

Resource Summary Report

Generated by [ASWG](#) on Apr 28, 2025

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, production service resource, service resource, analysis service resource

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

Keywords: bio.tools

Funding:

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: 20250428T053637+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 102 mentions in open access literature.

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

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.

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*.

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.

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

Pickering AC, et al. (2021) Evolutionary and Functional Analysis of Coagulase Positivity among the Staphylococci. *mSphere*, 6(4), e0038121.

Nelson DR, et al. (2021) Large-scale genome sequencing reveals the driving forces of viruses in microalgal evolution. *Cell host & microbe*, 29(2), 250.

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.

Ma X, et al. (2021) Structural and Evolutionary Adaptation of NOD-Like Receptors in Birds. *BioMed research international*, 2021, 5546170.

Jia H, et al. (2021) Direct Molecular Evidence for an Ancient, Conserved Developmental Toolkit Controlling Posttranscriptional Gene Regulation in Land Plants. *Molecular biology and evolution*, 38(11), 4765.