

Resource Summary Report

Generated by SPARC SAWG on Aug 9, 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 / aminiacid sequences, intuitive, fast and leightweight. 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: 20260808T185755+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 [SPARC SAWG](#) .

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.

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).

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

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.

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.

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.

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.

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.

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).

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).

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.

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).

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).

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).

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.

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).

Ndenga BA, et al. (2026) Serendipitous detection of invasive malaria vector *Anopheles stephensi* in Kisumu, Kenya in June 2022. *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.