

Resource Summary Report

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prank

RRID:SCR_017228

Type: Tool

Proper Citation

prank (RRID:SCR_017228)

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: data processing software, software toolkit, software resource, alignment software, image analysis software, software application

Defining Citation: [PMID:24170401](#), [PMID:21110866](#)

Keywords: multiple, nucleotide, sequence, alignment, DNA, codon, amino acid, phylogenetic, gap, predict, location, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: prank

Resource ID: SCR_017228

Alternate IDs: biotools:prank, SCR_024174, OMICS_12425

Alternate URLs: <https://www.ebi.ac.uk/goldman-srv/webprank/>, <https://ariloytynoja.github.io/prank-msa/>, <https://bio.tools/prank>

Old URLs: <https://omictools.com/prank-tool>

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260731T043017+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 253 mentions in open access literature.

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

Nachtigall PG, et al. (2026) The Golden Lancehead Genome Reveals Distinct Selective Processes Acting on Venom Genes of an Island Endemic Snake. *Genome biology and evolution*, 18(1).

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. *GigaScience*, 14.

Wang T, et al. (2025) Evolutionary analysis and population dynamics in the global transmission of Kaposi's sarcoma-associated herpesvirus. *Archives of virology*, 170(5), 92.

Liu Z, et al. (2025) The fourspine stickleback (*Apeltes quadracus*) has an XY sex chromosome system with polymorphic inversions on both X and Y chromosomes. *PLoS genetics*, 21(5), e1011465.

Arnce LR, et al. (2025) Comparative functional and evolutionary analysis of essential germline stem cell genes across the genus *Drosophila* and two outgroup species. *bioRxiv* : the preprint server for biology.

Legrand A, et al. (2025) Ancient convergence with prokaryote defense and recent adaptations to lentiviruses in primates characterize the ancestral immune factors SAMD9s. *bioRxiv* : the preprint server for biology.

Ishii Y, et al. (2025) Positive Selection of a Starch Synthesis Gene and Phenotypic Differentiation of Starch Accumulation in Symbiotic and Free-Living Coral Symbiont Dinoflagellate Species. *Genome biology and evolution*, 17(7).

Tareq MMI, et al. (2025) Development of a potential vaccine against Capripox virus implementing reverse vaccinology and pan-genomic immunoinformatics. *PloS one*, 20(7), e0326310.

Brabham HJ, et al. (2025) Discovery of functional NLRs using expression level, high-throughput transformation and large-scale phenotyping. *Nature plants*, 11(10), 2100.

Gong W, et al. (2025) Genomic analyses identify distinct patterns of selection in game fowl and Nami chicken. *Poultry science*, 104(12), 106095.

Sharma SP, et al. (2025) Genome Assembly of Gangetic Dolphin (*Platanista gangetica*) Reveals Signature of Regressive Evolution. *Genome biology and evolution*, 17(12).

Zheng Y, et al. (2025) Evolutionary relaxation and functional change of INSL3 and RXFP2 may underlie natural cryptorchidism in mammals. *EMBO reports*, 26(24), 6418.

Ruiz-Ruano FJ, et al. (2025) Programmed DNA elimination drives rapid genomic innovation in two thirds of all bird species. *bioRxiv : the preprint server for biology*.

Korneenko E, et al. (2025) Antibiotic resistance and viral co-infection in children diagnosed with pneumonia caused by *Mycoplasma pneumoniae* admitted to Russian hospitals during October 2023-February 2024. *BMC infectious diseases*, 25(1), 363.

Yuan H, et al. (2025) Novel genomics insights into the molecular evolution of long-distance migratory mammals. *BMC genomics*, 26(1), 795.

Colombi E, et al. (2025) Adaptative and ancient co-evolution of integrons with *Xanthomonas* genomes. *Microbial genomics*, 11(9).

Cai M, et al. (2025) Genome identification of NAC gene family and its gene expression patterns in responding to salt and drought stresses in *Rhododendron delavayi*. *BMC plant biology*, 25(1), 924.

Zhou Y, et al. (2025) Chromosome-level echidna genome illuminates evolution of multiple sex chromosome system in monotremes. *GigaScience*, 14.

Fusca DD, et al. (2025) Dynamic Birth and Death of Argonaute Gene Family Functional Repertoire Across *Caenorhabditis* Nematodes. *Genome biology and evolution*, 17(6).

Zhou G, et al. (2025) Whole-genome probe capture sequencing reveals genomic diversity and characteristics of *Mycoplasma pneumoniae* in Nanjing, China. *Frontiers in microbiology*, 16, 1589971.