

Resource Summary Report

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Comparative Fungal Genomics Platform

RRID:SCR_012910

Type: Tool

Proper Citation

Comparative Fungal Genomics Platform (RRID:SCR_012910)

Resource Information

URL: <http://cfgp.riceblast.snu.ac.kr/main.php>

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Description: The CFGP (Comparative Fungal Genomics Platform) was designed for comparative genomics projects with diverse fungal genomes. The CFGP provides important bioinformatic tools, such as BLAST search, ClustalW analysis, InterPro Scan, SignalP, and PSORT2, which are very common tools for the researchers in the field of genomics. Many of them have been executed in the unix environment, so some specific computing knowledge is required. In the CFGP, users can use these tools simply by clicking their mouse button. In addition, all of the results of the analysis will be stored in the CFGP, so you can easily share those results with other members.

Synonyms: CFGP

Resource Type: data or information resource, database

Keywords: fungal genome, comparative genomics, genomics

Resource Name: Comparative Fungal Genomics Platform

Resource ID: SCR_012910

Alternate IDs: nif-0000-02653

Alternate URLs: <http://cfgp.snu.ac.kr>

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260821T194004+0000

Ratings and Alerts

No rating or validation information has been found for Comparative Fungal Genomics Platform.

No alerts have been found for Comparative Fungal Genomics Platform.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Kim Y, et al. (2024) MoNOT3 Subunit Has Important Roles in Infection-Related Development and Stress Responses in *Magnaporthe oryzae*. International journal of molecular sciences, 25(6).

Raigh KS, et al. (2022) CFTR bearing variant p.Phe312del exhibits function inconsistent with phenotype and negligible response to ivacaftor. JCI insight, 7(6).

Sun Q, et al. (2022) MagicalRsQ: Machine-learning-based genotype imputation quality calibration. American journal of human genetics, 109(11), 1986.

Shin JH, et al. (2022) CsPOM1, a DYRK Family Kinase, Plays Diverse Roles in Fungal Development, Virulence, and Stress Tolerance in the Anthracnose Pathogen *Colletotrichum scovillei*. Frontiers in cellular and infection microbiology, 12, 861915.

Mushtaq A, et al. (2021) Carbamoyl Phosphate Synthase Subunit CgCPS1 Is Necessary for Virulence and to Regulate Stress Tolerance in *Colletotrichum gloeosporioides*. The plant pathology journal, 37(3), 232.

Sadat MA, et al. (2021) The Membrane-Bound Protein, MoAfo1, Is Involved in Sensing Diverse Signals from Different Surfaces in the Rice Blast Fungus. The plant pathology journal, 37(2), 87.

Sadat MA, et al. (2021) Genome-wide identification of F-box proteins in *Macrophomina phaseolina* and comparison with other fungus. Journal, genetic engineering & biotechnology, 19(1), 46.

Wu J, et al. (2020) Comparative Genomics Platform and Phylogenetic Analysis of Fungal Laccases and Multi-Copper Oxidases. Mycobiology, 48(5), 373.

Jin JH, et al. (2020) Genome-wide functional analysis of phosphatases in the pathogenic fungus *Cryptococcus neoformans*. Nature communications, 11(1), 4212.

Li J, et al. (2020) Secretome-Wide Analysis of Lysine Acetylation in *Fusarium oxysporum* f. sp. *lycopersici* Provides Novel Insights Into Infection-Related Proteins. Frontiers in microbiology, 11, 559440.

Lim YJ, et al. (2018) SUMOylation is required for fungal development and pathogenicity in the rice blast fungus *Magnaporthe oryzae*. *Molecular plant pathology*, 19(9), 2134.

Goh J, et al. (2017) ER retention receptor, MoERR1 is required for fungal development and pathogenicity in the rice blast fungus, *Magnaporthe oryzae*. *Scientific reports*, 7(1), 1259.

Zhou Z, et al. (2017) ABC protein CgABCF2 is required for asexual and sexual development, appressorial formation and plant infection in *Colletotrichum gloeosporioides*. *Microbial pathogenesis*, 110, 85.

Choi J, et al. (2017) Comparative analysis of genome sequences of the conifer tree pathogen, *Heterobasidion annosum* s.s. *Genomics data*, 14, 106.

Kim KT, et al. (2016) Kingdom-Wide Analysis of Fungal Small Secreted Proteins (SSPs) Reveals their Potential Role in Host Association. *Frontiers in plant science*, 7, 186.

Lee KT, et al. (2016) Systematic functional analysis of kinases in the fungal pathogen *Cryptococcus neoformans*. *Nature communications*, 7, 12766.

Jung KW, et al. (2015) Systematic functional profiling of transcription factor networks in *Cryptococcus neoformans*. *Nature communications*, 6, 6757.

Choi J, et al. (2015) dbHiMo: a web-based epigenomics platform for histone-modifying enzymes. *Database : the journal of biological databases and curation*, 2015, bav052.

Kuo HC, et al. (2015) Potential roles of laccases on virulence of *Heterobasidion annosum* s.s. *Microbial pathogenesis*, 81, 16.

Sadat A, et al. (2014) Analysis of in planta Expressed Orphan Genes in the Rice Blast Fungus *Magnaporthe oryzae*. *The plant pathology journal*, 30(4), 367.