

Resource Summary Report

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FunGAP

RRID:SCR_023213

Type: Tool

Proper Citation

FunGAP (RRID:SCR_023213)

Resource Information

URL: <https://github.com/CompSynBioLab-KoreaUniv/FunGAP>

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Description: Software tool to predict protein coding genes in fungal genome assembly. Performs gene prediction on given genome assembly and RNA-seq reads. Runs multiple gene predictors, evaluates all predicted genes, and assembles gene models that are highly supported by homology to known sequences.

Abbreviations: FunGAP

Synonyms: Fungal Genome Annotation Pipeline

Resource Type: simulation software, software application, software resource

Defining Citation: [PMID:28582481](#)

Keywords: Genome annotation, predict protein-coding genes, fungal genome assembly, RNA-seq reads, gene prediction

Funding: Rural Development Administration ;
Republic of Korea ;
School of Life Sciences and Biotechnology for BK21 PLUS ;
Korea University

Availability: Free, Available for download, Freely available

Resource Name: FunGAP

Resource ID: SCR_023213

Record Creation Time: 20230201T050208+0000

Record Last Update: 20260821T194236+0000

Ratings and Alerts

No rating or validation information has been found for FunGAP.

No alerts have been found for FunGAP.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Rafiqi M, et al. (2023) Endophytic fungi related to the ash dieback causal agent encode signatures of pathogenicity on European ash. IMA fungus, 14(1), 10.

Mena E, et al. (2022) Comparative genomics of plant pathogenic Diaporthe species and transcriptomics of Diaporthe caulivora during host infection reveal insights into pathogenic strategies of the genus. BMC genomics, 23(1), 175.