# Resource Summary Report

Generated by RRID 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 RRID.

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).

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.

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

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

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

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.

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

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.