**ProbCons**

**RRID:** SCR_011813  
**Type:** Tool

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**Proper Citation**

ProbCons (RRID:SCR_011813)

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**Resource Information**

**URL:** [http://probcons.stanford.edu/](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, analysis service resource, service resource

**Defining Citation:** [PMID:15687296](https://www.ncbi.nlm.nih.gov/pubmed/15687296), [DOI:10.1101/gr.2821705](https://doi.org/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://bio.tools/probcons), [https://sources.debian.org/src/probcons/](https://sources.debian.org/src/probcons/)

**Record Creation Time:** 20220129T080306+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 98 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.


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.


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.


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


Spadar A, et al. (2021) Flavivirus integrations in Aedes aegypti are limited and highly conserved across samples from different geographic regions unlike integrations in Aedes albopictus. Parasites & vectors, 14(1), 332.
