

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 processing software, data analysis 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: 20260801T042822+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 113 mentions in open access literature.

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

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

Wang L, et al. (2025) Metagenomic analysis reveals distinct patterns of gut microbiota features with diversified functions in *C. difficile* infection (CDI), asymptomatic carriage and non-CDI diarrhea. *Gut microbes*, 17(1), 2505269.

Yan Z, et al. (2025) Dietary microbiota-mediated shifts in gut microbial ecology and pathogen interactions in giant pandas (*Ailuropoda melanoleuca*). *Communications biology*, 8(1), 864.

Wang J, et al. (2025) Impact of intragastric administration of donkey milk on mouse immunity utilizing gut microbiomics and plasma metabolomics. *Frontiers in veterinary science*, 12, 1486406.

Zhang W, et al. (2025) Dynamics of the gut microbiome and resistome in response to prophylactic antibiotic treatment in post-surgical giant pandas. *Scientific reports*, 15(1), 43425.

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).

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.

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

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.

Yang R, et al. (2025) *Lactocaseibacillus rhamnosus* GR-1 prevents autism-like behaviors by reshaping the maternal and offspring microbiome. *NPJ biofilms and microbiomes*, 11(1), 187.

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).

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

Li H, et al. (2025) Unraveling gut microbiome alterations and metabolic signatures in hereditary transthyretin amyloidosis. *Microbiology spectrum*, 13(7), e0230224.

Jia X, et al. (2025) Metagenomic analysis reveals the abundance changes of bacterial communities and antibiotic resistance genes in the influent and effluent of hospital wastewater. *PloS one*, 20(10), e0335723.

Dong L, et al. (2025) Metagenomic insights reveal the differences in the community composition and functional characteristics of the sea turtle microbiomes based on host species and tissue region. *Frontiers in microbiology*, 16, 1652229.

Deng Y, et al. (2025) Symbiotic *Enterococcus faecalis* potentiates viral pathogenesis via fructose-1,6-bisphosphate-mediated insect gut epithelial damage. *NPJ biofilms and microbiomes*, 11(1), 215.

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.

Liang Y, et al. (2025) The molecular basis of octocoral calcification revealed by genome and skeletal proteome analyses. *GigaScience*, 14.

Shen Y, et al. (2025) Comparative microbiomic analysis of fecal microbiota associated with abdominal fat in ducks. *Poultry science*, 104(8), 105282.