

Resource Summary Report

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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](#)

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: 20260725T190530+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 945 mentions in open access literature.

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

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.

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

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.

Nascimento JPM, et al. (2026) Arrival of Oropouche Virus in a Nonendemic Area in Northeastern Brazil, 2024. *Journal of medical virology*, 98(1), e70780.

Han B, et al. (2025) Evolutionarily diverse caveolins share a common structural framework built around amphipathic disks. *The Journal of cell biology*, 224(9).

Martín-Carrascosa MDC, et al. (2025) A phylogenetic analysis of the CDKL protein family unravels its evolutionary history and supports the *Drosophila* model of CDKL5 deficiency disorder. *Frontiers in cell and developmental biology*, 13, 1582684.

Carrasco-Montalvo A, et al. (2025) Entomo-Virological Surveillance and Genomic Insights into DENV-2 Genotype III Circulation in Rural Esmeraldas, Ecuador. *Pathogens (Basel, Switzerland)*, 14(6).

Goya S, et al. (2025) Distinct Evolutionary Signatures of Human Parainfluenza Viruses 2 and 4 Reveal Host Antagonism Divergence and Phylogenetic Discordance. *Molecular biology and evolution*, 42(10).

Guadano-Procesi I, et al. (2025) Enterocytozoon bienewisi in Italian water buffalo calves (*Bubalus bubalis*): An exploratory haplotype analysis within Bovidae family in the European context. *Food and waterborne parasitology*, 40, e00273.

Shamsudin NA, et al. (2025) Morphological and molecular identification of endophytic fungi from roots of epiphyte orchid *Aerides odorata* Lour in Sabah. *Scientific reports*, 15(1), 33908.

Tang Y, et al. (2025) Comparative and Phylogenetic Analysis of Complete Chloroplast Genomes of Five Mangifera Species. *Genes*, 16(6).

Niu KY, et al. (2025) ?Three new species of *Sanguinoderma* (Ganodermataceae, Basidiomycota) from Southwest China revealed by morphology and phylogenetic analysis. *MycoKeys*, 118, 245.

Rollins RE, et al. (2025) Analysis of ticks (Acari: Ixodida) and associated microorganisms collected on the North Sea Island of Heligoland. *Parasitology research*, 124(3), 34.

Lu L, et al. (2025) ?Unveiling fungal diversity associated with coffee trees in China using a polyphasic approach and a global review of coffee saprobic fungi. *IMA fungus*, 16, e144874.

Sánchez-Serna G, et al. (2025) Less, but More: New Insights From Appendicularians on Chordate Fgf Evolution and the Divergence of Tunicate Lifestyles. *Molecular biology and evolution*, 42(1).

Nyathi S, et al. (2025) Geographic origin and evolution of dengue virus serotypes 1 and 3 circulating in Africa. *Virus evolution*, 11(1), veae116.

Horsman S, et al. (2025) Molecular Epidemiological Characteristics of *Staphylococcus pseudintermedius*, *Staphylococcus coagulans*, and Coagulase-Negative *Staphylococci* Cultured from Clinical Canine Skin and Ear Samples in Queensland. *Antibiotics (Basel, Switzerland)*, 14(1).

Shahid A, et al. (2025) A simple phylogenetic approach to analyze hypermutated HIV proviruses reveals insights into their dynamics and persistence during antiretroviral therapy. *Virus evolution*, 11(1), veae094.

Yang X, et al. (2025) ?Morphology and multigene phylogeny revealed four new species of *Geastrum* (Geastrales, Basidiomycota) from China. *MycoKeys*, 113, 73.

Büttner KA, et al. (2025) *Chlamydia trachomatis* genomes from rectal samples: description of a new clade comprising ompA-genotype L4 from Argentina. *Microbial genomics*, 11(2).