation, identification and genomic analysis of *Mycobacterium caprae* strain SY-1 from Chinese sika deer (*Cervus nippon*). *BMC genomics*, 27(1), 184.

Wan S, et al. (2026) Multidimensional characterization of a novel porcine *Klebsiella pneumoniae* phage Pkp-1. *BMC microbiology*, 26(1), 131.

Shehla S, et al. (2026) Shotgun Metagenomics Reveals Microbial Diversity, Resistome, and Plasmidome in Dairy Cattle Feces. *Veterinary sciences*, 13(3).

Wang Y, et al. (2026) Microbial Contamination, Degradation Characteristics of Dominant Bacteria on the Hull of the Nanhai No. 1 Shipwreck. *International journal of molecular sciences*, 27(12).

Pan J, et al. (2025) Unraveling the microbiome-aroma Nexus: a metagenomic and volatile compound analysis of Yunnan cigars. *Frontiers in microbiology*, 16, 1597501.

Wei M, et al. (2025) Elevated phenylacetylglutamine caused by gut dysbiosis associated with type 2 diabetes increases neutrophil extracellular traps formation and exacerbates brain infarction. *Clinical science (London, England : 1979)*, 139(12), 717.

Ma R, et al. (2025) The bacterial diversity and potential pathogenic risks of giant panda-infesting ticks. *Microbiology spectrum*, 13(7), e0219724.

Zheng YY, et al. (2025) *Algoriphagus aurantiacus* sp. nov. and *Algoriphagus persicinus* sp. nov., two novel species isolated from the shore soil of salt lake. *International journal of systematic and evolutionary microbiology*, 75(6).

Cao L, et al. (2025) Comparative analysis of metagenomics between high- and medium-temperature daqu, and microbial succession in Jiang-Nong Jianxiang Baijiu fermentation. *BMC genomics*, 26(1), 852.