

Resource Summary Report

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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: sequence analysis software, software resource, software application, data 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: 20260808T185730+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 5032 mentions in open access literature.

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

Hong YJ, et al. (2026) Identification of a De Novo MAGEL2 Pathogenic Variant in Schaaf-Yang Syndrome and the Importance of Paternal Allele Confirmation. Journal of clinical laboratory analysis, 40(3), e70152.

Huang JY, et al. (2026) A Large Dengue Outbreak in Taiwan, 2023: Driven by Imported Cases, Serotype Cocirculation, and Climate Variability. Open forum infectious diseases, 13(3), ofag070.

Spörri L, et al. (2026) Linking the microbiome to the complement system in geographic atrophy. NPJ genomic medicine, 11(1).

Khalid AB, et al. (2026) MEK inhibitor mirdametinib promotes fracture healing in osteofibrous dysplasia RASopathy. The Journal of clinical investigation, 136(9).

Montes-Rodríguez JM, et al. (2026) Morphological and molecular identification of symphylans (Myriapoda, Symphyla) from Colombian pineapple crops, with descriptions of two new species. ZooKeys, 1268, 281.

He S, et al. (2026) An individual with multiple high-risk links uncovered: an epidemiological investigation based on molecular network analysis. Frontiers in public health, 14, 1715356.

Buonafine CP, et al. (2026) Prevalence Rates, Species Distribution and Antifungal Susceptibility of Rare Candida and Related Saccharomycotina Yeasts Causing Bloodstream Infections in 28 Medical Centres. Mycoses, 69(3), e70149.

Alqahtani S, et al. (2026) Molecular characterization and genotypic diversity of human astroviruses among patients with gastroenteritis in Saudi Arabia, 2022-2023. Virus genes, 62(3), 271.

Sirkisson S, et al. (2026) Coreceptor usage of plasma and cerebrospinal fluid-derived HIV-1 subtype C variants. Virology journal, 23(1).

Wulan WN, et al. (2026) Protocol for the identification of recent HIV infection in newly diagnosed individuals. *STAR protocols*, 7(2), 104504.

Mirbadie SR, et al. (2026) Reinfection dynamics of owned dogs with *Echinococcus granulosus sensu lato* in endemic rural areas of central Iran: Implications for cystic echinococcosis control. *PLoS neglected tropical diseases*, 20(6), e0014451.

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

He J, et al. (2026) HIV-1 genetic diversity and pretreatment drug resistance in Xishuangbanna, a China-Myanmar-Laos border region. *BMC infectious diseases*, 26(1).

Ruiz-Guzmán G, et al. (2026) Infestation by Phorid Flies Disrupts Behavior and Immune Function in Honey Bees Monitored by Radio-frequency Identification. *Neotropical entomology*, 55(1), 12.

Gallego-Giraldo C, et al. (2026) Gene-specific double-stranded RNAs induce mortality in the South African mealybug *Delottococcus aberiae*. *Pest management science*, 82(6), 5184.

Lee SJ, et al. (2026) DNA Barcoding for Herbarium Specimens of the Red Alga *Meristotheca pilulaora* and Molecular Marker Development for Species Identification. *Biology*, 15(5).

Shirai T, et al. (2026) Temporal genetic changes in human bocavirus 1 in Fukushima, Japan, from 2018 to 2024. *Journal of medical microbiology*, 75(5).

Wu Z, et al. (2026) HIV-1 molecular transmission networks among MSM in Ningxia, China (2018-2024): insights into local transmission dynamics and drug resistance. *Frontiers in microbiology*, 17, 1766785.

Aliabadi F, et al. (2026) Taxonomy and phylogeny of the epiphytic sooty molds in family Metacapnodiaceae (class Eurotiomycetes, subclass Chaetothyriomycetidae). *MycKeys*, 129, 163.

Gunnar J, et al. (2026) Exploring the role of apolipoprotein ?4 in progressive myoclonic epilepsy type 1. *Epileptic disorders : international epilepsy journal with videotape*, 28(1), 55.