

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

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 40 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

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 ?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).

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

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

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

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

Mikhailov KV, et al. (2022) Genomic analysis reveals cryptic diversity in aphelids and sheds light on the emergence of Fungi. Current biology : CB, 32(21), 4607.

Jumper J, et al. (2021) Highly accurate protein structure prediction with AlphaFold. Nature, 596(7873), 583.

Crisci MA, et al. (2021) Closely related Lak megaphages replicate in the microbiomes of diverse animals. iScience, 24(8), 102875.

Tunyasuvunakool K, et al. (2021) Highly accurate protein structure prediction for the human proteome. Nature, 596(7873), 590.

Iha C, et al. (2021) Genomic adaptations to an endolithic lifestyle in the coral-associated alga *Ostreobium*. Current biology : CB, 31(7), 1393.

Lasso G, et al. (2021) A Sweep of Earth's Virome Reveals Host-Guided Viral Protein Structural Mimicry and Points to Determinants of Human Disease. Cell systems, 12(1), 82.

von Kügelgen A, et al. (2021) Complete atomic structure of a native archaeal cell surface. Cell reports, 37(8), 110052.

Jalal ASB, et al. (2020) Diversification of DNA-Binding Specificity by Permissive and Specificity-Switching Mutations in the ParB/Noc Protein Family. Cell reports, 32(3), 107928.

Mahdi LK, et al. (2020) Discovery of a Family of Mixed Lineage Kinase Domain-like Proteins in Plants and Their Role in Innate Immune Signaling. Cell host & microbe, 28(6), 813.