

Resource Summary Report

Generated by [dkNET](#) on Sep 9, 2026

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: 20260905T132536+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 [dkNET](#) .

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).