

Resource Summary Report

Generated by T1D on Sep 20, 2026

AliView

RRID:SCR_002780

Type: Tool

Proper Citation

AliView (RRID:SCR_002780)

Resource Information

URL: <https://github.com/AliView>

Proper Citation: AliView (RRID:SCR_002780)

Description: Software for aligning viewing and editing dna / aminic acid sequences, intuitive, fast and lightweight. It has been designed to meet the requirements of next generation sequencing era phylogenetic datasets.

Resource Type: software resource

Defining Citation: [PMID:25095880](https://pubmed.ncbi.nlm.nih.gov/25095880/)

Keywords: unix/linux, mac os x, windows, java

Availability: Free, Freely available

Resource Name: AliView

Resource ID: SCR_002780

Alternate IDs: OMICS_05209

Alternate URLs: <http://www.ormbunkar.se/aliview/>

License: GNU General Public License, v3

Record Creation Time: 20220129T080215+0000

Record Last Update: 20260919T195005+0000

Ratings and Alerts

No rating or validation information has been found for AliView.

No alerts have been found for AliView.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1039 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Francette AM, et al. (2026) Evolutionary analysis of transcription elongation factors reveals conserved and lineage-specific regulatory domains. *PLoS biology*, 24(6), e3003855.

Cho A, et al. (2026) Aerobic sister lineage of breviate has gene-rich mitochondrial genomes. *Current biology : CB*, 36(6), 1481.

Šikutová S, et al. (2026) Molecular Screening of Black Flies (Diptera: Simuliidae) for Vector-Borne Zoonotic Pathogens, South Moravia, Czech Republic. *Zoonoses and public health*, 73(1), 95.

Magri MS, et al. (2026) Deep conservation of cis-regulatory elements and chromatin organization in echinoderms uncover ancestral regulatory features of animal genomes. *Nature ecology & evolution*, 10(2), 355.

Cleveland ME, et al. (2026) Toward the Bioremediation of Nylon Waste Materials: Genome Mining Leads to the Identification of a Thermostable Laurolactamase From *Thermopolyspora flexuosa*. *ChemSusChem*, 19(1), e202501964.

Bakamutumaho B, et al. (2026) Hyperendemicity of Rift Valley Fever in Southwestern Uganda Associated With the Rapidly Evolving Lineage C Viruses. *The Journal of infectious diseases*, 233(1), e77.

Bonomo M, et al. (2026) Non-Invasive Underwater DNA Sampling Illuminates Red Sea Echinoderm Diversity. *Molecular ecology resources*, 26(1), e70059.

Pless LL, et al. (2026) Emergence and epidemiology of dominant variants of human metapneumovirus in the United States between 2016 and 2021. *mBio*, 17(2), e0261925.

Cosentino MAC, et al. (2026) Coronavirus Detection in Bats Captured on the Deforestation Arc of Mato Grosso, Brazil. *Zoonoses and public health*, 73(3), 281.

Harada M, et al. (2026) Four genetically distinct types of rabies virus exist in Vietnam, including the SEA1 and SEA3 subclades within the Asian clade. *Scientific reports*, 16(1).

Rathwell C, et al. (2026) Hi-C Links Reveal Viral Activity and Infection Within the Free-Living Microbial Community of a Secondary Chlorophyll Maximum in the Eastern Tropical North Pacific. *Environmental microbiology*, 28(4), e70274.

Ali MZ, et al. (2026) Two decades (2005 to 2025) of avian influenza research trends, knowledge gaps and distribution of emerging H5N1 2.3.4.4b clade in South Asia. *One health outlook*, 8(1).

Waheed A, et al. (2026) Genomic Insights into Chromosomal Colistin Resistance and Virulence-Resistance Convergence in MDR/XDR *Klebsiella pneumoniae* from Tertiary Hospitals in Peshawar, Pakistan. *Pathogens* (Basel, Switzerland), 15(2).

Whymys SE, et al. (2026) Repellent activity against *Aedes aegypti* and metabolomic profiling of *Myrica gale* L. essential oils from Irish boglands. *Scientific reports*, 16(1).

Telles-de-Deus J, et al. (2026) Evolution and spillover dynamics of yellow fever at the forest-urban interface in Brazil. *Nature microbiology*, 11(4), 877.

Garcia LE, et al. (2026) Genomic Footprints of Multiple Host Lineages in the Mitochondrial and Nuclear Genomes of the Holoparasite *Prosopanche americana*. *Plants* (Basel, Switzerland), 15(7).

Branda F, et al. (2026) Influenza A(H3N2) Subclade K (J.2.4.1): Molecular Characterization, Antigenic Divergence, and Global Spread During the 2025/26 Season. *Infectious disease reports*, 18(2).

Horá?ek N, et al. (2026) Expansion of the geranylgeranyl pyrophosphate synthase gene family underlies the evolution of terpenoid biosynthesis in termites. *PLoS biology*, 24(4), e3003648.

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.

Madhushan A, et al. (2026) Diversity, Taxonomy, and Pathogenicity of Members of *Fusarium tricinctum* Species Complex Associated with Wild Rosaceae Fruits. *Journal of fungi* (Basel, Switzerland), 12(5).