

Resource Summary Report

Generated by [NIF](#) on May 15, 2025

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

Funding:

Availability: GNU General Public License, v3

Resource Name: AliView

Resource ID: SCR_002780

Alternate IDs: OMICS_05209

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

Record Creation Time: 20220129T080215+0000

Record Last Update: 20250420T014122+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 811 mentions in open access literature.

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

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).

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.

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

Yang K, et al. (2025) Genetic diversity of highly pathogenic avian influenza H5N6 and H5N8 viruses in poultry markets in Guangdong, China, 2020-2022. *Journal of virology*, 99(1), e0114524.

Magalhães TBS, et al. (2025) First Detection of Alphacoronavirus in Bats from the World's Largest Wetland, the Pantanal, Brazil. *Pathogens (Basel, Switzerland)*, 14(1).

Richard G, et al. (2025) Major change in swine influenza virus diversity in France owing to emergence and widespread dissemination of a newly introduced H1N2 1C genotype in 2020. *Virus evolution*, 11(1), veae112.

Peng T, et al. (2025) ?Novel *Helicosporium* and *Neohelicomyces* (Tubeufiaceae, Tubeufiales) species from terrestrial habitats in China and Thailand. *MycKeys*, 112, 81.

Fajardo SN, et al. (2025) *Phytophthora* Species and Their Associations with Chaparral and

Oak Woodland Vegetation in Southern California. *Journal of fungi* (Basel, Switzerland), 11(1).

Y?ld?r?m Y, et al. (2025) Molecular Detection and Phylogenetic Analysis of Orf Virus From Dermatological Lesions in the Teats of Goats. *Veterinary medicine and science*, 11(1), e70139.

Sevinc Temizkan S, et al. (2025) Complete Genome Characterization of Canine Adenovirus From Türkiye With Next-Generation Sequencing. *Veterinary medicine and science*, 11(1), e70163.

Frankenberg SR, et al. (2025) Unearthing the secrets of Australia's most enigmatic and cryptic mammal, the marsupial mole. *Science advances*, 11(1), eado4140.

de Sousa LLF, et al. (2025) Phylogenetic inferences reveal multiple intra- and interhost genetic diversity among bat rabies viruses circulating in northeastern Brazil. *One health outlook*, 7(1), 1.

Willemsen A, et al. (2025) Novel High-Quality Amoeba Genomes Reveal Widespread Codon Usage Mismatch Between Giant Viruses and Their Hosts. *Genome biology and evolution*, 17(1).

Gao Y, et al. (2025) Identification and Pathogenicity of *Fusarium* Species from Herbaceous Plants on Grassland in Qiaojia County, China. *Microorganisms*, 13(1).

Bakhache W, et al. (2025) Deep mutation, insertion and deletion scanning across the Enterovirus A proteome reveals constraints shaping viral evolution. *Nature microbiology*, 10(1), 158.

Palka MV, et al. (2025) Ultrastructure of *Olkasia polycarbonata* (Euglenozoa, Euglenida) demonstrates cytoskeletal innovations associated with the feeding and flagellar apparatuses. *The Journal of eukaryotic microbiology*, 72(1), e13074.

Dagba Gbessin EH, et al. (2025) HIV-1 resistance mutations and genetic diversity among children failing antiretroviral treatment in five healthcare facilities in Benin, West Africa. *PLoS one*, 20(1), e0317882.

Dong J, et al. (2025) ?Molecular phylogeny and morphology reveal four new wood-inhabiting fungi of *Asterostroma* and *Radulomyces* (Basidiomycota) from Southwestern China. *MycoKeys*, 112, 35.

Denoeud F, et al. (2024) Evolutionary genomics of the emergence of brown algae as key components of coastal ecosystems. *Cell*, 187(24), 6943.