Resource Summary Report

Generated by NIF on May 16, 2025

SMALT

RRID:SCR_005498
Type: Tool

Proper Citation

SMALT (RRID:SCR_005498)

Resource Information

URL: http://www.sanger.ac.uk/resources/software/smalt/

Proper Citation: SMALT (RRID:SCR_005498)

Description: Software that aligns DNA sequencing reads with a reference genome. Reads from a wide range of sequencing platforms, for example Illumina, Roche-454, Ion Torrent, PacBio or ABI-Sanger, can be processed including paired reads.

Abbreviations: SMALT

Resource Type: software resource

Funding:

Resource Name: SMALT

Resource ID: SCR_005498

Alternate IDs: OMICS_00686

Record Creation Time: 20220129T080230+0000

Record Last Update: 20250420T014253+0000

Ratings and Alerts

No rating or validation information has been found for SMALT.

No alerts have been found for SMALT.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 494 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Coll F, et al. (2025) The mutational landscape of Staphylococcus aureus during colonisation. Nature communications, 16(1), 302.

Coetzee JL, et al. (2024) Assessing the propensity of TB clinical isolates to form viable but non-replicating subpopulations. Scientific reports, 14(1), 27686.

Kostygov AY, et al. (2024) A novel strain of Leishmania braziliensis harbors not a toti- but a bunyavirus. PLoS neglected tropical diseases, 18(12), e0012767.

Eraso JM, et al. (2024) Integrative genomic, virulence, and transcriptomic analysis of emergent Streptococcus dysgalactiae subspecies equisimilis (SDSE) emm type stG62647 isolates causing human infections. mBio, 15(11), e0257824.

Kirchner M, et al. (2024) Use of transcriptomics and genomics to assess the effect of disinfectant exposure on the survival and resistance of Escherichia coli O157:H7, a human pathogen. Frontiers in microbiology, 15, 1477683.

Wallace BA, et al. (2024) Globally distributed bacteriophage genomes reveal mechanisms of tripartite phage-bacteria-coral interactions. The ISME journal, 18(1).

Connor R, et al. (2024) Recommendations for Uniform Variant Calling of SARS-CoV-2 Genome Sequence across Bioinformatic Workflows. Viruses, 16(3).

Ortiz-Vasco CC, et al. (2024) The stringent response regulates the poly-?-hydroxybutyrate (PHB) synthesis in Azotobacter vinelandii. PloS one, 19(4), e0299640.

Alobaidallah MSA, et al. (2024) Enhancing the Efficacy of Chloramphenicol Therapy for Escherichia coli by Targeting the Secondary Resistome. Antibiotics (Basel, Switzerland), 13(1).

Wellner SM, et al. (2024) Genome-wide identification of fitness-genes in aminoglycoside-resistant Escherichia coli during antibiotic stress. Scientific reports, 14(1), 4163.

Hedskog C, et al. (2024) No Remdesivir Resistance Observed in the Phase 3 Severe and Moderate COVID-19 SIMPLE Trials. Viruses, 16(4).

Lekhuleni C, et al. (2024) Impact of pneumococcal conjugate vaccines on invasive pneumococcal disease-causing lineages among South African children. Nature communications, 15(1), 8401.

Tran TA, et al. (2024) Combining machine learning with high-content imaging to infer ciprofloxacin susceptibility in isolates of Salmonella Typhimurium. Nature communications, 15(1), 5074.

Stiffler AK, et al. (2024) Genomic and induction evidence for bacteriophage contributions to sargassum-bacteria symbioses. Microbiome, 12(1), 143.

Rajan KS, et al. (2024) Structural and mechanistic insights into the function of Leishmania ribosome lacking a single pseudouridine modification. Cell reports, 43(5), 114203.

Barno AR, et al. (2024) Snow viruses and their implications on red snow algal blooms. mSystems, 9(5), e0008324.

Sullivan GJ, et al. (2024) A method to correct for local alterations in DNA copy number that bias functional genomics assays applied to antibiotic-treated bacteria. mSystems, 9(4), e0066523.

An Y, et al. (2024) Genome-wide identification of the sorghum OVATE gene family and revelation of its expression characteristics in sorghum seeds and leaves. Scientific reports, 14(1), 15123.

Kosugi M, et al. (2024) Characterization of the far-red light absorbing light-harvesting chlorophyll a/b binding complex, a derivative of the distinctive Lhca gene family in green algae. Frontiers in plant science, 15, 1409116.

Heeren S, et al. (2024) Evolutionary genomics of Leishmania braziliensis across the neotropical realm. Communications biology, 7(1), 1587.