

Resource Summary Report

Generated by [kravitz2](#) on Jul 30, 2026

HHpred

RRID:SCR_010276

Type: Tool

Proper Citation

HHpred (RRID:SCR_010276)

Resource Information

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

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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: data or information resource, database, software resource

Resource Name: HHpred

Resource ID: SCR_010276

Alternate IDs: nlx_156935

Record Creation Time: 20220129T080257+0000

Record Last Update: 20260729T044244+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 972 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Nath R, et al. (2025) Lineage-Specific Class-A GPCR Dynamics Reflect Diverse Chemosensory Adaptations in Lophotrochozoa. *Molecular biology and evolution*, 42(3).

van Hooff JJE, et al. (2025) Repeated duplications and losses shaped SMC complex evolution from archaeal ancestors to modern eukaryotes. *Cell reports*, 44(7), 115855.

Xu L, et al. (2025) DNA polymerase actively and sequentially displaces single-stranded DNA-binding proteins. *Nature communications*, 16(1), 7431.

Pratt OS, et al. (2025) AlphaFold 2, but not AlphaFold 3, predicts confident but unrealistic α -solenoid structures for repeat proteins. *Computational and structural biotechnology journal*, 27, 467.

Washington JM, et al. (2025) Expanding the Diversity of Actinobacterial Tectiviridae: A Novel Genus from Microbacterium. *Viruses*, 17(1).

Santini S, et al. (2025) Pacmanvirus isolated from the Lost City hydrothermal field extends the concept of transpoviron beyond the family Mimiviridae. *The ISME journal*, 19(1).

Timinskas K, et al. (2025) Common themes in architecture and interactions of prokaryotic PolB2 and Pol V mutasomes inferred from in silico studies. *Computational and structural biotechnology journal*, 27, 401.

Buchan A, et al. (2025) Unlocking the genomic repertoire of a cultivated megaphage. *Npj viruses*, 3(1), 71.

Barcyt D, et al. (2025) Expanded diversity of pedinophytes provides a window into the evolution of the genetic code in organelles. *PLoS genetics*, 21(10), e1011901.

Jivaji AM, et al. (2025) Giant endogenous viral elements in the genome of the model protist *Euglena gracilis* reveal past interactions with giant viruses. *Journal of virology*, 99(9), e0071325.

Antoine R, et al. (2025) Multinuclear non-haem iron-dependent oxidative enzymes: landscape of their substrates, partner proteins and biosynthetic gene clusters. *Microbial genomics*, 11(7).

Shaw DR, et al. (2025) Independently evolved extracellular electron transfer pathways in ecologically diverse Desulfobacterota. *The ISME journal*, 19(1).

Gil-Gomez A, et al. (2025) Proteome remodeling in the zoospore-to-vegetative cell transition of the stramenopile *Aurantiochytrium limacinum* reveals candidate ectoplasmic network proteins. *PLoS one*, 20(7), e0326651.

Yoshida M, et al. (2025) "Paraxenoviridae", a putative family of globally distributed marine bacteriophages with double-stranded RNA genomes. *The ISME journal*, 19(1).

Gomez-Raya-Vilanova MV, et al. (2025) Transcriptional landscape of the cell cycle in a model thermoacidophilic archaeon reveals similarities to eukaryotes. *Nature communications*, 16(1), 5697.

Isaac AM, et al. (2025) Genomic characterization of novel lytic phage vB_Sal_S6 with putative host FhuA interaction and its application for *Salmonella* biocontrol in milk. *Scientific reports*, 15(1), 40777.

Castelo-Branco R, et al. (2025) Phosphorylation of peptides by a kinase domain in cyanobactin pathways. *Nature communications*, 16(1), 10279.

Xu T, et al. (2025) Discovery and characterization of complete genomes of 38 head-tailed proviruses in four predominant phyla of archaea. *Microbiology spectrum*, 13(1), e0049224.

Monteiro Guedes M, et al. (2025) Repurposing statins for the treatment of larval cestodiasis: in silico evaluation of statin-HMG-CoA reductase interactions and assessment of statin effects on a cestode model. *Parasitology*, 152(8), 787.

Namias A, et al. (2025) Recombination, truncation and horizontal transfer shape the diversity of cytoplasmic incompatibility patterns. *bioRxiv : the preprint server for biology*.