

Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 9, 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: production service resource, software resource, data analysis service, analysis service resource, service resource

Availability: Academic License Agreement

Resource Name: GeneMark

Resource ID: SCR_011930

Alternate IDs: OMICS_01485

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260808T185937+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 [SPARC SAWG](#) .

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.

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.

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).

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

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).

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

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).

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).