Resource Summary Report

Generated by FDI Lab - SciCrunch.org on May 1, 2025

MacVector

RRID:SCR_015700 Type: Tool

Proper Citation

MacVector (RRID:SCR_015700)

Resource Information

URL: http://macvector.com

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Description: Software application that provides sequence editing, primer design, internet database searching, protein analysis, sequence confirmation, multiple sequence alignment, phylogenetic reconstruction, coding region analysis, agarose gel simulation and a variety of other functions.

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

Keywords: vector, sequence, sequence alignment, sequence editing, primer design, phylogenetic reconstruction, FASEB list

Funding:

Availability: Commercially available, Available for purchase, Runs on Mac OS, Free version available

Resource Name: MacVector

Resource ID: SCR_015700

Record Creation Time: 20220129T080327+0000

Record Last Update: 20250501T081251+0000

Ratings and Alerts

No rating or validation information has been found for MacVector.

No alerts have been found for MacVector.

Data and Source Information

Source: <u>SciCrunch Registry</u>

Usage and Citation Metrics

We found 1463 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Olson CS, et al. (2025) Neuronal segmentation in cephalopod arms. Nature communications, 16(1), 443.

Delgado KN, et al. (2025) Development and utilization of Treponema pallidum expressing green fluorescent protein to study spirochete-host interactions and antibody-mediated clearance: expanding the toolbox for syphilis research. mBio, 16(1), e0325324.

Desalegn G, et al. (2025) A broad spectrum Shigella vaccine based on VirG53-353 multiepitope region produced in a cell-free system. NPJ vaccines, 10(1), 6.

Okwumabua O, et al. (2025) Detection of SARS-CoV-2 and a possible variant in shelter cats. PloS one, 20(1), e0317104.

Shi Y, et al. (2024) Mutations accumulated in the Spike of SARS-CoV-2 Omicron allow for more efficient counteraction of the restriction factor BST2/Tetherin. PLoS pathogens, 20(1), e1011912.

Ordóñez A, et al. (2024) Protocol for iterative enrichment of integrated sgRNAs via derivative CRISPR-Cas9 libraries from genomic DNA of sorted fixed cells. STAR protocols, 5(4), 103493.

Chávez-Larrea MA, et al. (2024) First Report of Trypanosoma vivax (Duttonella), Babesia bovis and Babesia bigemina DNA in Cattle from the Galapagos Islands, Ecuador, and Its Relationship with Anaplasma marginale. Pathogens (Basel, Switzerland), 13(10).

Wilson MH, et al. (2024) Zebrafish are resilient to the loss of major diacylglycerol acyltransferase enzymes. The Journal of biological chemistry, 300(12), 107973.

Emanuelli G, et al. (2024) Functional validation of EIF2AK4 (GCN2) missense variants associated with pulmonary arterial hypertension. Human molecular genetics, 33(17), 1495.

Wang L, et al. (2024) Complete Mitogenome sequencing of the fish louse Argulus japonicus (Crustacea: Branchiura): Comparative analyses and phylogenetic implications. Frontiers in

veterinary science, 11, 1376898.

Olson CS, et al. (2024) Neuronal segmentation in cephalopod arms. bioRxiv : the preprint server for biology.

Zhu N, et al. (2024) Utility of protein-protein binding surfaces composed of anti-parallel alphahelices and beta-sheets selected by phage display. The Journal of biological chemistry, 300(5), 107283.

Fu G, et al. (2024) The MBO2/FAP58 heterodimer stabilizes assembly of inner arm dynein b and reveals axoneme asymmetries involved in ciliary waveform. Molecular biology of the cell, 35(5), ar72.

Schember I, et al. (2024) Conserved and novel enhancers in the Aedes aegypti singleminded locus recapitulate embryonic ventral midline gene expression. PLoS genetics, 20(4), e1010891.

Bi C, et al. (2024) PMAT: an efficient plant mitogenome assembly toolkit using low-coverage HiFi sequencing data. Horticulture research, 11(3), uhae023.

Halawani AJ, et al. (2024) Investigation of Wright Blood Group Alleles and Genotypes in Malaria-Endemic Area in Southwestern Saudi Arabia. International journal of general medicine, 17, 5175.

Abbasi A, et al. (2024) Molecular Basis for the Differential Function of HAVCR1 Mucin Variants. Biomedicines, 12(11).

Tung J, et al. (2024) A genome-wide CRISPR/Cas9 screen identifies calreticulin as a selective repressor of ATF6?. eLife, 13.

Cassar O, et al. (2024) Southern African Origin of HTLV-1 in Romania. PLoS neglected tropical diseases, 18(8), e0012337.

Ma L, et al. (2024) Development of Highly Efficient Universal Pneumocystis Primers and Their Application in Investigating the Prevalence and Genetic Diversity of Pneumocystis in Wild Hares and Rabbits. Journal of fungi (Basel, Switzerland), 10(5).