

Resource Summary Report

Generated by [kravitz2](#) on Sep 4, 2026

PRANK

RRID:SCR_024174

Type: Tool

Proper Citation

PRANK (RRID:SCR_024174)

Resource Information

URL: <http://wasabiapp.org/software/prank/>

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Description: Software application as probabilistic multiple alignment program for DNA, codon and amino-acid sequences. Allows for defining potential structure for sequences to be aligned and then, simultaneously with the alignment, predicts the locations of structural units in the sequences.

Synonyms: prank

Resource Type: alignment software, software resource, software application, image analysis software, data processing software

Defining Citation: [PMID:24170401](#)

Keywords: Phylogeny aware alignment, DNA sequences, codon and amino-acid sequences,

Availability: Free, Available for download, Freely available,

Resource Name: PRANK

Resource ID: SCR_024174

Alternate IDs: OMICS_12425

Alternate URLs: <https://sources.debian.org/src/prank/>,
<https://github.com/ariloytynoja/prank-msa/issues>

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260903T235934+0000

Ratings and Alerts

No rating or validation information has been found for PRANK.

No alerts have been found for PRANK.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 19 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#).

Bénitière F, et al. (2024) Random genetic drift sets an upper limit on mRNA splicing accuracy in metazoans. *eLife*, 13.

He J, et al. (2024) Multiple Origins of Bioluminescence in Beetles and Evolution of Luciferase Function. *Molecular biology and evolution*, 41(1).

Xu M, et al. (2024) Molecular epidemiology of *Mycoplasma pneumoniae* pneumonia in children, Wuhan, 2020-2022. *BMC microbiology*, 24(1), 23.

Layoun P, et al. (2024) Flexible genomic island conservation across freshwater and marine Methylophilaceae. *The ISME journal*, 18(1).

Hannon-Hatfield JA, et al. (2024) Evolution of a Restriction Factor by Domestication of a Yeast Retrotransposon. *Molecular biology and evolution*, 41(3).

Park YS, et al. (2024) Identification and expression analyses of B3 genes reveal lineage-specific evolution and potential roles of REM genes in pepper. *BMC plant biology*, 24(1), 201.

Tea YK, et al. (2024) The spotted parrotfish genome provides insights into the evolution of a coral reef dietary specialist (Teleostei: Labridae: Scarini: *Cetoscarus ocellatus*). *Ecology and evolution*, 14(3), e11148.

Xu L, et al. (2024) Evolution and expression patterns of the neo-sex chromosomes of the crested ibis. *Nature communications*, 15(1), 1670.

Sakamoto F, et al. (2024) Detection of evolutionary conserved and accelerated genomic regions related to adaptation to thermal niches in *Anolis* lizards. *Ecology and evolution*, 14(3), e11117.

Krishnappa M, et al. (2024) An Integrated Computational and Experimental Approach to Formulate Tamanu Oil Bigels as Anti-Scarring Agent. *Pharmaceuticals (Basel, Switzerland)*, 17(1).

Merényi Z, et al. (2023) Genomes of fungi and relatives reveal delayed loss of ancestral gene families and evolution of key fungal traits. *Nature ecology & evolution*, 7(8), 1221.

Chen X, et al. (2023) Comparative Genomic Analysis Reveals Genetic Diversity and Pathogenic Potential of *Haemophilus seminalis* and Emended Description of *Haemophilus seminalis*. *Microbiology spectrum*, 11(4), e0477222.

Eldem V, et al. (2023) Global expression pattern of genes containing positively selected sites in European anchovy (*Engraulis encrasicolus* L.) may shed light on teleost reproduction. *PloS one*, 18(8), e0289940.

Wenzel M, et al. (2023) Wolbachia infection at least partially rescues the fertility and ovary defects of several new *Drosophila melanogaster* bag of marbles protein-coding mutants. *PLoS genetics*, 19(10), e1011009.

Li S, et al. (2023) Integrating genomic and multiomic data for *Angelica sinensis* provides insights into the evolution and biosynthesis of pharmaceutically bioactive compounds. *Communications biology*, 6(1), 1198.

Gu TT, et al. (2023) Genomic analysis reveals a cryptic pangolin species. *Proceedings of the National Academy of Sciences of the United States of America*, 120(40), e2304096120.

Tan X, et al. (2023) Phylogenomics Reveals High Levels of Incomplete Lineage Sorting at the Ancestral Nodes of the Macaque Radiation. *Molecular biology and evolution*, 40(11).

Beliavskaia A, et al. (2023) Metagenomics of culture isolates and insect tissue illuminate the evolution of *Wolbachia*, *Rickettsia* and *Bartonella* symbionts in *Ctenocephalides* spp. fleas. *Microbial genomics*, 9(7).

Li Z, et al. (2023) Behavioural individuality determines infection risk in clonal ant colonies. *Nature communications*, 14(1), 5233.