Resource Summary Report

Generated by NIF on Aug 20, 2026

VelvetOptimiser

RRID:SCR_024376
Type: Tool

Proper Citation

VelvetOptimiser (RRID:SCR_024376)

Resource Information

URL: https://github.com/tseemann/VelvetOptimiser/

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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 resource, software application

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: 20260818T043738+0000

Ratings and Alerts

No rating or validation information has been found for VelvetOptimiser.

No alerts have been found for VelvetOptimiser.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 60 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF .

Halperin AV, et al. (2026) In Vitro Restoration of Colistin Susceptibility by Ivacaftor Synergy with Limited Reproducibility in a Murine Pneumonia Model. Antibiotics (Basel, Switzerland), 15(4).

Li Y, et al. (2026) Whole-genome sequencing-based pathogen characterization for streptococcal infection directly from positive blood culture samples. Journal of clinical microbiology, 64(1), e0112625.

Postma A, et al. (2026) Genome and transcriptome-based identification and expression profiling of chemosensory gene families across developmental stages and tissues in Sirex noctilio (Hymenoptera: Siricidae). Insect molecular biology, 35(3), 270.

Njoroge SM, et al. (2025) Genomic profiling of enterotoxigenic Escherichia coli toxins and adhesins in livestock isolates from Kenya. Microbial genomics, 11(9).

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.

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

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.

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.

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.

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

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.

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.

Argim??n 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).

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).