Resource Summary Report

Generated by dkNET on Apr 30, 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 dkNET.

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.

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.

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.

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

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.

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).

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

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

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).

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.