

Resource Summary Report

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ProtHint

RRID:SCR_021167

Type: Tool

Proper Citation

ProtHint (RRID:SCR_021167)

Resource Information

URL: <https://github.com/gatech-genemark/ProtHint>

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Description: Software pipeline for predicting and scoring hints (in form of introns, start and stop codons) in genome of interest by mapping and spliced aligning predicted genes to database of reference protein sequences.

Resource Type: software toolkit, software resource

Keywords: Predicting and scoring hints, form of introns, start and stop codons, genome, mapping, spliced aligning, predicted genes, database, reference protein sequences

Availability: Free, Available for download, Freely available

Resource Name: ProtHint

Resource ID: SCR_021167

License URLs: <https://github.com/gatech-genemark/ProtHint/blob/master/LICENSE>

Record Creation Time: 20220129T080354+0000

Record Last Update: 20260803T040805+0000

Ratings and Alerts

No rating or validation information has been found for ProtHint.

No alerts have been found for ProtHint.

Data and Source Information

Usage and Citation Metrics

We found 45 mentions in open access literature.

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

Caron T, et al. (2025) Identification of quantitative trait loci (QTLs) for key cheese making phenotypes in the blue-cheese mold *Penicillium roqueforti*. PLoS genetics, 21(4), e1011669.

Omufwoko KS, et al. (2025) Developmental transcriptomes predict adult social behaviours in the socially flexible sweat bee, *Lasioglossum baleicum*. Molecular ecology, 34(15), e17244.

Beaulieu C, et al. (2025) The *Marchantia polymorpha* pangenome reveals ancient mechanisms of plant adaptation to the environment. Nature genetics, 57(3), 729.

Cadavid Sánchez IC, et al. (2025) Harnessing genetic diversity: The genomic and transcriptomic insights of *Eugenia uniflora* for environmental resilience. PloS one, 20(11), e0333437.

Zhu JP, et al. (2025) A chromosome-scale assembly of *Ormosia boluoensis* (Fabaceae). Scientific data, 12(1), 1659.

Gonçalves C, et al. (2025) Stable Hypermutators Revealed by the Genomic Landscape of Genes Involved in Genome Stability Among Yeast Species. Molecular biology and evolution, 42(11).

Laczkó L, et al. (2025) An updated reference genome of *Barbatula barbatula* (Linnaeus, 1758). Scientific data, 12(1), 137.

Chen M, et al. (2025) The genome of *Hippophae salicifolia* provides new insights into the sexual differentiation of sea buckthorn. GigaScience, 14.

Shaw PL, et al. (2025) Chromosome-level genome assemblies for the latent pine pathogen, *Diplodia sapinea*, reveal two accessory chromosomes with distinct genomic features and evolutionary dynamics. G3 (Bethesda, Md.), 15(12).

Yu N, et al. (2024) Chromosome-level genome of spider *Pardosa pseudoannulata* and cuticle protein genes in environmental stresses. Scientific data, 11(1), 121.

Weng YM, et al. (2024) Evolutionary genomics of three agricultural pest moths reveals rapid evolution of host adaptation and immune-related genes. GigaScience, 13.

Markee A, et al. (2024) De Novo Long-Read Genome Assembly and Annotation of the Luna Moth (*Actias luna*) Fully Resolves Repeat-Rich Silk Genes. Genome biology and evolution, 16(7).

Russo A, et al. (2024) Genome of the early spider-orchid *Ophrys sphegodes* provides insights into sexual deception and pollinator adaptation. *Nature communications*, 15(1), 6308.

Gao Y, et al. (2024) Chromosome-level genome assembly of *Ajuga decumbens*. *Frontiers in plant science*, 15, 1413468.

Lee SJ, et al. (2024) Chromosome-level genome assembly and annotation of the Patagonian toothfish *Dissostichus eleginoides*. *Scientific data*, 11(1), 1240.

Nagy NA, et al. (2024) The updated genome of the Hungarian population of *Aedes koreicus*. *Scientific reports*, 14(1), 7545.

Yang M, et al. (2024) Adaptation of *Fusarium* Head Blight Pathogens to Changes in Agricultural Practices and Human Migration. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 11(36), e2401899.

Schultz DT, et al. (2024) Acceleration of genome rearrangement in clitellate annelids. *bioRxiv : the preprint server for biology*.

Frail S, et al. (2024) Genomes of nitrogen-fixing eukaryotes reveal a non-canonical model of organellogenesis. *bioRxiv : the preprint server for biology*.

Sylvester T, et al. (2024) A reference quality genome assembly for the jewel scarab *Chrysina gloriosa*. *G3* (Bethesda, Md.), 14(6).