

# Resource Summary Report

Generated by RRID on Apr 28, 2025

## FGENESH

RRID:SCR\_011928

Type: Tool

### Proper Citation

FGENESH (RRID:SCR\_011928)

### Resource Information

**URL:** <http://nhjy.hzau.edu.cn/kech/swxxx/jakj/dianzi/Bioinf6/GeneFinding/GeneFinding2.htm>

**Proper Citation:** FGENESH (RRID:SCR\_011928)

**Description:** THIS RESOURCE IS NO LONGER IN SERVICE. Documented on August 10, 2020. Data analysis service for Hidden Markov Model (HMM)-based gene structure prediction (multiple genes, both chains).

**Abbreviations:** FGENESH

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

**Keywords:** bio.tools

**Funding:**

**Availability:** THIS RESOURCE IS NO LONGER IN SERVICE

**Resource Name:** FGENESH

**Resource ID:** SCR\_011928

**Alternate IDs:** biotools:fgenesh, OMICS\_01483

**Alternate URLs:** <https://bio.tools/fgenesh>

**Record Creation Time:** 20220129T080307+0000

**Record Last Update:** 20250428T053639+0000

## Ratings and Alerts

No rating or validation information has been found for FGENESH.

No alerts have been found for FGENESH.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 328 mentions in open access literature.

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

Tang R, et al. (2024) Tandemly expanded OR17b in Himalaya ghost moth facilitates larval food allocation via olfactory reception of plant-derived tricosane. International journal of biological macromolecules, 268(Pt 1), 131503.

Gong Y, et al. (2024) CRISPR/Cas9 system is a suitable gene targeting editing tool to filamentous fungus *Monascus pilosus*. Applied microbiology and biotechnology, 108(1), 154.

You Y, et al. (2024) Locust Pathogen *Aspergillus oryzae* XJ1 Is Different from *Aspergillus oryzae* and *Aspergillus flavus* Based on Genomics Comparisons. Microorganisms, 12(12).

Dutta TK, et al. (2024) Induced knockdown of Mg-odr-1 and Mg-odr-3 perturbed the host seeking behavior of *Meloidogyne graminicola* in rice. Heliyon, 10(4), e26384.

Zheng L, et al. (2024) PP2 gene family in *Phyllostachys edulis*: identification, characterization, and expression profiles. BMC genomics, 25(1), 1081.

Zhang Y, et al. (2024) Genomic Features of *Taiwanofungus gaoligongensis* and the Transcriptional Regulation of Secondary Metabolite Biosynthesis. Journal of fungi (Basel, Switzerland), 10(12).

Zhang Z, et al. (2024) Integrative multi-omics analysis reveals the contribution of neoVTX genes to venom diversity of *Synanceia verrucosa*. BMC genomics, 25(1), 1210.

Meng Y, et al. (2024) E3 ubiquitin ligase TaSDIR1-4A activates membrane-bound transcription factor TaWRKY29 to positively regulate drought resistance. Plant biotechnology journal, 22(4), 987.

Tang R, et al. (2024) A ghost moth olfactory prototype of the lepidopteran sex communication. GigaScience, 13.

Xie J, et al. (2024) Evolution and related pathogenic genes of *Pseudodiploöspora longispora*

on *Morchella* based on genomic characterization and comparative genomic analysis. *Scientific reports*, 14(1), 18588.

Li M, et al. (2024) Genome sequencing, comparative analysis, and gene expression responses of cytochrome P450 genes in *Oryzias curvinotus* provide insights into environmental adaptation. *Ecology and evolution*, 14(6), e11565.

Liu Z, et al. (2024) Molecular Phylogenetic and Comparative Genomic Analysis of *Pleurocordyceps fusiformispora* sp. nov. and *Perennicordyceps elaphomyceticola* in the Family Polycephalomycetaceae. *Journal of fungi* (Basel, Switzerland), 10(4).

Zhang H, et al. (2024) ZNF740 facilitates the malignant progression of hepatocellular carcinoma via the METTL3/HIF?1A signaling axis. *International journal of oncology*, 65(5).

Bellino C, et al. (2024) Molecular Evolution of RAMOSA1 (RA1) in Land Plants. *Biomolecules*, 14(5).

Ryu JS, et al. (2024) Quantitative trait loci analysis for molecular markers linked to agricultural traits of *Pleurotus ostreatus*. *PloS one*, 19(8), e0308832.

Jaqueth JS, et al. (2024) Pentatricopeptide repeat 153 (PPR153) restores maize C-type cytoplasmic male sterility in conjunction with RF4. *PloS one*, 19(7), e0303436.

Neupane S, et al. (2024) Discovery of unguisin J, a new cyclic peptide from *Aspergillus heteromorphus* CBS 117.55, and phylogeny-based bioinformatic analysis of UngA NRPS domains. *Beilstein journal of organic chemistry*, 20, 321.

Majka M, et al. (2023) The chromatin determinants and Ph1 gene effect at wheat sites with contrasting recombination frequency. *Journal of advanced research*, 53, 75.

Vannier N, et al. (2023) Genome-resolved metatranscriptomics reveals conserved root colonization determinants in a synthetic microbiota. *Nature communications*, 14(1), 8274.

Lu J, et al. (2023) Genome-Wide Identification and Expression Pattern of Cytochrome P450 Genes in the Social Aphid *Pseudoregma bambucicola*. *Insects*, 14(2).