

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 17, 2026

[prank](#)

RRID:SCR_017228

Type: Tool

Proper Citation

prank (RRID:SCR_017228)

Resource Information

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

Proper Citation: prank (RRID:SCR_017228)

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

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: 20260912T195850+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 281 mentions in open access literature.

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

Mohn RA, et al. (2026) Origin of subgenomes in the circumboreal, allopolyploid, carnivorous plant *Drosera anglica*. *American journal of botany*, 113(3), e70170.

Wang Z, et al. (2026) Genomic adaptations for tail-length evolution in arboreal snakes. *Molecular biology and evolution*, 43(2).

Kijpornyongpan T, et al. (2026) Gene presence-absence and evolutionary signals of positive selection associated with virulence divergence in *Beauveria* fungi. *Microbial genomics*, 12(6).

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).

Bono JM, et al. (2026) Evolution of the reproductive interactome and the origins of postmating-prezygotic reproductive divergence. *BMC biology*, 24(1).

Martins TW, et al. (2026) Sequencing of the invasive *E. coli* strain BEN2908 isolated from poultry: A comparative investigation of genomic regions shared with intestinal and extraintestinal model *E. coli* strains. *PloS one*, 21(2), e0342894.

Wang M, et al. (2026) A naturally synonymous mutation modulates an ERK-centered regulatory network to mediate thermotolerance divergence in *Crassostrea* oysters. *Communications biology*, 9(1).

Saber MA, et al. (2026) Pan-genome and reverse vaccinology for a multi-epitope vaccine against circulating post-2022 Monkeypox virus strains. *PloS one*, 21(6), e0351881.

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect *Cryptophyllum westwoodii* provide insights into the evolution of leaf-like masquerade. *GigaScience*, 15.

Luan Y, et al. (2026) Mechanisms of Aristolochic Acid Resistance in Specialist Butterflies and Evolutionary Insights for Potential Protective Pathways. *Advanced science*

(Weinheim, Baden-Wurttemberg, Germany), e18072.

Gu TT, et al. (2026) Large-scale genomic phylogeography provides insights into evolutionary history and conservation priorities of the white-bellied pangolin (*Phataginus tricuspis*). *Molecular biology and evolution*, 43(3).

Wang YY, et al. (2026) A Near Telomere-to-Telomere Genome of *Belamcanda chinensis* Provides Insights Into Genome Evolution and the Biosynthesis of Characteristic Isoflavones. *Plant biotechnology journal*, 24(6), 4285.

Salve BG, et al. (2026) Chromosomal rearrangements and segmental deletions contribute to gene loss in squamates. *BMC biology*, 24(1).

Oubassou EZ, et al. (2026) Genome sequencing and comparative analysis of *Nocardiopsis moroccensis* sp. nov., a halotolerant Actinomycetota from Moroccan hypersaline ecosystem. *BMC microbiology*, 26(1).

Griem-Krey H, et al. (2026) Transposable elements hitchhike on Starships across fungal genomes. *Nature communications*, 17(1).

Xu H, et al. (2026) The evolution of the immune system of bees is defined by conservation, expansions, and losses. *BMC biology*, 24(1).

Stewart RJ, et al. (2026) On the dynamic caddisfly silk H-fibroin gene: a population study in a net-spinning species. *Molecular biology and evolution*, 43(6).

Valdivia C, et al. (2026) Isolation and characterization of broad-range *Staphylococcus epidermidis* sephunaviruses. *Microbiology (Reading, England)*, 172(5).

Rinke S, et al. (2026) Genomic Insights Into the Evolution of Parental Care in Weevils. *Genome biology and evolution*, 18(6).

McCarthy ML, et al. (2026) Genomic Insights Into the Evolutionary History of *Berardius* Beaked Whales: Speciation Driven by Resource Specialization, Gigantism and Thermal Barriers? *Molecular ecology*, 35(12), e70426.