

Resource Summary Report

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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: analysis service resource, service resource, data analysis service, production service resource

Keywords: bio.tools

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: 20260728T043359+0000

Ratings and Alerts

No rating or validation information has been found for FGENESH.

No alerts have been found for FGENESH.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 330 mentions in open access literature.

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

Mochales-Riaño G, et al. (2025) Chromosome-level reference genome for the medically important Arabian horned viper (*Cerastes gasperettii*). *GigaScience*, 14.

Guang X, et al. (2025) Telomere-to-telomere African wild rice (*Oryza longistaminata*) reference genome reveals segmental and structural variation. *GigaScience*, 14.

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.

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.

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

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.

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).

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

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

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).

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.

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.

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