

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: service resource, production service resource, analysis service resource, data analysis service

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: 20260731T042841+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 106 mentions in open access literature.

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

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.

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*.

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

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).

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

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

Jiang M, et al. (2021) In silico analysis of glycosyltransferase 2 family genes in duckweed (Spirodela polyrhiza) and its role in salt stress tolerance. Open life sciences, 16(1), 583.

Scossa F, et al. (2021) Ancestral sequence reconstruction - An underused approach to understand the evolution of gene function in plants? Computational and structural biotechnology journal, 19, 1579.

Li W, et al. (2021) Protomer alignment modulates specificity of RNA substrate recognition by Ire1. eLife, 10.