

Resource Summary Report

Generated by [kravitz2](#) on Sep 5, 2026

Infernal

RRID:SCR_011809

Type: Tool

Proper Citation

Infernal (RRID:SCR_011809)

Resource Information

URL: <http://infernal.janelia.org/>

Proper Citation: Infernal (RRID:SCR_011809)

Description: Software for searching DNA sequence databases for RNA structure and sequence similarities.

Abbreviations: Infernal

Synonyms: Infernal: inference of RNA alignments, INFERENCE of RNA Alignment

Resource Type: software resource

Defining Citation: [PMID:24008419](#), [DOI:10.1093/bioinformatics/btp157](#)

Keywords: FASEB list

Availability: GNU General Public License, v3

Resource Name: Infernal

Resource ID: SCR_011809

Alternate IDs: OMICS_00977

Alternate URLs: <https://sources.debian.org/src/infernal/>

Record Creation Time: 20220129T080306+0000

Record Last Update: 20260903T235119+0000

Ratings and Alerts

No rating or validation information has been found for Infernal.

No alerts have been found for Infernal.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 772 mentions in open access literature.

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

Lu Z, et al. (2026) The *Rhus chinensis* Genome Provides Insights Into Tannin, Flavonoid Biosynthesis, and Glandular Trichome Development. *Plant biotechnology journal*, 24(3), 988.

Dong Z, et al. (2026) Fungal photobiont and microbiome genome composition in the *Cladonia uncialis* tripartite symbiosis. *Scientific data*, 13(1).

Mu D, et al. (2026) The genome of the medicinal plant *Uncaria rhynchophylla* provides new insights into monoterpenoid indole alkaloid metabolism and its molecular regulatory mechanism. *Molecular horticulture*, 6(1), 9.

Dong H, et al. (2026) The genome of *Phlebotomus chinensis*, the primary vector of visceral leishmaniasis in China: insights from chromosome-level assembly and comparative analysis. *Infectious diseases of poverty*, 15(1), 20.

Chen L, et al. (2026) Animal-associated jumbo phages as widespread and active modulators of gut microbiome ecology and metabolism. *Science advances*, 12(6), eaeb6265.

Albarrán-Cuitiño C, et al. (2026) Development of a plant growth-promoting bacterial EcoBiome derived from desert soil isolates. *Applied and environmental microbiology*, 92(5), e0010326.

Idrissi Azami A, et al. (2026) Comprehensive re-assembly and annotation dataset for the argan tree (*Argania spinosa* L., Sapotaceae) genome. *Scientific data*, 13(1), 267.

Rich KD, et al. (2026) Phylogenomics and gene association analysis support probiotic potential in a subset of *Staphylococcus xylosus* isolates. *Microbial genomics*, 12(4).

Zhao S, et al. (2026) Multi-Omics Insights Into Anthraquinone Biosynthesis in *Rheum tanguticum*. *Plant biotechnology journal*, 24(6), 3953.

Sun W, et al. (2026) Comparative Genomics Reveals Host-Specific Adaptation of *Pyricularia oryzae* Strains Isolated from Rice and Barnyard Grass. *Journal of fungi (Basel, Switzerland)*, 12(2).

Li H, et al. (2026) Comparative genome analysis provides a foundation for defining salvinatorin A biosynthesis in *Salvia divinorum*. *Nature communications*, 17(1).

Ma Q, et al. (2026) The pan-genome provides insights into evolutionary dynamics and fatty acid metabolism in Aceraceae family. *Genome biology*, 27(1).

Lee SC, et al. (2026) Functional divergence of the gut microbiome associated with lifestyle and helminth infection in Indigenous Peninsular Malaysian. *Research square*.

Yang Z, et al. (2026) Copy number evolution of conserved noncoding RNA gene families across mammals. *Mammalian genome : official journal of the International Mammalian Genome Society*, 37(1).

Wu L, et al. (2026) Chromosome-level genome assembly of triploid *Cyperus rotundus* uncovers allelic expression patterns and herbicide resistance mechanisms. *Plant communications*, 7(2), 101624.

Zou R, et al. (2026) A chromosome-level genome assembly of *Cistanche deserticola* provides insights into its evolution and molecular mechanisms of parasitism. *Plant communications*, 7(1), 101581.

Nguyen TNG, et al. (2026) Splicing regulation and intron evolution in the short-intron ciliate model of endosymbiosis *Paramecium bursaria*. *Nucleic acids research*, 54(3).

Yan Y, et al. (2026) *Bacillus subtilis* G01: A Multifunctional Agent with Broad-Spectrum Antimicrobial Activity and Digestive Enzymes for Sustainable Agriculture and Animal Husbandry. *Journal of microbiology and biotechnology*, 36, e2510049.

Wu H, et al. (2026) A high-quality chromosome-level genome assembly of the low chilling requirement mulberry, *Morus macroura*. *Scientific data*, 13(1).

Wan Y, et al. (2026) Chromosome-scale assembly and annotation of *Phytophthora capsici* isolate BYA5. *Scientific data*, 13(1), 184.