

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

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 [FDI Lab - SciCrunch.org](#).

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.

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).

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.

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

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

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

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

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.

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.

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.

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