

Resource Summary Report

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ProbCons

RRID:SCR_011813

Type: Tool

Proper Citation

ProbCons (RRID:SCR_011813)

Resource Information

URL: <http://probcons.stanford.edu/>

Proper Citation: ProbCons (RRID:SCR_011813)

Description: Efficient protein multiple sequence alignment program, which has demonstrated a statistically significant improvement in accuracy compared to several leading alignment tools.

Abbreviations: ProbCons

Synonyms: ProbCons: Probabilistic Consistency-based Multiple Alignment of Amino Acid Sequences

Resource Type: data analysis service, service resource, analysis service resource, production service resource

Defining Citation: [PMID:15687296](#), [DOI:10.1101/gr.2821705](#)

Keywords: bio.tools

Resource Name: ProbCons

Resource ID: SCR_011813

Alternate IDs: OMICS_00986, biotools:probcons

Alternate URLs: <https://bio.tools/probcons>, <https://sources.debian.org/src/probcons/>

Record Creation Time: 20220129T080306+0000

Record Last Update: 20260810T040547+0000

Ratings and Alerts

No rating or validation information has been found for ProbCons.

No alerts have been found for ProbCons.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 109 mentions in open access literature.

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

Petruk G, et al. (2026) The conserved N-terminal histidine in an engineered peptide mediates sepsis treatment efficacy via dual binding to CD14 and LPS. *Molecular therapy : the journal of the American Society of Gene Therapy*, 34(1), 407.

Ali N, et al. (2026) The Rpd3 histone deacetylase is a critical regulator of temperature-mediated morphogenesis and virulence in the human fungal pathogen *Histoplasma*. *PLoS biology*, 24(3), e3003341.

Hoang M, et al. (2026) Fast, accurate construction of multiple sequence alignments from protein language embeddings. *bioRxiv : the preprint server for biology*.

Salgado MG, et al. (2025) The auxin phenylacetic acid induces NIN expression in the actinorhizal plant *Datisca glomerata*, whereas cytokinin acts antagonistically. *PloS one*, 20(2), e0315798.

Voorhies M, et al. (2025) "Select and Resequence" Methods Enable a Genome-Wide Association Study of the Dimorphic Human Fungal Pathogen *Coccidioides posadasii*. *Genome biology and evolution*, 17(7).

Finegan TM, et al. (2025) Alternative splicing repurposes the *Drosophila* mitotic regulator Mud for meiotic functions. *Genetics*, 231(2).

Hu H, et al. (2025) Structure and mechanism of the Zorya anti-phage defence system. *Nature*, 639(8056), 1093.

Snyder LF, et al. (2024) Evolution of a Eukaryotic Transcription Factor's co-TF Dependence Involves Multiple Intrinsically Disordered Regions Affecting Activation and Autoinhibition. *bioRxiv : the preprint server for biology*.

Coulon PG, et al. (2024) High frequencies of alpha common cold coronavirus/SARS-CoV-2 cross-reactive functional CD4+ and CD8+ memory T cells are associated with protection from symptomatic and fatal SARS-CoV-2 infections in unvaccinated COVID-19 patients. *Frontiers in immunology*, 15, 1343716.

Kotb HM, et al. (2024) FaSTPACE: a fast and scalable tool for peptide alignment and consensus extraction. *NAR genomics and bioinformatics*, 6(3), lqae103.

Voorhies M, et al. (2024) Inferring the composition of a mixed culture of natural microbial isolates by deep sequencing. *bioRxiv : the preprint server for biology*.

McWhite CD, et al. (2023) Leveraging protein language models for accurate multiple sequence alignments. *Genome research*, 33(7), 1145.

Burch CL, et al. (2023) Empirical Evidence That Complexity Limits Horizontal Gene Transfer. *Genome biology and evolution*, 15(6).

Jacques F, et al. (2023) Roadmap to the study of gene and protein phylogeny and evolution-A practical guide. *PloS one*, 18(2), e0279597.

Rozman Grinberg I, et al. (2022) A nucleotide-sensing oligomerization mechanism that controls NrdR-dependent transcription of ribonucleotide reductases. *Nature communications*, 13(1), 2700.

Azimova D, et al. (2022) Cbp1, a fungal virulence factor under positive selection, forms an effector complex that drives macrophage lysis. *PLoS pathogens*, 18(6), e1010417.

Sarkar C, et al. (2022) Extracellular Domains of Transmembrane Proteins Defy the Expression Level-Evolutionary Rate Anticorrelation. *Genome biology and evolution*, 14(1).

Takusagawa M, et al. (2021) HBD1 protein with a tandem repeat of two HMG-box domains is a DNA clip to organize chloroplast nucleoids in *Chlamydomonas reinhardtii*. *Proceedings of the National Academy of Sciences of the United States of America*, 118(20).

Chang JM, et al. (2021) Incorporating alignment uncertainty into Felsenstein's phylogenetic bootstrap to improve its reliability. *Bioinformatics (Oxford, England)*, 37(11), 1506.

Hu T, et al. (2021) Bioinformatics resources for SARS-CoV-2 discovery and surveillance. *Briefings in bioinformatics*, 22(2), 631.