

Resource Summary Report

Generated by [RRID](#) on Aug 8, 2026

HHpred

RRID:SCR_010276

Type: Tool

Proper Citation

HHpred (RRID:SCR_010276)

Resource Information

URL: <http://toolkit.tuebingen.mpg.de/hhpred>

Proper Citation: HHpred (RRID:SCR_010276)

Description: The primary aim in developing HHpred was to provide biologists with a method for sequence database searching and structure prediction that is as easy to use as BLAST or PSI-BLAST and that is at the same time much more sensitive in finding remote homologs. In fact, HHpred's sensitivity is competitive with the most powerful servers for structure prediction currently available. HHpred is the first server that is based on the pairwise comparison of profile hidden Markov models (HMMs). Whereas most conventional sequence search methods search sequence databases such as UniProt or the NR, HHpred searches alignment databases, like Pfam or SMART. This greatly simplifies the list of hits to a number of sequence families instead of a clutter of single sequences. All major publicly available profile and alignment databases are available through HHpred.

Synonyms: Homology detection & structure prediction by HMM-HMM comparison

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

Resource Name: HHpred

Resource ID: SCR_010276

Alternate IDs: nlx_156935

Record Creation Time: 20220129T080257+0000

Record Last Update: 20260808T185926+0000

Ratings and Alerts

No rating or validation information has been found for HHpred.

No alerts have been found for HHpred.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1032 mentions in open access literature.

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

Black JJ, et al. (2026) The Legionella pneumophila effector SidL is an adenylyltransferase that modifies the glycolytic intermediate 3-phosphoglycerate. Molecular cell.

Leonardo IC, et al. (2026) A novel temperate phage from Alicyclobacillus: first evidence in this genus of genomic identity to a sigK-integrated prophage. Microbiology spectrum, 14(5), e0374725.

Desjardins JB, et al. (2026) An ART-fold Rhs toxin from Pluralibacter gergoviae defines Tne5, a novel family of NAD(P) glycohydrolases effectors. The Journal of biological chemistry, 302(7), 113182.

Nagar A, et al. (2026) Plasmodium ARK1 regulates spindle formation during atypical mitosis and forms a divergent chromosomal passenger complex. Nature communications, 17(1).

Gomaa SE, et al. (2026) Evaluating Proteus mirabilis phage vB_PmiA_PM1 efficacy against catheter-associated urinary tract infections in artificial urine and laboratory media. BMC microbiology, 26(1).

Roy FA, et al. (2026) Hybrid genome assembly of the cannabis powdery mildew agent Golovinomyces ambrosiae uncovers important resources for deciphering virulence factors. BMC genomics, 27(1).

Parra-Calisto A, et al. (2026) Type VI Secretion Systems in Salmonella Encode New Effectors with Putative Antibacterial and Anti-Eukaryotic Activities. Microorganisms, 14(6).

Qiu K, et al. (2026) pLM-Repeat: Exploiting the sequence representations of protein language models for sensitive repeat detection. Protein science : a publication of the Protein Society, 35(5), e70541.

Liu Y, et al. (2026) Systematic discovery of bacterial anti-phage systems through a protein domain-centric strategy. Nucleic acids research, 54(6).

Rakesh S, et al. (2026) Expanding the landscape of BREX diversity: uncovering multi-layered functional frameworks and identification of novel BREX-related defense systems. Nucleic acids research, 54(3).

Timinskas K, et al. (2026) Diversity and distribution of bacterial DNA polymerases. Nucleic acids research, 54(4).

Pedersen JS, et al. (2026) The first single-stranded DNA virus targeting *Pectobacterium* belongs to the family Microviridae and demonstrates a broad host range to *Pectobacterium brasiliense* soft rot pathogens. *Archives of virology*, 171(3).

Jing S, et al. (2026) Programmable *Klebsiella pneumoniae* Phage Tropism Enabled by Scalable Receptor-Binding Protein Mining and Modular Assembly. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(21), e14511.

Han X, et al. (2026) Ribosomal RNA cleavage by the previously unidentified RelS-RelI toxin-antitoxin system controls growth of *Mycobacterium tuberculosis*. *Nucleic acids research*, 54(12).

Tajuelo A, et al. (2026) KpFhaB/FhaC is a virulence-associated TPS system of the globally-disseminated *Klebsiella pneumoniae* ST15 high-risk clone. *Frontiers in cellular and infection microbiology*, 16, 1787622.

Zhu X, et al. (2026) Preparation and application of Taq DNA polymerase monoclonal antibody guided by structural domain analysis. *PloS one*, 21(3), e0345402.

Badawy S, et al. (2026) Genomic analysis of jumbo coliphage fEgEco12. *Archives of virology*, 171(5).

Obado SO, et al. (2026) Division of labor in trypanosome RNA processing and export through expanded Mex67 paralogs. *Nucleic acids research*, 54(1).

Sharar NS, et al. (2026) Multiple prophage acquisition events over the course of an outbreak drive lysogenic conversion of capsular polysaccharides produced by carbapenem-resistant *Acinetobacter baumannii* isolates. *Microbiology spectrum*, 14(6), e0408425.

Jdeed G, et al. (2026) A qPCR-Based Screening Platform for Exploratory Assessment of Phage Training Outcomes in *Enterobacter cloacae* and *Stenotrophomonas maltophilia*. *Viruses*, 18(6).