

Resource Summary Report

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HH-suite

RRID:SCR_016133

Type: Tool

Proper Citation

HH-suite (RRID:SCR_016133)

Resource Information

URL: <https://github.com/soedinglab/hh-suite>

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Description: Software package for sensitive protein sequence searching based on the pairwise alignment of hidden Markov models (HMMs). Used for sequence-based protein function and structure prediction what depends on sequence-search sensitivity and accuracy of the resulting sequence alignments.

Resource Type: data processing software, sequence analysis software, software toolkit, data analysis software, software resource, software application

Defining Citation: [DOI:10.1186/s12859-019-3019-7](https://doi.org/10.1186/s12859-019-3019-7)

Keywords: protein, sensitive sequence search, pairwise alignment, multiple database, homologous structure, prediction, modeling, bio.tools

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Availability: Free, Available for download, Freely available

Resource Name: HH-suite

Resource ID: SCR_016133

Alternate IDs: biotools:hh-suite

Alternate URLs: <https://bio.tools/hh-suite>

Old URLs: <http://toolkit.genzentrum.lmu.de/sections/search>

License: GPLv3

Record Creation Time: 20220129T080329+0000

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Ratings and Alerts

No rating or validation information has been found for HH-suite.

No alerts have been found for HH-suite.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 49 mentions in open access literature.

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

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.

Citu C, et al. (2025) Identification and catalog of viral transcriptional regulators in human diseases. *iScience*, 28(3), 112081.

Cuevas Zuviría B, et al. (2025) Structural evolution of nitrogenase over 3 billion years. *eLife*, 14.

Zhu Y, et al. (2025) In-depth analysis of 17,115 rice transcriptomes reveals extensive viral diversity in rice plants. *Nature communications*, 16(1), 1559.

Zhang Y, et al. (2025) Protein language model identifies disordered, conserved motifs implicated in phase separation. *eLife*, 14.

Tahmid MT, et al. (2025) TransBind allows precise detection of DNA-binding proteins and residues using language models and deep learning. *Communications biology*, 8(1), 568.

Zhang Y, et al. (2025) Protein Language Model Identifies Disordered, Conserved Motifs Implicated in Phase Separation. *bioRxiv : the preprint server for biology*.

Zhao Q, et al. (2025) The unique architecture of umbrella toxins permits a two-tiered molecular bet-hedging strategy for interbacterial antagonism. *Cell*.

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.

Soh TK, et al. (2024) A proteome-wide structural systems approach reveals insights into protein families of all human herpesviruses. *Nature communications*, 15(1), 10230.

Andersen JS, et al. (2024) Uncovering structural themes across cilia microtubule inner proteins with implications for human cilia function. *Nature communications*, 15(1), 2687.

Hardies SC, et al. (2023) Identification of Structural and Morphogenesis Genes of Sulfitobacter Phage ϕ GT1 and Placement within the Evolutionary History of the Podoviruses. *Viruses*, 15(7).

Cao W, et al. (2023) A sequence-based evolutionary distance method for Phylogenetic analysis of highly divergent proteins. *Scientific reports*, 13(1), 20304.

Pavlopoulos GA, et al. (2023) Unraveling the functional dark matter through global metagenomics. *Nature*, 622(7983), 594.

Fossa SL, et al. (2023) A novel family of sugar-specific phosphodiesterases that remove zwitterionic modifications of GlcNAc. *The Journal of biological chemistry*, 299(12), 105437.

Sharaf A, et al. (2022) Phylogenetic profiling resolves early emergence of PRC2 and illuminates its functional core. *Life science alliance*, 5(7).

Bhowmick S, et al. (2022) In Silico Protein Folding Prediction of COVID-19 Mutations and Variants. *Biomolecules*, 12(11).

Hespanhol JT, et al. (2022) Antibacterial T6SS effectors with a VRR-Nuc domain are structure-specific nucleases. *eLife*, 11.

Rousset F, et al. (2022) Phages and their satellites encode hotspots of antiviral systems. *Cell host & microbe*, 30(5), 740.

Vanni C, et al. (2022) Unifying the known and unknown microbial coding sequence space. *eLife*, 11.