

Resource Summary Report

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TIGRFAMS

RRID:SCR_005493

Type: Tool

Proper Citation

TIGRFAMS (RRID:SCR_005493)

Resource Information

URL: <http://www.jcvi.org/cgi-bin/tigrfams/index.cgi>

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Description: Consists curated multiple sequence alignments, Hidden Markov Models (HMMs) for protein sequence classification, and associated information designed to support automated annotation of (mostly prokaryotic) proteins. Starting with release 10.0, TIGRFAMS models use HMMER3, which provides excellent search speed as well as exquisite search sensitivity. See the "TIGRFAMS Complete Listing" page to review the accession, protein name, model type, and EC number (if assigned) of all models. TIGRFAMS is a member database in InterPro. The HMM libraries and supporting files are available to download and use for free from our FTP site.

Abbreviations: JCVI TIGRFAMS, TIGRFAM

Synonyms: TIGRFAMS

Resource Type: database, data or information resource, data set

Defining Citation: [PMID:23197656](#)

Keywords: sequence alignment, hidden markov model, protein sequence, classification, protein, protein family, sequence homology, sequence, homology, function, bio.tools

Availability: Free

Resource Name: TIGRFAMS

Resource ID: SCR_005493

Alternate IDs: nif-0000-03560, OMICS_01700, biotools:tigrfams

Alternate URLs: <https://bio.tools/tigrfams>

Old URLs: <http://www.tigr.org/TIGRFAMs>

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260728T043218+0000

Ratings and Alerts

No rating or validation information has been found for TIGRFAMS.

No alerts have been found for TIGRFAMS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 135 mentions in open access literature.

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

Costa VA, et al. (2025) Phylogenetic Diversity and Geographic Distribution of Atlantic Salmon Calicivirus in Major Salmon Farming Regions. *Journal of fish diseases*, 48(6), e14107.

Jung D, et al. (2025) Comparative genomic analysis of *Escherichia coli* isolated from cases of bovine clinical mastitis and the dairy farm environment. *Microbial genomics*, 11(6).

Mukherjee I, et al. (2025) Cultivation, genomics, and giant viruses of a ubiquitous and heterotrophic freshwater cryptomonad. *The ISME journal*, 19(1).

Smith NT, et al. (2025) Phylogenetic and biochemical analysis of the evolution and interdomain modularity of bifunctional L-fucokinase/GDP-fucose pyrophosphorylases. *The Journal of biological chemistry*, 301(12), 110937.

Menozzi E, et al. (2025) Exploring the relationship between GBA1 host genotype and gut microbiome in the GBA1 L444P/WT mouse model: implications for Parkinson's disease pathogenesis. *Frontiers in neuroscience*, 19, 1546203.

Galib M, et al. (2025) Identification of robust species-specific marker genes for the demarcation of the *Klebsiella pneumoniae*-*quasipneumoniae*-*variicola* complex. *Journal of medical microbiology*, 74(11).

Degnan PH, et al. (2025) Coupled evolutionary rates shape a Hawaiian insect-symbiont system. *BMC genomics*, 26(1), 336.

Du S, et al. (2025) House dust microbiome differentiation and phage-mediated antibiotic resistance and virulence dissemination in the presence of endocrine-disrupting chemicals

and pharmaceuticals. *Microbiome*, 13(1), 96.

Saeed H, et al. (2025) Characterization of holins, the membrane proteins of coliphage ASEC2201: a genomewide in silico approach. *Frontiers in microbiology*, 16, 1550594.

Ba?c? C, et al. (2025) Ultra-deep long-read metagenomics captures diverse taxonomic and biosynthetic potential of soil microbes. *GigaScience*, 14.

Costa VA, et al. (2025) Limited similarity in microbial composition among coral reef fishes from the Great Barrier Reef, Australia. *FEMS microbiology ecology*, 101(3).

Zhu X, et al. (2025) Virulence and Antibiotic Resistance of Pathogenic *Aeromonas caviae* from Diseased *Macrobrachium rosenbergii*. *Microorganisms*, 13(6).

Wu Y, et al. (2024) Evolution of two metabolic genes involved in nucleotide and amino acid metabolism in *Pseudomonas aeruginosa*. *PloS one*, 19(12), e0315931.

Cai Y, et al. (2024) Genome analysis of *Shewanella putrefaciens* 4H revealing the potential mechanisms for the chromium remediation. *BMC genomics*, 25(1), 136.

Arikan M, et al. (2024) gNOMO2: a comprehensive and modular pipeline for integrated multi-omics analyses of microbiomes. *GigaScience*, 13.

Valentin-Alvarado LE, et al. (2024) Complete genomes of Asgard archaea reveal diverse integrated and mobile genetic elements. *Genome research*, 34(10), 1595.

Jung H, et al. (2024) Genomic epidemiology and molecular characteristics of bla_{NDM-1}-positive carbapenem-resistant *Pseudomonas aeruginosa* belonging to international high-risk clone ST773 in the Gauteng region, South Africa. *European journal of clinical microbiology & infectious diseases* : official publication of the European Society of Clinical Microbiology, 43(4), 627.

Dmitrijeva M, et al. (2024) A global survey of prokaryotic genomes reveals the eco-evolutionary pressures driving horizontal gene transfer. *Nature ecology & evolution*, 8(5), 986.

Mancilla-Rojano J, et al. (2024) A bioinformatic approach to identify confirmed and probable CRISPR-Cas systems in the *Acinetobacter calcoaceticus*-*Acinetobacter baumannii* complex genomes. *Frontiers in microbiology*, 15, 1335997.

Glendinning L, et al. (2024) Infectious bronchitis virus vaccination, but not the presence of XCR1, is correlated with large differences in chicken caecal microbiota. *Microbial genomics*, 10(9).