

# Resource Summary Report

Generated by [dkNET](#) on Aug 5, 2026

## VelvetOptimiser

RRID:SCR\_024376

Type: Tool

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### Proper Citation

VelvetOptimiser (RRID:SCR\_024376)

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### Resource Information

**URL:** <https://github.com/tseemann/VelvetOptimiser/>

**Proper Citation:** VelvetOptimiser (RRID:SCR\_024376)

**Description:** Software tool to run as wrapper script for Velvet assembler and to assist with optimising the assembly. Used to search supplied hash value range for optimum, estimates expected coverage and then searches for optimum coverage cutoff. Estimates insert lengths for paired end libraries. Can optimise assemblies by default optimisation condition or by user supplied one. It outputs the results to subdirectory and records all its operations in logfile.

**Synonyms:** velvetoptimiser, perl-velvetoptimiser

**Resource Type:** software application, software resource

**Keywords:** wrapper script, Velvet assembler, optimising assembly, optimum search, search supplied hash value range, optimum coverage cutoff,

**Availability:** Free, Available for download, Freely available,

**Resource Name:** VelvetOptimiser

**Resource ID:** SCR\_024376

**Alternate IDs:** OMICS\_14601

**Alternate URLs:** <https://sources.debian.org/src/velvetoptimiser/>  
<https://sources.debian.org/src/vsearch/>

**License:** GNU General Public License v2.0

**Record Creation Time:** 20230830T050217+0000

**Record Last Update:** 20260805T044531+0000

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## Ratings and Alerts

No rating or validation information has been found for VelvetOptimiser.

No alerts have been found for VelvetOptimiser.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 55 mentions in open access literature.

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

Yassine I, et al. (2025) Understanding the population structure of *Moraxella catarrhalis* using core genome multilocus sequence typing (cgMLST) and a life identification number (LIN) code classification system. *bioRxiv : the preprint server for biology*.

Carasso S, et al. (2024) Inflammation and bacteriophages affect DNA inversion states and functionality of the gut microbiota. *Cell host & microbe*, 32(3), 322.

White RT, et al. (2024) Genomic epidemiology reveals geographical clustering of multidrug-resistant *Escherichia coli* ST131 associated with bacteraemia in Wales. *Nature communications*, 15(1), 1371.

Ferreira-Neto JRC, et al. (2023) Bridging the Gap: Combining Genomics and Transcriptomics Approaches to Understand *Stylosanthes scabra*, an Orphan Legume from the Brazilian Caatinga. *Plants (Basel, Switzerland)*, 12(18).

Unoarumhi Y, et al. (2023) A novel invasive *Streptococcus pyogenes* variant sublineage derived through recombinational replacement of the emm12 genomic region. *Scientific reports*, 13(1), 21510.

Calderon Toledo C, et al. (2023) Circulation of enterotoxigenic *Escherichia coli* (ETEC) isolates expressing CS23 from the environment to clinical settings. *mSystems*, 8(5), e0014123.

van Tonder AJ, et al. (2023) Colonization and transmission of *Staphylococcus aureus* in schools: a citizen science project. *Microbial genomics*, 9(4).

Forster SC, et al. (2022) Strain-level characterization of broad host range mobile genetic elements transferring antibiotic resistance from the human microbiome. *Nature communications*, 13(1), 1445.

Sikorski MJ, et al. (2022) Persistence of Rare *Salmonella* Typhi Genotypes Susceptible to First-Line Antibiotics in the Remote Islands of Samoa. *mBio*, 13(5), e0192022.

Mellor KC, et al. (2022) Contrasting long-term dynamics of antimicrobial resistance and virulence plasmids in *Salmonella* Typhimurium from animals. *Microbial genomics*, 8(8).

Xu Z, et al. (2022) Molecular Epidemiology of *Staphylococcus aureus* in China Reveals the Key Gene Features Involved in Epidemic Transmission and Adaptive Evolution. *Microbiology spectrum*, 10(5), e0156422.

Beresford-Jones BS, et al. (2022) The Mouse Gastrointestinal Bacteria Catalogue enables translation between the mouse and human gut microbiotas via functional mapping. *Cell host & microbe*, 30(1), 124.

Argimón S, et al. (2021) A global resource for genomic predictions of antimicrobial resistance and surveillance of *Salmonella* Typhi at pathogenwatch. *Nature communications*, 12(1), 2879.

Seibert BA, et al. (2021) *Chlamydia buteonis* in birds of prey presented to California wildlife rehabilitation facilities. *PloS one*, 16(10), e0258500.

Putonti C, et al. (2021) Genome Investigation of Urinary *Gardnerella* Strains and Their Relationship to Isolates of the Vaginal Microbiota. *mSphere*, 6(3).

Blundell-Hunter G, et al. (2021) Characterisation of Bacteriophage-Encoded Depolymerases Selective for Key *Klebsiella pneumoniae* Capsular Exopolysaccharides. *Frontiers in cellular and infection microbiology*, 11, 686090.

Di Gregorio S, et al. (2021) Genomic Epidemiology of CC30 Methicillin-Resistant *Staphylococcus aureus* Strains from Argentina Reveals Four Major Clades with Distinctive Genetic Features. *mSphere*, 6(2).

Masim ML, et al. (2021) Genomic surveillance of methicillin-resistant *Staphylococcus aureus* in the Philippines, 2013-2014. *Western Pacific surveillance and response journal : WPSAR*, 12(1), 6.

MacLennan JM, et al. (2021) Meningococcal carriage in periods of high and low invasive meningococcal disease incidence in the UK: comparison of UKMenCar1-4 cross-sectional survey results. *The Lancet. Infectious diseases*, 21(5), 677.

Wang X, et al. (2021) Genetic Analysis and Serological Detection of Novel O-Antigen Gene Clusters of *Plesiomonas shigelloides*. *Journal of microbiology and biotechnology*, 31(4), 520.