

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 analysis software, data processing software, sequence analysis software, service resource, software application, software 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: 20260905T132811+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 69 mentions in open access literature.

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

Eshak MIY, et al. (2026) Continuous in silico screening of fish, amphibians, reptiles, and birds expands the diversity of bornavirids and reveals unexpected genomic architectures. *Virus evolution*, 12(1), veag033.

Dai Z, et al. (2026) Discovery of a novel orthototivirus-like virus in patients with vulvovaginal candidiasis. *Frontiers in cellular and infection microbiology*, 16, 1779554.

Dai Z, et al. (2026) Identification of novel CRESS-DNA viruses in the human vaginal microbiome. *Frontiers in microbiology*, 17, 1790643.

Saghrouchni H, et al. (2026) Morphological and complete genome analysis of a novel *Clostridium perfringens* phage CpP_VarHS, isolated from wastewater. *Frontiers in pharmacology*, 17, 1807000.

Shi K, et al. (2026) Systemic remodeling of the multi-organ virome following *Echinococcus* infection in mice. *BMC microbiology*, 26(1).

Song X, et al. (2025) Maternal health status is associated with paired maternal and cord blood virome and mother-to-infant transmission. *NPJ biofilms and microbiomes*, 12(1), 14.

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.

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.

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.

Zhang E, et al. (2025) Viral Metagenomics of the Bharal (*Pseudois nayaur*) within the Qinghai-Tibet Plateau Revealed Diverse Viruses. *Polish journal of microbiology*, 74(2), 143.

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.

Abd-El-Haleem DAM, et al. (2024) Uncovering novel polyhydroxyalkanoate biosynthesis genes and unique pathway in yeast *hanseniaspora valbyensis* for sustainable bioplastic production. *Scientific reports*, 14(1), 27162.

Mifsud JCO, et al. (2024) A novel papillomavirus in a New Zealand fur seal (*Arctocephalus forsteri*) with oral lesions. *Npj viruses*, 2(1), 10.

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.

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.

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.

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*.