

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

BioEdit

RRID:SCR_007361

Type: Tool

Proper Citation

BioEdit (RRID:SCR_007361)

Resource Information

URL: <http://www.mbio.ncsu.edu/BioEdit/bioedit.html>

Proper Citation: BioEdit (RRID:SCR_007361)

Description: Software tool as biological sequence alignment editor written for Windows 95/98/NT/2000/XP/7 and sequence analysis program. Provides sequence manipulation and analysis options and links to external analysis programs to view and manipulate sequences with simple point and click operations., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Resource Type: data processing software, sequence analysis software, data analysis software, software resource, image analysis software, alignment software, software application

Keywords: sequence, alignment, editor, analysis, program

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: BioEdit

Resource ID: SCR_007361

Alternate IDs: nlx_156845

Record Creation Time: 20220129T080241+0000

Record Last Update: 20260731T042736+0000

Ratings and Alerts

No rating or validation information has been found for BioEdit.

No alerts have been found for BioEdit.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 13339 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Kim DG, et al. (2025) Genetic characteristics of novel extreme alkaline-inducible promoter located in five prime upstream region of peptidyl-prolyl cis/trans isomerase from *Vibrio anguillarum*. Scientific reports, 15(1), 21372.

Striewe LC, et al. (2025) Increasing prevalence of *Diphylobothrium* cestodes in seals from the North and Baltic Sea over 26?years. Frontiers in veterinary science, 12, 1574830.

Bell JA, et al. (2025) Haemosporidian infection risk and community structure determined by duck feeding guild. Parasitology, 152(2), 217.

Zubair A, et al. (2025) Targeting HIV-1 conserved regions: An immunoinformatic pathway to vaccine innovation for the Asia. PloS one, 20(3), e0317382.

Nouri S, et al. (2025) Evolutionary Dynamics and Population Genetics of Ash Shoestring-Associated Virus in a European-Wide Survey. Microorganisms, 13(3).

Lo Presti A, et al. (2025) Phylogenetic Analysis of Chikungunya Virus Eastern/Central/South African-Indian Ocean Epidemic Strains, 2004-2019. Viruses, 17(3).

Angsujinda K, et al. (2025) Evaluation of recombinant extracellular enveloped virion protein candidates for the detection of serological responses to lumpy skin disease virus in cattle. The veterinary quarterly, 45(1), 1.

Wang W, et al. (2025) Cryo-EM Analysis of a Tri-Heme Cytochrome-Associated RC-LH1 Complex from the Marine Photoheterotrophic Bacterium *Dinoroseobacter* *Shibae*. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 12(18), e2413456.

Ramirez-Castrillon M, et al. (2025) Tropical lakes as a novel source of oleaginous yeasts with lipid profiles for biodiesel, oleochemical, and nutraceutical applications. World journal of microbiology & biotechnology, 41(3), 105.

Liao C, et al. (2025) ?Unveiling four new taxa and *Nigrosynnemanatarajanensis* comb. nov. in *Stachybotryaceae* (Hypocreales) from monocotyledon plants in Guangdong Province, China. MycoKeys, 114, 299.

Ndiaye N, et al. (2025) An outbreak of atypical hand, foot and mouth disease associated Cocksackievirus A6 in children from Cape Verde, 2023. Virology journal, 22(1), 48.

Changbunjong T, et al. (2025) Species classification of *Tabanus* (Diptera: Tabanidae) in Western Thailand: Integrating DNA barcoding and modern morphometrics. Current research in parasitology & vector-borne diseases, 7, 100243.

Feng WC, et al. (2025) Species Diversity of Gymnopus Section Levipedes in Southwestern China, with a Description of Three New Species. *Journal of fungi* (Basel, Switzerland), 11(2).

Popovi? Milovanovi? T, et al. (2025) Biocontrol of Seedborne Fungi on Small-Grained Cereals Using *Bacillus halotolerans* Strain B33. *Journal of fungi* (Basel, Switzerland), 11(2).

Ren M, et al. (2025) Identification and genetic characterization of Xiabuqu River virus: A novel member of the Iflaviridae family detected in soft ticks from Tibet, China. *Virus research*, 354, 199543.

Gomes KA, et al. (2025) Multi-Province Outbreak of Acute Gastroenteritis Linked to Potential Novel Lineage of GII.17 Norovirus in Argentina in 2024. *Viruses*, 17(2).

Zhu P, et al. (2025) Epidemiological Study and Genetic Diversity Assessment of Porcine Epidemic Diarrhea Virus (PEDV) in Yunnan Province, China. *Viruses*, 17(2).

Li Y, et al. (2025) Population genetic structure and historical demography of *Saccostrea echinata* in the Northern South China sea and Beibu Gulf. *Scientific reports*, 15(1), 8261.

Changbunjong T, et al. (2025) Molecular detection and characterization of haemoparasites in captive tigers (*Panthera tigris*) from Thailand. *Current research in parasitology & vector-borne diseases*, 7, 100249.

Kim JY, et al. (2025) Reinfection of SARS-CoV-2 Variants in Immunocompromised Patients with Prolonged or Relapsed Viral Shedding. *Infection & chemotherapy*, 57(1), 81.