

Resource Summary Report

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SeqTrace

RRID:SCR_005580

Type: Tool

Proper Citation

SeqTrace (RRID:SCR_005580)

Resource Information

URL: <http://code.google.com/p/seqtrace/>

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Description: A software application for viewing and processing DNA sequencing chromatograms (trace files) that makes it easy to quickly generate high-quality finished sequences from a large number of trace files. SeqTrace can automatically identify, align, and compute consensus sequences from matching forward and reverse traces, filter low-quality base calls, and perform end trimming of finished sequences. The finished DNA sequences can then be exported to common sequence file formats, such as FASTA. SeqTrace also includes a full-featured trace file viewer and editor. You can view your sequencing chromatograms at a variety of scales and zoom levels, simultaneously view matching forward and reverse traces, edit the called bases, and export individual DNA sequences as well as forward/reverse alignments. SeqTrace supports popular trace file formats, including ABIF, SCF, and ZTR.

Abbreviations: SeqTrace

Synonyms: Seqtrace - User-friendly software for viewing and processing DNA sequencing trace files

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

Defining Citation: [PMID:22942788](#)

Keywords: dna sequencing trace file, dna sequencing, trace file, trace, python, gtk, chromatogram, graphic, sequence analysis, bio.tools

Availability: GNU General Public License, v3

Resource Name: SeqTrace

Resource ID: SCR_005580

Alternate IDs: OMICS_01021, biotools:seqtrace

Alternate URLs: <https://bio.tools/seqtrace>

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260727T040402+0000

Ratings and Alerts

No rating or validation information has been found for SeqTrace.

No alerts have been found for SeqTrace.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 62 mentions in open access literature.

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

Bonomo M, et al. (2026) Non-Invasive Underwater DNA Sampling Illuminates Red Sea Echinoderm Diversity. *Molecular ecology resources*, 26(1), e70059.

Elidrissi El Yallouli N, et al. (2025) Selected rhizobacteria strains improved the tolerance of *Vicia faba* plants to microcystins contaminated irrigation water and reduced human health risk. *Environmental science and pollution research international*, 32(47), 27101.

Lunda SL, et al. (2025) Pilot-scale depuration demonstrates the suitability of non-pathogenic *Vibrio parahaemolyticus* as a surrogate for commercial-scale validation studies. *PloS one*, 20(10), e0334240.

Tagliaferri TL, et al. (2025) CRISPR-Cas9 targeting the blaKPC gene in a clinical isolate of *Klebsiella michiganensis*: Reduction of imipenem resistance and changes in genomic carbapenem resistance determinants. *PloS one*, 20(8), e0328521.

Echavarria-Correa SM, et al. (2025) Distribution of CCR5-?32 and HLA-B*57:01 alleles in HIV-seropositive and HIV-exposed seronegative Peruvian individuals. *Human genome variation*, 12(1), 15.

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.

Staiano I, et al. (2025) Plant-microbe synergy: employing coastal plant bacteria for wheat prosperity under combined saline and heat stress. *Applied microbiology and biotechnology*, 109(1), 285.

Rosa F, et al. (2024) Island hitchhikers: pathogen agents of Madeira and Azores ticks. *Parasitology research*, 123(7), 261.

Everly V, et al. (2024) Metabolite from supernatant of soil and plant-associated bacteria control biofilm of fish pathogens. *BMC research notes*, 17(1), 311.

Rodrigues BL, et al. (2024) Hidden diversity in anthropophilic sand flies of the Monticola Series (Diptera, Psychodidae). *Scientific reports*, 14(1), 27215.

Quansah E, et al. (2024) Low nucleotide diversity of the *Plasmodium falciparum* AP2-EXP2 gene among clinical samples from Ghana. *Parasites & vectors*, 17(1), 453.

Ramírez-Pool JA, et al. (2024) *Bacillus* Strains as Effective Biocontrol Agents Against Phytopathogenic Bacteria and Promoters of Plant Growth. *Microbial ecology*, 87(1), 76.

Andrade AS, et al. (2024) Association Between Single-Nucleotide Polymorphisms in Toll-like Receptor 3 (tlr3), tlr7, tlr8 and tirap Genes with Severe Symptoms in Children Presenting COVID-19. *Viruses*, 17(1).

Neves RL, et al. (2023) Increased Risk of American Tegumentary Leishmaniasis in an Urban and Rural Area of Caratinga, Brazil between 2016 and 2021. *The American journal of tropical medicine and hygiene*, 109(4), 791.

Zarate-Sulca Y, et al. (2023) Single-nucleotide polymorphisms in *ialB*, *gltA* and *rpoB* genes of *Bartonella bacilliformis* isolated from patients in endemic Peruvian regions. *PLoS neglected tropical diseases*, 17(10), e0011615.

Rodrigues BL, et al. (2023) Morphological and DNA-based description of *Trichophoromyia peixotoi* n. sp. (Diptera: Psychodidae), a new sand fly species from the Brazilian Amazon. *Parasites & vectors*, 16(1), 240.

Vilkamaa P, et al. (2023) The Genus *Spinopygina* gen. nov. (Diptera, Sciaridae) from Western North America: Preliminary Molecular Phylogeny and Description of Seven New Species. *Insects*, 14(2).

Posada-López L, et al. (2023) Ecological interactions of sand flies, hosts, and *Leishmania panamensis* in an endemic area of cutaneous leishmaniasis in Colombia. *PLoS neglected tropical diseases*, 17(5), e0011316.

Okoi C, et al. (2022) Pulmonary non-tuberculous mycobacteria in colonisation and disease in The Gambia. *Scientific reports*, 12(1), 19523.

Elfahmi , et al. (2021) Expression of Two Key Enzymes of Artemisinin Biosynthesis FPS and ADS genes in *Saccharomyces cerevisiae*. *Advanced pharmaceutical bulletin*, 11(1), 181.