

Resource Summary Report

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Velvet

RRID:SCR_010755

Type: Tool

Proper Citation

Velvet (RRID:SCR_010755)

Resource Information

URL: <http://www.molecularrevolution.org/software/genomics/velvet>

Proper Citation: Velvet (RRID:SCR_010755)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on February 28,2023. Software package as de novo genomic assembler for short read sequencing technologies using de Bruijn graphs. Takes in short read sequences, removes errors, then produces high quality unique contigs, retrieves repeated areas between contigs. Can leverage very short reads in combination with read pairs to produce useful assemblies. Operating system Unix/Linux., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: Velvet

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource

Defining Citation: [PMID:18349386](#), [DOI:10.1101/gr.074492.107](#)

Keywords: de novo, genomic, assembly, short, read, sequencing, de Bruijn, graph, bio.tools

Funding: EMBL

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Velvet

Resource ID: SCR_010755

Alternate IDs: OMICS_00038, biotools:velvet

Alternate URLs: <https://www.ebi.ac.uk/~zerbino/velvet/>, <https://bio.tools/velvet>, <https://sources.debian.org/src/velvet/>

License: GNU General Public License version 2.0

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260919T195159+0000

Ratings and Alerts

No rating or validation information has been found for Velvet.

No alerts have been found for Velvet.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1039 mentions in open access literature.

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

Whitmire JM, et al. (2025) A unique *Helicobacter pylori* strain to study gastric cancer development. *Microbiology spectrum*, 13(1), e0216324.

Grobecker P, et al. (2025) A dedicated caller for DUX4 rearrangements from whole-genome sequencing data. *BMC medical genomics*, 18(1), 24.

González-Serrano F, et al. (2025) Amphibian skin bacteria contain a wide repertoire of genes linked to their antifungal capacities. *World journal of microbiology & biotechnology*, 41(3), 78.

Denoeud F, et al. (2024) Evolutionary genomics of the emergence of brown algae as key components of coastal ecosystems. *Cell*, 187(24), 6943.

Baroncelli R, et al. (2024) Genome evolution and transcriptome plasticity is associated with adaptation to monocot and dicot plants in *Colletotrichum* fungi. *GigaScience*, 13.

Frank T, et al. (2024) Antibiotic resistance and molecular characterization of non-invasive clinical *Haemophilus influenzae* isolates in Germany 2019 and 2020. *JAC-antimicrobial resistance*, 6(6), dlac197.

Strakova N, et al. (2024) Genotyping of *Campylobacter jejuni* and prediction tools of its antimicrobial resistance. *Folia microbiologica*, 69(1), 207.

Palma L, et al. (2024) Genome Sequence Analysis of Native *Xenorhabdus* Strains Isolated from Entomopathogenic Nematodes in Argentina. *Toxins*, 16(2).

Cagape CMS, et al. (2024) Genetic variation, structural analysis, and virulence implications of BimA and BimC in clinical isolates of *Burkholderia pseudomallei* in

Thailand. Scientific reports, 14(1), 24966.

Minařík M, et al. (2024) Identification of multiple transcription factor genes potentially involved in the development of electrosensory versus mechanosensory lateral line organs. *Frontiers in cell and developmental biology*, 12, 1327924.

Schmidt AK, et al. (2024) Targeted deletion of Pf prophages from diverse *Pseudomonas aeruginosa* isolates has differential impacts on quorum sensing and virulence traits. *Journal of bacteriology*, 206(5), e0040223.

Ndhlovu GON, et al. (2024) Investigating genomic diversity of *Staphylococcus aureus* associated with pediatric atopic dermatitis in South Africa. *Frontiers in microbiology*, 15, 1422902.

Jansen van Rensburg MJ, et al. (2024) Development of the Pneumococcal Genome Library, a core genome multilocus sequence typing scheme, and a taxonomic life identification number barcoding system to investigate and define pneumococcal population structure. *Microbial genomics*, 10(8).

Jonca J, et al. (2024) Comprehensive phenomic and genomic studies of the species, *Pectobacterium cacticida* and proposal for reclassification as *Alcorniella cacticida* comb. nov. *Frontiers in plant science*, 15, 1323790.

Park S, et al. (2024) Dynamic changes in the plastid and mitochondrial genomes of the angiosperm *Corydalis pauciovulata* (Papaveraceae). *BMC plant biology*, 24(1), 303.

Lehmkuhl J, et al. (2024) Role of membrane vesicles in the transmission of vancomycin resistance in *Enterococcus faecium*. *Scientific reports*, 14(1), 1895.

Park S, et al. (2024) Comparative and Adaptive Analyses of the Complete Chloroplast Genome Diversity in *Sium serra*. *Genes*, 15(12).

Xiong Y, et al. (2024) Extensive transcriptome data providing great efficacy in genetic research and adaptive gene discovery: a case study of *Elymus sibiricus* L. (Poaceae, Triticeae). *Frontiers in plant science*, 15, 1457980.

Jimenez J, et al. (2024) Single torradovirus infections explain the mysterious cassava frogskin disease in the Americas. *Scientific reports*, 14(1), 29648.

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.