

Resource Summary Report

Generated by [ASWG](#) on Sep 19, 2026

GeneMark

RRID:SCR_011930

Type: Tool

Proper Citation

GeneMark (RRID:SCR_011930)

Resource Information

URL: <http://opal.biology.gatech.edu/GeneMark/>

Proper Citation: GeneMark (RRID:SCR_011930)

Description: A family of gene prediction programs developed at Georgia Institute of Technology.

Abbreviations: GeneMark

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

Availability: Academic License Agreement

Resource Name: GeneMark

Resource ID: SCR_011930

Alternate IDs: OMICS_01485

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260912T195742+0000

Ratings and Alerts

No rating or validation information has been found for GeneMark.

No alerts have been found for GeneMark.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 805 mentions in open access literature.

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

Ma Y, et al. (2026) The hidden Markov model and its applications in bioinformatics analysis. *Genes & diseases*, 13(1), 101729.

Mu D, et al. (2026) The genome of the medicinal plant *Uncaria rhynchophylla* provides new insights into monoterpenoid indole alkaloid metabolism and its molecular regulatory mechanism. *Molecular horticulture*, 6(1), 9.

Sch??n ME, et al. (2026) Strain-level diversity of giant viruses infecting chlorarachniophyte algae in the subtropical North Pacific. *The ISME journal*, 20(1).

Wang Z, et al. (2026) Haplotype-Resolved Genome Assembly and Population Genomics Reveal Evolutionary History and Agronomic Traits of Mulberry. *Plant biotechnology journal*, 24(4), 2105.

Safi H, et al. (2026) Elucidating the protein interaction network of one of the largest icosahedral capsids in the virosphere. *The EMBO journal*, 45(10), 3514.

Yao W, et al. (2026) Chromosome-level genome assemblies of two maize inbred lines with contrasting plant architectures. *Scientific data*, 13(1), 276.

Human ZR, et al. (2026) Seasonality of composition, genomic potential and activity of coniferous forest soil microbiomes. *Scientific data*, 13(1).

Li Y, et al. (2026) Clinical Characteristics, Antimicrobial Resistance Profiles and Carbapenemases Genotypes of *Providencia rettgeri*: A 5-Year Retrospective Study in a Tertiary Teaching Hospital in Northern China. *Infection and drug resistance*, 19, 605665.

Zhou Z, et al. (2026) Chromosome-level genome provides novel insights into the starch metabolism regulation and evolutionary history of *Tetraselmis helgolandica*. *Journal of advanced research*, 79, 251.

Coleine C, et al. (2026) Genomic and Ecological Flexibility Shape the Global Distribution of a Black Fungus. *Environmental microbiology*, 28(4), e70301.

Baek K, et al. (2026) Genomic and in vitro characterization of two lytic bacteriophages infecting multidrug-resistant *Erwinia* sp. strain AnSW2-5. *Scientific reports*, 16(1).

Stellwagen SD, et al. (2026) Genome of Facultatively Parthenogenetic Harvester (Opiliones) Indicates Frequent Mitonuclear Sequence Transfer and Novel Full-Length Insertions. *Genome biology and evolution*, 18(5).

Kijpornyongpan T, et al. (2026) Gene presence-absence and evolutionary signals of positive selection associated with virulence divergence in *Beauveria* fungi. *Microbial genomics*, 12(6).

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

Dexter E, et al. (2026) Rapid evolution of a large structural polymorphism during a bacterial epidemic. *Heredity*, 135(1), 1.

Pedersen JS, et al. (2026) The first single-stranded DNA virus targeting *Pectobacterium* belongs to the family Microviridae and demonstrates a broad host range to *Pectobacterium brasiliense* soft rot pathogens. *Archives of virology*, 171(3).

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

Tagirdzhanova G, et al. (2026) Chromosome-level genome assembly of the photobiont microalga *Trebouxia* sp. 'A48' from the lichen *Xanthoria parietina*. *The New phytologist*, 249(2), 1036.

Shi Q, et al. (2026) Human messenger RNA harbors widespread noncoding splice isoforms. *Briefings in bioinformatics*, 27(1).

Huo Z, et al. (2026) Overcoming prokaryotic toxicity: a SUMO-fused secretory platform in *Komagataella phaffii* for high-yield production of phage holin Hol41. *Microbial cell factories*, 25(1).