## **Resource Summary Report**

Generated by dkNET on Apr 29, 2025

# **VMware**

RRID:SCR\_011878 Type: Tool

**Proper Citation** 

VMware (RRID:SCR\_011878)

#### **Resource Information**

URL: http://www.vmware.com/

Proper Citation: VMware (RRID:SCR\_011878)

**Description:** Software that virtualizes computing, from the data center to the cloud to mobile devices, to help customers be more agile, responsive, and profitable.

Abbreviations: VMware

Resource Type: software resource

Keywords: cloud, computing

Funding:

Resource Name: VMware

Resource ID: SCR\_011878

Alternate IDs: OMICS\_01209

Record Creation Time: 20220129T080307+0000

Record Last Update: 20250420T014601+0000

#### **Ratings and Alerts**

No rating or validation information has been found for VMware.

No alerts have been found for VMware.

## Data and Source Information

Source: SciCrunch Registry

### **Usage and Citation Metrics**

We found 21 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>dkNET</u>.

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.

Arshinoff BI, et al. (2022) Echinobase: leveraging an extant model organism database to build a knowledgebase supporting research on the genomics and biology of echinoderms. Nucleic acids research, 50(D1), D970.

Jacob D, et al. (2017) NMRProcFlow: a graphical and interactive tool dedicated to 1D spectra processing for NMR-based metabolomics. Metabolomics : Official journal of the Metabolomic Society, 13(4), 36.

Kiar G, et al. (2017) Science in the cloud (SIC): A use case in MRI connectomics. GigaScience, 6(5), 1.

Agrawal S, et al. (2017) CloVR-Comparative: automated, cloud-enabled comparative microbial genome sequence analysis pipeline. BMC genomics, 18(1), 332.

Denaxas S, et al. (2017) Methods for enhancing the reproducibility of biomedical research findings using electronic health records. BioData mining, 10, 31.

Jang JW, et al. (2016) Detecting and classifying method based on similarity matching of Android malware behavior with profile. SpringerPlus, 5, 273.

Post AR, et al. (2016) Metadata-driven Clinical Data Loading into i2b2 for Clinical and Translational Science Institutes. AMIA Joint Summits on Translational Science proceedings. AMIA Joint Summits on Translational Science, 2016, 184.

Hurley DG, et al. (2015) Virtual Reference Environments: a simple way to make research reproducible. Briefings in bioinformatics, 16(5), 901.

Adamczyk B, et al. (2015) Achieving High Resolution Timer Events in Virtualized Environment. PloS one, 10(7), e0130887.

Hu R, et al. (2015) G2LC: Resources Autoscaling for Real Time Bioinformatics Applications in IaaS. Computational and mathematical methods in medicine, 2015, 549026.

Kinger S, et al. (2014) Prediction based proactive thermal virtual machine scheduling in green clouds. TheScientificWorldJournal, 2014, 208983.

Moorhouse MJ, et al. (2014) ImmunoGlobulin galaxy (IGGalaxy) for simple determination and quantitation of immunoglobulin heavy chain rearrangements from NGS. BMC immunology, 15, 59.

Schilling LM, et al. (2013) Scalable Architecture for Federated Translational Inquiries Network (SAFTINet) Technology Infrastructure for a Distributed Data Network. EGEMS (Washington, DC), 1(1), 1027.

White JR, et al. (2013) CloVR-ITS: Automated internal transcribed spacer amplicon sequence analysis pipeline for the characterization of fungal microbiota. Microbiome, 1(1), 6.

Dinov ID, et al. (2011) Applications of the pipeline environment for visual informatics and genomics computations. BMC bioinformatics, 12, 304.

Angiuoli SV, et al. (2011) Resources and costs for microbial sequence analysis evaluated using virtual machines and cloud computing. PloS one, 6(10), e26624.

Dinov I, et al. (2010) Neuroimaging study designs, computational analyses and data provenance using the LONI pipeline. PloS one, 5(9).

Stein LD, et al. (2010) The case for cloud computing in genome informatics. Genome biology, 11(5), 207.

Moran LB, et al. (2008) Towards a pathway definition of Parkinson's disease: a complex disorder with links to cancer, diabetes and inflammation. Neurogenetics, 9(1), 1.