Resource Summary Report

Generated by RRID on Apr 17, 2025

PHAge Search Tool

RRID:SCR_005184
Type: Tool

Proper Citation

PHAge Search Tool (RRID:SCR_005184)

Resource Information

URL: http://phast.wishartlab.com/

Proper Citation: PHAge Search Tool (RRID:SCR_005184)

Description: A web server designed to rapidly and accurately identify, annotate and graphically display prophage sequences within bacterial genomes or plasmids. It accepts either raw DNA sequence data or partially annotated GenBank formatted data and rapidly performs a number of database comparisons as well as phage cornerstone feature identification steps to locate, annotate and display prophage sequences and prophage features. Relative to other prophage identification tools, PHAST is up to 40 times faster and up to 15% more sensitive. It is also able to process and annotate both raw DNA sequence data and Genbank files, provide richly annotated tables on prophage features and prophage quality and distinguish between intact and incomplete prophage. PHAST also generates downloadable, high quality, interactive graphics that display all identified prophage components in both circular and linear genomic views. Databases available for download include Virus DB, Prophage and virus DB, Bacteria DB, and PHAST result DB. Pre-calculated genomes for viewing are also available.

Abbreviations: PHAST

Synonyms: PHAST - PHAge Search Tool

Resource Type: data analysis service, data set, data or information resource, analysis service resource, production service resource, service resource

Defining Citation: PMID:21672955

Keywords: prophage sequence, genome, prophage, sequence, bacterial genome, plasmid, dna sequence, graph, phage, annotate, virus, nucleotide sequence, fasta, annotated genome, genbank, bio.tools, FASEB list

Funding:

Availability: Acknowledgement requested

Resource Name: PHAge Search Tool

Resource ID: SCR_005184

Alternate IDs: biotools:phast, OMICS_00180

Alternate URLs: https://bio.tools/phast

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250417T065216+0000

Ratings and Alerts

No rating or validation information has been found for PHAge Search Tool.

No alerts have been found for PHAge Search Tool.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 221 mentions in open access literature.

Listed below are recent publications. The full list is available at RRID.

Wright SN, et al. (2025) State of the interactomes: an evaluation of molecular networks for generating biological insights. Molecular systems biology, 21(1), 1.

Ivankovi? M, et al. (2024) A comparative analysis of planarian genomes reveals regulatory conservation in the face of rapid structural divergence. Nature communications, 15(1), 8215.

Li Y, et al. (2024) A novel pathogenic species of genus Stenotrophomonas: Stenotrophomonas pigmentata sp. nov. Frontiers in cellular and infection microbiology, 14, 1410385.

Lei H, et al. (2024) Evolutionary origin of germline pathogenic variants in human DNA mismatch repair genes. Human genomics, 18(1), 5.

Eastment RV, et al. (2024) Convergent genomic signatures associated with vertebrate viviparity. BMC biology, 22(1), 34.

Wang J, et al. (2024) Pathogenic and genomic characterization of rabbit-sourced Pasteurella multocida serogroup F isolates recovered from dead rabbits with respiratory disease. Microbiology spectrum, 12(4), e0365423.

de Los Santos MR, et al. (2024) Divergent landscapes of A-to-I editing in postmortem and living human brain. medRxiv : the preprint server for health sciences.

Ou JH, et al. (2024) Complex genetic architecture of the chicken Growth1 QTL region. PloS one, 19(5), e0295109.

Silvestro D, et al. (2024) Toward a Semi-Supervised Learning Approach to Phylogenetic Estimation. Systematic biology, 73(5), 789.

Kim BY, et al. (2024) Single-fly genome assemblies fill major phylogenomic gaps across the Drosophilidae Tree of Life. PLoS biology, 22(7), e3002697.

Kuderna LFK, et al. (2024) Identification of constrained sequence elements across 239 primate genomes. Nature, 625(7996), 735.

Tian R, et al. (2024) Sirenian genomes illuminate the evolution of fully aquatic species within the mammalian superorder afrotheria. Nature communications, 15(1), 5568.

Sakamoto F, et al. (2024) Detection of evolutionary conserved and accelerated genomic regions related to adaptation to thermal niches in Anolis lizards. Ecology and evolution, 14(3), e11117.

Cossette ML, et al. (2024) Comparative Genomics of the World's Smallest Mammals Reveals Links to Echolocation, Metabolism, and Body Size Plasticity. Genome biology and evolution, 16(11).

Cahn J, et al. (2024) MaizeCODE reveals bi-directionally expressed enhancers that harbor molecular signatures of maize domestication. Nature communications, 15(1), 10854.

Ma W, et al. (2024) A Novel Strain of Bacillus cereus with a Strong Antagonistic Effect Specific to Sclerotinia and Its Genomic and Transcriptomic Analysis. Microorganisms, 12(3).

Li X, et al. (2024) The Genome of Bifidobacterium longum subsp. infantis YLGB-1496 Provides Insights into Its Carbohydrate Utilization and Genetic Stability. Genes, 15(4).

Örmälä-Tiznado A-M, et al. (2024) Molecular characteristics, fitness, and virulence of high-risk and non-high-risk clones of carbapenemase-producing Klebsiella pneumoniae. Microbiology spectrum, 12(2), e0403622.

Zhu C, et al. (2024) Convergent Degenerated Regulatory Elements Associated with Limb Loss in Limbless Amphibians and Reptiles. Molecular biology and evolution, 41(11).

Xue M, et al. (2024) Identification and characterization of a potential strain for the production of polyhydroxyalkanoate from glycerol. Frontiers in microbiology, 15, 1413120.