

Resource Summary Report

Generated by [T1D](#) on Jul 31, 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: 20260725T190605+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 507 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

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.

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

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.

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.

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).

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.

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

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

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).

Sancho-Sánchez E, et al. (2025) Reactivation of hidden-latent *Brucella* infection after doxycycline and streptomycin treatment in mice. *Antimicrobial agents and chemotherapy*, 69(2), e0130224.

- 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.
- Coetzee JL, et al. (2024) Assessing the propensity of TB clinical isolates to form viable but non-replicating subpopulations. *Scientific reports*, 14(1), 27686.
- Connor R, et al. (2024) Recommendations for Uniform Variant Calling of SARS-CoV-2 Genome Sequence across Bioinformatic Workflows. *Viruses*, 16(3).
- Wallace BA, et al. (2024) Globally distributed bacteriophage genomes reveal mechanisms of tripartite phage-bacteria-coral interactions. *The ISME journal*, 18(1).
- 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.
- 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.
- Alobaidallah MSA, et al. (2024) Enhancing the Efficacy of Chloramphenicol Therapy for *Escherichia coli* by Targeting the Secondary Resistome. *Antibiotics (Basel, Switzerland)*, 13(1).