

Resource Summary Report

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SMALT

RRID:SCR_005498

Type: Tool

Proper Citation

SMALT (RRID:SCR_005498)

Resource Information

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

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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

Resource Name: SMALT

Resource ID: SCR_005498

Alternate IDs: OMICS_00686

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260815T182307+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 516 mentions in open access literature.

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

Freixeiro P, et al. (2026) Pre-clinical efficacy of a candidate outer membrane vesicle gonococcal vaccine in comparison with 4CMenB. *NPJ vaccines*, 11(1).

Cai J, et al. (2026) Discovery of H2 Receptor Antagonists as Colistin Enhancers by Targeting Acid Stress Response. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(26), e14165.

De Luca DG, et al. (2026) Phylogenomic analysis and genetic mechanisms of antifungal resistance in clinical isolates of *Candida glabrata* (*Nakaseomyces glabratus*) from across Canada, 2013-2020. *Microbiology spectrum*, 14(1), e0180325.

Grandmond-Lemire S, et al. (2026) Environmental effects on constructed wetland microbial diversity and function in the context of wastewater management. *Microbiology spectrum*, 14(6), e0022925.

Gonzaga-Pérez MC, et al. (2026) *Azotobacter vinelandii* AmrZ is a global regulator linking alginate production and c-di-GMP homeostasis. *Microbiology* (Reading, England), 172(3).

Abdelmalek N, et al. (2026) Profiling of genetic determinants required for fitness of community-associated methicillin-resistant *Staphylococcus aureus* in human blood. *Microbiology spectrum*, 14(6), e0358525.

Geerts MM, et al. (2026) Disentangled Assembly Graphs Reveal Hidden Eukaryotic Diversity in eDNA Metagenomic Data. *Molecular ecology resources*, 26(3), e70128.

Lekhuleni C, et al. (2026) Clonal expansion of global pneumococcal sequence cluster 3 within serotype 8 after 13-valent pneumococcal conjugate vaccine introduction, South Africa. *Microbial genomics*, 12(6).

Katsburg M, et al. (2026) What makes them stick? A genetic analysis of biofilm formation of an infective endocarditis-causing *Streptococcus canis* strain using transposon directed insertion-site sequencing. *Frontiers in cellular and infection microbiology*, 16, 1777632.

Pitts J, et al. (2025) Oral dosing of the nucleoside analog obeldesivir is efficacious against RSV infection in African green monkeys. *Nature communications*, 16(1), 6437.

Hansen D, et al. (2025) Impact of HIV-1 capsid polymorphisms on viral infectivity and susceptibility to lenacapavir. *mBio*, 16(5), e0018725.

Padilla JJ, et al. (2025) Characterization of the Antibiotic and Copper Resistance of Emergent Species of Onion-Pathogenic *Burkholderia* Through Genome Sequence Analysis and High-Throughput Sequencing of Differentially Enriched Random Transposon Mutants. *Pathogens* (Basel, Switzerland), 14(3).

Cervantes-Echeverría M, et al. (2025) Human-derived fecal virome transplantation (FVT) reshapes the murine gut microbiota and virome, enhancing glucose regulation. *PloS one*, 20(12), e0337760.

Wallace BA, et al. (2025) High microbial diversity, functional redundancy, and prophage enrichment support the success of the yellow pencil coral, *Madracis mirabilis*, in Curaçao's coral reefs. *mSystems*, 10(11), e0120825.

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

Sanches Ferreira AD, et al. (2025) Investigating two decades of *Streptococcus pneumoniae* bacteraemia in the Gelderland area, the Netherlands, using whole-genome sequencing. *Microbial genomics*, 11(3).

Galili-Kostin B, et al. (2025) TblncRNA-23, a long non-coding RNA transcribed by RNA polymerase I, regulates developmental changes in *Trypanosoma brucei*. *Nature communications*, 16(1), 3697.

Eraso JM, et al. (2025) Analysis of *Streptococcus dysgalactiae* subspecies *equisimilis* gene transcripts during experimental primate necrotizing myositis. *mBio*, 16(8), e0134925.

Akintayo I, et al. (2025) Tracking clonal and plasmid transmission in colistin- and carbapenem-resistant *Klebsiella pneumoniae*. *mSystems*, 10(2), e0112824.

Negash AA, et al. (2025) Genomic characterization of *Streptococcus pneumoniae* isolates obtained from carriage and disease among paediatric patients in Addis Ababa, Ethiopia. *Microbial genomics*, 11(3).