

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 17, 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: 20260912T195741+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 [SPARC SAWG](#) .

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).