

Resource Summary Report

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VecScreen

RRID:SCR_016577

Type: Tool

Proper Citation

VecScreen (RRID:SCR_016577)

Resource Information

URL: <https://www.ncbi.nlm.nih.gov/tools/vecscreen/>

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Description: Software tool to screen a nucleic acid sequence for vector contamination. Detects foreign DNAs such as vector, linker, adapter, and primer regions involved in nucleotide sequences by using blast search against vector sequence database. The main unit of this tool is vecscreen program obtainable from NCBI.

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

Keywords: screen, sequence, nucleic acid, segment, vector, contamination

Availability: Free, Available for download, Freely available

Resource Name: VecScreen

Resource ID: SCR_016577

Alternate URLs: <https://www.ddbj.nig.ac.jp/vecscreen-help-e.html>

Record Creation Time: 20220129T080331+0000

Record Last Update: 20260805T044356+0000

Ratings and Alerts

No rating or validation information has been found for VecScreen.

No alerts have been found for VecScreen.

Data and Source Information

Usage and Citation Metrics

We found 48 mentions in open access literature.

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

Lu X, et al. (2025) Virome characteristics of small mammals and their associated environments in pastoral areas on the Qinghai-Tibet Plateau. NPJ biofilms and microbiomes, 11(1), 168.

Lu X, et al. (2025) Metagenomic analysis reveals the diversity of the vaginal virome and its association with vaginitis. Frontiers in cellular and infection microbiology, 15, 1582553.

Madrigal G, et al. (2025) Klumpy: A tool to evaluate the integrity of long-read genome assemblies and illusive sequence motifs. Molecular ecology resources, 25(1), e13982.

Goodheart JA, et al. (2024) A chromosome-level genome for the nudibranch gastropod *Berghia stephanieae* helps parse clade-specific gene expression in novel and conserved phenotypes. BMC biology, 22(1), 9.

Bukhman YV, et al. (2024) Chromosome level genome assembly of the Etruscan shrew *Suncus etruscus*. Scientific data, 11(1), 176.

Dhar SK, et al. (2024) Novel *Bacillus* and *Prestia* isolates from Dwarf century plant enhance crop yield and salinity tolerance. Scientific reports, 14(1), 14645.

Lu X, et al. (2024) Metagenomic analysis reveals high diversity of gut viromes in yaks (*Bos grunniens*) from the Qinghai-Tibet Plateau. Communications biology, 7(1), 1097.

Tempone AJ, et al. (2024) Rhabdoviral Endogenous Sequences Identified in the Leishmaniasis Vector *Lutzomyia longipalpis* Are Widespread in Sandflies from South America. Viruses, 16(3).

Al-Madboly LA, et al. (2024) Characterization of GQA as a novel β -lactamase inhibitor of CTX-M-15 and KPC-2 enzymes. Microbial cell factories, 23(1), 221.

Bao S, et al. (2023) Viral metagenomics of the gut virome of diarrheal children with Rotavirus A infection. Gut microbes, 15(1), 2234653.

Parashar M, et al. (2023) Two Novel Plant-Growth-Promoting *Lelliottia amnigena* Isolates from *Euphorbia prostrata* Aiton Enhance the Overall Productivity of Wheat and Tomato. Plants (Basel, Switzerland), 12(17).

Naveenarani M, et al. (2023) Isolation and Characterization of *Erianthus arundinaceus* Phosphate Transporter 1 (PHT1) Gene Promoter and 5' Deletion Analysis of Transcriptional Regulation Regions under Phosphate Stress in Transgenic Tobacco. Plants (Basel, Switzerland), 12(21).

Pan J, et al. (2023) Metagenomic analysis of herbivorous mammalian viral communities in the Northwest Plateau. *BMC genomics*, 24(1), 568.

Goodheart JA, et al. (2023) A chromosome-level genome for the nudibranch gastropod *Berghia stephanieae* helps parse clade-specific gene expression in novel and conserved phenotypes. *bioRxiv : the preprint server for biology*.

Aidoo OF, et al. (2023) First report on the presence of huanglongbing vectors (*Diaphorina citri* and *Trioza erytreae*) in Ghana. *Scientific reports*, 13(1), 11366.

Brosnan EB, et al. (2023) Novel Genome Sequences of *Ophidiomyces ophidiicola*, the Causative Agent of Snake Fungal Disease. *Microbiology resource announcements*, 12(7), e0009323.

Jiang X, et al. (2023) Virome of high-altitude canine digestive tract and genetic characterization of novel viruses potentially threatening human health. *mSphere*, 8(5), e0034523.

Yang Z, et al. (2023) Virome diversity of ticks feeding on domestic mammals in China. *Virologica Sinica*, 38(2), 208.

Vaidya M, et al. (2023) Analysis of regulatory sequences in exosomal DNA of NANOGP8. *PloS one*, 18(1), e0280959.

He J, et al. (2023) Establishing *Physalis* as a Solanaceae model system enables genetic reevaluation of the inflated calyx syndrome. *The Plant cell*, 35(1), 351.