

Resource Summary Report

Generated by [dkNET](#) on Aug 16, 2026

GenePath

RRID:SCR_007974

Type: Tool

Proper Citation

GenePath (RRID:SCR_007974)

Resource Information

URL: <http://www.genepath.org/>

Proper Citation: GenePath (RRID:SCR_007974)

Description: GenePath is a web-enabled intelligent assistant for the analysis of genetic data and for discovery of genetic networks. GenePath uses abductive inference to elucidate network constraints and logic to derive consistent networks. Typically, it starts with a set of genetic experiments, uses a set of embedded rules (patterns) to infer relations between genes and outcome, and based on these relations constructs a genetic network.

Synonyms: GenePath

Resource Type: data or information resource, database

Keywords: genetic, data, network

Resource Name: GenePath

Resource ID: SCR_007974

Alternate IDs: nif-0000-20848

Record Creation Time: 20220129T080244+0000

Record Last Update: 20260815T182905+0000

Ratings and Alerts

No rating or validation information has been found for GenePath.

No alerts have been found for GenePath.

Data and Source Information

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Kwiatkowski P, et al. (2026) Phenotypic and Genotypic Characteristics of Staphylococcus aureus Nasal Strains Isolated from Students of the Pomeranian Medical University in Szczecin, Poland: A Cross-Sectional Study. Toxins, 18(5).

Matra S, et al. (2025) Wastewater surveillance of open drains for mapping the trajectory and succession of SARS-CoV-2 lineages in 23 cities of Maharashtra state (India) during June 2022 to May 2023. Heliyon, 11(4), e42534.

Shravya MS, et al. (2025) Biallelic Variant, c.644-13_644-9del in UNC50 Is Associated With Congenital Myasthenia Syndrome. American journal of medical genetics. Part A, 197(8), e64086.

Wacharapluesadee S, et al. (2024) Comparative Performance in the Detection of Four Coronavirus Genera from Human, Animal, and Environmental Specimens. Viruses, 16(4).

Patankar SB, et al. (2022) Efficacy and safety of polyherbal formulation as an add-on to standard-of-care in mild-to-moderate COVID-19: A randomized, double-blind, placebo-controlled trial. Journal of Ayurveda and integrative medicine, 13(4), 100653.

Widerström M, et al. (2022) Heterogeneity of Staphylococcus epidermidis in prosthetic joint infections: time to reevaluate microbiological criteria? European journal of clinical microbiology & infectious diseases : official publication of the European Society of Clinical Microbiology, 41(1), 87.

Yaren O, et al. (2021) Ultra-rapid detection of SARS-CoV-2 in public workspace environments. PloS one, 16(2), e0240524.

Aumeran C, et al. (2021) A prospective study on the pathogenesis of catheter-associated bacteriuria in critically ill patients. BMC microbiology, 21(1), 86.

Kwiatkowski P, et al. (2020) Antibacterial Activity of Selected Essential Oil Compounds Alone and in Combination with β -Lactam Antibiotics Against MRSA Strains. International journal of molecular sciences, 21(19).

Yaren O, et al. (2017) Point of sampling detection of Zika virus within a multiplexed kit capable of detecting dengue and chikungunya. BMC infectious diseases, 17(1), 293.

Li J, et al. (2016) Characterization of clinical extensively drug-resistant Pseudomonas aeruginosa in the Hunan province of China. Annals of clinical microbiology and antimicrobials, 15(1), 35.

Li J, et al. (2016) An Outbreak of Infections Caused by a Klebsiella pneumoniae ST11 Clone Coproducing Klebsiella pneumoniae Carbapenemase-2 and RmtB in a Chinese

Teaching Hospital. Chinese medical journal, 129(17), 2033.

Diop A, et al. (2016) First Description of the Extended Spectrum-Beta-Lactamase Gene blaCTX-M-109 in *Salmonella* Grumpensis Strains Isolated from Neonatal Nosocomial Infections in Dakar, Senegal. PloS one, 11(6), e0157683.

Al-Bayssari C, et al. (2015) MUS-2, a novel variant of the chromosome-encoded β -lactamase MUS-1, from *Myroides odoratimimus*. New microbes and new infections, 7, 67.

Wu W, et al. (2015) Transition of blaOXA-58-like to blaOXA-23-like in *Acinetobacter baumannii* Clinical Isolates in Southern China: An 8-Year Study. PloS one, 10(9), e0137174.

Wang X, et al. (2014) Analysis of ventilator-associated pneumonia infection route by genome macrorestriction-pulsed-field gel electrophoresis and its prevention with combined nursing strategies. Experimental and therapeutic medicine, 8(6), 1922.