Resource Summary Report

Generated by dkNET on Apr 29, 2025

VirtualBox

RRID:SCR_011876
Type: Tool

Proper Citation

VirtualBox (RRID:SCR_011876)

Resource Information

URL: https://www.virtualbox.org/

Proper Citation: VirtualBox (RRID:SCR_011876)

Description: A general-purpose full virtualizer for x86 and AMD64/Intel64 hardware, targeted at server, desktop and embedded use.

Abbreviations: VirtualBox

Resource Type: software resource

Funding:

Availability: GNU General Public License, v2

Resource Name: VirtualBox

Resource ID: SCR_011876

Alternate IDs: OMICS_01208

Record Creation Time: 20220129T080307+0000

Record Last Update: 20250420T014601+0000

Ratings and Alerts

No rating or validation information has been found for VirtualBox.

No alerts have been found for VirtualBox.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 90 mentions in open access literature.

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

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.

Zhang H, et al. (2024) ProcGCN: detecting malicious process in memory based on DGCNN. PeerJ. Computer science, 10, e2193.

Lee JY, et al. (2024) Multi-omics analysis sandbox toolkit for swift derivations of clinically relevant genesets and biomarkers. BMB reports, 57(12), 521.

Bashour H, et al. (2024) Biophysical cartography of the native and human-engineered antibody landscapes quantifies the plasticity of antibody developability. Communications biology, 7(1), 922.

Lötsch J, et al. (2024) Machine learning and biological validation identify sphingolipids as potential mediators of paclitaxel-induced neuropathy in cancer patients. eLife, 13.

Tsebriy O, et al. (2023) Machine learning-based phenotypic imaging to characterise the targetable biology of Plasmodium falciparum male gametocytes for the development of transmission-blocking antimalarials. PLoS pathogens, 19(10), e1011711.

Rischke S, et al. (2023) Machine learning identifies right index finger tenderness as key signal of DAS28-CRP based psoriatic arthritis activity. Scientific reports, 13(1), 22710.

Chouliaras N, et al. (2023) A novel autonomous container-based platform for cybersecurity training and research. PeerJ. Computer science, 9, e1574.

Ilca LF, et al. (2023) Enhancing Cyber-Resilience for Small and Medium-Sized Organizations with Prescriptive Malware Analysis, Detection and Response. Sensors (Basel, Switzerland), 23(15).

Mahmud I, et al. (2022) Performance Evaluation of MPTCP on Simultaneous Use of 5G and 4G Networks. Sensors (Basel, Switzerland), 22(19).

Xu Y, et al. (2022) Validating the knowledge bank approach for personalized prediction of survival in acute myeloid leukemia: a reproducibility study. Human genetics, 141(9), 1467.

Huang M, et al. (2022) Spatiotemporal dynamics and functional characteristics of the composition of the main fungal taxa in the root microhabitat of Calanthe sieboldii

(Orchidaceae). BMC plant biology, 22(1), 556.

Johansen B, et al. (2022) First Evidence of a Combination of Terpinen-4-ol and ?-Terpineol as a Promising Tool against ESKAPE Pathogens. Molecules (Basel, Switzerland), 27(21).

González-Ramírez M, et al. (2022) A computational pipeline to learn gene expression predictive models from epigenetic information at enhancers or promoters. STAR protocols, 4(1), 101948.

Mills WT, et al. (2022) SCRAP: a bioinformatic pipeline for the analysis of small chimeric RNA-seq data. RNA (New York, N.Y.), 29(1), 1.

Zugman A, et al. (2022) Mega-analysis methods in ENIGMA: The experience of the generalized anxiety disorder working group. Human brain mapping, 43(1), 255.

Greenberg JM, et al. (2022) Microbiota of the Pregnant Mouse: Characterization of the Bacterial Communities in the Oral Cavity, Lung, Intestine, and Vagina through Culture and DNA Sequencing. Microbiology spectrum, 10(4), e0128622.

Liu Q, et al. (2021) Small noncoding RNA discovery and profiling with sRNAtools based on high-throughput sequencing. Briefings in bioinformatics, 22(1), 463.

Liu Q, et al. (2021) Response of Sugarcane Rhizosphere Bacterial Community to Drought Stress. Frontiers in microbiology, 12, 716196.

Ducoli L, et al. (2021) LETR1 is a lymphatic endothelial-specific lncRNA governing cell proliferation and migration through KLF4 and SEMA3C. Nature communications, 12(1), 925.