

Resource Summary Report

Generated by [ASWG](#) on Aug 23, 2026

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

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: 20260815T182436+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 99 mentions in open access literature.

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

Liu Z, et al. (2026) Metagenomic analysis of the DNA virome communities in swine lungs. *Frontiers in microbiology*, 17, 1798033.

Gkarane V, et al. (2026) Towards real-time pork breed and boar taint classification using rapid evaporative ionisation mass spectrometry. *NPJ science of food*, 10(1), 37.

Hriez S, et al. (2026) Measuring the impact of virtualization and containerization on the environment when using GPUs for processing the AI models. *Frontiers in big data*, 9, 1838191.

Settelmeier J, et al. (2025) MultiOmicsAgent: Guided Extreme Gradient-Boosted Decision Trees-Based Approaches for Biomarker-Candidate Discovery in Multiomics Data. *Journal of proteome research*, 24(6), 2816.

Block KT, et al. (2025) MRI4ALL: A Week-Long Hackathon for the Development of an Open-Source Ultra-Low-Field MRI System. *Journal of magnetic resonance imaging : JMRI*, 62(4), 959.

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).

Djaffardjy M, et al. (2023) Developing and reusing bioinformatics data analysis pipelines using scientific workflow systems. *Computational and structural biotechnology journal*, 21, 2075.

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.

Antunes AM, et al. (2022) A Pipeline for the Development of Microsatellite Markers using Next Generation Sequencing Data. *Current genomics*, 23(3), 175.

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