

Resource Summary Report

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Fgenesh plus plus

RRID:SCR_018928

Type: Tool

Proper Citation

Fgenesh plus plus (RRID:SCR_018928)

Resource Information

URL:

http://www.softberry.com/berry.phtml?topic=fgenesh_plus_plus&group=help&subgroup=pipelines

Proper Citation: Fgenesh plus plus (RRID:SCR_018928)

Description: Software tool as pipeline for automatic prediction of genes in eukaryotic genomes based on Softberry gene finding software.

Synonyms: Fgenesh Plus Plus, FGENESH plus plus, FGENESH Plus Plus

Resource Type: simulation software, software application, software resource

Defining Citation: [PMID:16925832](#)

Keywords: Automatic gene prediction, eukaryotic genomes, Softberry software, gene finding

Availability: Restricted

Resource Name: Fgenesh plus plus

Resource ID: SCR_018928

License: Softberry license

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260912T195907+0000

Ratings and Alerts

No rating or validation information has been found for Fgenesh plus plus.

No alerts have been found for Fgenesh plus plus.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Kojima Y, et al. (2025) Adsorption Capacity of CBM104s Appended to Different Types of Catalytic Domains. *Journal of applied glycoscience*, 72(4), 7204101.

Silver LW, et al. (2024) A reference genome, mitochondrial genome and associated transcriptomes for the critically endangered swift parrot (*Lathamus discolor*). *F1000Research*, 13, 251.

Angosto-Bazarra D, et al. (2022) Evolutionary analyses of the gasdermin family suggest conserved roles in infection response despite loss of pore-forming functionality. *BMC biology*, 20(1), 9.

Peel E, et al. (2022) Genome assembly of the numbat (*Myrmecobius fasciatus*), the only termitivorous marsupial. *GigaByte (Hong Kong, China)*, 2022, gigabyte47.

Peel E, et al. (2021) A reference genome for the critically endangered woylie, *Bettongia penicillata ogilbyi*. *GigaByte (Hong Kong, China)*, 2021, gigabyte35.

Voelker J, et al. (2021) A high-quality draft genome for *Melaleuca alternifolia* (tea tree): a new platform for evolutionary genomics of myrtaceous terpene-rich species. *GigaByte (Hong Kong, China)*, 2021, gigabyte28.

Brandies PA, et al. (2020) The first *Antechinus* reference genome provides a resource for investigating the genetic basis of semelparity and age-related neuropathologies. *GigaByte (Hong Kong, China)*, 2020, gigabyte7.