

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

Sequencher

RRID:SCR_001528

Type: Tool

Proper Citation

Sequencher (RRID:SCR_001528)

Resource Information

URL: <http://genecodes.com/sequencher>

Proper Citation: Sequencher (RRID:SCR_001528)

Description: Software for Next-Generation DNA sequencing, Sanger DNA analysis, and RNA sequencing. It contains sequence analysis tools which include reference-guided alignments, de novo assembly, variant calling, and SNP analyses. It has integrated the Cufflinks suite for in-depth transcript analysis and differential gene expression of RNA-Seq data.

Abbreviations: Sequencher sequence analysis software

Synonyms: Sequencher sequence analysis software

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

Keywords: dna, sequencing, sequence analysis software, NGS, sanger, data visualization

Availability: Available for download

Resource Name: Sequencher

Resource ID: SCR_001528

Alternate IDs: OMICS_01817

Alternate URLs: <http://genecodes.com/sequencher-features>

License: Commercial license

Record Creation Time: 20220129T080208+0000

Record Last Update: 20260801T190131+0000

Ratings and Alerts

No rating or validation information has been found for Sequencher.

No alerts have been found for Sequencher.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4965 mentions in open access literature.

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

Page ER, et al. (2026) Functional synergy and genomic linkage of glyphosate resistance traits in Canada fleabane. *Pest management science*, 82(1), 305.

Zeng Y, et al. (2026) Endophyte *Acrocalymma vagum* establishes the holobiont with rice to attract beneficial microorganisms and promote disease resistance. *Journal of advanced research*, 79, 161.

Wetherby K, et al. (2025) Identification of an elusive SERPING1 deletion in a family with hereditary angioedema type I utilizing soft clipping. *Frontiers in allergy*, 6, 1565283.

Xue J, et al. (2025) An HIV fusion-inhibitory lipopeptide provides robust post-exposure prophylaxis and prevents viral reservoir seeding in macaques. *Cell reports*, 44(9), 116228.

Wu D, et al. (2025) Phylogeographic history of *Parthenocissus* (Vitaceae) in North America based on chloroplast and nuclear DNA sequences. *Frontiers in plant science*, 16, 1521784.

Frøvoll TL, et al. (2025) Measuring cytokines in Eurasian tundra reindeer (*Rangifer tarandus tarandus*) with a bovine bead-based multiplex immunoassay and real-time PCR. *Acta veterinaria Scandinavica*, 67(1), 34.

Ngo HT, et al. (2025) Diet of Critically Endangered Black-Eyed Bent-Toed Gecko, *Cyrtodactylus nigriocularis*, Nguyen, Orlov & Darevsky, 2006 From Vietnam. *Ecology and evolution*, 15(7), e71645.

Garbino GST, et al. (2025) Phylogeographic analysis of long-legged bats, *Macrophyllum macrophyllum*, with notes on roosting behavior and natural history. *PeerJ*, 13, e19432.

Jacinto J, et al. (2025) Exploring skeletal disorders in cattle and sheep: a WGS-based framework for diagnosis and classification. *Genetics, selection, evolution : GSE*, 57(1), 51.

Drögemüller M, et al. (2025) LMF1 frameshift deletion in Franches-Montagnes horses with hypertriglyceridemia-induced pancreatitis. *Scientific reports*, 15(1), 28667.

Ye S, et al. (2025) Genetic analysis using long-read sequencing to overcome the difficulties in VWF gene. *Research and practice in thrombosis and haemostasis*, 9(4), 102888.

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

De Elías-Escribano A, et al. (2025) Wide Variation of *Aedes albopictus* Genotypes First Introduced into Canary Islands Assessed by rDNA Internal Transcribed Spacer Region and mtDNA *cox1* Sequencing and Cloning. *Tropical medicine and infectious disease*, 10(2).

Park MS, et al. (2025) Rare Non-Cryptic NUP98 Rearrangements Associated With Myeloid Neoplasms and Their Poor Prognostic Impact. *Annals of laboratory medicine*, 45(1), 53.

Liu R, et al. (2025) Transcriptome analysis of nitrogen assimilation preferences in *Burkholderia* sp. M6-3 and *Arthrobacter* sp. M7-15. *Frontiers in microbiology*, 16, 1559884.

Minna Z, et al. (2025) Divergent transmission dynamics and drug resistance evolution of HIV-1 CRF01_AE and CRF07_BC in Tianjin, China (2013-2022). *Virology journal*, 22(1), 137.

Polevoi A, et al. (2025) ?New species of *Plesioaxymyia* Sinclair (Diptera, Axymyiidae) from the Palaearctic Region, including an updated molecular phylogeny of the family. *ZooKeys*, 1236, 297.

Cheema AN, et al. (2025) Search for the elusive haplotype of the APOE polymorphism associated with Alzheimer's disease. *Scientific reports*, 15(1), 16923.

Blasco-Aróstegui J, et al. (2025) Mito-nuclear discordance reveals introgressive hybridization following vicariance and secondary contact in Iberian scorpions (Buthidae: *Buthus*). *BMC ecology and evolution*, 25(1), 112.

Millanes AM, et al. (2025) Different Patterns of Frequency, Lichen Specificity and Thallus Location Between the Yeast and Filamentous Phases of Two Lichen-Inhabiting Basidiomycetes. *Environmental microbiology*, 27(11), e70203.