

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 analysis software, data processing software, sequence analysis software, software application, software resource, software toolkit

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

Funding: Excellence Initiative of the Bundesministerium für Bildung und Forschung ; Ludwig-Maximilians Universität Munich ; the Deutsche Forschungsgemeinschaft grant SFB646

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

Record Last Update: 20260905T133007+0000

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 53 mentions in open access literature.

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

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.

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

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.

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

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.

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).

Redl I, et al. (2023) ADOPT: intrinsic protein disorder prediction through deep bidirectional transformers. *NAR genomics and bioinformatics*, 5(2), lqad041.

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.

Tubiana J, et al. (2022) Reduced B cell antigenicity of Omicron lowers host serologic response. *Cell reports*, 41(3), 111512.

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