Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 27, 2024

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

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 799 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Berry MA, et al. (2024) Diverse domain architectures of CheA histidine kinase, a central component of bacterial and archaeal chemosensory systems. Microbiology spectrum, 12(1), e0346423.

Kawato S, et al. (2024) Integrase-associated niche differentiation of endogenous large DNA viruses in crustaceans. Microbiology spectrum, 12(1), e0055923.

Pramono AK, et al. (2024) Bacterial community and genome analysis of cytoplasmic incompatibility-inducing Wolbachia in American serpentine leafminer, Liriomyza trifolii. Frontiers in microbiology, 15, 1304401.

Cao Yao JC, et al. (2024) Complete Genome Sequences of Four Mycobacteriophages Involved in Directed Evolution against Undisputed Mycobacterium abscessus Clinical Strains. Microorganisms, 12(2).

Costa AR, et al. (2024) Accumulation of defense systems in phage-resistant strains of Pseudomonas aeruginosa. Science advances, 10(8), eadj0341.

Makarova KS, et al. (2024) Computational analysis of genes with lethal knockout phenotype and prediction of essential genes in archaea. mBio, 15(2), e0309223.

Rakesh S, et al. (2024) Reappraisal of the DNA phosphorothioate modification machinery: uncovering neglected functional modalities and identification of new counter-invader defense systems. Nucleic acids research, 52(3), 1005.

Gao W, et al. (2024) Genome characteristics and the ODV proteome of a second distinct alphabaculovirus from Spodoptera litura. BMC genomics, 25(1), 91.

Makhsous N, et al. (2024) Within-Host Rhinovirus Evolution in Upper and Lower Respiratory Tract Highlights Capsid Variability and Mutation-Independent Compartmentalization. The Journal of infectious diseases, 229(2), 403.

Mercado-Evans V, et al. (2024) Gestational diabetes augments group B Streptococcus infection by disrupting maternal immunity and the vaginal microbiota. Nature

communications, 15(1), 1035.

Cortés-Martín A, et al. (2024) Isolation and characterization of a novel lytic Parabacteroides distasonis bacteriophage ?PDS1 from the human gut. Gut microbes, 16(1), 2298254.

Karlin DG, et al. (2024) Parvovirus B19 and Human Parvovirus 4 Encode Similar Proteins in a Reading Frame Overlapping the VP1 Capsid Gene. Viruses, 16(2).

Evseev PV, et al. (2024) Characterisation of New Foxunavirus Phage Murka with the Potential of Xanthomonas campestris pv. campestris Control. Viruses, 16(2).

Mondragón-Rosas F, et al. (2024) Characterization of Tau95 led to the identification of a four-subunit TFIIIC complex in trypanosomatid parasites. Applied microbiology and biotechnology, 108(1), 109.

Zamba-Campero M, et al. (2024) Broadly conserved FlgV controls flagellar assembly and Borrelia burgdorferi dissemination in mice. bioRxiv : the preprint server for biology.

Nakonieczna A, et al. (2024) New bacteriophage-derived lysins, LysJ and LysF, with the potential to control Bacillus anthracis. Applied microbiology and biotechnology, 108(1), 76.

Dutta TK, et al. (2024) Induced knockdown of Mg-odr-1 and Mg-odr-3 perturbed the host seeking behavior of Meloidogyne graminicola in rice. Heliyon, 10(4), e26384.

Palumbo R, et al. (2024) Remote homology identification of the Drosophila melanogaster ortholog of the RNA Polymerase I subunit Rpa34/POLR1G. microPublication biology, 2024.

Burroughs AM, et al. (2023) New biochemistry in the Rhodanese-phosphatase superfamily: emerging roles in diverse metabolic processes, nucleic acid modifications, and biological conflicts. NAR genomics and bioinformatics, 5(1), lqad029.

Patil PR, et al. (2023) Mechanism and evolutionary origins of alanine-tail C-degron recognition by E3 ligases Pirh2 and CRL2-KLHDC10. Cell reports, 42(9), 113100.