

Resource Summary Report

Generated by [dkNET](#) on Sep 1, 2026

[skesa](#)

RRID:SCR_024341

Type: Tool

Proper Citation

skesa (RRID:SCR_024341)

Resource Information

URL: <https://github.com/ncbi/SKESA>

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Description: Software de-novo sequence read assembler for microbial genomes. Designed to create breaks at repeat regions in the genome. This leads to excellent sequence quality without significantly compromising contiguity. SKESA contigs could be connected into GFA graph using GFA connector.

Synonyms: SKESA

Resource Type: software application, software resource

Defining Citation: [PMID:30286803](#)

Keywords: de-novo sequence read assembler, microbial genomes, create breaks at repeat regions in genome,

Availability: Free, Available for download, Freely available,

Resource Name: skesa

Resource ID: SCR_024341

Alternate URLs: <https://sources.debian.org/src/skesa/>

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260829T183140+0000

Ratings and Alerts

No rating or validation information has been found for skesa.

No alerts have been found for skesa.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

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

Tinggaard M, et al. (2026) Periorbital infections caused by Group A streptococci: a case series. BMC infectious diseases, 26(1), 317.

Di Pilato V, et al. (2026) Genomic landscape of *Candidozyma auris* in Italy, 2019 to 2025: emerging diversity of clade I sub-lineages associated with inter-facility transmission and cross-border transfers. Euro surveillance : bulletin Europeen sur les maladies transmissibles = European communicable disease bulletin, 31(18).

Thirumoorthy TP, et al. (2025) Emergence of carbapenem-resistant *Salmonella* Typhi harboring bla NDM-5 in India: genomic evidence from a multicenter study. Frontiers in microbiology, 16, 1685068.

Smith AM, et al. (2025) Whole-genome sequencing for surveillance of *Salmonella* at a public health institution in South Africa. African journal of laboratory medicine, 14(1), 2900.

Lazzari R, et al. (2025) *Vibrio fluvialis* cholangitis with bacteremia and refractory septic shock: a case report and review of the literature. Infection, 53(6), 2883.

Forth LF, et al. (2025) An inter-laboratory study characterizes the impact of bioinformatic approaches on genome-based cluster detection for foodborne bacterial pathogens. Frontiers in microbiology, 16, 1629731.

Sadeesh Kumar L, et al. (2025) Population structure and antimicrobial resistance of *Corynebacterium diphtheriae* in Victoria, Australia. Microbial genomics, 11(10).

Abdalla SE, et al. (2025) Genomic Insights of Antibiotic-Resistant *Escherichia coli* Isolated from Intensive Pig Farming in South Africa Using 'Farm-to-Fork' Approach. Antibiotics (Basel, Switzerland), 14(5).

Sia CM, et al. (2025) Distinct adaptation and epidemiological success of different genotypes within *Salmonella enterica* serovar Dublin. eLife, 13.

Hammerum AM, et al. (2024) Surveillance of vancomycin-resistant enterococci reveals shift in dominating clusters from vanA to vanB *Enterococcus faecium* clusters, Denmark, 2015 to 2022. Euro surveillance : bulletin Europeen sur les maladies transmissibles = European communicable disease bulletin, 29(23).

Vesty A, et al. (2024) The Emergence and Impact of the M1UK Lineage on Invasive Group A *Streptococcus* Disease in Aotearoa New Zealand. Open forum infectious diseases,

11(8), ofae457.

Cribb DM, et al. (2024) Genomic diversity of *Campylobacter jejuni* and *Campylobacter coli* isolates recovered from human and poultry in Australia and New Zealand, 2017 to 2019. *Microbial genomics*, 10(11).

Khasapane NG, et al. (2023) Three novel sequencing types from seventeen *Staphylococcus aureus* genomes isolated from dairy cows milk in the Free State Province of South Africa. *Microbiology resource announcements*, 12(12), e0073923.

Forth LF, et al. (2023) Impact of wet-lab protocols on quality of whole-genome short-read sequences from foodborne microbial pathogens. *Frontiers in microbiology*, 14, 1253362.

Wyres KL, et al. (2020) Genomic surveillance for hypervirulence and multi-drug resistance in invasive *Klebsiella pneumoniae* from South and Southeast Asia. *Genome medicine*, 12(1), 11.