

Resource Summary Report

Generated by [dkNET](#) on Aug 25, 2026

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

Resource Name: VMware

Resource ID: SCR_011878

Alternate IDs: OMICS_01209

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260815T182425+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 23 mentions in open access literature.

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

Cong X, et al. (2026) Ethanol Regulates Bitterness Perception of the Trp-Ile-Lys-Lys (WIKK) Peptide by Activating the Human Bitter Receptor T2R47. *Foods* (Basel, Switzerland), 15(4).

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

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.

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.

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.

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.

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

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.

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

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

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

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

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).