

Resource Summary Report

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PathoFact2

RRID:SCR_027650

Type: Tool

Proper Citation

PathoFact2 (RRID:SCR_027650)

Resource Information

URL: <https://gitlab.com/uniluxembourg/lcsb/systems-ecology/pathofact2>

Proper Citation: PathoFact2 (RRID:SCR_027650)

Description: Software integrative pipeline for antimicrobial resistance genes, virulence factors, toxins, and biosynthetic gene clusters prediction in metagenomes. Used for predicting microbiome-based pathogenicity and resistance to better understand and address challenges posed by antimicrobial resistance and infectious diseases.

Synonyms: PathoFact 2.0

Resource Type: software application, software resource

Defining Citation: [DOI:10.1101/2024.12.09.627531](https://doi.org/10.1101/2024.12.09.627531)

Keywords: predicting microbiome-based pathogeni, antimicrobial resistance genes, virulence factors, toxin-related proteins, biosynthetic gene clusters, metagenomes

Funding: Pélican grant from the Mie and Pierre Hippert-Faber Pélican Foundation ; Luxembourg National Research Fund FNR CORE/23/BM/15886415; European Research Council ERC-CoG 863664; Luxembourg National Research Fund FNR CORE/23/BM/15886415; Luxembourg Government CoVaLux program

Availability: Free, Available for download, Freely available

Resource Name: PathoFact2

Resource ID: SCR_027650

License: GNU GPL v3.0

Record Creation Time: 20251113T055906+0000

Record Last Update: 20260810T040944+0000

Ratings and Alerts

No rating or validation information has been found for PathoFact2.

No alerts have been found for PathoFact2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Delgado LF, et al. (2026) PathoFact 2.0: an integrative pipeline for the prediction of antimicrobial resistance genes, virulence factors, toxins and toxin-associated proteins, and biosynthetic gene clusters in metagenomes. GigaScience, 15.

Lu Z, et al. (2026) Tick-vectored mobilization of antibiotic resistance genes: transboundary dissemination across wildlife-livestock-vector-environment interfaces. NPJ biofilms and microbiomes, 12(1).

Correa F, et al. (2025) Early antimicrobial regimen shapes gut microbiota and health trajectories in pigs: a longitudinal study from weaning to finishing. Animal microbiome, 7(1), 110.

Zadjelovic V, et al. (2023) Microbial hitchhikers harbouring antimicrobial-resistance genes in the riverine plastisphere. Microbiome, 11(1), 225.